



- (51) **International Patent Classification:**
C07K 14/00 (2006.01) *A61P 35/00* (2006.01)
- (21) **International Application Number:**
PCT/US2017/023901
- (22) **International Filing Date:**
23 March 2017 (23.03.2017)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
62/312,419 23 March 2016 (23.03.2016) US
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- (81) **Designated States** (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY,

BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

- (84) **Designated States** (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- with international search report (Art. 21(3))
- before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))
- with sequence listing part of description (Rule 5.2(a))

(54) **Title:** TREATMENT OF CANCER BY ACTIVATING ENDOGENOUS CRYPTIC AMYLOIDOGENIC AGGREGATING PEPTIDES

(57) **Abstract:** The present disclosure relates, in general, to therapy using toxic amyloidogenic aggregating peptides for treating cancer or preventing recurrence of cancer diseases such as lung cancer, prostate cancer, breast cancer, hepatocellular cancer, esophageal cancer, colorectal cancer, pancreatic cancer, bladder cancer, kidney cancer, ovarian cancer, stomach cancer, fibrotic cancer, glioma and melanoma, and metastases thereof.



TREATMENT OF CANCER BY ACTIVATING ENDOGENOUS CRYPTIC AMYLOIDOGENIC AGGREGATING PEPTIDES

FIELD OF THE INVENTION

[0001] The invention relates, in general, to materials and methods for cancer treatment and prevention.

BACKGROUND

[0002] Cancer is a group of diseases characterized by the uncontrolled growth and spread of abnormal cells. Cancer is the second leading cause of human death next to coronary disease (Health, United States, 2014: At a Glance, *National Center for Health Statistics*, CDC). According to statistics from the American Cancer Society, approximately 600,000 Americans are expected to die of cancer in 2016 (Cancer Facts & Figures 2016, *American Cancer Society*). Cancer therapeutic resistance occurs as cancers develop resistance to treatments such as chemotherapy, radiotherapy and targeted therapies, through numerous different mechanisms. Therefore, there is an urgent need for the development of effective anticancer agents to target difficult to treat cancers that fail to respond to current cancer therapy.

[0003] Abnormal protein aggregation is observed as a newly uncovered general response to cellular stress (Audas et al., *Developmental Cell* (2016)) and a long recognized mechanism in neurodegenerative disorders (Koo *et al.*, *PNAS* (1999) 96: 9989-90). Protein aggregates usually adopt high-ordered beta sheet quaternary structures forming insoluble fibrils termed amyloids. The term “amyloid” is generically used for all proteins capable of forming large, insoluble fibrils. Amyloid pathology has been extensively described in diseases correlated with aging and aging itself. In cancer, a disease of aging, prion-like aggregation of mutant p53 has been observed (Costa et al., *Cold Spring Harb Perspect Biol.* (2016) 8(10): a023614). Parkinson disease is characterized by inclusions known as Lewy bodies present in the cytoplasm of neurons. In Alzheimer’s disease, aggregates can occur both extracellular as neuritic plaques composed of A β peptide, and intracellular as neurofibrillary tangles of hyperphosphorylated TAU protein. In Amyotrophic lateral sclerosis (ALS) aggregation of ubiquitinated proteins, including FUS, TDP-43 and OPTN, occurs in degenerating motor neurons. Interestingly, these aggregated ubiquitinated proteins co-occur with perikaryal inclusions of neurofilament (NF). Abnormal NF aggregation and misassembly has also been reported in other motor neuron diseases such as giant axonal neuropathy (GAN) and Charcot-Marie-Tooth disease (CMT). However, the causes for NF accumulation appear to be heterogeneous and not fully understood.

SUMMARY OF THE INVENTION

[0004] All ‘naturally’ occurring amyloidogenic protein pathology relies on expression of ‘aggregate-prone’ proteins from a given genome. Gene expression and protein translation are guided

by well-known molecular mechanisms. We discovered in all vertebrate genomes, including human genomes, that specific non-coding DNA sequences downstream of regular termination codons contain sequence motives (cryptic amyloidogenic elements), which, after translation into proteins, act as effective amyloidogenic seeds (Rebelo *et al.*, *Am J Hum Genet* (2016) 98(4):597–614). Described herein, is a specific type of such proteins originating from elongated translation of the original reading frame into the 3'-UTR or by switching into alternative reading frames that omit the natural termination codon and thus also read into the 3'-UTR until a new termination codon appears.

[0005] Such artificially forced expression of elongated, and now amyloidogenic, proteins will result in cellular aggregates and cause cancer cells to revert into a dormant state or enter apoptosis. Identified and described below are proteins that contain such elements, how they are to be confirmed as targets *in vitro*, and how the *in vivo* activation is possible, including DNA editing, such as using guided CRISPR/Cas9, and pharmacological induced read-through.

[0006] The invention provides various materials, methods, and uses relating to treatment of undesirable neoplastic cells, such as cancer cells. While amyloid aggregation is detrimental to nerve cell survival, it is of practical use to reduce viability of cancer cells as described herein. In particular, the present disclosure relates to materials and methods for treating or preventing the reoccurrence of cancer using toxic amyloidogenic aggregating proteins or fragments thereof. In particular, the specific amyloidogenic proteins in question are artificially created by incorporating specific downstream (3'-UTR) amyloidogenic elements into an elongated protein isoform.

[0007] For example, one aspect of the invention is a method of treating a mammalian subject to inhibit growth of neoplastic cells. An exemplary method comprises:

administering to the subject a composition that comprises an agent selected from the group consisting of:

- a. an agent that comprises an amyloidogenic peptide;
- b. an agent that comprises a nucleotide sequence that encodes the amyloidogenic peptide; and
- c. an agent that induces expression of an endogenous nucleotide sequence that encodes the amyloidogenic peptide.

[0008] Amyloidogenic peptides are peptides that have a propensity to fold into an improper or undesirable shape and form ordered aggregates referred to as fibrils. In preferred variations of the invention, the amyloidogenic peptide (relevant to either (a) or (b) or (c) above) is either:

(i) a Cryptic Amyloidogenic Element ("CAE") encoded by nucleic acid in a 3'-untranslated region ("3'-UTR") of a gene in the neoplastic cell; or

(ii) comprises an amino acid sequence that is at least 70% identical to the CAE and that retains the property of amyloidogenic aggregation.

[0009] In some variations, the amyloidogenic peptide has an amino acid sequence at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98%, or at least 99% identical to the CAE. In some variations, the amyloidogenic peptide has an amino acid sequence identical to the CAE except at 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acid positions. Preferred variants from the naturally occurring CAE differ with conservative substitutions and/or differ with substitutions that increase the propensity of the peptide to form toxic amyloid fibrils.

[0010] The term “Cryptic Amyloidogenic Element” refers to a peptide sequence that has amyloidogenic properties; that is encoded by nucleic acid in the genome of an organism; and that is not normally expressed in healthy cells because its coding sequence resides in an untranslated region of the genome, such as a 3'-untranslated region of a gene. A CAE that is located in a 3' untranslated region is expressed when the gene is mutated to eliminate the natural (wild type) termination codon (e.g., missense mutation or frameshift mutation), or when the cell is subjected to an agent or condition that causes termination codon read-through during mRNA translation.

[0011] Aspects of the invention that are described or claims as methods can alternatively be described or claims as uses.

[0012] For instance, a related aspect of the invention is the use of a composition that comprises an agent to inhibit growth of neoplastic cells in a mammalian subject, wherein the agent is selected as described in the preceding paragraphs.

[0013] Similarly, another related aspect of the invention is the use of a composition that comprises an agent for the manufacture of a medicament to inhibit growth of neoplastic cells in a mammalian subject, wherein the agent is selected as described in the preceding paragraphs.

[0014] In some variations, the agent is administered in an amount effective to slow or halt the growth of the neoplastic cells. In some variations, the agent is administered in an amount effective to kill neoplastic cells in the subject.

[0015] A “mammalian subject” can be any mammal. Particularly contemplated include animals of agricultural importance, such as bovine, equine, and porcine animals; animals important as domestic pets, including canines and felines; animals important in research, including rodents and primates; large endangered species and zoo animals such as primates, felines, giraffes, elephants, rhinos. Especially contemplated are humans.

[0016] It is contemplated that the invention is applicable to the treatment of any neoplastic condition. In some variations, the neoplastic cells are malignant. Treatment of all cancers and tumor types are contemplated. In some variations, the neoplastic cells are from a cancer of neurogenic

origin or a glia-derived tumor. For instance, treatment of each of neuroblastomas, central neurocytomas, and retinoblastomas is contemplated. For these particular neoplastic targets, it is specifically contemplated that the amyloidogenic peptide is encoded by the 3'-UTR of an NEFH or NEFL gene.

[0017] More generally, in some variations of the invention, the agent is selected based on an analysis of proteins that are determined to be, or determined to be likely to be, highly expressed in the target neoplastic cells.

[0018] Thus, in some variations a CAE is selected that is located in a gene that is highly expressed in the neoplastic cells, but not expressed or expressed at very low levels in normal cells. All variety of techniques are contemplated for determining genes that are highly expressed in the neoplastic cells. Some techniques analyze a sample of the neoplastic cells, e.g., from a biopsy, to provide highly personalized and targeted care for the individual. Other variations rely on data taken from similar neoplastic cells (e.g., from databases) or from healthy counterpart cells (data from the individual or from a database).

[0019] Thus, in some variations, the method or use of the invention further comprises additional steps of: screening the neoplastic cells to identify one or more genes that are highly expressed therein; and selecting, as the amyloidogenic peptide, a peptide that is encoded by a CAE that is located in the 3'-UTR of one of the highly expressed genes.

[0020] In some embodiments, this screening of the neoplastic cells comprises measuring protein and/or mRNA in a sample of the neoplastic cells. In other embodiments, the screening of the neoplastic cells comprises: pathological examination to characterize the neoplastic cells. e.g., to identify the type of cancer or tumor; and identifying genes that are highly expressed in a database of gene expression data for the neoplastic cell type, or for healthy cells of the type from which the neoplastic cells arose.

[0021] When one or more highly expressed genes are identified, the list can be screened for candidates having a CAE in the 3'-UTR. For example, in some variations, the selecting of the amyloidogenic peptide comprises analyzing the 3'-UTR of the genes identified as highly expressed; and selecting from that set of genes a gene having a 3'-UTR containing an open reading frame that encodes a peptide with amyloidogenic properties.

[0022] In some variations, the selecting of a gene having the CAE entails analysis of the 3'-UTR sequence of the mRNA (or cDNA) for evidence of amyloidogenic motifs, as described below in detail. However, such analysis has already been performed herein, and thousands of putative CAE's identified, as set forth below in Table 1. Thus, in some variations, the selecting of the amyloidogenic peptide comprises selected a gene from the list in Table 1 below that is among the genes identified as highly expressed in the neoplastic cells.

[0023] In some variations of the invention, the CAE is present in the 3'-UTR of a gene set forth in Table 1. More particularly, in some variations, the CAE is in the 3'-UTR of a gene selected from the group consisting of APOA2, ATXN2, B2M, FGB, FUS, IAPP, LYZ, NOTCH3, PRNP, RHO, SAA1, SNCA, NEFH, NEFL, BSCL2, MAPT, and TTR, as presented in Table 3, and also Table 4. Still more particularly, in some variations the CAE is in the 3'-UTR of a gene is selected from NEFH, NEFL, and FUS. Still more particularly, in some variations the amyloidogenic peptide comprises the amino acid sequence QFSLFSL. Still more particularly, in some variations the amyloidogenic peptide comprises an amino acid sequence at least 70% identical (or at least 75%, 80%, 85%, 90%, 95%, or 100% identical) to the sequence SSRIRVTQFSLFSLCKKKLLR, and retains the property of amyloidogenic aggregation.

[0024] In some variation of the invention the amyloidic element is in close proximity of an Arginine/Histidine-rich region of ~20 bases. This region may serve as anchor for Amyloid body formation, a specific form of aggregation (Audas *et al.*, *Developmental Cell* (2016) 39:155-168).

[0025] In some embodiments of the invention, the amyloidogenic peptide is introduced to the cell exogenously, by administering to the subject in need of the treatment either a composition comprising the peptide, or a composition comprising a nucleotide sequence that encodes the peptide and that is capable of being expressed in the cell.

[0026] Thus, in some variations, the agent of the method or use of the invention comprises a nucleotide sequence that encodes the amyloidogenic peptide. In some particular embodiments, the agent comprises cDNA or mRNA encoding the amyloidogenic peptide.

[0027] In embodiments where the agent is a nucleic acid, suitable expression control sequences (such as promoters, enhancers, polyadenylation signals sequences, etc.) are included in some variations, to promote expression of the encoded amyloidogenic peptide. Thus, in some variations, the agent further comprises a promoter operatively linked to the nucleotide sequence that encodes the amyloidogenic peptide. Optionally, the promoter is a tissue-selective promoter that promotes expression of genes in the neoplastic cells more readily than other cell types. In highly preferred embodiments, a tissue-specific promoter is selected. Fewer side-effects are expected with more selective promoters.

[0028] In some embodiments, the agent comprises a vector that comprises the nucleotide sequence that encodes the amyloidogenic peptide. All variety of gene therapy vectors are contemplated.

[0029] When the agent (nucleic acid or peptide) is administered exogenously, sequence variation from an endogenous CAE is possible. In some variations, the amyloidogenic peptide comprises an amino acid sequence at least 70% identical to the amino acid sequence of the CAE and retains the property of amyloidogenic aggregation. Greater degrees of similarity, e.g., at least 75%, 80%, 85%,

90%, 95%, or 100% identical, are also specifically contemplated, where the peptide retains amyloidogenic properties.

[0030] In other embodiments of the methods and uses of the invention, the selected agent is neither the amyloidogenic peptide or coding sequence per se, but rather, an agent which causes one or more endogenous CAE to be expressed in the target neoplastic cells. In some variations of this embodiment, the agent is a chemical agent that causes, induces, or promotes translation through natural stop codons, leading to translation of a gene product that includes the CAE located in the 3'-UTR. In other variations, the agent comprises one or more molecules that cause targeted genetic modification of the target cell. The targeted genetic modification can be a missense modification of a stop codon into a codon for an amino acid. The targeted genetic modification also can be an insertion or deletion in the stop codon or upstream of the stop codon that leads to a frameshift and translation of a modified protein that includes the CAE from the 3'-UTR of the wild type gene.

[0031] Thus, for example, in some embodiments of the method or use of the invention, the amyloidogenic peptide comprises the CAE, and the agent causes expression of an endogenous nucleotide sequence that encodes the CAE. For instance, in some variations, the agent causes expression by causing translation of mRNA beyond the regular stop codon of the gene. Exemplary agents that are specifically contemplated include an aminoglycoside antibiotic that induces translational read-through. Examples of cancer related genes suitable for this approach are given in Table 6 – those genes contain the CAE in the first reading frame.

[0032] In some embodiments of the method or use of the invention, the agent induces expression of the amyloidogenic peptide by modifying chromosomal DNA of the neoplastic cells to create a modified gene that includes the CAE in-frame with the start codon, uninterrupted by a stop codon. A variety of tools now exist to achieve such targeted modification.

[0033] In some variations, the agent comprises a CRISPR Cas9 protein and one or more guide RNA molecules to introduce a site-specific modification of the chromosomal DNA to create a modified gene that includes the CAE in-frame with the start codon, uninterrupted by a stop codon. Optionally, the agent further includes a template nucleic acid for homology directed repair. In some variations, the agent comprises a zinc finger nuclease (ZFN) or a transcription activator-like effector nuclease (TALEN) to introduce a site-specific modification of the chromosomal DNA to create a modified gene that includes the CAE in-frame with the start codon, uninterrupted by a stop codon.

[0034] In some variations, chromosomal DNA is modified by eliminating the regular stop codon of the gene. In some variations, the chromosomal DNA is modified by changing the reading frame of the gene such that the CAE is in-frame with the start codon free of interruption by a stop codon.

[0035] As described herein in detail, many putative CAE elements have been identified, and in some variations of the invention, two or more are enlisted for treatment simultaneously. In some

variations, two or all three of the following are employed: a. an agent that comprises an amyloidogenic peptide; b. an agent that comprises a nucleotide sequence that encodes the amyloidogenic peptide; and c. an agent that induces expression of an endogenous nucleotide sequence that encodes the amyloidogenic peptide. In other variations, two or more of the same category are employed.

[0036] CRISPR provides an especially appealing tool for inducing expression of two or more endogenous nucleotide sequences that encode amyloidogenic peptides, because a single CRISPR construct can be constructed to deliver Cas9 (gene or protein), two or more guide RNA's, and optionally two or more templates for homology directed repair.

[0037] All routes and vehicles for administration are contemplated. In some variations, the agent is formulated with one or more pharmaceutically acceptable carriers. In some variations, the agent is locally administered to a tumor that comprises the neoplastic cells. For example, if the tumor is in the eye or brain, then the agent is locally administered intracranially or intraocularly or intravitreally.

[0038] Still further embodiments of the invention include materials that are useful as therapeutic agents and/or useful for practicing methods of the invention.

[0039] For example, an embodiment of the invention is a polynucleotide comprising a nucleotide sequence that encodes an amyloidogenic peptide fused in-frame with an expression control sequence to promote expression of the amyloidogenic peptide in mammalian cells, wherein the amyloidogenic peptide is either:

[0040] (i) a Cryptic Amyloidogenic Element ("CAE") encoded by nucleic acid in a 3'-untranslated region ("3'-UTR") of a gene in the neoplastic cell; or

[0041] (ii) comprises an amino acid sequence at least 80% identical to the CAE and retains the property of amyloidogenic aggregation.

[0042] For this embodiment of the invention, particular embodiments are contemplated in which the CAE is present in the 3'-UTR of a genome-wide gene set forth in Table 1. More particularly, the putative CAE in the 3'-UTR of any of the following genes is specifically contemplated: APOA2, ATXN2, B2M, FGB, FUS, IAPP, LYZ, NOTCH3, PRNP, RHO, SAA1, SNCA, NEFH, NEFL, BSCL2, MAPT, and TTR. In very particular embodiments, the CAE is in the 3'-UTR of a gene is selected from NEFH, NEFL, and FUS. Known aggregation prone gene targets found to also encode non-coding CAE elements are listed in Table 3 and oncogene targets found to contain CAE elements are listed Table 4. These lists of genes are contemplated for use in the instant invention, as groups (genera), and individually. All subgroups from these tables are specifically contemplated as subgroups suitable for practicing the instant invention, as if each such subgroup were individually listed here.

[0043] In some variations, the invention includes an expression vector comprising any of the foregoing polynucleotides. In particular embodiments, the vector comprises a viral vector. Exemplary vectors that are specifically contemplated include retroviral, adenoviral, adeno-associated viral (AAV), and herpes simplex viral vectors.

[0044] In some variations, the invention is directed to a composition that comprises any of the foregoing polynucleotides or vectors and a pharmaceutically acceptable carrier.

[0045] Still additional aspects of the invention include CRISPR agents. For example, the invention includes a polynucleotide comprising a nucleotide sequence of a crRNA sequence operably linked to a tracrRNA sequence, wherein the crRNA sequence targets a 3' end of a gene set forth in Table 1. In particular embodiments, the gene to be targeted is selected from the group consisting of APOA2, ATXN2, B2M, FGB, FUS, IAPP, LYZ, NOTCH3, PRNP, RHO, SAA1, SNCA, NEFH, NEFL, BSCL2, MAPT, and TTR. In highly specific embodiments, the gene is selected from NEFH, NEFL, and FUS.

[0046] In the context of oligonucleotides useful for directing CRISPR Cas9 nucleases to a sequence targeted for cleavage, a crRNA can be operably linked to a tracrRNA sequences in the manner that occurs in nature. Specifically, the two nucleotides in nature are made as separate strands which have segments that share reverse complement homology, such that one strand partially anneals to the other to form a double-stranded region held together by hydrogen bonds. Alternatively, crRNA and tracrRNA can be formed in a single polynucleotide strand, e.g., as described by Jinek *et al.*, "A Programmable Dual-RNA-Guided DNA Endonuclease in Adaptive Bacterial Immunity," *Science* 337: 816 (2012), incorporated herein by reference in its entirety. As described therein, essential features from crRNA and trRNA can be engineered into a single, chimeric RNA molecule, with the crRNA at the 5' end and tracrRNA at the 3' end. In some embodiments, a spacer, such as a GAAA tetraloop, is included between the 3' end of the crRNA and the 5' end of the tracrRNA. As described herein and in CRISPR scientific literature, the targeting function of the targeting domain of crRNA is manifested by near-perfect or perfect sequence complementarity to a selected target site in the genome. This region of complementarity is selected to be, for example, 15-40 nucleotides in length, and more preferably 15-30, 15-25, or 17-20 nucleotides in length. All integer lengths in these ranges are individually contemplated as embodiments of the invention.

[0047] In particular variations, the crRNA sequence targets a site upstream of, and within 100 nucleotides of, the natural stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence of a Cas9 protein. Targeting within 90, or 80, or 70, or 60, or 50, or 40, or 30, or 20, or 10 nucleotides of the stop codon is specifically contemplated, as is targeting the stop codon itself.

[0048] Genes suitable for targeting with CRISPR Cas9 (or other genetic modification techniques) include those listed in Tables 1, 3, and 4, for example. Using the parameters described herein with respect to the type of modification desired, software tools exist for designing suitable targeting nucleic acids from model human genome sequences or, in some embodiments, from a subject's own sequenced genome. Exemplary targeting sequences for some of the genes identified herein are set forth in Table 5 and in SEQ ID NOs: 1-42. Thus, in some variations, the polynucleotide of the invention comprises a nucleotide targeting sequence which comprises or consists essentially of or consists of 17-20 nucleotides from a sequence set forth in any of SEQ ID NO. 1-42.

[0049] For polynucleotides described herein, sequences generally have been presented using A/G/C/T for adenine, guanine, cytosine, and thymine as is conventional IUPAC practice. However, as described herein and known in the art, CRISPR Cas9 operates as an RNA-driven nuclease, and natural RNA comprises U/uracil rather than T/thymine. The presentation of sequences with "T" should be understood in all cases to include and represent the equivalent RNA/"U" sequence, unless context unambiguously states otherwise. Both single stranded and double stranded polynucleotides are contemplated.

[0050] In some embodiments, the invention includes a polynucleotide comprising:

(a) a nucleotide sequence of a crRNA sequence, said crRNA sequence including:

(i) a nucleotide targeting sequence of 17-20 nucleotides that hybridizes to a 3' end ("target site") of a gene set forth in Table 1, and (ii) a nucleotide sequence that hybridizes to a tracrRNA recognized by a Cas9 protein, wherein (i) is disposed 5' relative to (ii) and wherein the targeting sequence targets a site inclusive or upstream of, and within 100 nucleotides of, the wild type stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence for said Cas9 protein; or (b) a nucleotide sequence encoding (a).

[0051] In some embodiments, the invention is a polynucleotide comprising:

(a) a nucleotide sequence of a CRISPR guide RNA including, from 5' to 3':

(i) a nucleotide targeting sequence of 17-20 nucleotides that hybridizes to a 3' end ("target site") of a gene set forth in Table 1, (ii) a linker sequence of 3-25 bases, such as a tetraloop sequence, and (iii) a nucleotide sequence of a tracrRNA recognized by a Cas9 protein, wherein the targeting sequence targets a site inclusive or upstream of, and within 100 nucleotides of, the wild type stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence for said Cas9 protein; or (b) a nucleotide sequence encoding (a).

[0052] For these embodiments, the genes set forth in Table 3 or Table 4 are among the preferred genes around which to design a targeting crRNA sequence.

[0053] In some variations of the polynucleotide of the invention, the crRNA sequence targets a site upstream of, and within 100 nucleotides of, the natural stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence for a Cas9 protein. As described herein, the target of course also can be the stop codon itself.

[0054] In still further variations, the invention includes a vector comprising the polynucleotide to be used as a CRISPR agent. Optionally, the vector further comprises a nucleotide sequence that encodes a Cas9 polypeptide that complexes with the tracrRNA sequence and that cleaves upstream of the PAM sequence. Optionally, the vector further comprises a nucleotide sequence of a crRNA sequence operably linked to a tracrRNA sequence, wherein the crRNA sequence targets a 3' end of a second gene set forth in Table 1; three, four, or more are specifically contemplated.

[0055] More generally, in some variations, the invention is a vector comprising a nucleotide sequence that comprises or that encodes one or more polynucleotides of the invention. In some variations, the vector is an expression vector. For instance, in the expression vector, the nucleotide sequence that encodes the polynucleotide is operably linked to an expression control sequence (e.g., a promoter) to promote expression of the polynucleotide as RNA in a human cell. In some variations, the expression control sequence comprises a constitutive promoter. Exemplary promoters include the U6, CMV, EF1 α , or CMV promoters.

[0056] In some variations, the expression vector is designed for use in a subject's cell, e.g., a human cell that is a neoplastic cell. In some variations, the cell has one or more genes that is highly expressed compared to a normal cell of the same cell type, and the expression control sequence that is selected for the vector comprises a promoter of one of the genes that is highly expressed. Differential expression between neoplastic versus control helps to focus the effects of the therapy on target neoplastic cells and reduce off-target side effects.

[0057] As described above, in some variations of the invention the crRNA and tracrRNA are fused as a synthetic single strand guide RNA. In other variations, the two functionalities are carried on separate strands. In the latter scenario, in some aspects of the invention where the expression vector that includes an expression cassette for the crRNA optionally further includes a promoter sequence operably linked to a nucleotide sequence encoding a tracrRNA.

[0058] In some variations, the expression vector according to the invention, further includes a promoter sequence operably linked to a nucleotide sequence encoding a Cas9 nuclease that complexes with tracrRNA that comprises the tracrRNA sequence to be used, and that cleaves upstream of the PAM sequence. In some preferred variations, the expression control sequence or coding sequence for the Cas9 nuclease further comprises a nuclear localization sequence (NLS).

[0059] Exemplary Cas9 nuclease for practice of the invention include those from *Streptococcus pyogenes*, *Listeria innocua*, *Staphylococcus aureus*, *Streptococcus thermophiles*, and synthetic

variants derived therefrom. Scientists have extensively studied Cas9 biology and have now designed many variants, e.g., by introducing mutations in the primary amino acid sequence to modulate specificity, nuclease functioning, and the like. Such variants are contemplated. Likewise, Cas9 has now been characterized in many other species of bacteria, and all such Cas9 are suitable and contemplated for practice of aspects of the invention. In some variations, the nucleotide sequence encoding the Cas9 nuclease is a codon-optimized sequence. In particular, the codons are optimized for mammalian (e.g., human expression, based on species codon usages). For example codon optimized Cas9 coding sequences of proteins derived from *Streptococcus pyogenes*, *Listeria innocua*, *Staphylococcus aureus*, or *Streptococcus thermophiles* are contemplated.

[0060] In some variations of the invention, the expression vector of the invention further includes a nucleotide sequence encoding a DNA repair template operably connected to a promoter. For example, in some variations, the DNA repair template includes a sequence to introduce a missense or frameshift mutation at point of cleavage by the Cas9 via homology-directed repair (HDR), and includes segments flanking said sequence that are homologous to the predicted site of Cas9 cleavage. In some variations, the DNA repair template includes sequence to introduce a missense mutation in a stop codon of the gene, or a frameshift mutation in the coding sequence of the gene.

[0061] In some variations, the vector of the invention is a vector selected from the group consisting of a retroviral, adenoviral, adeno-associated viral (AAV), and herpes simplex viral vectors.

[0062] Other tools for delivering CRISPR/Cas9 reagents of the invention are contemplated as well. For example, in some variations, the invention includes a lipid nanoparticle comprising or containing a polynucleotide of the invention, or a vector of the invention.

[0063] In still further variations, the invention includes a composition comprising a polynucleotide or vector or a nanoparticle or other therapeutic agent described herein, and a pharmaceutically acceptable carrier.

[0064] Likewise, it should be appreciated that therapeutic agents described herein are suitable and intended for use in therapeutic method and uses described herein. Thus, still other aspects of the invention are any of the methods or uses that use an agent as described herein as aspects of the invention, wherein the agent comprises a polynucleotide, vector, nanoparticle, or composition as described herein.

[0065] Methods and materials of the invention can be combined with standard-of-care cancer therapies to achieve a therapeutic effect greater than either approach on its own. Thus, in some variations, methods and uses of the invention further comprise administration of a standard of care therapy before, during, or after the method or use described above. Kits and combinations of agents are likewise contemplated as materials of the invention.

[0066] Aspects of the invention that have been described herein as methods also can be described as “uses,” and all such uses are contemplated as aspects of the invention. Likewise, compositions described herein as having a “use” can alternatively be described as processes or methods of using, which are contemplated as aspects of the invention. It should be understood that details described herein in the context of describing a method are applicable to “uses,” and vice versa.

[0067] Reference throughout this specification to “one embodiment”, “some embodiments” or “an embodiment” means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present disclosure. The particular features, structures, or characteristics described herein may be combined in any suitable manner, and all such combinations are contemplated as aspects of the invention.

[0068] Unless otherwise specified the use of the ordinal adjectives “first”, “second”, “third”, etc., to describe a common object, merely indicate that different instances of like objects are being referred to, and are not intended to imply that the objects so described must be in a given sequence, either temporally, spatially, in ranking, or in any other manner.

[0069] The invention includes, as an additional aspect, all embodiments of the invention narrower in scope in any way than the variations defined by specific paragraphs above. For example, where certain aspects of the invention that are described as a genus or set, it should be understood that every member of a genus or set is, individually, an aspect of the invention. Likewise, every individual subset is intended as an aspect of the invention. By way of example, if an aspect of the invention is described as a members selected from the group consisting of 1, 2, 3, and 4, then subgroups (e.g., members selected from {1,2,3} or {1,2,4} or {2,3,4} or {1,2} or {1,3} or {1,4} or {2,3} or {2,4} or {3,4}) are contemplated and each individual species {1} or {2} or {3} or {4} is contemplated as an aspect or variation of the invention. Likewise, if an aspect of the invention is characterized as a range, such as a temperature range, then integer sub-ranges are contemplated as aspects or variations of the invention.

[0070] The headings herein are for the convenience of the reader and not intended to be limiting. Additional aspects, embodiments, and variations of the invention will be apparent from the Detailed Description and/or Drawing and/or claims.

[0071] Although the Applicant invented the full scope of the invention described herein, the Applicant does not intend to claim subject matter described in the prior art work of others. Therefore, in the event that statutory prior art within the scope of a claim is brought to the attention of the Applicants by a Patent Office or other entity or individual, the Applicant reserves the right to exercise amendment rights under applicable patent laws to redefine the subject matter of such a claim to specifically exclude such statutory prior art or obvious variations of statutory prior art from the scope

of such a claim. Variations of the invention defined by such amended claims also are intended as aspects of the invention.

BRIEF DESCRIPTION OF THE FIGURES

[0072] **Figure 1** shows NEFH protein domains and mutations associated with diseases. Coding KSP deletions and insertions from reported ALS cases represented by triangles. CMT frameshift variants from UK1 and F2 are pointed by the arrows.

[0073] **Figures 2A-2D** shows the identification of cryptic amyloidogenic elements (CAEs) in the NEFH and NEFL-3'UTRs. (**Fig. 2A**) Clustal Omega multiple-sequence alignment of wild-type NEFH (SEQ ID NO. 43) and frameshift variants harbored by the CMT-affected families (ASP1004Glnfs*56: SEQ ID NO. 44; Pro1008Alafs*54: SEQ ID NO. 45). Translation of the NEFH-3' UTR open reading frames (ORFs) for ORF1 (SEQ ID NO. 46), ORF2 (SEQ ID NO. 47), and ORF3 (SEQ ID NO. 48) are illustrated. (**Fig. 2B**) Consensus sequence of positive residues (asterisks) for all aggregation predictors tested for NEFH 3'-UTR ORF3 (SEQ ID NO.48),. (**Fig. 2C**) TANGO score of NEFL 3'-UTR ORF1 (SEQ ID NO.49), ORF2 (SEQ ID NO.50), and ORF3 (SEQ ID NO.51). (**Fig. 2D**) Consensus sequence of positive residues (asterisks) for all aggregation predictors tested for NEFL 3'-UTR ORF1 (SEQ ID NO.49).

[0074] **Figure 3** shows NEFH Co-immunoprecipitation: Cell lysates were immunoprecipitated with an antibody against either GFP or Myc and IgG as a negative control. Both GFP-WT-NEFH and GFP-FS-NEFH were co-immunoprecipitated with NEFL-myc. Kinesin was also present in the co-immunoprecipitate.

[0075] **Figure 4** shows confocal microscopy time lapse images of Neuro-2a cells expressing NEFH-CAE. Cells lose neuronal-like projection and adopt a more rounded shape before detaching from plate.

[0076] **Figure 5** shows effect of NEFH-CAE expression *in vivo* in vertebrate model Zebrafish embryos injected with RNA encoding GFP-NEFH-CAE do not show major morphological defects at 48 hpf. Quantification of the average axon length shows a decrease in GFP-FS-NEFH injected fishes compared to both GFP-WT-NEFH injected and uninjected larvae. Axon length is not significantly different between GFP-WT-NEFH injected fishes and uninjected control fish. The average axon length per fish was calculated from the first four myotomes. Data was compiled from three independent experiments and significance was determined by a one-way ANOVA with Bonferroni correction test. P-values are *0.024 and **0.014.

DETAILED DESCRIPTION

Definitions

[0077] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting.

[0078] “Cryptic amyloidogenic element (CAE)” as used herein in, refers to a stretch of amino acids, of any length or combination, predicted to self-aggregate and/or induce amyloid aggregation and proteotoxicity in a target cell, and that has the additional properties summarized in [0009].

[0079] “Fragment” as used herein in the context a of an amyloidogenic peptide or its corresponding coding sequence means a portion of a reference peptide or polypeptide or nucleic acid sequence that retains a pertinent biological property (e.g. a portion that is effective to aggregate or directly or indirectly induce amyloidogenic peptide aggregation and proteotoxicity).

[0080] “Frameshift mutation” as used herein, refers to a genetic mutation caused by indels (insertions or deletions) of a number of nucleotides in a DNA sequence that is not divisible by three and that results in a change of codon reading frame of a sequence of nucleic acids. As described herein, of particular interest are frameshift mutations that result in translation read-through of a wild type stop codon.

[0081] “Guide RNA” as used herein, refers to the polynucleotide sequence that contains a targeting sequence (also referred to as guide sequence or CRISPR RNA sequence [crRNA]) that specifies the target site and the trans-activating CRISPR [tracrRNA] or tracr sequence.

[0082] “3'-UTR” as used herein refers to the 3' untranslated region (UTR) of a gene of interest. UTRs of a gene are transcribed but not translated. The 3'-UTR starts immediately following the natural or wild type stop codon and continues until the transcriptional termination signal. For the purposes of this invention, 3'-UTR includes portions of a complete 3'-UTR that includes a CAE.

[0083] “Peptide” or “polypeptide” as used herein, refers to a linked sequence of amino acids and may be natural, synthetic, or a modification or combination of natural and synthetic.

[0084] “TANGO” is a statistical mechanics algorithm, to predict protein aggregation (Fernandez-Escamilla *et al.*, *Nat Biotechnol.* 2004 22(10):1302-6, incorporated by reference in its entirety).

[0085] “Treating,” “treatment,” or “to treat” each refer to administration of a therapeutic agent or process to a mammalian subject to alleviate, suppress, repress, eliminate or slow the appearance of symptoms, clinical signs, or underlying pathology of cancer/tumor on a temporary or permanent basis. Successful prevention is demonstrated by a statistically significant reduction of occurrence in a population study over a finite and clinically meaningful period of time. In the context of an individual, prevention occurs if the cancer/tumor does not occur over a measurable period of time (e.g. weeks or months) following administration of an agent shown to have prevention properties in a population study. Repressing the cancer involves administering an agent of the present invention to a subject after clinical appearance of the disease resulting in a measurable and statistically significant

reduction in growth and/or size of a tumor. Slowing the progression of disease, as measurable by a statistically significant reduction of occurrence in a population study over a finite and clinically meaningful period of time, is indicative of an agent useful to treat.

[0086] A “biological sample” from an organism comprises any tissue, cell, or fluid which can be analyzed for a trait of interest, such as nucleic acid. A “nucleic acid sample” refers to a biological sample obtained from an individual that contains nucleic acid (DNA or RNA).

[0087] The disclosed methods are useful for treating cancer, for example, inhibiting cancer growth, including complete cancer remission, for inhibiting cancer metastasis, and for promoting cancer resistance. The term “cancer growth” generally refers to any one of a number of indices that suggest change within the cancer to a more developed form. Thus, indices for measuring an inhibition of cancer growth include but are not limited to a decrease in cancer cell survival, a decrease in tumor volume or morphology (for example, as determined using computed tomographic (CT), sonography, or other imaging method), a delayed or slowed tumor growth, a destruction of tumor vasculature, an increase in the activity of cytolytic T-lymphocytes, and a decrease in levels of tumor-specific antigens.

[0088] The term “therapeutically effective amount” refers to an amount of a compound sufficient exhibit a detectable treatment, amelioration, or inhibitory effect in a patient or in an experimental trial involving multiple patients compared to a placebo or control. In the context of a therapy for a subject with a neoplastic condition, evidence of a therapeutic effect includes shrinkage of the neoplasm, a slowing or halting of growth/progression, inhibiting metastasis, increased survival, increased progression-free survival, increased quality of life during period of survival (e.g., reduction of symptoms/discomfort), and other accepted measures.

[0089] A dose of administration will depend on factors such as route of administration (local vs. systemic), patient characteristics (e.g., gender, weight, health, side effects); the nature and extent of the condition; and the therapeutic or combination of therapeutics selected for administration. Therapeutically effective amounts for a given situation can be estimated from in vitro studies to determine, e.g., IC50 concentrations, pre-clinical studies and clinical studies in animals and humans, and the like, and determined by routine experimentation that is within the skill and judgment of the clinician.

[0090] Abnormal protein aggregation is observed in an expanding number of neurodegenerative diseases. The origins of these aggregates are diverse; however, they share similar structures and overlapping mechanisms of cellular toxicity in different diseases. Protein aggregates usually adopt high-ordered beta sheet quaternary structures forming insoluble fibrils termed amyloids (Aguzzi *et al.*, *Nature reviews Drug discovery* (2010) 9:237-248). Disclosed herein is a mechanism of treating and/or preventing the reoccurrence of cancer by using intracellular toxic amyloidogenic peptide

aggregation induced by a mutation event, such as a mutation characterized herein, in axonal neuropathy families.

[0091] The inventors have determined that previously unrecognized cryptic amyloidogenic elements (CAE) in the 3'-UTR of NEFH are expressed under certain circumstances (e.g. familial mutation), leading to aggregation and neuronal degeneration in certain familial neurodegenerative diseases. Described herein is the use of these amyloidogenic elements, including nucleic acids that encode them, to inhibit the growth and survival of cancerous cells. Specific frameshift variants in NEFH in CMT2 families result in stop-loss and translation of a CAE in the 3'-UTR.

[0092] Expression of the mutant NEFH resulted in prominent abnormal protein aggregates, disruption of the NF network, and altered cell dynamics. Interestingly, the same aggregation phenomenon was induced by triggering the translation of the 3'-UTR of NEFL and FUS. *In vivo* and *in vitro* results show that translation of CAE in the 3'-UTR of NFs cause axonopathy and could be of broader impact for neurodegenerative diseases.

Genome editing techniques

[0093] Aspects of the invention involve the administration of an agent or agents to modify the genome of mammalian cells. In some embodiments, these agents can be used to induce the endogenous expression of CAEs.

[0094] Genome-editing is a method of genetic engineering in which DNA is inserted, deleted or replaced in the genome of an organism using engineered nucleases. Genome-editing techniques such as designer zinc fingers, transcription activator-like effectors nucleases (TALENs), or CRISPR-Cas (clustered regularly interspaced short palindromic repeats-CRISPR associated) systems are contemplated for producing targeted genome modification.

[0095] Genome editing may be used to induce missense or frameshift mutations in target genomic loci by single base modification (single nucleotide base change, insertion, or deletion) or by insertions or deletions of a number of nucleotides in a DNA sequence that is not divisible by three, respectively. A frameshift mutation will, in general, cause the reading of the codons after the mutation to code for different amino acids. In some embodiments, missense or frameshift mutations are used to eliminate stop codons. For example, a gene is modified to mutate a stop codon or introduce a change in reading frame, leading to translation of a CAE in the 3'-UTR of the target gene.

[0096] Aspects of the invention involve targeted genetic modification of cells. A variety of techniques are suitable including Zinc-finger nucleases (ZFNs) and TALENs and CRISPR-Cas systems.

Zinc-finger nucleases (ZFNs) and Transcription activator-like effector nucleases (TALENs)

[0097] Zinc-fingers nucleases (ZFNs) and Transcription activator-like effector nucleases (TALENs) are customizable DNA-binding proteins that comprise DNA-modifying enzymes. Both can be designed and targeted to specific sequences in a variety of organisms (Esvelt and Wang, *Mol Syst Biol.* (2013) 9: 641, which is incorporated by reference in its entirety). ZFNs and TALENs can be used to introduce a broad range of genetic modifications by inducing DNA double-strand breaks that stimulate error-prone nonhomologous end joining or homology-directed repair at specific genomic locations. The versatility of ZFNs and TALENs arises from the ability to customize the DNA-binding domain to recognize virtually any sequence. These DNA-binding modules can be combined with numerous effector domains to affect genomic structure and function, including nucleases, transcriptional activators and repressors, recombinases, transposases, DNA and histone methyltransferases, and histone acetyltransferases. Thus, the ability to execute genetic alterations depends largely on the DNA-binding specificity and affinity of designed zincfinger and TALE proteins (Gaj *et al.*, *Trends in Biotechnology*, (2013) 31(7):397-405). The following U.S. granted patents, incorporated by reference, describe the use of ZFNs and TALENs in mammalian cells, U.S. 8,685,737 and U.S. 8,697,853.

CRISPR

[0098] CRISPR–Cas (clustered regularly interspaced short palindromic repeats–CRISPR associated) is an RNA-mediated adaptive immune system found in bacteria and archaea, which provides adaptive immunity against foreign nucleic acids (Wiedenheft *et al.*, *Nature* (2012) 482:331–8; Jinek *et al.*, *Science* (2012) 337:816–21). However, multiple research groups have demonstrated how the biological components of this system can be harnessed to introduce directed modification to the genome of mammalian cells (Cong *et al.*, *Science* (2013) 339:819-23; Mali *et al.*, *Science* (2013) 339(6121):823-6; Jinek *et al.*, *Elife.* (2013); 2:e00471). CRISPR–Cas systems are generally defined by a genomic locus called the CRISPR array, a series of 20–50 base-pair (bp) direct repeats separated by unique “spacers” of similar length and preceded by an AT-rich “leader” sequence (Wright *et al.*, *Cell* (2016) 164:29-44).

[0099] Three types of CRISPR/Cas systems exist, type I, II and III. The Type II CRISPR–Cas systems require a single protein, Cas9, to catalyze DNA cleavage (Sapranaukas *et al.*, *Nucleic Acids Res.* (2011) 39(21): 9275–9282). Cas9 serves as an RNA-guided DNA endonuclease. Cas9 generates blunt double-strand breaks (DSBs) at sites defined by a 20-nucleotide guide sequence (also known as targeting nucleotide sequence or protospacer) which are homologous to target sequences in a genome of interest. The guide sequences are contained within an associated CRISPR RNA (crRNA) transcript. Cas9 can be programmed to cleave double-stranded DNA at any site defined by the guide RNA sequence and next to the protospacer-adjacent (PAM) motif, a short sequence required by and recognized by the CRISPR complex (Sapranaukas *et al.*, *Nucleic Acids Res.* (2011) 39(21): 9275–9282; Jinek *et al.*, *Science* (2012) 337:816–21). The precise sequence and length requirements for the

PAM differ depending on the Cas9 (or other Cas enzyme) ortholog used, but PAMs are typically 2-5 base pair sequences adjacent the protospacer (that is, the target sequence). For example, the PAM sequence 5' NNAGAAW 3' is required for *Streptococcus pyogenes* Cas9 target binding, the PAM sequence 5' NNGRRT 3' or 5' NNGRR(N) 3' are required for *Staphylococcus aureus* Cas9 target binding, the PAM sequence 5' NNGRRT 3 is required for *Streptococcus thermophilus* Cas9 target binding. Cas9 requires both the guide crRNA and a trans-activating crRNA (tracrRNA) that is partially complementary to the crRNA for site-specific DNA recognition and cleavage (Jinek *et al.*, *Science* (2012) 337:816–21). The mature crRNA that is base-paired to tracrRNA forms a two-RNA structure that directs the CRISPR-associated protein Cas9 to introduce DSBs in target DNA. Tracr sequences for use with type II CRISPR-Cas systems are described in Jinek *et al.*, *Science* (2012) 337:816–21 and Chylinski *et al.*, *RNA Biol* (2013) 10(5): 726–737 which are incorporated by reference in their entirety, and specifically for their teachings regarding crRNA and Tracr sequences and guide RNAs referenced in the following paragraph.

[00100] Recent experiments showed that the crRNA:tracrRNA complex can be synthesized as a single transcript (single-guide RNA or sgRNA or chimeric guide RNA) encompassing the features required for both Cas9 binding and DNA target site recognition. Sequences of suitable sgRNAs are described in Jinek *et al.*, *Science* (2012) 337:816–21 and are adaptable to the instant invention. Using sgRNA, Cas9 from *streptococcus pyogenes* can be programmed to cleave double-stranded DNA at any site defined by the guide RNA sequence and including a GG protospacer-adjacent (PAM) motif (Sapranauskas *et al.*, *Nucleic Acids Res.* (2011) 39(21): 9275–9282; Jinek *et al.*, *Science* (2012) 337:816–21). Cas9 from other bacterial species utilize alternative PAM sequences, thereby increasing the number of CRISPR-targetable loci. The DSBs instigate either non-homologous end-joining (NHEJ), which is error-prone and conducive to frameshift mutations that knock out gene alleles, or homology-directed repair (HDR), which can be exploited with the use of an exogenously introduced double-strand or single-strand DNA repair template to knock in or correct a mutation in the genome. Therefore, in the presence of a homologous repair donor, the CRISPR/Cas9 system may be used to generate precise and defined modifications and insertions at a targeted locus through the HDR process. In some variations, the cell targeted to undergo the RNA-guided, site-specific cleavage of DNA will also be given a DNA repair template. For example, the donor DNA repair template that has the desired modification (e.g., missense codon change) or insertion (e.g., frameshift) is flanked by segments of DNA homologous to the blunt ends of the cleaved DNA (Mali *et al.*, *Science* (2013) 33: 823-826). In some variations of the instant invention, the donor DNA repair template encodes a missense modification of a stop codon into a codon for a translated amino acid or it encodes an insertion in the stop codon or upstream of the stop codon that leads to a frameshift mutation and translation of a modified protein that includes the CAE from the 3'-UTR of the wild type gene. In still another variation, the donor DNA repair template encodes a toxic amyloidogenic peptide

sequence that will be translated along with the native amino acid sequence of a highly expressed protein.

[00101] In the absence of a homologous repair donor, single DSBs generated by CRISPR/Cas9 are repaired through the error-prone NHEJ, which sometimes results in insertion or deletion (indel) mutations. Indel mutations in coding exons may introduce premature stop codons or frame-shift mutations, thereby inactivating the corresponding proteins.

[00102] The ability to easily target specific gene loci make CRISPR a useful tool for introducing genetic modifications for the invention, for example, to promote transcription of the CAE in the 3'-UTR of target genes.

[00103] Other publications describing the CRISPR systems and Cas9, include the following Cong *et al. Science* (2013) 339:819-23; Jinek *et al., Elife.* (2013) 2:e00471; Lei *et al. Cell* (2013) 152: 1173–1183; Gilbert *et al. Cell* (2013) 154:442-51; Lei *et al. Elife* (2014) 3:e04766; Perez-Pinela *et al. Nat Methods* (2013) 10: 973–976; Maider *et al. Nature Methods* (2013) 10, 977–979 which are incorporated by reference. The following U.S. and international patents and patent applications describe the methods of use of CRISPR, 8,697,359; 8,771,945; 8,795,965; 8,865,406; 8,871,445; 8,889,356; 8,895,308; 8,906,616; 8,932,814; 8,945,839; 8,993,233; 8,999,641; 2014/0068797; and WO 2014/197568, all incorporated by reference in their entirety.

[00104] The CRISPR related protein, Cas9, can be from any number of species including but not limited to *Streptococcus pyogenes*, *Listeria innocua*, *Staphylococcus aureus* and *Streptococcus thermophiles* and optionally codon-optimized to express in the target cell of interest. The nucleotide sequences of Cas9 orthologs are described in the art, for example, in international patent application WO 2015048577A2 and US patent application 2014/0068797A1.

[00105] In one aspect, the invention uses CRISPR-Cas system comprising a Cas9 protein and one or more guide RNAs and optionally repair templates to modify eukaryotic genes that contain a CAE in the 3'-UTR of the gene. Exemplary genes are identified in Table 1. In some variations, CRISPR-Cas systems are used to modify *NEFH* or *NEFL* genes in a eukaryotic cell so that the 3'-UTR of *NEFH* or *NEFL* are translated *in vivo*.

[00106] The CRISPR-Cas reagents (e.g. CRISPR-Cas9) used to modify the genes are themselves an aspect of the invention. For example, the invention includes a guide RNA molecule, e.g., an isolated or non-naturally occurring gRNA molecule, comprising a targeting domain which is complementary with a target domain from the *NEFH* or *NEFL* genes. Particularly complemented are targeting domains including or just upstream of the stop-codon.

[00107] In one aspect, the invention uses CRISPR-Cas reagents (e.g. CRISPR-Cas9 and induce DSBs, NHEJ and frameshift mutation(s) in eukaryotic genes that contain a CAE in the 3'-UTR of the

gene. Exemplary genes are identified in Table 1. In some variations, the exemplary genes identified in Table 3 or in Table 4, or subsets of those genes, are selected.

[00108] It will be understood from these Tables and from the description herein that the nature of the modification differs slightly, depending on the reading frame of a CAE. If a CAE falls in the same reading frame as the wild type protein (frame 1), then a missense or deletion of the stop codon achieves read-through. If a CAE falls in a different reading frame (frame 2 or frame 3) then a frameshift mutation achieves read-through. In some variations the frameshift occurs with a stop codon mutation. In some variations, a frameshift is introduced upstream of the stop codon, preferably in the exon that encodes the stop codon and/or the amino acids immediately upstream of the stop codon.

[00109] In another aspect, the invention uses CRISPR-Cas reagents (e.g. CRISPR-Cas9 homologous repair donor) induce DSBs, HDR and modification and insertion of nucleotide bases of stop codons in target eukaryotic genes that contain a CAE in the 3'-UTR of the gene. Exemplary genes are identified in Table 1.

[00110] In another aspect, CRISPR-Cas reagents (e.g. CRISPR-Cas9) are designed and made and used to alter the non-coding sequence of any gene listed in Table 1 to alter the expression of a CAE located in the 3'-UTR of the gene by targeting, e.g., a promoter, an enhancer, an intron, 3'UTR, and/or polyadenylation signal.

[00111] The agent may encode the wild-type sequence of the CRISPR related protein or a variant CRISPR related protein. The agent can include either the wild-type codon usage or codon usage optimized for a particular application, e.g., human codon optimization for human therapeutics. The type II CRISPR Cas9 systems are particularly preferred.

[00112] In some embodiments, DNA encoding Cas9 molecules (e.g., eaCas9 molecules) and/or gRNA molecules, are delivered into cells by art-known methods or as described herein. For example, Cas9-encoding and/or gRNA-encoding DNA are delivered, e.g., by vectors (e.g., viral or non-viral vectors), non-vector based methods (e.g., using naked DNA or DNA complexes), or a combination thereof.

[00113] Preferably, the vector is a viral vector, such as a lenti- or baculo- or preferably adeno-viral/adeno-associated viral vectors (AAV), but other means of delivery are known (such as yeast systems, microvesicles, gene guns/means of attaching vectors to gold nanoparticles) and are provided. In some embodiments, one or more of the viral or plasmid vectors may be delivered via liposomes, nanoparticles, exosomes, microvesicles, hydrodynamic-based gene delivery or a gene-gun. Cas9 and gRNA can be present in a single lentiviral transfer vector or separate transfer vectors. Adenoviral delivery of the CRISPR/Cas9 system is described in Holkers *et al.*, *Nature Methods* (2014), 11(10):1051-1057 which is incorporated by reference in its entirety.

[00114] In certain embodiments the invention provides a method of treating cancer in a subject (e.g., mammal or human) or a non-human subject (e.g., mammal) in need thereof comprising modifying the subject or a non-human subject by manipulation of the target sequence comprising providing treatment comprising: delivering a non-naturally occurring or engineered composition comprising an AAV or lentivirus vector system comprising one or more AAV or lentivirus vectors operably encoding a composition for expression thereof, wherein the target sequence is manipulated by the composition when expressed.

[00115] In some embodiments, CRISPR/Cas9 multiplexing may be used to target multiple genomic loci wherein 2 or more guide RNAs are expressed as described in CRISPR 101:A Desktop Resource (1st Edition), *Addgene*, January 2016 which is incorporated by reference in its entirety.

Gene expression analysis

[00116] In an embodiment of the present invention, gene expression data are used to determine genomic targets. Expression data in the database derived from cells as closely related to the neoplastic cells of interest is preferably selected. Examples of databases include, but not limited to, Genbank public domain database available on the Internet at www.ncbi.nlm.nih.gov/Genbank; The Cancer Genome Atlas (<http://cancergenome.nih.gov/>); Gene Expression across Normal and Tumor tissue (GENT) database (<http://medicalgenome.kribb.re.kr/GENT/>); Achilles Project (<http://www.broadinstitute.org/achilles>); Cancer Cell Line Factory (CCLF) (www.broadinstitute.org/cellfactory); Connectivity Map (CMap) (<http://www.broadinstitute.org/cmap>).

[00117] In an alternative embodiment of the present invention, gene expression analysis of cells from a patient's tumor(s) to determine a molecular signature is performed using methods described in the art (Ramaswamy et al., *PNAS* (2001) 98: 15149-15154; Ramaswamy et al., *Nat Genet.* (2003) 33(1):49-54; Fehrmann et al., *Nature Genetics* (2015) 47, 115–125, which are incorporated by reference. Exemplary analyses include mRNA measurement and/or protein measurements and/or protein activity measurements.

Gene expression constructs

[00118] In some embodiments of the present invention, gene expression constructs such as promoter expression plasmids are used to transform target neoplastic cells *in vivo* to express amyloidogenic peptides. The constructs described herein include a promoter (e.g. cytomegalovirus (CMV) promoter), the coding and or non-coding (e.g. 3'-UTR) regions from multiple genes encoding one or more wildtype or modified proteins (e.g. mutated), inteins, transcription termination or regulator elements sequences. In some embodiments tissue specific promoters may be used. For example, the Cre-loxP system may be utilized to express amyloidogenic peptides in specific tissues. In some cases the Cre-loxP gene expression construct is inducible.

[00119] In some embodiments, a target cell is screened to identify a gene that is highly expressed, and a promoter for the highly expressed gene is selected as a promoter for the gene expression construct. In some embodiments, a target neoplastic cell and corresponding healthy cells are screened to identify a gene that is highly expressed in the neoplastic cells but not highly expressed in the healthy control cells, and the promoter for such a gene is selected for the gene expression construct.

Identification of cryptic amyloidogenic elements (CAEs)

[00120] In an embodiment of the present invention, potential cryptic amyloidogenic elements (CAEs) are identified using *in silico* analysis. Bioinformatics aggregation prediction analysis of all 3'-UTR sequences in a genome of interest is performed using RefSeq transcripts from the National Center for Biotechnology Information (NCBI) database and aggregation prediction programs, TANGO and PASTA. Described in detail in example 6.

Methods of Treatment

[00121] Provided herein is a method of inhibiting or reducing the growth, progression and/or reoccurrence of cancer.

[00122] Although more than one route can be used to administer an agent of the present invention, a particular route can provide a more immediate and more effective reaction than another route. Depending on the circumstances, a pharmaceutical composition comprising the agent is applied or introduced into body cavities, absorbed through the skin or mucous membranes, ingested, inhaled, and/or introduced into circulation. For example, in certain circumstances, it will be desirable to deliver the pharmaceutical composition orally; through injection or infusion by intravenous, intratumoral, intraperitoneal, intracerebral (intra-parenchymal), intracerebroventricular, intramuscular, intra-ocular, intraarterial, intraportal, intralesional, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, urethral, vaginal, or rectal means; by controlled, delayed, sustained or otherwise modified release systems; or by implantation devices. In one aspect, drug exposure can be optimized by maintaining constant drug plasma concentrations over time. Such a steady-state is generally accomplished in clinical settings by continuous drug infusion at doses depending on the drug clearance and the plasma concentration to be sustained. If desired, the composition is administered regionally via intratumoral, administration, intrathecal administration, intracerebral (intra-parenchymal) administration, intracerebroventricular administration, or intraarterial or intravenous administration targeting the region of interest. Alternatively, the antibiotics, peptides and/or induction agents are administered locally via implantation of a matrix, membrane, sponge, or another appropriate material onto which the desired compound has been absorbed or encapsulated. Where an implantation device is used, the device is, in one aspect, implanted into any suitable tissue or organ, and delivery of the desired compound is, for example, via diffusion, timed-release bolus, or continuous administration.

[00123] In some preferred embodiments involving genetic modification, the polynucleotide guide sequences and Cas9 polynucleotide or polypeptide sequence described herein are administered using adeno-associated virus (AAV) vectors or lipid nanoparticles. AAV-mediated CRISPR delivery is described in Wang *et al.*, *Int J Mol Sci.* 17(5): 626 (2016); Gaj and Schaffer, *Cold Spring Harb Protoc* (11):086868 (2016). Lipid nanoparticle-mediated CRISPR delivery is described Zuris *et al.*, *Nature Biotechnology* 33, 73–80 (2015); Yin *et al.*, *Nature Biotechnology* 34, 328–333 (2016); Wang *et al.*, *Int J Mol Sci.* 17(5): 626 (2016) which are incorporated by reference.

Aminoglycoside antibiotics

[00124] In some variations of the invention, a composition is administered to a subject in need of treatment, wherein the composition includes an agent that decreases translational fidelity and results in increased read-through of stop codons. Exemplary agents of this class include aminoglycoside antibiotics. See, e.g., Heier *et al.*, “Translational readthrough by the aminoglycoside geneticin (G418) modulates SMN stability *in vitro* and improves motor function in SMA mice *in vivo*,” *Hum Mol Genet.* 2009 Apr 1; 18(7): 1310–1322; 27; Stephenson J. “Antibiotics show promise as therapy for genetic disorders,” *J. Am. Med. Assoc.* 2001;285:2067–2068; Zingman *et al.*, “Aminoglycoside-induced translational read-through in disease: overcoming nonsense mutations by pharmacogenetic therapy,” *Clin. Pharmacol. Ther.* 2007;81:99–103; Bidou *et al.*, “Sense from nonsense: therapies for premature stop codon diseases,” *Trends Mol Med.* 2012 Nov;18(11):679-88; Nudelman *et al.*, “Redesign of aminoglycosides for treatment of human genetic diseases caused by premature stop mutations,” *Bioorg Med Chem Lett.* 2006 Dec 15;16(24):6310-5; Keeling *et al.*, “Therapeutics based on stop codon readthrough,” *Annu Rev Genomics Hum Genet.* 2014;15:371-94; and Gomez-Grau *et al.*, “Evaluation of Aminoglycoside and Non-Aminoglycoside Compounds for Stop-Codon Readthrough Therapy in Four Lysosomal Storage Diseases,” *PLoS One* 10(8):e0135873 (2015), all incorporated herein by reference in their entirety, and specifically for their descriptions of compounds that promote stop-codon read-through and how to use them.

[00125] Exemplary agents that are specifically contemplated include an aminoglycoside antibiotic that increases or induces translational read-through in cells exposed to the antibiotic. Aminoglycoside antibiotics or aminoglycosides exhibit concentration-dependent bactericidal activity. They mode of action includes binding to the 30S ribosome to inhibit bacterial protein synthesis. Examples of aminoglycoside antibiotics for use in the instant invention but not limited to, include the following: paromomycin, tobramycin, gentamicin, amikacin, kanamycin, neomycin, dibekacin, sisomicin, netilmicin and streptomycin.

Formulation

[00126] In some variations, gene editing is contemplated as a method to activate CAE in 3'-UTRs. Any standard gene editing approach for *in vivo* applications that is able to introduce small insertions

and deletions at a targeted locus or provide precise nucleotide exchanges will suffice. Typically, AAV particles from small scale and large scale AAV packaging is applied directly for *in vivo* animal injection. The recommended titer for *in vivo* animal injection is 10^{11} GC per mouse or 2×10^9 GC/g (body weight). For local injections (e.g. into brain) a smaller quantity of AAV viruses can be applied.

[00127] In some variations agents of the present invention, e.g., aminoglycoside antibiotics are formulated as a composition comprising one or more pharmaceutically acceptable carriers. The phrase “pharmaceutically (or pharmacologically) acceptable” refers to molecular entities and compositions that do not produce allergic, or other adverse reactions when administered using routes well-known in the art, as described below. “Pharmaceutically acceptable carriers” include any and all clinically useful solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like.

[00128] Suitable methods of administering a physiologically-acceptable composition, such as a pharmaceutical composition comprising a compound and/or micelle described herein, are well known in the art.

Combination therapy

[00129] It is contemplated the two or more agents of the present invention may be given simultaneously, in the same formulation. It is further contemplated that the two or more agents are administered in separate formulations and administered either separately or concurrently, with concurrently referring to agents given within 30 minutes of each other.

[00130] The agents of the invention may be administered as a monotherapy or simultaneously or metronomically with other treatments, which may be a surgery or removal of a tumor. The term “simultaneous” or “simultaneously” as used herein, means that the two treatments are administered within 48 hours (h), preferably 24 h, more preferably 12 h, yet more preferably 6 h, and most preferably 3 h or less, of each other. The term “metronomically” as used herein means the administration of the agent at times different from the other treatment and at a certain frequency relative to repeat administration.

[00131] Concurrent administration of two therapeutic agents does not require that the agents be administered at the same time or by the same route, as long as there is an overlap in the time period during which the agents are exerting their therapeutic effect. Simultaneous or sequential administration is contemplated, as is administration on different days or weeks.

[00132] In some variations of the invention, agent of the invention is administered as a co-therapy in combination with a standard-of-care therapy for a neoplastic condition. Exemplary standard-of-care anti-neoplastic therapies include antitumor agents and chemotherapeutic agents such as an aromatase inhibitor, an anti-estrogen, an anti-androgen, a gonadorelin agonist, a topoisomerase I

inhibitor, a topoisomerase II inhibitor, a microtubule active agent, an alkylating agent, a retinoid, a carotenoid, a tocopherol, a cyclooxygenase inhibitor, an MMP inhibitor, a mTOR inhibitor, an antimetabolite, a platin compound, a methionine aminopeptidase inhibitor, a bisphosphonate, an antiproliferative antibody, a heparanase inhibitor, an inhibitor of Ras oncogenic isoforms, a telomerase inhibitor, a proteasome inhibitor, a compound used in the treatment of hematologic malignancies, a Flt-3 inhibitor, an Hsp90 inhibitor, a kinesin spindle protein inhibitor, a MEK inhibitor, an antitumor antibiotic, a nitrosourea, a compound targeting/decreasing protein or lipid kinase activity, a compound targeting/decreasing protein or lipid phosphatase activity, any further anti-angiogenic compound, and combinations thereof. Specific examples of antitumor agents include, but are not limited to, azacitidine, axathioprine, bevacizumab, bleomycin, capecitabine, carboplatin, chlorabucil, cisplatin, cyclophosphamide, cytarabine, daunorubicin, docetaxel, doxifluridine, doxorubicin, epirubicin, etoposide, fluorouracil, gemcitabine, herceptin, idarubicin, mechlorethamine, melphalan, mercaptopurine, methotrexate, mitoxantrone, oxaliplatin, paclitaxel, tafluposide, teniposide, tioguanine, retinoic acid, valrubicin, vinblastine, vincristine, vindesine, vinorelbine, receptor tyrosine kinase inhibitors, and combinations thereof. Additional examples of antitumor or chemotherapeutic agents are known in the art.

[00133] Second agent choice is dictated by the standard of care for a given cancer type, cancer progression/stage such as isolated versus metastatic and surgical or morbidity status.

[00134] It is further contemplated that other adjunct therapies may be administered, where appropriate. For example, the patient may also be administered an extracellular matrix degrading protein, surgical therapy, chemotherapy, a cytotoxic agent, or radiation therapy where appropriate.

Dosage

[00135] The method may comprise administering a therapeutically effective amount of one or more agents consisting of a aminoglycoside antibiotics to a patient in need thereof. The therapeutically effective amount required for use in therapy varies with the nature of the cancer being treated, and the age/condition of the patient. In general, however, doses employed for adult human treatment typically are in the range of 7.5 mg/kg (Wagner *et al.*, *Ann Neurol.* 2001 49(6):706-11) to about 15 mg/kg per day. The dose may be about 0.1mg/kg to about 15 mg/kg per day. The desired dose may be conveniently administered in a single dose, or as multiple doses administered at appropriate intervals, for example as two, three, four or more sub-doses per day. Multiple doses may be desired, or required.

Cancer types

[00136] The invention also provides for methods of treating, inhibiting and preventing tumor growth and cancers such as, e.g. brain tumors (including meningiomas, glioblastoma multiforme, anaplastic astrocytomas, cerebellar astrocytomas, other high-grade or low-grade astrocytomas, brain

stem gliomas, oligodendrogliomas, mixed gliomas, other gliomas, cerebral neuroblastomas, craniopharyngiomas, diencephalic gliomas, germinomas, medulloblastomas, ependymomas, choroid plexus tumors, pineal parenchymal tumors, gangliogliomas, neuroepithelial tumors, neuronal or mixed neuronal glial tumors), lung tumors (including small cell carcinomas, epidermoid carcinomas, adenocarcinomas, large cell carcinomas, carcinoid tumors, bronchial gland tumors, mesotheliomas, sarcomas or mixed tumors), prostate cancers (including adenocarcinomas, squamous cell carcinoma, transitional cell carcinoma, carcinoma of the prostatic utricle, or carcinosarcomas), breast cancers (including adenocarcinomas or carcinoid tumors), or gastric, intestinal, or colon cancers (including adenocarcinomas, invasive ductal carcinoma, infiltrating or invasive lobular carcinoma, medullary carcinoma, ductal carcinoma in situ, lobular carcinoma in situ, colloid carcinoma or Paget's disease of the nipple), skin cancer (including melanoma, squamous cell carcinoma, tumor progression of human skin keratinocytes, basal cell carcinoma, hemangiopericytoma and Kaposi's sarcoma), lymphoma (including Hodgkin's disease and non-Hodgkin's lymphoma), sarcomas (including osteosarcoma, chondrosarcoma and fibrosarcoma) as well as for the treatment of nervous system disorders.

Subject

[00137] In some variations the subject is a mammal (e.g. mice, rat, rabbit, bird, guinea pig, dog or cat). In some variations the subject is a human. Other subjects are contemplated, as set forth in the summary of the invention above.

Kit

[00138] Provided herein is a kit, which may be used for inhibiting or reducing the growth, progression and/or reoccurrence of cancer. The kit may comprise one or more agents consisting of a toxic aggregating peptide, a nucleotide sequence that encodes the toxic aggregating peptide and/ or an agent that induces expression of an endogenous nucleotide sequence that encodes the toxic aggregating peptide. The agents may be part of a pharmaceutical composition. The kit may further comprise instructions for using the kit and conducting the administering the said agents or formulation.

EXAMPLES

[00139] The following Examples are merely illustrative and are not intended to limit the scope or content of the invention in any way.

Example 1: Identification of NEFH frameshift variants in CMT2 families.

[00140] Whole exome sequencing was performed on three affected individuals belonging to different generations of a British family (UK1) diagnosed with autosomal-dominant CMT2. Exome data was analyzed with a strict filtering approach for segregation of non-synonymous heterozygous

variants using the F2 Genomes Management Application (GEM.app) software (Gonzalez *et al.*, *Human mutation* (2013) 34, 842-846). A heterozygous frameshift variant in NEFH was identified as a top candidate for the disease from a list containing six additional variants (Table 2).

[00141] Table 2: List of candidate genes from UK1 family's exome data

seattleseq_gene	MIM	pos	Ref	genotype	protein_notation	polyphen	gerp_score
NEFH	162230	29886637	AAG/AAG	AAG/A	p.Asp1004fs*56		
DNAH17	610063	76440872	G/G	G/A	p.S3781L	0.679	5.12
LYST	606897	235944236	C/C	C/T	p.E1715K	0.856	5.05
MED20	612915	41877152	A/A	A/G	p.V93A	0.309	5.91
PFKFB3	605319	6258150	T/T	T/C	p.I101T	0.995	5.11
SPAG5	615562	26905701	C/C	C/T	p.G1063S	1	3.49
TRAF4	602464	27076455	G/G	G/A	p.G425S	0.025	6.11

[00142] NEFH was selected because NF abnormalities have been previously reported in neurodegenerative diseases, including ALS (Liu *et al.*, *CMLS* (2004) 61, 3057-3075). In addition, mutations in NEFL, another major NF component, also cause CMT (Jordanova *et al.*, *Brain: a journal of neurology* (2003) 126, 590-597). The variant co-segregated with the phenotype across three generations in this family. This variant, (c.3010_3011delGA, p.Asp1004Glnfs*58, chr22:29,886,637) affects the last coding exon and shifts translation into an alternative open reading frame (ORF) resulting in continued translation of an additional 40 amino acids beyond the stop codon in the original ORF (Figure 2A). The mutant protein retains its major functional domains, including the head, rod and tail domains (Figure 1). An additional screen 322 CMT families was subsequently performed with whole exome sequencing. This screen identified another CMT2 family (F2) with four affected individuals carrying a nearby heterozygous frameshift variant in NEFH (c.3017_3020dup, p.Pro1008Alafs*56, chr22:29,886,645). This insertion interestingly also resulted in a stop-loss mutation and translation of the identical ORF as observed in family UK1. Co-segregation of the distinct variants with the phenotype was confirmed by Sanger sequencing in both families. Sequencing of DNA from the deceased parent in family F2, who was likely a carrier of the pathogenic variant was not possible. These mutations were not observed in approximately 5,000 additional exomes (Gonzalez *et al.*, *Human mutation* (2015) 36, 950-956), with a wide range of clinical phenotypes, including other neuropathies, from our own collection and no other frameshift variants in the last exon of NEFH were found.

Example 2: Identification of cryptic amyloidogenic elements in NEFH and NEFL 3'-UTRs.

[00143] Because NFs have a considerable tendency to aggregate in neurodegenerative diseases, the intrinsic aggregation propensity of the extension of amino acids present in NEFH in the two CMT2 families was investigated. The web-based aggregation prediction tool TANGO28 was used to analyze aggregation-prone segments based on the physico-chemical principles of beta-sheet formation. According to this algorithm a segment is predicted to aggregate when it contains at least five consecutive residues with a TANGO score above 5% (Fernandez-Escamilla, *Nature biotechnology*

(2004) 22, 1302-1306 incorporated by reference). Analysis of the 3'-UTR extension of amino acids present in the NEFH mutant p.Asp1004Glnfs*58, showed a hot spot for aggregation in eight stretches of amino acids (QFSLFSL) with a combined score of 250 (Figure 2A). Aggregation propensity was also analyzed with other prediction tools including AGGRESCAN29, FoldAmyloid30 and PASTA 2.031 that use different algorithms to predict aggregation. All tested tools detected aggregation and an amyloidogenic region in an overlapping stretch of amino acids of the mutant extension (Figure 2B). This stretch of amino acids predicted to induce aggregation is herein referred to as a cryptic amyloidogenic element (CAE) because it is located in a 3'-UTR and not normally translated in the absence of a genetic mutation or stop codon read-through. Prediction analysis of the other two open reading frames of the NEFH-3'UTR resulted in no aggregation for ORF1 and high aggregation scores for ORF2. These data suggest that any frameshift variants resulting in loss of the NEFH stop codon and translation of cryptic amyloidogenic elements in 3'-UTR would have the potential to cause protein aggregation.

[00144] Investigation of the *in silico* the aggregation propensity of the NEFL 3'-UTR region, revealed that only ORF1 of the 3'-UTR was positive for aggregation prediction with a high TANGO score of 443 comprising the motif ISLIISGII (Figure 2D). Positive scores for ORF1 were also obtained with AGGRESCAN, FoldAmyloid, and PASTA2.0. *In silico* results for NEFL suggested that only missense mutations affecting the STOP codon resulting in translation of 3'-UTR ORF1 have the potential to cause aggregation.

Example 3: Prominent aggregation in cultured Neuro-2a cells expressing neurofilaments (NFs) encoding 3'-UTR CAEs

[00145] Following *in silico* analysis, the potential of the 3'-UTR CAEs identified in affected individuals to cause aggregation in Neuro-2a cells was investigated. Constructs were created encoding GFP-tagged wild type protein (*GFP-WT-NEFH*) and frameshift mutant protein encoding 40 additional amino acids of ORF3 (*GFP-FS-NEFH*). *GFP-WT-NEFH* transfection led to evenly distributed expression in the cytoplasm of Neuro-2a cells. Expression of *GFP-FS-NEFH* revealed prominent abnormal perinuclear aggregation after 24hrs post transfection. Quantification showed that over 75% of cells transfected with *GFP-FS-NEFH* contained aggregates compared to less than 1% in *GFP-WT-NEFH* cells. Cells transfected with wild-type NEFH retained their typical Neuro-2a cell morphology with 'axon-like' projections extending from the cell body. By contrast, *GFP-FS-NEFH* expressing cells were round-shaped and their axon-like projections were significantly reduced.

[00146] In order to experimentally identify which of the additional 40 amino acids are responsible for the aggregation, a series of truncated constructs harboring stop codons (STOP1-STOP4) at different positions throughout the extension of amino acids was created. Cells were transfected with constructs STOP1, STOP2, and STOP3 did not form aggregation in cells and their subcellular

distribution pattern was identical to *GFP-WT-NEFH*. Aggregates were observed in a small proportion of cells (20%) transfected with the longest construct, *GFP-STOP4-NEFH*; however, aggregation was still more severe in the full-length extension described above (*GFP-FS-NEFH*). To further characterize the predicted CAE, the most distal 22 amino acids predicted to cause aggregation (SSRIRVTQFSLFLSLCKKKLLR) were cloned directly *in frame* with the C-terminus end of the *GFP-WT-NEF* to create the *GFP-NEFH-CAE* construct. As expected, cells transfected with the *GFP-NEFH-CAE* construct caused prominent aggregation at the same level observed in cells transfected with the *GFP-FS-NEFH*. These results prove that the most distal 22 amyloidogenic amino acids are sufficient and necessary for the formation of aggregates.

[00147] The ability of the 3'-UTR CAE present in the *NEFL* to cause aggregation in cells was also investigated. Neuro-2a cells were transfected with constructs encoding GFP-tagged NEFL (*GFP-WT-NEFL*), NEFL without Stop codon fused *in-frame* with the NEFL-3'-UTR containing the predicted CAE (*GFP-NEFL-ORF1*), and NEFL fused with the ORF3 3'-UTR, which was not predicted to contain CAE (*GFP-NEFL-ORF3*). Although a few cells transfected with GFP-WT-NEFL presented aggregates due to the self-assembly nature of NEFL, a large portion of cells adopted NF-like structures, an indication of NF assembly, in about 45% of transfected cells. These filamentous structures can also be explained by the ability of NEFL to self-assemble, in contrast to NEFH, which is an obligate heteropolymer and it requires interaction with either NEFL or NEFM in order to assemble into NFt structures (Evgrafov *et al. Nature genetics* (2004) 36, 602-606). However, all cells transfected with *GFP-NEFL-ORF1* formed prominent aggregation and adopted a rounded shape without forming filamentous structures. In contrast, cells transfected with *GFP-NEFL-ORF3* resulted in NFs structures comparable with the *GFP-WT-NEFL*. The results suggest that specific translation of 3'-UTR CAE present in the first open reading-frame of NEFL is required for the formation of aggregates.

Example 4: Evaluation of cells expressing the NEFH-3'-UTR CAE

[00148] As a dramatic difference in cell shape and viability was observed in cells expressing GFP-FS-NEFH compared to wild-type NEFH, the cellular features were quantified. Western blots were performed to show that the levels of protein expression in Neuro-2a cells transfected with GFP-WT-NEFH and GFP-FS-NEFH were similar. Therefore, differences in aggregation cannot be due to protein expression levels. These cells were analyzed using the Incucyte imaging system with time-lapse images taken every 3 hours between 24-48hrs post transfection. It was observed that the average green (GFP) object area (μm^2) per cell was smaller in cells expressing GFP-FS-NEFH ($\sim 120 \mu\text{m}^2$) compared to GFP-WT-NEFH ($>250 \mu\text{m}^2$), suggesting that GFP-FS-NEFH cells were about 2X smaller. The percentage of confluence of GFP-WT-NEFH positive cells increased with time from 2 % to 6.5 %, while the confluence of GFP-FS-NEFH remained below 2 %. This indicates decreased cell viability after GFP-FS-NEFH transfection. In addition, 48h post transfection, cells expressing

GFP-FS-NEFH started to detach from plates, whereas cells transfected with the GFP-WT-NEFH were still attached and viable several days after transfection. The average green object eccentricity, a parameter that measures object roundness from 0 to 1, where 0 represents a perfect circle, confirmed that GFP-FS-NEFH cells have a more rounded shape. Therefore abnormal aggregation of mutant NEFH may cause a toxic gain-of-function effect leading to loss of neuronal characteristics and loss of cell viability.

[00149] To further characterize the NEFH aggregation structures, cells were stained with thioflavin T, a dye commonly used to stain amyloid fibrils with beta-sheet structures in individual tissues (Gonzalez *et al.*, *Human mutation* (2015) Innovative Genomic Collaboration Using the GENESIS (GEM.app) Platform; Groenning *et al.*, *Journal of chemical biology* (2010) 3, 1-18). Confocal fluorescent imaging showed strong thioflavin T staining of NEFH aggregates, suggesting a fibrillary amyloid-like type of structure. In order to further understand the composition of the aggregates, transmission electron microscopy was performed in transfected Neuro-2a cells. In cells transiently expressing GFP-FS-NEFH, disordered arrays of filaments of approximately 10nm in diameter consistent with NF size, were observed. Similar disordered NF inclusion structures were previously reported in the anterior horn cells in an individual with ALS harboring a SOD1 (MIM: 147450) mutation (Kokubo *et al.*, *Archives of neurology* (1999) 56, 1506-1508). These disordered arrays of filaments were observed in 12/100 images of cells expressing GFP-FS-NEFH in no less than 5 different cells and were never observed in 0/40 GFP-WT-NEFH images or 0/20 images of untransfected cells. Although it was not possible to distinguish untransfected from transfected cells in the EM images, transfection efficiency was ~70% and close to 20 rounded cells transfected with GFP-FS-NEFH were analyzed, which is a feature of cells containing severe aggregates. Based on the frequency of this feature in cells expressing GFP-FS-NEFH and absence in cells expressing GFP-WT-NEFH or untransfected cells, these structures were likely to be the aggregate.

Example 5: Expression of NEFH mutant protein disrupts the neurofilament (NF) network in cultured Neuro-2a cells.

[00150] In order to see the effect of the expression of the mutant NEFH on the NF network, *GFP-NEFH* constructs with a plasmid encoding NEFL fused to a Myc-tag at the C-terminus (NEFL-Myc) were co-transfected. As expected, the *GFP-WT-NEFH* co-localized with NEFL-Myc protein and assembled into organized NF-like structures. The GFP-FS-NEFL also co-localized with NEFL-Myc, but within the massive aggregates, suggesting arrest and co-aggregation of NEFL and consequently disruption of the NF network. Co-immunoprecipitation experiments were performed to confirm interaction between the mutant NEFH and NEFL. Cell lysates were immunoprecipitated with an anti-GFP antibody to pull-down NEFH. Western blot confirmed that NEFL-Myc was co-immunoprecipitated in cells transfected with either *GFP-WT-NEFH* or *GFP-FS-NEFH* (Figure 3). The reverse co-immunoprecipitation with NEFL-Myc pull-down also confirmed the interaction.

Kinesin was further detected in the co-immunoprecipitate in cells transfected with either wild-type or mutant NEFH (Figure 3).

[00151] These results suggest that the mutant NEFH is trapping NEFL, kinesins and possibly other interacting proteins into the aggregates and consequently blocking these proteins from performing their proper functions. Hence, this stop-loss NEFH mutation found in individuals with CMT2 is most likely a toxic gain-of-function mutation. To determine whether the aggregates were affecting exclusively the NF network or additional cytoskeleton components, cells were stained with a tubulin antibody. The microtubule network was normally distributed and assembled in cells transfected with either *GFP-WT-NEFH* or *GFP-FS-NEFH* indicating it was not affected by the aggregates.

[00152] The NF network has been shown to be important for the spatial subcellular distribution of mitochondria (Wagner *et al.*, *The Journal of neuroscience : the official journal of the Society for Neuroscience* (2003) 23:9046-58). Therefore cells were stained with an antibody against the mitochondrial outer membrane protein TOM20 (MIM: 601848) to evaluate the effect of the stop-loss mutation. Mitochondria were evenly distributed in cells expressing *GFP-WT-NEFH*; however, in cells expressing *GFP-FS-NEFH*, mitochondria accumulated adjacently to the NEFH aggregates. Similarly, it has been shown that *NEFL* mutations linked to CMT cause altered mitochondrial distribution and co-localization with aggregates Perez-Olle *et al.*, *Journal of neurochemistry* (2005) 93:861-74. The results support the importance of NF integrity in proper mitochondrial distribution.

Example 6: Expression of CAE induces formation of Amyloid bodies upon physiological stress

[00126] Amyloid bodies are nuclear protein foci that induce a state of cellular dormancy (Audas *et al.*, *Developmental Cell* (2016) 39:155-168). Amyloid bodies formation is an important cellular mechanism during stress, such as high temperature, hypoxia and acidosis, conditions prevalent in tumor microenvironment. MCF-7, breast cancer cells transfected with GFP-CAE (TOPO GFP vector, *Invitrogen*) shows cytoplasmic puncta expression under standard growth conditions (37°C, 5% CO₂) compared with a positive control VHL-GFP. When such cells were placed under different environmental stresses, heat shock (43°C), acidosis and hypoxia (pH 6.0, 1% O₂) (3 hours), GFP-CAE changes from cytoplasmic puncta to co-localization with Congo Red, amyloid marker, positive foci in the nucleus. VHL-GFP was also targeted to amyloid bodies during stress as previously reported. This data supports the hypothesis that CAE aggregates can force growing cells to enter a state of dormancy.

Example 7: Genome-wide analysis of human 3'-UTR CAE

[00153] In order to identify potential candidate genes for causing aggregation through expression of a cryptic amyloidogenic element in the 3'-UTR, bioinformatics aggregation prediction analysis of all human 3'-UTR sequences was performed. Human 3'-UTR sequences were acquired from the UTRef section of UTRdb, a curated collection of eukaryotic 5' and 3'-UTRs. The UTRef section

contains 34,619 3'-UTR sequences from genes retrieved from the National Center for Biotechnology Information (NCBI) RefSeq transcripts (Grillo et al., *Nucleic acids research* (2010) 38, D75-80). These sequences were translated into the three forward reading-frames to simulate stop-loss mutations caused by either missense (frame 1) or frameshift (frames 2 and 3) mutations. After filtering out amino acid sequences with over 90% similarity and genes of uncertain function (LOC symbols), approximately 12,400 genes per reading-frame were annotated with the aggregation prediction programs, TANGO and PASTA.

[00154] Next, sequences were filtered for highly stringent threshold aggregation scores, above 200 for TANGO and below -4 for PASTA. These score cutoffs were based on the aggregation prediction scores obtained for the NEFH-3'-UTR. Sequences that lack an alternative stop codon were filtered-out since they would likely be degraded by the non-stop decay mechanism. It has been reasoned that the stability of stop-loss mRNAs and/or proteins decreases as the distance between the mutated stop codon and the next alternative stop codon increases (Hamby *et al.*, *Human genomics* (2011) 5, 241-264). Therefore, only sequences containing an alternative stop codon within 50 amino acids were considered.

[00155] After these filter criteria were applied, we obtained 4,861 genes, approximately 1,600 genes per reading-frame, containing a 3'-UTR sequence that has a high potential for aggregation if translated. Table 1 contains a list of the putative CAE's identified, MIM number corresponding to the Online Mendelian Inheritance in Man (OMIM®) catalog of human genes, TANGO and PASTA score for protein aggregation, University of California, Santa Cruz (UCSC) genome browser transcript ID and human genome version 19 (Hg19) chromosome location reference number for use on Genome Reference Consortium (GRC), NCBI website. The frame 1, 2 or 3 are also indicated in Table 1 for each of these genomic loci.

[00156] Although our results suggest that a large number of genes have the potential to cause aggregation as the result of a stop-loss mutation, several physiological factors that vary in different intracellular micro environments influence aggregation, such as, temperature, pH, pressure and protein concentration (Huang *et al.*, *Archives of biochemistry and biophysics* 568, 46-55). Moreover, the frequency of stop-loss caused by a missense mutation within the stop codon (frame 1) is very low, 0.027% (609 of 2,207,918 variants) as observed in the NHLBI GO Exome Sequencing Project. Finally, in order to cause significant protein aggregation disease, the protein must be expressed in cells that can be negatively impacted by aggregations such as postmitotic neurons, and protein expression levels must overwhelm the cell's ability to clear aggregations.

Next, disease-associated genes previously reported to aggregate that contain a predicted 3'-UTR-CAE in any frame were identified. A list with the top 21 high-risk aggregation genes was compiled as shown in Table 3.

[00157] Table 3: List of aggregation disease genes predicted to contain a 3'-UTR CAE.

Gene	Gene MIM Number	Disease	Protein Size (aa)	Frame 1			Frame 2			Frame 3		
				TAAGG	PASGA	TAAGG	PASGA	TAAGG	PASGA	TAAGG	PASGA	PASGA
AF042	101610	Angiodysplasia A-2 deficiency	143800	182.8	no	0.0	no	0.0	no	0.0	no	no
A7962	601517	Spirochaetosis strain 2	183000	883.1	-7.9	76.5	no	833.0	-2.7	833.0	-2.7	-2.7
B294	103703	Amyloidosis	105200	no	no	2285.7	-17.8	181.1	no	181.1	no	no
F08	134830	Hypobulbinemia, congenital	202400	388.3	-3.5	988.2	-13.9	no	no	no	no	no
F08	137070	Angiodysplasia lateral sclerosis (ALD)	608010	1323.0	no	no	no	48.4	no	48.4	no	no
PAEP	147940	Type 8 diabetes	125830	no	no	341.1	-10.9	no	no	no	no	no
L12	133480	Amyloidosis	105200	183.1	no	962.9	-8.9	180.7	-5.7	180.7	-5.7	-5.7
NEFH	603276	Cerebral arteriosclerosis	105310	no	no	no	no	568.0	-5.1	568.0	-5.1	-5.1
PRNP	176640	Prion disease	605600	0.0	no	896.1	-10.3	no	no	no	no	no
NEFL	180360	Retinitis pigmentosa	613731	687.1	-7.9	no	no	no	no	no	no	no
SAA1	104750	Amyloidosis	105210	no	no	no	no	326.2	-4.1	326.2	-4.1	-4.1
SACA	163880	Parkinson's disease	168801	no	no	4.4	no	1442.5	-9.0	1442.5	-9.0	-9.0
SOD1	147450	Angiodysplasia lateral sclerosis (ALD)	105400	no	no	568.1	-7.0	6.7	no	6.7	no	no
TAF089	603078	Angiodysplasia lateral sclerosis (ALD)	612909	714.6	-5.8	no	no	466.6	-10.0	466.6	-10.0	-10.0
NEFL	162280	Charcot-Marie-Tooth	607734	449.6	-8.7	no	no	5.5	-2.9	5.5	-2.9	-2.9
BSCL2	608158	Neuropathy, distal hereditary motor	600794	136.7	no	0.6	no	1.2	no	1.2	no	no
PAEP	157140	Parkinson disease	168800	no	no	156.6	no	8.7	no	8.7	no	no
Y78	176300	Amyloidosis	105210	0.0	no	0.0	no	112.3	no	112.3	no	no

[00158] The aggregation of 5 genes (NEFH, NEFL, FUS, TDP43 and SOD1) from the list of aggregation disease genes containing 3'UTR CAEs was tested. Aggregation was confirmed in three of those genes (NEFH, NEFL and FUS) in transfected cells. Neuro-2a cells transfected with FUS

fused in frame with its predicted 3'-UTR-CAE frame 1 (GFP-FUS-CAE) showed prominent aggregation in the cytoplasm and neuronal projections of transfected cells. In comparison, wild-type FUS (GFP-WT-FUS) localized to the nucleus. Cells transfected with SOD1 and TARDBP fused with their respective 3'-UTR-CAE did not result in protein aggregation. These results showed that aggregation induced by translation of the 3-UTR CAE is not a NF exclusive phenomenon; however, it is important to validate the bioinformatics aggregation prediction of the 3'-UTR-CAE since other intrinsic protein factors may interfere with protein structure.

Example 8: Time lapse images shows toxic effect of aggregates in Neuro-2a cells

[00159] Time-lapse of Z-stacked images of Neuro-2a cells expressing the NEFH-FS-CAE aggregates as described in Example 7, depicted progressive loss of neuronal projections before cell rounding and detachment (Figure 4). The abnormal aggregation of mutant NEFH might cause a toxic gain-of-function effect leading to loss of neuronal characteristics and loss of cell viability. It was concluded that cells become 'dormant' as described by (Audas *et al.*, *Developmental Cell* (2016) 39:155-168). However, as our cells detach, they do not remain viable for a long time.

Example 9: Analysis of 3'-UTR-CAE of human genes that undergo functional translational read-through (FTR)

[00160] Translation of mRNA usually terminates at the first in-frame stop codon, however, translational read-through can occur, when translation bypasses the first termination codon and continues until the next stop codon in the 3'-UTR, resulting in protein extension. This phenomenon is commonly observed in less complex organisms, but very rare in mammals. Although prone to errors, translation termination error rate is below 0.1% in humans. However, some termination suppressor drugs such as aminoglycosides can significantly increase this error. Interestingly, a few mammalian genes have been shown to undergo a programmed translational read-through mechanism termed functional translational read-through (FTR) (Schueren and Thoms, *PLoS Genet* (2016) 12(8):e1006196). This mechanism allows the generation of distinct protein isoforms that can modulate function of the regular-sized protein. Because evolution would be expected to suppress translation of toxic cryptic amyloidogenic elements in FTR genes, the aggregation propensity of the 3-UTR of these genes was evaluated. Tango was calculated for 13 genes with confirmed FTR and as expected none of those genes have a positive CAE at frame 1. Fisher's exact test demonstrated that the number of FTR genes with absent CAE was statistically significant ($p=0.003865$).

Example 10: Determining the ability of amyloidogenic aggregates to inhibit cancer cell growth *in vitro*

[00161] Cancer cells heavily depend on the autophagic and proteasomal pathways to scavenge nutrients that are essential for their growth and survival. Therefore in hypoxic tumor cells, impaired clearance of the protein aggregates will result in apoptotic cell death.

[00162] The ability of toxic amyloidogenic peptide aggregates to inhibit the growth and survival of *in vitro* models of cancer is investigated. Amyloidogenic peptide aggregates are exogenously-expressed in neuroblastoma cells and cell morphology growth and survival is evaluated under both hypoxic and normal culture conditions.

[00163] Neuroblastoma cancer cells (Neuro-2a cells) are maintained in DMEM (supplemented with 10% fetal bovine serum and 1% antibiotic/antimycotic agent) at 37°C in 5% CO₂ and 21% O₂. For hypoxia experiments, the cells are incubated in a hypoxia chamber (5% CO₂ and 1% O₂) at 37°C. Cells are transfected with mammalian expression vectors encoding GFP-tagged wild type protein (*GFP-WT-NEFH*) or NEFL without a stop codon fused *in-frame* with the NEFL-3'-UTR containing the predicted CAE, toxic protein aggregate construct (*GFP-NEFL-ORF1*, cDNA cDNA encoding for the most distal 22 amino acids predicted to cause aggregation, SSRIRVTQFSLFLSLCKKKLLR). Cells will subjected to hypoxic conditions or maintained in normal culture conditions. Following 24 h post transfection, cell morphology is analyzed by fluorescence microscopy. The percentage of cells displaying aggregation is quantified. These cells are then analyzed using the Incucyte imaging system with time-lapse images taken every 3 h between 24-48 h post transfection. Average green (GFP) object area (μm^2) per cell and average green object eccentricity, a parameter that measures object roundness from 0 to 1, where 0 represents a perfect circle, is measured. Cell viability is determined by measuring apoptosis (Caspase activity), autophagy (autophagy markers), membrane integrity (permeability assay), metabolic activity (MTT assay) and cell proliferation (BrdU staining), cell monolayer confluence and detachment from the culture dish. In addition, protein expression levels are determined by Western blotting.

Example 11: Expression of human 3'-UTR CAE in cancer cell lines

[00164] Glioblastoma cells are affected by toxicity mediated by CAE expression. Lentivirus was produced in order to obtain stable and inducible expression of cytotoxic amyloidogenic protein in glioblastoma. The mutant NEFH-CAE (as described in example 5 and as shown in Figure 2) was cloned in the pLVX-TRE3G vector (Clontech) under the control of a TRE (tetracycline response element) inducible promoter that expresses high levels of protein, but only in the presence of doxycycline (Dox) and Tet-On 3G transactivator protein (pLVX-Tet3G). When bound to Dox, the constitutively expressed Tet-on 3G protein undergoes a conformational change that allows it to bind to the TRE sequence and activate transcription. The GFP-TRE3G vector expressing only GFP was also generated to be used as an experimental control. Preliminary results in glioblastoma cells co-transfected with NEFH-CAE-TRE3G and pLVX-Tet3G in the presence and absence of Dox showed tight regulation of the gene and formation of aggregates after 48 hr exposure to Dox. No leakage of expression was observed in the absence of Dox.

[00165] These preclinical data demonstrate the effectiveness of an inducible CAE under the control of a response element in models of cancer whereby the amyloidogenic protein was able to induce controllable cytotoxicity in cancer cells. The results also demonstrate the feasibility of using an inducible promoter, which is contemplated as an aspect of the invention.

Example 12: Generation of CRISPR guide RNAs to induce the activation of CAE in oncogenes highly expressed in tumors

[00166] Oncogenes and tumor associated genes that contain a predicted 3'UTR-CAE in any frame were filtered and selected for study. Those genes were retrieved from the Tumor Associated Gene (TAG) database. A list with 105 candidate genes with high aggregation prediction scores was compiled as shown in Table 4.

[00167] Those genes are potential good targets to activate toxic aggregates in specific types of cancer cells. A list of genes highly expressed in tumors in different types of cancer (based on immunohistochemistry) was collected using the Human Protein Atlas (www.proteinatlas.org/). CRISPR guide RNAs (gRNAs) were designed to genes targets using Deskgen (<https://www.deskgen.com/>) to target the terminal end of the last exons to activate the expression of the CAE in different type of cancer including glioblastoma, breast cancer, melanoma, pancreatic cancer and liver cancer as shown in Table 5. Guide RNAs were designed to have the PAM site immediately upstream (less than 20 nucleotide) or right at the stop codon. Guide RNAs were designed for the following genes: ABL2, BCL9, BIRC5, CCNE1, CEP55, CSF1R, FUS, IRF2, MYB, NUMA1, SALL4, SEMA3E, SERTAD2, SPHK1, TACC3, TIAM1 (Table 5). The same approach is suitable for design of guide RNAs for other genes with CAE's described herein.

[00168] To summarize, Table 5 provides the following information: 1) the oncogenes and tumor associated genes containing CAE and that are highly expressed in particular tumors; 2) OMIM reference sequence; 3) the CAE reading frame; 4) NCBI reference sequence; 5) the cancer type in which the gene is highly expressed; 6) the associated 'guide RNA' DNA target sequence; 7) the protospacer adjacent motif sequence (PAM); 8) the target exon number in the gene of interest.

Example 13: Expression of human 3'-UTR NEFH-CAE in vertebrate zebrafish

[00169] In order to assess the effects of the *NEFH*-CAE variant *in vivo*, RNA was injected into one-cell stage zebrafish embryos. Equal amounts of RNA encoding either *GFP-WT-NEFH* or *GFP-NEFH-CAE* were injected into transgenic Tg(*Olig2:DsRed*) (Kucenas et al., *Neuron Glia Biol* (2008) 4:71–81) embryos at a dosage at which there was no apparent effect on body morphology, but a measurable difference in motor neuron outgrowth. The common path of the caudal anterior primary motor neurons at 48 hours post fertilization (hpf) was assessed. The *GFP-NEFH-CAE* RNA injected embryos were found to have significantly decreased axon lengths compared to both *GFP-WT-NEFH* and uninjected larvae (Figure 5), while there is no significant difference between the motor neurons

lengths of the uninjected embryos and embryos injected with *GFP-WT-NEFH* RNA. These data indicate that the addition of the 3'-UTR CAE can function through a toxic mechanism. Such agents containing a nucleotide sequence that encodes the amyloidogenic peptide could be used to inhibit growth of neoplastic (e.g. cancer) cells in mammals by inducing cytotoxicity through exogenous expression of the amyloidogenic peptide.

Example 14: Determining the ability of amyloidogenic aggregates to inhibit cancer cell growth *in vivo*.

[00170] Prolonged use of aminoglycoside antibiotics, such as gentamicin could potentially induce aggregation of NEFL. Therefore the effect of aminoglycoside antibiotics on growth rate of Neuro-2a cells are investigated using a xenograft model.

[00171] C57/BL6 mice (6-8 week old) are purchased from Charles River Laboratory and used according to an approved protocol. Mice (n=8 mice per group) are injected with 1×10^6 Neuro-2a cancer cells into the appropriate matching tissue. Once tumors reached 150 mm^2 (30 days), mice are randomized and divided by multiple case and control groups and each group received the treatment. The treatment with control agent and aminoglycoside antibiotic is performed daily for 7 days. The aminoglycoside antibiotics and vehicle control are delivered via tail vein injection. Control agent is injected at FDA recommended dosage per body weight. The aminoglycoside antibiotics are injected at FDA approved dosages per body weight. Tumor sizes are subsequently measured using a caliper. Animals are sacrificed once the tumor reached 2000 mm^3 in size. Protein aggregation can be detected by immunostaining and/or by blue native polyacrylamide gel electrophoresis to detect high molecular weight aggregates complexes.

Example 15: Determining the ability of NEFL stop codon mutation to induce NEFL aggregation and inhibit cancer cell growth *in vitro*.

[00172] The effect of CRISPR/Cas9-mediated mutation of the Stop codon *NEFL* gene, on the growth rate of Neuro-2a cells is investigated. Cells are infected with Adv-CRISPR/Cas9 and single guide RNA and growth rate and survival is measured *in vitro*.

[00173] Neuroblastoma cancer cells (Neuro-2a cells) are maintained in as previously described. For hypoxia experiments, the cells are incubated in a hypoxia chamber (5 % CO_2 and 1 % O_2) at 37 °C. Neuro-2a cells are seeded at a density of 8.0×10^4 cells per well in 24-well plates. The following day, the cells are transduced with Adv.Cas9 (150 TCID₅₀/cell), Adv.gRNA for the stop codon of NEFL (targeted to 50 TCID₅₀/cell) and Adv.Δ2.donor (10 TU/cell). To serve as negative controls, cells are either mock-transduced or are transduced with Adv.Cas9 (150 TCID₅₀/cell) and Adv.Δ2.donor (10 TU/cell). Following 24 h post transduction, cell morphology is analyzed by fluorescence microscopy. The percentage of cells displaying aggregation is quantified. These cells are then analyzed using the IncuCyte live-cell imaging system (Essen Instruments) with time-lapse images

taken every 3 h between 24-48 h post transduction. Average green (GFP) object area (μm^2) per cell and average green object eccentricity, a parameter that measures object roundness from 0 to 1, where 0 represents a perfect circle, is measured using the IncuCyte Zoom software. A total of 36 images are acquired per well for each time point. Cell viability is determined by measuring apoptosis (Caspase activity), autophagy (autophagy markers), membrane integrity (permeability assay), metabolic activity (MTT assay) and cell proliferation (BrdU staining), cell monolayer confluence and detachment from the culture dish. In addition, protein expression levels are determined by Western blotting.

[00174] To confirm genetic modification, surveyor assay and sequencing analysis is performed on lysates of cells infected with plasmid DNA as described above. After infection, the cells are incubated at 37 °C for 72 h before genomic DNA extraction. Genomic DNA is extracted using the QuickExtract DNA extraction kit (Epicentre) following the manufacturer's protocol. Briefly, cells are resuspended in QuickExtract solution and incubated at 65 °C for 15 minutes and 98 °C for 10 minutes. Extracted genomic DNA is immediately processed or stored at -20°C.

[00175] The genomic region surrounding a CRISPR target site for each gene is PCR amplified, and products are purified using QiaQuick Spin Column (Qiagen) following manufacturer's protocol. A total of 400 ng of the purified PCR products are mixed with 2 μL 10X Taq polymerase PCR buffer (Enzymatics) and ultrapure water to a final volume of 20 μL , and subjected to a re-annealing process to enable heteroduplex formation: 95 °C for 10 min, 95 °C to 85 °C ramping at -2 °C/s, 85 °C to 25 °C at -0.25 °C/s, and 25 °C hold for 1 minute. Following re- annealing, products are treated with Surveyor nuclease and Surveyor enhancer S (Transgenomics) following the manufacturer's recommended protocol, and analyzed on 4-20 % Novex TBE poly-acrylamide gels (Life Technologies). Gels are stained with SYBR Gold DNA stain (Life Technologies) for 30 minutes and imaged with a Gel Doc gel imaging system (Bio-rad). Quantification is based on relative band intensities, as a measure of the fraction of cleaved DNA.

Example 16: Determining the ability of NEFL stop codon mutation to induce NEFL aggregation and inhibit cancer cell growth *in vivo*.

[00176] Glioblastoma Multiforme (GBM) is recognized as one of the most deadly cancers characterized by cellular atypia, severe necrosis, and high rate of angiogenesis (Chen *et al.*, *Biochim Biophys Acta*. (2013) 1836(1):158-65). The U87 glioma mouse xenograft is a commonly used model of GBM.

[00177] Swiss nude mice (4– 6 weeks old) are purchased from Charles River Laboratory and used according to an approved protocol. Mice (n=10 mice per group) are subjected to intracranial implantation of human 1×10^5 U87 cells (suspended in 10 μL of sterile PBS) into the right frontal hemisphere using a stereotactic fixation device. Implants were placed 2 mm from the midline, 3 mm anterior to the bregma, and 3 mm deep. Cells were slowly injected over 120–180 sec.

[00178] Once tumors develop, mice are treated with CRISPR constructs, AdV.Cas9 (150 TCID₅₀/cell), AdV.gRNA for the stop codon of NEFL (targeted to 50 TCID₅₀/cell) and AdV.Δ2.donor (10 TU/cell) via transcranial injection. To serve as negative controls, mice are injected with vector controls without guide RNA. Tumor sizes are subsequently measured using a caliper. Following completion of the study, animals are sacrificed and tumor cells are analyzed. Protein aggregation can be detected by immunostaining and/or by blue native polyacrylamide gel electrophoresis to detect high molecular weight aggregates complexes. Cell viability is determined by measuring apoptosis (Caspase activity), autophagy (autophagy markers), and membrane integrity (permeability assay). In addition, protein expression levels are determined by Western blotting. To confirm genetic modification, surveyor assay and sequencing analysis is performed on extracted tumor lysates as described above.

Table 1

Table 1	Frame 1				Frame 2				Frame 3					
	Gene	MM Number	TANGO	PASTA	UCSC Transcript ID	Hg19 Location	TANGO	PASTA	UCSC Transcript ID	Hg19 Location	TANGO	PASTA	UCSC Transcript ID	Hg19 Location
A2M		103950	NA	NA	NA	NA	444.572	-4.840821	uc001qvkl.1	chr12:9220304-9220418	NA	NA	NA	NA
AACS		614364	NA	NA	NA	NA	479.236	-8.254097	uc001uhc.3	chr12:125626776-125627871	481.525	-8.254097	uc001uhc.3	chr12:125626776-125627871
AADACL3		NA	NA	NA	NA	NA	NA	NA	NA	NA	729.366	-6.520575	uc001aug.1	chr1:12785964-12788726
AAED1		NA	808.469	-11.059608	uc004awm.3	chr9:99403533-99404040	NA	NA	NA	NA	NA	NA	NA	NA
AAK1		616405	NA	NA	NA	NA	348.205	-16.518709	uc010fdm.1	chr2:69771371-69771526	NA	NA	NA	NA
AARS		601085	NA	NA	NA	NA	NA	NA	NA	NA	331.065	-4.734393	uc010vlu.1	chr16:70286297-70286623
AARSD1		613212	NA	NA	NA	NA	461.255	-5.153679	uc002icd.3	chr17:41102543-41102609	NA	NA	NA	NA
AASDH		614365	713.979	-13.239747	uc010hnb.3	chr4:57204457-57204567	NA	NA	NA	NA	1407.39	-12.190286	NA	NA
AASS		605113	582.035	-7.439998	uc003vka.3	chr7:121713598-121716542	637.449	-7.620471	uc003vka.3	chr7:121713598-121716542	500.27	-4.941699	uc003vka.3	chr7:121713598-121716542
ABCA1		600046	NA	NA	NA	NA	388.284	-4.521932	uc004bcl.3	chr9:107543284-107546595	820.407	-4.653754	uc004bcl.3	chr9:107543284-107546595
ABCA10		612508	NA	NA	NA	NA	328.634	-6.503525	uc010wqs.1	chr17:67144148-67144967	NA	NA	NA	NA
ABCA13		607807	238.481	-6.088288	uc003lop.2	chr7:48267027-48269729	NA	NA	NA	NA	NA	NA	NA	NA
ABCA3		601615	1103.92	-1.072616	uc002cpy.1	chr16:2325879-2326674	433.694	-7.71141	uc002cpy.1	chr16:2325879-2326674	NA	NA	NA	NA
ABCA5		612503	1698.08	-13.121301	uc002jlb.2	chr17:67240576-67243677	1263.96	-5.626877	uc002jlb.2	chr17:67240576-67243677	663.697	-6.410467	uc002jlb.2	chr17:67240576-67243677
ABCA6		612504	786.504	-12.259205	uc002jhw.1	chr17:67074847-67075113	258.66	-6.915899	uc002jhy.3	chr17:67131365-67132134	NA	NA	NA	NA
ABCA8		612505	NA	NA	NA	NA	1835.46	-4.341029	uc002jhp.3	chr17:66863431-66864225	1461.34	-10.227365	uc002jhp.3	chr17:66863431-66864225
ABCA9		612507	271.367	-7.774992	uc010dez.3	chr17:66970773-66972055	320.413	-2.497322	uc010dez.3	chr17:66970773-66972055	NA	NA	NA	NA
ABCB11		603201	449.027	-5.647562	uc010zda.1	chr2:169779449-169780131	NA	NA	NA	NA	NA	NA	NA	NA
ABCB4		171060	253.859	-3.877531	NA	NA	240.091	-7.230367	uc003uij.3	chr7:87081712-87082255	NA	NA	NA	NA
ABCB5		611785	735.569	-13.100493	uc003suw.4	chr7:20698713-20700017	NA	NA	NA	NA	NA	NA	NA	NA
ABCB6		605452	NA	NA	NA	NA	NA	NA	NA	NA	814.821	-6.721982	uc002kvc.2	chr2:220074488-220074659
ABCC2		601107	NA	NA	NA	NA	753.088	-8.857978	uc001kql.2	chr10:101611389-101611662	NA	NA	NA	NA
ABCC3		604323	1177.17	-3.596524	uc002isl.3	chr17:48768562-48769063	NA	NA	NA	NA	449.528	-6.51192	uc002isl.3	chr17:48768562-48769063
ABCC4		605250	972.818	-14.03781	uc010eaj.3	chr13:95672083-95673828	NA	NA	NA	NA	NA	NA	NA	NA
ABCC5		605251	239.31	-6.379406	uc003fmh.3	chr3:183701541-183702682	NA	NA	NA	NA	294.71	-1.424308	uc003fmh.3	chr3:183701541-183702682
ABCG2		603756	NA	NA	NA	NA	NA	NA	NA	NA	1424.91	-14.381849	uc003hmf.3	chr4:89011416-89013385
ABHD12B		NA	NA	NA	NA	NA	NA	NA	NA	NA	566.71	-7.528861	uc001wvq.3	chr14:51371085-51371688
ABHD13		NA	NA	NA	NA	NA	NA	NA	NA	NA	1320.81	-9.520672	uc001vqq.3	chr13:108882581-108886603
ABHD16A		142620	NA	NA	NA	NA	NA	NA	NA	NA	657.55	-4.909684	uc003nvx.2	chr6:31654726-31654988
ABHD17B		NA	NA	NA	NA	NA	NA	NA	NA	NA	378.643	-4.252365	uc004ail.3	chr9:74477368-74477496
ABHD3		612197	NA	NA	NA	NA	NA	NA	NA	NA	749.093	-10.060514	uc002hkt.2	chr18:19230858-19231551
ABI1		603050	NA	NA	NA	NA	504.03	-5.957448	uc010qdg.2	chr10:27035525-27037498	NA	NA	NA	NA
ABI3BP		606279	611.542	-5.030571	uc003duj.3	chr3:100468179-100469338	NA	NA	NA	NA	NA	NA	NA	NA
ABL2		164690	239.103	-3.707258	uc001gmh.3	chr1:179085983-179086398	222.186	-6.350043	uc009wwe.3	chr1:179079716-179079939	NA	NA	NA	NA
ABLIM3		611305	NA	NA	NA	NA	214.821	-9.927634	uc003lpy.2	chr5:148637968-148639999	NA	NA	NA	NA
ABRACL		NA	1303.28	-12.261925	uc003qil.2	chr6:139364041-139364439	1251.97	-10.879057	uc003qil.2	chr6:139364041-139364439	536.08	-6.256734	uc003qil.2	chr6:139364041-139364439
ABT1		NA	367.166	-5.924138	uc003nli.3	chr6:26598874-26600277	821.258	-5.181718	uc003nli.3	chr6:26598874-26600277	NA	NA	NA	NA
ABTB1		608308	330.242	-4.901486	uc003ejr.3	chr3:127399319-127399769	NA	NA	NA	NA	948.29	-8.83878	uc003ejr.3	chr3:127399319-127399769
ACAD10		611181	479.2	-4.621561	uc001lsc.3	chr12:112194278-112194911	543.092	-3.435728	uc009zvw.2	chr12:112147510-112148121	NA	NA	NA	NA
ACAD8		604773	1540.84	-2.777604	uc009zdc.3	chr11:134129078-134129819	230.064	-5.678102	uc010lsc.1	chr11:134129742-134131073	486.637	-5.57642	uc009zdc.3	chr11:134129078-134129819
ACAD9		611103	NA	NA	NA	NA	698.927	-2.283534	uc003ala.4	chr3:128631451-128631957	451.749	-2.073016	uc010hsw.1	chr3:128627112-128627942
ACAT1		607809	456.646	-6.245965	uc001plw.1	chr11:108006851-108007666	1051.57	-8.685169	uc001plw.1	chr11:108006851-108007666	1111.32	-8.330367	uc001plw.1	chr11:108006851-108007666
ACBD3		606809	NA	NA	NA	NA	NA	NA	NA	NA	672.713	-7.216864	uc001hpy.3	chr1:226332380-226334310
ACBD5		616618	NA	NA	NA	NA	NA	NA	NA	NA	503.216	-8.008755	uc010qdp.2	chr10:27484143-27486358
ACCS		608405	372.662	-4.538341	uc010rfm.1	chr11:44098926-44101170	NA	NA	NA	NA	226.938	-7.053404	uc009yxs.1	chr11:44105343-44105569
ACD		609377	NA	NA	NA	NA	NA	NA	NA	NA	373.642	-4.966819	uc002etp.4	chr16:67691415-67691508
ACE2		300335	NA	NA	NA	NA	748.984	-12.960602	uc004cxa.1	chrX:15579156-15580027	NA	NA	NA	NA

Table 1

[illegible]

Table 1

ADAMTS5	605007	496.474	-9.440545	uc002ymg.3	chr21:28290231-28296371	NA	NA	NA	NA	NA	NA	1182.65	NA	NA	NA	chr5:64510225-64510468
ADAMTS6	605008	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADAMTS9	605421	1001.21	-14.96224	uc011bfp.1	chr3:64507157-64507344	602.119	-1.164763	uc011bfp.1	chr3:64507157-64507344	NA	NA	793.966	NA	NA	NA	chr9:18684803-18684952
ADAMTSL1	609198	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	555.351	NA	NA	NA	chr1:150532673-150533412
ADAMTSL4	610113	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADAT1	604230	NA	NA	NA	NA	386.125	-4.423724	uc002leo.2	chr16:75632247-75634113	NA	NA	NA	NA	NA	NA	NA
ADCY10	605205	NA	NA	NA	NA	685.055	-10.012084	uc001gpr.3	chr1:167778625-167778914	NA	NA	NA	NA	NA	NA	NA
ADCV2	103071	207.824	-5.703427	uc003jdz.1	chr5:7826985-7830194	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADCV8	103070	1120.56	-15.695436	uc003ydl.4	chr8:131792547-131792635	1391.32	-14.878036	uc003ydl.4	chr8:131792547-131792635	1180.96	-9.226396	NA	NA	NA	NA	chr8:131792547-131792635
ADCV9	603302	691.119	-8.202348	uc002cvx.3	chr16:4012650-4015775	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADGB	614630	NA	NA	NA	NA	1050.46	-9.009208	uc003qlp.3	chr6:147136354-147136597	NA	NA	NA	NA	NA	NA	NA
ADGRE3	606101	NA	NA	NA	NA	316.395	-8.14128	uc002mzi.4	chr19:14730051-14730244	NA	NA	NA	NA	NA	NA	NA
ADGRF2	NA	NA	NA	NA	NA	421.326	-5.633664	uc003oyy.3	chr6:47662726-47665533	NA	NA	NA	NA	NA	NA	NA
ADGRG3	NA	685.432	-6.880478	uc010cdc.3	chr16:57712265-57712751	NA	NA	NA	NA	NA	NA	650.891	-6.042059	uc002aia.4	NA	chr16:57609451-57611100
ADGRG5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	356.231	-4.435621	uc003hcc.4	NA	chr4:62935888-62938168
ADGRL3	616417	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADGRL4	616419	NA	NA	NA	NA	564.397	-5.908999	uc001dlq.4	chr1:79355449-79356838	NA	NA	NA	NA	NA	NA	NA
ADH1A	103700	647.721	-0.931022	uc003hur.2	chr4:100197523-100197780	984.541	-7.456647	uc003hur.2	chr4:100197523-100197780	NA	NA	NA	NA	NA	NA	NA
ADH1B	103720	NA	NA	NA	NA	575.393	-5.678532	uc003hus.4	chr4:10027527-10028996	NA	NA	NA	NA	NA	NA	NA
ADH4	103740	NA	NA	NA	NA	603.553	-7.227677	uc011ced.2	chr4:100044833-100045592	NA	NA	NA	NA	NA	NA	NA
ADH5	103710	452.092	-9.977706	uc003huk.1	chr4:9996376-99997415	NA	NA	NA	NA	NA	NA	705.212	-4.299435	uc003hup.4	NA	chr4:100125879-100126077
ADH6	103735	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADH7	600086	710.698	-9.368407	uc021xqj.1	chr4:100333418-100334304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADI1	613400	470.128	-4.791654	uc002xpx.4	chr2:3501690-3502733	NA	NA	NA	NA	NA	NA	447.739	-7.909151	uc001jwi.3	NA	chr10:76468204-76469061
ADK	102750	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADORA2B	600446	494.701	-7.626874	uc002gpd.1	chr17:15878657-15879210	NA	NA	NA	NA	NA	NA	612.767	-6.035027	uc001ebf.3	NA	chr1:112025970-112026308
ADORA3	600445	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	487.965	-5.933672	uc002ave.4	NA	chr15:73043708-73044681
ADPGK	611861	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADPRH	603081	790.356	-8.775883	uc003ecs.3	chr3:119306726-119308792	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ADPRM	NA	NA	NA	NA	NA	497.11	-6.759758	uc002gmt.3	chr17:10614462-10614875	NA	NA	NA	NA	NA	NA	NA
ADRA1A	104221	NA	NA	NA	NA	294.121	-5.226475	uc003xfc.1	chr8:28605667-28606106	NA	NA	NA	NA	NA	NA	NA
ADRB2	109690	NA	NA	NA	NA	426.898	-5.842956	uc003jpr.2	chr5:148207637-148208197	NA	NA	NA	NA	NA	NA	NA
ADRBK1	109635	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	499.662	-9.620672	uc009ym.1	NA	chr11:67052922-67054029
ADTRP	614348	1047.92	-11.977491	uc003nab.3	chr6:11713888-11714710	623.671	-4.003574	uc003nab.3	chr6:11713888-11714710	674.969	-7.215103	NA	NA	NA	NA	chr6:11713888-11714710
AEBP2	NA	551.538	-5.447398	uc001ree.2	chr12:19671052-19675173	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AEN	610177	454.286	-4.809185	uc010bni.2	chr15:89170047-89170572	1308.82	-8.506475	uc010bni.2	chr15:89170047-89170572	NA	NA	NA	NA	NA	NA	NA
AFAP1L2	612420	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1158.34	-5.451382	uc001lbn.3	NA	chr10:116054583-116055800
AFI1	159557	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	782.31	-8.587524	uc011ccx.2	NA	chr4:87968840-87969201
AFF2	300806	NA	NA	NA	NA	630.194	-8.348309	uc004fco.3	chrX:147985793-147985907	NA	NA	NA	NA	NA	NA	NA
AFG3L2	604581	740.898	-7.023342	uc002kqz.2	chr18:12328943-12329563	509.45	-4.270726	uc002kqz.2	chr18:12328943-12329563	579.044	-5.114649	NA	NA	NA	NA	chr18:12328943-12329563
AFMID	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	669.618	-8.098637	uc002jvb.3	NA	chr17:76202992-76203782
AFP	104150	376.027	-7.547135	uc003hgz.1	chr4:74321348-74321492	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGA	613228	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	471.495	-6.301065	uc003luu.2	NA	chr4:178351929-178352861
AGAP6	NA	907.015	-6.949954	uc001jix.4	chr10:51769947-51770259	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGAP9	NA	NA	NA	NA	NA	571.029	-7.747569	uc009xnl.2	chr10:48237211-48237508	NA	NA	NA	NA	NA	NA	NA
AGBL2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	601.081	-5.305395	uc001nrg.3	NA	chr11:47681143-47681724
AGF G1	600862	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1252.94	-11.456195	uc002vpc.2	NA	chr2:228419212-228425938
AGF1	608464	952.013	-5.243169	uc003ket.3	chr5:76359078-76361058	498.817	-7.301877	uc003kes.3	chr5:76331584-76331878	NA	NA	NA	NA	NA	NA	NA
AGL	610860	NA	NA	NA	NA	307.473	-5.162082	uc001dsi.1	chr1:100387208-100389579	NA	NA	NA	NA	NA	NA	NA

Table 1

AG02	606229	424.967	-5.654323	uc003yvn.3	chr8:141541264-141542142	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGPAT1	603099	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGPAT5	614796	NA	NA	NA	NA	228.58	-5.151283	uc003wqo.3	chr8:6614910-6619021	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGPS	603051	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGR2	606358	NA	NA	NA	NA	380.214	-8.477037	uc003str.3	chr7:16832264-16832531	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AGRN	103320	NA	NA	NA	NA	258.61	-3.774371	uc001ack.2	chr1:990362-991499	1146.18	-10.042644	uc001ack.2	chr1:990362-991499	NA	NA	NA	NA	NA	NA
AGTRAP	608729	NA	NA	NA	NA	594.833	-6.857241	uc001asu.3	chr1:11810162-11810828	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AHCTF1	610853	463.989	-4.613284	uc001lbv.2	chr1:247002402-247004107	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AHR	600253	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AHS42	NA	290.348	-6.742453	uc002sbb.2	chr2:61413922-61414686	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AHSG	138680	NA	NA	NA	NA	239.356	-4.281995	uc003tqj.3	chr3:186335305-186335490	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AIFM2	605159	599.288	-4.511345	uc010djb.2	chr10:71857979-71859375	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AIMTL	NA	546.035	-6.090322	uc001bmd.4	chr1:26648350-26648458	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AIMP1	603605	NA	NA	NA	NA	1457.35	-6.347748	uc011cfig.2	chr4:107268850-107270381	477.99	-6.827829	uc011cfig.2	chr4:107268850-107270381	NA	NA	NA	NA	NA	NA
AK1	103000	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AK4	103030	NA	NA	NA	NA	956.855	-16.875932	uc001dby.3	chr1:65691861-65697828	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AK9	615358	1674.55	-15.107617	uc003ptr.4	chr6:109952900-109954113	1242.49	-13.557257	uc003ptr.4	chr6:109952900-109954113	1756.19	-24.936199	uc011eas.1	chr6:109814059-109814571	NA	NA	NA	NA	NA	NA
AKAP1	602449	1100.25	-7.144316	uc002lux.3	chr17:55197686-55198710	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKAP11	604696	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKAP12	604698	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKAP14	300462	547.65	-4.880603	uc004esd.3	chrX:119037559-119037620	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKAP5	604688	880.743	-6.412715	uc001xhd.4	chr14:64936397-64941221	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKAP6	604691	1022.74	-3.77998	uc010aml.3	chr14:33201888-33203819	1266.11	-5.444838	uc010aml.3	chr14:33201888-33203819	536.53	-9.371549	uc010aml.3	chr14:33201888-33203819	NA	NA	NA	NA	NA	NA
AKAP9	604001	441.827	-7.533427	uc003uid.4	chr7:91625130-91625366	240.029	-5.532238	uc003ule.2	chr7:91670228-91671095	565.947	-7.550122	uc003ule.2	chr7:91670228-91671095	NA	NA	NA	NA	NA	NA
AKR1B10	604007	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKR1B15	616336	NA	NA	NA	NA	383.94	-4.37522	uc011kpr.2	chr7:134264302-134264592	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKR1C3	603966	587.591	-8.577187	uc001lhr.3	chr10:5149696-5149878	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKR7A2	603418	NA	NA	NA	NA	339.705	-5.292473	uc001bbw.3	chr1:19629202-19630718	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKR7A3	608477	NA	NA	NA	NA	319.082	-8.796156	uc001bbv.1	chr1:19609057-19609224	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AKT3	611223	NA	NA	NA	NA	1108.45	-10.380657	uc001iab.2	chr1:243663021-243668550	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALB	103600	NA	NA	NA	NA	842.026	-13.754001	uc011lsg.2	chr9:75515578-75516175	841.842	-6.89653	uc003hgs.4	chr4:74286809-74287129	NA	NA	NA	NA	NA	NA
ALDH1A1	100640	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALDH3A2	609523	270.655	-7.292776	uc002gwa.1	chr17:19578871-19580908	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALDH6A1	603178	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALDOC	103870	539.976	-6.457156	uc002hbp.3	chr17:26900135-26900543	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALG13	300776	611.856	-5.920844	uc004epi.2	chrX:110931230-110933623	333.719	-14.075961	uc022ccn.1	chrX:110931115-110933623	896.348	-8.461835	uc022ccn.1	chrX:110931115-110933623	NA	NA	NA	NA	NA	NA
ALG14	612866	526.33	-7.360435	uc001dra.2	chr1:95448279-95448631	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALG2	607905	NA	NA	NA	NA	808.078	-11.828651	uc004azf.3	chr9:101978707-101980215	626.239	-6.793333	uc004azf.3	chr9:101978707-101980215	NA	NA	NA	NA	NA	NA
ALG5	604565	NA	NA	NA	NA	925.397	-8.563312	uc001luyv.3	chr13:37523908-37524078	990.773	-11.701294	uc001luyv.3	chr13:37523908-37524078	NA	NA	NA	NA	NA	NA
ALG9	606941	NA	NA	NA	NA	919.403	-8.179035	uc001ply.3	chr11:111652919-111657120	937.226	-5.064702	uc001ply.3	chr11:111652919-111657120	NA	NA	NA	NA	NA	NA
ALKBH5	613303	296.645	-5.224656	uc010cpw.3	chr17:18111711-18113267	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALLC	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALMS1P	NA	NA	NA	NA	NA	902.32	-4.079886	uc010yri.2	chr2:73912218-73912694	617.834	-10.792376	uc010wt.3	chr2:3750154-3750260	NA	NA	NA	NA	NA	NA
ALOX5AP	603700	NA	NA	NA	NA	803.367	-8.95589	uc010ldr.2	chr13:31338244-31338565	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALS2	606352	1362.19	-13.030073	uc002uyv.4	chr2:202586713-202587753	308.953	-4.803593	uc002uyo.3	chr2:202564986-202566573	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALS2CR12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ALX1	601527	762.036	-6.751349	uc001tae.4	chr12:85695254-85695561	661.801	-12.364502	uc001tae.4	chr12:85695254-85695561	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AMACR	604489	438.163	-4.032429	uc003ijk.2	chr5:33997112-33997355	585.045	-6.349009	uc003jlg.3	chr5:33987091-33989197	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
AMBN	601259	NA	NA	NA	NA	487.762	-6.729336	uc003hli.3	chr4:71472448-71473004	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

AMBP	176870	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	581.029	-7.381495	uc004bie.4	chr9:116822408-116822518
AMELY	410000	NA	NA	NA	NA	NA	283.558	-5.212522	uc004iqz.3	NA	chrY:673959-6734113	NA	NA	NA	NA
AMICA1	NA	586.95	7.011785	uc001psg.2	NA	chr11:118064442-118065039	NA	NA	NA	NA	chrX:109437414-109441747	NA	NA	NA	NA
AMMECR1	300195	NA	NA	NA	NA	NA	524.486	-5.394369	uc004eop.3	NA	chr2:128619207-128622667	NA	NA	NA	NA
AMMECR1L	NA	NA	NA	NA	NA	NA	466.589	-5.071615	uc002ipl.3	NA	chr12:31824071-31825237	NA	NA	NA	NA
AMN1	NA	NA	NA	NA	NA	NA	1466.05	-16.466447	uc001rko.4	NA	chrX:112018105-112021794	NA	NA	NA	NA
AMOT	300410	NA	NA	NA	NA	NA	385.85	-6.464716	uc004epr.3	NA	NA	1543.08	-10.475448	uc010ovr.1	chr1:110173775-110174677
AMPD2	102771	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	305.567	-4.895548	uc010bz.1	chr11:10527432-10529126
AMPD3	102772	818.811	-7.752449	uc010rbz.1	NA	chr11:10527432-10529126	NA	NA	NA	NA	NA	712.359	-6.576645	uc003hfk.1	chr4:71398183-71398459
AMTN	610912	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	784.738	-5.646233	uc001vww.4	chr14:21162168-21162345
ANG	105850	NA	NA	NA	NA	NA	316.136	-3.864586	uc001vxx.4	NA	chr14:21162168-21162345	NA	NA	NA	NA
ANGEL2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	388.44	-5.09284	uc010pho.2	chr1:213165524-213168382
ANGPT1	601667	NA	NA	NA	NA	NA	821.848	-9.055921	uc011llv.2	NA	chr8:108261710-108264082	NA	NA	NA	NA
ANGPT2	601922	NA	NA	NA	NA	NA	344.727	-9.271782	uc003wvj.4	NA	chr8:6357175-6360621	NA	NA	NA	NA
ANH	NA	687.656	-7.978357	uc010lcl.2	NA	chr12:133794898-133795470	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANKH	605145	NA	NA	NA	NA	NA	1077.43	-11.35707	uc003jfm.4	NA	chr5:14704909-14711305	NA	NA	NA	NA
ANKHD1	610500	NA	NA	NA	NA	NA	397.842	-6.449907	uc003lfr.3	NA	chr5:139919004-139919441	NA	NA	NA	NA
ANKMY1	NA	710.728	-8.062947	uc002vzf.3	NA	chr2:241492166-241492228	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANKRA2	605787	767.844	-11.615776	uc003kcu.2	NA	chr5:72848025-72848621	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANKRD11	611192	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	455.414	-4.355335	uc002hfr.1	chr16:89365283-89367221
ANKRD13A	615123	NA	NA	NA	NA	NA	1114.61	-12.884117	uc009zvm.2	NA	chr12:110458965-110460255	NA	NA	NA	NA
ANKRD17	615929	393.775	-7.71959	uc011cbd.1	NA	chr4:73978801-73978986	624.054	-6.545105	uc003hgo.3	NA	chr4:73940502-73941947	261.047	-5.135784	uc003hgo.3	chr4:73940502-73941947
ANKRD20ASP	NA	340.647	-5.409111	uc010xag.2	NA	chr18:14184108-14185386	583.575	-4.056875	uc010xag.2	NA	chr18:14184108-14185386	NA	NA	NA	NA
ANKRD26	610855	1433.5	-13.245119	uc001llg.2	NA	chr10:27293045-27294518	NA	NA	NA	NA	NA	1406.11	-8.665963	uc001llg.2	chr10:27293045-27294518
ANKRD28	611122	218.829	-6.560457	uc011avy.1	NA	chr3:15708744-15711776	NA	NA	NA	NA	NA	652.133	-9.955255	uc003kdo.2	chr5:74364122-74364343
ANKRD31	NA	2051.18	-18.17751	uc003kdo.2	NA	chr5:74364122-74364343	NA	NA	NA	NA	NA	235.199	-8.365459	uc002bet.3	chr15:79587235-79590581
ANKRD34C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	700.046	-7.298207	uc002iso.3	chr17:48770551-48773357
ANKRD40	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	231.68	-3.64839	uc009yvi.2	chr11:82923706-82926242
ANKRD42	NA	898.042	-9.833575	uc009yvi.2	NA	chr11:82923706-82926242	NA	NA	NA	NA	NA	1279.16	-6.026144	uc002litz.4	chr2:197831741-197832162
ANKRD44	NA	1079.61	-5.257466	uc002litz.4	NA	chr2:197831741-197832162	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANKRD45	NA	NA	NA	NA	NA	NA	303.662	-4.732646	uc001lga.1	NA	chr1:173577475-173579283	NA	NA	NA	NA
ANKRD49	NA	NA	NA	NA	NA	NA	772.87	-6.450876	uc001pew.3	NA	chr11:94231698-94232744	NA	NA	NA	NA
ANKRD50	NA	NA	NA	NA	NA	NA	252.236	-5.06163	uc010lmw.3	NA	chr4:125585204-125588669	NA	NA	NA	NA
ANKRD6	610583	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	390.278	-6.46399	uc003pne.4	chr6:90340724-90343553
ANKRD7	610731	NA	NA	NA	NA	NA	249.167	-4.448399	uc003yji.3	NA	chr7:117882403-117882784	285.108	-3.450736	uc003yji.3	chr7:117882403-117882784
ANKS4B	609901	334.94	-6.973966	uc010bwp.1	NA	chr16:21262142-21263750	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANO1	610108	608.89	-1.475041	uc001opj.3	NA	chr11:70034111-70035652	1057.62	-9.425129	uc001opj.3	NA	chr11:70034111-70035652	NA	NA	NA	NA
ANO4	610111	634.713	-6.013856	uc001llhw.2	NA	chr12:101521639-101524219	1215.31	-8.672186	uc001mqj.2	NA	chr11:22301312-22304913	NA	-5.490211	uc001llhw.2	chr12:101521639-101522419
ANO5	608662	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ANO6	608663	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	2040.2	-9.488139	uc001roo.3	chr12:45823095-45826134
ANO7	605096	NA	NA	NA	NA	NA	342.41	-5.296089	uc002wax.2	NA	chr2:242163569-242164791	NA	NA	NA	NA
ANP32B	NA	NA	NA	NA	NA	NA	415.007	-8.032003	uc004aya.3	NA	chr9:100777714-100778224	NA	NA	NA	NA
ANXA1	151690	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	501.654	-6.105755	uc004ajf.1	chr9:75785024-75785307
ANXA3	106490	635.139	-3.923796	uc003hld.3	NA	chr4:79531270-79531605	1691.93	-10.747866	uc003hld.3	NA	chr4:79531270-79531605	NA	NA	NA	NA
ANXA5	131230	NA	NA	NA	NA	NA	206.891	-6.255208	uc003ldu.4	NA	chr4:122589152-122589622	NA	NA	NA	NA
ANXA7	186360	NA	NA	NA	NA	NA	632.426	-5.04571	uc001jtz.2	NA	chr10:75135189-75135852	513.002	-5.575595	uc001jtz.2	chr10:75135189-75135852
AOC2	602268	NA	NA	NA	NA	NA	873.793	-12.432538	uc002ltn.3	NA	chr17:41002366-41002724	NA	NA	NA	NA
AOX1	602841	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	516.271	-4.050784	uc002lwx.3	chr2:201535403-201536217
AP1G1	603533	494.064	-5.973242	uc002faz.3	NA	chr16:71762905-71766960	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

AP2A2	607242	NA	NA	NA	NA	844,592	-7,370,147	uc001lss.3	chr11:1010626-1012245	NA	NA	NA	NA
AP3M1	610366	451,442	-7,290,908	uc001jwl.3	chr10:75880015-75883567	NA	NA	NA	NA	NA	NA	NA	NA
AP4E1	607244	1089,1	-9,153,814	NA	NA	NA	NA	NA	NA	282,864	-4,926,208	uc001zyx.2	chr15:51294860-51298097
AP4S1	607243	NA	NA	NA	NA	NA	NA	NA	NA	271,002	-4,681	uc001wqw.4	chr14:31554089-31555008
AP5M1	614368	NA	NA	NA	NA	1641,13	-6,642,618	uc001xcu.4	chr14:57741743-57742175	1089,82	-15,622,121	uc001kcu.4	chr14:57741743-57742175
AP5S1	614824	354,576	-6,011,422	uc002wjl.3	chr20:3804945-3805580	NA	NA	NA	NA	NA	NA	NA	NA
APAF1	602233	NA	NA	NA	NA	647,448	-8,408,864	uc001lpc.3	chr12:99126260-99129211	NA	NA	NA	NA
APBA1	602414	NA	NA	NA	NA	975,827	-12,902,824	uc004alh.2	chr9:72042449-72046242	NA	NA	NA	NA
APBA2	602712	NA	NA	NA	NA	626,836	-5,244	uc001zcm.1	chr15:29394123-29394962	806,637	-12,058,342	uc001zcm.1	chr15:29394123-29394962
APBA3	604262	NA	NA	NA	NA	493,96	-6,972,095	uc002lpo.1	chr19:3750771-3751023	NA	NA	NA	NA
APBB1IP	609036	271,513	-4,507,734	uc001lsr.3	chr10:26790107-26790867	NA	NA	NA	NA	NA	NA	NA	NA
APFH	102645	685,725	-9,056,655	uc003cxl.3	chr3:49720776-49720934	NA	NA	NA	NA	NA	NA	NA	NA
API5	609774	864,582	-12,477,097	uc001mxf.2	chr11:43364006-43366080	NA	NA	NA	NA	1139,47	-10,786,537	uc001mxf.2	chr11:43364006-43366080
APIP	612491	NA	NA	NA	NA	348,586	-5,135,784	uc010reo.1	chr11:34896714-34896830	NA	NA	NA	NA
APLP2	104776	NA	NA	NA	NA	NA	NA	NA	NA	631,171	-7,164,445	uc001dcp.3	chr11:130013344-130014706
APOA5	606368	NA	NA	NA	NA	585,826	-4,418,834	uc001ppr.3	chr11:116660086-116660843	NA	NA	NA	NA
APOB	107730	318,78	-4,098,363	uc002red.3	chr2:21224301-21224601	396,406	-5,268,298	uc002red.3	chr2:21224301-21224601	NA	NA	NA	NA
APOBEC3C	607750	466,341	-5,283,477	uc003awr.3	chr22:39414393-39414825	NA	NA	NA	NA	NA	NA	NA	NA
APOE	107741	NA	NA	NA	NA	NA	NA	NA	NA	301,876	-5,925,51	uc002pab.3	chr19:45412508-45412650
APOH	138700	NA	NA	NA	NA	408,75	-7,843,125	uc002jfn.4	chr17:64208147-64208250	NA	NA	NA	NA
APOL2	607252	758,563	-7,263,197	uc011amm.2	chr22:36622255-36623449	NA	NA	NA	NA	NA	NA	NA	NA
APPL1	604299	707,545	-5,288,662	uc010nbb.3	chr3:57301866-57302049	NA	NA	NA	NA	NA	NA	NA	NA
AQP10	606578	719,654	-7,410,811	uc001feu.3	chr1:154296957-154297801	NA	NA	NA	NA	NA	NA	NA	NA
AQP9	602914	703,744	-5,331,671	uc010ugx.1	chr15:58476335-58478110	693,546	-7,839,81	uc010ugx.1	chr15:58476335-58478110	NA	NA	NA	NA
AQR	610548	NA	NA	NA	NA	443,142	-5,602,549	uc001zhv.3	chr15:35148552-35148992	379,732	-5,527,587	uc003gsq.2	chr4:36067620-36069528
ARAP2	606645	NA	NA	NA	NA	NA	NA	NA	NA	766,008	-4,854,909	uc001hrr.3	chr1:228285715-228286913
ARF1	103180	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ARF6	600464	NA	NA	NA	NA	658,523	-9,832,598	uc001wvg.4	chr14:50360983-50363772	NA	NA	NA	NA
ARFGAP1	608377	NA	NA	NA	NA	NA	NA	NA	NA	332,536	-4,109,288	uc011aas.1	chr20:61919226-61920848
ARFGAP2	606908	NA	NA	NA	NA	NA	NA	NA	NA	510,89	-6,793,713	uc010rhd.2	chr11:47194649-47194866
ARHGEF1	604141	573,884	-8,648,408	uc003xxm.2	chr8:68109894-68111168	782,151	-0,728,39	uc003xxm.2	chr8:68109894-68111168	NA	NA	NA	NA
ARHFP1	605928	NA	NA	NA	NA	339,665	-4,340,257	uc003imz.3	chr4:153831372-153833063	NA	NA	NA	NA
ARHFP2	601638	1049,74	-4,586,033	uc001mdk.3	chr11:6495913-6498342	NA	NA	NA	NA	NA	NA	NA	NA
ARG1	608313	NA	NA	NA	NA	NA	NA	NA	NA	861,219	-14,338,252	uc003qco.2	chr6:131904948-131905465
ARGFX	611164	NA	NA	NA	NA	NA	NA	NA	NA	1619,53	-11,933,535	uc003eef.3	chr3:121305448-121309469
ARHGAP10	609746	471,426	-9,236,217	uc003lle.1	chr4:148778812-148779639	NA	NA	NA	NA	NA	NA	NA	NA
ARHGAP11A	610589	590,501	-14,721,695	uc010ubw.1	chr15:32930047-32931868	545,869	-4,135,009	uc001zgw.3	chr15:32928140-32928382	NA	NA	NA	NA
ARHGAP18	613351	NA	NA	NA	NA	1068,66	-9,253,961	uc003qbr.3	chr6:129898240-129899657	NA	NA	NA	NA
ARHGAP21	609870	623,056	-6,472,77	uc001lsl.1	chr10:24917943-24918846	NA	NA	NA	NA	NA	NA	NA	NA
ARHGAP29	610496	1328,32	-13,234,418	uc001ldq.4	chr1:94634463-94639424	1481,78	-2,102,763	uc001ldq.4	chr1:94634463-94639424	1498,07	-3,625,596	uc001ldq.4	chr1:94634463-94639424
ARHGAP32	608541	485,072	-7,188,398	uc009zco.3	chr11:128834955-128838801	NA	NA	NA	NA	639,843	-7,604,816	uc009zco.3	chr11:128834955-128838801
ARHGAP33	614902	596,063	-5,597,539	uc002obs.2	chr19:36279332-36279724	540,237	-5,334,934	uc002obs.2	chr19:36279332-36279724	NA	NA	NA	NA
ARHGAP42	615936	600,289	-7,300,864	uc001pge.2	chr11:100859533-100861656	NA	NA	NA	NA	NA	NA	NA	NA
ARHGAP6	300118	497,673	-5,601,986	uc004cum.1	chrX:11155663-11156982	NA	NA	NA	NA	NA	NA	NA	NA
ARHGEF12	604763	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ARHGEF15	608504	NA	NA	NA	NA	588,111	-9,013,614	uc002glb.2	chr17:8216063-8217349	NA	NA	NA	NA
ARHGEF16	NA	NA	NA	NA	NA	572,903	-5,814,258	uc009vli.1	chr1:3390213-3391021	NA	NA	NA	NA
ARHGEF28	612790	NA	NA	NA	NA	991,164	-20,859,578	uc010zfr.3	chr5:73236839-73237818	NA	NA	NA	NA
ARHGEF3	612115	NA	NA	NA	NA	NA	NA	NA	NA	307,134	-5,264,453	uc011bev.1	chr3:56761446-56763297

Table 1

ARHGEF35	NA	NA	NA	NA	NA	551,466	-4,698665	uc003wdz.2	chr7:143883176-143884021	1025.27	-8,23548	uc003wdz.2	chr7:143883176-143884021
ARHGEF38	NA	NA	NA	NA	NA	803,666	-5,778281	uc003hxx.3	chr4:106552207-106552837	NA	NA	NA	NA
ARHGEF4	605216	NA	NA	NA	NA	NA	NA	NA	NA	1217.03	-5,511759	uc002trz.1	chr2:131704259-131704803
ARID1B	614556	NA	NA	NA	NA	NA	NA	NA	NA	1163.4	-11,711323	uc003qqq.1	chr6:157470147-157473538
ARID2	609539	748,131	-3,647276	uc001tros.1	chr12:46298862-46301819	458,524	-4,323699	uc001rol.1	chr12:46233285-46236017	NA	NA	NA	NA
ARID5A	611583	NA	NA	NA	NA	NA	NA	NA	NA	243,483	-4,748682	uc0023we.3	chr2:97218051-97218371
ARL13B	608922	NA	NA	NA	NA	NA	NA	NA	NA	459,796	-5,490174	uc0033rd.3	chr3:93772108-93774522
ARL14EPL	NA	NA	NA	NA	NA	450,012	-6,208547	uc021yct.1	chr5:115394645-115394827	1099.32	-9,973846	uc021yct.1	chr5:115394645-115394827
ARL15	NA	NA	NA	NA	NA	NA	NA	NA	NA	1354.14	-12,232902	uc003pgg.1	chr5:53180614-53182390
ARL17A	NA	NA	NA	NA	NA	377,564	-5,267015	uc002khi.4	chr17:44376500-44376811	NA	NA	NA	NA
ARL4A	604786	NA	NA	NA	NA	1192,97	-5,089979	uc003ssp.3	chr7:12728483-12730558	NA	NA	NA	NA
ARL5B	608909	346,451	-4,37522	uc001lqi.1	chr10:18964146-18966940	NA	NA	NA	NA	NA	NA	NA	NA
ARL6P1	607669	NA	NA	NA	NA	349,582	-6,040094	uc010van.1	chr16:18802991-18804573	NA	NA	NA	NA
ARL6P6	616495	NA	NA	NA	NA	513,919	-7,641352	uc002tyn.3	chr2:153616355-153617767	NA	NA	NA	NA
ARL8B	616596	NA	NA	NA	NA	626,989	-4,117285	uc003bqg.3	chr3:5220399-5222601	278,075	-3,471118	uc003bqg.3	chr3:5220399-5222601
ARMCX5	NA	NA	NA	NA	NA	1393,15	-13,368919	uc004eig.3	chrX:101858747-101859085	NA	NA	NA	NA
ARNTL	602550	374,488	-6,281078	uc001mko.3	chr11:13408304-13408812	NA	NA	NA	NA	1157,58	-8,860753	uc001mko.3	chr11:13408304-13408812
ARNTL2	614517	1444,54	-11,222628	uc001rhi.2	chr12:27573466-27578746	NA	NA	NA	NA	NA	NA	NA	NA
ARPC3	604225	1085,21	-8,487821	uc001lqi.3	chr12:110872706-110872959	NA	NA	NA	NA	NA	NA	NA	NA
ARRDC4	NA	532,714	-7,347509	uc002bul.4	chr15:98514418-98517068	1778,2	-10,378009	uc002bul.4	chr15:98514418-98517068	NA	NA	NA	NA
ARRDC5	NA	260,005	-4,845527	uc002nbn.3	chr19:4890449-4891057	NA	NA	NA	NA	NA	NA	NA	NA
ARSA	607574	212,333	-4,682161	uc003bna.4	chr22:51061182-51063572	NA	NA	NA	NA	NA	NA	NA	NA
ARSB	611542	1430,63	-11,448138	uc003kfq.3	chr5:78073037-78076219	NA	NA	NA	NA	NA	NA	NA	NA
ARSE	300180	NA	NA	NA	NA	NA	NA	NA	NA	769,679	-9,56035	uc004erc.4	chrX:2852673-2852872
ART4	110600	NA	NA	NA	NA	660,984	-4,837777	uc001rcl.1	chr12:14982245-14982304	773,985	-8,083501	uc001rcl.1	chr12:14982245-14982304
ARV1	611647	NA	NA	NA	NA	417,429	-6,384341	uc009xfl.1	chr1:2311133010-2311133147	507,526	-5,849707	uc001huh.3	chr1:2311135884-231136479
ASAP1	605953	NA	NA	NA	NA	399,088	-6,623233	uc003ysz.2	chr8:131064351-131066976	NA	NA	NA	NA
ASB1	605758	782,918	-6,278528	uc002vvg.3	chr2:239355153-239360891	NA	NA	NA	NA	NA	NA	NA	NA
ASB11	300626	NA	NA	NA	NA	NA	NA	NA	NA	316,166	-6,422245	uc004cwo.2	chrX:15299831-15301626
ASB16	615056	NA	NA	NA	NA	777,825	-4,660612	uc002fll.1	chr17:42255759-42256451	NA	NA	NA	NA
ASB17	NA	NA	NA	NA	NA	NA	NA	NA	NA	762,986	-8,695003	uc001dhe.2	chr1:76384558-76384636
ASB7	615052	643,587	-2,207764	uc002bwj.3	chr15:101170256-101170414	582,774	-12,640694	uc002bwj.3	chr15:101170256-101170414	NA	NA	NA	NA
ASMTL	300162	209,512	-5,012961	uc004cpk.2	chrX:1522032-1522161	NA	NA	NA	NA	NA	NA	NA	NA
ASNSD1	NA	581,213	-9,207436	uc002uql.3	chr2:190535453-190535557	NA	NA	NA	NA	NA	NA	NA	NA
ASPA	608034	704,701	-9,561641	uc010ckg.3	chr17:3402389-3402700	NA	NA	NA	NA	NA	NA	NA	NA
ASPDH	NA	NA	NA	NA	NA	215,226	-4,7723	uc010denz.3	chr19:51014857-51014986	NA	NA	NA	NA
ASPH	600582	NA	NA	NA	NA	496,231	-5,797451	uc011leg.2	chr8:62413115-62415917	NA	NA	NA	NA
ASPM	605481	579,048	-7,543463	uc001glw.4	chr1:197057248-197057334	NA	NA	NA	NA	NA	NA	NA	NA
ASS1	603470	NA	NA	NA	NA	NA	NA	NA	NA	700,494	-11,03023	uc004bzm.3	chr9:133376409-133376661
ASTE1	NA	1105,42	-9,631582	uc010htm.1	chr3:130732721-130732900	NA	NA	NA	NA	NA	NA	NA	NA
ASTN1	600904	NA	NA	NA	NA	776,727	-5,953168	uc001glb.1	chr1:176828441-176828746	NA	NA	NA	NA
ASTN2	612856	NA	NA	NA	NA	457,558	-4,805341	uc004bjp.2	chr9:119187504-119188129	NA	NA	NA	NA
ASXL1	612990	678,249	-9,511004	uc002wxt.3	chr20:30959973-30960352	NA	NA	NA	NA	1044,05	-13,683314	uc0023wt.3	chr20:30959973-30960352
ASZ1	605797	NA	NA	NA	NA	NA	NA	NA	NA	867,616	-7,877995	uc003vjp.2	chr7:117003276-117003649
ATAD2	611941	NA	NA	NA	NA	1233,45	-16,054851	uc011lil.2	chr8:124332091-124333373	625,6	-12,722897	uc011lil.2	chr8:124332091-124333373
ATAD5	609534	849,499	-17,394089	uc002hfs.1	chr17:29221932-29222295	NA	NA	NA	NA	NA	NA	NA	NA
ATE1	607103	NA	NA	NA	NA	NA	NA	NA	NA	532,504	-9,827832	uc001lfp.3	chr10:123502625-123503194
ATF1	123803	361,076	-8,81154	uc001rww.4	chr12:51213563-51214943	NA	NA	NA	NA	NA	NA	NA	NA
ATF3	603148	NA	NA	NA	NA	NA	NA	NA	NA	473,6	-5,034036	uc001hjf.3	chr1:212792898-212794119

Table 1

ATF7IP	613644	1227.63	-9.06265	uc001rbu.3	chr12:14628959-14629347	1772.4	-3.498198	uc001rbu.3	chr12:14628959-14629347	1237.47	-5.440922	uc001rbu.3	chr12:14628959-14629347
ATF7IP2	613645	1770.3	-21.277169	uc002czu.3	chr16:10576107-10577495	1745.23	-0.334273	uc002czu.3	chr16:10576107-10577495	NA	NA	NA	NA
ATG101	615089	NA	NA	NA	NA	1244.58	-4.644222	uc001tzu.4	chr12:52470975-52471279	NA	NA	NA	NA
ATG12	609608	NA	NA	NA	NA	756.377	-5.710038	uc003kth.3	chr5:115163894-115167500	NA	NA	NA	NA
ATG14	613515	NA	NA	NA	NA	798.303	-7.972395	uc001xbw.2	chr14:558333109-55836336	NA	NA	NA	NA
ATG2B	616226	587.622	-8.462493	uc001yfi.3	chr14:96747595-96752091	NA	NA	NA	NA	NA	NA	NA	NA
ATG4D	611340	NA	NA	NA	NA	NA	NA	NA	NA	759.658	-7.554543	uc002nov.3	chr19:10663744-10664094
ATIC	601731	709.812	-4.283927	uc002vex.4	chr2:216214379-216214496	NA	NA	NA	NA	610.193	-6.569674	uc002vex.4	chr2:216214379-216214496
ATL2	609368	754.984	-5.197475	uc010ynn.2	chr2:38522029-38523624	573.499	-3.895191	uc010ynn.2	chr2:38522029-38523624	698.796	-5.609656	uc010ynn.2	chr2:38522029-38523624
ATH	607585	646.266	-7.148427	uc001pkb.1	chr11:108236236-108239826	NA	NA	NA	NA	781.042	-2.846765	uc001pkd.4	chr11:108160533-108161367
ATOH8	NA	NA	NA	NA	NA	727.169	-5.541324	uc002sqm.4	chr2:86000032-86002336	NA	NA	NA	NA
ATP10A	605855	NA	NA	NA	NA	395.584	-4.163003	uc010ayu.3	chr15:25923860-25924487	481.682	-6.025016	uc010ayu.3	chr15:25923860-25924487
ATP11C	300516	NA	NA	NA	NA	667.511	-7.828659	uc004lax.3	chrX:138808505-138811121	NA	NA	NA	NA
ATP13A3	610232	NA	NA	NA	NA	981.603	-11.22549	uc003ftx.4	chr3:194123403-194126647	NA	NA	NA	NA
ATP13A4	609556	NA	NA	NA	NA	418.512	-5.892502	uc003fld.3	chr3:193119866-193120440	NA	NA	NA	NA
ATP1A2	182340	NA	NA	NA	NA	302.554	-5.034847	uc001fvb.2	chr1:160106826-160106992	NA	NA	NA	NA
ATP1B2	182331	NA	NA	NA	NA	599.842	-5.413352	uc002gfi.1	chr17:7559214-7561089	NA	NA	NA	NA
ATP1B3	601867	NA	NA	NA	NA	521.92	-7.867919	uc003eug.1	chr3:141644544-141645382	NA	NA	NA	NA
ATP1B4	NA	NA	NA	NA	NA	1147.99	-10.76458	uc004esq.3	chrX:119513490-119517104	963.792	-7.108402	uc004esq.3	chrX:119513490-119517104
ATP2B2	108733	NA	NA	NA	NA	743.813	-6.759495	uc010hdp.2	chr3:10429568-10429919	716.295	-6.832539	uc010hdp.2	chr3:10429568-10429919
ATP2B4	108732	NA	NA	NA	NA	224.275	-4.927504	uc001gzx.3	chr1:203708983-203713209	1832.15	-13.611216	uc001gzx.3	chr1:203708700-203713209
ATP2C2	613082	NA	NA	NA	NA	449.322	-7.666387	uc002flx.3	chr16:84497339-84497793	NA	NA	NA	NA
ATP5A1	164360	NA	NA	NA	NA	849.11	-13.792353	uc002lbt.1	chr18:43664110-43664247	NA	NA	NA	NA
ATP5B	102910	1042.86	-8.657256	uc001slr.3	chr12:57031959-57032106	NA	NA	NA	NA	NA	NA	NA	NA
ATP5C1	108729	649.173	-5.903855	uc010qbb.2	chr10:7841162-7841605	762.549	-6.033502	uc001ljj.3	chr10:7849626-7849762	762.346	-6.033502	uc001ljj.3	chr10:7849622-7849762
ATP5G1	603192	259.648	-5.146556	uc002log.3	chr17:46973132-46973232	643.468	-6.226567	NA	NA	360.958	-5.826945	uc002log.3	chr17:46973132-46973232
ATP5G2	603193	NA	NA	NA	NA	589.535	-6.486772	uc001sec.3	chr12:54058944-54059097	NA	NA	NA	NA
ATP5G3	602736	NA	NA	NA	NA	782.429	-13.6922	uc002luz.4	chr2:176040986-176043015	NA	NA	NA	NA
ATP5J2	NA	NA	NA	NA	NA	376.482	-10.229359	uc003uql.3	chr7:99055784-99055949	NA	NA	NA	NA
ATP6AP1	300197	523.666	-5.693356	uc004lff.1	chrX:153664238-153664862	NA	NA	NA	NA	NA	NA	NA	NA
ATP6V0A2	611716	273.444	-5.503612	uc001ufq.1	chr12:124221900-124222049	NA	NA	NA	NA	NA	NA	NA	NA
ATP6V0B	603717	NA	NA	NA	NA	875.694	-5.423566	uc001clf.3	chr1:44443084-44443967	401.476	-4.37522	uc001clf.3	chr1:44443680-44443972
ATP6V0D1	607028	970.324	-17.166689	uc010vjr.1	chr16:67471917-67472430	NA	NA	NA	NA	1493.42	-17.594665	uc010vjr.1	chr16:67471917-67472430
ATP6V0E2	611019	NA	NA	NA	NA	515.607	-6.06863	uc003wgr.3	chr7:1495767-149577787	NA	NA	NA	NA
ATP6V1A	607027	NA	NA	NA	NA	NA	NA	NA	NA	1372.17	-14.425225	uc003sao.3	chr3:113528275-113530905
ATP6V1B2	606939	NA	NA	NA	NA	962.554	-8.872884	uc003wzp.3	chr8:20077914-20079207	958.921	-11.537631	uc003wzp.3	chr8:20077914-20079207
ATP6V1C1	603097	NA	NA	NA	NA	NA	NA	NA	NA	994.969	-7.72899	uc003ylz.4	chr8:104080976-104085285
ATP6V1C2	NA	NA	NA	NA	NA	853.121	-8.0664	uc002ras.3	chr2:10923390-10925236	NA	NA	NA	NA
ATP6V1D	609398	NA	NA	NA	NA	256.951	-6.846554	uc001xlf.3	chr14:67804581-67805337	NA	NA	NA	NA
ATP6V1E1	108746	NA	NA	NA	NA	NA	NA	NA	NA	326.487	-6.120118	uc002mr.1	chr22:18074903-18075439
ATP6V1F	607160	NA	NA	NA	NA	1152.61	-5.246955	uc003voc.2	chr7:128508633-128509503	NA	NA	NA	NA
ATP6V1G1	607296	486.683	-6.216275	uc004bjc.3	chr9:117360024-117361152	NA	NA	NA	NA	NA	NA	NA	NA
ATP6V1G3	NA	NA	NA	NA	NA	869.114	-1.207919	uc009wzd.3	chr1:198492352-198492520	1129.38	-2.751467	uc009wzd.3	chr1:198492352-198492520
ATP7A	300011	716.68	-1.819641	uc004ecw.2	chrX:77264911-77268087	1105.75	-7.025999	uc004ecw.2	chrX:77264911-77268087	698.288	-3.097801	uc004ecw.2	chrX:77264911-77268087
ATP8B1	602397	NA	NA	NA	NA	412.713	-5.368716	uc002lgw.3	chr18:55313659-55315719	NA	NA	NA	NA
ATP8B2	605867	588.7	-7.016366	uc001few.3	chr1:154310151-154310322	1214.63	-7.809032	uc001few.3	chr1:154310151-154310322	1016.17	-5.237598	uc001few.3	chr1:154310151-154310322
ATP8B3	605866	NA	NA	NA	NA	472.667	-5.698418	uc002lly.1	chr19:1798760-1799649	NA	NA	NA	NA
ATP8B4	609123	1301.08	-9.643518	uc001tzt.3	chr15:50150435-50152390	NA	NA	NA	NA	NA	NA	NA	NA
ATP	601215	NA	NA	NA	NA	NA	NA	NA	NA	417.49	-7.543463	uc003euy.1	chr3:142168080-142171897

Table 1

ATRLN1	612869	1077.76	-8.421552	uc001lbg.3	chr10:117704291-117708496	911.465	-6.151088	uc001lbg.3	chr10:117704291-117708496	523.868	-8.90812	uc001lbg.3	chr10:117704291-117708496
ATXN1	601556	1122.85	-11.197959	uc003nbl.3	chr6:16299343-16306559	NA	NA	NA	NA	852.962	-7.708961	uc001sh.3	chr12:111890018-111890615
ATXN2	601517	989.088	-7.910787	uc001tsh.3	chr12:111890018-111890615	NA	NA	NA	NA	1040.81	-4.127988	uc003dlw.4	chr3:63985144-63989136
ATXN7	607640	NA	NA	NA	NA	1391.47	0.013457	uc003dlv.3	chr3:63982178-63982295	NA	NA	NA	NA
ATXN7L2	NA	NA	NA	NA	NA	933.235	-7.859073	uc001dtr.3	chr1:110035223-110035420	NA	NA	NA	NA
AUP1	602434	772.871	-4.812433	uc002sme.3	chr2:74753775-74753926	501.509	-7.3683	uc021vjm.1	chr2:74754088-74754203	1651.08	-11.321314	uc002sme.3	chr2:74753775-74753926
AURKB	604970	1325.91	-8.488097	NA	NA	812.25	-10.995927	uc010cnu.3	chr17:8108049-8108188	NA	NA	NA	NA
AURKC	603495	502.069	-4.968085	uc002qoc.3	chr19:57746786-57746916	1206.83	-9.151295	uc002qoc.3	chr19:57746786-57746916	810.654	-7.756988	uc002qoc.3	chr19:57746786-57746916
AVIL	613397	NA	NA	NA	NA	NA	NA	NA	NA	273.732	-2.918401	uc001sqj.2	chr12:58191160-58191664
AZJ2	609916	NA	NA	NA	NA	NA	NA	NA	NA	486.004	-7.766873	uc003cee.4	chr3:28367995-28368293
B2M	109700	NA	NA	NA	NA	2265.65	-17.597682	uc001zuc.3	chr15:45009805-45010357	NA	NA	NA	NA
B3GALT1	603093	510.843	-5.064142	uc002udz.1	chr2:168726531-168727366	878.802	-9.395031	uc002udz.1	chr2:168726531-168727366	NA	NA	NA	NA
B3GALT4	603095	NA	NA	NA	NA	NA	NA	NA	NA	631.528	-6.642339	uc003odr.3	chr6:33246334-33246602
B3GNT4	605864	NA	NA	NA	NA	NA	NA	NA	NA	497.574	-5.924138	uc001lbu.3	chr12:122691936-122692084
B4GALNT2	111730	687.515	-7.151568	uc010wll.1	chr17:47247091-47247351	NA	NA	NA	NA	NA	NA	NA	NA
B4GALT4	604015	NA	NA	NA	NA	NA	NA	NA	NA	917.872	-5.847207	uc003ece.1	chr3:118930587-118935082
B4GALT6	604017	214.016	-5.651533	uc002kwz.4	chr18:29202209-29205576	NA	NA	NA	NA	NA	NA	NA	NA
BABAM1	612766	NA	NA	NA	NA	579.864	-5.030886	uc002ntu.3	chr19:17389858-17390162	NA	NA	NA	NA
BAGE3	NA	810.03	-1.802787	uc002yit.1	chr21:11049450-11049570	314.788	-7.851233	uc002yit.1	chr21:11026723-11026839	526.583	-6.212389	uc002yit.1	chr21:11020813-11020917
BARD1	601593	312.898	-9.173472	uc010zjm.1	chr2:215593275-215593593	NA	NA	NA	NA	NA	NA	NA	NA
BAX	600040	1110.13	-6.56381	uc002plf.1	chr19:49464355-49464519	677.648	-6.681534	uc002plj.3	chr19:49464894-49465055	NA	NA	NA	NA
BAZ1B	605681	431.128	-9.307547	uc003yc.3	chr7:72854728-72856023	NA	NA	NA	NA	NA	NA	NA	NA
BAZ2A	605682	NA	NA	NA	NA	NA	NA	NA	NA	695.084	-7.711833	uc001slo.1	chr12:56989380-56992401
BAZ2B	605683	673.512	-9.585952	uc002uao.3	chr2:160175490-160176775	NA	NA	NA	NA	720.511	-3.126428	uc002lar.1	chr2:160260901-160261329
BBS4	600374	NA	NA	NA	NA	609.132	-5.423575	uc002avb.3	chr15:73029929-73030817	NA	NA	NA	NA
BBS5	603650	NA	NA	NA	NA	NA	NA	NA	NA	823.529	-10.7821	uc002uet.3	chr2:170361093-170363165
BBS9	607968	NA	NA	NA	NA	1028.62	-6.847433	uc011kan.1	chr7:33353924-33354183	NA	NA	NA	NA
BCAP29	NA	NA	NA	NA	NA	931.25	-8.14343	uc003vej.2	chr7:107258809-107263762	NA	NA	NA	NA
BCAR3	604704	NA	NA	NA	NA	731.154	-4.394389	uc009wdm.1	chr1:94036889-94037097	1290.56	-9.593388	uc009wdm.1	chr1:94036889-94037097
BCAR4	613746	NA	NA	NA	NA	358.675	-5.755202	uc010uyv.2	chr16:11913692-11913776	NA	NA	NA	NA
BCAS4	607471	NA	NA	NA	NA	NA	NA	NA	NA	1237.53	-13.639567	uc002xvq.3	chr20:49493073-49493714
BCCIJP	611883	NA	NA	NA	NA	314.325	-5.332107	uc001ljb.4	chr10:127524844-127525124	542.377	-4.232466	uc021qar.1	chr10:1275252543-127523219
BCL10	603517	NA	NA	NA	NA	NA	NA	NA	NA	568.04	-5.636385	uc021opd.1	chr1:85731460-85733309
BCL11A	606557	699.926	-2.465276	uc002sab.3	chr2:60678302-60679709	NA	NA	NA	NA	699.15	-9.206331	uc002sab.3	chr2:60678302-60679709
BCL2	151430	664.489	-1.553062	uc002ilt.1	chr18:60790579-60795857	NA	NA	NA	NA	NA	NA	NA	NA
BCL2A1	601056	NA	NA	NA	NA	NA	NA	NA	NA	224.821	-4.888625	uc002bfc.4	chr15:80253232-80253408
BCL2L11	603827	258.078	-1.764485	uc002tgt.1	chr2:111886329-111886423	515.498	-1.486703	uc002igu.1	chr2:111891809-111892622	1163.32	-4.345747	uc002tgt.1	chr2:111886329-111886423
BCL2L12	610837	768.01	-6.755666	uc002ppa.3	chr19:50177006-50177173	NA	NA	uc001rae.3	chr12:12247526-12247864	499.996	-5.844576	uc001rac.3	chr12:12251923-12252627
BCL2L14	606126	276.118	-3.366852	uc001rac.3	chr12:12251923-12252627	222.933	-4.336641	uc001edw.3	chr1:114419436-114423744	NA	NA	NA	NA
BCL2L15	NA	NA	NA	NA	NA	354.478	-7.584491	uc001edw.3	chr1:114419436-114423744	NA	NA	NA	NA
BCL7B	605846	NA	NA	NA	NA	674.704	-6.698924	uc003yfl.2	chr7:72950683-72951627	NA	NA	NA	NA
BCL9	602597	NA	NA	NA	NA	416.91	-4.866935	uc001epq.3	chr1:147096761-147098015	NA	NA	NA	NA
BCLAF1	612588	NA	NA	NA	NA	785.956	-8.790764	uc011edb.1	chr6:136578001-136582247	NA	NA	NA	NA
BCO2	611740	721.442	-10.096836	uc001pne.1	chr11:112085728-112086460	NA	NA	NA	NA	NA	NA	NA	NA
BCOR	300465	731.897	-5.237521	uc010nhb.3	chrX:39910499-39911653	NA	NA	NA	NA	NA	NA	NA	NA
BCORL1	300688	491.957	-4.805341	uc022cdlu.1	chrX:129190112-129192058	NA	NA	NA	NA	NA	NA	NA	NA
BCORP1	NA	236.897	-2.917374	uc011nav.1	chrY:21628342-21628913	273.478	-3.159389	uc011nav.1	chrY:21628342-21628913	276.128	-4.912083	uc011nav.1	chrY:21628342-21628913
BCR	151410	NA	NA	NA	NA	NA	NA	NA	NA	802.894	-5.02011	uc002zww.3	chr22:23657710-23660224
BDH1	603063	NA	NA	NA	NA	NA	NA	NA	NA	955.054	-12.226262	uc003fv.3	chr3:197236654-197238765

Table 1

BDH2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	712.546	-7.80583	uc003hwr.3	chr4:103998782-104000858	
BOKRB2	113503	NA	NA	NA	NA	NA	985.943	-7.617296	uc010avl.2	chr14:96704154-96710503	432.142	-3.854518	uc010avl.2	chr14:96704154-96710503	
BDNE	113505	NA	NA	NA	NA	NA	855.71	-10.029552	uc010rdu.2	chr11:27676442-27679367	NA	NA	NA	NA	
BDP1	607012	NA	NA	NA	NA	NA	246.195	-4.971255	uc003kbn.1	chr5:70807039-70807178	1390.92	-9.777427	uc003kbp.1	chr5:70806713-70863649	
BEND2	NA	NA	NA	NA	NA	NA	506.373	-4.539498	uc004cyl.4	chrX:18181051-18183128	683.399	-7.950195	uc004cyl.4	chrX:18181051-18183128	
BEND7	NA	NA	NA	NA	NA	NA	877.388	-5.245182	uc001imm.2	chr10:13480484-13481171	515.959	-3.321475	uc001imm.2	chr10:13480484-13481171	
BET1	605456	NA	NA	NA	NA	NA	NA	NA	NA	NA	307.239	-6.987781	uc003unf.1	chr7:93621000-93623541	
BEX2	300691	974.327	-11.135713	uc004eka.3	chrX:102564274-102564517	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BEX4	300692	2172.07	-13.596293	uc004ejv.4	chrX:102471445-102472128	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BEX5	300693	681.834	-11.776508	uc010niz.3	chrX:101408679-101408901	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BHLHB9	300921	970.057	-7.034284	uc004ejo.3	chrX:102005568-102007369	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BHLHE22	613483	NA	NA	NA	NA	NA	NA	NA	NA	NA	486.785	-6.379406	uc003xvl.3	chr8:65494494-65496191	
BHMT	602888	NA	NA	NA	NA	NA	NA	NA	NA	NA	256.743	-7.305491	uc003kfu.4	chr5:78426940-78428113	
BHMT2	605932	583.828	-5.604559	uc003kft.3	chr5:78394398-783985897	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BICD1	602204	NA	NA	NA	NA	NA	NA	NA	NA	NA	370.386	-7.126125	uc001ku.3	chr12:32530562-32531141	
BIC	603392	NA	NA	NA	NA	NA	323.232	-6.495135	uc003bdk.3	chr22:43525312-43525718	NA	NA	NA	NA	
BIN3	606396	NA	NA	NA	NA	NA	NA	NA	NA	NA	698.134	-5.785125	uc003xcl.3	chr8:22477947-22478934	
BIRC5	603352	NA	NA	NA	NA	NA	208.345	-4.748612	uc002jvc.3	chr17:76210933-76211066	NA	NA	NA	NA	
BIRC7	605737	NA	NA	NA	NA	NA	986.737	-7.249729	uc002vei.3	chr20:61871608-61871854	NA	NA	NA	NA	
BIRC8	NA	NA	NA	NA	NA	NA	1105.67	-13.275275	uc002qbk.3	chr19:53792854-53792916	NA	NA	NA	NA	
BIVM	NA	703.823	-16.055454	uc001vps.3	chr13:103492216-103493888	NA	NA	NA	NA	NA	715.127	-11.941018	uc001vps.3	chr13:103492216-103493888	
BLM	604610	422.855	-5.846009	uc002bpr.3	chr15:91358510-91358686	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BLOC1S6	604310	1632.8	-15.269262	uc001zqv.3	chr15:45898713-45901909	492.777	-5.437051	uc001zqv.3	chr15:45898713-45901909	NA	NA	NA	NA	NA	NA
BLZF1	608692	502.157	-7.409111	uc001gtw.3	chr1:169346275-169346621	423.951	-2.366946	uc001gtw.3	chr1:1693462421-169357539	806.212	-5.765459	uc001gtw.3	chr1:169346275-169346621		
BMP10	608748	1251.25	-11.708709	uc002sez.1	chr2:69092813-69092762	NA	NA	NA	NA	NA	725.168	-9.439893	uc002sez.1	chr2:69092613-69092762	
BMP2	NA	NA	NA	NA	NA	NA	214.806	-4.712115	uc003hij.3	chr4:79800084-79800594	NA	NA	NA	NA	
BMP3	112263	NA	NA	NA	NA	NA	906.206	-8.728905	uc003hmg.4	chr4:81974691-81978685	NA	NA	NA	NA	
BMP8	602284	NA	NA	NA	NA	NA	1735.49	-16.322899	uc001cdz.1	chr1:40223903-40226090	NA	NA	NA	NA	
BMP1A	601299	594.033	-9.978637	uc001kdy.3	chr10:88683477-88684945	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BMP1B	603248	NA	NA	NA	NA	NA	592.382	-5.378547	uc003hlm.4	chr4:96075825-96079601	NA	NA	NA	NA	
BMPR2	600799	NA	NA	NA	NA	NA	249.417	-8.849914	uc002uzf.4	chr2:203424670-203432474	NA	NA	NA	NA	
BNIP2	603292	699.896	-6.59091	uc010uhb.2	chr15:59955062-59956267	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BNIP3	603293	NA	NA	NA	NA	NA	NA	NA	NA	NA	892.771	-5.227471	uc001lkr.1	chr10:133781204-133782027	
BOC	608708	1210.67	-8.025358	uc003dzw.1	chr3:112969779-112970852	493.329	-0.557048	uc003dzw.3	chr3:113005710-113006305	NA	NA	NA	NA	NA	NA
BOLA3	613183	1484.14	-14.188083	uc002skd.1	chr2:74362528-74362648	984.163	-11.119094	uc002skd.1	chr2:74362528-74362648	475.71	-9.198202	uc002skc.1	chr2:74362528-74362719		
BPH1	603156	254.752	-4.203343	uc003muy.3	chr6:3152810-3153432	796.9	-8.706554	uc003muy.3	chr6:3152810-3153432	NA	NA	NA	NA	NA	NA
BPY2B	NA	1211.4	-18.3382	uc004kvj.3	chrY:25144416-25144521	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BRD1	604589	NA	NA	NA	NA	NA	587.304	-6.332884	uc011arf.2	chr22:50166937-50167880	1375.83	-13.524208	uc011arf.2	chr22:50166937-50167880	
BRD3	601541	203.206	-5.507344	uc004csw.3	chr9:136895446-136898711	NA	NA	NA	NA	NA	1718.57	-2.327148	uc004csw.3	chr9:136895446-136898711	
BRD7	NA	973.867	-11.224285	uc002ege.2	chr16:50352929-50353121	1352.95	-10.857087	uc002ege.2	chr16:50352929-50353121	NA	NA	NA	NA	NA	NA
BRD9	NA	NA	NA	NA	NA	NA	989.161	-0.047985	uc003jpl.3	chr5:863850-864582	1056.92	-16.080428	uc003jpl.3	chr5:863850-864582	
BRNP1	602865	603.735	-4.430811	uc004bxc.2	chr9:121928908-121929361	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BRNP3	NA	NA	NA	NA	NA	NA	859.799	-8.418148	uc010pat.1	chr1:190066797-190067147	NA	NA	NA	NA	NA
BRU1	NA	2062.3	-16.146846	uc003jiz.3	chr5:34920034-34922014	NA	NA	NA	NA	NA	398.02	-14.91091	uc003jiz.3	chr5:34920034-34922014	
BRWD1	NA	1117.52	-17.496422	uc002ym.3	chr21:40688363-40670343	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BSPR1	NA	NA	NA	NA	NA	NA	975.45	-8.424514	uc004bhtg.4	chr9:116132423-116133513	NA	NA	NA	NA	NA
BST1	600387	NA	NA	NA	NA	NA	310.4	-9.760163	uc003gph.4	chr4:15733469-15733796	1399.18	-8.522056	uc003gph.4	chr4:15733469-15733796	
BTAF1	605191	1019.06	-11.144936	uc001khr.3	chr10:93788691-93790080	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BTBD10	615933	NA	NA	NA	NA	NA	NA	NA	NA	NA	1411.48	-7.305804	uc010rcl.2	chr11:13409556-13410377	

Table 1

BTBD17	NA	382,874	-4,798,624	uc002jkn.2	chr17:72352555-72352795	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BTBD7	610386	514,524	-7,460,051	uc010aur.3	chr14:93703896-93708618	583,013	-8,110,752	uc001yba.4	chr14:93721866-93723507	NA	NA	NA	NA	NA	NA	NA
BTD	609019	NA	NA	NA	NA	345,301	-6,047,635	uc011avv.2	chr3:15868996-15867325	NA	NA	NA	NA	NA	NA	NA
BTf3	602542	464,992	-8,486,968	uc010zdi.1	chr5:72795205-72795476	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BTg2	601597	717,932	-9,776,032	uc001grz.3	chr1:203276567-203278729	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BTN2A2	613591	645,862	2,248,946	uc003nhs.3	chr6:26394558-26395100	523,827	-0,444,406	uc003nhs.3	chr6:26394558-26395100	NA	NA	NA	NA	NA	NA	NA
BTN3A3	613595	NA	NA	NA	NA	NA	NA	NA	NA	419,415	-8,815,144	uc003niz.3	chr6:26452640-26453643	NA	NA	NA
BUB1	602452	380,956	-6,294,105	uc002gd.2	chr2:111418445-111419154	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BUB1B	602860	463,231	-8,913,968	uc001zlx.4	chr15:40512961-40513337	NA	NA	NA	NA	890,287	-5,076,864	uc001lhf.4	chr10:124922349-124924881	NA	NA	NA
BUB3	603719	1178,44	-8,822,235	uc001lhc.2	chr10:124923352-124924886	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
BUD13	NA	379,807	-6,370,781	uc009yzc.3	chr11:116631167-116631411	1141,76	-8,528,545	uc003stin.1	chr7:16725731-16727179	566,803	-6,877,934	uc003stj.2	chr7:16745714-16746148	NA	NA	NA
BZW2	NA	NA	NA	NA	NA	NA	NA	NA	NA	1325,26	-10,820,286	uc001inw.3	chr10:15137384-15138355	NA	NA	NA
C10orf111	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C10orf131	NA	886,612	-7,190,301	uc010qpo.2	chr10:97697967-97698415	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C10orf32	NA	NA	NA	NA	NA	590,732	-8,350,209	uc001kwh.2	chr10:104623487-104624718	NA	NA	NA	NA	NA	NA	NA
C10orf63	NA	NA	NA	NA	NA	408,516	-4,766,32	uc001jlc.3	chr10:50902649-50902948	NA	NA	NA	NA	NA	NA	NA
C10orf82	NA	NA	NA	NA	NA	NA	NA	NA	NA	1189,36	-8,809,932	uc001lcr.3	chr10:118423207-118423680	NA	NA	NA
C10orf88	NA	964,364	-10,208,94	uc001lgw.2	chr10:124690419-124691942	NA	NA	NA	NA	630,663	-7,755,551	uc001lgw.2	chr10:124690419-124691942	NA	NA	NA
C11orf24	610880	482,642	-5,457,377	uc001onr.4	chr11:68028803-68029112	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C11orf57	NA	NA	NA	NA	NA	NA	NA	NA	NA	744,957	-8,506,944	uc001pmr.4	chr11:111953697-111955874	NA	NA	NA
C11orf58	NA	NA	NA	NA	NA	NA	NA	NA	NA	437,873	-11,470,382	uc001mmk.2	chr11:16776652-16779901	NA	NA	NA
C11orf68	NA	NA	NA	NA	NA	485,316	-7,167,761	uc001ogi.3	chr11:65684283-65684929	NA	NA	NA	NA	NA	NA	NA
C11orf70	NA	932,259	-7,339,459	uc001pgp.3	chr11:101953931-101955291	636,676	-10,993,456	uc001pgp.3	chr11:101946636-101946842	979,126	-13,928,117	uc001pgc.3	chr11:101946636-101946842	NA	NA	NA
C11orf88	NA	NA	NA	NA	NA	713,331	-3,645,097	uc001plb.1	chr11:111405194-111407755	704,527	-4,598,357	uc001pln.4	chr11:111407553-111407756	NA	NA	NA
C12orf29	NA	344,188	-7,904,757	uc001lao.3	chr12:88442200-88443937	740,991	-12,345,314	uc001lao.3	chr12:88442200-88443937	NA	NA	NA	NA	NA	NA	NA
C12orf39	NA	427,174	-7,655,648	uc001lam.1	chr12:88373816-88374107	1178,62	-7,826,097	uc001lan.3	chr12:88377174-88379609	NA	NA	NA	NA	NA	NA	NA
C12orf60	NA	NA	NA	NA	NA	1079,94	-16,052,856	uc001trj.4	chr12:14976608-14976791	NA	NA	NA	NA	NA	NA	NA
C12orf65	613541	NA	NA	NA	NA	NA	NA	NA	NA	371,873	-4,531,871	uc001uen.3	chr12:123741579-123742506	NA	NA	NA
C12orf73	NA	NA	NA	NA	NA	386,125	-8,260,024	uc009zuj.2	chr12:104343981-104345300	NA	NA	NA	NA	NA	NA	NA
C14orf1	604576	1247,85	-5,465,797	uc001xrl.3	chr14:76117233-76117897	1738,18	-9,598,907	uc001xrt.3	chr14:76117233-76117897	NA	NA	NA	NA	NA	NA	NA
C14orf105	NA	NA	NA	NA	NA	NA	NA	NA	NA	202,583	-6,325,793	uc001xcy.2	chr14:57936595-57938072	NA	NA	NA
C14orf159	NA	NA	NA	NA	NA	NA	NA	NA	NA	908,756	-7,399,268	uc001xyv.2	chr14:91691178-91691703	NA	NA	NA
C14orf2	604573	NA	NA	NA	NA	NA	NA	NA	NA	862,641	-7,171,605	uc001yol.4	chr14:104378625-104379002	NA	NA	NA
C14orf28	NA	1163,44	-8,819,935	uc001wvp.1	chr14:45373737-45376459	806,385	-7,937,769	uc001wva.3	chr14:45374754-45376460	NA	NA	NA	NA	NA	NA	NA
C14orf37	NA	252,526	-5,129,985	uc001xdc.3	chr14:58470808-58471453	1259,64	-6,887,74	uc001xdc.3	chr14:58470808-58471453	221,268	-3,711,218	uc001xde.3	chr14:58582866-58583043	NA	NA	NA
C14orf39	NA	NA	NA	NA	NA	706,618	-9,015,63	uc001xez.4	chr14:60902674-60903562	NA	NA	NA	NA	NA	NA	NA
C15orf32	NA	NA	NA	NA	NA	613,47	-4,749,643	uc002brc.1	chr15:93043631-93044347	NA	NA	NA	NA	NA	NA	NA
C15orf40	NA	NA	NA	NA	NA	315,202	-4,694,998	uc002bjm.3	chr15:83673145-83674348	216,3	-4,126,155	uc010uon.2	chr15:83657715-83657825	NA	NA	NA
C15orf57	NA	1078,37	-15,687,712	uc001zlv.3	chr15:40823538-40824497	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C15orf59	NA	NA	NA	NA	NA	873,177	-12,644,019	uc002avy.3	chr15:74032141-74032257	NA	NA	NA	NA	NA	NA	NA
C15orf61	NA	1080,75	-10,270,435	uc002aqz.3	chr15:67818884-67819641	NA	NA	NA	NA	1041,24	-8,414,177	uc002aqz.3	chr15:67818884-67819641	NA	NA	NA
C15orf65	NA	NA	NA	NA	NA	370,763	-6,418,252	uc002ada.3	chr15:55710769-55710910	NA	NA	NA	NA	NA	NA	NA
C16orf59	NA	599,344	-5,736,782	uc002cqq.2	chr16:2514294-2514964	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C16orf62	NA	NA	NA	NA	NA	754,541	-8,636,282	uc002dgm.2	chr16:19628263-19628490	NA	NA	NA	NA	NA	NA	NA
C16orf74	NA	323,84	-3,576,385	uc002jfc.4	chr16:85741124-85741613	611,114	-5,901,6	uc002jfc.4	chr16:85741124-85741613	NA	NA	NA	NA	NA	NA	NA
C16orf83	NA	875,194	-10,969,079	uc002djp.3	chr16:30771358-30771539	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C17orf104	NA	603,232	-7,197,1	uc002zha.3	chr17:42751565-42753165	NA	NA	NA	NA	309,363	-5,202,03	uc002lgr.3	chr17:42746907-42748590	NA	NA	NA
C17orf86	NA	NA	NA	NA	NA	559,926	-5,334,583	uc010wdq.2	chr17:36827959-36829608	NA	NA	NA	NA	NA	NA	NA
C18orf42	616427	NA	NA	NA	NA	NA	NA	NA	NA	1486,47	-12,293,73	uc010wzc.1	chr18:5143672-5145560	NA	NA	NA

Table 1

C1orf63	NA	NA	NA	NA	NA	665.513	-4.181136	uc002ljj.3	chr18:72023716-72026422	NA	NA	-5.671791	NA	NA	chr19:16628813-16629430
C1orf44	NA	NA	NA	NA	NA	779.613	-9.191134	uc002nmt.2	chr19:10198103-10198936	216.777	-5.661259	uc002nmt.2	NA	NA	chr19:10198103-10198936
C1orf66	NA	581.16	-3.912914	uc002nmt.2	chr19:10198103-10198936	746.339	-6.51408	uc002sea.4	chr2:68269332-68270020	NA	NA	NA	NA	NA	NA
C1orf66	606997	NA	NA	NA	NA	1256.77	-10.580497	uc010klm.1	chr7:7274197-7274928	NA	NA	NA	NA	NA	NA
C1orf11	610555	NA	NA	NA	NA	1189.84	-10.243501	uc001tqj.1	chr10:16555742-16556526	NA	NA	NA	NA	NA	NA
C1QL3	615227	NA	NA	NA	NA	1723.6	-6.227595	uc001iai.3	chr1:244803230-244803662	812.542	-13.112159	uc001iak.1	NA	NA	chr1:244773674-244773890
C1orf101	NA	NA	NA	NA	NA	799.924	-11.013517	uc009wvu.1	chr1:169821195-169821378	426.765	-13.267141	uc001lgo.3	NA	NA	chr1:169773390-169773526
C1orf112	NA	913.818	-11.573	uc010plu.1	chr1:169798487-169798955	585.961	-4.310151	uc001hul.3	chr1:231359509-231360024	NA	NA	NA	NA	NA	NA
C1orf131	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C1orf140	NA	269.494	-6.606572	uc001hmv.1	chr1:221503270-221507177	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C1orf216	NA	463.867	-3.90834	uc001bzh.1	chr1:36179477-36181232	528.395	-7.791242	uc001bzh.1	chr1:36179477-36181232	362.989	-9.283392	uc001bzh.1	NA	NA	chr1:36179477-36181232
C1orf27	609335	211.675	-7.084357	uc021pgg.1	chr1:186375281-186375400	NA	NA	NA	NA	1145.56	-9.31031	uc021pgg.1	NA	NA	chr1:186388141-186390503
C1orf35	NA	NA	NA	NA	NA	751.506	-6.083935	uc001hrx.3	chr1:228288428-228288831	NA	NA	NA	NA	NA	NA
C1orf53	NA	762.536	-8.348763	uc001guh.3	chr1:197876351-197876497	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C2orf173	NA	NA	NA	NA	NA	NA	NA	NA	NA	411.666	-7.879615	uc002xcp.2	NA	NA	chr20:34114799-34115078
C21orf59	615494	NA	NA	NA	NA	260.52	-4.945564	uc002yqc.3	chr21:33973984-33974172	NA	NA	NA	NA	NA	NA
C2orf39	NA	NA	NA	NA	NA	NA	NA	NA	NA	941.947	-5.498829	uc002pk.2	NA	NA	chr22:19430673-19431787
C2CD2	NA	NA	NA	NA	NA	311.994	-5.774047	uc002yqx.1	chr21:43321062-43321658	NA	NA	NA	NA	NA	NA
C2CD3	615944	632.048	-8.844149	uc001ouu.2	chr11:73745480-73745642	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C2CD4A	610343	NA	NA	NA	NA	NA	NA	NA	NA	570.55	-9.63106	uc002ahf.4	NA	NA	chr15:62360923-62363116
C2CD4B	610344	NA	NA	NA	NA	NA	NA	NA	NA	479.309	-4.159832	uc002ahg.2	NA	NA	chr15:62455737-62456088
C2CD5	NA	NA	NA	NA	NA	NA	NA	NA	NA	1289.04	-10.117767	uc009hvj.1	NA	NA	chr12:22630962-22631186
C2orf42	NA	NA	NA	NA	NA	NA	NA	NA	NA	796.429	-9.828334	uc002zgh.3	NA	NA	chr2:70377017-70377487
C2orf43	NA	NA	NA	NA	NA	NA	NA	NA	NA	568.202	-6.53487	uc002rec.3	NA	NA	chr2:20884818-20886662
C2orf47	NA	NA	NA	NA	NA	794.961	-6.809271	uc002juvm.3	chr2:200828535-200828847	NA	NA	NA	NA	NA	NA
C2orf49	NA	NA	NA	NA	NA	NA	NA	NA	NA	1702.25	-19.684259	uc002tcs.1	NA	NA	chr2:105961829-105961984
C2orf57	NA	NA	NA	NA	NA	227.766	-5.388806	uc002vrz.3	chr2:232458851-232458994	NA	NA	NA	NA	NA	NA
C2orf72	NA	NA	NA	NA	NA	684.133	-5.651462	uc010zme.2	chr2:231911954-231914427	412.346	-5.466334	uc010zme.2	NA	NA	chr2:231911954-231914427
C2orf78	NA	683.899	-9.615335	uc002sjr.1	chr2:74044120-74044274	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C2orf80	615536	947.675	-7.221694	uc002vcr.3	chr2:209030071-209030530	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C3orf22	NA	NA	NA	NA	NA	1286.04	-5.694355	uc003ejb.3	chr3:126268519-126268710	NA	NA	NA	NA	NA	NA
C3orf50	NA	441.242	-3.544189	uc011blw.1	chr3:118870140-118870206	NA	NA	NA	NA	673.893	-9.241189	uc003ccb.1	NA	NA	chr3:118870140-118870302
C3orf53	NA	NA	NA	NA	NA	1321.82	-12.43413	uc003fal.1	chr3:155480401-155481305	NA	NA	NA	NA	NA	NA
C3orf36	NA	NA	NA	NA	NA	273.392	-5.222337	uc003epz.1	chr3:133646990-133647149	NA	NA	NA	NA	NA	NA
C3orf58	612200	430.162	-5.593289	uc003evo.3	chr3:143708684-143711210	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C3orf70	NA	525.116	-4.553848	uc003pjd.3	chr3:184795838-184800794	392.369	-5.535506	uc003pjd.3	chr3:184795838-184800794	1005.46	-11.979047	uc003fpd.3	NA	NA	chr3:184795838-184800794
C4BPA	120830	1488.15	-15.053295	uc001hfo.3	chr1:207318063-207318317	218.437	-7.083614	uc001hfo.3	chr1:207318063-207318317	NA	NA	NA	NA	NA	NA
C4BPB	120831	558.183	-7.195297	uc010pse.1	chr1:207268914-207269240	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C4orf17	NA	NA	NA	NA	NA	1091.92	-8.221619	uc003huw.3	chr4:100463267-100463460	NA	NA	NA	NA	NA	NA
C4orf26	614829	NA	NA	NA	NA	490.523	-4.710729	uc003hip.2	chr4:76489650-76491103	NA	NA	NA	NA	NA	NA
C4orf27	NA	NA	NA	NA	NA	NA	NA	NA	NA	210.255	-6.369736	uc003isl.4	NA	NA	chr4:170650619-170650728
C4orf29	NA	1905.37	-18.738954	uc021xrt.1	chr4:128951832-128952455	989.319	-6.889342	uc021xrt.1	chr4:128951832-128952455	1134.53	-7.232481	uc003fft.3	NA	NA	chr4:128956969-128957476
C5	120900	426.604	-8.247029	uc010nmv.1	chr9:123761957-123762182	722.454	-9.376068	uc004bvv.3	chr9:123714614-123715016	NA	NA	NA	NA	NA	NA
C5AR1	113995	NA	NA	NA	NA	NA	NA	NA	NA	1203.45	-7.54251	uc002pgl.1	NA	NA	chr19:47824088-47825327
C5orf22	NA	834.056	-5.690852	uc003hjj.4	chr5:31553010-31555165	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C5orf46	NA	725.764	-5.281261	uc003bov.4	chr5:147281100-147281187	NA	NA	NA	NA	409.746	-2.463336	uc010lbp.3	NA	NA	chr5:147269579-147269787
C5orf56	NA	1411.41	-12.310437	uc003kwz.2	chr5:131811625-131811736	NA	NA	NA	NA	699.638	-7.933695	uc003kwz.2	NA	NA	chr5:131811625-131811736
C5orf58	NA	NA	NA	NA	NA	984.201	-10.945709	uc010ijn.3	chr5:169673118-169673235	NA	NA	NA	NA	NA	NA
C6orf11	611419	781.538	-9.570472	uc003ojf.3	chr6:34214157-34214290	332.159	-5.703903	uc003ojf.3	chr6:34214157-34214290	NA	NA	NA	NA	NA	NA

Table 1

C6orf132	NA	453.151	-3.3676	uc003onw.2	chr6:42068857-42071498	833.714	-7.723433	uc003onw.2	chr6:42068857-42071498	NA	NA	NA	NA
C6orf201	NA	NA	NA	NA	NA	590.112	-8.283425	uc011dhw.1	chr6:4125218-4126353	NA	NA	NA	NA
C6orf226	NA	NA	NA	NA	NA	1154.51	-9.405406	uc003osw.3	chr6:42858003-42858220	NA	NA	NA	NA
C6orf62	NA	742.84	-7.617432	uc003nel.3	chr6:24705090-24706364	1039.01	-5.570147	uc003nel.3	chr6:24705090-24706364	NA	NA	NA	NA
C7orf131	616071	673.167	-5.708272	uc003sxn.1	chr7:25174316-25175590	NA	NA	NA	NA	551.093	-6.453775	uc003sxn.1	chr7:25174316-25175590
C7orf34	NA	NA	NA	NA	NA	NA	NA	NA	NA	448.101	-6.867483	uc003wca.2	chr7:142637675-142637957
C7orf62	NA	NA	NA	NA	NA	369.575	-4.06856	uc003ujv.3	chr7:98423420-88423494	NA	NA	NA	NA
C7orf73	NA	676.322	-8.255527	uc003vsv.3	chr7:135358914-135361160	NA	NA	NA	NA	NA	NA	NA	NA
C8orf34	NA	807.741	-10.160973	uc010lyk.2	chr8:69358737-69360245	NA	NA	NA	NA	NA	NA	NA	NA
C8orf48	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
C9orf131	NA	NA	NA	NA	NA	NA	NA	NA	NA	595.848	-10.44353	uc003wvp.3	chr8:13425461-13425797
C9orf139	NA	NA	NA	NA	NA	NA	NA	NA	NA	370.403	-5.746329	uc003rvu.3	chr9:35045867-35045988
C9orf156	NA	NA	NA	NA	NA	NA	NA	NA	NA	628.628	-8.43788	uc004ckp.1	chr9:139929507-139931234
C9orf24	NA	NA	NA	NA	NA	844.025	-7.494372	uc022bku.1	chr9:100673200-100675183	1218.44	-4.147975	uc004axv.1	chr9:100666772-100667014
C9orf3	NA	NA	NA	NA	NA	NA	NA	NA	NA	213.407	-4.268978	uc003urf.1	chr9:34379017-34379073
C9orf47	NA	NA	NA	NA	NA	455.47	-7.482689	uc004aux.2	chr9:97694037-97695955	442.075	-8.233932	uc004aux.2	chr9:97694037-97695955
C9orf64	611342	NA	NA	NA	NA	624.671	-8.107551	uc004aqc.2	chr9:91606904-91611057	NA	NA	NA	NA
C9orf84	NA	NA	NA	NA	NA	569.235	-6.841088	uc004arb.3	chr9:86553227-86554425	NA	NA	NA	NA
C9orf91	NA	NA	NA	NA	NA	915.006	-9.474843	uc004bfq.3	chr9:114448901-114449049	562.091	-0.300984	uc004bfq.3	chr9:114448901-114449049
CA2	611492	203.577	-9.116049	uc003ydk.2	chr8:86393019-86393721	NA	NA	NA	NA	NA	NA	NA	NA
CA3	114750	1704.68	-8.844461	uc003ydl.3	chr8:86360383-86361267	NA	NA	NA	NA	NA	NA	NA	NA
CAB5	300230	NA	NA	NA	NA	1005.16	-5.302802	uc004cxe.3	chrX:15800788-15805748	612.695	-4.999425	uc004cxe.3	chrX:15800788-15805748
CAB39L	612175	993.047	-10.308831	uc001vcw.3	chr13:49882786-49884949	786.102	-10.007189	uc001vcw.3	chr13:49882786-49884949	451.099	-6.36467	uc001vcw.3	chr13:49882786-49884949
CABLES1	609194	554.411	-2.606597	uc002kub.2	chr18:20837332-20840434	292.764	-4.497664	uc002kub.2	chr18:20837332-20840434	1220.06	-3.867449	uc002kub.2	chr18:20837332-20840434
CABS1	NA	367.249	-5.164006	uc003hff.3	chr4:71201945-71202063	NA	NA	NA	NA	NA	NA	NA	NA
CACNB2	600003	2094.98	-2.272591	uc001lpr.2	chr10:18828654-18830688	691.997	-2.879673	uc001lpr.2	chr10:18828654-18830688	1047.67	-3.9971	uc001lpr.2	chr10:18828654-18830688
CADM1	605686	NA	NA	NA	NA	576.467	-6.680857	uc001ppf.4	chr11:115039951-115040308	NA	NA	NA	NA
CALCA	114130	NA	NA	NA	NA	NA	NA	NA	NA	891.812	-5.036312	uc001mtl.2	chr11:114988215-14988647
CALCB	114160	398.563	-5.778329	uc001mlk.1	chr11:15099629-15100177	NA	NA	NA	NA	NA	NA	NA	NA
CALD1	114213	NA	NA	NA	NA	NA	NA	NA	NA	251.334	-10.429201	uc003vrz.3	chr7:134653097-134655480
CALHM2	612235	696.037	-4.181136	uc001ksa.3	chr10:105206543-105206908	NA	NA	NA	NA	NA	NA	NA	NA
CALM2	114182	1372.97	-9.290608	uc002rvl.2	chr2:47387221-47387914	236.674	-9.952222	uc002rvl.2	chr2:47387221-47387914	NA	NA	NA	NA
CALM3	114182	630.72	-6.470214	uc002pew.3	chr19:47112411-47114039	NA	NA	NA	NA	NA	NA	NA	NA
CAMK1	604998	301.407	-6.98675	uc003bst.3	chr3:9799029-9799222	1239.48	-6.053941	uc003bst.3	chr3:9799031-9799200	NA	NA	NA	NA
CAMK2A	114078	NA	NA	NA	NA	976.369	-9.783965	uc010jhe.2	chr5:149617852-149618050	899.232	-2.988636	uc010jhe.2	chr5:149617852-149618050
CAMK2D	607708	NA	NA	NA	NA	321.463	-5.179688	uc003lby.3	chr4:114372188-114375667	321.046	-9.882362	uc003lby.3	chr4:114372188-114375671
CAMK4	114080	428.792	-4.419144	uc003kpf.3	chr5:110820165-110820748	NA	NA	NA	NA	NA	NA	NA	NA
CAMKK2	615002	NA	NA	NA	NA	668.622	-6.917556	uc001lzu.3	chr12:121675495-121678501	NA	NA	NA	NA
CAMLG	601118	NA	NA	NA	NA	NA	NA	NA	NA	463.124	-4.343469	uc003kzt.3	chr5:134086641-134087850
CAMTA1	611501	NA	NA	NA	NA	321.856	-8.101593	uc001ach.3	chr1:6931826-6932107	NA	NA	NA	NA
CANT1	613165	NA	NA	NA	NA	NA	NA	NA	NA	901.027	-9.066449	uc002lwl.3	chr17:76987798-76989631
CAP1	NA	NA	NA	NA	NA	740.111	-4.140747	uc001cey.4	chr1:40537206-40538321	NA	NA	NA	NA
CAPN7	606400	471.632	-4.712115	uc003bzn.3	chr3:15292768-15294423	NA	NA	NA	NA	NA	NA	NA	NA
CAPN9	606401	279.33	-3.754366	uc001htz.1	chr1:230937343-230937749	NA	NA	NA	NA	251.966	-6.492262	uc001htz.1	chr1:230937343-230937749
CAPN1	114170	321.012	-4.041162	uc002odi.1	chr19:36640728-36641251	NA	NA	NA	NA	NA	NA	NA	NA
CARD18	605354	NA	NA	NA	NA	1051.1	-9.560057	uc021qpy.1	chr11:105008448-105008825	NA	NA	NA	NA
CASC5	609173	NA	NA	NA	NA	NA	NA	NA	NA	412.791	-5.397901	uc010bbs.1	chr15:40954387-40954881
CASP1	147678	276.932	-4.277097	uc021qpt.1	chr11:104986237-104986327	NA	NA	NA	NA	NA	NA	NA	NA
CASP3	606636	944.164	-7.969538	uc003lwh.3	chr4:185548850-185550425	1622.03	-7.457599	uc003lwh.3	chr4:185548850-185550425	NA	NA	NA	NA

Table 1

CASP4	602664	961.837	-7.758603	NA	NA	497.853	-6.779521	uc001plb.1	chr11:104813594-104813700	NA	NA	1037.46	NA	NA	uc002uwp.1	NA	chr2:202151318-202152434
CASP8	601763	NA	NA	NA	NA	344.255	0.185686	uc021vuy.1	chr2:202137383-202137499	NA	NA	526.363	NA	NA	uc001awm.2	NA	chr1:15817324-15820278
CASP9	602234	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CASS4	NA	314.339	-4.990961	uc002exp.2	chr20:55033804-55034396	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CAS1	114090	862.737	-7.60557	uc003kl.3	chr5:96108344-96110385	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CATSPER2	607249	965.187	-10.673052	uc001zsh.3	chr15:43922772-43922898	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CATSPERB	611169	232.812	-3.995125	uc010aub.1	chr14:92047118-92047232	1245.5	-13.032093	uc010aub.1	chr14:92047118-92047232	NA	NA	NA	NA	NA	NA	NA	NA
CATSPERG	613452	NA	NA	NA	NA	1083.31	-5.671908	uc002off.4	chr19:38861433-38861589	NA	NA	633.928	NA	NA	NA	NA	chr7:116199342-116201239
CAV1	601047	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CAV2	601048	NA	NA	NA	NA	845.023	-8.459895	uc003vld.3	chr7:116146176-116148595	NA	NA	NA	NA	NA	NA	NA	NA
CBLB	604491	NA	NA	NA	NA	392.771	-5.672775	uc003dwa.3	chr3:105377109-105377813	787.309	NA	NA	NA	NA	uc003dwa.3	NA	chr3:105377109-105377813
CBL1	606872	NA	NA	NA	NA	520.717	-6.550353	uc003veq.3	chr7:107399624-107402083	NA	NA	NA	NA	NA	NA	NA	NA
CBLN3	612978	NA	NA	NA	NA	208.715	-4.469281	uc001wpg.4	chr14:24895740-24896994	NA	NA	NA	NA	NA	NA	NA	NA
CBR1	114830	502.493	-8.360496	uc010gmx.1	chr21:37443496-37443881	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CBR4	NA	991.57	-10.475706	uc003iny.3	chr4:169908742-169911300	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CBWD1	611078	1371.84	-15.02735	uc011lir.1	chr9:122843-123162	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CBWD2	611079	334.38	-4.951907	uc002jli.2	chr2:114201445-114201594	1407.5	-17.504002	uc002jli.2	chr2:114201445-114201594	NA	NA	NA	NA	NA	NA	NA	NA
CBX3	604477	1242.7	-13.305525	uc003sxl.3	chr7:26251829-26253227	706.802	-6.77192	uc003sxl.3	chr7:26251829-26253227	1769.39	NA	NA	NA	NA	uc003sxl.3	NA	chr7:26251829-26253227
CBX5	604478	549.687	-5.902245	uc001slh.4	chr12:54624731-54635538	NA	NA	NA	NA	NA	NA	261.382	NA	NA	uc001sfh.4	NA	chr12:54624731-54635538
CBX7	608457	231.132	-7.162001	uc003axb.3	chr22:39526779-39529895	1223.73	-6.499796	uc003axb.3	chr22:39526779-39529895	NA	NA	NA	NA	NA	NA	NA	NA
CC2D2A	612013	591.344	-6.806973	uc003gnr.4	chr4:15482837-15483887	NA	NA	NA	NA	275.777	-5.958384	NA	NA	NA	uc003gnr.4	NA	chr4:15482910-15483887
CCBL2	610656	356.236	-8.128401	uc001dmp.2	chr1:89401456-89401865	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC108	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	756.554	NA	NA	uc002vjm.3	NA	chr2:219882978-219883717
CCDC109B	NA	1096.97	-13.146703	uc011cis.2	chr4:110608749-110608872	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC110	609488	NA	NA	NA	NA	861.184	-6.131047	uc011ckl.1	chr4:186378923-186379256	NA	NA	NA	NA	NA	NA	NA	NA
CCDC126	NA	NA	NA	NA	NA	NA	NA	NA	NA	274.292	-5.603029	NA	NA	NA	uc003swl.3	NA	chr7:23682735-23684327
CCDC134	NA	237.073	-8.016744	uc003bbh.1	chr22:42221828-42222303	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC144A	NA	NA	NA	NA	NA	601.397	-8.177433	uc002gmk.1	chr17:16876844-16878311	NA	NA	NA	NA	NA	NA	NA	NA
CCDC144NL	NA	622.537	-4.876265	uc002gyf.3	chr17:20766708-20768727	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC148	NA	854.999	-11.965892	uc002tzi.3	chr2:159027869-159028624	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC150	NA	NA	NA	NA	NA	NA	NA	NA	NA	218.738	-4.855898	NA	NA	NA	uc002lro.1	NA	chr2:197531656-197532658
CCDC152	NA	NA	NA	NA	NA	NA	NA	NA	NA	1009.55	-10.198354	NA	NA	NA	uc003jmx.3	NA	chr5:42799884-42802539
CCDC158	NA	NA	NA	NA	NA	1786.65	-5.53953	uc003hkb.4	chr4:77234192-77234322	NA	NA	NA	NA	NA	NA	NA	NA
CCDC169	NA	1462.49	-3.007245	uc010abm.3	chr13:36804912-36805329	254.548	-5.033115	uc010tqj.2	chr13:36801179-36801337	NA	NA	NA	NA	NA	NA	NA	NA
CCDC174	NA	NA	NA	NA	NA	NA	NA	NA	NA	505.172	-7.032316	NA	NA	NA	uc003byw.3	NA	chr3:14712702-14714166
CCDC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	685.023	-5.496666	NA	NA	NA	uc021rtw.1	NA	chr14:59971785-59971956
CCDC176	NA	NA	NA	NA	NA	NA	NA	NA	NA	292.274	-5.109962	NA	NA	NA	uc010tup.2	NA	chr14:74531403-74532796
CCDC180	NA	1151.18	-9.145948	uc021topx.1	chr1:93744035-93744287	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC180	NA	691.604	-9.070769	uc004axf.3	chr9:100105850-100105925	NA	NA	NA	NA	456.933	-3.535729	NA	NA	NA	uc004axf.3	NA	chr9:100105850-100105925
CCDC184	NA	NA	NA	NA	NA	356.192	-5.175553	uc001lrj.2	chr12:48578491-48579709	NA	NA	NA	NA	NA	NA	NA	NA
CCDC25	NA	NA	NA	NA	NA	NA	NA	NA	NA	295.205	-5.693168	NA	NA	NA	uc003agc.3	NA	chr8:27590833-27593732
CCDC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	279.513	-6.786744	NA	NA	NA	uc001liq.1	NA	chr10:12938625-12940415
CCDC34	612324	1067.64	-12.717417	uc001mnh.1	chr11:27360061-27360367	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC36	NA	NA	NA	NA	NA	282.437	-5.495056	uc003cwl.4	chr3:49282296-49283171	NA	NA	NA	NA	NA	NA	NA	NA
CCDC58	NA	1044.85	-10.599849	uc003eey.3	chr3:122078436-122078715	893.08	-9.078997	uc003eey.3	chr3:122078436-122078715	1201.47	-10.054687	NA	NA	NA	uc003eey.3	NA	chr3:122078436-122078715
CCDC6	601985	NA	NA	NA	NA	NA	NA	NA	NA	314.035	-8.067419	NA	NA	NA	uc001jks.4	NA	chr10:61348506-61552674
CCDC80	NA	787.912	-7.057914	uc001tix.3	chr12:119978521-119978852	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCDC86	NA	246.676	-4.355081	uc003dhw.2	chr3:56603391-56604774	703.694	-11.459369	uc003dhw.2	chr3:56603391-56604774	NA	NA	NA	NA	NA	NA	NA	NA
CCDC7	NA	NA	NA	NA	NA	NA	NA	NA	NA	626.628	-6.763677	NA	NA	NA	uc001lwl.1	NA	chr10:33165322-33165508

Table 1

CDCD70	NA	561.533	-4.113323	uc001vlu.4	chr13:52440217-52440372	NA	NA	NA	NA	NA	NA	532.296	NA	NA	NA	chr11:32701408-32705033
CDCD73	612328	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CDCD80	608298	299.126	-4.394565	uc011bhv.2	chr3:112323409-112324263	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CDCD81	NA	NA	NA	NA	NA	1136.63	-7.257027	uc001pbw.2	chr11:86133758-86134151	961.096	-10.50038	NA	NA	NA	NA	chr11:86133758-86134151
CDCD83	NA	NA	NA	NA	NA	875.871	-8.843158	uc001pbg.1	chr11:85630554-85631051	NA	NA	NA	NA	NA	NA	NA
CDCD88A	609736	327.418	-6.056234	uc002tyl.2	chr2:55514978-55518300	NA	NA	NA	NA	429.525	-7.791389	NA	NA	NA	NA	chr2:555151313-55515491
CDCD88B	611205	NA	NA	NA	NA	259.542	-6.278528	uc001nzz.1	chr11:64117198-64118167	NA	NA	NA	NA	NA	NA	NA
CDCD88C	611204	NA	NA	NA	NA	1646.96	-12.285305	uc001xzl.3	chr14:91737667-91738968	252.176	-8.644124	NA	NA	NA	NA	chr14:91805454-91805617
CDCD89	NA	511.248	-5.961301	uc001pau.1	chr11:85394893-85396048	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CDCD9	NA	NA	NA	NA	NA	1227.24	-20.191221	uc010xym.2	chr19:47774936-47775210	NA	NA	NA	NA	NA	NA	NA
CDCD90B	NA	NA	NA	NA	NA	230.497	-3.818793	uc001pac.3	chr11:82972502-82972952	839.29	-7.592701	NA	NA	NA	NA	chr11:82972502-82972952
CDCD91	NA	496.536	-7.487713	uc001hio.3	chr12:28702107-28703099	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CDCD96	NA	NA	NA	NA	NA	1807.38	-13.194786	uc003gju.2	chr14:7042576-7042997	1627.99	-11.696693	NA	NA	NA	NA	NA
CCK	118440	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL1	182281	1052.02	-11.565785	uc002hid.1	chr17:32687398-32687577	208.144	-3.026875	uc002hid.1	chr17:32687398-32687577	NA	NA	NA	NA	NA	NA	NA
CCL2	158105	422.435	-4.526567	uc002hiv.3	chr17:32583847-32584220	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL20	601960	599.8	-4.820696	uc002vpl.2	chr2:228681800-228682280	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL23	602494	817.293	-9.385681	uc002hks.1	chr17:34340097-34340236	359.509	-6.165506	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL25	602565	NA	NA	NA	NA	405.742	-4.824262	uc002mjc.4	chr19:8127110-8127547	NA	NA	NA	NA	NA	NA	NA
CCL5	187011	711.949	-4.757201	uc002hki.3	chr17:34198496-34199380	NA	NA	NA	NA	1139.2	-8.620127	NA	NA	NA	NA	chr17:34198496-34199380
CCNB1	123836	982.939	-16.626952	uc003ym.3	chr5:68473459-68474070	NA	NA	NA	NA	1273.56	-15.112176	NA	NA	NA	NA	NA
CCNB2	602765	NA	NA	NA	NA	444.652	-4.130216	uc002atfz.3	chr15:59417077-59417244	1507.84	-17.585865	NA	NA	NA	NA	chr15:59417077-59417244
CCNB3	300456	NA	NA	NA	NA	890.205	-11.527604	uc001qmo.3	chr12:4409176-4414522	836.409	-7.285364	NA	NA	NA	NA	chr15:50094703-50094911
CCND2	123833	NA	NA	NA	NA	485.131	-6.916269	uc001zqv.3	chr15:43487040-43489375	NA	NA	NA	NA	NA	NA	chr12:4409176-4414522
CCNDBP1	607089	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCNE1	123837	621.915	-6.999868	uc002insn.3	chr19:30314685-30315215	NA	NA	NA	NA	442.899	-5.757108	NA	NA	NA	NA	chr10:97817999-97820625
CCNF	600227	NA	NA	NA	NA	231.808	-4.33271	uc002cqd.1	chr16:2507022-2508859	NA	NA	NA	NA	NA	NA	NA
CCNG2	603203	NA	NA	NA	NA	1256.31	-6.651738	uc003hmq.4	chr4:78087078-78091213	NA	NA	NA	NA	NA	NA	NA
CCNJ	NA	NA	NA	NA	NA	NA	NA	NA	NA	424.337	-5.603029	NA	NA	NA	NA	chr10:97817999-97820625
CCNJL	NA	NA	NA	NA	NA	753.23	-7.695143	uc001ygi.4	chr14:99977120-99977852	NA	NA	NA	NA	NA	NA	chr5:159678671-159680384
CCNK	603544	NA	NA	NA	NA	NA	NA	NA	NA	408.234	-5.706638	NA	NA	NA	NA	chr3:156865586-156866029
CCNL1	613384	913.927	-5.632346	uc003bce.3	chr3:156865586-156866029	NA	NA	NA	NA	741.912	-9.240699	NA	NA	NA	NA	chr12:490832241-49086815
CCNT1	143055	NA	NA	NA	NA	516.801	-3.647738	uc001rsd.4	chr12:49082241-49086815	618.928	-8.150906	NA	NA	NA	NA	chr2:135712119-135716915
CCNT2	603862	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCNY	612786	NA	NA	NA	NA	1334.86	-7.613279	uc001iyu.4	chr10:35858098-35860847	NA	NA	NA	NA	NA	NA	NA
CCR2	601267	NA	NA	NA	NA	450.802	-11.882534	uc003cpm.4	chr3:46400102-46400868	385.327	-8.607589	NA	NA	NA	NA	NA
CCRN4L	NA	1785.59	-17.03841	uc003lth.1	chr4:139964542-139965034	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:139964542-139965034
CCSER2	NA	1389.61	-9.850715	uc001kdg.1	chr10:86133682-86133761	213.609	-4.956776	uc001svb.1	chr12:69995106-69995357	NA	NA	NA	NA	NA	NA	NA
CTC7	605139	NA	NA	NA	NA	747.607	-9.606266	uc011cmq.2	chr5:10261984-10262313	NA	NA	NA	NA	NA	NA	NA
CTC75	610150	NA	NA	NA	NA	1517.61	-5.779502	uc002szz.3	chr2:73479990-73480150	845.417	-5.525511	NA	NA	NA	NA	chr2:73479990-73480150
CCT7	605140	745.133	-4.375428	uc002szz.3	chr2:73479990-73480150	833.883	-6.34101	uc011aap.2	chr21:30428648-30428795	NA	NA	NA	NA	NA	NA	NA
CCT8	NA	NA	NA	NA	NA	360.678	-5.649508	uc002zlp.1	chr22:17071648-17071766	NA	NA	NA	NA	NA	NA	NA
CCT8L2	NA	NA	NA	NA	NA	926.307	-6.256458	uc003sqy.2	chr7:6862353-6864043	576.764	-8.609823	NA	NA	NA	NA	chr7:6862353-6864043
CCZ1B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CD164	603356	564.233	-10.018052	uc003pid.3	chr6:109687717-109689481	NA	NA	NA	NA	968.03	-6.625238	NA	NA	NA	NA	chr1:158227481-158228058
CD14C	188370	NA	NA	NA	NA	386.733	-8.709097	uc001fru.3	chr1:158263267-158264564	NA	NA	NA	NA	NA	NA	NA
CD1C	188340	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CD1E	188411	1028.9	-15.661571	uc001fry.3	chr1:158326687-158327343	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CD200R1	607546	NA	NA	NA	NA	472.952	-4.355516	uc003daj.1	chr3:112641532-112642523	NA	NA	NA	NA	NA	NA	NA

Table 1

CD200R1L	NA	778.193	-7.301218	uc003dzl.1	chr3:112534556-112534809	538.403	-4.791895	uc003dzl.1	chr3:112534556-112534809	652.152	-4.150229	uc003dzl.1	chr3:112534556-112534809
CD226	605397	NA	NA	NA	NA	1023.86	-8.288795	uc010dqp.3	chr18:67530193-67531549	NA	NA	NA	NA
CD244	605554	NA	NA	NA	NA	727.559	-8.388554	uc001fxa.3	chr1:160799950-160801136	546.605	-4.770657	uc001fxa.3	chr1:160799950-160801136
CD2AP	604241	NA	NA	NA	NA	658.235	-12.190102	uc003oyw.3	chr6:47591964-47594996	665.828	-7.207507	uc003oyw.3	chr6:47591964-47594996
CD2BP2	604470	NA	NA	NA	NA	784.722	-6.793448	uc002dkr.3	chr16:30362087-30364305	NA	NA	NA	NA
CD300LG	610520	NA	NA	NA	NA	559.053	-7.32423	uc010czk.3	chr17:41935197-41935602	NA	NA	NA	NA
CD33	159590	NA	NA	NA	NA	NA	NA	NA	NA	540.17	-6.616247	uc010oes.1	chr19:51739087-51742993
CD36	173510	593.18	-8.780672	uc003uhf.4	chr7:80305700-80308593	NA	NA	NA	NA	1213.82	-13.779237	uc003jhc.3	chr7:80303464-80303734
CD40LG	300386	NA	NA	NA	NA	565.894	-8.009249	uc004faa.3	chrX:135741575-135742549	693.856	-9.392037	uc004faa.3	chrX:135741575-135742549
CD55	125240	NA	NA	NA	NA	1031.64	-5.595792	uc001hfr.4	chr1:207532956-207534311	1172.59	-4.162373	uc001hfr.4	chr1:207532956-207534311
CD56	153420	NA	NA	NA	NA	NA	NA	NA	NA	488.634	-5.017189	uc010owy.2	chr1:117061322-117061848
CD69	107273	417.698	-4.959153	uc010sgu.2	chr12:9906735-9907178	421.463	-5.500072	uc001qwk.3	chr12:9905082-9906076	NA	NA	NA	NA
CD72	107272	NA	NA	NA	NA	331.493	-4.37522	uc010mkl.1	chr9:35609976-35610297	NA	NA	NA	NA
CD79A	112205	NA	NA	NA	NA	NA	NA	NA	NA	911.382	-6.954196	uc002onu.3	chr19:42385048-42385439
CD80	112203	NA	NA	NA	NA	741.198	-5.316169	uc003ecq.3	chr3:119243140-119244596	NA	NA	NA	NA
CD9	143030	NA	NA	NA	NA	NA	NA	NA	NA	219.973	-18.577082	uc011qng.2	chr12:63465995-6347437
CD98L2	300846	623.307	-6.576836	uc004fek.3	chrX:149934809-149937506	NA	NA	NA	NA	NA	NA	NA	NA
CDADC1	NA	NA	NA	NA	NA	NA	NA	NA	NA	637.04	-6.276476	uc001veu.3	chr13:49865894-49867622
CDC123	NA	NA	NA	NA	NA	NA	NA	NA	NA	1351.49	-6.676111	uc009xja.2	chr10:12257853-12258491
CDC14A	603504	507.379	-5.416632	uc001dlg.4	chr1:100983837-100985833	1552.26	-4.079213	uc001dte.4	chr1:100950023-100950926	1626.37	-4.732985	uc009wec.1	chr1:100856495-100856616
CDC16	603461	358.531	-7.053353	uc001vuik.1	chr13:115038039-115038150	NA	NA	NA	NA	786.91	-1.065824	uc010hkm.1	chr13:115007791-115008823
CDC20	603618	NA	NA	NA	NA	651.744	-7.763979	uc001cik.3	chr1:43828801-43828873	672.955	-8.126236	NA	NA
CDC23	603462	631.528	-6.75899	uc003lcm.1	chr5:137541563-137542151	NA	NA	NA	NA	NA	NA	NA	NA
CDC37L1	610346	NA	NA	NA	NA	726.828	-6.142166	uc003zbp.3	chr9:4706113-4706594	1497.94	-15.378742	uc003zbp.3	chr9:4706113-4706594
CDC40	605585	NA	NA	NA	NA	NA	NA	NA	NA	1024.92	-7.272968	uc003pua.3	chr6:110551335-110553422
CDC42SE2	NA	NA	NA	NA	NA	NA	NA	NA	NA	672.539	-8.287405	uc003kvh.3	chr5:130726785-130730360
CDC5L	602868	NA	NA	NA	NA	NA	NA	NA	NA	1213.04	-9.123901	uc003oxl.3	chr6:444144449-44418161
CDC7	603311	NA	NA	NA	NA	NA	NA	NA	NA	479.001	-4.762079	uc001dec.3	chr1:91989993-91991321
CDCA4	612270	NA	NA	NA	NA	500.71	-8.741178	uc001yqa.2	chr14:105475910-105476970	NA	NA	NA	NA
CDCA5	609374	1071.132	-8.199776	uc001ocp.2	chr11:64844927-64846578	NA	NA	NA	NA	NA	NA	NA	NA
CDCATL	609685	NA	NA	NA	NA	743.751	-7.947492	uc003sve.4	chr7:21940517-21941939	NA	NA	NA	NA
CDCP1	611735	545.54	-4.271943	uc003con.3	chr3:45151731-45151956	1376.01	-10.049214	uc003com.3	chr3:45123769-45127129	NA	NA	NA	NA
CDH1	192090	NA	NA	NA	NA	712.676	-8.464332	uc002ewg.1	chr16:68867403-68869444	433.341	-4.362234	uc002ewg.1	chr16:68867403-68869444
CDH13	601364	NA	NA	NA	NA	230.759	-4.014158	uc021tlw.1	chr16:83214475-83214630	259.58	-4.997563	uc010chh.3	chr16:83214565-83214630
CDH17	603017	NA	NA	NA	NA	580.898	-8.462248	uc003ygh.2	chr8:95139394-95140467	NA	NA	NA	NA
CDH18	603019	NA	NA	NA	NA	209.43	-5.49047	uc021xwu.1	chr5:19473155-19473825	1195.72	-12.032067	NA	NA
CDH23	605516	NA	NA	NA	NA	575.193	-0.787664	uc009xql.3	chr10:73377238-73377362	NA	NA	NA	NA
CDH5	601120	NA	NA	NA	NA	690.788	-6.313894	uc002eon.1	chr16:66426291-66426888	NA	NA	NA	NA
CDH6	603007	915.634	-6.143871	uc003jhe.2	chr5:31323416-31329253	NA	NA	NA	NA	269.379	-7.120567	uc003jhd.2	chr5:31318142-31318435
CDH7	605806	1151.49	-11.828811	uc002lka.3	chr18:63530183-63531361	310.473	-7.042182	uc002ljp.3	chr18:63548131-63548175	NA	NA	NA	NA
CDH8	603008	968.8	-6.639862	uc002eog.2	chr16:61685915-61687511	NA	NA	NA	NA	NA	NA	NA	NA
CDK1	116940	726.739	-21.285142	uc010qli.2	chr10:62545558-62547988	1698.74	-19.560287	uc001jht.3	chr10:62553734-62554610	NA	NA	NA	NA
CDK13	603309	NA	NA	NA	NA	493.739	-5.015324	uc003lth.4	chr7:40134580-40136733	NA	NA	NA	NA
CDK17	603440	NA	NA	NA	NA	297.15	-9.131762	uc001tep.2	chr12:96672039-96674019	NA	NA	NA	NA
CDKRAP1	608200	777.293	-14.948345	uc002wzb.1	chr20:31946647-31948114	NA	NA	NA	NA	NA	NA	NA	NA
CDKL3	608459	574.306	-3.568908	uc011cxm.1	chr5:133541305-133541558	452.516	-3.26535	uc011cxm.1	chr5:133541305-133541558	979.568	-10.284501	uc011cxq.2	chr5:133634115-133634401
CDKL4	NA	781.421	-7.327679	uc002rrm.3	chr2:39405688-39406306	NA	NA	NA	NA	580.947	-7.50327	uc002rrm.3	chr2:39405688-39406306
CDKN1A	116899	NA	NA	NA	NA	1718.27	-18.614253	uc021lyzb.1	chr6:36653578-36655116	216.346	-6.173846	uc021lyzb.1	chr6:36653578-36655116
CDKN1B	600778	NA	NA	NA	NA	NA	NA	NA	NA	469.435	-7.506124	uc001rat.2	chr12:12873970-12875305

Table 1

CDKN1C	600856	NA	NA	NA	NA	459.963	-4.006339	uc001lwr.4	chr11:2904448-2905140	458.424	-4.006339	uc001lwr.4	chr11:2904448-2905140
CDKN2AIP	615914	344.867	-6.648004	uc003lvp.1	chr4:184368581-184369049	NA	NA	NA	NA	NA	NA	NA	NA
CDKN2AIPNL	NA	NA	NA	NA	NA	NA	NA	NA	NA	442.417	-9.622014	uc011cxs.2	chr5:133737756-133738605
CDKN2C	603369	NA	NA	NA	NA	NA	NA	NA	NA	410.212	-4.122947	uc001csf.3	chr1:51439943-51440309
CDON	608707	NA	NA	NA	NA	560.794	-8.852866	uc001qdb.4	chr11:125826713-125830836	NA	NA	NA	NA
CDR2	117340	NA	NA	NA	NA	NA	NA	NA	NA	706.237	-6.08278	uc002dkn.3	chr16:22357257-22358285
CDSN	602593	NA	NA	NA	NA	561.92	-7.935349	uc011fzy.2	chr6_dbb_hap3:2380037-2380970	NA	NA	NA	NA
CDV3	NA	NA	NA	NA	NA	387.421	-9.117455	uc003epp.4	chr3:133306019-133309118	NA	NA	NA	NA
CDX1	600746	NA	NA	NA	NA	NA	NA	NA	NA	848.736	-6.745981	uc003lra.3	chr5:149563244-149564121
CEACAM1	109770	NA	NA	NA	NA	633.407	-6.420475	uc002atv.3	chr19:43011458-43013260	901.716	-1.504843	uc002atv.3	chr19:43011458-43013260
CEACAM21	NA	204.249	-5.409518	uc002ore.4	chr19:42092817-42093197	NA	NA	NA	NA	NA	NA	NA	NA
CEACAM4	NA	NA	NA	NA	NA	236.094	-5.175553	uc002orh.1	chr19:42125344-42125702	NA	NA	NA	NA
CEACAM5	114890	234.617	-4.056795	NA	NA	767.203	-4.465697	uc010ahz.1	chr19:42219414-42219789	NA	NA	NA	NA
CEACAM8	615747	NA	NA	NA	NA	758.707	-6.293504	uc002oud.2	chr19:43084395-43085505	NA	NA	NA	NA
CEBPZ	612828	546.142	-11.658577	uc002pz.3	chr2:37428775-37428906	NA	NA	NA	NA	NA	NA	NA	NA
CELA3B	NA	NA	NA	NA	NA	307.151	-4.98961	uc001blk.3	chr1:22315773-22315847	NA	NA	NA	NA
CELF5	612680	775.281	-7.753551	uc002kl.2	chr19:3293333-3297073	NA	NA	NA	NA	648.143	-5.757253	uc002kl.2	chr19:3293333-3297073
CELSR2	604265	NA	NA	NA	NA	344.952	-6.449887	uc001dxa.4	chr1:109816672-109818378	NA	NA	NA	NA
CENPC	117141	NA	NA	NA	NA	640.978	-6.406897	uc003hdd.1	chr4:68337989-68338322	413.617	-8.771709	uc003hdd.1	chr4:68337989-68338322
CENPE	117143	414.884	-4.519712	uc003hxb.1	chr4:104026963-104027378	NA	NA	NA	NA	731.896	-6.120114	uc003hxb.1	chr4:104026963-104027378
CENPH	605607	NA	NA	NA	NA	1471.61	-12.70313	uc003jvp.3	chr5:68505627-68506184	NA	NA	NA	NA
CENPO	611506	NA	NA	NA	NA	323.6	-9.566223	uc003ozh.1	chr6:49459989-49460820	NA	NA	NA	NA
CENPV	608139	570.276	-7.504018	uc002gpw.3	chr17:16245848-16246130	NA	NA	NA	NA	NA	NA	NA	NA
CENPW	611264	NA	NA	NA	NA	NA	NA	NA	NA	1070.06	-9.372888	uc003qao.3	chr6:126669639-126669754
CEP120	613446	NA	NA	NA	NA	1543.12	-14.611696	uc003klk.3	chr5:122680579-122682212	NA	NA	NA	NA
CEP135	611423	400.241	-4.242707	uc010lgz.1	chr4:56832053-56832746	NA	NA	NA	NA	NA	NA	NA	NA
CEP152	613529	1317.79	-11.427382	uc001zxa.2	chr15:49033345-49033783	NA	NA	NA	NA	NA	NA	NA	NA
CEP162	610201	NA	NA	NA	NA	521.028	-4.634588	uc003pki.4	chr6:84833960-84834788	NA	NA	NA	NA
CEP164	614848	350.97	-4.852798	uc001prg.1	chr11:117280846-117281417	NA	NA	NA	NA	NA	NA	NA	NA
CEP170	613023	1270.69	-7.950231	uc021pls.1	chr1:243374515-243375032	NA	NA	NA	NA	NA	NA	NA	NA
CEP290	610142	498.579	-7.830195	uc001laq.3	chr12:88442790-88442960	NA	NA	NA	NA	NA	NA	NA	NA
CEP44	NA	608.935	-12.850309	uc003lir.3	chr4:175238535-175241482	1857.28	-5.245797	uc003lir.3	chr4:175238535-175241482	250.357	-5.795954	uc010lro.2	chr4:175252747-175254531
CEP55	610000	NA	NA	NA	NA	606.546	-8.696259	uc009kug.3	chr10:95287911-95288849	NA	NA	NA	NA
CEP57	607951	NA	NA	NA	NA	445.18	-4.485099	uc001plo.2	chr11:95555149-955556379	NA	NA	NA	NA
CEP57L1	NA	409.887	-5.972452	uc003psx.4	chr6:109483953-109485115	NA	NA	NA	NA	NA	NA	NA	NA
CEP63	614724	639.376	-9.657021	uc003aeq.1	chr3:134280378-134283870	861.192	-2.406554	uc003aeq.3	chr3:134293734-134293855	NA	NA	NA	NA
CEP70	614310	NA	NA	NA	NA	1567.14	-5.86213	uc003esi.3	chr3:138213187-138213856	NA	NA	NA	NA
CEP72	616475	NA	NA	NA	NA	993.094	-8.442764	uc003jlr.3	chr5:653269-653666	NA	NA	NA	NA
CEP78	NA	823.232	-5.211948	uc011lsp.1	chr9:80863834-80865369	460.016	-5.354181	uc004aky.4	chr9:80881679-80881983	NA	NA	NA	NA
CEP83	615847	866.274	-8.158815	uc001tdd.3	chr12:94702056-94702588	NA	NA	NA	NA	203.578	-1.861905	uc001tdd.3	chr12:94702056-94702588
CEP89	615470	498.939	-8.452835	uc002nua.3	chr19:33422133-33422292	NA	NA	NA	NA	NA	NA	NA	NA
CEP97	615864	519.491	-6.749008	uc003dvk.1	chr3:101484396-101486181	NA	NA	NA	NA	NA	NA	NA	NA
CERS3	615276	NA	NA	NA	NA	423.489	-4.174426	uc002bvz.3	chr15:100940600-100942917	NA	NA	NA	NA
CES1P1	NA	NA	NA	NA	NA	245.243	-6.071173	uc002eik.3	chr16:55807487-55808826	906.605	-8.752191	uc002eik.3	chr16:55807487-55808826
CES5A	NA	NA	NA	NA	NA	736.716	-5.814373	uc002elo.2	chr16:55880066-55880362	953.872	-8.866658	uc002elo.2	chr16:55880066-55880362
CETN1	603187	NA	NA	NA	NA	973.356	-9.016836	uc002kko.1	chr18:580928-581524	NA	NA	NA	NA
CETN2	300006	530.907	-4.054336	uc004fga.3	chrX:151995871-151996384	507.036	-6.482968	uc004fga.3	chrX:151995871-151996384	NA	NA	NA	NA
CETN3	602907	923.371	-12.426121	uc003kp.3	chr5:89689529-89689880	NA	NA	NA	NA	NA	NA	NA	NA
CFAP20	NA	NA	NA	NA	NA	1961.08	-16.308774	uc002emb.1	chr16:58147497-58147928	NA	NA	NA	NA

Table 1

CFAP43	NA	646.88	-8.260514	uc009xxq.3	chr10:105889646-105889896	1455.09	-9.327977	uc009xxq.3	chr10:105889646-105889896	528.11	-5.490174	uc009xxq.3	chr10:105889646-105889896
CFAP44	NA	NA	NA	NA	NA	349.138	-8.93029	uc010hql.2	chr3:113005777-113010403	813.92	-8.334461	uc010hql.2	chr3:113005777-113010403
CFAP45	605152	NA	NA	NA	NA	306.878	-2.830685	uc001fui.3	chr1:159842154-159842274	NA	NA	NA	NA
CFAP47	NA	1148.55	-6.189839	uc004ddk.1	chrX:36162927-36163187	215.568	-3.607941	uc004ddk.1	chrX:36162927-36163187	NA	NA	NA	NA
CFAP53	614759	1683.34	-11.128728	uc002lee.2	chr18:47753563-47753750	1550.93	-17.353677	uc002lee.2	chr18:47753563-47753750	NA	NA	NA	NA
CFAP61	NA	NA	NA	NA	NA	691.894	-9.128699	uc002wru.3	chr20:20341055-20341346	NA	NA	NA	NA
CFAP70	NA	272.509	-3.873459	uc009xrd.1	chr10:75053021-75056781	NA	NA	NA	NA	458.263	-5.253225	uc001tv.4	chr10:75013516-75013732
CFAP97	616047	1257.04	-9.015977	uc003kpg.3	chr4:186090180-186091452	NA	NA	NA	NA	988.725	-9.591056	uc003xvf.4	chr4:186080819-186083951
CFH1	134370	NA	NA	NA	NA	1419.08	-19.118384	uc001gjf.4	chr1:196716444-196716634	930.267	-9.491429	uc001gjt.4	chr1:196716444-196716634
CFHR1	134371	NA	NA	NA	NA	254.801	-10.917978	uc001gim.3	chr1:196801130-196801319	1419.92	-15.580586	uc001gim.3	chr1:196801130-196801319
CFHR2	600889	NA	NA	NA	NA	NA	NA	NA	NA	2031.6	-20.389126	uc001gta.1	chr1:196928211-196928356
CFHR3	605336	313.428	-9.7788	uc001glt.3	chr1:19675961-196759152	NA	NA	NA	NA	NA	NA	NA	NA
CFHR5	608593	845.421	-10.595342	uc001gls.4	chr1:196977814-196978803	781.599	-9.32009	uc001gls.4	chr1:196977814-196978803	NA	NA	NA	NA
CFI1	217030	NA	NA	NA	NA	1020.25	-12.326294	uc003hzz.3	chr4:110661848-110662048	NA	NA	NA	NA
CFP1	300383	NA	NA	NA	NA	NA	NA	NA	NA	201.186	-6.706005	uc004dlg.4	chrX:47483612-47483673
CGA1	118850	NA	NA	NA	NA	NA	NA	NA	NA	982.272	-5.610066	uc003plj.2	chr6:87795216-87795473
CGGBP1	603363	1539.59	-12.990028	uc003dqs.3	chr3:88101100-88104622	554.243	-9.118596	uc002rkk.1	chr2:54001663-54002287	NA	NA	NA	NA
CHAC2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CHCHD4	611077	NA	NA	NA	NA	NA	NA	NA	NA	1029.72	-13.224546	uc003byl.4	chr3:14153577-14154386
CHD1	602118	NA	NA	NA	NA	NA	NA	NA	NA	887.816	-6.179804	uc010bn.3	chr5:98190908-98192083
CHD2	602119	613.999	-1.558496	uc002bsn.3	chr15:93492311-93492463	648	-1.123285	uc002bsm.2	chr15:93486366-93488095	NA	NA	NA	NA
CHD6	616114	708.649	-11.616953	uc002xjp.1	chr20:40031170-40033232	1242.95	-14.036454	uc002xkb.1	chr20:40064665-40065865	NA	NA	NA	NA
CHD8	610528	NA	NA	NA	NA	NA	NA	NA	NA	386.421	-5.409259	uc001war.2	chr14:21853353-21853771
CHEK2	604373	1503.82	-9.546017	uc003ads.1	chr22:29083731-29083884	NA	NA	NA	NA	NA	NA	NA	NA
CHGB	118920	NA	NA	NA	NA	NA	NA	NA	NA	215.73	-4.895349	uc002wmg.3	chr20:5905696-5906005
CHIC2	604332	NA	NA	NA	NA	1502.2	-15.369036	uc003haj.2	chr4:54875958-54876261	741.821	-7.162204	uc003haj.2	chr4:54875958-54876261
CHKA	118491	NA	NA	NA	NA	NA	NA	NA	NA	454.913	-5.439775	uc001onj.3	chr11:67820326-67821454
CHMP2B	609512	895.543	-11.330334	uc003dqp.4	chr3:87302973-87304698	NA	NA	NA	NA	572.065	-8.501789	uc003dqp.4	chr3:87302973-87304698
CHMP4A	610051	NA	NA	NA	NA	565.933	-5.353179	uc001wni.3	chr14:24678787-24679082	NA	NA	NA	NA
CHMP6	610901	342.1	-4.990321	uc002jyw.4	chr17:78972954-78973933	NA	NA	NA	NA	NA	NA	NA	NA
CHMP7	611130	698.856	-8.565907	uc003xdc.2	chr8:23118113-23119512	NA	NA	NA	NA	NA	NA	NA	NA
CHODL	607247	NA	NA	NA	NA	919.532	-10.61904	uc002ykr.3	chr21:19638356-19639687	NA	NA	NA	NA
CHORDC1	604353	NA	NA	NA	NA	NA	NA	NA	NA	231.139	-11.746528	uc001pdg.2	chr11:89933597-89935572
CHPT1	NA	318.195	-4.62131	uc001lip.1	chr12:102102024-102123424	936.498	-10.341375	uc001tim.3	chr12:102122724-102122846	710.395	-1.828518	uc001tin.3	chr12:102122724-102122846
CHRD12	613127	588.828	-6.879416	NA	NA	617.653	-6.879416	uc001ovg.3	chr11:74407474-74407553	617.335	-12.403018	uc001owh.3	chr11:74407474-74407542
CHRM3	118494	431.187	-6.899372	uc001hyp.3	chr1:240072525-240072717	NA	NA	NA	NA	NA	NA	NA	NA
CHRM5	118496	632.539	-8.422437	uc001zhk.1	chr15:34356518-34357287	NA	NA	NA	NA	NA	NA	NA	NA
CHRNA	100730	355.101	-9.41261	uc010ydl.3	chr2:233406244-233406592	NA	NA	NA	NA	NA	NA	NA	NA
CHST11	610128	NA	NA	NA	NA	957.582	-14.80168	uc001iky.3	chr12:105151582-105155792	NA	NA	NA	NA
CHST12	610129	NA	NA	NA	NA	NA	NA	NA	NA	1264.8	-5.855737	uc003smc.3	chr7:2473520-2474216
CHST8	610190	NA	NA	NA	NA	NA	NA	NA	NA	461.506	-5.143917	uc002nus.4	chr19:34263969-34264414
CHSY1	608183	204.234	-5.671791	uc010usd.2	chr15:101715928-101717592	NA	NA	NA	NA	1552.64	-10.659597	uc010usd.2	chr15:101715928-101717592
CHSY3	609863	1627.88	-20.267391	uc003kvd.3	chr5:129521485-129522327	NA	NA	NA	NA	NA	NA	NA	NA
CHTF8	613202	NA	NA	NA	NA	NA	NA	NA	NA	646.261	-6.058024	uc002ewo.2	chr16:69151912-69152756
CHTOP1	614206	NA	NA	NA	NA	223.989	-5.118764	uc009woj.2	chr1:153614926-153615872	NA	NA	NA	NA
CHURC1	608577	980.505	-10.700957	uc001xhw.2	chr14:65398949-65402084	NA	NA	NA	NA	1806.37	-29.380444	uc001xhw.2	chr14:65398949-65402084
CIAPIN1	608943	279.202	-4.548486	uc002ell.1	chr16:57462087-57463081	NA	NA	NA	NA	NA	NA	NA	NA
CIDEA	604440	NA	NA	NA	NA	658.294	-5.459286	uc002kqt.4	chr18:12272720-12277594	NA	NA	NA	NA
CILP1	603489	674.424	-6.782484	uc002aon.2	chr15:65488337-65489068	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

	CIPC:	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr14:77580662-77583629	
	CIR1:	605228	564625	-6.230108	uc002um.3	chr2:175212878-175213224	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CIRH1A:	NA	528 044	-8.323079	uc002ewr.2	chr16:69199475-69201745	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CISD2:	611509	NA	NA	NA	NA	NA	NA	609 294	-6.412487	uc003hwf.4	chr4:103808588-103813963	731.843	-14.229902	uc003hwf.4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:103808588-103813963
	CKAP2:	611569	NA	NA	NA	NA	NA	NA	911.074	-9.427165	uc001vgu.2	chr13:53049277-53050763	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CKLF:	616074	NA	NA	NA	NA	NA	NA	1996.04	-19.48529	uc002eol.3	chr16:66599915-66600190	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CKMT1B:	123290	NA	NA	NA	NA	NA	NA	665.823	-11.567842	uc01oudv.1	chr15:43889595-43890525	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CKS1B:	118900	NA	NA	NA	NA	NA	NA	523.057	-4.766854	uc001fgb.3	chr11:154951254-154951725	1182.07	-11.469886	uc001fgb.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr1:154951254-154951725	
	CKS2:	118901	526624	-10.127995	uc004aqh.3	chr9:91931341-91931618	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLASP1:	605852	1207.02	-10.223343	uc002lmf.3	chr2:122121706-122122627	828 264	-6.22512	uc002lmy.3	chr2:122098352-122098436	297 035	-3.982861	uc002lmg.1	chr2:122159085-122159198	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr2:122159085-122159198	
	CLASP2:	605853	513.861	-5.111101	uc003cfr.3	chr3:33643935-33644028	932 203	-11.040496	uc003cfs.3	chr3:335537739-335540122	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr1:86965729-86965974	
	CLCA:	603906	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLCN3:	600580	855.927	-1.593137	uc003ish.3	chr4:170641217-170644338	457 453	-4.264037	uc003ish.3	chr4:170641217-170644338	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLDN11:	601326	601.321	-0.968871	uc003igx.3	chr3:170150545-170152479	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr3:170577772-170578169	
	CLDN14:	605608	NA	NA	NA	NA	871.309	-8.593999	uc002yvl.1	chr21:37832920-37833273	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLDN22:	NA	650.25	-7.216864	uc010lsa.1	chr4:184239220-184240708	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLDN6:	615798	NA	NA	NA	NA	1394.76	-8.594202	uc002csu.4	chr16:3064713-3065359	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLDN7:	609131	NA	NA	NA	NA	579.84	-4.062675	uc002gfm.4	chr17:7163222-7163692	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLDN8:	611231	NA	NA	NA	NA	333.26	-6.844158	uc002ynu.2	chr21:31586324-31587565	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLDN1:	NA	488 627	-11.309752	uc003dso.2	chr3:98225321-98225577	933 307	-8.992724	uc003dsp.3	chr3:98234317-98235502	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLEC18B:	616572	1126.38	-5.070206	uc010vnu.1	chr16:74444434-74445938	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLEC4A:	605306	NA	NA	NA	NA	1137.73	-5.702827	uc001qlz.1	chr12:8290884-8291203	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLEC4D:	609964	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLEC6A:	613579	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLEC9A:	612252	371.832	-4.45596	uc001qxa.3	chr12:10218232-10218565	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr12:8673868-8674960	
	CLEC1:	607467	NA	NA	NA	NA	523.918	-4.53937	uc001qwj.3	chr12:9875089-9875221	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr12:8630061-8630926	
	CLIC2:	300138	NA	NA	NA	NA	1015.41	-8.940642	uc004fnf.3	chrX:154505500-154507191	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr12:10218232-10218565	
	CLIC6:	615321	704.263	-6.093815	uc002yuf.1	chr21:36088781-36090519	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr21:36088781-36090519	
	CLK1:	601951	NA	NA	NA	NA	272.411	-4.995621	uc010zhi.1	chr2:201717732-201718028	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLK2:	602989	NA	NA	NA	NA	1472.71	-6.687955	uc001fjw.3	chr1:155232659-155233008	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLK2P1:	NA	NA	NA	NA	NA	673.943	-7.276272	uc003swk.2	chr7:23624335-23624680	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLK3:	602990	377.082	-2.79134	uc010ulm.1	chr15:74912803-74914557	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLK4:	607969	338.586	-11.463417	uc003njf.1	chr5:178029665-178030617	1780.39	-6.703617	uc011dgg.1	chr5:178029665-178030758	522.819	-9.184256	uc003mjf.1	chr5:178029665-178030617	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLMN:	611121	832.831	-6.091105	uc001yef.2	chr14:95648276-95657900	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLMP:	611693	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLN5:	608102	1330.34	-7.615349	uc001vkc.3	chr13:77575105-77576652	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLNK:	611434	NA	NA	NA	NA	970.555	-0.15257	uc003gmo.4	chr4:10491838-10492090	1596.82	-9.065956	uc003gmo.4	chr4:10491838-10492090	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLPB:	616254	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLRN1:	606397	247.397	-4.792627	uc003eyk.1	chr3:150644354-150645722	312.126	-5.109962	uc003eyj.3	chr3:150643950-150644638	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CLRN3:	NA	838.318	-11.115052	uc001ljl.1	chr10:129676114-129676412	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr1:47842418-47844511	
	CLTA:	118960	840.252	-10.553577	uc0003zc.3	chr8:36211772-36212059	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr3:99897233-99897476	
	CMC2:	NA	837.407	-9.294135	uc002flu.3	chr16:81009699-81009989	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr16:66622023-66622177	
	CMPK1:	191710	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
	CMSS1:	NA	408.802	-10.612987	uc003dhl.3	chr3:99897233-99897476	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr3:99897233-99897476	
	CMTM2:	607885	1074.81	-8.795019	uc002ept.3	chr16:66622023-66622177	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr16:66622023-66622177	
	CMTR2:	616190	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr16:71316203-71317510	
	CNGA1:	123825	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:47937994-47938437	
	CNHI1:	611287	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA							

Table 1

CNN2	602373	NA	NA	NA	1220.56	-5.652832	uc002lqu.3	chr19:1037900-1039064	NA	NA	NA	NA	NA
CNN3	602374	1331.88	-10.230977	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CNOT4	604911	NA	NA	NA	981.966	-6.820699	uc003vsu.2	chr7:135071822-135073545	NA	NA	NA	NA	NA
CNOT6	NA	716.164	-5.268188	NA	817.353	-3.320933	uc011ccd.2	chr4:78634541-78641584	NA	NA	NA	NA	NA
CNOT7	604913	728.762	-8.410521	uc003wxh.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
CNP	123830	605.309	-7.074092	uc002hyl.1	NA	NA	NA	NA	1149.9	-11.263273	uc002hyl.1	chr17:40125943-40129754	NA
CNPY1	612493	NA	NA	NA	661.797	-7.525995	uc003wmc.1	chr7:155293953-155295762	NA	NA	NA	NA	NA
CNPY2	605861	611.272	-6.703869	uc001sku.2	NA	NA	NA	NA	584.411	-5.446144	uc001sku.2	chr12:56704213-56704335	NA
CNRP1	NA	993.001	-4.732762	uc002sej.4	NA	NA	NA	NA	652.619	-1.407842	uc002sej.4	chr2:68511303-68511559	NA
CNTD2	NA	NA	NA	NA	356.694	-5.216751	uc010xvi.2	chr19:40728115-40728958	NA	NA	NA	NA	NA
CNTF	118945	412.908	-6.153975	uc001nna.4	NA	NA	NA	NA	NA	NA	NA	NA	NA
CNTLN	611870	309.08	-3.555114	uc003zmx.4	NA	NA	NA	NA	232.65	-4.658954	uc003zmx.2	chr9:17166979-17167372	NA
CNTN3	601325	NA	NA	NA	483.329	-6.549115	uc003dpm.1	chr3:74311722-74313551	1875.87	-9.812783	uc003dpm.1	chr3:74311722-74313551	NA
CNTN4	607280	NA	NA	NA	402.166	-3.441979	uc003bpc.3	chr3:3097905-3099645	572.286	-4.554289	uc003bpd.1	chr3:3079021-3079360	NA
CNTN5	607219	NA	NA	NA	1088.47	-13.388474	uc009yvw.2	chr11:100095571-100096179	NA	NA	NA	NA	NA
CNTN6	607220	NA	NA	NA	1410.95	-18.775715	uc010hbo.2	chr3:1339680-1340053	872.121	-6.819105	uc010hbo.2	chr3:1339680-1340053	NA
CNTRL	605496	217.914	-10.875735	uc004bkc.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
CNTRQB	611425	858.771	-4.193113	uc002gjp.3	NA	NA	NA	NA	739.639	-11.600749	uc002gjp.3	chr17:7852829-7853237	NA
COA5	613920	NA	NA	NA	NA	NA	NA	NA	672.932	-6.641836	uc002zyz.3	chr2:99215786-99217214	NA
COBL1	610318	NA	NA	NA	NA	NA	NA	NA	613.584	-7.645332	uc002ucn.3	chr2:165541258-165542455	NA
COG4	606976	NA	NA	NA	429.383	-4.548676	uc002ezc.3	chr16:70514472-70514912	NA	NA	NA	NA	NA
COL12A1	120320	NA	NA	NA	NA	NA	NA	NA	252.315	-5.513544	uc021zbv.1	chr6:75794042-75796262	NA
COL13A1	120350	NA	NA	NA	NA	NA	NA	NA	1033.2	-13.771831	uc001gjk.2	chr10:71718458-71718904	NA
COL19A1	120165	1227.28	-8.390266	uc003pic.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
COL21A1	610002	NA	NA	NA	NA	NA	NA	NA	814.409	-5.710016	uc003pcr.3	chr6:555921388-55922454	NA
COL23A1	610043	NA	NA	NA	NA	NA	NA	NA	754.306	-9.498056	uc010jkt.2	chr5:177664617-177665698	NA
COL3A1	120180	505.905	-6.246893	uc002uql.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
COL4A1	120130	NA	NA	NA	NA	NA	NA	NA	1207.74	-8.722427	uc001vqw.4	chr13:110801310-110802709	NA
COL4A2	120090	NA	NA	NA	NA	NA	NA	NA	1152.19	-9.710903	uc001vqx.3	chr13:111164539-111165373	NA
COL4A3	120070	NA	NA	NA	NA	NA	NA	NA	573.829	-6.356593	uc002vom.2	chr2:228176587-228179508	NA
COL4A3BP	604677	NA	NA	NA	NA	NA	NA	NA	660.308	-7.147229	uc003kds.3	chr5:74666928-74670016	NA
COL6A3	120250	699.003	-6.884633	uc002vwj.2	NA	NA	NA	NA	NA	NA	NA	NA	NA
COLLEC10	607620	592.596	-6.445321	uc003yoc.3	240.672	-3.155209	uc003yoc.3	chr8:120118431-120119202	859.994	-15.435508	uc003yoc.3	chr8:120118431-120119202	NA
COLGAL12	NA	1245.74	-7.712518	uc010poj.1	725.039	-8.476284	uc001gqp.3	chr1:183904986-183907894	520.677	-6.2762	uc010poj.1	chr1:183898796-183899362	NA
COMMD10	NA	NA	NA	NA	NA	NA	NA	NA	627.314	-7.430117	uc003krt.1	chr5:115628187-115628978	NA
COMMD6	612377	294.866	-7.309197	uc001vjp.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
COMMD8	616656	NA	NA	NA	NA	NA	NA	NA	797.599	-6.784494	uc003gxi.3	chr4:47452811-47453661	NA
COPB2	606990	910.078	-5.81851	uc003elig.3	NA	NA	NA	NA	541.645	-6.795238	uc011bmw.2	chr3:139076433-139076704	NA
COPB4	616008	NA	NA	NA	949.115	-10.491934	uc003hca.3	chr4:83996584-83996971	NA	NA	NA	NA	NA
COP58	616011	770.974	-8.785368	uc002vwg.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
COQ10B	NA	NA	NA	NA	617.721	-5.95853	uc002uuh.1	chr2:198338649-198339851	1357.3	-8.998711	uc002uuh.1	chr2:198338649-198339851	NA
COQ2	609825	NA	NA	NA	NA	NA	NA	NA	511.471	-5.290866	uc003hog.3	chr4:84184977-84185351	NA
COQ3	605196	NA	NA	NA	1001.08	-9.764987	uc003ppk.3	chr6:99817348-99817475	NA	NA	NA	NA	NA
COQ4	612898	NA	NA	NA	623.322	-7.940053	uc004bur.4	chr9:131095925-131096351	NA	NA	NA	NA	NA
CORIN	605236	NA	NA	NA	1500.88	-13.674753	uc011bzi.1	chr4:47663505-47663722	399.012	-4.708516	uc011bzf.2	chr4:47596018-47597737	NA
CORO2A	602159	NA	NA	NA	NA	NA	NA	NA	472.595	-4.362155	uc004ayk.3	chr9:100883257-100887055	NA
COX10	602125	NA	NA	NA	464.417	-8.741827	uc002gpf.4	chr17:14110531-14111996	NA	NA	NA	NA	NA
COX16	NA	NA	NA	NA	684.056	-6.092115	uc001xmb.3	chr14:70791798-70793049	980.197	-12.301669	uc001xmb.3	chr14:70791798-70793049	NA
COX7A2	123996	663.645	-8.130103	uc003phv.2	NA	NA	NA	NA	720.478	-5.458301	uc003phv.2	chr6:75947391-75947645	NA

Table 1

COXA2L	605771	204.652	-3.172767	uc002rsk.3	chr2:42577645-42578358	451.902	-4.477337	uc002rsk.3	chr2:42577645-42578358	NA	NA	NA	NA	NA	NA	NA
COXB2	609811	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:46736847-46736963
COXB6	NA	479.981	-4.487595	uc001ybl.1	chr14:93814467-93814700	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CP	117700	933.168	-11.689376	uc010hvf.1	chr3:148903853-148904292	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	606688	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr7:129916651-129916872
CPA2	609562	NA	NA	NA	NA	610.485	-6.142054	uc003xxs.2	chr8:6898517-68985992	NA	NA	NA	NA	NA	NA	NA
CPAMD8	608841	NA	NA	NA	NA	285.801	-5.810792	uc002nfb.3	chr19:17003762-17003918	NA	NA	NA	NA	NA	NA	NA
CPB1	114852	1700.2	-7.647771	uc003ewl.3	chr3:148577790-148577972	NA	NA	NA	NA	773.145	-5.710244	NA	NA	NA	NA	chr3:148577790-148577972
	603107	NA	NA	NA	NA	NA	NA	NA	NA	1102.1	-8.555592	uc001vaw.3	NA	NA	NA	chr13:46627322-46627748
CPB2	610607	1066.84	-7.175414	uc010lju.2	chr5:173980309-173983823	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CPB4	605033	1018.77	-9.117283	uc003nde.1	chr5:175307049-175311023	1057.86	-6.538364	uc003nde.1	chr5:175307049-175311023	NA	NA	NA	NA	NA	NA	NA
CPLX2	609585	359.715	-4.523019	uc002ayu.1	chr15:75122696-75124136	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CPN1	603103	695.242	-5.603875	uc001kql.2	chr10:101802065-101802183	1087.25	-8.433296	NA	NA	514.886	-8.522531	NA	NA	NA	NA	NA
CPNE1	604205	NA	NA	NA	NA	337.875	-5.872445	uc010zvj.2	chr20:34213953-34214162	NA	NA	NA	NA	NA	NA	NA
CPNE2	604206	606.873	-11.461281	uc002ekl.1	chr16:57180288-57181876	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CPNE3	604207	NA	NA	NA	NA	NA	NA	NA	NA	495.839	-5.717069	uc003ydv.2	NA	NA	NA	chr8:87570639-87573726
CPNE4	604208	661.101	-9.8835	uc003eoj.3	chr3:131253577-131254038	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CPPED1	615603	NA	NA	NA	NA	805.524	-6.456126	uc002dca.4	chr16:12753656-12758742	803.495	-6.259272	uc002dca.4	NA	NA	NA	chr16:12753656-12758742
CPSE2	606028	NA	NA	NA	NA	816.076	-6.059901	uc001yeh.2	chr14:92628089-92630543	NA	NA	NA	NA	NA	NA	NA
CPSE7	NA	365.409	-5.908002	uc009ynp.2	chr11:61188420-61188801	NA	NA	NA	NA	655.151	-5.175258	uc001nnp.3	NA	NA	NA	chr11:61170120-61172176
CPT1B	601987	NA	NA	NA	NA	NA	NA	NA	NA	539.136	-5.397706	uc003bmk.4	NA	NA	NA	chr22:51007290-51007510
CPTP	615467	794.599	-4.845648	uc001aao.3	chr1:1263144-1264276	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CPZ	603105	NA	NA	NA	NA	483.271	-5.143917	uc003glm.3	chr4:8621345-8621488	NA	NA	NA	NA	NA	NA	NA
	180230	NA	NA	NA	NA	NA	NA	NA	NA	574.611	-7.26967	uc002bdp.2	NA	NA	NA	chr15:78640320-78640572
CRABP1	614178	NA	NA	NA	NA	NA	NA	NA	NA	559.554	-7.427761	uc001qmj.2	NA	NA	NA	chr12:3757109-3757637
CRACR2A	606121	NA	NA	NA	NA	1448.07	-13.092824	uc003lus.3	chr7:65617345-65619553	NA	NA	NA	NA	NA	NA	NA
CREB3L2	608834	NA	NA	NA	NA	NA	NA	NA	NA	630.499	-4.112428	uc003rvv.3	NA	NA	NA	chr7:137559725-137565221
CREB5	NA	291.513	-4.944841	uc011jzr.2	chr7:28763989-28764776	221.677	-3.09101	uc003szo.3	chr7:28858897-28865511	NA	NA	NA	NA	NA	NA	NA
CREBRF	NA	1746.71	-7.57385	uc003mcf.3	chr5:172518437-172519333	586.759	-11.842591	uc003mch.3	chr5:172560749-172566291	NA	NA	NA	NA	NA	NA	NA
CREM	123812	1206	-6.923832	uc001hcz.3	chr10:35500327-35501886	NA	NA	NA	NA	569.903	-3.870552	uc001ivx.3	NA	NA	NA	chr10:35500732-35501886
CRHBP1	122559	657.115	-7.318598	uc010hcz.3	chr5:76254739-76254847	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CRIPAK	610203	NA	NA	NA	NA	NA	NA	NA	NA	316.176	-5.505275	uc003gdf.2	NA	NA	NA	chr4:1389641-1389782
CRISP1	601193	NA	NA	NA	NA	1209.89	-6.382111	uc003ozw.2	chr6:49801979-49803028	639.41	-5.673029	uc003ozw.2	NA	NA	NA	chr6:49801979-49803028
CRISP1D2	612434	1581.68	-8.004311	uc002fik.4	chr16:84872582-84873626	807.304	-7.970899	uc002fik.4	chr16:84872582-84873626	939.721	-8.472077	uc002fik.2	NA	NA	NA	chr16:84879515-84879756
CRK	164762	NA	NA	NA	NA	787.286	-6.122336	uc002zsl.3	chr17:1324647-1328806	NA	NA	NA	NA	NA	NA	NA
CRKL	602007	303.225	-5.60498	uc002ztl.2	chr22:21304134-21308037	279.288	-7.858606	uc002ztl.2	chr22:21304134-21308037	308.904	-3.22987	uc002ztl.2	NA	NA	NA	chr22:21304134-21308037
CRLF3	614853	541.032	-4.731745	uc002hfr.4	chr17:29109702-29111204	377.806	-5.024132	uc002hfr.4	chr17:29109702-29111204	241.072	-5.666301	uc002hfr.4	NA	NA	NA	chr17:29109702-29111204
CRLS1	608188	NA	NA	NA	NA	271.302	-5.713495	uc002wmm.4	chr20:6017805-6020697	NA	NA	NA	NA	NA	NA	NA
CRNKL1	610952	353.89	-8.035045	uc002wrs.3	chr20:20015012-20016838	919.675	-9.479613	uc002wrs.3	chr20:20015012-20016838	NA	NA	NA	NA	NA	NA	NA
CRNN	611312	NA	NA	NA	NA	NA	NA	NA	NA	509.282	-6.42302	uc001exx.2	NA	NA	NA	chr1:152381719-152382069
CRTPAP	605497	NA	NA	NA	NA	NA	NA	NA	NA	373.917	-5.428603	uc003cfl.4	NA	NA	NA	chr3:33183941-33189265
CRYAA	123580	NA	NA	NA	NA	NA	NA	NA	NA	546.94	-5.948126	uc002zdd.1	NA	NA	NA	chr21:44592391-44592913
CRYBA4	123631	710.618	-5.94855	uc003aciz.4	chr22:27026452-27026636	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CRYGS	123730	NA	NA	NA	NA	920.699	-4.507734	uc003qe.3	chr3:186256232-186256484	NA	NA	NA	NA	NA	NA	NA
CSAD	616569	534.851	-4.355081	uc021tqy.1	chr12:53551447-53552294	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CSF1R	164770	NA	NA	NA	NA	NA	NA	NA	NA	688.995	-7.060863	uc011dof.2	NA	NA	NA	chr5:149456467-149456695
CSF2RA	306250	324.06	-4.84583	uc004cpn.2	chrX:1428373-1428828	NA	NA	NA	NA	807.893	-13.307158	uc004cpn.2	NA	NA	NA	chrX:1428373-1428828
CSF3	138970	NA	NA	NA	NA	NA	NA	NA	NA	744.975	-8.771447	uc002hto.3	NA	NA	NA	chr17:38173213-38174066
CSH2	118820	407.693	-9.564075	NA	NA	570.379	-5.15376	uc002gi.3	chr17:61949372-61949888	NA	NA	NA	NA	NA	NA	NA

Table 1

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CYB5B	611964	618.221	-6.143686	uc002exf.3	chr16:69482095-69484124	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CYB5D1	NA	NA	NA	NA	NA	200.72	-4.750343	uc002gjb.4	chr17:7762931-7765600	NA	NA	NA	NA	NA	NA	NA	NA
CYB5E2	608342	NA	NA	NA	NA	852.503	-2.676455	uc001mfm.3	chr11:7686326-7686604	431.422	-8.598565	uc001mfm.3	chr11:7686326-7686604	NA	NA	NA	NA
CYB5R4	608343	NA	NA	NA	NA	704.169	-6.295885	uc003pkf.3	chr6:94669598-84670146	NA	NA	NA	NA	NA	NA	NA	NA
CYFIP1	606322	NA	NA	NA	NA	NA	NA	NA	NA	641.022	-8.560023	uc001yus.3	chr15:23003041-23003603	NA	NA	NA	NA
CYL2	604035	NA	NA	NA	NA	775.97	-8.25712	uc004bbs.2	chr9:105780607-105780770	NA	NA	NA	NA	NA	NA	NA	NA
CYLD	605018	1736.44	0.437262	uc002ego.3	chr16:50818367-50820674	NA	NA	NA	NA	802.094	-8.611595	uc002ego.3	chr16:50818367-50820674	NA	NA	NA	NA
CYP19A1	107910	NA	NA	NA	NA	620.377	-7.528639	uc001tyz.4	chr15:51500254-51503004	303.837	-3.677465	uc001tyz.4	chr15:51500254-51503004	NA	NA	NA	NA
CYP1A1	108330	NA	NA	NA	NA	NA	NA	NA	NA	1322.6	-11.844586	uc010bj.1	chr15:75013061-75013303	NA	NA	NA	NA
CYP1A2	124060	NA	NA	NA	NA	767.437	-5.161176	uc002ayr.1	chr15:75047430-75048941	NA	NA	NA	NA	NA	NA	NA	NA
CYP1B1	601771	NA	NA	NA	NA	NA	NA	NA	NA	630.418	-5.163575	uc002qpo.2	chr2:38294746-38297864	NA	NA	NA	NA
CYP20A1	NA	NA	NA	NA	NA	NA	NA	NA	NA	943.659	-9.285444	uc002uzv.4	chr2:204161632-204170563	NA	NA	NA	NA
CYP21A2	613815	NA	NA	NA	NA	294.213	-4.823852	uc003nze.2	chr6:32008912-32009447	NA	NA	NA	NA	NA	NA	NA	NA
CYP24A1	126065	NA	NA	NA	NA	436.611	-4.032327	uc002xwu.1	chr20:52769988-52771300	NA	NA	NA	NA	NA	NA	NA	NA
CYP27B1	609506	NA	NA	NA	NA	NA	NA	NA	NA	942.975	-8.666374	uc001sqb.1	chr12:58158161-58158301	NA	NA	NA	NA
CYP2C9	601130	633.449	-7.529759	uc001kz.3	chr10:96702107-96703022	417.617	-4.060501	uc001kka.4	chr10:96748786-96749148	258.71	-4.834918	uc001kz.3	chr10:96702107-96703022	NA	NA	NA	NA
CYP2E1	124040	NA	NA	NA	NA	373.895	-8.472378	uc001fij.1	chr10:135352469-135352620	NA	NA	NA	NA	NA	NA	NA	NA
CYP3A5	605325	NA	NA	NA	NA	283.268	-5.622688	uc003urt.3	chr7:99268845-99269396	286.356	-4.133205	uc003urq.3	chr7:99245813-99245927	NA	NA	NA	NA
CYP46A1	604087	NA	NA	NA	NA	515.48	-7.533667	uc001ygn.1	chr14:100174043-100179774	NA	NA	NA	NA	NA	NA	NA	NA
CYP4F12	611485	629.633	-1.929685	uc010xoo.2	chr19:15791495-15791754	447.481	-7.8522	uc010xoo.2	chr19:15791495-15791754	NA	NA	NA	NA	NA	NA	NA	NA
CYP4F3	601270	NA	NA	NA	NA	NA	NA	NA	NA	343.624	-6.258253	uc002njb.3	chr19:15770196-15771570	NA	NA	NA	NA
CYP4F8	611545	NA	NA	NA	NA	685.675	-7.854855	uc010xoi.1	chr19:15729198-15730572	NA	NA	NA	NA	NA	NA	NA	NA
CYP4V2	608614	NA	NA	NA	NA	490.319	-5.090941	uc003jyw.4	chr4:187131796-187134617	NA	NA	NA	NA	NA	NA	NA	NA
CYP4X1	614999	NA	NA	NA	NA	447.33	-4.106452	uc001tqr.3	chr4:147515847-47516423	NA	NA	NA	NA	NA	NA	NA	NA
CYP4Z1	NA	NA	NA	NA	NA	295.974	-5.233557	uc001tqu.1	chr14:147583607-47583992	NA	NA	NA	NA	NA	NA	NA	NA
CYP51A1	601637	NA	NA	NA	NA	673.092	-10.440726	uc003lulm.4	chr7:91741463-91742978	NA	NA	NA	NA	NA	NA	NA	NA
CYSLTR2	605666	NA	NA	NA	NA	688.469	-8.972358	uc001vck.2	chr13:49281995-49283498	NA	NA	NA	NA	NA	NA	NA	NA
CYTH1	182115	277.993	-4.63134	uc002jwv.3	chr17:76670130-76672172	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CYTH2	602488	1260.18	-6.391384	uc010xzc.1	chr19:48975873-48976236	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CYTIIP	604448	556.997	-7.722992	uc002tjz.1	chr2:158271131-158272188	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
CYR1	616020	NA	NA	NA	NA	NA	NA	NA	NA	541.551	-4.28772	uc002ymd.3	chr21:27838528-27840819	NA	NA	NA	NA
DACT1	607861	NA	NA	NA	NA	NA	NA	NA	NA	244.938	-5.936957	uc010hrv.2	chr14:59113853-59115038	NA	NA	NA	NA
DACT2	608966	NA	NA	NA	NA	NA	NA	NA	NA	225.831	-8.16927	uc003qwd.3	chr6:168707584-168708111	NA	NA	NA	NA
DAND5	609068	NA	NA	NA	NA	593.023	-4.067544	uc010dyz.1	chr19:13084203-13085567	NA	NA	NA	NA	NA	NA	NA	NA
DAPK1	600831	620.783	-6.749656	uc004apc.3	chr9:90322280-90323549	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DAPP1	605768	NA	NA	NA	NA	286.066	-5.758828	uc003hvf.4	chr4:100789343-100791346	568.437	-5.988957	uc011cek.2	chr4:100784927-100785442	NA	NA	NA	NA
DARS	603084	325.411	-4.024679	uc002lux.1	chr2:136664254-136664885	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DAZL	601486	NA	NA	NA	NA	NA	NA	NA	NA	654.627	-5.189693	uc003cba.3	chr3:16628301-16630166	NA	NA	NA	NA
DBF4	604281	903.142	-8.625398	uc003ujf.1	chr7:87537479-87538856	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DBI	125950	NA	NA	NA	NA	NA	NA	NA	NA	1064.77	-10.898804	uc002hvv.3	chr2:120129895-120130122	NA	NA	NA	NA
DBR1	607024	1156.92	-9.485672	uc003ert.3	chr3:137879830-137880730	1323.06	-14.673025	uc003ert.3	chr3:137879830-137880730	NA	NA	NA	NA	NA	NA	NA	NA
DCAF12	NA	NA	NA	NA	NA	NA	NA	NA	NA	1216.33	-8.258806	uc003ttt.2	chr9:34086381-34088347	NA	NA	NA	NA
DCAF12L2	NA	NA	NA	NA	NA	1392.34	-10.768565	uc004euk.2	chrX:125297482-125298515	NA	NA	NA	NA	NA	NA	NA	NA
DCAF13	616196	1408.61	-13.240869	uc003yin.3	chr8:104455111-104455680	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DCAF16	NA	NA	NA	NA	NA	999.771	-6.921306	uc003gpn.3	chr4:17802278-17805113	NA	NA	NA	NA	NA	NA	NA	NA
DCAF5	603812	1072.51	-11.185222	uc001kx.4	chr14:69555921-69557771	NA	NA	NA	NA	1379.79	-9.270454	uc001kxp.3	chr14:69517637-69520573	NA	NA	NA	NA
DCAF6	610494	NA	NA	NA	NA	NA	NA	NA	NA	632.703	-8.611271	uc001gev.3	chr1:168044674-168045083	NA	NA	NA	NA
DCAKD	NA	645.574	-7.896472	uc002lhx.2	chr17:43100706-43101800	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DCBLD1	NA	NA	NA	NA	NA	452.656	-13.535796	uc003pxr.1	chr6:117869070-117870960	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

DCBLD2	608698	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	624.529	-7.237003	uc003dtd.3	chr3:98514814-98518215
DOCK	125450	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	480.265	-5.773908	uc003hfk.3	chr4:71895096-71896629
DOLK1	604742	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	526.546	-7.81021	uc001lue.4	chr13:36342789-36348778
DCN	125255	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	850.482	-11.832845	uc001lbo.3	chr12:91539035-91539834
DCP1B	609843	348.257	-5.97131	uc001lqk.1	chr12:2055214-2055371	NA	NA	NA	NA	NA	NA	869.9	0.089781	uc010sdy.1	chr12:2050757-2050957
DC1	191275	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DCTD	607638	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	442.989	-8.067711	uc003wif.3	chr4:183811244-18381251
DCTP1	615840	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	550.497	-5.531388	uc002dyf.3	chr16:30435019-30435553
DCUN1D1	605905	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	376.573	-8.960392	uc003fid.1	chr3:18260559-182662881
DCX	300121	1460.17	-15.900862	uc004epd.3	chrX:110537007-110544914	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDA11	604743	1761.87	-12.814762	uc010osb.2	chr1:85784168-85787134	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDH01	614603	970.37	-9.085704	uc001xag.3	chr14:53503458-53513485	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDH02	615003	275.594	-6.287877	uc003xla.2	chr8:38095790-38096610	NA	NA	NA	NA	NA	NA	447.862	-6.822783	uc001aww.3	chr1:15960065-15960796
DDI2	NA	573.172	-8.429707	uc001awx.2	chr1:15986332-15987552	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDN	610588	618.798	-5.490174	uc001trsv.1	chr12:49388933-49390522	1178.69	-6.411042	uc001rsv.1	chr12:49388933-49390522	NA	NA	NA	NA	NA	NA
DDOST	602202	448.293	-7.264193	uc001bdo.1	chr1:20978260-20978871	870.689	-9.553412	uc001bdo.1	chr1:20978260-20978871	NA	NA	NA	NA	NA	NA
DDRGK1	616177	444.45	-5.509458	uc002wic.3	chr20:3171012-3171298	528.769	-7.006966	uc002wic.3	chr20:3171012-3171298	NA	NA	NA	NA	NA	NA
DDT	602750	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	675.886	-11.182104	uc002zyz.4	chr22:24313554-24313739
DDX17	608469	1784.67	-13.445906	uc003avw.4	chr22:38879443-38881939	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDX18	606355	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	686.938	-7.224684	uc002tlh.1	chr2:118588301-118589953
DDX31	616533	829.837	-6.165336	uc004cbq.1	chr9:135468676-135470252	NA	NA	NA	NA	NA	NA	690.491	-4.410208	uc004cbq.1	chr9:135469676-135470252
DDX3Y	400010	NA	NA	NA	NA	1057.01	-5.569501	uc010mwv.1	chrY:15026580-15026743	NA	NA	NA	NA	NA	NA
DDX4	605281	629.852	-7.595238	uc003fig.4	chr5:55112369-55112974	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDX47	615428	NA	NA	NA	NA	655.096	-7.103075	uc001rav.3	chr12:12982489-12982915	NA	NA	NA	NA	NA	NA
DDX5	180630	1335.83	-13.263429	uc010deh.2	chr17:62494374-62496040	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDX52	612500	548.717	-7.206606	uc002hoht.2	chr17:35972363-35974340	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DDX55	NA	NA	NA	NA	NA	975.709	-6.450349	uc001lufh.3	chr12:124104021-124104255	NA	NA	NA	NA	NA	NA
DDX59	615464	781.681	-8.136568	uc009wzk.3	chr1:200613165-200613381	562.416	-8.596412	uc010ppl.1	chr1:200610119-200610276	NA	NA	NA	NA	NA	NA
DDX6	600326	1099.42	-6.227878	uc001puu.2	chr11:118618473-118622806	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DECR1	222745	NA	NA	NA	NA	773.017	-8.16059	uc003yek.1	chr8:91064126-91064227	NA	NA	NA	NA	NA	NA
DEF46	60471	675.215	-8.389447	uc003wql.3	chr8:6782216-6782339	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DEFB129	NA	NA	NA	NA	NA	572.708	-4.466028	uc002wda.3	chr20:210413-210527	NA	NA	NA	NA	NA	NA
DEGS2	610862	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	594.775	-9.068463	uc001yrg.2	chr14:100612753-100613097
DENND1B	613292	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	765.802	-4.807437	uc021pgu.1	chr1:197473879-197479589
DENND2C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	578.519	-8.747386	uc001efc.1	chr1:115127196-115128220
DENND4A	600382	965.819	-4.343313	uc002aph.3	chr15:65952957-65954188	152.13	-13.657735	uc010uji.1	chr15:66007413-66007785	NA	NA	NA	NA	NA	NA
DENND4C	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	288.004	-5.459773	uc003znr.3	chr9:19369990-19374137
DENND5B	NA	721.565	-4.37695	uc001rkl.3	chr12:31585311-31586043	NA	NA	NA	NA	NA	NA	436.577	-5.574706	uc001rkl.1	chr12:31535157-31540536
DEPDC1B	616073	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	343.008	-7.070358	uc003jsh.3	chr5:59892739-59893579
DEPDC5	614191	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DEPDC7	612294	527.57	-6.369407	uc010reg.1	chr11:33047705-33048263	548.903	-4.874114	uc011als.2	chr22:32302484-32303020	NA	NA	NA	NA	NA	NA
DERA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	235.613	-4.589976	uc001dec.3	chr12:16189681-16190315
DERL2	610304	NA	NA	NA	NA	1329.6	-8.25838	uc002gpc.1	chr17:5377613-5378003	NA	NA	NA	NA	NA	NA
DFFA	601882	1008.9	-7.721187	uc001tarj.3	chr1:10520603-10521546	444.792	-5.303749	uc001tarj.3	chr1:10520603-10521546	702.658	-3.637846	uc001tarj.3	NA	NA	NA
DFFB	601893	NA	NA	NA	NA	1659.64	-16.558377	uc001ala.1	chr1:3782868-3782962	NA	NA	NA	NA	NA	NA
DGAT2	606983	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	305.988	-5.309166	uc001ova.3	chr11:75511554-75512581
DGCR6	601279	594.478	-5.477706	uc002zoh.4	chr22:18899203-18899601	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DGKB	604070	274.583	-8.230584	uc003ssz.3	chr7:14184674-14188755	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DGKH	604071	864.705	-4.577431	uc010fh.2	chr13:42803288-42803891	894.565	-11.205163	uc010fh.2	chr13:42803288-42803891	894.731	-7.136125	uc010fh.2	NA	NA	NA

Table 1

DHFR11	616588	982,962	-8,429,723	uc003dri.3	chr3:93776766-93779791	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DHPS	600944	582,911	-5,636,885	uc002mug.2	chr19:12786531-12786651	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DHRS1	610410	718,851	-4,630,178	uc001woj.2	chr14:24759804-24760064	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DHRS11	616159	NA	NA	NA	NA	894,039	-8,637,033	uc002hnd.3	chr17:34956633-34957233	NA	NA	NA	NA	NA	NA
DHRS7	612833	NA	NA	NA	NA	244,111	-3,650,219	uc001xes.3	chr14:60611500-60611683	388,341	-4,578,215	uc001xes.3	chr14:60611500-60611683	NA	NA
DHRS7B	616160	NA	NA	NA	NA	792,518	-4,477,78	uc002gyo.3	chr17:21094467-21095285	NA	NA	NA	NA	NA	NA
DHX30	616423	967,982	-5,268,378	uc003cns.2	chr3:47983246-47984169	NA	NA	NA	NA	571,196	-4,799,69	uc003cns.2	chr3:47983246-47984169	NA	NA
DHX32	607960	NA	NA	NA	NA	750,456	-5,650,058	uc001lje.1	chr10:127524909-127525255	NA	NA	NA	NA	NA	NA
DHX33	614405	750,894	-5,908,518	uc002gbz.3	chr17:5344232-5347524	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DHX35	NA	448,165	-7,534,375	uc002xjh.3	chr20:37667187-37668366	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DHX40	607570	696,753	-6,137,96	uc002kni.2	chr17:57684534-57685713	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DHX57	NA	NA	NA	NA	NA	NA	NA	NA	NA	1809,4	-14,814,332	uc002rld.4	chr2:39024876-39025440	NA	NA
DHX9	603115	NA	NA	NA	NA	1201,48	-11,775,117	uc001gpr.3	chr1:182856570-182857117	NA	NA	NA	NA	NA	NA
DICER1	606241	1661,91	-11,931,692	uc010avh.1	chr14:95552566-95556834	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DIEXF	NA	221,794	-7,613,252	uc001thir.2	chr1:210024793-210030910	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DIMT1	612499	1127,43	-8,616,824	uc003lia.3	chr5:61684351-61684836	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DIO1	147892	NA	NA	NA	NA	NA	NA	NA	NA	260,92	-5,589,298	uc001cwb.3	chr1:54375673-54376759	NA	NA
DIO2	601413	NA	NA	NA	NA	212,292	-6,632,222	uc001xut.3	chr14:80663868-80669631	NA	NA	NA	NA	NA	NA
DIP2A	607711	1003,03	-0,243,268	uc002zjl.3	chr21:47965920-47966219	685,863	-6,582,904	uc002zjm.3	chr21:47966960-47967120	623,185	-5,761,203	uc002zjn.3	chr21:47969832-47970023	NA	NA
DIP2C	611380	916,377	-3,202,008	uc001lip.3	chr10:320130-323264	445,25	-7,083,457	uc001lip.3	chr10:320130-323264	793,04	2,480,958	uc009xhi.1	chr10:386420-386610	NA	NA
DIRA3	605193	NA	NA	NA	NA	1217,86	-9,928,79	uc001ded.3	chr1:68511645-68512290	NA	NA	NA	NA	NA	NA
DIRC1	606423	NA	NA	NA	NA	1355,96	-11,237,693	uc002uqi.1	chr2:189598465-189599332	699,826	-10,800,752	uc002uqi.1	chr2:189598465-189599332	NA	NA
DIS3L	614183	473,948	-10,463,499	uc002app.3	chr15:66625651-66626236	NA	NA	NA	NA	739,829	-7,089,5	NA	NA	NA	NA
DIXO2	610493	357,58	-4,696,435	uc001pmk.3	chr11:111845712-111846719	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DKFZP434K028	604258	229,482	-6,298,196	uc011kxx.1	chr8:12940872-129433319	NA	NA	NA	NA	300,509	-6,604,706	uc001nsd.3	chr11:61521501-61521917	NA	NA
DLC1	238331	496,813	-6,195,754	uc003vet.3	chr7:107559705-107561643	548,171	-5,375,663	uc003vet.3	chr7:107559705-107561643	849,881	-1,712,748	uc011kxx.1	chr8:12940872-129433319	NA	NA
DLEU7	NA	NA	NA	NA	NA	NA	NA	NA	NA	700,763	-4,889,924	uc001vez.3	chr13:51397046-51397449	NA	NA
DLG1	601014	458,282	-6,156,304	uc011bub.2	chr3:196769431-196771493	1563,36	-8,320,321	uc010rsw.1	chr11:83166056-83170860	483,081	-5,764,825	uc011bub.2	chr3:196769431-196771493	NA	NA
DLG2	603583	851,421	-10,890,656	uc010rsw.1	chr11:83166056-83170860	NA	NA	NA	NA	1054,69	-7,651,467	uc010rb.1	chr11:83172595-83173015	NA	NA
DLG4	602887	540,129	-6,993,796	uc002geu.3	chr17:7106037-7106108	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DLG5	604090	370,062	-3,921,482	uc001jzl.3	chr10:79550549-79552197	349,491	-5,246,477	uc001jzl.4	chr10:79575791-79575929	NA	NA	NA	NA	NA	NA
DLGAP5	NA	NA	NA	NA	NA	NA	NA	NA	NA	1085,46	-6,572,52	uc001xbs.3	chr14:55614834-55615068	NA	NA
DLK1	176290	NA	NA	NA	NA	447,075	-7,563,602	uc003ova.3	chr6:43418090-43418276	1446,84	-13,401,035	uc001yhu.4	chr14:101201234-101201464	NA	NA
DLK2	NA	NA	NA	NA	NA	NA	NA	NA	NA	220,19	-4,299,868	uc010zdk.1	chr2:172965873-172966120	NA	NA
DLX2	126255	NA	NA	NA	NA	339,212	-4,336,061	uc003uon.3	chr7:96649702-96650047	1163,95	-4,845,83	uc003uon.3	chr7:96649702-96650047	NA	NA
DLX5	600028	NA	NA	NA	NA	587,919	-4,069,49	uc010bks.1	chr1:44809096-44881440	NA	NA	NA	NA	NA	NA
DMAP1	605077	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DMBT1	601969	556,926	-4,585,484	uc001lqk.1	chr10:124402915-124403252	637,37	-8,341,886	uc004dco.1	chrX:31137345-31139949	NA	NA	NA	NA	NA	NA
DMD	300377	583,476	-2,809,975	uc004dcm.1	chrX:31137345-31140035	1056,69	-7,514,724	uc021uwb.1	chr19:46272976-46273738	NA	NA	NA	NA	NA	NA
DMPK	605377	NA	NA	NA	NA	NA	NA	NA	NA	375,175	-9,825,844	uc003zpp.1	chr9:22451911-22452472	NA	NA
DMRT1	602424	673,593	-6,418,252	uc003zgv.3	chr9:968140-968090	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
DMRTA1	614803	NA	NA	NA	NA	319,81	-5,207,294	uc010oma.2	chr1:50883223-50884336	NA	NA	NA	NA	NA	NA
DMRTA2	614804	NA	NA	NA	NA	505,055	-6,511,92	uc001cvq.1	chr1:53932336-53933158	316,958	-3,730,877	uc001cvq.1	chr1:53932336-53933158	NA	NA
DMRTB1	614805	NA	NA	NA	NA	408,936	-7,848,24	uc003ksd.2	chr5:118582915-118584822	NA	NA	NA	NA	NA	NA
DMXL1	605671	846,036	-6,421,941	uc003ksd.2	chr5:118582915-118584822	824,368	-11,650,011	uc002abd.3	chr15:51739921-51741180	676,628	-6,448,375	uc002abd.3	chr15:51739921-51741180	NA	NA
DMXL2	612186	622,682	-5,425,405	uc002abd.3	chr15:51739921-51741180	NA	NA	NA	NA	514,661	-7,514,009	uc002pv.3	chr2:230222345-230223255	NA	NA
DNER	607299	334,361	-4,462,42	uc002pv.3	chr2:230222345-230223255	236,858	-4,821,863	uc001mdp.3	chr11:6541342-6542097	NA	NA	NA	NA	NA	NA
DNHD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

[illegible]

Table 1

DUSP8	602038	NA	NA	NA	NA	483.622	-6.479288	uc001lts.2	chr11:1575281-1577747	494.151	-8.799424	uc001lts.2	chr11:1575281-1577747
DUT	601266	1062.54	-6.736045	uc001zws.3	chr15:48634276-48635570	NA	NA	NA	NA	NA	NA	NA	NA
DUXA	611168	1233.3	-7.633809	uc002qoa.1	chr19:57663094-57665779	NA	NA	NA	NA	NA	NA	NA	NA
DVL3	601368	NA	NA	NA	NA	752.027	-7.820199	uc003fms.3	chr3:18388544-183891314	431.247	-4.620109	uc003fms.3	chr3:18388544-183891314
DYM	607461	NA	NA	NA	NA	1204.44	-6.49732	uc002ldl.1	chr18:46570172-46570424	1272.42	-2.520133	uc002ldl.1	chr18:46570172-46570424
DYNC1H1	600112	382.123	-5.840876	uc001yts.2	chr14:102516901-102517135	NA	NA	NA	NA	NA	NA	NA	NA
DYNC1L1	615890	606.211	-4.658034	uc003ctb.4	chr3:32567463-32568290	NA	NA	NA	NA	NA	NA	NA	NA
DYNC2L1	NA	567.962	-6.720737	uc002dth.3	chr2:44021882-44022316	298.427	-16.563237	uc002dth.3	chr2:44019930-44022322	837.569	-5.844674	uc002dth.3	chr2:44036907-44037149
DYNLT1	601554	1081.04	-5.254383	uc003qtm.2	chr6:159057507-159057858	NA	NA	NA	NA	NA	NA	NA	NA
DYRK1A	600855	NA	NA	NA	NA	611.055	-7.520362	uc002ywi.3	chr21:38884214-38887679	606.627	-4.549532	uc002ywi.3	chr21:38878611-38878657
DYRK3	603497	NA	NA	NA	NA	1033.86	-6.287354	uc001hei.3	chr1:206822311-206822542	861.737	-8.641795	uc001hei.3	chr1:206822311-206822542
DYRK4	609181	NA	NA	NA	NA	NA	NA	NA	NA	217.382	-8.23963	uc001qmx.3	chr12:4722920-4723041
DYTN	NA	NA	NA	NA	NA	NA	NA	NA	NA	486.423	-6.615056	uc002vbr.1	chr2:207516345-207516541
DZ1P1	608671	567.604	-5.603994	uc001vmj.3	chr13:96230456-96234487	NA	NA	NA	NA	NA	NA	NA	NA
DZ1P3	608672	561.452	-7.413131	uc003dxf.1	chr3:108409745-108410234	479.751	-5.546902	uc003dxf.1	chr3:108409745-108410234	316.973	-6.597742	uc003dxf.1	chr3:108412207-108413693
E2F5	600967	286.263	-5.248158	uc003ycz.4	chr8:86126098-86126753	NA	NA	NA	NA	NA	NA	NA	NA
EAF1	608315	NA	NA	NA	NA	567.722	-6.762516	uc003bzu.3	chr3:15480663-15484120	NA	NA	NA	NA
EAPP	609486	572.769	-10.282138	uc001wsd.1	chr14:34985135-34985515	NA	NA	NA	NA	NA	NA	NA	NA
EAR52	612799	617.831	-8.366133	uc002dlf.4	chr16:235333334-23535691	299.78	-3.881119	uc002dlf.4	chr16:235333334-23535691	NA	NA	NA	NA
EBF2	609934	459.333	-6.416353	uc003xel.2	chr8:25889866-25890596	NA	NA	NA	NA	233.179	-5.057655	uc003xes.2	chr8:25699246-257021124
EBI3	605816	NA	NA	NA	NA	289.261	-4.079749	uc002zlu.3	chr19:4237086-4237524	NA	NA	NA	NA
EBLN1	613249	540.054	-6.407206	uc021pob.1	chr10:22497743-22497811	NA	NA	NA	NA	NA	NA	NA	NA
EBPL	NA	658.264	-5.428213	uc001vdl.3	chr13:50234810-50235344	NA	NA	NA	NA	NA	NA	NA	NA
ECM2	603479	NA	NA	NA	NA	NA	NA	NA	NA	2505.86	-20.421797	uc004asf.4	chr9:952555829-952556364
ECSIT	608388	NA	NA	NA	NA	582.499	-6.357429	uc010dyv.2	chr19:11616731-11617243	NA	NA	NA	NA
EDA2R	300276	NA	NA	NA	NA	681.641	-4.575303	uc004dwl.2	chrX:65815482-65817935	NA	NA	NA	NA
EDC3	609842	572.35	-6.037678	uc002aym.3	chr15:74922898-74924952	NA	NA	NA	NA	NA	NA	NA	NA
EDC4	606030	NA	NA	NA	NA	NA	NA	NA	NA	569.887	-6.190109	uc002eur.3	chr16:67918052-67918417
EDN1	131240	NA	NA	NA	NA	545.625	-8.79093	uc010jpb.3	chr6:12292747-12293113	NA	NA	NA	NA
EDN3	131242	468.869	-5.108479	uc002vap.3	chr20:57899751-57901047	NA	NA	NA	NA	NA	NA	NA	NA
EDNRB	131244	813.132	-5.433751	uc001vko.2	chr13:78469616-78472334	786.956	-8.545551	uc001vko.2	chr13:78469616-78472334	923.921	-8.589803	uc001vko.2	chr13:78469616-78472334
EDRF1	NA	1318.5	-14.619822	uc001lio.1	chr10:127452042-127452712	1566.13	-16.658293	uc001lin.3	chr10:127436624-127437652	538.29	-5.622688	uc001lio.1	chr10:127452042-127452712
EFCAB11	NA	977.138	-7.686403	uc001xxw.2	chr14:90389670-90391002	563.822	-5.1118	uc001xxs.3	chr14:90263469-90263586	NA	NA	NA	NA
EFCAB14	NA	NA	NA	NA	NA	628.518	-5.787714	uc010dmj.2	chr1:47140831-47144132	NA	NA	NA	NA
EFCAB3	NA	NA	NA	NA	NA	1840.12	-19.237885	uc010wpc.2	chr17:60493691-60493839	NA	NA	NA	NA
EFCAB5	NA	NA	NA	NA	NA	NA	NA	NA	NA	1406.13	-14.753148	uc002het.3	chr17:28435043-28435470
EFCAB7	NA	221.099	-7.898175	uc001dbf.3	chr1:64038188-64038364	NA	NA	NA	NA	NA	NA	NA	NA
EFHB	NA	377.909	-4.501018	uc003cbl.4	chr3:19920966-19921122	NA	NA	NA	NA	NA	NA	NA	NA
EFHC2	300817	846.797	-9.936115	uc002bvg.1	chrX:44007128-44008040	808.194	-9.697979	uc022bvg.1	chrX:44007128-44008040	NA	NA	NA	NA
EFNB1	300035	NA	NA	NA	NA	930.437	-9.84382	uc004dxd.4	chrX:68060498-68062006	NA	NA	NA	NA
EFNB2	600527	334.159	-4.391684	uc001vql.3	chr13:107142079-107145387	NA	NA	NA	NA	NA	NA	NA	NA
EFNB3	602297	NA	NA	NA	NA	521.23	-4.254039	uc002gis.3	chr17:7612895-7614693	NA	NA	NA	NA
EFTUD1	NA	NA	NA	NA	NA	1023.07	-8.71403	uc002bgt.1	chr15:82422561-82422713	996.066	-12.502846	uc002bgt.1	chr15:82422561-82422713
EFTUD2	NA	NA	NA	NA	NA	NA	NA	NA	NA	377.487	-5.15376	uc002lhn.2	chr17:42927655-42928641
EGFEM1P	NA	341.259	-5.715728	uc003flh.4	chr3:168547033-168548374	NA	NA	NA	NA	NA	NA	NA	NA
EGFL6	300239	1697.5	-12.053467	uc004cvi.3	chrX:13651215-13651694	NA	NA	NA	NA	495.428	-9.285163	uc004cvi.3	chrX:13651215-13651694
EGLN1	606425	NA	NA	NA	NA	511.562	-7.43534	uc001huu.3	chr1:231499497-231502156	358.577	-5.690497	uc001huu.3	chr1:231499497-231502156
EHBP1	609922	NA	NA	NA	NA	896.401	-10.495377	uc010lq.1	chr2:63053408-63053716	532.85	-15.484832	uc010lq.1	chr2:63272636-63273621
EHD3	605891	NA	NA	NA	NA	NA	NA	NA	NA	435.874	-8.031125	uc002nu.3	chr2:31489571-31491260

Table 1

EHD4:	605892	586.436	-7.230777	uc001zoi.3	chr15:42191639-42192842	NA	NA	NA	NA	NA	NA	NA	NA	NA
EID1:	605894	739.312	-4.803936	uc001zxc.1	chr15:49170938-49172380	NA	NA	NA	NA	NA	NA	NA	NA	NA
EID2:	609773	NA	NA	NA	NA	442.73	-6.036513	uc002oma.3	chr19:40029447-40030008	NA	NA	NA	NA	NA
EID3:	612986	1101.04	-8.130276	uc001lkw.3	chr12:104698715-104698982	NA	NA	NA	NA	NA	NA	NA	NA	NA
EIF1AD:	NA	542.606	-4.818991	uc001ogm.2	chr11:65764016-65766069	NA	NA	NA	NA	NA	NA	NA	NA	NA
EIF1AX:	300186	565.952	-7.934214	uc004czi.3	chrX:20142636-20146423	261.596	-5.04028	uc004czi.3	chrX:20142636-20146423	NA	NA	NA	NA	NA
EIF1AY:	400014	NA	NA	NA	NA	614.58	-6.923764	uc004fik.3	chrY:22754233-22755040	NA	NA	NA	NA	NA
EIF2AK4:	609280	696.407	-5.257692	uc001zkl.3	chr15:40265984-40267625	579.136	-7.028584	uc001zkl.3	chr15:40265984-40267625	541.583	-5.063079	uc001zkl.3	chr15:40265984-40267625	NA
EIF2B4:	606687	NA	NA	NA	NA	NA	NA	NA	NA	521.906	-8.508304	uc002kfi.1	chr2:27589089-27591481	NA
EIF2D:	613709	480.947	-4.615429	uc001heh.2	chr11:206764974-206765106	883.254	-6.328861	uc001heh.2	chr11:206764974-206765106	866.722	-8.29099	uc001heh.2	chr11:206764974-206765106	NA
EIF2S1:	603907	NA	NA	NA	NA	NA	NA	NA	NA	205.219	-4.919721	uc001jig.3	chr14:67850158-67853233	NA
EIF2S2:	603908	NA	NA	NA	NA	861.653	-5.97446	uc002xaf.3	chr20:32676115-32677535	NA	NA	NA	NA	NA
EIF2S3:	300161	NA	NA	NA	NA	895.451	-5.449679	uc004dbc.3	chrX:24094903-24096927	NA	NA	NA	NA	NA
EIF3G:	603913	833.222	-6.04034	uc002mnd.3	chr19:10225690-10225789	NA	NA	NA	NA	NA	NA	NA	NA	NA
EIF3H:	603912	NA	NA	NA	NA	1521.34	-13.976626	uc011hz.1	chr8:117670488-117671046	1328.18	-11.143041	uc011hz.1	chr8:117670488-117671046	NA
EIF3IP1:	NA	575.943	-7.129522	uc003vip.1	chr7:109599284-109599680	NA	NA	NA	NA	NA	NA	NA	NA	NA
EIF3J:	603910	896.946	-7.168892	uc001zlv.3	chr15:44853348-44855001	704.344	-8.175658	uc001zlv.3	chr15:44853348-44855001	1212.39	-8.965148	uc001zlv.3	chr15:44853348-44855001	NA
EIF3L:	NA	NA	NA	NA	NA	NA	NA	NA	NA	358.478	-4.884203	uc003auf.3	chr22:38284472-38284789	NA
EIF4A2:	601102	NA	NA	NA	NA	NA	NA	NA	NA	260.807	-6.483717	uc003fqg.3	chr3:186507059-186507685	NA
EIF4A3:	608546	NA	NA	NA	NA	1090.5	-6.630955	uc010wuc.2	chr17:778109013-78109288	NA	NA	NA	NA	NA
EIF4B:	603928	550.648	-4.497684	uc001sbh.4	chr12:53434008-53435993	NA	NA	NA	NA	501.382	-4.879666	uc001sbh.4	chr12:53434008-53435993	NA
EIF4E:	133440	734.043	-4.904694	uc011cec.1	chr4:99807502-99808217	NA	NA	NA	NA	443.651	-5.549346	uc011cea.1	chr4:99799607-99802178	NA
EIF4E2:	605895	NA	NA	NA	NA	NA	NA	NA	NA	1079.82	-11.646689	uc002vdb.1	chr2:233445654-233448349	NA
EIF4EBP2:	602224	NA	NA	NA	NA	593.566	-5.722133	uc001jrb.3	chr10:72181504-72188374	NA	NA	NA	NA	NA
EIF5AL1:	NA	840.144	-9.244323	uc009rxr.3	chr10:81272871-81276192	NA	NA	NA	NA	NA	NA	NA	NA	NA
ELAVL4:	163860	NA	NA	NA	NA	NA	NA	NA	NA	386.873	-5.219938	uc009vyu.3	chr1:50663144-50663232	NA
ELF2:	NA	577.819	-5.858704	uc011chc.1	chr4:139978871-139980136	NA	NA	NA	NA	NA	NA	NA	NA	NA
ELF5:	605169	674.87	-2.896435	uc001mvo.1	chr11:34500342-34501764	NA	NA	NA	NA	626.728	-6.99685	uc001mvq.2	chr11:34513144-34514963	NA
ELK4:	600246	NA	NA	NA	NA	NA	NA	NA	NA	1024.36	-8.317603	uc001hcz.3	chr1:205588396-205588955	NA
ELL3:	609885	NA	NA	NA	NA	NA	NA	NA	NA	330.213	-4.568145	uc001zsv.1	chr15:44064798-44065313	NA
ELMOD1:	615456	465.619	-6.414065	uc001pjm.3	chr11:107535924-107537505	NA	NA	NA	NA	NA	NA	NA	NA	NA
ELMOD2:	610196	1252.62	-19.980105	uc003lik.3	chr4:141471530-141474924	NA	NA	NA	NA	1180.61	-10.152742	uc003lik.3	chr4:141471530-141474924	NA
ELN:	130160	NA	NA	NA	NA	313.059	-5.127891	uc003lzn.3	chr7:73483031-73484236	NA	NA	NA	NA	NA
ELOVL7:	614451	NA	NA	NA	NA	497.512	-6.095497	uc011tqo.2	chr5:60047616-60050450	NA	NA	NA	NA	NA
ELP2:	616054	NA	NA	NA	NA	289.598	-6.510954	uc002kzk.2	chr18:33754605-33754688	NA	NA	NA	NA	NA
ELP4:	606985	200.217	-4.961186	uc001imb.3	chr11:31805073-31805329	NA	NA	NA	NA	NA	NA	NA	NA	NA
ELSPBP1:	607443	NA	NA	NA	NA	587.068	-7.482145	uc002pht.3	chr19:48528209-48528410	NA	NA	NA	NA	NA
EMBP1:	NA	1149.42	-9.59363	uc009whl.1	chr11:121310592-121313686	228.346	-3.984669	uc009whl.1	chr11:121310592-121313686	NA	NA	NA	NA	NA
EMC10:	614545	617.505	-7.963835	uc002psk.3	chr19:50985406-50986608	NA	NA	NA	NA	NA	NA	NA	NA	NA
EMC2:	607722	708.434	-9.793651	uc003ymw.1	chr8:109498828-109499136	NA	NA	NA	NA	NA	NA	NA	NA	NA
EMC3:	NA	793.002	-8.813713	uc003buo.3	chr3:10010345-10011270	NA	NA	NA	NA	NA	NA	NA	NA	NA
EMC4:	616245	NA	NA	NA	NA	375.083	-5.248158	uc001zth.3	chr15:34521990-34522352	758.816	-5.248158	uc001zth.3	chr15:34521990-34522352	NA
EMCN:	608350	NA	NA	NA	NA	NA	NA	NA	NA	200.533	-4.275788	uc003hvr.3	chr4:101316498-101319530	NA
EMLIN2:	608928	422.655	-4.750617	uc002kin.3	chr18:2913403-2914090	NA	NA	NA	NA	NA	NA	NA	NA	NA
EML1:	602033	NA	NA	NA	NA	NA	NA	NA	NA	813.741	-9.802606	uc010tww.2	chr14:100406450-100408395	NA
EML4:	607442	272.079	-6.456969	uc002rsl.4	chr2:42488442-42488639	NA	NA	NA	NA	233.012	-4.416075	uc002rsl.3	chr2:42557348-42559688	NA
EMP2:	602334	999.453	-17.202225	uc002czk.3	chr16:10622279-10626761	NA	NA	NA	NA	NA	NA	NA	NA	NA
ENDOD1:	NA	NA	NA	NA	NA	1438.69	-9.334802	uc001pjh.3	chr11:94862744-94865815	NA	NA	NA	NA	NA
ENDOV:	NA	NA	NA	NA	NA	NA	NA	NA	NA	682.555	-11.897688	uc002yjl.1	chr17:78393850-78394333	NA

Table 1

ENGASE	611898	657.935	-6.600342	uc002jwu.1	chr17:77078328-77078959	NA	NA	NA	NA	NA	362.928	NA	NA	NA	chr12:7031964-7032859
EN02	131360	NA	NA	NA	NA	380.577	-6.029878	uc001qru.1	chr12:7031964-7032859	NA	NA	NA	NA	NA	chr12:7031964-7032859
ENOPH1	NA	NA	NA	NA	NA	390.545	-14.687345	uc003hmv.3	chr4:83381274-83382244	NA	NA	NA	NA	NA	NA
ENPEP	138297	651.452	-7.654804	uc003lab.4	chr4:111482715-111484493	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ENPP2	601060	1477.21	-15.956141	uc011lic.2	chr8:120569317-120569760	868.132	-10.83832	uc011lic.2	chr8:120569317-120569760	NA	NA	NA	NA	NA	NA
ENPP3	602182	713.996	-11.633901	uc003qcu.4	chr6:132068097-132068550	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ENPP4	NA	484.053	-4.948872	uc003oxy.3	chr6:46111378-46114436	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ENSA	603061	NA	NA	NA	NA	483.935	-6.252863	uc001evf.3	chr1:150595754-150598113	NA	NA	NA	NA	NA	NA
ENTHD1	NA	521.358	-7.772913	uc003avg.3	chr22:40139049-40139683	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ENTPD1	601752	NA	NA	NA	NA	NA	NA	NA	NA	NA	517.392	-8.299582	uc001lle.1	chr10:97605441-97605843	NA
ENTPD4	607577	280.747	-4.013073	uc011kzv.1	chr8:23291606-23291825	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ENY2	NA	NA	NA	NA	NA	748.503	-12.044533	uc003ync.3	chr8:110355711-110358189	NA	NA	NA	NA	NA	NA
EOGT	614789	NA	NA	NA	NA	NA	NA	NA	NA	NA	447.67	-7.564841	uc003dnj.3	chr3:69024368-69026768	NA
EP300	602700	850.608	-10.309157	uc003azi.4	chr22:41574961-41576081	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EP400NL	NA	NA	NA	NA	NA	834.309	-5.450347	uc001ujs.4	chr12:132593300-132593444	NA	NA	NA	NA	NA	NA
EPB41L1	602879	NA	NA	NA	NA	479.244	-5.878943	uc002xeu.3	chr20:34817263-34820721	NA	NA	NA	NA	NA	NA
EPB41L4B	610340	NA	NA	NA	NA	820.291	-5.679652	uc004bdz.1	chr9:111934254-111936833	NA	NA	NA	NA	NA	NA
EPB41L5	611730	NA	NA	NA	NA	NA	NA	NA	NA	755.1	-4.183678	uc010flk.3	chr2:120861817-120864492	NA	NA
EPDR1	NA	228.949	-6.803556	uc003flg.3	chr7:37989806-37991542	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPG5	615068	1550.16	-10.608766	uc002lbn.3	chr18:43427574-43432431	760.54	-6.642035	uc002lbo.1	chr18:43487830-43487910	585.057	-11.361198	uc002lbn.3	chr18:43427574-43432431	NA	NA
EPHA2	178946	NA	NA	NA	NA	756.654	-6.354258	uc001aya.2	chr1:16450832-16451709	NA	NA	NA	NA	NA	NA
EPHA3	179611	409.756	-6.894712	uc003dqp.1	chr3:89448657-89449495	NA	NA	NA	NA	609.209	-6.762516	uc003dqp.1	chr3:89448657-89449495	NA	NA
EPHA4	602188	NA	NA	NA	NA	655.497	-4.767512	uc002vmq.3	chr2:222289929-222290747	NA	NA	NA	NA	NA	NA
EPHA5	600004	NA	NA	NA	NA	735.645	-6.579983	uc003poe.3	chr6:93949740-93953143	403.336	-5.266298	uc003hda.2	chr4:66196279-66197686	NA	NA
EPHA7	602190	NA	NA	NA	NA	432.138	-8.999419	uc002nap.3	chr19:15337730-15338247	NA	NA	NA	NA	NA	NA
EPHX3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPHX4	NA	498.656	-5.830931	uc001don.2	chr1:32528844-92529093	NA	NA	NA	NA	777.622	-6.481523	uc010khr.3	chr6:145946440-145948630	NA	NA
EPM2A	607566	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPN2	607263	320.064	-6.42791	uc002gvd.4	chr17:19237568-19240028	NA	NA	NA	NA	1584.25	-16.369205	uc003zaa.1	chr8:144939912-144940158	NA	NA
EPKP1	607553	1751.77	-20.879433	uc003zaa.1	chr8:144939912-144940158	NA	NA	NA	NA	328.01	-6.758649	uc001hly.1	chr1:220141942-220142147	NA	NA
EPRS	138295	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPS15	600051	1288.32	-13.627571	uc001csp.3	chr1:51819935-51822371	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPS8	600206	1867.58	-14.287032	uc010slv.2	chr12:15773075-15774250	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPS8L2	614988	984.948	-8.124649	uc010qwj.1	chr11:721940-722302	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPYC	601657	266.888	-7.274096	uc001lbt.3	chr12:91357456-91357932	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ERAP1	606832	NA	NA	NA	NA	1409.37	-10.238285	uc003kml.3	chr5:96096514-96098903	NA	NA	NA	NA	NA	NA
ERB84	600543	613.759	-7.258569	uc002veg.1	chr2:212240442-212248339	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ERC1	607127	714.979	-6.427947	uc001qlb.2	chr12:1599397-1605099	829.795	-9.264101	uc009zdp.3	chr12:1353793-1354122	NA	NA	NA	NA	NA	NA
ERCC3	133510	646.992	-6.16928	uc002boe.1	chr2:128014866-128015171	465.09	-3.739966	uc010ljy.3	chr2:128047272-128047809	NA	NA	NA	NA	NA	NA
ERCC4	133520	793.641	-7.814146	uc010bva.3	chr16:14026160-14027104	741.777	-8.71745	uc010bva.3	chr16:14026160-14027104	NA	NA	NA	NA	NA	NA
ERCC6L	300687	NA	NA	NA	NA	327.312	-5.6571	uc004eap.1	chrX:71424507-71424863	NA	NA	NA	NA	NA	NA
ERCC8	609412	NA	NA	NA	NA	437.933	-6.702474	uc003jsn.3	chr5:60199187-60199406	463.567	-7.049464	uc003isl.3	chr5:60169659-60170441	NA	NA
EREG	602061	825.373	-15.782308	uc003hid.3	chr4:75246859-75247703	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ERIGC3	NA	405.955	-6.193279	NA	NA	476.063	-4.946302	uc010zvq.2	chr20:34144130-34144209	NA	NA	NA	NA	NA	NA
ER11	608739	457.734	-7.81021	uc003wsk.2	chr8:8887545-8890849	227.936	-5.680285	uc010bwh.2	NA	NA	NA	NA	NA	NA	NA
ER12	NA	NA	NA	NA	NA	669.518	-8.271131	uc001dgi.4	chr1:75055011-75055297	NA	NA	NA	NA	NA	NA
ERIC3	NA	NA	NA	NA	NA	745.997	-6.737641	uc010ojw.1	chr1:43304655-43305384	NA	NA	NA	NA	NA	NA
ERMAP	609017	573.695	-7.841324	uc010ojw.1	chr1:43304655-43305384	1210.75	-5.457567	uc010zci.2	chr2:158175125-158177782	NA	NA	NA	NA	NA	NA
ERMIN	610072	NA	NA	NA	NA										

Table 1

ERP29	602287	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	350.937	-5.61809	uc001hkk.1	chr12:112460457-112461024
ERP44	609170	994.64	-13.737964	uc004bam.3	chr9:102741463-102744893	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ESCO2	609353	NA	NA	NA	NA	263.301	-6.931236	uc003xkg.3	chr8:27860956-27862424	NA	NA	NA	NA	NA	NA
ESF1	NA	NA	NA	NA	NA	466.439	-5.455059	uc002zwoj.3	chr20:13694969-13695520	NA	NA	NA	NA	NA	NA
ESPL1	604143	385.492	-4.45297	uc001scj.2	chr12:53687259-53687427	NA	NA	NA	NA	490.643	-3.832978	uc001scj.2	-3.832978	uc001scj.2	chr12:53687259-53687427
ESRRA	601998	NA	NA	NA	NA	NA	NA	NA	NA	303.868	-4.856061	uc001lnsq.1	-4.856061	uc001lnsq.1	chr11:64083439-64084210
ESX1	300154	292.657	-7.840127	uc004ely.3	chrX:103494719-103494908	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ESYT2	616691	695.412	-11.607894	uc003wnz.1	chr7:158523689-158526897	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ETFB	130410	NA	NA	NA	NA	378.419	-5.439337	uc002pwg.3	chr19:51848409-51848464	NA	NA	NA	NA	NA	NA
ETNKF	609858	530.996	-3.667603	uc001rfs.3	chr12:222797239-22797349	NA	NA	NA	NA	596.548	-4.659142	uc001rft.3	-4.659142	uc001rft.3	chr12:22837889-22843608
ETV1	600541	937.692	-3.075469	uc021zzw.1	chr7:13946055-13946137	1074.2	-5.283375	uc021zzl.1	chr7:13300856-13935490	NA	NA	NA	NA	NA	NA
ETV5	601600	437.962	-5.857318	uc003fpy.3	chr3:185764106-185766427	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EVC2	607261	NA	NA	NA	NA	535.229	-7.119264	uc003gjl.3	chr4:5564146-5564574	NA	NA	NA	NA	NA	NA
EVL5	NA	521.651	-5.143917	uc002min.3	chr19:7928589-7929862	NA	NA	NA	NA	243.854	-3.885436	uc002mio.1	-3.885436	uc002mio.1	chr19:7921871-7924076
EVPL	601590	572.197	-7.400201	uc002qil.2	chr17:74002927-74003183	385.5	-5.285101	uc002qil.2	chr17:74002927-74003183	NA	NA	NA	NA	NA	NA
EXOC4	608185	1087.54	-8.103812	uc003vri.3	chr7:133164901-133165805	NA	NA	NA	NA	977.208	-12.986352	uc003vrk.3	-12.986352	uc003vrk.3	chr7:133749282-133750513
EXOC6	609672	344.392	-7.398995	uc010qmr.2	chr10:94818113-94819251	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
EXOC7	608163	NA	NA	NA	NA	753.122	-7.058542	uc002qjp.2	chr17:74077086-74079757	618.563	-3.988751	uc010dgv.2	-3.988751	uc010dgv.2	chr17:74077086-74079728
EXOC8	615283	1017.64	-10.284304	uc001huq.3	chr1:231468482-231471313	NA	NA	NA	NA	1116.54	-6.218359	uc001huq.3	-6.218359	uc001huq.3	chr1:231468482-231471313
EXOSC10	605960	NA	NA	NA	NA	767.099	-8.251079	uc009vmy.1	chr1:11139768-11140816	976.105	-8.322627	uc001jasa.3	-8.322627	uc001jasa.3	chr1:11126676-11126774
EXOSC8	606019	NA	NA	NA	NA	272.46	-11.434782	uc001uwa.3	chr13:37583437-37583751	NA	NA	NA	NA	NA	NA
EXOSC9	606180	NA	NA	NA	NA	523.38	-10.641849	uc003idz.3	chr4:122738012-122738176	NA	NA	NA	NA	NA	NA
EYA4	603550	416.615	-5.210592	uc011ecq.2	chr6:133849944-133853258	NA	NA	NA	NA	841.256	-3.579343	uc011ecq.2	-3.579343	uc011ecq.2	chr6:133849944-133853258
EZH1	601674	339.421	-5.250511	uc010cyo.1	chr17:40855441-40855743	616.738	-7.080547	uc002iaz.3	chr17:40852293-40854549	766.538	-0.41409	uc002iaz.3	-0.41409	uc002iaz.3	chr17:40852293-40854549
EZH2	601573	NA	NA	NA	NA	333.636	-6.693194	uc022aov.1	chr7:148504464-148504737	NA	NA	NA	NA	NA	NA
EZR	123900	NA	NA	NA	NA	485.701	-6.2637	uc011tfr.2	chr6:159186773-159187945	NA	NA	NA	NA	NA	NA
F11R	605721	NA	NA	NA	NA	551.86	-5.244337	uc010piv.2	chr1:160965001-160968660	360.423	-8.223133	uc010piv.2	-8.223133	uc010piv.2	chr1:160965001-160968660
FAH2	300654	NA	NA	NA	NA	NA	NA	NA	NA	722.032	-16.297911	uc004wv.3	-16.297911	uc004wv.3	chrX:57515366-57515629
FABP1	134650	NA	NA	NA	NA	NA	NA	NA	NA	243.513	-12.171129	uc002sst.2	-12.171129	uc002sst.2	chr2:88422508-88422572
FABP4	600434	NA	NA	NA	NA	NA	NA	NA	NA	1685	-10.218914	uc003ycd.2	-10.218914	uc003ycd.2	chr8:823390732-823391099
FABP7	602965	236.097	-7.737058	uc003pzd.3	chr6:123102493-123104039	1014.81	-4.286046	uc003pzd.3	chr6:123102493-123104039	NA	NA	NA	NA	NA	NA
FADD	602457	904.1	-7.115195	uc001opm.2	chr11:70052580-70053508	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FAF2	NA	NA	NA	NA	NA	933.351	-16.476217	uc003mej.4	chr5:175933952-175937075	575.315	-6.645377	uc003mej.4	-6.645377	uc003mej.4	chr5:175933952-175937075
FAHD1	616320	NA	NA	NA	NA	248.59	-2.30319	uc002cnc.1	chr16:1877906-1878908	272.608	-9.451525	uc002cnc.1	-9.451525	uc002cnc.1	chr16:1877906-1878908
FAM104A	NA	553.647	-4.06257	uc002jji.4	chr17:71203492-71205667	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FAM110B	611394	251.28	-7.606873	uc003xjl.1	chr8:59059903-59062277	215.506	-5.081129	uc003xjl.1	chr8:59059903-59062277	NA	NA	NA	NA	NA	NA
FAM111A	615292	NA	NA	NA	NA	NA	NA	NA	NA	534.164	-5.315011	uc001mnc.3	-5.315011	uc001mnc.3	chr11:58920978-58922511
FAM117B	NA	643.13	-3.809107	uc010zhw.2	chr2:203589757-203589955	2794.24	-6.317217	uc010zhw.2	chr2:203589757-203589955	668.866	-5.604784	uc010zhw.2	-5.604784	uc010zhw.2	chr2:203630488-203634480
FAM120AS	NA	953.087	-5.703267	uc004alu.4	chr9:96208782-96209892	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FAM122B	NA	NA	NA	NA	NA	201.039	-5.346047	uc004ext.3	chrX:133903596-133905314	NA	NA	NA	NA	NA	NA
FAM126A	610531	NA	NA	NA	NA	NA	NA	NA	NA	275.4	-7.84276	uc003svm.4	-7.84276	uc003svm.4	chr7:22980878-22985207
FAM126B	NA	NA	NA	NA	NA	NA	NA	NA	NA	583.968	-12.737066	uc002lws.4	-12.737066	uc002lws.4	chr2:201838441-201845992
FAM134C	616498	219.038	-4.195707	uc002lal.2	chr17:40733057-40733830	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FAM135A	NA	852.277	-7.021129	uc003pjh.3	chr6:71269625-71270877	618.164	-6.716301	uc003pjh.3	chr6:71269625-71270877	687.071	-2.933073	uc003prk.3	-2.933073	uc003prk.3	chr6:71233866-71234306
FAM135B	NA	NA	NA	NA	NA	355.14	-7.283888	uc003yva.3	chr8:139155103-139155250	NA	NA	NA	NA	NA	NA
FAM13B	609371	NA	NA	NA	NA	2570.92	-19.566165	uc003lhz.2	chr5:137273642-137275913	NA	NA	NA	NA	NA	NA
FAM13C	NA	288.584	-5.968631	uc001jkn.3	chr10:61005889-61007373	NA	NA	NA	NA	458.457	-7.298557	uc010qif.1	-7.298557	uc010qif.1	chr10:61010929-61011246
FAM149A	NA	356.623	-5.742345	uc001cla.1	chr4:187088443-187088484	362.14	-8.913186	uc010isj.2	chr4:187079202-187079564	NA	NA	NA	NA	NA	NA
FAM149B1	NA	NA	NA	NA	NA	484.555	-6.916269	uc009qxz.3	chr10:75000778-75001939	NA	NA	NA	NA	NA	NA

Table 1

FAM151B	NA	NA	NA	NA	NA	1467.52	-12.066363	uc003kgv.2	chr5:79837652-79838382	748.131	-8.338082	uc003kgv.2	chr5:79837652-79838382
FAM153C	NA	981.353	-11.253161	uc011dge.2	chr5:177475666-177476088	NA	NA	NA	NA	499.572	-5.804305	uc011dge.2	chr5:177475666-177476088
FAM160A1	NA	602.036	-9.943427	uc003lmj.2	chr4:152585907-152584784	NA	NA	NA	NA	NA	NA	NA	NA
FAM160A2	NA	275.455	-4.624329	uc001mck.4	chr11:6232564-6232735	NA	NA	NA	NA	506.453	-5.384782	uc001mck.4	chr11:6232564-6232735
FAM162A	608017	NA	NA	NA	NA	369.079	-5.656457	uc011bjq.1	chr3:122126291-122126811	NA	NA	NA	NA
FAM163A	611727	NA	NA	NA	NA	NA	NA	NA	NA	815.154	-6.686591	uc009wjl.3	chr1:179783325-179785333
FAM166A	NA	334.37	-3.71663	uc004cmi.1	chr9:140138037-140138151	406.028	-6.281993	uc004cmi.1	chr9:140138037-140138151	NA	NA	NA	NA
FAM166B	NA	NA	NA	NA	NA	239.206	-4.37522	uc010mkr.3	chr9:35561827-35562003	NA	NA	NA	NA
FAM168B	NA	NA	NA	NA	NA	NA	NA	NA	NA	775.6	-4.023616	uc002tsd.3	chr2:131805449-131810025
FAM169A	615769	NA	NA	NA	NA	732.258	-11.970916	uc010izm.3	chr5:74073399-74077284	NA	NA	NA	NA
FAM171B	NA	NA	NA	NA	NA	811.201	-10.509981	uc002upr.1	chr2:187627551-187628335	721.276	-7.390355	uc002upr.1	chr2:187627551-187628335
FAM172A	NA	283.385	-4.499109	uc010bd.3	chr5:92953431-92956692	427.233	-8.210142	uc010bd.3	chr5:92953431-92956692	NA	NA	NA	NA
FAM172BP	NA	NA	NA	NA	NA	208.256	-4.779559	uc003duy.1	chr3:101241824-101242731	NA	NA	NA	NA
FAM175A	611143	NA	NA	NA	NA	473.443	-2.969149	uc003hou.2	chr4:84382094-84383621	1832.87	-11.049168	uc003hou.2	chr4:84382094-84383621
FAM177A1	NA	1488.87	-10.861595	uc001wsp.3	chr14:35550435-35552589	NA	NA	NA	NA	NA	NA	NA	NA
FAM177B	NA	NA	NA	NA	NA	398.801	-5.102033	uc001hnt.3	chr1:222923401-222924002	NA	NA	NA	NA
FAM179A	NA	312.473	-4.990424	uc002rms.1	chr2:29268405-29270413	965.487	-9.350703	uc002rms.1	chr2:29268405-29270413	1065.95	-11.30611	uc010ezl.3	chr2:29274960-29275096
FAM179B	NA	433.834	-5.463865	uc010anb.1	chr14:45465144-45466607	961.905	-2.876145	uc001wvu.3	chr14:45475492-45477346	NA	NA	NA	NA
FAM180A	NA	766.331	-9.081762	uc003vid.3	chr7:135418394-135418722	NA	NA	NA	NA	NA	NA	NA	NA
FAM184A	NA	NA	NA	NA	NA	481.302	-5.598799	uc003pyj.3	chr6:119280996-119281287	NA	NA	NA	NA
FAM189A2	607710	NA	NA	NA	NA	307.375	-5.371038	uc010moo.1	chr9:72006675-72007370	666.229	-6.158318	uc010mon.1	chr9:72006721-72007370
FAM189B	NA	NA	NA	NA	NA	496.217	-6.502594	uc001fqj.1	chr1:155222540-155223343	1247.63	-8.866505	uc001fqj.1	chr1:155222540-155223343
FAM193A	NA	NA	NA	NA	NA	NA	NA	NA	NA	378.919	-4.387198	uc01oick.3	chr4:27333596-2734302
FAM198A	NA	1267.21	-5.103611	uc003cmp.4	chr3:43097879-43099207	NA	NA	NA	NA	NA	NA	NA	NA
FAM198B	NA	1414.15	-7.870705	uc003ppp.4	chr4:159045732-159048558	NA	NA	NA	NA	NA	NA	NA	NA
FAM199X	NA	NA	NA	NA	NA	NA	NA	NA	NA	734.102	-12.254555	uc004clw.3	chrX:103434460-103440582
FAM200A	NA	312.101	-4.982461	uc003ura.3	chr7:99143923-99144308	NA	NA	NA	NA	NA	NA	NA	NA
FAM208A	616493	NA	NA	NA	NA	1255.92	-3.565784	uc003dlb.4	chr3:56654160-56657064	2323.21	-12.721424	uc003dlb.4	chr3:56654160-56657064
FAM20B	611063	NA	NA	NA	NA	370.258	-4.84583	uc001gmc.3	chr1:179041280-179045702	NA	NA	NA	NA
FAM210B	NA	NA	NA	NA	NA	NA	NA	NA	NA	1162.51	-11.02533	uc002xsc.3	chr20:54941344-54943718
FAM213A	NA	278.129	-5.954095	uc021pux.1	chr10:82191856-82192753	1167.11	-13.056718	uc021pux.1	chr10:82191856-82192753	NA	NA	NA	NA
FAM213B	NA	870.187	-4.949832	uc021oex.1	chr1:2520919-2522908	NA	NA	NA	NA	NA	NA	NA	NA
FAM215A	NA	536.705	-5.76815	uc010wiq.1	chr17:41995024-41995355	NA	NA	NA	NA	NA	NA	NA	NA
FAM216A	NA	NA	NA	NA	NA	679.05	-5.4696	uc001tqu.4	chr12:110927943-110928192	NA	NA	NA	NA
FAM216B	NA	1080.2	-7.953717	uc010lft.2	chr13:43362927-43365685	NA	NA	NA	NA	NA	NA	NA	NA
FAM219B	NA	NA	NA	NA	NA	NA	NA	NA	NA	230.672	-5.087947	uc002azh.4	chr15:75192328-75194959
FAM21C	613631	1273.94	-11.847784	uc001jcu.3	chr10:46287849-46288412	NA	NA	NA	NA	NA	NA	NA	NA
FAM221A	NA	1477.99	-17.796224	uc003swo.4	chr7:23741784-23742269	NA	NA	NA	NA	NA	NA	NA	NA
FAM222B	NA	619.993	-6.315861	uc002hcl.1	chr17:27082996-27085287	NA	NA	NA	NA	NA	NA	NA	NA
FAM227B	NA	NA	NA	NA	NA	NA	NA	NA	NA	489.329	-5.296089	uc001xrl.2	chr15:49620592-49620764
FAM24A	NA	205.074	-5.777951	uc001lgy.3	chr10:124672471-124672627	1433.65	-10.131519	uc001lgy.3	chr10:124672471-124672627	NA	NA	NA	NA
FAM24B	NA	497.151	-8.072033	uc001lgl.3	chr10:124608610-124608762	NA	NA	NA	NA	NA	NA	NA	NA
FAM26E	NA	NA	NA	NA	NA	NA	NA	NA	NA	1679.59	-8.24003	uc003pwy.3	chr6:116837153-116839709
FAM3D	608619	NA	NA	NA	NA	NA	NA	NA	NA	460.335	-4.96181	uc003dkq.3	chr3:58619670-58620005
FAM46A	611357	612.19	-5.988155	uc003pjl.3	chr6:82455447-82459411	NA	NA	NA	NA	NA	NA	NA	NA
FAM47A	NA	1618.07	-17.231484	uc004ddg.3	chrX:34147869-34148019	1183.69	-6.095428	uc004ddg.3	chrX:34147869-34148019	NA	NA	NA	NA
FAM47B	NA	1470.7	-14.785593	uc004ddi.2	chrX:34962887-34963034	1189.87	-8.055785	uc004ddi.2	chrX:34962887-34963034	NA	NA	NA	NA
FAM47C	NA	1432.13	-15.900546	uc004ddi.2	chrX:37029592-37029739	NA	NA	NA	NA	NA	NA	NA	NA
FAM49A	NA	NA	NA	NA	NA	NA	NA	NA	NA	678.117	-9.29512	uc010wmn.2	chr2:16730730-16734203

Table 1

FAM50B	614686	NA	NA	NA	NA	NA	NA	NA	NA	NA	302,229	-5,703,427	uc003mvlv.3	chr6:3851024-3851551
FAM57A	611627	NA	NA	NA	NA	NA	NA	NA	NA	NA	299,267	-7,350,018	uc002frp.3	chr17:644811-646075
FAM65C	614542	567,272	-5,755,502	uc002xvm.3	chr20:49202647-49203768	NA	NA	NA	NA	NA	NA	NA	NA	NA
FAM69A	614542	NA	NA	NA	NA	NA	NA	NA	NA	NA	457,466	-6,755,109	uc001dpc.3	chr1:932398286-932398576
FAM72B	614711	NA	NA	NA	NA	NA	NA	NA	NA	NA	706,493	-8,756,299	uc009whp.3	chr1:120854587-120855681
FAM73A	NA	278,309	-7,997,543	uc001dhy.1	chr1:78324782-78327860	1584,09	-8,287,003	uc001dhy.1	chr1:78324782-78327860	NA	NA	NA	NA	NA
FAM73B	NA	681,683	-0,760,026	uc011mbn.1	chr9:131830813-131831254	1476,26	-5,680,441	uc011mbn.1	chr9:131830813-131831254	1357,51	-3,542,979	uc011mbn.1	chr9:131830813-131831254	
FAM76A	NA	NA	NA	NA	NA	NA	NA	NA	NA	995,69	-7,452,681	uc009vxb.3	chr1:28086169-28086275	
FAM76B	NA	NA	NA	NA	NA	853,112	-6,965,41	uc001pfn.2	chr11:95502106-95504724	NA	NA	NA	NA	
FAM81A	NA	NA	NA	NA	NA	NA	NA	NA	NA	1030,32	-11,057,328	uc010lha.2	chr15:59752583-59752749	
FAM81B	NA	748,733	-8,921,045	uc003kla.1	chr5:94785987-94786144	NA	NA	NA	NA	NA	NA	NA	NA	NA
FAM83D	NA	713,008	-2,777,772	uc002xfj.3	chr20:37570803-37574842	874,944	-9,617,066	uc002xfj.3	chr20:37581164-37581703	NA	NA	NA	NA	NA
FAM89A	NA	NA	NA	NA	NA	671,467	-6,979,481	uc001hul.2	chr1:231154704-231155608	NA	NA	NA	NA	NA
FAM91A1	NA	328,638	-9,606,683	uc011llk.1	chr8:124822631-124822719	1087,17	-7,070,14	uc003yqv.3	chr8:124824945-124827690	970,639	-5,968,708	uc011llk.1	chr8:124822631-124822719	
FAM92A1	NA	NA	NA	NA	NA	590,992	-8,787,469	uc022ayc.1	chr8:94730903-94731016	NA	NA	NA	NA	
FAM9A	300477	NA	NA	NA	NA	722,141	-8,760,234	uc0022bsk.1	chrX:8758837-8759213	NA	NA	NA	NA	
FAM9C	300479	1019,8	-3,303,881	uc004cvg.3	chrX:13053736-13056559	496,42	-6,905,571	uc004cvg.3	chrX:13053736-13056559	NA	NA	NA	NA	
FANCA	607139	NA	NA	NA	NA	216,733	-6,212,881	uc002fou.1	chr16:89803959-89805008	NA	NA	NA	NA	
FANCD2	613984	665,139	-4,543,067	uc003buu.3	chr3:10081561-10083246	618,67	-7,048,315	uc003buu.3	chr3:10081561-10083246	NA	NA	NA	NA	
FANCE	613976	529,387	-5,110,535	uc003oko.1	chr6:35434123-35434881	NA	NA	NA	NA	679,091	-6,674,369	uc001mqj.1	chr11:22644079-22646231	
FANCF	613897	552,323	-7,425,937	uc001mqj.1	chr11:22644079-22646231	NA	NA	NA	NA	1117,07	-20,640,92	uc001wvc.2	chr14:45636375-45636626	
FANCM	609644	NA	NA	NA	NA	NA	NA	NA	NA	870,421	-5,981,804	uc001ljh.4	chr10:127698008-127698161	
FANK1	611640	NA	NA	NA	NA	511,917	-6,870,795	uc001ljh.4	chr10:127698008-127698161	NA	NA	NA	NA	
FAP	604003	NA	NA	NA	NA	842,047	-5,856,117	uc010lpc.3	chr2:163027200-163027488	NA	NA	NA	NA	
FARP1	602654	275,098	-4,390,561	uc001vnh.3	chr13:99100572-99102023	557,756	-6,863,112	uc001vnh.3	chr13:99100572-99102023	447,946	-5,128,135	uc001vnh.3	chr13:99100572-99102023	
FASTKD1	NA	950,169	-13,085,491	uc002uev.4	chr2:170386263-170386334	NA	NA	NA	NA	NA	NA	NA	NA	
FASTKD2	612322	NA	NA	NA	NA	410,57	-6,990,853	uc002vbu.3	chr2:207656527-207660911	NA	NA	NA	NA	
FASTKD3	NA	NA	NA	NA	NA	NA	NA	NA	NA	287,522	-4,876,333	uc011cmp.2	chr5:7859272-7859547	
FAT2	604269	574,531	-3,225,304	uc003lud.4	chr5:150883653-150885125	869,533	-6,111,992	uc003lud.4	chr5:150883653-150885125	NA	NA	NA	NA	
FAU	134690	NA	NA	NA	NA	588,661	-6,011,357	uc001ocx.3	chr11:64888099-64888152	NA	NA	NA	NA	
FAXDC2	NA	NA	NA	NA	NA	NA	NA	NA	NA	408,384	-6,327,885	uc003lvs.4	chr5:154198052-154199875	
FBL11	NA	1006,28	-12,356,662	uc011dep.2	chr5:167957515-167957639	1737,79	-11,180,242	uc011dep.2	chr5:167957515-167957639	1560,58	-15,837,406	NA	NA	
FBLN2	135821	899,288	-12,747,037	uc011auz.2	chr3:13679420-13679922	441,463	-4,817,318	uc011auz.2	chr3:13679420-13679922	292,2	-4,628,603	uc011auz.2	chr3:13679420-13679922	
FBN2	612570	NA	NA	NA	NA	NA	NA	NA	NA	677,687	-7,464,141	uc003kuv.2	chr5:127663781-127664337	
FBP1	611570	NA	NA	NA	NA	NA	NA	NA	NA	212,126	-5,087,692	uc004auw.4	chr9:97365421-97365562	
FBP2	603027	NA	NA	NA	NA	478,448	-7,841,707	uc004auv.3	chr9:97321003-97321219	NA	NA	NA	NA	
FBXL13	609080	NA	NA	NA	NA	NA	NA	NA	NA	607,961	-5,432,569	uc010liq.1	chr7:102453308-102453788	
FBXL17	609083	843,43	-9,917,67	uc003kan.4	chr5:107213952-107216563	NA	NA	NA	NA	NA	NA	NA	NA	
FBXL22	609088	NA	NA	NA	NA	1432,94	-6,021,958	uc002amr.2	chr15:63891393-63892933	NA	NA	NA	NA	
FBXL3	605653	NA	NA	NA	NA	1019,68	-14,675,279	uc001vkd.3	chr13:77679389-77681279	NA	NA	NA	NA	
FBXL4	605654	321,422	-8,102,104	uc003ppf.1	chr6:99321601-99322153	452,089	-7,862,84	uc010kcp.3	chr6:99322468-99323138	NA	NA	NA	NA	
FBXL5	605655	807,02	-10,998,024	uc010dlw.2	chr4:15606007-15607345	NA	NA	NA	NA	NA	NA	NA	NA	
FBXL6	609076	392,601	-4,010,76	uc003zbx.3	chr8:145579088-145579190	NA	NA	NA	NA	NA	NA	NA	NA	
FBXO11	607871	776,295	-4,855,062	uc010fbk.3	chr2:48034059-48035256	NA	NA	NA	NA	696,547	-6,367,636	uc002rwg.2	chr2:48045556-480455913	
FBXO15	609093	NA	NA	NA	NA	NA	NA	NA	NA	1602,49	-8,788,476	uc002lle.2	chr18:71740588-717406095	
FBXO21	609095	376,19	-7,212,301	uc001hwj.3	chr12:117581585-117583891	NA	NA	NA	NA	NA	NA	NA	NA	
FBXO22	609096	346,582	-5,387,853	uc002bbj.2	chr15:76222428-76223208	NA	NA	NA	NA	892,645	-11,571,23	uc002bbj.2	chr15:76222428-76223208	
FBXO25	609098	389,569	-7,067,585	uc003wox.3	chr8:418805-419875	NA	NA	NA	NA	NA	NA	NA	NA	
FBXO30	609101	NA	NA	NA	NA	364,711	-10,293,061	uc003qla.3	chr6:146119272-146121241	NA	NA	NA	NA	

Table 1

FBXO33	609103	743.068	-11.858334	uc001wvk.3	chr14:39865577-39868719	NA	NA	NA	NA	NA	NA	515.227	NA	NA	NA	NA	chr17:6690748-6690965
FBXO39	609106	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FBXO42	609109	674.74	-7.801615	uc001ayf.3	chr1:16576559-16577164	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FBXO43	609110	NA	NA	NA	NA	455.812	-6.351615	uc003yjd.3	chr8:101145588-101146029	303.616	-4.084102	NA	NA	NA	NA	NA	chr8:101145588-101146029
FBXO5	606013	NA	NA	NA	NA	519.849	-7.21788	uc003qpg.3	chr6:153291658-153292297	NA	NA	NA	NA	NA	NA	NA	NA
FBXO7	605648	921.064	-9.899164	uc003amq.3	chr22:32894518-32894818	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FBXW11	605651	704.871	-6.476772	uc011day.1	chr5:171288556-171291105	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FBXW7	606278	825.861	-11.042294	uc003imu.3	chr4:153332312-153332424	787.213	-9.381955	uc003imu.3	chr4:153332312-153332424	NA	NA	NA	NA	NA	NA	NA	NA
FCER1A	147140	NA	NA	NA	NA	956.17	-6.981329	uc001ftq.3	chr1:159277723-159278014	NA	NA	NA	NA	NA	NA	NA	NA
FCER1G	147139	NA	NA	NA	NA	1020.61	-8.878375	uc001fyz.1	chr1:161188734-161189038	NA	NA	NA	NA	NA	NA	NA	NA
FCGR1A	146760	817.451	-6.342293	uc001esp.4	chr1:149763074-149764074	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FCGR2A	146790	742.747	-9.566993	uc001gam.3	chr1:161487939-161489360	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FCHO2	613438	NA	NA	NA	NA	540.378	-4.661996	uc011csk.1	chr5:72333827-72333938	NA	NA	NA	NA	NA	NA	NA	NA
FCHSD2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	618.373	-6.549	uc001csh.4	NA	NA	chr11:72547790-72549835
FCRL3	606510	631.85	-5.997229	uc001fra.3	chr1:157647978-157648499	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FCRLB	609251	982.874	-3.068911	uc001gbh.3	chr1:161697453-161697933	NA	NA	NA	NA	NA	NA	606.777	-7.838316	uc001gbh.3	NA	NA	chr1:161697453-161697933
FDFT1	184420	NA	NA	NA	NA	1504.72	-8.931724	uc001pkx.3	chr11:110333193-110335608	1096.34	-10.848559	NA	NA	uc003wuh.3	NA	NA	chr8:11696119-11696818
FDX1	103260	NA	NA	NA	NA	661.499	-6.056115	uc001pmc.4	chr11:111744780-111745645	NA	NA	NA	NA	NA	NA	NA	NA
FDXACB1	NA	NA	NA	NA	NA	481.204	-5.556089	uc001nsg.3	chr11:61563977-61564714	NA	NA	NA	NA	NA	NA	NA	NA
FEN1	600393	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FER1L5	NA	407.464	-5.978523	uc002swr.2	chr2:97317767-97320635	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FERMT1	607900	NA	NA	NA	NA	430.287	-6.110874	uc002wmq.3	chr20:60556492-6057819	NA	NA	NA	NA	NA	NA	NA	NA
FEZ1	604825	1998.29	-10.408843	uc001qbx.3	chr11:125315641-125315990	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FGB	134830	358.31	-3.541012	uc003baa.4	chr4:155491803-155493915	998.238	-13.942872	uc003ica.4	chr4:155491803-155493915	NA	NA	NA	NA	NA	NA	NA	NA
FGD4	611104	NA	NA	NA	NA	253.853	-3.480662	uc001rlc.3	chr12:32793468-32798984	457.451	-9.6022	NA	NA	uc001rlc.3	NA	NA	chr12:32793468-32798984
FGF1	131220	653.205	-5.469545	uc003lmq.3	chr5:141971743-141974854	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FGF14	601515	NA	NA	NA	NA	640.936	-5.998116	uc001vpe.2	chr13:102373205-102375180	NA	NA	NA	NA	NA	NA	NA	NA
FGF20	605558	861.158	-7.06114	uc003wxc.1	chr8:16850334-16850580	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FGF21	609436	1643.77	-6.711043	uc002pkn.1	chr19:49261478-49261582	NA	NA	NA	NA	NA	NA	1639.53	-17.893559	NA	NA	NA	NA
FGF7	148180	NA	NA	NA	NA	767.527	-9.129266	uc001zxn.3	chr15:49776702-49779523	NA	NA	NA	NA	NA	NA	NA	NA
FGFR1OP	605392	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	460.806	-9.720122	uc011tegr.1	NA	NA	chr6:167453608-167453926
FGL1	605776	NA	NA	NA	NA	939.966	-5.431716	uc003wxx.3	chr8:17721900-17722100	425.101	-4.088876	NA	NA	uc003wxx.3	NA	NA	chr8:17721900-17722100
FGL2	605351	NA	NA	NA	NA	740.261	-7.243553	uc003ugb.3	chr7:76822688-76825595	NA	NA	NA	NA	NA	NA	NA	NA
FHL2	602633	492.159	-4.682318	uc002tct.3	chr2:105977283-105977739	1149.03	-10.829891	uc002tct.3	chr2:105977283-105977739	1317.91	-7.489084	NA	NA	uc002tde.1	NA	NA	chr2:105988004-105989986
FHL5	605126	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	457.833	-7.256791	uc003pos.2	NA	NA	chr6:97063649-97064512
FIBIN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	493.196	-4.699684	uc001mrd.3	NA	NA	chr11:27016710-27018632
FIGN1	300091	378.795	-4.551301	uc004cwl.2	chrX:15363713-15364254	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FIGNL1	615393	657.614	-6.886462	uc003lps.3	chr7:50511832-50512960	300.538	-9.155832	uc003lps.3	chr7:50511832-50512960	NA	NA	NA	NA	NA	NA	NA	NA
FILIP1	607307	291.652	-5.457279	uc003phy.1	chr6:76004607-76005625	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FILIP1L	612993	NA	NA	NA	NA	250.621	-4.557543	uc003dtn.3	chr3:99666772-99667117	811.214	-7.895483	NA	NA	uc010hpf.3	NA	NA	chr3:99551988-99552078
FIP1L1	607686	625.106	-5.446964	uc011bzt.1	chr4:54306937-54307150	826.105	-8.115755	uc003gzy.3	chr4:54325617-54326103	NA	NA	NA	NA	NA	NA	NA	NA
FIS1	609003	783.085	-6.060458	uc003uyj.4	chr7:100882893-100883086	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FITM2	612029	895.259	-7.561535	uc002xlr.1	chr20:42935197-42935264	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FKBP15	NA	747.008	-10.68648	uc004bgr.2	chr9:115927800-115928357	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FKBP6	604839	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	562.567	-5.826351	uc003twr.2	NA	NA	chr7:7272190-72727641
FKRP	606596	479.68	-4.773948	uc002pfn.2	chr19:47260196-47261832	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
FKSG29	NA	NA	NA	NA	NA	1537.06	-8.738476	uc010aay.1	chr13:100004106-100004281	NA	NA	NA	NA	NA	NA	NA	NA
FLCN	607273	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1016.39	-14.954518	uc002gra.4	NA	NA	chr17:17115527-17116968
FLJ10038	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	488.362	-7.110787	uc001pyg.3	NA	NA	chr15:50641135-50646482

Table 1

FLJ13224	NA	NA	NA	NA	NA	490,542	-6,237078	uc001rkf.1	chr12:31478258-31478879	NA	NA	NA	NA
FLJ30679	NA	627,059	-8,836901	uc010vos.1	chr16:86589345-86590905	NA	NA	NA	NA	NA	NA	NA	NA
FLJ33360	NA	1702,76	-8,174818	uc003dtn.1	chr5:6310554-6312482	NA	NA	NA	NA	NA	NA	NA	NA
FLJ44635	NA	302,009	-2,880372	uc004eal.2	chrX:71380103-71381600	425,448	-5,199318	uc004eal.2	chrX:71380103-71381600	NA	NA	NA	NA
FLNB	603381	1053,27	-9,12147	uc003djl.2	chr3:58156490-58157982	982,981	-9,502373	uc003djl.2	chr3:58156490-58157982	751,361	-9,488768	uc003djl.2	chr3:58156490-58157982
FLT4	136352	NA	NA	NA	NA	NA	NA	NA	NA	908,216	-6,552282	uc003mma.4	chr5:180034753-180035280
FLVCR1	609144	689,147	-9,842755	uc001hjt.3	chr1:213068633-21307205	NA	NA	NA	NA	NA	NA	NA	NA
FMN2	606373	NA	NA	NA	NA	NA	NA	NA	NA	1129,02	-8,865061	uc010pyd.2	chr1:240637455-240638489
FMOD	600245	NA	NA	NA	NA	NA	NA	NA	NA	494,091	-6,740556	uc001gtr.3	chr1:203309752-203311470
FN1	135600	NA	NA	NA	NA	NA	NA	NA	NA	939,179	-9,601432	uc002vez.3	chr2:216225179-216226277
FN3KRP	611683	1223,56	-6,739879	uc002klu.3	chr17:80685048-80685893	NA	NA	NA	NA	NA	NA	NA	NA
FNBP4	615265	NA	NA	NA	NA	NA	NA	NA	NA	951,412	-11,825676	uc001ngl.3	chr11:47738069-47738973
FNDC3A	615794	NA	NA	NA	NA	1632,47	-10,783082	uc001vcl.1	chr13:49720076-49720983	NA	NA	NA	NA
FNDC3B	611909	1039,45	-15,759713	uc003fla.3	chr3:172055230-172056104	NA	NA	NA	NA	NA	NA	NA	NA
FNFA	134635	590,746	-5,443081	uc003xps.3	chr8:42940426-42940932	NA	NA	NA	NA	NA	NA	NA	NA
FOLR1	136430	NA	NA	NA	NA	514,93	-5,35717	uc001tor.2	chr11:71907222-71907367	NA	NA	NA	NA
FOLR2	136425	NA	NA	NA	NA	428,406	-4,624517	uc001ose.4	chr11:71932807-71932994	NA	NA	NA	NA
FOPNL	NA	752,289	-12,342722	uc002dec.1	chr16:15959577-15961296	611,986	-5,594917	uc002dec.1	chr16:15959577-15961296	NA	NA	NA	NA
FOXA3	602295	2000,62	-12,034165	uc002ptr.3	chr19:46376317-46377055	NA	NA	NA	NA	NA	NA	NA	NA
FOXK2	147685	NA	NA	NA	NA	356,128	-0,602221	uc002klm.1	chr17:80553717-80554067	441,531	-7,543716	uc010dlu.3	chr17:80559281-80562483
FOXN3	602628	NA	NA	NA	NA	1863,03	-18,201903	uc001xxn.4	chr14:89622516-89628757	NA	NA	NA	NA
FOXP1	605515	NA	NA	NA	NA	1026,69	-8,206464	uc003doi.3	chr3:71003865-71008397	NA	NA	NA	NA
FOXP2	605317	331,38	-8,663074	uc003vgw.3	chr7:114268769-114269032	597,673	-5,44009	uc003vgx.2	chr7:114284849-114285885	NA	NA	NA	NA
FGPS	138510	NA	NA	NA	NA	NA	NA	NA	NA	846,978	-7,136163	uc004bpg.1	chr9:130575884-130576556
FGT3	603609	NA	NA	NA	NA	698,925	-4,684035	uc001dgb.2	chr1:74671517-74674148	NA	NA	NA	NA
FRA10AC1	608866	1703,2	-1,827337	uc001kpb.1	chr10:95448837-95451720	569,95	-8,40106	uc001kjb.1	chr10:95448837-95451720	1224,8	-7,525986	uc009xuh.1	chr10:95451529-95452398
FREM1	608944	NA	NA	NA	NA	NA	NA	NA	NA	596,884	-7,088693	uc003zll.3	chr9:14734664-14737393
FREM2	608945	NA	NA	NA	NA	495,446	-7,223484	uc001uww.3	chr13:39438765-39439063	NA	NA	NA	NA
FRG1	601278	265,75	-4,307423	uc003zts.3	chr4:190884285-190884359	1155,47	-10,400992	NA	NA	1090,99	-8,532667	uc003zts.3	chr4:190884285-190884359
FRG1B	NA	NA	NA	NA	NA	271,503	-4,19588	uc010zlk.1	chr20:29652155-29653908	NA	NA	NA	NA
FRG2EP	NA	NA	NA	NA	NA	NA	NA	NA	NA	235,695	-4,814194	uc003dpr.4	chr3:75715193-75716368
FRMD4B	NA	210,192	-3,533304	uc003dnu.2	chr3:69219146-69221011	645,832	-9,020197	uc003dnu.2	chr3:69219146-69221011	NA	NA	NA	NA
FRMD6	614555	1679,68	-10,35757	uc001wzc.3	chr14:52194748-52197444	NA	NA	NA	NA	NA	NA	NA	NA
FRMD7	300628	NA	NA	NA	NA	368,446	-6,15846	uc022cdy.1	chrX:131211021-131211899	NA	NA	NA	NA
FRMD8	NA	NA	NA	NA	NA	NA	NA	NA	NA	233,211	-5,387098	uc001edu.4	chr11:65178832-65180995
FRMPD2	613323	NA	NA	NA	NA	NA	NA	NA	NA	716,916	-7,073337	uc001jgg.3	chr10:49364601-49365364
FRMPD2B	NA	NA	NA	NA	NA	NA	NA	NA	NA	464,764	-6,266805	uc001fy.4	chr10:48844036-48844799
FRRS1L	604574	NA	NA	NA	NA	NA	NA	NA	NA	701,85	-7,929096	uc004bdw.1	chr9:111899581-111899734
FRSL	607743	1282,05	-5,629612	uc001suy.3	chr12:69968736-69973562	281,453	-8,049302	uc001suy.3	chr12:69968736-69973562	NA	NA	NA	NA
FRYL	NA	2347,31	-6,484739	uc003gyt.1	chr4:48619621-48621200	NA	NA	NA	NA	274,035	-4,164841	uc003gym.1	chr4:48621544-48622651
FRZB	605083	NA	NA	NA	NA	703,864	-8,698223	uc002upa.2	chr2:183698005-183698975	NA	NA	NA	NA
FSP1	615795	242,825	-5,600257	uc001zki.3	chr15:39892232-39893080	567,686	-11,220535	uc001zki.3	chr15:39892232-39893080	220,54	-4,179799	uc001zki.3	chr15:39892232-39893080
FSTL3	605343	453,133	-4,37522	uc002ljk.1	chr19:681705-683392	NA	NA	NA	NA	NA	NA	NA	NA
FSTL4	NA	1384,62	-7,528398	uc003kym.1	chr5:132532152-132534786	717,631	-4,355081	uc003kym.1	chr5:132532152-132534786	NA	NA	NA	NA
FTHL17	300308	822,368	-6,735242	uc004dcl.1	chrX:31089358-31089518	NA	NA	NA	NA	NA	NA	NA	NA
FTMT	608847	NA	NA	NA	NA	NA	NA	NA	NA	611,867	-6,379406	uc003kss.3	chr5:121188388-121188523
FTSJ2	606906	NA	NA	NA	NA	NA	NA	NA	NA	660,441	-9,866254	uc003slm.3	chr7:2273926-2274756
FUBP1	603444	NA	NA	NA	NA	NA	NA	NA	NA	1229,93	-9,787264	uc001dli.3	chr1:78413591-78414450
FUBP3	603536	1360,58	-10,539367	uc004bzt.1	chr9:133512410-133513739	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

FUCA1	612280	NA	NA	NA	NA	355,597	-6,230,619	uc001bie.3	chr1:241,717,157,217,241,722,04	NA	NA	NA	NA
FUCA2	136820	593,396	-7,287,561	uc003qjm.3	chr6:1438,15949-1438,16843	NA	NA	NA	NA	NA	NA	NA	NA
FUND02	NA	NA	NA	NA	NA	NA	NA	NA	NA	523,766	-5,296,089	uc004fmw.3	chrX:154282948-154,285,191
FUND02P2	NA	NA	NA	NA	NA	641,955	-5,519,41	uc010ffz.1	chr2:945,18399-845,19324	NA	NA	NA	NA
FUOM	NA	585,318	-4,393,945	uc001lms.2	chr10:135,16858-135,169002	NA	NA	NA	NA	NA	NA	NA	NA
FUS	137070	522,526	-7,680,538	uc010vfi.2	chr16:31,194,165-31,194,671	NA	NA	NA	NA	688,693	-4,840,821	uc010vfi.2	chr16:31,194,165-31,194,671
FUT10	NA	NA	NA	NA	NA	NA	NA	NA	NA	835,767	-4,498,625	uc003jic.3	chr8:332,834-332,300,94
FUT11	NA	NA	NA	NA	NA	478,678	-5,591,052	uc001juy.1	chr10:75533,108-755,348,81	304,448	-6,493,437	uc001jva.3	chr10:755,354,44-755,359,76
FUT14	104230	NA	NA	NA	NA	790,225	-8,222,126	uc001pez.3	chr11:942,788,93-942,830,64	NA	NA	NA	NA
FUT9	608865	289,782	-6,659,611	uc003pop.4	chr6:96652,112-966,634,88	NA	NA	NA	NA	NA	NA	NA	NA
FUT1	610622	363,437	-5,612,617	NA	NA	352,869	-6,295,051	uc002ppq.2	chr19:503,101,24-503,104,07	NA	NA	NA	NA
FXN	608829	NA	NA	NA	NA	NA	NA	NA	NA	315,878	-5,652,384	uc004agz.2	chr9:7,168,762,9-7,169,393
FXYD5	606669	NA	NA	NA	NA	NA	NA	NA	NA	493,555	-7,094,459	uc010xsq.2	chr19:35,657,327-35,657,664
FYB	602731	587,639	-6,635,598	uc003jis.3	chr5:39,105,354-39,107,544	NA	NA	NA	NA	1138,85	-9,754,634	uc003jis.3	chr5:39,105,354-39,107,544
FZD10	606147	1070,13	-6,897,438	uc001uul.3	chr12:130,649,234-130,650,285	NA	NA	NA	NA	1650,6	-10,873,198	uc001luil.3	chr12:130,649,234-130,650,285
FZD2	606667	508,326	-5,105,848	uc002lpx.2	chr17:426,637,55-426,386,30	449,525	-4,941,699	uc002lpx.2	chr17:426,637,55-426,386,30	NA	NA	NA	NA
FZD4	604579	NA	NA	NA	NA	NA	NA	NA	NA	307,351	-6,776,111	uc001pcc.3	chr11:86,656,717-86,662,183
FZD6	603409	1448,3	-12,985,985	uc003yfh.3	chr8:104,934,738-104,934,5094	NA	NA	NA	NA	NA	NA	NA	NA
G2E3	611299	590,655	-4,641,665	uc010lpe.1	chr14:3,107,711,9-3,107,727,5	NA	NA	NA	NA	NA	NA	NA	NA
G3BP2	NA	328,283	-6,619,905	uc003hnr.3	chr4:76,667,953-76,657,061,3	1101,64	-13,402,13	uc003hnr.3	chr4:76,667,953-76,657,061,3	1940,46	-14,661,271	uc003hnr.3	chr4:76,657,953-76,657,061,3
GAB3	300482	NA	NA	NA	NA	897,779	-6,792,263	uc004fmj.1	chrX:153,903,527-153,906,454	NA	NA	NA	NA
GAB4	NA	NA	NA	NA	NA	557,326	-6,962,161	uc002zlw.3	chr22:17,442,2827-17,443,622	NA	NA	NA	NA
GABPB1	600610	846,739	-12,765,153	uc001zyc.3	chr15:50,578,077-50,578,216	1198,17	-10,664,636	uc001zyc.3	chr15:50,578,077-50,578,216	NA	NA	NA	NA
GABRA1	137160	NA	NA	NA	NA	964,987	-12,787,44	uc010jiw.3	chr5:16,132,442,9-16,132,896,5	440,105	-6,984,171	uc010jiw.3	chr5:16,132,442,9-16,132,896,5
GABRA6	137143	NA	NA	NA	NA	1094,08	-7,291,649	uc003jyu.2	chr5:16,112,8780-16,112,959,8	NA	NA	NA	NA
GABRG2	137164	NA	NA	NA	NA	1011,24	-11,912,703	uc003lvy.4	chr5:16,158,037,5-16,158,254,5	NA	NA	NA	NA
GABRR1	137161	372,088	-7,282,323	uc003pna.2	chr6:89,887,723-89,888,488	NA	NA	NA	NA	NA	NA	NA	NA
GADD45A	126335	348,53	-7,805,044	uc009wbc.2	chr1:68,153,381-68,154,021	NA	NA	NA	NA	NA	NA	NA	NA
GALC	606890	990,353	-7,036,64	uc001xvi.3	chr14:883,993,558-884,010,75	592,377	-9,367,979	uc001xvi.3	chr14:883,993,558-884,010,75	NA	NA	NA	NA
GALNS	612222	NA	NA	NA	NA	642,369	-7,308,81	uc002fma.3	chr16:88,921,536-88,921,794	834,369	-6,906,133	uc002fma.3	chr16:88,921,536-88,921,794
GALNT13	603869	647,707	-2,263,375	uc002tyr.4	chr2:15,530,7064-15,531,048,9	959,633	-6,087,396	uc002tyr.4	chr2:15,530,7064-15,531,048,9	297,384	-3,800,905	uc010fcc.1	chr2:15,525,656,94-15,526,585,2
GALNT15	615131	1552,45	-9,585,602	uc003caq.4	chr3:16,269,008-16,271,253	NA	NA	NA	NA	NA	NA	NA	NA
GALNT3	601756	499,705	-8,586,398	uc010phi.1	chr2:16,660,431,3-16,660,529,0	NA	NA	NA	NA	NA	NA	NA	NA
GALNT8	176257	NA	NA	NA	NA	607,972	-4,765,543	NA	NA	635,617	-8,723,398	uc001qne.1	chr12:4,881,764-4,881,892
GALP	611178	NA	NA	NA	NA	771,237	-6,893,114	uc002qmo.1	chr19:56,686,640-56,687,144	460,58	-1,352,47	uc002qmo.1	chr19:56,686,640-56,687,144
GALR1	600377	NA	NA	NA	NA	NA	NA	NA	NA	370,443	-5,866,022	uc002lms.4	chr18:74,980,859-74,982,096
GAPT	NA	NA	NA	NA	NA	NA	NA	NA	NA	398,497	-7,736,926	uc003jro.1	chr5:5,779,083,8-5,779,218,5
GAR1	606468	NA	NA	NA	NA	NA	NA	NA	NA	655,206	-5,301,186	uc003hzt.3	chr4:11,074,558-11,074,589,3
GARNL3	NA	NA	NA	NA	NA	430,098	-1,599,478	uc011mad.2	chr9:130,155,534-130,155,82,8	351,537	-5,234,056	uc004bqt.1	chr9:130,106,658-130,107,617
GART	138440	1053,27	-8,068,135	uc002yrk.3	chr21:34,876,238-34,876,430	NA	NA	NA	NA	NA	NA	NA	NA
GAS2	602835	NA	NA	NA	NA	NA	NA	NA	NA	851,976	-11,062,559	uc009yle.3	chr11:22,833,563-22,834,547
GAS2L1	602128	894,436	-5,190,394	uc010gvm.1	chr22:29,708,487-29,708,770	NA	NA	NA	NA	NA	NA	NA	NA
GAS8	605178	545,955	-2,432,912	uc002qih.2	chr16:90,109,754-90,111,379	502,768	-2,402,873	uc002qih.2	chr16:90,109,754-90,111,379	NA	NA	NA	NA
GATA1	305371	NA	NA	NA	NA	261,925	-5,031,061	uc004dkq.4	chrX:4,865,257,2-4,865,271,7	NA	NA	NA	NA
GATS	NA	NA	NA	NA	NA	785,879	-10,853,379	uc003uua.4	chr7:99,798,278-99,800,226	NA	NA	NA	NA
GBAS	603004	NA	NA	NA	NA	206,811	-4,605,375	uc003ire.2	chr7:56,066,766-56,067,875	NA	NA	NA	NA
GBE1	607839	661,112	-6,214,096	uc021xav.1	chr3:81,538,850-81,539,657	NA	NA	NA	NA	NA	NA	NA	NA
GBP3	600413	NA	NA	NA	NA	355,344	-5,805,202	uc001dmt.3	chr1:894,723,60-894,734,06	NA	NA	NA	NA
GBP5	611467	772,782	-7,022,278	uc001dnc.3	chr1:897,246,34-897,263,86	627,735	-5,574,275	uc001dnc.3	chr1:897,246,34-897,263,86	NA	NA	NA	NA

Table 1

GBP6	612467	602.591	-5.102371	uc001dnt.2	chr1:89851029-89853719	NA	NA	NA	NA	NA	NA	414.586	-10.684653	NA	NA	chr1:89597434-89597831
GBP7	612468	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GCA	607030	331.054	-8.815	uc002ucg.3	chr2:163216754-163219148	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GCC2	612711	1537.17	-16.631634	uc002lec.3	chr2:109124087-109125854	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GCH1	600225	1017.44	-7.49047	uc001xbh.1	chr14:55308724-55309772	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GCLC	606857	489.131	-9.716712	uc003pbv.1	chr6:53362140-53363553	NA	NA	NA	NA	NA	NA	1356.12	-9.692521	uc003pbv.1	NA	chr6:53362140-53363553
GCN1L1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	718.516	-7.577541	uc001bxo.3	NA	chr12:120565014-120565652
GCNT7	NA	1180.81	-8.739465	NA	NA	504.912	-4.114195	uc010zzg.1	chr20:55066548-55066612	873.676	-8.057442	uc010zcg.1	NA	NA	NA	chr20:55066548-55066612
GDA	139260	NA	NA	NA	NA	1001.15	-3.608502	uc011lse.2	chr9:74863259-74867140	1009.33	-4.307779	uc011lse.2	NA	NA	NA	chr9:74863259-74867140
GDAP1	606598	NA	NA	NA	NA	329.676	-5.818446	uc003yah.3	chr8:75276603-75279335	NA	NA	NA	NA	NA	NA	NA
GDF15	605312	NA	NA	NA	NA	NA	NA	NA	NA	1055.78	-11.622865	uc002niv.2	NA	NA	NA	chr19:18499746-18499986
GDNF	600837	686.512	-5.458576	uc011cpd.2	chr5:37812779-37815752	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GDPD1	616317	512.614	-1.780268	uc002ikj.3	chr17:57350249-57350382	NA	NA	NA	NA	336.464	-5.678282	uc002mk.2	NA	NA	NA	chr17:57351135-57353330
GDPD5	609632	381.985	-7.312371	uc009yue.1	chr11:75153809-75154117	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GEMIN7	607419	NA	NA	NA	NA	692.939	-7.349378	uc002pdp.1	chr19:45593769-45594782	NA	NA	NA	NA	NA	NA	NA
GEMIN8	300962	NA	NA	NA	NA	NA	NA	NA	NA	1131.02	-4.980835	uc004cwh.3	NA	NA	NA	chrX:14024845-14027031
GEM1	612449	NA	NA	NA	NA	NA	NA	NA	NA	854.405	-7.545694	uc002rct.2	NA	NA	NA	chr2:17963207-17966632
GFM1	606639	631.119	-10.963277	uc003fcd.3	chr3:158399959-158400222	1187.51	-17.205622	uc003gcd.3	chr3:158399959-158400222	NA	NA	NA	NA	NA	NA	NA
GGA2	606005	372.756	-4.474012	uc002dlq.3	chr16:23474863-23478910	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GGT5	137168	590.948	-6.591359	uc002zrq.4	chr22:24615622-24616084	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GHLR	605353	808.446	-5.806062	uc010hdc.2	chr3:10327434-10327558	NA	NA	NA	NA	868.58	-4.605842	uc003bjv.1	NA	NA	NA	chr3:10327434-10327527
GID4	NA	NA	NA	NA	NA	500.777	-5.296089	uc002gsg.1	chr17:17968558-17971718	NA	NA	NA	NA	NA	NA	NA
GID8	611625	NA	NA	NA	NA	NA	NA	NA	NA	316.656	-4.031126	uc002dyd.3	NA	NA	NA	chr20:61576265-61579827
GLF	609342	509.076	-6.433731	uc001mol.3	chr11:59596746-59596956	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GIMAP2	608085	569.59	-6.69738	uc003who.3	chr7:150390389-150390728	NA	NA	NA	NA	412.609	-6.407206	uc003who.3	NA	NA	NA	chr7:150390389-150390728
GIMAP4	608087	NA	NA	NA	NA	1137.09	-5.471148	uc011kuu.2	chr7:150270149-150270308	1090.19	-8.427373	uc011kuu.2	NA	NA	NA	chr7:150270149-150270308
GIN53	610610	498.933	-6.040669	uc002ent.4	chr16:58438634-58440048	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GIPC2	NA	NA	NA	NA	NA	761.653	-9.047105	uc001dik.3	chr1:78601428-78603112	NA	NA	NA	NA	NA	NA	NA
GIT2	608564	NA	NA	NA	NA	578.792	-5.597539	uc001tpq.2	chr12:110367607-110370782	347.697	-6.887039	uc001tpq.2	NA	NA	NA	chr12:110367607-110370782
GJA3	121015	NA	NA	NA	NA	NA	NA	NA	NA	594.313	-8.586587	uc001umx.1	NA	NA	NA	chr13:20712395-20716119
GJB3	603324	NA	NA	NA	NA	464.944	-4.629077	uc001bxv.3	chr1:35251177-35251967	NA	NA	NA	NA	NA	NA	NA
GJC1	608655	NA	NA	NA	NA	NA	NA	NA	NA	546.21	-8.060838	uc002hj.3	NA	NA	NA	chr17:42875816-42881994
GJC3	611925	597.309	-7.899391	uc011kpl.2	chr7:99520892-99521167	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GKAP1	611356	NA	NA	NA	NA	NA	NA	NA	NA	385.637	-5.461205	uc004amy.3	NA	NA	NA	chr9:86354336-86354611
GLA	300644	NA	NA	NA	NA	388.238	-10.788676	uc011mrj.1	chrX:100656118-100656530	NA	NA	NA	NA	NA	NA	NA
GLDN	608603	240.079	-4.620964	uc002aba.3	chr15:51696952-51700209	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GLE1	603371	NA	NA	NA	NA	NA	NA	NA	NA	838.893	-7.369056	uc004bvj.3	NA	NA	NA	chr9:131303450-131304580
GLG1	600753	NA	NA	NA	NA	NA	NA	NA	NA	1282.86	-10.380517	uc002fcw.4	NA	NA	NA	chr16:74481326-74485953
GLI2	165230	NA	NA	NA	NA	NA	NA	NA	NA	374.052	-4.609851	uc010vyu.1	NA	NA	NA	chr2:121709030-121709339
GLI3	165240	677.321	-6.553227	uc011kbg.2	chr7:42000548-42003927	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GLIPR2	607141	784.96	-2.814864	uc011lpj.1	chr9:36151033-36151768	NA	NA	NA	NA	740.209	-8.203101	uc011lpj.1	NA	NA	NA	chr9:36151033-36151768
GLIS3	610192	936.278	-5.799423	uc010mhf.1	chr9:3824128-3828271	807.78	-9.246272	uc003zhy.1	chr9:3855437-3855967	552.569	-7.744022	uc010mhf.1	NA	NA	NA	chr9:3824128-3828271
GLRA2	305990	NA	NA	NA	NA	543.498	-6.989327	uc004cwe.4	chrX:14748608-14749933	NA	NA	NA	NA	NA	NA	NA
GLRA3	600421	NA	NA	NA	NA	NA	NA	NA	NA	947.907	-12.449671	uc003fty.1	NA	NA	NA	chr4:175563198-175564936
GLRA4	NA	NA	NA	NA	NA	NA	NA	NA	NA	859.062	-8.585353	uc010nou.2	NA	NA	NA	chrX:102973502-102973888
GLRB	138492	NA	NA	NA	NA	NA	NA	NA	NA	449.626	-6.470214	uc003lpj.2	NA	NA	NA	chr4:158091881-158093242
GLRX	600443	NA	NA	NA	NA	NA	NA	NA	NA	519.337	-4.565581	uc003kln.4	NA	NA	NA	chr5:95149553-95150661
GLRX2	606820	NA	NA	NA	NA	NA	NA	NA	NA	679.554	-10.139386	uc001gsz.2	NA	NA	NA	chr1:193065595-193065754
GLRX3	612754	NA	NA	NA	NA	NA	NA	NA	NA	208.41	-4.641606	uc001lkn.2	NA	NA	NA	chr10:131978377-131978646

Table 1

GLRX5	609588	NA	NA	NA	NA	555.405	-7.675977	uc001yem.1	chr14:96010463-96011055	NA	NA	NA	NA
GLS	138280	NA	NA	NA	NA	915.295	-11.581377	uc002usd.2	chr2:191760002-191761227	NA	NA	NA	NA
GM2A	613109	628.067	-5.948531	uc003lir.4	chr5:150647013-150649953	NA	NA	NA	NA	NA	NA	NA	NA
GMEB1	604409	NA	NA	NA	NA	NA	NA	NA	NA	1483.91	-17.804893	uc001bqz.3	chr1:29041286-29042115
GMPPB	615320	550.579	-7.533205	uc003cxk.1	chr3:497589932-49759184	NA	NA	NA	NA	NA	NA	NA	NA
GNB2L1	176981	NA	NA	NA	NA	828.664	-9.456162	uc011dhl.2	chr5:180668873-180667312	NA	NA	NA	NA
GNB3	139130	NA	NA	NA	NA	237.906	-6.473777	uc001qrc.3	chr12:6956063-6956557	NA	NA	NA	NA
GNB4	610863	NA	NA	NA	NA	636.955	-5.936995	uc003jfv.4	chr3:179113876-179119000	NA	NA	NA	NA
GNB7	604430	NA	NA	NA	NA	1311.29	-9.456005	uc002lwd.2	chr19:2511218-2515019	819.106	-10.023752	uc002lwd.2	chr19:2511218-2515019
GNL1	143024	NA	NA	NA	NA	212.891	-4.441025	uc011dmi.2	chr6:30509155-30513848	666.722	-3.901655	uc011dmi.2	chr6:30509155-30513848
GNL3	608011	NA	NA	NA	NA	650.285	-6.299344	uc003dfd.3	chr3:52728292-52728510	823.569	-8.203496	uc003dfd.3	chr3:52728292-52728510
GNN		NA	NA	NA	NA	227.006	-5.26967	uc009zuh.2	chr12:104307805-104309225	NA	NA	NA	NA
GNPTAB	607840	NA	NA	NA	NA	NA	NA	NA	NA	408.546	-7.350016	uc001htt.3	chr12:102139275-102140941
GNRHR	138850	NA	NA	NA	NA	853.116	-7.358474	uc003hdm.3	chr4:68603099-68606306	NA	NA	NA	NA
GNS	607664	NA	NA	NA	NA	326.351	-8.724808	uc001ssf.3	chr12:65107222-65110520	NA	NA	NA	NA
GOLGA3	602581	1312.16	-14.043839	uc001lukz.1	chr12:133345495-133349690	266.169	-2.815295	uc001ukz.1	chr12:133345495-133349690	NA	NA	NA	NA
GOLGA8B	NA	274.284	-8.757456	uc010uks.1	chr15:72958684-72959738	NA	NA	NA	NA	NA	NA	NA	NA
GOLGA6L10	NA	531.124	-11.55694	uc021ssn.1	chr15:82633123-82635129	NA	NA	NA	NA	536.439	-0.526154	uc021ssn.1	chr15:82633123-82635129
GOLGA8IP	NA	466.089	-6.674369	uc001yyh.1	chr15:23262503-23262743	NA	NA	NA	NA	NA	NA	NA	NA
GOLPH3	612207	NA	NA	NA	NA	812.452	-7.2485	uc003jnp.1	chr5:32124824-32126317	NA	NA	NA	NA
GOLT1B	615078	275.602	-8.368115	uc001rez.2	chr12:21668642-21671337	NA	NA	NA	NA	NA	NA	NA	NA
GON4L	610393	581.207	-3.545006	uc001fly.1	chr1:155719510-155720374	NA	NA	NA	NA	1465.21	-16.83926	uc001fmc.3	chr1:155734576-155734673
GORASP2	608693	NA	NA	NA	NA	1999.34	-15.973411	uc002ugj.3	chr2:171822641-171823643	NA	NA	NA	NA
GOSR1	604026	NA	NA	NA	NA	NA	NA	NA	NA	1061.94	-10.747866	uc002hfc.1	chr17:28811892-28812280
GOSR2	604027	NA	NA	NA	NA	642.859	-2.288994	uc002iky.3	chr17:45012647-45014205	NA	NA	NA	NA
GP6	605546	NA	NA	NA	NA	477.888	-4.551622	uc002qli.3	chr19:55525075-55525449	NA	NA	NA	NA
GPALPP1	NA	NA	NA	NA	NA	NA	NA	NA	NA	707.396	-4.582683	uc001uzq.3	chr13:45602139-45602404
GPAM	602395	NA	NA	NA	NA	1003.13	-7.103233	uc001kzq.1	chr10:113914758-113916994	NA	NA	NA	NA
GPC3	300037	NA	NA	NA	NA	1411.16	-16.024273	uc004exe.2	chrX:132669776-132670151	1145.21	-10.450789	uc004exe.2	chrX:132669776-132670151
GPC5	602446	851.283	-10.241773	uc010lif.2	chr13:93518693-93519487	NA	NA	NA	NA	NA	NA	NA	NA
GPC6	604404	214.994	-3.411675	uc001vlt.3	chr13:95055472-95060273	223.857	1.985351	uc010lig.1	chr13:94958513-94958788	960.96	-8.751567	uc001vlt.1	chr13:94482868-94484342
GPCPD1	614124	NA	NA	NA	NA	370.783	-11.2352	uc002wmd.4	chr20:5525080-5528306	671.138	-8.302363	uc002wmd.4	chr20:5525080-5528306
GPHA2	609651	NA	NA	NA	NA	NA	NA	NA	NA	633.004	-5.68575	uc001lcca.3	chr11:64701943-64702244
GPHN	603930	NA	NA	NA	NA	1656.65	-6.922271	uc001xiw.3	chr14:67525557-67525733	NA	NA	NA	NA
GPKOW	NA	NA	NA	NA	NA	NA	NA	NA	NA	539.771	-5.144435	uc004dmr.3	chrX:4896902-48970558
GPLD1	602515	758.828	-8.948163	uc010jpr.1	chr6:24447759-24448093	222.364	-4.499585	uc010jpr.1	chr6:24447759-24448093	NA	NA	NA	NA
GPMEA	601275	NA	NA	NA	NA	546.6	-6.224167	uc011ckj.2	chr4:176554088-176556055	NA	NA	NA	NA
GNP3	NA	NA	NA	NA	NA	285.124	-4.421335	uc001lqr.3	chr12:110890291-110890838	NA	NA	NA	NA
GPR1	600239	799.161	-9.667094	uc002vbl.4	chr2:207040042-207040903	NA	NA	NA	NA	395.275	-3.439412	uc002vbl.4	chr2:207040042-207040903
GPR137C	NA	757.374	-11.828064	uc001wzl.4	chr14:53101834-53104431	NA	NA	NA	NA	NA	NA	NA	NA
GPR157	NA	NA	NA	NA	NA	NA	NA	NA	NA	508.056	-5.101542	uc001apr.3	chr1:9169158-9171214
GPR171	NA	NA	NA	NA	NA	346.069	-7.007312	uc003eyq.4	chr3:150915619-150916213	NA	NA	NA	NA
GPR19	602927	586.762	-8.979627	uc001rar.3	chr12:12813995-12814134	NA	NA	NA	NA	NA	NA	NA	NA
GPR35	602646	NA	NA	NA	NA	NA	NA	NA	NA	465.086	-4.819481	uc010fzh.2	chr2:241570300-241570676
GPR37L1	NA	249.015	-4.794158	uc001gxj.3	chr1:202097685-202098634	NA	NA	NA	NA	NA	NA	NA	NA
GPR4	600551	903.261	-8.124066	uc002pcm.3	chr19:46093023-46094035	NA	NA	NA	NA	NA	NA	NA	NA
GPR45	604838	NA	NA	NA	NA	251.641	-4.15004	uc002lco.1	chr2:105859435-105859924	NA	NA	NA	NA
GPR63	606915	1134.99	-12.644913	uc003pou.3	chr6:97241998-97246347	1096.24	-10.97671	uc003pou.3	chr6:97241998-97246347	NA	NA	NA	NA
GPR75	606704	1327.86	-9.686062	uc002rxo.3	chr2:54080050-54080270	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

GPR32	300748	566.831	-9.504369	uc004dfl.3	chrX:41587291-41589388	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GPR34	606383	269.256	-7.635547	uc001slu.3	chr12:54756229-54756444	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GPR87	606379	330.89	-3.48427	uc003eyt.2	chr3:151011876-151011956	794.18	-8.335227	NA	NA	NA	NA	573.915	-5.801158	uc003eyt.2	chr3:151011876-151011956	NA	NA
GPRASP1	300417	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	585.914	-6.558034	uc004ejl.4	chrX:101913030-101914010	NA	NA
GPRIN3	611241	NA	NA	NA	NA	1402.16	-8.007053	uc003hsm.1	chr4:30165429-90168930	NA	NA	NA	NA	NA	NA	NA	NA
GPM2	609245	743.058	-3.327729	uc010ovc.2	chr1:109472583-109473044	444.655	-4.699884	uc010ovc.2	chr1:109472583-109473044	719.784	-0.823285	uc010ovc.2	-0.823285	uc010ovc.2	chr1:109472563-109473044	NA	NA
GPX1	138320	259.836	-5.881273	uc021wxw.1	chr3:49394609-49394820	NA	NA	NA	NA	615.166	-7.258569	uc021wxw.1	-7.258569	uc021wxw.1	chr3:49394609-49394820	NA	NA
GPX8	NA	NA	NA	NA	NA	NA	NA	NA	NA	281.34	-6.998558	uc003jpr.2	-6.998558	uc003jpr.2	chr5:54459952-54463129	NA	NA
GRAMD2	NA	NA	NA	NA	NA	550.368	-4.820783	uc010ukh.2	chr15:72452147-72454349	NA	NA	NA	NA	NA	NA	NA	NA
GRAMD3	NA	NA	NA	NA	NA	NA	NA	NA	NA	229.647	-4.482767	uc011twc.2	-4.482767	uc011twc.2	chr5:125828649-125829853	NA	NA
GRAMD4	613691	NA	NA	NA	NA	1054.4	-7.404716	uc003bhx.3	chr22:47073149-47075688	1200.48	-10.957936	uc003bhx.3	-10.957936	uc003bhx.3	chr22:47073149-47075688	NA	NA
GRAP2	604518	NA	NA	NA	NA	NA	NA	NA	NA	715.278	-7.248455	uc003ayh.2	-7.248455	uc003ayh.2	chr22:40367089-40367384	NA	NA
GREB1L	NA	NA	NA	NA	NA	NA	NA	NA	NA	420.649	-2.431635	uc002ktf.1	-2.431635	uc002ktf.1	chr18:19034599-19035091	NA	NA
GRHL2	608576	222.941	-2.428788	uc010mbt.1	chr8:102555788-102556298	NA	NA	NA	NA	440.862	-5.490174	uc010mbt.1	-5.490174	uc010mbt.1	chr8:102555788-102556298	NA	NA
GRIA2	138247	478.105	-4.37695	uc011ciu.1	chr4:158282726-158282804	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GRIA3	305915	1736.1	-15.383554	uc004etq.4	chrX:122622564-122624766	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GRI4	138246	650.823	-8.438075	uc001piu.1	chr11:105782635-105784231	NA	NA	NA	NA	563.307	-6.678257	uc010qmf.1	-6.678257	uc010qmf.1	chr10:87359312-87362029	NA	NA
GRID1	610659	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GRIK1	138245	707.712	-11.248785	uc002ymt.3	chr21:30909254-30909550	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GRIK2	138244	1410.42	-4.070226	uc021zdl.1	chr6:102192585-102193018	1251.7	-6.487024	uc003pqn.3	chr6:102337743-102338007	777.659	-1.386778	uc021zdl.1	-1.386778	uc021zdl.1	chr6:102192585-102193018	NA	NA
GRIN3A	606650	NA	NA	NA	NA	627.249	-7.840127	uc004bbq.1	chr9:104337982-104340045	NA	NA	NA	NA	NA	NA	NA	NA
GRM7	604101	NA	NA	NA	NA	743.9	-10.867232	uc003bqm.2	chr3:7782094-7783218	NA	NA	NA	NA	NA	NA	NA	NA
GRM8	601116	338.353	-6.836101	uc003vir.2	chr7:126078652-126079172	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GRP	137260	818.068	-11.220853	uc002lhu.3	chr18:56897690-56898002	809.861	-11.220853	uc002lhu.3	chr18:56897690-56898002	NA	NA	NA	NA	NA	NA	NA	NA
GRPEL2	NA	644.539	-4.553067	uc003lqj.3	chr5:148730846-148734146	832.479	-4.141222	uc003lqj.3	chr5:148730846-148734146	583.489	-5.443081	uc003lqj.3	-5.443081	uc003lqj.3	chr5:148730846-148734146	NA	NA
GRSF1	604851	NA	NA	NA	NA	1111.23	-9.644448	uc011caz.1	chr4:71681499-71686578	NA	NA	NA	NA	NA	NA	NA	NA
GRTP1	NA	1033.47	-6.486554	uc001vtn.3	chr13:113978505-113978802	NA	NA	NA	NA	664.001	-4.486431	NA	NA	NA	NA	NA	NA
GRXCR1	613283	1189.06	-16.082854	uc003gwt.3	chr4:43032558-43032675	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GSDMB	611221	NA	NA	NA	NA	965.377	-6.703814	uc010cwi.3	chr17:38060848-38061064	NA	NA	NA	NA	NA	NA	NA	NA
GSDMC	608384	NA	NA	NA	NA	567.414	-6.215394	uc003ysr.3	chr8:130760442-130760746	NA	NA	NA	NA	NA	NA	NA	NA
GSR	138300	NA	NA	NA	NA	1640.99	-15.053228	uc003xrh.2	chr8:30535580-30537036	NA	NA	NA	NA	NA	NA	NA	NA
GSTA1	138359	NA	NA	NA	NA	NA	NA	NA	NA	523.709	-6.476277	uc003paz.3	-6.476277	uc003paz.3	chr6:52656178-52656655	NA	NA
GSTM2	138380	818.093	-6.737641	uc010ovt.2	chr1:110225829-110226619	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GSTM3	138390	NA	NA	NA	NA	746.462	-6.673209	uc001dyo.2	chr1:110278554-110279692	NA	NA	NA	NA	NA	NA	NA	NA
GSTM4	138333	557.652	-10.354395	uc009wfl.2	chr1:110199547-110199958	NA	NA	NA	NA	773.153	-4.352682	uc001dyn.3	-4.352682	uc001dyn.3	chr1:110260049-110260890	NA	NA
GSTM5	138385	NA	NA	NA	NA	549.625	-6.054358	uc002ivo.3	chr2:1447703581-1447704702	484.01	-13.616393	uc010qgw.1	-13.616393	uc010qgw.1	chr10:106048393-106048815	NA	NA
GTDC1	610165	666.982	-10.455262	uc002lvo.3	chr2:1447703581-1447704702	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GTF2A2	600519	NA	NA	NA	NA	NA	NA	NA	NA	1132.57	-7.260382	uc002zgg.3	-7.260382	uc002zgg.3	chr15:59930261-59931330	NA	NA
GTF2E2	189964	603.028	-6.011422	uc003xlg.3	chr8:30436031-30436437	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GTF2H2C	NA	548.867	-10.493739	uc003jwx.4	chr5:68888026-68888729	NA	NA	NA	NA	281.659	-7.915613	uc003jww.1	-7.915613	uc003jww.1	chr5:68874584-68874629	NA	NA
GTF2I	601679	906.229	-10.355831	uc003uat.3	chr7:74131276-74131386	1268.65	-10.088877	uc003uat.3	chr7:74131276-74131386	1221.5	-5.455973	uc003uba.2	-5.455973	uc003uba.2	chr7:74173169-74175020	NA	NA
GTF2IRD2B	608900	NA	NA	NA	NA	422.827	-4.4703	uc003ubs.4	chr7:74539125-74540018	NA	NA	NA	NA	NA	NA	NA	NA
GTF3C3	604888	NA	NA	NA	NA	205.683	-6.119731	uc002ult.3	chr2:197627756-197629286	NA	NA	NA	NA	NA	NA	NA	NA
GTF3C6	611784	456.111	-6.351604	uc003pum.3	chr6:111288994-111289091	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GTPBP2	607434	869.923	-5.418562	uc010jyv.3	chr6:43588218-43589350	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GTPBP4	NA	1288.89	-10.044339	uc001ift.3	chr10:1063168-1063708	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GTPBP6	300124	635.265	-7.463472	uc004cpe.1	chrX:221426-221740	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
GTSF1	NA	NA	NA	NA	NA	1197.86	-11.818668	uc001sgb.3	chr12:54849736-54849937	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

GUCA1A	600364	1122.55	-13.049034	uc003onx.3	chr6:42147142-42147794	NA	NA	NA	NA	609.245	-6.359267	uc003onx.3	chr6:42147142-42147794
GUCY1A3	139396	969.772	-7.017034	uc003lov.3	chr4:156651384-156659214	NA	NA	NA	NA	NA	NA	NA	NA
GUF1	NA	606.411	-7.451648	uc003gww.4	chr4:44700699-44702697	385.801	-4.93645	uc003gww.4	chr4:44700699-44702697	NA	NA	NA	NA
GULP1	608165	656.015	-16.476089	uc002uql.3	chr2:189458689-189460652	NA	NA	NA	NA	NA	NA	NA	NA
GUSB	611499	NA	NA	NA	NA	NA	NA	NA	NA	604.112	-7.304119	uc003tun.3	chr7:65425673-65425883
GUSBP1	NA	1001.99	-8.432764	uc003jgl.3	chr5:21470807-21471090	NA	NA	NA	NA	750.716	-5.3711	uc003jgl.3	chr5:21470807-21471090
GYG1	603942	302.975	-4.089288	uc011bnp.2	chr3:148741953-148742059	NA	NA	NA	NA	948.431	-3.215325	uc003wmw.3	chr3:148744721-148745456
GYG2	300198	661.412	-6.137429	uc004cqs.1	chrX:2799255-2800861	NA	NA	NA	NA	NA	NA	NA	NA
GYG2P1	NA	NA	NA	NA	NA	NA	NA	NA	NA	1151.16	-7.772186	uc022cjl.1	chrY:14517915-14518274
GYPE1	138590	NA	NA	NA	NA	NA	NA	NA	NA	1028.84	-5.799805	uc003ljj.3	chr4:144792019-144793405
GZF1	613842	560.696	-7.635321	uc002wsy.3	chr20:23351079-23353683	NA	NA	NA	NA	NA	NA	NA	NA
GZMK	600784	NA	NA	NA	NA	722.612	-8.298611	uc003jpl.1	chr5:54329755-54329960	NA	NA	NA	NA
H1F0	142708	NA	NA	NA	NA	NA	NA	NA	NA	1323.99	-10.044178	uc003aty.3	chr22:38202137-38203443
H1FX	602785	773.185	-6.755107	uc003ek.3	chr3:129033614-129034103	NA	NA	NA	NA	654.284	-6.85454	uc003ek.3	chr3:129033614-129034103
H2AFY	610054	NA	NA	NA	NA	235.151	-5.804303	uc003lam.1	chr5:134670071-134670665	NA	NA	NA	NA
H2AFZ	142763	250.618	-5.622688	uc003hvo.1	chr4:100869244-100869618	714.97	-7.821444	uc003hvn.1	chr4:100869243-100870603	1115.95	-4.529025	uc003hvn.1	chr4:100869243-100870603
H3F3C	616134	423.505	-6.710187	uc001rkr.3	chr12:31944119-31944692	NA	NA	NA	NA	NA	NA	NA	NA
HACD3	615940	248.654	-4.06825	uc002apc.3	chr15:65868718-65870693	NA	NA	NA	NA	NA	NA	NA	NA
HACD4	615941	NA	NA	NA	NA	225.269	-8.49867	uc010miq.2	chr9:21003623-21007035	NA	NA	NA	NA
HADHA	600890	NA	NA	NA	NA	280.368	-6.706005	uc010ykt.1	chr2:26434806-26435369	NA	NA	NA	NA
HAGH	138760	400.755	-4.620363	uc002cmz.3	chr16:1859104-1859283	NA	NA	NA	NA	NA	NA	NA	NA
HAD1	605023	969.455	-3.749254	uc002wmw.1	chr20:7863631-7864239	836.527	-9.767606	uc002wmw.1	chr20:7863631-7864239	907.79	-2.680614	uc002wmw.1	chr20:7863631-7864239
HAP1	600947	1641.66	-12.465227	uc002hxm.1	chr17:39878891-39880952	NA	NA	NA	NA	NA	NA	NA	NA
HARS	142810	NA	NA	NA	NA	329.968	-4.314917	uc003lgu.3	chr5:140053490-140053841	NA	NA	NA	NA
HARS2	600783	495.555	-5.163575	uc003lpx.3	chr5:140078138-140078890	NA	NA	NA	NA	NA	NA	NA	NA
HAS2	601636	NA	NA	NA	NA	NA	NA	NA	NA	452.084	-8.858592	uc003yph.2	chr8:122625271-122626348
HAS3	602428	NA	NA	NA	NA	NA	NA	NA	NA	878.021	-6.750959	uc010cft.3	chr16:69149170-69151570
HAT1	603053	919.158	-12.130504	uc010fiq.2	chr2:172844358-172845768	NA	NA	NA	NA	NA	NA	NA	NA
HAUS2	613429	NA	NA	NA	NA	555.61	-5.128775	uc001lze.3	chr15:42859015-42862190	NA	NA	NA	NA
HAUS3	613430	563.613	-5.861762	uc011bvj.1	chr4:2229191-2230137	NA	NA	NA	NA	NA	NA	NA	NA
HAUS4	613431	NA	NA	NA	NA	797.1	-9.780509	uc001wht.3	chr14:23415437-23415733	NA	NA	NA	NA
HAUS8	613434	1011.5	-16.975417	uc002nle.3	chr19:17160571-17160682	NA	NA	NA	NA	NA	NA	NA	NA
HAVCR1	606518	NA	NA	NA	NA	476.708	-5.594051	uc011ddl.1	chr5:156456531-156456598	NA	NA	NA	NA
HAVCR2	606652	NA	NA	NA	NA	1451.7	-16.894046	uc003lwk.2	chr5:156512843-156514112	1018.94	-7.264807	uc003lwk.2	chr5:156512843-156514112
HBBI	141900	272.765	-4.783462	uc001mae.1	chr11:5246696-5246827	NA	NA	NA	NA	NA	NA	NA	NA
HBG1	142200	NA	NA	NA	NA	1292.27	-8.499943	uc001mah.1	chr11:5269502-5269588	NA	NA	NA	NA
HBG2	142250	NA	NA	NA	NA	468.41	-4.294229	uc001mai.1	chr11:5269502-5269588	NA	NA	NA	NA
HBP1	NA	707.129	-3.232032	uc011klv.2	chr7:106841877-106842974	NA	NA	NA	NA	844.066	-5.659931	uc011klv.2	chr7:106841877-106842974
HCCS	300056	NA	NA	NA	NA	493.94	-4.919721	uc004cuj.3	chrX:11139931-11141204	NA	NA	NA	NA
HCFC2	607926	567.08	-8.713057	uc001tkj.4	chr12:104497052-104500304	NA	NA	NA	NA	NA	NA	NA	NA
HCM1	602780	NA	NA	NA	NA	NA	NA	NA	NA	896.746	-8.295173	uc003jok.3	chr5:45255052-45262022
HCRTR1	602392	NA	NA	NA	NA	NA	NA	NA	NA	238.217	-4.925141	uc009vrx.2	chr1:32092582-32092919
HDAC1	601241	1114.36	-10.665396	uc001bvb.1	chr1:32798646-32799224	NA	NA	NA	NA	NA	NA	NA	NA
HDAC11	607226	425.649	-3.397031	uc010neb.3	chr3:13545978-13547924	499.568	-7.300275	uc003bvy.3	chr3:13546184-13547924	NA	NA	NA	NA
HDAC5	605315	468.205	-5.539813	uc002lfd.1	chr17:42154121-42155743	NA	NA	NA	NA	289.983	-10.674499	uc003qaa.1	chr6:125596496-125597291
HDDC2	NA	NA	NA	NA	NA	221.264	-5.985994	uc003qaa.1	chr6:125596496-125597291	416.882	-6.391384	uc002lcs.3	chr18:44633781-446335052
HDHD2	NA	NA	NA	NA	NA	NA	NA	NA	NA	678.416	-4.868837	uc002waz.3	chr2:242166682-242169015
HDLBP	142695	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HDX	NA	479.116	-5.551374	uc004eek.2	chrX:83572882-83576896	267.539	-5.733285	uc004eek.2	chrX:83572882-83576896	NA	NA	NA	NA

Table 1

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HEATR1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1354.11	-17.402569	uc009xgh.2	chr1:236712305-236714201
HEATRA	NA	NA	NA	NA	NA	NA	743.345	-5.923901	uc010ipk.1	chr14:31803518-31803606	NA	NA	NA	NA
HEATRB	NA	991.452	-13.547208	uc010czy.1	chr2:37208153-37208632	NA	NA	NA	NA	NA	603.061	-5.432614	uc010ezy.1	chr2:37208153-37208632
HEATR9	NA	444.842	-5.591052	uc002hke.1	chr17:34181960-34182066	296.258	296.258	-3.56398	uc002hke.1	chr17:34181960-34182066	NA	NA	NA	NA
HECA	607977	NA	NA	NA	NA	NA	2242.09	-21.730613	uc003qin.3	chr6:139498243-139501946	NA	NA	NA	NA
HECTD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	408.483	-5.724804	uc001wra.1	chr14:31569324-31570135
HECTD2	NA	300.935	-8.212902	uc001kth.2	chr10:933221966-933222967	504.901	-7.264428	uc001kth.2	uc001kth.2	chr10:933221966-933222967	986.993	-7.728285	uc001kth.2	chr10:933221966-933222967
HECTD3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	472.745	-4.570054	uc001cmx.4	chr1:45468220-45469163
HECTD4	NA	943.174	-9.121611	uc001ttt.3	chr12:112687361-112687931	NA	NA	NA	NA	NA	NA	NA	NA	NA
HELLS	603946	NA	NA	NA	NA	NA	NA	NA	NA	NA	684.372	-9.271534	uc001kjs.3	chr10:96361380-96361856
HELQ	606769	1409.43	-10.815639	uc003hom.3	chr4:84328499-84328605	NA	NA	NA	NA	NA	NA	NA	NA	NA
HELZ	606699	NA	NA	NA	NA	640.27	-4.137071	uc002jrk.4	uc002jrk.4	chr17:65066554-65074367	601.445	-6.541207	uc010der.3	chr17:65104267-65104546
HEPACAM2	614133	NA	NA	NA	NA	NA	NA	NA	NA	NA	311.766	-5.603029	uc010Hf.3	chr7:92817899-92818539
HEPH	300167	NA	NA	NA	NA	1089.47	-7.263028	uc011moz.2	uc011moz.2	chrX:65486515-65487230	NA	NA	NA	NA
HERC1	605109	639.61	-9.796354	uc002amp.3	chr15:63900817-63901279	NA	NA	NA	NA	NA	NA	NA	NA	NA
HERC2	605837	530.16	-5.038391	uc001zbn.1	chr15:28435347-28436077	NA	NA	NA	NA	NA	NA	NA	NA	NA
HERC4	609248	454.693	-6.571994	uc021pr.1	chr10:69724549-69726415	722.99	-7.705469	uc009xpq.3	uc009xpq.3	chr10:69681656-69682687	NA	NA	NA	NA
HEXB	606873	258.939	-7.773584	uc003kdd.3	chr5:74017001-74017113	NA	NA	NA	NA	NA	NA	NA	NA	NA
HEXDC	NA	NA	NA	NA	NA	255.801	-5.0142	uc010wvn.1	uc010wvn.1	chr17:80398117-80398408	NA	NA	NA	NA
HEXIM1	607328	NA	NA	NA	NA	346.194	-7.93743	uc002lig.3	uc002lig.3	chr17:43227638-43229468	NA	NA	NA	NA
HHIP	606178	213.402	-4.052466	uc003jir.2	chr4:145581123-145581180	943.94	-7.878725	uc003jls.2	uc003jls.2	chr4:145659110-145659881	NA	NA	NA	NA
HIATL1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	292.197	-5.767179	uc004aur.3	chr9:97221695-97223202
HIGD1A	NA	NA	NA	NA	NA	1625.03	-10.161489	uc010hid.3	uc010hid.3	chr3:42824400-42826762	NA	NA	NA	NA
HILPDA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	574.707	-6.05046	uc003vne.4	chr7:128097515-128098472
HIP1R	605613	NA	NA	NA	NA	NA	NA	NA	NA	NA	402.888	-4.676168	uc001ludg.1	chr12:123341796-123342447
HIPK1	608003	426.473	-4.37522	uc001oem.3	chr1:114516135-114520491	NA	NA	NA	NA	NA	234.361	-5.10492	uc001eem.3	chr1:114516135-114520491
HISTH2AB	602795	270.781	-4.116528	NA	NA	643.996	-4.373225	uc003nft.1	uc003nft.1	chr6:26033320-26033403	NA	NA	NA	NA
HIVEP1	194540	906.098	-12.092224	uc003nac.3	chr6:12164695-12165232	999.223	-6.385728	uc003nac.3	uc003nac.3	chr6:12164695-12165232	1145.13	-10.720855	uc003nac.3	chr6:12164695-12165232
HIVEP2	143054	1291.41	-8.577927	uc003qjd.3	chr6:143072604-143074243	NA	NA	NA	NA	NA	590.38	-7.042919	uc003qjd.3	chr6:143072604-143074243
HJURP	612667	1496.48	-9.264957	uc002vvg.3	chr2:234745486-234746222	NA	NA	NA	NA	NA	634.485	-7.534397	uc002vvg.3	chr2:234745486-234746222
HKR1	165250	510.586	-12.129491	uc002ofy.3	chr19:37854678-37855357	NA	NA	NA	NA	NA	264.521	-8.162035	uc002ofz.3	chr19:37850588-37850676
HLF	142385	980.928	-7.016767	uc002lug.1	chr17:53398241-53402426	NA	NA	NA	NA	NA	NA	NA	NA	NA
HLTF	603257	NA	NA	NA	NA	591.192	-4.146581	uc003ewq.1	uc003ewq.1	chr3:148747904-148749150	NA	NA	NA	NA
HMBX1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	713.649	-8.716263	uc010lvd.3	chr8:28906632-28906838
HMB5	609806	NA	NA	NA	NA	NA	NA	NA	NA	NA	922.199	-7.905713	uc009aoa.2	chr11:118962904-118963521
HMCE5	NA	1051.82	-8.505098	uc003elt.3	chr3:129023669-129024135	788.633	-8.431328	uc003elt.3	uc003elt.3	chr3:129023669-129024135	NA	NA	NA	NA
HMG20A	605534	NA	NA	NA	NA	NA	NA	NA	NA	NA	503.862	-5.723396	uc002bcq.1	chr15:77756739-77757355
HMG42	600698	NA	NA	NA	NA	257.017	-4.072378	uc001issu.1	uc001issu.1	chr12:66308695-66309227	NA	NA	NA	NA
HMG81	163905	1213.58	-6.735242	uc001lsv.3	chr13:31032879-31035670	678.647	-4.412205	uc001lsv.3	uc001lsv.3	chr13:31035776-31035819	NA	NA	NA	NA
HMG82	163906	NA	NA	NA	NA	533.776	-5.458538	uc011ckc.1	uc011ckc.1	chr4:174252527-174253230	NA	NA	NA	NA
HMGCLL1	NA	688.848	-9.096557	uc003pcn.3	chr6:55299171-55300459	NA	NA	NA	NA	NA	571.064	-6.558203	uc003pcp.3	chr6:55376873-55378835
HMGN1	163920	NA	NA	NA	NA	NA	NA	NA	NA	NA	634.55	-10.179042	uc002yxo.3	chr21:40714241-40715037
HMGN2	163910	NA	NA	NA	NA	869.866	-9.501937	uc001bnp.4	uc001bnp.4	chr1:26801640-26803133	NA	NA	NA	NA
HMGN3	604502	NA	NA	NA	NA	NA	NA	NA	NA	NA	598.104	-8.382585	uc003pit.3	chr6:79910962-79911404
HMGN4	NA	NA	NA	NA	NA	777.836	-11.107483	uc003nig.3	uc003nig.3	chr6:26545708-26547164	NA	NA	NA	NA
HMGXB4	604702	803.146	-8.289808	uc003ank.3	chr22:35689645-35691800	466.37	-9.592067	uc003ank.3	uc003ank.3	chr22:35689645-35691800	1219.36	-12.421436	uc003ank.3	chr22:35689645-35691800
HMH41	601155	NA	NA	NA	NA	534.978	-4.667753	uc002lra.1	uc002lra.1	chr19:1086006-1086627	NA	NA	NA	NA
HMMR	600936	1427.08	-15.72479	uc003lzf.3	chr5:162918171-162918953	1778.43	-23.870699	uc003lzf.3	uc003lzf.3	chr5:162918171-162918953	NA	NA	NA	NA
HN1	NA	1087.27	-8.488559	uc002jrb.1	chr17:73131344-73132096	1051.92	-7.228869	uc002jrz.1	uc002jrz.1	chr17:73131344-73132196	954.565	-10.996879	uc002jrz.1	chr17:73131344-73132196

Table 1

HNF1B	189907	712,161	-7,367,194	uc021lvu.1	chr17:36046434-36047374	NA	NA	NA	NA	NA	NA	NA	336,459	NA	NA	NA	chr5:137087073-137088837
HNRNPA0	609409	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	406,165	NA	NA	NA	chr14:21678927-21679495
HNRNPD	164020	NA	NA	NA	NA	476,725	-6,960,962	uc001vzw.3	chr14:21677296-21679381	NA	NA	NA	NA	NA	NA	NA	uc010thr.2
HNRNPD	601324	1467,23	-19,1491	uc010jir.1	chr4:83275908-83276486	556,923	-8,355,371	uc010jir.1	chr4:83275908-83276486	NA	NA	NA	NA	NA	NA	NA	NA
HNRNPH3	602324	251,297	-5,760,401	uc001jnw.4	chr10:70101812-70102953	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HNRNPK	600712	621,666	-7,169,206	uc001lsw.2	chr9:86582998-86584321	542,973	-5,639,248	uc004land.4	chr9:86582998-86584264	NA	NA	NA	1272,78	NA	NA	NA	NA
HNRNPL	603083	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-7,672,685	NA	NA	NA	uc002ojk.3
HNRNPLL	611208	805,374	-8,483,596	uc002rqv.3	chr2:38790328-38791323	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HNRNPM	160994	656,076	-9,916,232	uc010dwd.3	chr19:8553739-8554002	1351,81	-12,245,255	uc010dwd.3	chr19:8553739-8554002	NA	NA	NA	NA	NA	NA	NA	NA
HOMER3	604800	NA	NA	NA	NA	216,706	-4,084,102	uc010beby.2	chr19:19040010-19040251	NA	NA	NA	NA	NA	NA	NA	NA
HOOK3	607825	1258,55	-9,324,166	uc010kxj.1	chr8:42852895-42853299	1029,17	-10,301,969	uc010kxj.1	chr8:42852895-42853299	825,372	-7,112,012	NA	825,372	NA	NA	NA	uc003xpr.3
HORMAD1	609824	419,1	-6,446,522	uc001evk.2	chr1:150670535-150671129	NA	NA	NA	NA	NA	NA	356,501	-10,053,011	NA	NA	NA	uc001evk.2
HORMAD2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	443,295	-6,302,889	NA	NA	NA	uc003agv.3
HOXA13	142959	NA	NA	NA	NA	616,608	-7,031,625	uc003szb.1	chr7:27236499-27237816	NA	NA	NA	NA	NA	NA	NA	NA
HOXA2	604685	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	660,524	-7,729,342	NA	NA	NA	uc003syh.3
HOXA4	142953	1139,01	-6,8996	uc003sym.4	chr7:27168126-27168843	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HOXB2	142967	339,441	-4,830,146	uc002lmm.3	chr17:46620019-46620429	NA	NA	NA	NA	NA	NA	240,319	-4,111,702	NA	NA	NA	uc002lmm.3
HOXC11	605559	847,792	-10,338,666	uc001sem.3	chr12:54369196-54369667	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HOXD10	142984	NA	NA	NA	NA	1345,05	-7,539,481	uc002ukj.3	chr2:176983960-176984670	NA	NA	NA	NA	NA	NA	NA	NA
HOXD3	142980	742,148	-7,656,091	uc002ukt.1	chr2:177037003-177037826	NA	NA	NA	NA	NA	NA	813,901	-9,137,874	NA	NA	NA	NA
HOXD8	142985	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	uc002ukn.3
HOXD9	142982	NA	NA	NA	NA	1509,47	-11,270,513	uc010zex.2	chr2:176988904-176989645	NA	NA	NA	NA	NA	NA	NA	NA
HPGD	601688	594,211	-4,666,856	uc011ckh.1	chr4:175411328-175413106	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HPGDS	602598	914,11	-9,605,569	uc003hte.1	chr4:95219707-95220630	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HPRT1	308000	NA	NA	NA	NA	686,904	-10,346,143	uc004exl.4	chrX:133634108-133634698	NA	NA	NA	NA	NA	NA	NA	NA
HP53	606118	650,977	-1,294,873	uc003sewu.1	chr3:148890010-148891305	NA	NA	NA	NA	NA	NA	890,305	-6,052,701	NA	NA	NA	uc021xfk.1
HRAS	190020	351,437	-4,164,841	uc010qvw.2	chr11:532242-532755	NA	NA	NA	NA	NA	NA	1064,78	-10,251,158	NA	NA	NA	NA
HS2ST1	604844	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	uc001dmc.4
HS3ST3A1	604057	508,11	-4,596,967	uc002gob.1	chr17:13399006-13399513	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HS3ST3B1	604058	1141,69	-10,153,695	uc002goh.1	chr17:14248964-14249492	604,67	-6,471,949	uc002goh.1	chr17:14248964-14249492	NA	NA	NA	NA	NA	NA	NA	NA
HSD17B12	609574	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	395,16	-5,492,512	NA	NA	NA	chr11:43876799-43878169
HSD17B4	601860	NA	NA	NA	NA	926,587	-8,609,898	uc003ksj.3	chr5:118877690-118878030	NA	NA	NA	NA	NA	NA	NA	NA
HSD17B7P2	NA	464,596	-2,263,132	uc010qew.1	chr10:38647460-38647980	539,713	-5,675,098	uc010qew.1	chr10:38647460-38647980	NA	NA	NA	NA	NA	NA	NA	NA
HSP2	140581	773,016	-8,970,337	uc003pyl.4	chr6:122741380-122741555	739,878	-7,713,877	uc003pyu.2	chr6:122753386-122754264	NA	NA	NA	NA	NA	NA	NA	NA
HSP4	602438	365,664	-4,470,918	uc002eri.2	chr16:67203689-67203848	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HSP5	NA	NA	NA	NA	NA	411,279	-4,131,464	uc002lwi.1	chr17:56497529-56499720	NA	NA	NA	NA	NA	NA	NA	NA
HSPX2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	220,966	-5,912,618	NA	NA	NA	chrX:148858449-148858528
HSP90AA1	140571	NA	NA	NA	NA	1518,57	-9,438,667	uc001yku.4	chr14:102547075-102548048	NA	NA	NA	NA	NA	NA	NA	NA
HSPA12A	610701	NA	NA	NA	NA	1362,33	-11,903,135	uc001lcl.3	chr10:118430703-118434291	NA	NA	NA	NA	NA	NA	NA	NA
HSPA1A	140550	NA	NA	NA	NA	599,961	-8,746,472	uc003nmj.3	chr6:31785460-31785719	NA	NA	NA	NA	NA	NA	NA	NA
HSPA1B	603012	1842,57	-8,280,465	uc003nxt.2	chr6:31797654-31798031	832,883	-5,944,426	uc003nxx.2	chr6:31797654-31798031	NA	NA	1315,15	-9,278,028	NA	NA	NA	NA
HSPA2	140560	1754,95	-11,056,129	uc001xhk.4	chr14:85009488-65009954	NA	NA	NA	NA	NA	NA	773,611	-11,470,192	NA	NA	NA	chr14:85009488-65009954
HSPA4L	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:128754030-128754526
HSPB1	602195	1156,39	-9,309,635	uc003uew.3	chr7:75933491-75933614	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HSPBAP1	608263	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	443,462	-8,427,644	NA	NA	NA	chr3:122474107-122474251
HSPC2	142461	601,618	-5,105,197	uc001bfl.3	chr1:22148737-22149808	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
HSPH1	610703	769,634	-9,306,382	uc001ujj.3	chr13:31710763-31711454	369,43	-5,293,671	uc010aax.1	chr13:31726467-31726959	510,23	-4,300,559	NA	NA	NA	NA	NA	chr13:31726467-31726959
HTATIP2	605628	NA	NA	NA	NA	492,458	-8,502,708	uc009yla.1	chr11:20404752-20405329	1114,68	-6,112,243	NA	NA	NA	NA	NA	chr11:20404752-20405329
HTN1	142701	NA	NA	NA	NA	486,373	-6,698,963	uc003hex.3	chr4:70924297-70924559	818,794	-7,951,881	NA	NA	NA	NA	NA	chr4:70924297-70924559

Table 1

HTR1D	182133	1020.86	-10.717626	uc001bgn.3	chr1:23518388-23519578	NA	NA	NA	NA	684.973	-8.349557	uc001bgn.3	chr1:23518388-23519578
HTR2B	601122	NA	NA	NA	NA	NA	NA	NA	NA	468.192	-6.237078	uc010fw.3	chr2:231972950-231973230
HTR3C	610121	NA	NA	NA	NA	674.111	-7.11863	uc0003fmk.3	chr3:183778141-183778461	442.516	-5.163575	uc0003fmk.3	chr3:183778141-183778461
HTR3D	610122	245.586	-6.90591	uc0003fmj.3	chr3:183756764-183757157	578.275	-5.201113	uc0003fmj.3	chr3:183756764-183757157	NA	NA	NA	NA
HTR4	602164	NA	NA	NA	NA	690.386	-6.910405	uc021yfg.1	chr5:147830595-147830835	254.357	-4.476225	uc021yfg.1	chr5:147830595-147830835
HTRA4	610700	744.875	-7.614987	uc0003xmj.3	chr8:38845618-38846181	NA	NA	NA	NA	NA	NA	NA	NA
HUS1B	609713	NA	NA	NA	NA	985.179	-6.951259	uc0003mtg.3	chr6:655939-656107	NA	NA	NA	NA
HYAL2	603551	NA	NA	NA	NA	NA	NA	NA	NA	449.008	-6.035312	uc010hjl.2	chr3:50356020-50356332
HYKK	614681	482.76	-8.99264	uc002bdt.3	chr15:78819926-78820606	NA	NA	NA	NA	NA	NA	NA	NA
HYPK	612784	572.273	-5.199055	uc0001zfg.1	chr15:44093779-44095241	NA	NA	NA	NA	NA	NA	NA	NA
IAH1	NA	444.823	-7.142982	uc002qzt.3	chr2:9628459-9628591	NA	NA	NA	NA	NA	NA	NA	NA
IAPP	147940	NA	NA	NA	NA	541.128	-10.861205	uc0001rev.3	chr12:21531361-21532914	NA	NA	NA	NA
ICAT1L	NA	544.74	-5.730053	uc0002uzj.3	chr2:203684329-203684417	NA	NA	NA	NA	NA	NA	NA	NA
ICAM1	147840	NA	NA	NA	NA	437.352	-8.241263	uc0002mmq.2	chr19:10395964-10397291	NA	NA	NA	NA
ICAM5	601852	NA	NA	NA	NA	NA	NA	NA	NA	1522.82	-10.821995	uc0002mnu.4	chr19:10407293-10407454
ICK	612325	313.51	-5.320226	uc0003pbh.2	chr6:52866098-52869946	609.151	-5.569369	uc0003pbj.3	chr6:52880346-52880832	586.538	-8.351957	uc0003pbh.2	chr6:52866098-52869946
ICMT	605851	1217.77	-9.404387	uc0001amk.3	chr1:6281253-6285139	NA	NA	NA	NA	NA	NA	NA	NA
ICT1	603000	593.38	-5.846009	uc0002jmm.3	chr17:73017101-73017356	NA	NA	NA	NA	NA	NA	NA	NA
ID2	600386	734.245	-8.552103	uc0002qza.3	chr2:8823815-8824583	NA	NA	NA	NA	NA	NA	NA	NA
IDH3A	601149	NA	NA	NA	NA	704.526	-6.744577	uc0002bdd.3	chr15:78461348-78462884	1026.2	-6.365787	uc0002bdd.3	chr15:78461348-78462884
IDO2	612129	729.512	-5.46729	uc010lwy.1	chr8:39873122-39873910	NA	NA	NA	NA	NA	NA	NA	NA
IER3P1	609382	NA	NA	NA	NA	929.077	-6.788403	uc0002lcu.3	chr18:444681390-44682547	1068.51	-14.262846	uc0002lcu.3	chr18:444681390-44682547
IFI16	147586	NA	NA	NA	NA	655.267	-6.442974	uc0001ftg.3	chr1:159024692-159024945	NA	NA	NA	NA
IFI35	600735	NA	NA	NA	NA	NA	NA	NA	NA	621.206	-6.403842	uc021bxx.1	chr17:41166317-41166476
IFI6	147572	NA	NA	NA	NA	NA	NA	NA	NA	602.01	-4.307831	uc0001bon.1	chr1:27992572-27992891
IFT3	604650	NA	NA	NA	NA	NA	NA	NA	NA	458.572	-8.097483	uc0001kgf.3	chr10:91099886-91100725
IFT5	616135	NA	NA	NA	NA	NA	NA	NA	NA	958.445	-10.549336	uc010qng.1	chr10:91178406-91178576
IFNL1	607403	NA	NA	NA	NA	659.835	-4.809185	uc0002okv.3	chr19:39789157-39789312	NA	NA	NA	NA
IFRD1	603502	NA	NA	NA	NA	1213.34	-8.133929	uc0003vgh.3	chr7:112115575-112117258	NA	NA	NA	NA
IFT172	607386	NA	NA	NA	NA	511.097	-3.793893	uc0002rkv.3	chr2:27694554-27695041	511.584	-8.201542	uc0002ku.3	chr2:27667240-27667298
IFT43	614068	NA	NA	NA	NA	304.222	-6.551024	uc0001xsg.2	chr14:76549921-76550092	NA	NA	NA	NA
IFT52	NA	1394.81	-15.233894	uc0002xkw.3	chr20:42275624-42275862	NA	NA	NA	NA	NA	NA	NA	NA
IFT57	606621	2118.27	-26.269368	uc021xoc.1	chr3:107879659-107881323	NA	NA	NA	NA	NA	NA	NA	NA
IFT81	605489	795.366	-6.473521	uc0001lbg.3	chr12:110605784-110606250	NA	NA	NA	NA	774.257	-7.293039	uc0001tgg.3	chr12:110605784-110606250
IFT88	600595	NA	NA	NA	NA	NA	NA	NA	NA	631.514	-5.772743	uc0001unh.3	chr13:21265315-21265576
IGFBP2	146731	NA	NA	NA	NA	257.509	-7.100463	uc010zju.2	chr2:217525615-217529156	NA	NA	NA	NA
IGFBP3	146732	689.45	-9.405339	uc0003tnr.3	chr7:45951844-45953433	NA	NA	NA	NA	NA	NA	NA	NA
IGFBP7	602867	439.722	-7.743469	uc0003hcn.3	chr4:57897237-57897482	NA	NA	NA	NA	NA	NA	NA	NA
IGIP	NA	477.035	-5.629777	uc0003flb.1	chr5:139508224-139508391	NA	NA	NA	NA	NA	NA	NA	NA
IGSF1	300137	NA	NA	NA	NA	505.509	-5.131939	uc0004ewd.3	chrX:130407483-130407769	356.811	-3.045307	uc0004ewd.3	chrX:130407483-130407769
IGSF10	NA	205.264	-4.147118	uc0011bob.2	chr3:151153778-151154476	NA	NA	NA	NA	NA	NA	NA	NA
IGSF21	NA	735.691	-7.147229	uc0001bau.2	chr1:18704821-18704977	NA	NA	NA	NA	989.536	-8.579008	uc0001bau.2	chr1:18704821-18704977
IGSF22	NA	304.693	-4.242692	uc0009yhl.2	chr11:18725852-18726014	NA	NA	NA	NA	651.403	-10.99586	uc0009yhl.2	chr11:18725852-18726014
IHH	600726	484.867	-4.852798	uc0002vjo.2	chr2:219919142-219919928	NA	NA	NA	NA	NA	NA	NA	NA
IKKB	603258	2037.39	-2.897924	uc0003xov.3	chr8:42174561-42174729	NA	NA	NA	NA	1763.76	-18.063942	uc010kh.2	chr8:42177023-42178362
IKZF1	603023	NA	NA	NA	NA	1074.94	-10.566495	uc0003low.4	chr7:50468326-50472798	267.626	-4.280797	uc0003tov.1	chr7:50436069-50437142
IL12A	161560	547.729	-8.923444	uc0003fcx.3	chr3:159713347-159713806	NA	NA	NA	NA	NA	NA	NA	NA
IL13	147683	NA	NA	NA	NA	NA	NA	NA	NA	510.692	-4.01612	uc0003kxj.1	chr5:131995975-131996801
IL13RA1	300119	1695.68	-7.215737	uc0004eqr.1	chrX:117895265-117895477	1382.31	-15.951354	uc0004eqr.1	chrX:117895265-117895477	879.426	-6.458981	uc0004eqr.1	chrX:117895265-117895477

Table 1

IL15:	600564	1073.81	-13.6481	uc003lis.3	chr4:142654002-142655140	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL16:	603035	NA	NA	NA	NA	892.579	-6.393712	uc010ump.2	chr15:81601140-81605104	NA	NA	NA	NA	NA	NA	NA	NA
IL17RD:	606807	NA	NA	NA	NA	246.979	-5.224909	uc003dik.3	chr3:57124010-57130420	NA	NA	NA	NA	NA	NA	NA	NA
IL18R1:	604494	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr2:103013347-103015217
IL1A:	147760	828.534	-10.851862	uc002lig.3	chr2:113531492-113532643	394.27	-6.194173	uc002tlg.3	chr2:113531492-113532643	NA	NA	NA	NA	NA	NA	NA	NA
IL1B:	147720	1118.38	-5.416822	uc002tlh.1	chr2:113587337-113587937	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL1RAP:	602626	NA	NA	NA	NA	486.166	-10.011083	uc003ism.2	chr3:190366495-190369308	1671.02	-12.176356	uc003ier.3	NA	NA	NA	NA	NA
IL2:	147680	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL2ORA:	605620	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL24:	604136	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IL26:	605679	479.82	-6.622714	uc001sik.1	chr12:68595129-68595624	NA	NA	NA	NA	1153.89	-8.991409	uc003chl.3	NA	NA	NA	NA	chr4:123372626-123372906
IL3:	147740	NA	NA	NA	NA	NA	NA	NA	NA	470.072	-5.163524	uc001hex.2	NA	NA	NA	NA	chr6:137321108-137322694
IL36G:	605542	483.916	-8.722053	uc002lio.1	chr2:113742627-113743227	608.337	-5.377847	uc003kwe.1	chr5:131398485-131398896	NA	NA	NA	NA	NA	NA	NA	chr1:207076331-207077484
IL5RA:	147851	NA	NA	NA	NA	238.596	-4.879666	uc010hbt.2	chr3:3131857-3131926	2518.7	-15.762921	uc010hbp.3	NA	NA	NA	NA	NA
IL6:	147620	NA	NA	NA	NA	NA	NA	NA	NA	267.509	-8.559155	uc003svj.4	NA	NA	NA	NA	chr7:22771193-22771621
IL6ST:	600694	NA	NA	NA	NA	592.065	-5.172253	uc010lwd.3	chr5:55230925-55236909	1532.07	-5.170405	NA	NA	NA	NA	NA	NA
IL9:	146931	NA	NA	NA	NA	689.875	-9.209554	uc003lbb.1	chr5:135227935-135228079	1491.46	-17.120129	uc003lbb.1	NA	NA	NA	NA	chr5:135227935-135228079
ILDR1:	609739	862.852	-4.758592	uc003eeq.3	chr3:121706170-121707213	NA	NA	NA	NA	623.378	-6.948033	uc003eeq.3	NA	NA	NA	NA	chr3:121706170-121707213
ILDR2:	NA	NA	NA	NA	NA	NA	NA	NA	NA	312.585	-4.869887	uc001gdk.2	NA	NA	NA	NA	chr1:166882441-166888591
ILF3:	603182	NA	NA	NA	NA	493.527	-7.045511	uc002mpn.3	chr19:10799989-10803095	494.774	-7.045511	uc002mpn.3	NA	NA	NA	NA	chr19:10799989-10803095
ILKAP:	NA	NA	NA	NA	NA	1083.23	-9.904259	uc002vsv.3	chr2:239079043-239079176	NA	NA	NA	NA	NA	NA	NA	NA
ILVBL:	605770	382.258	-4.551745	uc002nam.3	chr19:15225785-15226062	NA	NA	NA	NA	777.432	-8.338848	uc002nam.3	NA	NA	NA	NA	chr19:15225785-15226062
IMP2A:	605922	1066.73	-11.926636	uc010dlb.2	chr18:12017831-12018284	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IMPACT:	615319	NA	NA	NA	NA	NA	NA	NA	NA	572.372	-7.321587	uc002khv.4	NA	NA	NA	NA	chr18:22030812-22033494
IMPDH2:	146691	444.588	-5.75435	uc003cvi.3	chr3:49061762-49061815	NA	NA	NA	NA	370.827	-2.846168	NA	NA	NA	NA	NA	NA
IMPQ2:	607056	NA	NA	NA	NA	NA	NA	NA	NA	573.678	-7.982004	uc011bhe.2	NA	NA	NA	NA	chr3:100941390-100945784
INCENP:	604411	NA	NA	NA	NA	NA	NA	NA	NA	812.149	-8.57109	uc001nsw.1	NA	NA	NA	NA	chr11:61919449-61920635
ING1:	601566	NA	NA	NA	NA	328.37	-7.161504	uc001vrg.3	chr13:111372280-111373421	NA	NA	NA	NA	NA	NA	NA	NA
ING2:	604215	NA	NA	NA	NA	994.176	-9.182658	uc003ivs.1	chr4:184432106-184432249	NA	NA	NA	NA	NA	NA	NA	NA
ING3:	607493	697.851	-14.639805	uc003vjrn.1	chr7:120596226-120597034	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
INHBC:	601233	NA	NA	NA	NA	286.751	-5.736782	uc001tsnv.1	chr12:57843806-57844609	NA	NA	NA	NA	NA	NA	NA	NA
INO80C:	NA	708.486	-7.355986	uc002kyx.4	chr18:33048291-33048574	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
INO80D:	NA	NA	NA	NA	NA	NA	NA	NA	NA	795.625	-6.689767	uc002vaz.4	NA	NA	NA	NA	chr2:206858445-206869091
INPP4A:	600916	NA	NA	NA	NA	NA	NA	NA	NA	472.704	-8.495112	uc002svk.3	NA	NA	NA	NA	chr2:99204072-99207496
INPP4B:	607494	NA	NA	NA	NA	759.997	-6.376647	uc003liw.4	chr4:142949182-142949934	NA	NA	NA	NA	NA	NA	NA	NA
INPP5J:	606481	NA	NA	NA	NA	NA	NA	NA	NA	583.715	-6.390218	uc010gwf.3	NA	NA	NA	NA	chr22:31523036-31523237
INPP5K:	607875	NA	NA	NA	NA	204.174	-3.241847	uc010cjs.2	chr17:1412417-1412616	490.172	-6.873754	uc010cjs.2	NA	NA	NA	NA	chr17:1412417-1412616
INSL5:	606413	NA	NA	NA	NA	NA	NA	NA	NA	1192.94	-11.98178	uc001dcw.3	NA	NA	NA	NA	chr1:67263424-67263695
INSM2:	614027	733.255	-3.508026	uc001whi.1	chr14:36005160-36006260	942.031	-6.263729	uc001whi.1	chr14:36005160-36006260	NA	NA	NA	NA	NA	NA	NA	NA
INSR:	147670	343.791	-6.159392	uc002mgf.3	chr19:7151995-7152708	290.506	-5.934216	uc002mgf.3	chr19:7151995-7152708	NA	NA	NA	NA	NA	NA	NA	NA
INSRR:	147671	NA	NA	NA	NA	818.255	-9.798998	uc009wsj.2	chr1:156820794-156820973	NA	NA	NA	NA	NA	NA	NA	NA
INTS10:	611353	238.989	-6.051403	uc003wzj.3	chr8:19709317-19709586	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
INTS12:	611355	515.313	-6.330751	uc003hxxw.3	chr4:106603785-106603889	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
INTS3:	611347	NA	NA	NA	NA	NA	NA	NA	NA	694.649	-6.241093	uc009wom.3	NA	NA	NA	NA	chr1:153745747-153746555
INTS5:	611349	NA	NA	NA	NA	NA	NA	NA	NA	417.124	-4.476812	uc001rud.3	NA	NA	NA	NA	chr1:62414320-62414491
INTS7:	611350	NA	NA	NA	NA	635.087	-7.638361	uc001hiw.2	chr1:212113741-212115165	NA	NA	NA	NA	NA	NA	NA	NA
INTS8:	611351	NA	NA	NA	NA	709.363	-7.946321	uc010mba.3	chr8:95892463-95892721	NA	NA	NA	NA	NA	NA	NA	NA
INTU:	610621	NA	NA	NA	NA	779.084	-8.239139	uc003fik.2	chr4:128637592-128637934	NA	NA	NA	NA	NA	NA	NA	NA
IP6K1:	606891	NA	NA	NA	NA	NA	NA	NA	NA	266.267	-4.174909	uc021wyl.1	NA	NA	NA	NA	chr3:49761728-49764554

Table 1

IP6K2	606992	240.226	-9.857403	uc003cur.3	chr3:48730884-48731581	NA	NA	NA	NA	NA	915.601	-10.001092	uc003cup.3	chr3:48725436-48725705
IP6K3	606993	966.315	-4.151662	uc003cufb.2	chr6:33689443-33690496	NA	NA	NA	NA	NA	622.028	-7.116467	uc003cufb.2	chr6:33689443-33690496
IPCEF1	609851	NA	NA	NA	NA	NA	NA	NA	NA	NA	736.322	-6.535875	uc003cpv.3	chr6:154475618-154480962
IPO13	609851	NA	NA	NA	NA	284.221	-5.15376	uc001jkb.3	chr10:59951278-59955836	NA	NA	NA	NA	NA
IPO5	610411	226.208	-5.131939	uc001ckx.3	chr1:44433355-44433694	NA	NA	NA	NA	NA	NA	NA	NA	NA
IPO6	602008	633.465	-6.185322	uc001vne.3	chr13:98674077-98676550	NA	NA	NA	NA	NA	893.145	-5.212678	uc001tuu.3	chr12:113633246-113633379
IPO7	605586	NA	NA	NA	NA	827.878	-14.07708	uc001mho.3	chr11:9466742-9469674	890.201	-9.080962	uc001mho.3	chr11:9466742-9469674	NA
IPO9	NA	721.691	-4.49076	uc001gwz.3	chr1:201845183-201853422	NA	NA	NA	NA	NA	NA	NA	NA	NA
IOCD	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
IOCG	612477	908.613	-2.613278	uc003fyn.3	chr3:197615946-197616450	872.866	-3.576795	uc003fyn.3	chr3:197615946-197616450	NA	NA	NA	NA	NA
IOCH	612523	NA	NA	NA	NA	506.489	-7.872273	uc002aqm.3	chr15:67599167-67599561	NA	NA	NA	NA	NA
IOCK	NA	NA	NA	NA	NA	491.008	-6.755109	uc010vat.2	chr16:19867812-19868859	NA	NA	NA	NA	NA
IQGA2P2	605401	NA	NA	NA	NA	277.834	-6.045029	uc003kek.3	chr5:76003139-76003957	788.859	-8.089559	uc003kek.3	chr5:76003139-76003957	NA
IRAK4	606883	NA	NA	NA	NA	NA	NA	NA	NA	NA	317.106	-5.56387	uc001rnt.3	chr12:44180519-44183346
IRF2	147576	1792.14	-13.227448	uc003lwf.4	chr4:185308876-185309911	1609.34	-10.44082	uc003lwf.4	chr4:185308876-185309911	NA	NA	NA	NA	NA
IRF4	601900	NA	NA	NA	NA	755.367	-6.683249	uc010jne.2	chr6:401816-402637	496.077	-5.244314	uc010jne.2	chr6:401816-402637	NA
IRF6	607199	NA	NA	NA	NA	350.771	-10.398505	uc0011hq.2	chr1:209958968-209961764	1773.57	-23.210979	uc001bhq.2	chr1:209958968-209961764	NA
IRF9	147574	NA	NA	NA	NA	NA	NA	NA	NA	503.706	-6.24246	uc001wmq.3	chr14:24635406-24635774	NA
IRS2	600797	715.797	-7.669286	uc001vqv.3	chr13:110406184-110408650	NA	NA	NA	NA	NA	NA	NA	NA	NA
IRX1	606197	517.408	-5.176329	uc003jde.3	chr5:3601155-3601517	NA	NA	NA	NA	NA	NA	NA	NA	NA
IRX2	606198	NA	NA	NA	NA	NA	NA	NA	NA	462.93	-5.118599	uc003jda.3	chr5:2746279-2746900	NA
IRX3	612985	NA	NA	NA	NA	760.89	-14.332879	uc002eht.1	chr16:54317212-54317597	NA	NA	NA	NA	NA
ISL1	600366	910.091	-6.759197	uc003por.3	chr5:50689445-50690563	NA	NA	NA	NA	NA	NA	NA	NA	NA
ISM1	615793	1091.52	-12.324546	uc010gce.1	chr20:13280107-13281297	NA	NA	NA	NA	NA	NA	NA	NA	NA
ISOC1	NA	NA	NA	NA	NA	240.605	-5.360344	uc003kva.3	chr5:128448695-128449719	NA	NA	NA	NA	NA
ITFC1	611803	NA	NA	NA	NA	NA	NA	NA	NA	437.331	-19.406737	uc010vgh.2	chr16:47189298-47189678	NA
ITFC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	508.634	-6.578222	uc002egf.3	chr16:315022-316119	NA
ITGA2	192974	NA	NA	NA	NA	NA	NA	NA	NA	829.555	-9.460145	uc003joy.3	chr5:52386430-52390609	NA
ITGA8	604063	NA	NA	NA	NA	445.559	-4.487595	uc001ioc.1	chr10:15559088-15559156	NA	NA	NA	NA	NA
ITGA9	603963	NA	NA	NA	NA	1245.49	-8.753277	uc003chtd.3	chr3:37860481-37861281	NA	NA	NA	NA	NA
ITGAE1	604682	NA	NA	NA	NA	NA	NA	NA	NA	463.565	-6.867557	uc002two.4	chr17:3617919-3618140	NA
ITGB1	135630	203.183	-6.174036	uc001lwr.4	chr10:33189246-33190563	725.606	-8.871923	uc001lwr.4	chr10:33189246-33190563	NA	NA	NA	NA	NA
ITGB3BP	605494	743.549	-4.880447	uc001dba.2	chr1:63906441-63906774	568.143	-7.676051	uc009wak.1	chr1:63919112-63919580	NA	NA	NA	NA	NA
ITIH2	146640	279.866	-12.122012	uc001ljs.3	chr10:7791298-7791483	NA	NA	NA	NA	NA	NA	NA	NA	NA
ITIH5	609783	NA	NA	NA	NA	1198.44	-10.865683	uc001ljr.2	chr10:7613368-7614284	NA	NA	NA	NA	NA
ITM2A	300222	230.733	-6.07173	uc004edh.3	chrX:78615881-78616585	NA	NA	NA	NA	NA	NA	NA	NA	NA
ITM2C	609554	483.479	-4.53937	uc002vqz.3	chr2:231742815-231743963	NA	NA	NA	NA	NA	NA	NA	NA	NA
ITPK1	601838	NA	NA	NA	NA	596.118	-6.888427	uc001ybf.3	chr14:93406068-93407905	NA	NA	NA	NA	NA
ITPKB	147522	NA	NA	NA	NA	NA	NA	NA	NA	691.288	-4.875821	uc010pyo.2	chr1:226819391-22682371	NA
ITPR1	147265	649.177	-10.117708	uc003bqc.3	chr3:4887910-4889524	NA	NA	NA	NA	NA	NA	NA	NA	NA
IVD	607036	NA	NA	NA	NA	580.804	-6.226191	uc001zlq.2	chr15:40710463-40713512	NA	NA	NA	NA	NA
JADE1	610514	NA	NA	NA	NA	265.351	-4.28772	uc003igk.3	chr4:129793418-129796379	NA	NA	NA	NA	NA
JAK2	147796	NA	NA	NA	NA	1588.76	-19.010233	uc010nhm.3	chr9:5126792-5128183	NA	NA	NA	NA	NA
JAKMIP1	611195	1291.74	-5.308066	uc010ldd.1	chr4:6027926-6028005	1071.84	-4.560272	uc003glu.4	chr4:6055482-6055701	650.995	0.703103	uc010ide.3	chr4:6055482-6055875	NA
JMY	604279	NA	NA	NA	NA	NA	NA	NA	NA	1269.85	-7.97121	uc003kfx.4	chr5:78617429-78623038	NA
JPH4	NA	950.64	-6.685653	uc010lnc.1	chr14:24037244-24038842	601.675	-6.912567	uc001wks.2	chr14:24044160-24044790	NA	NA	NA	NA	NA
JRK	603210	NA	NA	NA	NA	NA	NA	NA	NA	514.038	-6.745981	uc003ywo.3	chr8:143738874-143740266	NA
JRKL	603211	978.023	-19.332694	uc001ply.2	chr11:96125389-96126727	761.377	-8.674533	uc001ply.2	chr11:96125389-96126727	1183.46	-9.231227	uc001prf.2	chr11:96125389-96126727	NA
KANSL1L	613833	933.627	-9.278384	uc002vdx.1	chr2:210908157-210908636	755.362	-12.023713	uc002vdy.1	chr2:211016129-211018214	781.669	-5.641856	uc002vds.3	chr2:210885435-210887672	NA

Table 1

KANSL2	615488	NA	NA	NA	NA	1375.59	-9.780064	uc001rnw.2	chr12:49046995-49047826	NA	NA	NA	NA
KANSL3	NA	NA	NA	NA	NA	974.194	-7.726172	uc002swo.3	chr2:97265390-97267316	NA	NA	NA	NA
KARS	601421	397.406	-2.820397	uc002feq.3	chr16:75661622-75661792	NA	NA	NA	NA	298.054	-7.248111	uc002feq.3	chr16:75661622-75661792
KAT2B	602303	NA	NA	NA	NA	NA	NA	NA	NA	203.263	-4.50214	uc003cbq.3	chr3:20194018-20195896
KAT7	609880	NA	NA	NA	NA	621.26	-6.428508	uc002ipl.2	chr17:47904865-47904658	NA	NA	NA	NA
KATNBL1	616235	NA	NA	NA	NA	NA	NA	NA	NA	639.961	-5.083785	uc010ubz.2	chr15:34438271-34439396
KAZN	NA	NA	NA	NA	NA	NA	NA	NA	NA	302.345	-4.782558	uc009vog.1	chr1:15392394-15394651
KBTBD2	NA	353.007	-4.989817	uc003tdb.2	chr7:32907778-32908956	NA	NA	NA	NA	254.75	-4.238367	uc003tdb.2	chr7:32907778-32908956
KBTBD4	NA	NA	NA	NA	NA	335.238	-4.216616	uc001nfw.2	chr11:47593749-47594481	NA	NA	NA	NA
KCNK1	176258	NA	NA	NA	NA	NA	NA	NA	NA	739.61	-7.527893	uc009yhc.1	chr11:17803282-17804602
KCND1	300281	532.142	-7.98407	uc004dlw.1	chrX:48818639-48819841	NA	NA	NA	NA	337.843	-3.117938	uc004dlw.1	chrX:48818639-48819841
KCNC3	606767	993.685	-8.503403	uc002rsm.3	chr2:42669157-42671073	NA	NA	NA	NA	NA	NA	NA	NA
KCNH5	605716	263.383	-7.70718	uc001xga.3	chr14:63416531-63416776	1906.06	-20.492517	uc001xfx.3	chr14:63173945-63174225	828.962	-6.455136	uc0014fx.1	chr14:63173945-63174225
KCNH7	608169	NA	NA	NA	NA	NA	NA	NA	NA	345.963	-7.000413	uc002uch.2	chr2:163227917-163228338
KCNJ13	603208	NA	NA	NA	NA	1391.06	-10.320448	uc002vto.3	chr2:233630512-233632900	NA	NA	NA	NA
KCNK10	605873	NA	NA	NA	NA	213.577	-10.016696	uc001xwm.3	chr14:88646452-88651878	NA	NA	NA	NA
KCNK12	607366	NA	NA	NA	NA	1386.97	-7.833361	uc002rwb.3	chr2:47747915-47748045	NA	NA	NA	NA
KCNK17	607370	208.971	-5.130159	uc003ooo.3	chr6:39266777-39267202	NA	NA	NA	NA	574.435	-9.506581	uc003ooo.3	chr6:39266777-39267202
KCNK6	603939	NA	NA	NA	NA	463.412	-4.133243	uc002olc.3	chr19:38818044-38819649	NA	NA	NA	NA
KCNK7	603940	NA	NA	NA	NA	NA	NA	NA	NA	494.258	-7.431088	uc001oes.3	chr11:65360326-65360475
KCNMB2	605214	NA	NA	NA	NA	NA	NA	NA	NA	670.3	-10.136079	uc003fjd.3	chr3:178560726-178562217
KCNRG	607947	934.526	-8.63731	uc001vdl.3	chr13:50594364-50595058	433.327	-4.626173	uc001vdu.3	chr13:50594591-50595058	NA	NA	NA	NA
KCNS1	602905	447.41	-6.230584	uc002xnc.3	chr20:43720950-43723510	NA	NA	NA	NA	NA	NA	NA	NA
KCNS3	603888	NA	NA	NA	NA	483.574	-4.280391	uc002rvv.3	chr2:18113752-18114225	NA	NA	NA	NA
KCNT2	610044	959.972	-11.5574	uc009wyu.3	chr1:196249674-196249977	NA	NA	NA	NA	NA	NA	NA	NA
KCNU1	615215	NA	NA	NA	NA	914.904	-9.653798	uc010lvw.3	chr8:36793439-36793643	NA	NA	NA	NA
KCTD1	613420	393.021	-5.912629	uc002kvy.3	chr18:24035684-24039577	NA	NA	NA	NA	1236.43	-5.917729	uc002kvy.3	chr18:24035684-24039577
KCTD18	NA	NA	NA	NA	NA	313.366	-7.282142	uc002uvs.3	chr2:201353684-201354822	NA	NA	NA	NA
KCTD20	615932	652.783	-4.943606	uc003ome.3	chr6:36454953-36458315	NA	NA	NA	NA	987.214	-6.398113	uc003ome.3	chr6:36454953-36458315
KCTD5	611285	NA	NA	NA	NA	NA	NA	NA	NA	749.925	-10.117853	uc002crd.3	chr16:2757329-2759031
KCTD6	NA	NA	NA	NA	NA	1414.48	-8.229314	uc003dlj.4	chr3:58487360-58488087	NA	NA	NA	NA
KCTD7	611725	268.402	-5.637918	uc003lvc.3	chr7:66104220-66108216	360.444	-6.540856	uc003lvd.4	chr7:66105382-66108216	838.931	-3.756676	uc003lvd.4	chr7:66105382-66108216
KDEL2	609024	579.629	-6.780667	uc003sqe.4	chr7:6500712-6502771	NA	NA	NA	NA	931.318	-6.616868	uc003sqf.4	chr7:6500712-6502596
KDM1A	609132	NA	NA	NA	NA	NA	NA	NA	NA	434.469	-4.849513	uc001bgl.2	chr1:23409858-23410184
KDM4E	616581	NA	NA	NA	NA	357.376	-4.13108	uc010ruf.1	chr11:94760243-94760760	NA	NA	NA	NA
KDM5A	180202	NA	NA	NA	NA	NA	NA	NA	NA	659.067	-4.563325	uc021qsr.1	chr12:389223-394828
KDM5D	426000	NA	NA	NA	NA	964.02	-2.583996	uc004fuf.3	chrY:21867301-21867880	906.923	-7.61484	uc004fuf.3	chrY:21867301-21867880
KEAP1	606016	NA	NA	NA	NA	536.565	-8.842705	uc002mop.1	chr19:10596796-10597327	459.359	-4.392235	uc002mop.1	chr19:10596796-10597327
KEL	613883	NA	NA	NA	NA	567.874	-5.355261	uc003wcb.3	chr7:142638201-142638338	NA	NA	NA	NA
KHDC1	611688	489.964	-5.080418	uc003pgn.4	chr6:73951038-73951251	NA	NA	NA	NA	NA	NA	NA	NA
KHDC1L	NA	NA	NA	NA	NA	494.219	-5.112054	uc003pgm.4	chr6:739333268-73933470	NA	NA	NA	NA
KHDRBS2	610487	681.676	-7.145035	uc003peg.2	chr6:62389865-62390867	NA	NA	NA	NA	NA	NA	NA	NA
KIAA0100	610664	1353.13	-2.175733	uc002hbu.3	chr17:26941458-26942081	NA	NA	NA	NA	1072.18	-8.413183	uc002hbu.3	chr17:26966079-26966322
KIAA0101	610696	NA	NA	NA	NA	NA	NA	NA	NA	504.02	-7.427867	uc002ank.3	chr15:64657211-64658228
KIAA0196	610657	548.898	-4.805341	uc003yrt.3	chr8:126036503-126036858	NA	NA	NA	NA	390.205	-5.550454	uc003yrt.3	chr8:126036503-126036858
KIAA0226	NA	650.318	-6.160363	uc003jyc.2	chr3:197398259-197401888	883.416	-10.352966	uc003jyc.2	chr3:197398259-197401888	415.523	-4.350569	uc003jyc.1	chr3:197403088-197403710
KIAA0368	616694	497.34	-7.791023	uc004ble.1	chr9:114122973-114124309	NA	NA	NA	NA	NA	NA	NA	NA
KIAA0408	NA	NA	NA	NA	NA	581.525	-5.358621	uc003qba.3	chr6:127759551-127765253	NA	NA	NA	NA
KIAA0513	611675	NA	NA	NA	NA	NA	NA	NA	NA	328.329	-4.435821	uc002ftt.3	chr16:85112614-85113362

Table 1

KIAA0586	610178	575.156	-11.705671	uc001xdl.4	chr14:59014651-59015549	568.392	-6.827958	uc001xdl.4	chr14:59014651-59015549	NA	NA	NA	NA	NA	NA	NA	NA
KIAA0754		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr1:39880222-39882154
KIAA0825		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr5:93486556-93489711
KIAA0895		NA	NA	NA	NA	592.762	-8.383723	uc003lfe.3	chr7:36394805-36396423	NA	NA	NA	NA	NA	NA	NA	
KIAA0922	616243	1156.62	-6.964402	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:15455729-154557862
KIAA1024		NA	NA	NA	NA	721.416	-3.744789	uc002baw.1	chr15:79760727-79764642	NA	NA	NA	NA	NA	NA	NA	
KIAA1107		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr1:92649888-92650280
KIAA1143		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr3:44790236-44794832
KIAA1147		NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr7:141356528-141362455
KIAA1191		NA	NA	NA	NA	399.619	-8.77982	uc003mdlw.3	chr5:175773066-175774602	NA	NA	NA	NA	NA	NA	NA	
KIAA1210		NA	960.002	-9.57114	uc004era.4	1268.04	-10.066452	uc004era.4	chrX:118212598-118215291	NA	NA	NA	NA	NA	NA	NA	chr4:57193971-57196890
KIAA1211		NA	783.994	-7.690833	uc003hbk.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIAA1217		NA	1137.35	-6.858569	uc001lrs.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr10:24835254-24836772
KIAA1257		NA	NA	NA	NA	272.378	-5.03552	uc003eli.4	chr3:128689782-128690067	NA	NA	NA	NA	NA	NA	NA	
KIAA1324	611298	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIAA1328	616480	NA	NA	NA	NA	471.208	-0.996908	uc021uiv.1	chr18:34465680-34466367	NA	NA	NA	NA	NA	NA	NA	chr1:109745635-109749403
KIAA1407		NA	NA	NA	NA	206.337	-5.490174	uc003ygo.2	chr8:95500005-95500933	616.056	-5.582211	uc002kzz.3	uc009wey.3	uc002kzz.3	uc003hbk.2	NA	chr18:34802191-34805288
KIAA1429	616447	NA	NA	NA	NA	1047.81	-7.776178	uc001lux.3	chr10:30301729-30306811	1381.9	-7.438897	uc003eaw.3	NA	NA	NA	NA	chr3:113682984-113684001
KIAA1462	614398	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIAA1468		NA	NA	NA	NA	NA	NA	NA	NA	304.691	-4.340257	uc002lil.3	NA	NA	NA	NA	chr1:109745635-109749403
KIAA1551		NA	NA	NA	NA	429.619	-5.539283	uc001lrs.3	chr12:32145470-32146043	564.85	-7.764018	uc001lrs.3	NA	NA	NA	NA	chr12:32145470-32146043
KIAA1586		NA	NA	NA	NA	675.408	-9.069655	uc003pdj.3	chr6:56919662-56920023	1080.08	-13.340759	uc003pdj.3	NA	NA	NA	NA	chr6:56919662-56920023
KIAA1598		NA	NA	NA	NA	507.129	-5.36657	uc021pz.1	chr10:118615739-118616492	NA	NA	NA	NA	NA	NA	NA	
KIAA1715	610236	NA	NA	NA	NA	NA	NA	NA	NA	494.356	-5.23998	uc002ukc.1	NA	NA	NA	NA	chr2:176790410-176794694
KIAA1755		NA	704.057	-4.433232	uc002xlv.1	NA	NA	NA	NA	672.605	-4.753566	uc002xhv.1	NA	NA	NA	NA	chr20:36838907-36841443
KIAA1841		NA	NA	NA	NA	612.256	-6.451747	uc002sav.4	chr2:61315656-61316639	NA	NA	NA	NA	NA	NA	NA	
KIAA1875		NA	832.178	-4.965117	uc011kz.1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIAA2013		NA	596.191	-5.986481	uc001all.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIAA2018		NA	NA	NA	NA	NA	NA	NA	NA	334.653	-6.928917	uc003eal.3	NA	NA	NA	NA	chr3:113367233-113373790
KIAA2022	300524	578.014	-10.608828	uc004ebv.3	chrX:73952691-73959239	752.901	-8.576447	uc004ebv.3	chrX:73952691-73959239	498.153	-5.995081	uc004ebv.3	NA	NA	NA	NA	chrX:73952691-73959239
KIF11	148760	514.585	-5.167591	uc001kic.3	chr10:94413554-94415152	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIF15		NA	NA	NA	NA	NA	NA	NA	NA	1067.06	-7.175229	uc003cnx.4	NA	NA	NA	NA	chr3:44894228-44894748
KIF16B		NA	NA	NA	NA	NA	NA	NA	NA	613.886	-8.785953	uc010gci.2	NA	NA	NA	NA	chr20:16347488-16347790
KIF17	605037	751.297	-5.284611	uc001bdp.4	chr1:20990507-20991076	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIF20B	605498	NA	NA	NA	NA	1502.92	-17.615404	uc001kgr.1	chr10:91533806-91534700	NA	NA	NA	NA	NA	NA	NA	
KIF23	605064	882.061	-6.249868	uc002asb.3	chr15:69740147-69740764	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIF25	603815	NA	NA	NA	NA	NA	NA	NA	NA	603.823	-6.747937	uc003qwk.1	NA	NA	NA	NA	chr6:168445677-168445769
KIF26B	614026	387.886	-7.606735	uc001lbt.1	chr1:245865909-245866428	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIF2B	615142	NA	NA	NA	NA	252.96	-5.341407	uc002lua.2	chr17:51902417-51902573	NA	NA	NA	NA	NA	NA	NA	
KIF5A	602821	538.279	-6.302238	uc001sor.1	chr1:245865909-245866428	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
KIFC1	603763	1576.87	-26.78724	uc003oef.4	chr12:57978001-57978554	NA	NA	NA	NA	1253.31	-22.622704	uc003oef.4	NA	NA	NA	NA	chr6:33377468-33377699
KIN	601720	NA	NA	NA	NA	NA	NA	NA	NA	1740.53	-12.832908	uc010qba.2	NA	NA	NA	NA	chr10:7801234-7801786
KIR2DL5B	615727	NA	NA	NA	NA	NA	NA	NA	NA	439.74	-5.622688	uc002quk.1	NA	NA	NA	NA	chr19:gil000209_random:95743-96246
KIR3DX1		NA	NA	NA	NA	NA	NA	NA	NA	358.231	-6.46399	uc010erm.2	NA	NA	NA	NA	chr19:55054792-55055195
KISS1R	604161	NA	NA	NA	NA	NA	NA	NA	NA	754.272	-9.014252	uc002lqk.4	NA	NA	NA	NA	chr19:920749-921015
KITLG	184745	496.458	-7.844421	uc009zsn.3	chr12:88886570-88890888	428.93	-10.028932	uc009zsn.3	chr12:88886570-88890888	473.93	-8.583759	NA	NA	NA	NA	NA	
KL	604824	NA	NA	NA	NA	NA	NA	NA	NA	592.971	-11.566181	uc001luus.3	NA	NA	NA	NA	chr13:33638324-33640282
KLF3	609392	709.181	-10.823703	uc003gig.2	chr4:38691505-38692372	NA	NA	NA	NA	230.992	-3.584488	uc003gtg.2	NA	NA	NA	NA	chr4:38691505-38692372
KLF4	602253	682.472	-5.102033	uc004bdl.2	chr9:110247133-110248031	582.265	-4.486817	uc004bdl.2	chr9:110247133-110248031	NA	NA	NA	NA	NA	NA	NA	

Table 1

KLF8	300286	261.43	-3.171367	uc010nkg.2	chrX:56292186-56295922	1476.46	-8.70384	uc010nkg.2	chrX:56292186-56295922	808.997	-7.819798	uc004dur.3	chrX:56310928-56314322
KLHDC1	611281	1340.26	-17.533052	uc001www.3	chr14:50218491-50219870	NA	NA	NA	NA	NA	NA	NA	NA
KLHDC10	615152	NA	NA	NA	NA	NA	NA	NA	NA	535.154	-6.114609	uc003vpi.2	chr7:129770587-129775560
KLHDC8B	613169	NA	NA	NA	NA	NA	NA	NA	NA	1531.55	-9.918008	uc003cwh.3	chr3:49213235-49213919
KLHL1	605332	1563.77	-13.303817	uc001vip.3	chr13:70274725-70275833	1089.43	-6.50114	uc001vip.3	chr13:70274725-70275833	NA	NA	NA	NA
KLHL10	60878	566.702	-5.234499	uc010mw.1	chr17:40002053-40002185	NA	NA	NA	NA	1014.89	-9.454426	NA	NA
KLHL12	614522	NA	NA	NA	NA	NA	NA	NA	NA	953.125	-13.214116	uc001aym.1	chr1:202860230-202861764
KLHL2	605774	NA	NA	NA	NA	NA	NA	NA	NA	561.619	-7.030205	uc003irb.3	chr4:166243213-166244308
KLHL20	NA	713.338	-5.267639	uc001gic.3	chr1:173754386-173755840	NA	NA	NA	NA	995.589	-9.69386	uc001gic.3	chr1:173754386-173755840
KLHL24	611295	NA	NA	NA	NA	NA	NA	NA	NA	666.037	-9.139646	uc003flv.3	chr3:183397075-183402304
KLHL25	NA	NA	NA	NA	NA	NA	NA	NA	NA	410.832	-5.091727	uc002bly.3	chr15:86302559-86304242
KLHL3	605775	NA	NA	NA	NA	704.325	-6.186347	uc003lbs.1	chr5:136996400-136997588	NA	NA	NA	NA
KLHL32	NA	NA	NA	NA	NA	233.472	-4.313838	uc003poy.3	chr6:97562445-97562618	NA	NA	NA	NA
KLHL36	NA	NA	NA	NA	NA	NA	NA	NA	NA	242.172	-4.975672	uc002fig.3	chr16:84695740-84695916
KLHL41	607701	NA	NA	NA	NA	NA	NA	NA	NA	702.892	-6.305672	uc010zdh.1	chr2:170382207-170382772
KLHL6	614214	NA	NA	NA	NA	NA	NA	NA	NA	426.339	-7.349544	uc003fft.1	chr3:183208894-183211994
KLK10	602673	512.228	-6.425521	uc002puv.3	chr19:51516000-51518055	NA	NA	NA	NA	NA	NA	NA	NA
KLK11	604434	NA	NA	NA	NA	1040.06	-9.007307	uc002pvc.4	chr19:51525487-51525800	NA	NA	NA	NA
KLK12	605539	NA	NA	NA	NA	845.803	-8.657449	uc010ycc.1	chr19:51532348-51532708	NA	NA	NA	NA
KLRC2	602891	NA	NA	NA	NA	836.026	-8.403813	uc010sthe.1	chr12:10579193-10579474	571.218	-6.036966	uc001qyk.2	chr12:10583206-10583715
KLRC4	602893	NA	NA	NA	NA	NA	NA	NA	NA	969.978	-9.978313	uc001qye.3	chr12:10559983-10560251
KLRD1	602894	1071.03	-3.515876	uc001qwx.4	chr12:10467393-10469850	NA	NA	NA	NA	NA	NA	NA	NA
KLRC2	NA	NA	NA	NA	NA	705.659	-6.44214	uc003wvb.3	chr7:139138088-139138332	659.267	-6.44214	uc003wvb.3	chr7:139138088-139138332
KMT2C	608833	350.129	-4.630178	uc003wkk.3	chr7:151832010-151833916	NA	NA	NA	NA	NA	NA	NA	NA
KMT2E	608444	480.701	-0.378577	uc003vcl.3	chr7:104731870-104732057	552.731	-6.357429	uc003vcl.3	chr7:104731870-104732057	NA	NA	NA	NA
KNG1	612358	919.417	-10.901619	uc011bsa.2	chr3:186460121-186460678	NA	NA	NA	NA	NA	NA	NA	NA
KPRP	613260	NA	NA	NA	NA	534.379	-6.272196	uc001flal.1	chr1:152733805-152734529	NA	NA	NA	NA
KRAS	190070	372.819	-4.225845	uc001rgp.1	chr12:25358180-25362845	NA	NA	NA	NA	NA	NA	NA	NA
KRBA2	NA	NA	NA	NA	NA	364.448	-9.110276	uc002gfl.1	chr17:8271973-8272451	NA	NA	NA	NA
KREMEN1	609898	NA	NA	NA	NA	503.875	-4.549532	uc010lev.1	chr7:91828283-91830049	367.93	-7.653458	uc003ael.3	chr22:29538101-29542808
KRT11	604214	NA	NA	NA	NA	206.86	-5.112054	uc001sau.1	chr12:53068520-53068976	NA	NA	NA	NA
KRT1	139350	NA	NA	NA	NA	1059.76	-7.476569	uc002hvk.2	chr17:39017430-39017912	NA	NA	NA	NA
KRT12	601687	NA	NA	NA	NA	940.325	-10.901081	uc010cxg.3	chr17:39081413-39081601	1044.64	-9.789248	uc002hvm.1	chr17:39078952-39079240
KRT23	606194	NA	NA	NA	NA	NA	NA	NA	NA	877.535	-11.130376	uc002whh.1	chr17:38948448-38948678
KRT28	616677	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
KRT173	608247	242.646	-5.091727	uc001sas.3	chr12:53001354-53001979	NA	NA	NA	NA	NA	NA	NA	NA
KRTCAP2	NA	865.644	-5.952069	uc001flhp.1	chr1:155143877-155145032	NA	NA	NA	NA	NA	NA	NA	NA
KSR1	601132	NA	NA	NA	NA	NA	NA	NA	NA	548.082	-5.264453	uc002gzm.3	chr17:25948962-25950718
KYNU	605197	1309.44	-11.326714	uc002ivk.3	chr2:143746911-143747106	NA	NA	NA	NA	NA	NA	NA	NA
L3HYDPDH	614811	413.438	-4.933639	uc010lrx.1	chr14:59945444-59946069	618.697	-11.405501	uc001xee.1	chr14:59939406-59939682	NA	NA	NA	NA
LACC1	613409	NA	NA	NA	NA	1371.37	-10.96318	uc010acg.3	chr13:44465585-44468068	NA	NA	NA	NA
LACE1	NA	NA	NA	NA	NA	1099.9	-16.617198	uc003psj.3	chr6:108843629-108844251	NA	NA	NA	NA
LACTB2	NA	607.268	-7.957961	uc003xyp.3	chr8:71549501-71550094	1738.32	-8.999381	uc003xyp.3	chr8:71549501-71550094	NA	NA	NA	NA
LAC3	153337	388.552	-4.825936	uc001lqqs.3	chr12:6884741-6884897	NA	NA	NA	NA	NA	NA	NA	NA
LALBA	149750	428.413	-5.499084	uc001rtl.3	chr12:48961467-48961739	NA	NA	NA	NA	NA	NA	NA	NA
LAMA2	156225	NA	NA	NA	NA	906.517	-9.149238	uc003qbn.3	chr6:129837493-129837710	NA	NA	NA	NA
LAMA5	601033	NA	NA	NA	NA	NA	NA	NA	NA	469.431	-4.589171	uc002ycq.3	chr20:60884121-60884391
LAMB4	616380	758.739	-4.568145	uc003vey.2	chr7:107663996-107664483	NA	NA	NA	NA	NA	NA	NA	NA
LAMP2	309060	460.246	-7.746153	uc004ess.4	chrX:119560003-119562338	771.212	-6.625496	uc004ess.4	chrX:119560003-119562338	NA	NA	NA	NA

Table 1

LAMTOR3	603296	890.596	-10.386552	uc003hvg.2	chr4:100799495-100803150	212.15	-7.092043	uc003hvg.2	chr4:100799495-100803150	NA	NA	NA	NA	NA	NA
LAPTM4A	NA	845.172	-5.944465	uc002rdm.3	chr2:20232411-20232965	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LARP1B	NA	689.253	-1.28018	uc003lly.3	chr4:129029058-129030056	NA	NA	NA	NA	1009.79	-4.191284	uc003lfx.3	NA	NA	chr4:129028558-129030056
LARP6	611300	NA	NA	NA	NA	512.237	-5.755202	uc002ass.3	chr15:71123889-71124390	NA	NA	NA	NA	NA	NA
LARS	151350	NA	NA	NA	NA	296.768	-6.345379	uc003lnw.1	chr5:145492589-145493668	368.341	-4.553691	uc003lnw.1	NA	NA	chr5:145492589-145493668
LASP1	602920	NA	NA	NA	NA	483.935	-6.096677	uc010wdy.1	chr17:37055079-37055453	NA	NA	NA	NA	NA	NA
LATS1	603473	963.649	-6.920701	uc003qmw.3	chr6:150004055-150004151	758.185	-8.290386	uc003qmw.3	chr6:150004055-150004151	NA	NA	NA	NA	NA	NA
LBR	600024	NA	NA	NA	NA	1651.9	-8.394796	uc001hoy.3	chr1:225589204-225591004	591.618	-6.773939	uc001hoy.3	NA	NA	chr1:225589204-225591004
LCA5	611408	234.832	-5.294173	uc003pk.3	chr6:80194708-80196720	643.097	-5.361305	uc011dyr.2	chr6:80222489-80222856	803.905	-7.839223	uc011dyr.2	NA	NA	chr6:80222489-80222856
LCE1B	612604	NA	NA	NA	NA	596.869	-5.920294	uc001faq.3	chr1:152785280-152785585	NA	NA	NA	NA	NA	NA
LCE1E	612607	NA	NA	NA	NA	582.176	-6.777891	uc001fan.3	chr1:152760133-152760901	NA	NA	NA	NA	NA	NA
LCE2A	612609	320.507	-4.45287	uc001faj.3	chr1:152671699-152671918	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LCE3D	612616	NA	NA	NA	NA	459.766	-4.588473	uc002mk.1	chr2:30829067-30830712	526.507	-5.216407	uc001fab.3	NA	NA	chr1:152551860-152552133
LCLAT1	614241	NA	NA	NA	NA	380.616	-4.355081	uc004kcc.3	chr9:139849226-139849949	NA	NA	NA	NA	NA	NA
LCN12	612905	NA	NA	NA	NA	601.835	-6.894172	uc001kmr.3	chr10:98718176-98724198	NA	NA	NA	NA	NA	NA
LCOR	607698	NA	NA	NA	NA	998.571	-20.203447	uc021xmq.1	chr4:17844839-17847343	655.71	-9.487061	uc021xmq.1	NA	NA	chr4:17844839-17847343
LCORL	611799	1525.42	-13.872596	uc021xmq.1	chr4:17844839-17847343	501.662	-4.343469	uc001kul.3	chr10:103868182-103868731	NA	NA	NA	NA	NA	NA
LDB1	603451	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LDLRAD3	NA	217.07	-6.369407	uc001mwk.1	chr11:36250948-36252841	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LDLRAD4	606571	NA	NA	NA	NA	NA	NA	NA	NA	798.024	-5.634334	uc002ksh.1	NA	NA	chr18:13645657-13652753
LDOC1	300402	NA	NA	NA	NA	518.406	-4.466028	uc004fhj.3	chrX:140269931-140270765	NA	NA	NA	NA	NA	NA
LEAP2	611373	NA	NA	NA	NA	NA	NA	NA	NA	684.928	-7.479592	uc003hyc.3	NA	NA	chr5:132210139-132210582
LEFTY1	603037	378.903	-4.477337	uc001hpo.3	chr1:226073982-226074426	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LEKR1	613536	NA	NA	NA	NA	NA	NA	NA	NA	359.476	-6.017368	uc021xgh.1	NA	NA	chr3:156763540-156763918
LEMD1	610480	1128.42	-6.387362	uc001hcl.2	chr1:205350506-205350862	NA	NA	NA	NA	1548.09	-1.964069	uc001hcl.2	NA	NA	chr1:205350506-205350862
LEMD3	607844	1206.3	-5.9547	uc001ssl.2	chr12:65640106-65642141	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LEO1	610507	831.311	-8.764199	uc002abo.3	chr15:52230222-52230362	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LEPROT	613461	NA	NA	NA	NA	NA	NA	NA	NA	456.844	-7.809576	uc009wao.3	NA	NA	chr1:65893487-65893692
LEPROTL1	607338	NA	NA	NA	NA	898.329	-12.283378	uc003xliw.4	chr8:29963379-29965587	NA	NA	NA	NA	NA	NA
LETM1	604407	NA	NA	NA	NA	NA	NA	NA	NA	605.562	-4.578215	uc003gdlv.3	NA	NA	chr4:1813206-1816150
LETMD1	NA	NA	NA	NA	NA	948.617	-5.505503	uc010sna.2	chr12:51450387-51450735	1227.37	-1.655602	uc010sna.2	NA	NA	chr12:51450387-51450735
LGALS13	608717	NA	NA	NA	NA	NA	NA	NA	NA	624.97	-7.722091	uc002omb.3	NA	NA	chr19:40097980-40098114
LGALS3	153619	407.462	-4.042018	uc001kbr.3	chr14:55611990-55612148	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LGALS8	606099	927.675	-10.702852	uc001hsw.2	chr1:236711462-236716279	767.442	-7.210276	uc001hsw.2	chr1:236711462-236716279	NA	NA	NA	NA	NA	NA
LG14	608303	NA	NA	NA	NA	844.553	-6.715664	uc002nxx.2	chr19:35615417-35616096	NA	NA	NA	NA	NA	NA
LHFP	606710	529.647	-8.710191	uc001uxf.3	chr13:39917028-39918072	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LHX8	604425	NA	NA	NA	NA	1592.21	-13.08933	uc001gui.1	chr1:197898390-197899273	289.899	-6.537418	uc001dgo.3	NA	NA	chr1:75626581-75627218
LHX9	606066	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LIG1	126391	NA	NA	NA	NA	NA	NA	NA	NA	559.471	-6.726625	uc010vze.1	NA	NA	chr19:48618703-48618905
LIG3	600940	NA	NA	NA	NA	739.618	-6.519317	uc002hij.3	chr17:333330068-33330191	381.161	-5.376514	uc002hik.2	NA	NA	chr17:333331526-33332088
LILRA1	604810	285.122	-7.432334	uc010yfh.2	chr19:55110760-55111185	441.019	-3.455055	uc010yfh.2	chr19:55110760-55111185	NA	NA	NA	NA	NA	NA
LILRA2	604812	NA	NA	NA	NA	1114.18	-2.452249	uc010dm.3	chr19:55098668-55099027	1349.04	-1.240736	uc010dm.3	NA	NA	chr19:55098668-55099027
LILRB2	604815	320.219	-4.215396	uc010erf.3	chr19:54777675-54778683	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LIMA1	608364	436.621	-5.254071	uc001rwg.4	chr12:50569563-50570846	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LIMCH1	NA	741.562	-5.98331	uc003gvl.1	chr4:41621462-41622311	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LIMK1	601329	NA	NA	NA	NA	NA	NA	NA	NA	475.634	-5.890821	uc003uac.1	NA	NA	chr7:73523496-73525770
LIMS1	602567	NA	NA	NA	NA	1080	-6.761596	uc002tel.3	chr2:109300456-109303702	524.368	-5.43496	uc002tel.3	NA	NA	chr2:109300456-109303702
LIN28A	611043	NA	NA	NA	NA	636.894	-5.312572	uc001brnj.3	chr1:26752950-26756219	399.569	-3.142143	uc001brnj.3	NA	NA	chr1:26752950-26756219
LINTB	612331	NA	NA	NA	NA	889.025	-7.133192	NA	NA	1456.95	-11.73772	uc002pmp.3	NA	NA	chr19:49621631-49621717

Table 1

LINC0167	612332	763.403	-6.825205	uc001mr1.3	chr11:27155965-27520195	NA	NA	NA	NA	NA	609.083	NA	NA	-5.315011	NA	NA	chr11:129873393-129875381
LINC00305	NA	NA	NA	NA	NA	1142.51	-11.395425	uc010dtk.2	chr18:61747243-61747535	NA	NA	NA	NA	NA	NA	NA	NA
LINC00493	NA	NA	NA	NA	NA	429.445	-8.941192	uc002wrd.4	chr20:18550050-18550203	NA	NA	NA	NA	NA	NA	NA	NA
LINC00657	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	363.928	-6.379406	uc002xet.3	chr20:34633540-346338313	NA	NA	NA
LINC00893	NA	1057.76	-5.003196	uc011mx1.1	chrX:148614964-148615450	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LINC00937	NA	NA	NA	NA	NA	792.425	-4.711658	uc001quk.4	chr12:8509560-8509621	300.316	-4.682225	NA	NA	NA	NA	NA	NA
LINC00998	NA	NA	NA	NA	NA	1196.01	-10.697528	uc011kmt.2	chr7:112756773-112757547	NA	NA	NA	NA	NA	NA	NA	NA
LINC01225	NA	228.97	-4.523737	uc021okn.1	chr1:31973448-31974167	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LINC01387	NA	513.96	-6.048592	uc021tugs.1	chr18:6590544-6590652	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LINC01559	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LINC01588	NA	NA	NA	NA	NA	709.54	-10.366445	uc001wxi.1	chr14:50448430-50449022	NA	264	-5.837604	uc001bs.2	chr12:13523605-135236137	NA	NA	NA
LIPF	601980	NA	NA	NA	NA	1154.58	-11.429777	uc009xtk.3	chr10:90428518-90429295	875.717	-8.686488	uc001Hfg.2	chr10:90438439-90438572	NA	NA	NA	NA
LIX1L	NA	465.506	-4.127138	uc001ent.3	chr1:145498779-145499091	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LMAN1	601567	426.858	-7.056036	uc002lhz.3	chr18:56995056-56998324	697.89	-4.746183	uc002lhz.3	chr18:56995056-56998324	352.317	-8.665676	uc002lhz.3	chr18:56995056-56998324	NA	NA	NA	NA
LMAN2	609551	NA	NA	NA	NA	541.13	-5.083871	uc003nge.3	chr5:176758563-176759086	NA	NA	NA	NA	NA	NA	NA	NA
LMAN2L	609552	NA	NA	NA	NA	NA	NA	NA	NA	NA	394.844	-5.421883	uc0023wu.3	chr2:9737371667-9737372992	NA	NA	NA
LMBR1	605522	595.619	-4.557091	uc003wmv.4	chr7:156473570-156476771	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LMBR1L	610007	NA	NA	NA	NA	NA	NA	NA	NA	NA	276.116	-6.40512	uc001rtg.4	chr12:49490923-49491454	NA	NA	NA
LMBRD1	612625	NA	NA	NA	NA	NA	NA	NA	NA	NA	1497.52	-7.558011	uc003pez.3	chr6:70385641-70386049	NA	NA	NA
LMLN	609380	NA	NA	NA	NA	1496.96	-8.755524	uc003jvt.3	chr3:197765539-197770591	906.081	-10.437612	uc003fyt.3	chr3:197765539-197770591	NA	NA	NA	NA
LMNB1	150340	NA	NA	NA	NA	NA	NA	NA	NA	NA	717.124	-5.990875	uc003kud.2	chr5:126171957-126172712	NA	NA	NA
LMNTD1	NA	477.755	-5.233399	uc009zjc.2	chr12:25652786-25652930	NA	NA	NA	NA	NA	746.338	-8.882417	uc001rdj.2	chr12:16701306-16704155	NA	NA	NA
LMO3	180386	597.343	-6.437445	uc001rdj.2	chr12:16701306-16704155	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LMO7	604362	395.721	-5.964015	uc010thv.2	chr13:76432080-76434006	1229.09	-9.859924	uc010thv.2	chr13:76432080-76434006	NA	643.998	-7.662825	uc003dtx.4	chr3:100174771-100175170	NA	NA	NA
LNP1	NA	NA	NA	NA	NA	377.745	-4.07697	uc003dtx.4	chr3:100174771-100175170	NA	NA	NA	NA	NA	NA	NA	NA
LNX2	609733	NA	NA	NA	NA	671.306	-5.489355	uc001turl.4	chr13:28120050-28122471	NA	NA	NA	NA	NA	NA	NA	NA
LONRF2	NA	680.04	-4.919167	uc002tal.4	chr2:100889753-100900759	277.639	-8.871164	uc002tal.4	chr2:100889753-100900759	NA	NA	NA	NA	NA	NA	NA	NA
LPA2	605110	NA	NA	NA	NA	322.546	-5.175553	uc002ma.4	chr19:19734466-19735064	NA	NA	NA	NA	NA	NA	NA	NA
LPA4	300086	NA	NA	NA	NA	706.262	-6.487599	uc010nme.3	chrX:78011480-78012578	NA	NA	NA	NA	NA	NA	NA	NA
LPCA4	612039	537.804	-5.137233	uc001zlg.3	chr15:34651089-34651327	750.42	-10.487956	uc001zlg.3	chr15:34651089-34651327	1019.46	-8.64513	uc001zlg.3	chr15:34651089-34651327	NA	NA	NA	NA
LPP1	600700	595.339	-7.424327	uc011bpg.2	chr3:188592268-188609460	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LPPR1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	332.321	-9.93722	uc004bbb.3	chr9:104086340-104087417	NA	NA	NA
LPPR5	NA	825.445	-6.123556	uc001dsb.3	chr1:99355801-99358627	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LRAT	604863	NA	NA	NA	NA	658.477	-15.322758	uc003lom.1	chr4:155670289-155674270	1302.97	-14.460577	uc003lom.1	chr4:155670289-155674270	NA	NA	NA	NA
LRBA	606453	486.923	-6.830625	uc003lik.2	chr4:151933981-151935566	282.531	-6.731226	uc003lik.4	chr4:151185811-151186873	NA	NA	NA	NA	NA	NA	NA	NA
LRCOL1	NA	609.117	-6.052808	uc021tgr.1	chr12:133179736-133179987	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LRMP	602003	NA	NA	NA	NA	NA	NA	NA	NA	NA	612.372	-10.643201	uc001rgh.3	chr12:25260995-25261269	NA	NA	NA
LRP11	NA	NA	NA	NA	NA	546.525	-5.386727	uc003qng.2	chr6:150139894-150141684	NA	NA	NA	NA	NA	NA	NA	NA
LRP12	NA	NA	NA	NA	NA	960.494	-7.841613	uc003yly.3	chr8:105501459-105502900	NA	NA	NA	NA	NA	NA	NA	NA
LRP1B	608766	661.759	-10.288328	uc002tvj.1	chr2:140988996-140990754	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LRP2	600073	NA	NA	NA	NA	NA	NA	NA	NA	NA	965.885	-13.031261	uc010df.1	chr2:170097260-170097453	NA	NA	NA
LRP2BP	NA	NA	NA	NA	NA	1617.05	-13.409775	uc003kji.2	chr4:186285032-186288333	1133	-7.588672	uc003kji.2	chr4:186285032-186288333	NA	NA	NA	NA
LRP4	604270	NA	NA	NA	NA	691.399	-8.751679	uc001ndm.4	chr11:46878268-46880533	NA	NA	NA	NA	NA	NA	NA	NA
LRPPRC	607544	757.21	-10.056367	uc002rtt.2	chr2:44113363-44115738	1482.5	-18.658574	uc002rtt.2	chr2:44113363-44115738	NA	NA	NA	NA	NA	NA	NA	NA
LRP1	609193	NA	NA	NA	NA	347.979	-5.937339	uc001wwo.3	chr14:50081133-50081390	427.47	-9.916191	uc001wwo.3	chr14:50081133-50081390	NA	NA	NA	NA
LRRC10	610846	NA	NA	NA	NA	NA	NA	NA	NA	NA	586.796	-7.437086	uc001sv.3	chr12:70002345-70003784	NA	NA	NA
LRRC2	607180	NA	NA	NA	NA	401.804	-6.20854	uc010hji.3	chr3:46558878-46560503	NA	NA	NA	NA	NA	NA	NA	NA
LRRC23	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	541.167	-6.066948	uc001trp.3	chr12:7023055-7023406	NA	NA	NA

Table 1

LRRC27	NA	824.384	-3.11674	uc001lilf.2	chr10:134166410-134166901	498.203	-4.048622	uc001lilf.2	chr10:134166410-134166901	755.009	-5.70302	uc010quuv.1	chr10:134166465-134166901
LRRC3	NA	NA	NA	NA	NA	743.282	-7.985589	uc002zfa.3	chr21:45877302-45878739	NA	NA	NA	NA
LRRC34	NA	980.137	-10.347876	uc003ffx.3	chr3:169511216-169511422	NA	NA	NA	NA	NA	NA	NA	NA
LRRC36	NA	NA	NA	NA	NA	447.368	-5.561929	uc002esv.3	chr16:67418993-67419109	590.496	-2.319103	uc002esv.3	chr16:67418993-67419109
LRRC37A4P	NA	NA	NA	NA	NA	NA	NA	NA	NA	814.737	-7.342178	uc010wyl.2	chr17_ctg5_hap1.1489501-1489848
LRRC4	610486	1209.6	-8.495508	uc003rmk.3	chr7:127867124-127868731	NA	NA	NA	NA	NA	NA	NA	NA
LRRC40	NA	NA	NA	NA	NA	998.669	-7.962972	uc001der.2	chr1:70610485-70611482	723.331	-7.055763	uc001der.2	chr1:70610485-70611482
LRRC46	NA	237.744	-5.813961	uc002ima.3	chr17:45914487-45915079	NA	NA	NA	NA	NA	NA	NA	NA
LRRC47	NA	NA	NA	NA	NA	685.736	-5.115382	uc001akx.1	chr11:3696784-3697651	NA	NA	NA	NA
LRRC69	614854	NA	NA	NA	NA	728.562	-6.944018	uc002qit.3	chr17:48458594-48460348	NA	NA	NA	NA
LRRC61	NA	292.554	-4.273567	uc003wgv.3	chr7:150034731-150035245	NA	NA	NA	NA	NA	NA	NA	NA
LRRC66	NA	536.16	-7.452762	uc003gzi.3	chr4:52859866-52860544	NA	NA	NA	NA	NA	NA	NA	NA
LRRC68	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LRRFP2	614043	1425.46	-10.538168	uc011ayf.1	chr3:37094117-37095341	NA	NA	NA	NA	348.083	-4.421226	uc003yev.1	chr8:92231229-92231464
LRRIC01	NA	564.221	-8.728813	uc001lad.3	chr12:85441300-85442338	NA	NA	NA	NA	NA	NA	NA	NA
LRRK2	609007	1040.72	-2.105601	uc001rmg.4	chr12:40761568-40763086	623.714	-7.817479	uc001rmi.3	chr12:40758936-40763086	552.454	-13.393013	uc001tac.3	chr12:85638720-85638883
LRRN1	NA	NA	NA	NA	NA	1486.11	-13.838965	uc003bpt.4	chr3:3888477-3889387	NA	NA	NA	NA
LRRTM1	610867	NA	NA	NA	NA	NA	NA	NA	NA	824.091	-6.058837	uc002sok.1	chr2:80529003-80529375
LRRTM2	610868	NA	NA	NA	NA	NA	NA	NA	NA	703.474	-7.341314	uc011cyz.1	chr5:138205079-138208698
LRTM1	NA	523.272	-5.371038	uc003dhl.3	chr3:54952381-54952485	NA	NA	NA	NA	NA	NA	NA	NA
LSM6	607286	639.088	-7.161855	uc003lkl.4	chr4:147110809-147111213	898.732	-8.420926	uc003lkl.4	chr4:147110809-147111213	NA	NA	NA	NA
LSM7	607287	220.475	-6.51192	uc002vlp.4	chr19:2321520-2321678	NA	NA	NA	NA	NA	NA	NA	NA
LSMEM2	NA	1292.26	-8.590169	uc003cyz.3	chr3:50324634-50325545	NA	NA	NA	NA	NA	NA	NA	NA
LSR	616582	1087.01	-13.121391	uc002nyl.3	chr19:35758763-35758867	NA	NA	NA	NA	NA	NA	NA	NA
LST1	109170	556.057	-8.242802	uc010jsw.3	chr6:31556518-31556686	NA	NA	NA	NA	NA	NA	NA	NA
LTV1	NA	539.288	-4.08791	uc003qjs.3	chr6:144184665-144184943	NA	NA	NA	NA	NA	NA	NA	NA
LUC7L2	613056	NA	NA	NA	NA	NA	NA	NA	NA	736.939	-8.786084	uc003vuz.1	chr7:139097331-139097571
LUM	600616	1464.68	-17.763327	uc001lbn.3	chr12:91497232-91497941	1752.72	-19.863609	uc001lbn.3	chr12:91497232-91497941	797.205	-8.951197	uc001lbn.3	chr12:91497232-91497941
LURAP1	616129	691.332	-8.603814	uc010oma.2	chr1:46685893-46686928	NA	NA	NA	NA	NA	NA	NA	NA
LURAP1L	616130	NA	NA	NA	NA	NA	NA	NA	NA	1528.87	-20.319084	uc003zkw.3	chr9:12821760-12823059
LUZP1	601422	462.591	-6.682476	uc001bgl.2	chr1:23410516-23415387	NA	NA	NA	NA	NA	NA	NA	NA
LUZP4	300616	1613.07	-9.499443	uc004epa.3	chrX:114541370-114542121	NA	NA	NA	NA	NA	NA	NA	NA
LVRN	610046	NA	NA	NA	NA	NA	NA	NA	NA	551.84	-6.335321	uc003kro.3	chr5:115361816-115363299
LY6K	615093	NA	NA	NA	NA	1200.32	-7.719585	uc011ljv.2	chr8:143784790-143785584	518.871	-5.783976	uc011ljw.2	chr8:143784408-143785584
LY75	604524	NA	NA	NA	NA	230.269	-5.886763	uc002ubc.4	chr2:160659868-160661554	216.154	-6.508649	uc002ubc.4	chr2:160659868-160661554
LYAR	NA	1026.03	-5.931364	uc011bvz.2	chr4:4269429-4269615	NA	NA	NA	NA	NA	NA	NA	NA
LYPD6	613359	NA	NA	NA	NA	NA	NA	NA	NA	405.439	-7.780598	uc021vqt.1	chr2:150327365-150330659
LYRM4	613311	NA	NA	NA	NA	495.646	-7.06625	uc003mwp.3	chr6:5108653-5109656	453.051	-3.240128	uc003mwp.3	chr6:5108653-5109656
LYRM7	615831	NA	NA	NA	NA	531.339	-8.478199	uc003kvg.1	chr5:130535295-130541119	239.038	-3.82979	uc003kvg.1	chr5:130535295-130541119
LYSMD3	NA	261.588	-5.094939	uc002kjp.3	chr5:89811445-89814635	NA	NA	NA	NA	261.745	-8.124103	uc010jaz.2	chr5:89811445-89814628
LYZ	153450	NA	NA	NA	NA	962.949	-6.518174	uc001suw.2	chr12:69747000-69748013	NA	NA	NA	NA
LYZL6	612751	NA	NA	NA	NA	NA	NA	NA	NA	635.989	-5.71832	uc002hij.2	chr17:34261523-34261799
LZIC	610458	1181.62	-11.077533	uc001laqm.3	chr1:9989776-9990456	776.499	-7.476231	uc001laqm.3	chr1:9989776-9990456	NA	NA	NA	NA
MAATS1	609910	NA	NA	NA	NA	NA	NA	NA	NA	527.697	-6.839046	uc010hqx.1	chr3:119428747-119429208
MACC1	612646	NA	NA	NA	NA	1643.98	-35.055769	uc003sus.4	chr7:20174279-20180568	NA	NA	NA	NA
MACF1	608271	671.633	-4.536509	uc021olt.1	chr1:39951467-39952810	503.573	-5.333482	uc010olt.1	chr1:39748051-39748740	518.011	-3.777244	uc021olt.1	chr1:39951467-39952810
MAD2L1BP	NA	NA	NA	NA	NA	NA	NA	NA	NA	385.753	-4.580107	uc003ovl.3	chr6:43608271-43608688
MAEL	611368	NA	NA	NA	NA	NA	NA	NA	NA	1167.35	-7.297603	uc021peh.1	chr1:166991093-166991447
MAF	177075	1281.56	-13.878332	uc002fjm.3	chr16:79627745-79628356	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

MAGEA10:	300343	454.317	-7.361481	uc004flk.3	chrX:151301783-151302982	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAGEB1:	300097	2067.34	-20.339829	uc004dcc.3	chrX:30269655-30270155	682.668	-5.030571	uc004dcc.3	chrX:30269655-30270155	NA	NA	NA	NA	NA	NA	NA	NA
MAGEB18:	NA	542.598	-4.196924	uc004dbq.2	chrX:26158297-26158853	522.629	-7.759387	uc004dbq.2	chrX:26158297-26158853	NA	NA	NA	NA	NA	NA	NA	NA
MAGEB2:	300098	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAGED1:	300224	572.23	-9.189668	uc004dpm.3	chrX:51645242-51645450	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAGEE1:	300759	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAGI3:	615943	565.328	-10.072857	uc001edi.4	chr1:114224884-114228545	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAGOH:	602603	1424.77	-8.698107	uc001cvf.2	chr1:53692564-53692716	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAGOHB:	NA	789.542	-7.938494	uc001qvy.2	chr12:10756364-10758873	1536.74	-15.001684	uc001qvy.2	chr12:10756364-10758873	NA	NA	NA	NA	NA	NA	NA	NA
MAK16:	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAL2:	603684	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MALT1:	604860	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAN1A2:	604345	275.216	-4.333211	uc001ehd.1	chr1:118065580-118068320	1066.54	-7.955933	uc001ehd.1	chr1:118065580-118068320	NA	NA	NA	NA	NA	NA	NA	NA
MAN1B1:	604346	437.606	-5.496767	uc004clf.1	chr9:140003044-140003639	292.407	-4.573173	uc004clf.1	chr9:140003044-140003639	NA	NA	NA	NA	NA	NA	NA	NA
MAN2A1:	154582	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MANEA:	612327	1716.62	-22.033931	uc003pon.3	chr6:96034913-96035254	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MANSC4:	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAOB:	309860	1128.91	-8.198852	uc011mkx.2	chrX:43625857-43626865	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP1LC3C:	609605	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP2:	157130	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP2K6:	601254	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP2K7:	603014	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP3K12:	600447	360.324	-7.292087	uc001sdm.2	chr12:53874276-53874965	998.826	-9.210452	uc001sdm.2	chr12:53874276-53874965	NA	NA	NA	NA	NA	NA	NA	NA
MAP3K15:	300820	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP3K5:	602448	486.085	-5.866681	uc011edj.2	chr6:136878187-136878895	356.93	-8.044757	uc004czl.2	chrX:19378176-19378966	NA	NA	NA	NA	NA	NA	NA	NA
MAP4K1:	601983	312.683	-4.035908	uc002oik.1	chr19:39078281-39078449	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP6:	601783	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP7D1:	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP7D2:	NA	348.522	-6.155233	uc004czq.2	chrX:20024831-20026516	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP7D3:	300930	473.287	-5.212678	uc004ezl.3	chrX:135298974-135300652	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAP9:	610070	NA	NA	NA	NA	700.774	-12.215267	uc003ios.3	chr4:156263812-156268934	1049.9	-7.079601	uc003ios.3	chr4:156263812-156268934	NA	NA	NA	NA
MAPK14:	600289	513.672	-2.297988	uc011dth.2	chr6:36063853-36065831	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAPK6:	602904	1749.78	-13.789411	uc002abp.3	chr15:52357198-52358462	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MAPK8:	601158	NA	NA	NA	NA	688.904	-9.986503	uc001lgo.3	chr10:49842939-49843183	NA	NA	NA	NA	NA	NA	NA	NA
MAPK8IP2:	607755	NA	NA	NA	NA	NA	NA	NA	NA	208.365	-4.210683	uc003mx.3	chr19:45783833-45783992	NA	NA	NA	NA
MAPK9:	602896	NA	NA	NA	NA	516.706	-5.867576	uc003mls.4	chr5:179660595-179663383	779.385	-6.165719	uc003mlt.4	chr5:179660595-179663514	NA	NA	NA	NA
MARK1:	606511	NA	NA	NA	NA	433.721	-7.988182	uc001hmm.4	chr1:220835509-220837799	NA	NA	NA	NA	NA	NA	NA	NA
MARK4:	606495	910.444	-5.723791	uc002pbb.2	chr19:45805968-45808541	NA	NA	NA	NA	476.955	-5.830366	uc002paz.2	chr19:45783833-45783992	NA	NA	NA	NA
MARS:	156560	NA	NA	NA	NA	NA	NA	NA	NA	1063.57	-9.388647	uc010vq.1	chr12:57909922-57910064	NA	NA	NA	NA
MARS2:	609728	994.117	-9.502248	uc002uuq.3	chr12:198571912-198573114	NA	NA	NA	NA	760.402	-5.953375	uc002luq.3	chr2:198571912-198573114	NA	NA	NA	NA
MARVELD2:	610572	805.404	-8.527594	uc003jwq.3	chr5:68737482-68737890	990.986	-8.80008	uc003jwq.3	chr5:68737482-68737890	NA	NA	NA	NA	NA	NA	NA	NA
MAS1:	165180	NA	NA	NA	NA	NA	NA	NA	NA	365.428	-5.783976	uc003qz.3	chr6:160328966-160329107	NA	NA	NA	NA
MAST3:	612258	NA	NA	NA	NA	293.17	-7.930334	uc002nhz.4	chr19:18260537-18262499	NA	NA	NA	NA	NA	NA	NA	NA
MAST4:	NA	NA	NA	NA	NA	1168.11	-9.937645	uc003jus.3	chr5:66410077-66410875	NA	NA	NA	NA	NA	NA	NA	NA
MAT1A:	610550	NA	NA	NA	NA	243.121	-4.775867	uc001kbw.3	chr10:82031576-82033536	NA	NA	NA	NA	NA	NA	NA	NA
MAT2A:	601468	NA	NA	NA	NA	1537.17	-12.278736	uc002spr.3	chr2:85770896-85772403	592.685	-4.038807	uc010vyr.2	chr2:85770162-85770775	NA	NA	NA	NA
MATN1:	115437	NA	NA	NA	NA	404.029	-5.703427	uc001brz.3	chr1:31184124-31186428	NA	NA	NA	NA	NA	NA	NA	NA
MATN2:	602108	NA	NA	NA	NA	846.521	-7.990106	uc003yib.1	chr8:99016041-99016514	265.391	-10.753516	uc003yib.1	chr8:99016041-99016514	NA	NA	NA	NA
MATN3:	602109	218.059	-2.353903	uc002rdl.3	chr2:20191813-20192871	NA	NA	NA	NA	1224.56	-12.562243	uc002rdl.3	chr2:20191813-20192871	NA	NA	NA	NA

Table 1

MATR3	164015	NA	NA	NA	NA	NA	NA	NA	NA	NA	773.238	-5.197222	uc003lct.3	chr5:138665085-138667366
MBD1	156535	NA	NA	NA	NA	NA	NA	NA	NA	NA	551.169	-5.349731	uc002lef.3	chr18:47793252-47793957
MBD2	603547	NA	NA	NA	NA	219.801	-8.741468	uc002lth.2	chr18:51729050-51729265	902.628	-9.138454	uc002fig.2	chr18:51677971-51681681	
MBD5	611472	NA	NA	NA	NA	1743.63	-11.598938	uc0002lwm.4	chr2:149270511-149271044	NA	NA	NA	NA	
MBIP	609431	944.464	-13.231176	uc001lwm.2	chr14:36767764-36768288	1474.81	-1.562794	uc001lwm.2	chr14:36767764-36768288	553.704	-5.568777	uc001lwm.2	chr14:36767764-36768288	
MBL2	154545	593.228	-10.598525	uc001ljl.3	chr10:54525140-54527896	NA	NA	NA	NA	634.209	-6.039178	uc0001ljl.3	chr10:54525140-54527896	
MBNL2	607327	564.104	-9.098986	uc001vnc.3	chr13:98009994-98011528	NA	NA	NA	NA	213.229	-5.656301	uc010ljl.2	chr13:98043704-98046374	
MBNL3	300413	903.775	-10.787246	uc004awl.3	chrX:131503343-131513693	NA	NA	NA	NA	NA	NA	NA	NA	
MC1R	155555	NA	NA	NA	NA	523.001	-8.234059	uc002lpe.4	chr16:89986621-89987385	NA	NA	NA	NA	
MC5R	600042	749.627	-5.616246	uc010xaf.2	chr18:13826743-13826861	1012.08	-8.299275	uc010xaf.2	chr18:13826743-13826861	NA	NA	NA	NA	
MCC	159350	571.478	-5.654323	uc003kql.4	chr5:112357796-112362998	NA	NA	NA	NA	NA	NA	NA	NA	
MCCC2	609014	NA	NA	NA	NA	NA	NA	NA	NA	298.394	-6.926032	uc003kbs.4	chr5:70952688-70954530	
MCF2	311030	NA	NA	NA	NA	316.908	-4.583737	uc010nsh.2	chrX:138663930-138664601	NA	NA	NA	NA	
MCFD2	607788	388.014	-6.330978	uc0002rvk.3	chr2:47129009-47132601	857.492	-7.521137	uc0002rvk.3	chr2:47129009-47132601	NA	NA	NA	NA	
MCHR2	606111	1287.28	-9.854367	uc003pqh.1	chr6:100367786-100368815	NA	NA	NA	NA	NA	NA	NA	NA	
MCM2	116945	NA	NA	NA	NA	NA	NA	NA	NA	1381.15	-6.25191	uc011bkn.2	chr3:127340617-127341278	
MCM3AP	603294	NA	NA	NA	NA	NA	NA	NA	NA	694.462	-6.506625	uc002rio.1	chr21:47655048-47655181	
MCMBP	610909	NA	NA	NA	NA	NA	NA	NA	NA	946.003	-8.090572	uc0001let.1	chr10:121602294-121602685	
MCMDC2	NA	NA	NA	NA	NA	NA	NA	NA	NA	436.65	-6.406623	uc0003xwv.3	chr8:67796264-67796854	
MCOLN3	607400	NA	NA	NA	NA	303.777	-3.295331	uc0001dko.3	chr1:85483765-85484805	201.168	-4.493057	uc0001dko.3	chr1:85483765-85484805	
MCPH1	607117	382.658	-4.810288	uc003wql.3	chr8:6303077-6304940	NA	NA	NA	NA	NA	NA	NA	NA	
MCRS1	609504	215.469	-4.933746	uc0001trul.1	chr12:49952086-49952425	NA	NA	NA	NA	NA	NA	NA	NA	
MCTP1	616296	NA	NA	NA	NA	856.491	-7.204207	uc003kku.2	chr5:94042289-94043200	NA	NA	NA	NA	
MCTST1	300587	NA	NA	NA	NA	815.102	-7.648517	uc0004esx.3	chrX:119746120-119755016	964.019	-9.733943	uc0004esx.3	chrX:119746120-119755016	
MDC1	607593	NA	NA	NA	NA	676.694	-6.785601	uc0003nrf.4	chr6:30667584-30668241	NA	NA	NA	NA	
MDFC	614511	1139.39	-14.446601	uc022akf.1	chr7:114563552-114563720	391.223	-5.492857	uc022akf.1	chr7:114563552-114563720	509.281	-7.57009	uc022akf.1	chr7:114563552-114563720	
MDM1	613813	319.328	-5.490174	uc0001sua.4	chr12:68718785-68720265	578.578	-11.738192	uc0001sua.4	chr12:68718785-68720265	NA	NA	NA	NA	
MECOM	165215	NA	NA	NA	NA	NA	NA	NA	NA	451.828	-6.677247	uc010hvk.1	chr3:168801287-168802831	
MECP2	300005	519.209	-4.783117	uc0004fiv.2	chrX:153287264-153295817	NA	NA	NA	NA	NA	NA	NA	NA	
MED12	300188	NA	NA	NA	NA	NA	NA	NA	NA	637.419	-7.732115	uc0004dyv.3	chrX:70362069-70362304	
MED17	603810	1007.95	-6.086082	uc0001pel.2	chr11:93521355-93522962	NA	NA	NA	NA	706.611	-1.889971	uc0001pel.2	chr11:93521355-93522962	
MED19	612385	NA	NA	NA	NA	NA	NA	NA	NA	435.541	-4.494564	uc0001hla.1	chr11:57471182-57471509	
MED22	185641	757.393	-4.525297	uc0004cdc.3	chr9:136207755-136208354	NA	NA	NA	NA	NA	NA	NA	NA	
MED28	610311	482.834	-6.449887	uc0003gpi.1	chr4:17625422-17626160	NA	NA	NA	NA	NA	NA	NA	NA	
MED30	610237	NA	NA	NA	NA	1244.27	-9.722781	uc0003voj.3	chr8:118552218-118552501	NA	NA	NA	NA	
MED31	NA	NA	NA	NA	NA	NA	NA	NA	NA	926.686	-10.09216	uc0002pde.4	chr17:6546633-6547786	
MED6	602984	695.616	-5.388268	uc0001xmf.3	chr14:71050957-71051529	542.917	-2.642949	uc0001xmf.3	chr14:71050957-71051529	319.836	-6.3261	uc0001xmf.3	chr14:71050957-71051529	
MED7	605045	1413.3	-11.947574	uc010ljk.3	chr5:156565451-156565740	NA	NA	NA	NA	NA	NA	NA	NA	
MEDAG	600660	475.331	-6.562262	uc0002bve.3	chr15:100252977-100256629	772.574	-5.917129	uc0002bve.3	chr15:100252977-100256629	355.579	-6.2151	uc0001uth.4	chr13:31498573-31499709	
MEF2A	600662	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
MEF2C	600662	NA	NA	NA	NA	NA	NA	NA	NA	1457.66	-11.119391	uc0003kjl.2	chr5:88014058-88018420	
MEGF10	612453	NA	NA	NA	NA	1292.66	-8.262511	uc0003kuh.4	chr5:126793011-126796910	NA	NA	NA	NA	
MEGF9	604268	540.67	-6.056652	uc0004bkk.4	chr9:123420280-123421647	385.551	-4.507734	uc0004bkk.4	chr9:123420280-123421647	NA	NA	NA	NA	
MEIG1	614174	1179.29	-22.694091	uc0009xjk.1	chr10:15014641-15014850	673.893	-6.549788	uc0009xjk.1	chr10:15014641-15014850	NA	NA	NA	NA	
MEIS3P1	NA	NA	NA	NA	NA	NA	NA	NA	NA	480.797	-5.175553	uc0002gpc.3	chr17:15691010-15693019	
MERTK	604705	NA	NA	NA	NA	815.72	-6.873205	uc010jzh.1	chr6:46806874-46807519	NA	NA	NA	NA	
MES1	601029	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
METAP1	610151	NA	NA	NA	NA	730.04	-4.111178	uc0003huf.4	chr4:99982469-99983960	NA	NA	NA	NA	

Table 1

METAP1D	610267	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	733.051	-6.20619	uc002uhk.3	chr2:172945135-172945587
METAP2	601870	NA	NA	NA	NA	604.145	-5.064142	uc001lec.3	chr12:9507681-95098613	NA	NA	NA	NA	NA	NA
METTL10	NA	NA	NA	NA	NA	471.345	-2.757144	uc001lhy.1	chr10:126447406-126449071	224.763	-5.318861	uc001lhy.1	NA	NA	chr10:126447406-126449071
METTL12	NA	NA	NA	NA	NA	1071.71	-12.883165	uc001nug.1	chr11:62434524-62434923	NA	NA	NA	NA	NA	NA
METTL14	616504	568.4	-6.121731	uc003cfc.3	chr4:119631458-119632077	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
METTL15	NA	591.836	-13.360446	uc001nsg.2	chr11:28351943-28355054	942.759	-14.555765	uc001nsg.2	chr11:28351943-28355054	696.467	-6.071581	uc001nsh.2	chr11:2835389-28355054	NA	NA
METTL16	NA	NA	NA	NA	NA	NA	NA	NA	NA	878.326	-5.728369	uc002fut.3	chr17:2319348-2323263	NA	NA
METTL21A	615257	981.441	-9.255038	uc002vcf.2	chr2:208473839-208477769	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
METTL21B	615258	NA	NA	NA	NA	821.991	-8.075247	uc001sag.3	chr12:58174430-58176324	NA	NA	NA	NA	NA	NA
METTL2A	NA	NA	NA	NA	NA	303.709	-6.906296	uc002lcv.2	chr17:60526091-60527454	NA	NA	NA	NA	NA	NA
METTL3	612472	NA	NA	NA	NA	1394.42	-15.469295	uc001olix.2	chr14:21969294-21969850	NA	NA	NA	NA	NA	NA
METTL4	NA	952.524	-10.6231	uc010dkj.3	chr18:2537524-2539135	351.67	-5.056668	uc010dkj.3	chr18:2537524-2539135	557.203	-9.868007	uc010dkj.3	chr18:2537524-2539135	NA	NA
METTL6	NA	NA	NA	NA	NA	401.029	-7.099132	uc003bztl.1	chr3:15455881-15456315	NA	NA	NA	NA	NA	NA
METTL8	609525	424.279	-3.444104	uc002lugs.4	chr2:172173913-172180872	201.44	-4.859142	uc002lugs.4	chr2:172173913-172180872	NA	NA	NA	NA	NA	NA
METTL9	609388	207.345	-5.027447	uc002dje.3	chr16:21668754-21668792	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MEX3C	611005	NA	NA	NA	NA	1093.51	-9.341261	uc001lzh.1	chr15:44096733-44097291	942.015	-11.833307	uc002lfc.4	chr18:48700920-48702720	NA	NA
MFAP1	600215	NA	NA	NA	NA	NA	NA	NA	NA	358.477	-3.559457	uc001lth.1	chr15:44096733-44097291	NA	NA
MFAP3L	616523	NA	NA	NA	NA	NA	NA	NA	NA	451.258	-6.246893	uc003lsh.4	chr4:170907748-170912528	NA	NA
MFHAS1	605352	NA	NA	NA	NA	714.464	-6.099793	uc003wsj.1	chr8:8641999-8643531	NA	NA	NA	NA	NA	NA
MFN1	608506	NA	NA	NA	NA	NA	NA	NA	NA	1160.38	-7.941416	uc003fjs.3	chr3:179109848-179111008	NA	NA
MFSD8	611124	NA	NA	NA	NA	1550.15	-12.313093	uc003lfp.3	chr4:128838960-128841784	464.494	-5.163575	uc011cgv.1	chr4:128842679-128842913	NA	NA
MGAR2	NA	260.866	-4.875288	uc003lhr.1	chr4:140187317-140187752	969.434	-12.373779	uc003lhr.1	chr4:140187317-140187752	NA	NA	NA	NA	NA	NA
MGAT2	602616	NA	NA	NA	NA	667.183	-8.025358	uc001lwr.3	chr14:50089331-50090199	295.377	-6.595879	uc001lwr.3	chr14:50089331-50090199	NA	NA
MGAT3	604621	NA	NA	NA	NA	NA	NA	NA	NA	338.01	-4.368459	uc003axv.4	chr22:39884955-39888199	NA	NA
MGAT4A	604623	NA	NA	NA	NA	705.514	-10.38458	uc002saze.3	chr2:99235569-99242028	NA	NA	NA	NA	NA	NA
MGAT5B	612441	NA	NA	NA	NA	581.839	-5.932271	uc002lth.3	chr17:74944921-74946471	642.989	-5.127132	uc002lth.4	chr17:74878385-74878607	NA	NA
MGME1	615076	NA	NA	NA	NA	459.062	-5.54896	uc002wqlh.3	chr20:17970753-17971762	NA	NA	NA	NA	NA	NA
MGST1	138330	NA	NA	NA	NA	1486.55	-8.429703	uc001lrf.3	chr12:16516976-16517344	NA	NA	NA	NA	NA	NA
MGST2	601733	808.664	-2.31517	uc021xse.1	chr4:140625170-140625406	1095.09	-5.35259	uc021xse.1	chr4:140625170-140625406	295.445	-3.118996	uc003lhy.3	chr4:140625303-140625406	NA	NA
MIAP2	608001	NA	NA	NA	NA	NA	NA	NA	NA	824.489	-8.748487	uc001wux.3	chr14:39722454-39722575	NA	NA
MICAL3	608882	NA	NA	NA	NA	623.456	-5.541424	uc002znh.2	chr22:18317101-18317215	NA	NA	NA	NA	NA	NA
MICB	602436	NA	NA	NA	NA	758.458	-5.514129	uc011lfcy.2	chr6_cox_hap2:2987358-2988570	NA	NA	NA	NA	NA	NA
MICU2	610632	NA	NA	NA	NA	566.563	-8.086002	uc010lct.2	chr13:22066828-22067387	673.871	-6.850497	uc010lct.2	chr13:22066828-22067387	NA	NA
MIEF1	615497	NA	NA	NA	NA	841.004	-10.385107	uc003axxx.3	chr22:39910329-39914137	NA	NA	NA	NA	NA	NA
MIEN1	611802	NA	NA	NA	NA	NA	NA	NA	NA	537.13	-5.335124	uc002hsq.3	chr17:37885409-37885774	NA	NA
MIEF1	NA	782.231	-5.869119	uc001lddc.2	chr1:67452157-67454302	712.907	-7.235581	uc001lddc.2	chr1:67452157-67454302	NA	NA	NA	NA	NA	NA
MINK1	609426	390.782	-5.78778	uc010vsk.2	chr17:4800583-4801356	631.388	-5.552811	uc010vsk.2	chr17:4800583-4801356	611.115	-3.244397	uc010vsk.2	chr17:4800583-4801356	NA	NA
MINPP1	605391	229.672	-5.468491	uc001kev.3	chr10:89311943-89313218	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MIOS	615359	NA	NA	NA	NA	NA	NA	NA	NA	811.71	-7.31556	uc003srf.3	chr7:7646724-7647110	NA	NA
MIEP2	602241	NA	NA	NA	NA	378.559	-5.92779	uc001uox.4	chr13:24304328-24304486	NA	NA	NA	NA	NA	NA
MIS18A	NA	218.187	-5.673029	uc002ypj.3	chr21:33640630-33641347	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MIS18BP1	NA	NA	NA	NA	NA	1157.21	-11.056193	uc001twf.3	chr14:45672393-45673311	NA	NA	NA	NA	NA	NA
MITD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	595.437	-6.921452	uc002szs.1	chr2:99785726-99785837	NA	NA
MITF	156845	583.2	-9.241189	uc003dnz.3	chr3:70014400-70017488	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MK67	176741	NA	NA	NA	NA	NA	NA	NA	NA	1102.72	-10.988088	uc001lke.3	chr10:129894925-129897453	NA	NA
MKLN1	605623	861.777	-12.494789	uc011kpl.2	chr7:131172488-131181398	NA	NA	NA	NA	524.957	-4.840405	uc011kpl.2	chr7:131172488-131181398	NA	NA
MKRN2	607754	NA	NA	NA	NA	348.322	-5.080409	uc003vuu.4	chr7:140155983-140156447	597.114	-4.93754	uc003vuu.4	chr7:140155983-140156447	NA	NA
MKRN2OS	NA	NA	NA	NA	NA	441.644	-4.616069	uc021wlc.1	chr3:12581280-12581691	NA	NA	NA	NA	NA	NA
MKSI1	609883	768.772	-9.434113	uc002ivr.2	chr17:56282797-56283439	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

MKX1	601332	855.782	-5.977701	uc001lix.4	chr10:27961803-27964157	NA	NA	NA	NA	NA	785.499	NA	NA	NA	chr12:121134349-121139667
MLEC	613802	344.14	-4.013345	uc001tyr.1	chr12:121134349-121139667	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLF1	601402	1055.4	-14.703596	uc003fbx.3	chr3:158322992-158324249	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLH1	120436	NA	NA	NA	NA	854.716	0.166689	uc003cgl.3	chr3:37092145-37092337	1070.49	-5.541789	uc003cgl.3	chr3:37092145-37092337	NA	NA
MLLT10	602409	NA	NA	NA	NA	NA	NA	NA	NA	1002.67	-7.352891	uc001lqs.3	chr10:22030868-22032559	NA	NA
MLLT11	604684	964.857	-7.940541	uc001ewq.3	chr1:151039974-151040973	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLLT3	159558	1121.3	-14.728143	uc011lne.1	chr9:20344968-20346440	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLLT4	159559	447.903	-6.204244	uc021zlj.1	chr6:168370616-168372700	NA	NA	NA	NA	NA	751.938	-7.985108	uc021zlj.1	chr6:168370616-168372700	NA
MMAA	607481	NA	NA	NA	NA	NA	NA	NA	NA	1456.64	-21.490569	uc003ikh.4	chr4:146576587-146581187	NA	NA
MMAHC	609831	393.3	-4.323811	uc009vxx.3	chr1:45874888-45976739	NA	NA	NA	NA	988.571	-6.465455	uc009vxx.3	chr1:45974888-45976739	NA	NA
MMAHCH	611935	NA	NA	NA	NA	1101.03	-12.193309	uc002lxc.3	chr2:150426147-150426487	2969.67	-20.15297	uc002lxc.3	chr2:150426147-150426487	NA	NA
MMD	604467	NA	NA	NA	NA	1156.59	-9.157682	uc002lul.3	chr17:53469974-53471694	NA	NA	NA	NA	NA	NA
MME	120520	558.147	-4.926569	uc010hvr.1	chr3:154898249-154901518	NA	NA	NA	NA	586.624	-8.10231	uc022cet.1	chrX:135044231-135047182	NA	NA
MMGT1	NA	NA	NA	NA	NA	NA	NA	NA	NA	1522.24	-16.869343	uc001phg.2	chr11:102641233-102641523	NA	NA
MMP10	185260	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MMP15	602261	NA	NA	NA	NA	446.862	-5.1118	uc002ena.3	chr16:58079351-58080804	NA	NA	NA	NA	NA	NA
MMP16	602262	1076.99	-5.776699	uc003yeb.4	chr8:89049460-89053688	664.669	-5.144157	uc003yeb.4	chr8:89049460-89053688	NA	NA	NA	NA	NA	NA
MMP7	178990	NA	NA	NA	NA	1741.98	-13.560378	uc001phb.3	chr11:102391239-102391506	1251.92	-4.011546	uc001phb.3	chr11:102391239-102391506	NA	NA
MMP8	120355	648.809	-5.895186	uc001phe.2	chr11:102582526-102584078	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MMRN1	601456	247.183	-6.379406	uc010ku.3	chr4:90874570-90875780	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MMRN2	608925	NA	NA	NA	NA	368.154	-6.446522	uc001kea.3	chr10:88695298-88696499	NA	NA	NA	NA	NA	NA
MMS2L	615614	NA	NA	NA	NA	205.408	-15.195844	uc011eaf.2	chr6:97590037-97594681	284.804	-7.008867	uc003ppc.3	chr6:97701352-97702354	NA	NA
MOB1A	609281	505.421	-6.434412	uc002skh.4	chr2:74383211-74383694	NA	NA	NA	NA	567.188	-8.175083	uc003hfv.2	chr4:71841039-71842460	NA	NA
MOB1B	609282	1700.59	-1.890743	uc003hfv.2	chr4:71841039-71842460	1879.17	-23.993816	uc003hfv.3	chr4:71847775-71853891	NA	NA	NA	NA	NA	NA
MOB3C	NA	486.778	-7.809358	uc001cqe.4	chr1:47073387-47075326	NA	NA	NA	NA	446.707	-7.726319	uc003opb.3	chr6:39872034-39874132	NA	NA
MOC51	603707	NA	NA	NA	NA	NA	NA	NA	NA	1206.1	-13.98207	uc011cdf.2	chr5:52397927-52398054	NA	NA
MOC52	603708	451.07	-1.905312	uc003poz.3	chr5:52393895-52394431	494.15	-3.696608	uc011cdf.2	chr5:52393895-52394497	975.933	-4.621561	uc003cyb.2	chr3:40946308-40947547	NA	NA
MON1A	611464	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MON1B	608954	NA	NA	NA	NA	473.972	-6.794786	uc002lecz.3	chr16:77232206-77233543	NA	NA	NA	NA	NA	NA
MORC2	616661	NA	NA	NA	NA	251.393	-6.209134	uc003aje.1	chr22:31322600-31322789	NA	NA	NA	NA	NA	NA
MORC4	NA	913.53	-6.405782	uc004emu.4	chrX:106183964-106184708	298.63	-6.004877	uc004temp.4	chrX:106057101-106058137	686.578	-7.650829	uc004ekw.3	chrX:102930426-102931088	NA	NA
MORF4L2	300409	702.689	-9.502926	uc004ekw.3	chrX:102330426-102331088	NA	NA	NA	NA	1310.41	-8.912094	uc011arq.1	chr22:50581765-50581881	NA	NA
MOV10L1	605794	NA	NA	NA	NA	NA	NA	NA	NA	920.662	-4.90022	uc002ghx.3	chr17:7490763-7491527	NA	NA
MPDU1	604041	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MPEG1	610390	661.091	-5.560352	uc001mnv.4	chr11:58975983-58978187	NA	NA	NA	NA	418.713	-5.305648	uc001umg.3	chr13:20245127-20245258	NA	NA
MPHOSPH8	611626	500.404	-2.170723	uc001umg.3	chr13:20245127-20245258	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MPP7	610973	726.408	-10.223326	uc001lua.1	chr10:28339923-28342993	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MPPD2	600911	NA	NA	NA	NA	360.793	-4.455897	uc001msr.3	chr11:30431618-30433014	NA	NA	NA	NA	NA	NA
MPR1P	612935	NA	NA	NA	NA	801.615	-8.110599	uc002ggu.2	chr17:17088137-17095962	NA	NA	NA	NA	NA	NA
MR1	600764	NA	NA	NA	NA	237.983	-7.818823	uc001lqq.2	chr1:181024402-181031074	NA	NA	NA	NA	NA	NA
MRAP	609196	NA	NA	NA	NA	1180.47	-7.67313	uc002ypk.3	chr21:338686965-33867094	NA	NA	NA	NA	NA	NA
MRE11A	600814	NA	NA	NA	NA	NA	NA	NA	NA	424.749	-6.040094	uc001peu.2	chr11:94150469-94153290	NA	NA
MRGPRX2	607228	NA	NA	NA	NA	NA	NA	NA	NA	413.015	-5.230157	uc001mph.3	chr11:19076003-19076956	NA	NA
MRM1	NA	345.925	-4.215284	uc002hne.3	chr17:34964852-34965407	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MROH7	NA	1241.5	-8.289133	uc001cxo.2	chr1:55129467-55129728	541.294	-4.353334	uc001cxo.2	chr1:55129467-55129728	NA	NA	NA	NA	NA	NA
MROH9	NA	821.977	-5.450956	uc001lgh.3	chr1:170967542-170967946	239.452	-5.36657	uc001lgh.3	chr1:170967542-170967946	NA	NA	NA	NA	NA	NA
MRPL11	611826	403.329	-9.019962	uc001ohy.4	chr11:66202550-66203583	339.352	-3.672304	uc001ohy.4	chr11:66202550-66203583	NA	NA	NA	NA	NA	NA
MRPL19	611832	NA	NA	NA	NA	NA	NA	NA	NA	371.363	-5.658348	uc002snl.3	chr2:75882412-75889334	NA	NA
MRPL2	611822	NA	NA	NA	NA	NA	NA	NA	NA	1547.44	-4.53294	uc003ots.1	chr6:43021767-43022011	NA	NA

Table 1

MRPL22	611835	NA	NA	NA	NA	788.527	-7.551554	uc003lvy.4	chr5:154346458-154348971	NA	NA	NA	NA
MRPL35	611841	948.259	-9.989012	uc002sig.4	chr2:86437792-86440477	382.741	-8.248625	uc002srf.4	chr2:86439550-86440477	1316.5	-14.609574	uc002arg.4	chr2:86437792-86440477
MRPL36	611842	NA	NA	NA	NA	471.574	-9.90122	uc003jcx.4	chr5:1798499-1798737	NA	NA	NA	NA
MRPL42	611847	1361.77	-14.748872	uc001lca.3	chr12:93894996-93897548	NA	NA	NA	NA	NA	NA	NA	NA
MRPL46	611851	NA	NA	NA	NA	210.812	-5.674106	uc002bmi.1	chr15:89002708-89007910	NA	NA	NA	NA
MRPL48	611853	NA	NA	NA	NA	NA	NA	NA	NA	508.791	-6.737641	uc001ouh.4	chr11:73575416-73575656
MRPL50	611854	439.895	-6.598085	uc004bbe.2	chr9:104152249-104152747	NA	NA	NA	NA	NA	NA	NA	NA
MRPL57	611997	NA	NA	NA	NA	NA	NA	NA	NA	600.758	-8.880167	uc001unw.3	chr13:21751365-21753220
MRPL9	611824	310.885	-5.04767	uc001eyv.3	chr1:151732123-151732525	473.687	-4.261176	uc001eyv.3	chr1:151732123-151732525	695.006	-4.375258	uc001leyv.3	chr1:151732123-151732525
MRPS14	611978	NA	NA	NA	NA	NA	NA	NA	NA	462.369	-4.507734	uc001gkk.3	chr1:174982094-174983804
MRPS16	609204	NA	NA	NA	NA	NA	NA	NA	NA	732.409	-6.408624	uc001jts.1	chr10:75008601-75010609
MRPS18C	611983	NA	NA	NA	NA	NA	NA	NA	NA	278.402	-4.874063	uc003hor.4	chr4:84382351-84382929
MRPS23	611985	1187.2	-5.637216	uc002lvc.3	chr17:55916287-55917143	NA	NA	NA	NA	578.264	-5.438736	uc002lvc.3	chr17:55916287-55917143
MRPS33	611993	NA	NA	NA	NA	722.865	-8.957283	uc003vwd.4	chr7:140705961-140706229	NA	NA	NA	NA
MRPS36	611996	NA	NA	NA	NA	450.952	-6.919258	uc003jqv.3	chr5:68525053-68525985	NA	NA	NA	NA
MRPS5	611972	823.59	-3.925327	uc002sub.3	chr2:95752952-95753101	NA	NA	NA	NA	207.398	-8.427206	uc002sub.3	chr2:95752952-95753101
MRPS6	611973	216.538	-8.89253	uc002yp.2	chr21:35514901-35515334	501.207	-7.396125	uc002yp.2	chr21:35514901-35515334	NA	NA	NA	NA
MS2	NA	689.93	-7.005284	uc003nea.3	chr6:24423285-24423705	621.06	-8.05039	uc003neb.3	chr6:24423285-24425816	NA	NA	NA	NA
MS4A1	112210	NA	NA	NA	NA	NA	NA	NA	NA	538.935	-5.196112	uc009ymy.1	chr11:60231286-60231785
MS4A13	NA	NA	NA	NA	NA	360.008	-5.178053	uc001nps.3	chr11:60310049-60310191	NA	NA	NA	NA
MS4A2	147138	NA	NA	NA	NA	NA	NA	NA	NA	228.979	-5.847175	uc001rop.3	chr11:59863130-59865940
MS4A4A	606547	886.209	-13.391437	uc001noz.3	chr11:60075652-60076445	NA	NA	NA	NA	NA	NA	NA	NA
MS4A6A	606548	NA	NA	NA	NA	1036.46	-4.782558	uc001noq.3	chr11:59939080-59939726	639.411	-3.042746	uc001noq.3	chr11:59939080-59939726
MISANTD3	NA	269.782	-4.624739	uc022bbz.1	chr9:103212839-103214016	NA	NA	NA	NA	NA	NA	NA	NA
MSH4	602105	NA	NA	NA	NA	958.946	-8.580759	uc001dhd.2	chr1:76378573-76378923	NA	NA	NA	NA
MSL1	614801	1391.75	-12.745392	uc002hua.4	chr17:38290623-38293045	NA	NA	NA	NA	571.452	-7.620023	uc002hua.4	chr17:38290623-38293045
MSL2	614802	1023.52	-6.773401	uc011bmb.1	chr3:135867760-135869988	750.899	-6.435021	uc011bmb.1	chr3:135867760-135869988	NA	NA	NA	NA
MSL3	300609	NA	NA	NA	NA	NA	NA	NA	NA	235.083	-6.444387	uc004cuw.3	chrX:11793199-11793872
MSRA	601250	1284.16	-10.315689	uc003wsx.3	chr8:10285823-10286401	NA	NA	NA	NA	NA	NA	NA	NA
MSX1	142983	NA	NA	NA	NA	233.526	-4.206923	uc003gfl.3	chr4:4864871-4865660	NA	NA	NA	NA
MT1A	156350	653.041	-6.786994	uc002ejr.3	chr16:56673863-56673999	NA	NA	NA	NA	NA	NA	NA	NA
MT1E	156351	NA	NA	NA	NA	367.733	-6.279567	uc002ejl.3	chr16:56660884-56661024	NA	NA	NA	NA
MT1F	156352	682.24	-6.698985	uc002ejl.3	chr16:566693077-566693215	NA	NA	NA	NA	NA	NA	NA	NA
MT1G	156353	NA	NA	NA	NA	760.054	-6.531752	uc002ejv.1	chr16:56700653-56700790	NA	NA	NA	NA
MT1H	156354	NA	NA	NA	NA	533.954	-6.704343	uc002ejw.3	chr16:56704902-56705041	NA	NA	NA	NA
MT1M	156357	NA	NA	NA	NA	1252.53	-5.421104	uc002ejn.3	chr16:56667755-56667898	568.486	-9.106859	uc002ejn.3	chr16:56667755-56667898
MT1X	156359	NA	NA	NA	NA	1008.58	-12.130377	uc002ejy.3	chr16:56717962-56718108	NA	NA	NA	NA
MT2A	156360	608.797	-3.913272	uc002ejh.3	chr16:56643267-56643409	672.533	-10.058801	uc002ejh.3	chr16:56643267-56643409	NA	NA	NA	NA
MTCP1	300116	NA	NA	NA	NA	786.117	-8.124339	uc004fmz.2	chrX:154292309-154293674	NA	NA	NA	NA
MTDH	610323	NA	NA	NA	NA	442.372	-6.234994	uc003yhz.3	chr8:98736899-98742488	361.118	-6.529536	uc003yhz.3	chr8:98736899-98742488
MTER2	NA	474.639	-4.529601	uc001tme.1	chr12:107371069-107371334	NA	NA	NA	NA	NA	NA	NA	NA
MTF2	609882	NA	NA	NA	NA	293.491	-6.462448	uc001dpi.4	chr1:93602585-93604638	NA	NA	NA	NA
MTFMT	611766	633.728	-9.755785	uc002aof.4	chr15:65293850-65295399	NA	NA	NA	NA	1098.24	-10.090352	uc002aof.4	chr15:65293850-65295399
MTFR1	NA	NA	NA	NA	NA	1031.05	-13.498363	uc011lep.2	chr8:66620361-66620573	NA	NA	NA	NA
MTG2	610919	NA	NA	NA	NA	572.866	-5.523039	uc002ycc.4	chr20:60776134-60777810	NA	NA	NA	NA
MTHFD2	604887	575.091	-6.025016	uc002skj.3	chr2:74441370-74442424	NA	NA	NA	NA	NA	NA	NA	NA
MTHFD2L	614047	NA	NA	NA	NA	1912.15	-17.854173	uc011cbj.2	chr4:75107325-75107916	508.043	-5.918091	uc011cbj.2	chr4:75107325-75107916
MTHFR	607093	524.224	-5.1118	uc001atb.1	chr1:11845787-11850736	NA	NA	NA	NA	NA	NA	NA	NA
MTHFS	604197	NA	NA	NA	NA	NA	NA	NA	NA	1013.31	-6.474058	uc021vvp.1	chr15:80135889-80137551

Table 1

MTMR11	300171	NA	NA	NA	NA	NA	1069.18	NA	NA	NA	NA	878.331	-7.728709	uc011mya.1	chrX:149931203-149933397
MTMR11	NA	776.707	-1.083355	uc001e1m.2	chr1:149900543-149900758	NA	NA	-8.667684	uc001e1l.4	chr1:149900543-149901020	1249.52	-8.667684	uc010pbm.1	chr1:149902257-149902831	
MTMR14	611089	NA	NA	NA	NA	NA	NA	NA	NA	NA	474.795	-5.131939	uc003brz.3	chr3:9743658-9744078	
MTMR6	603561	645.7	-5.381745	uc001urqe.1	chr13:25802307-25802677	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MTMP8	NA	401.35	-4.992822	uc004dvs.3	chrX:63487961-63488416	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MTMP9	606260	NA	NA	NA	NA	NA	599.944	-5.585691	uc003wfm.3	chr8:11180298-11185654	NA	NA	NA	NA	NA
MTOR	601231	NA	NA	NA	NA	NA	NA	NA	NA	NA	315.005	-6.175893	uc001asc.3	chr1:11166588-11167541	
MTR	156570	NA	NA	NA	NA	NA	859.695	-1.609293	uc001hyi.4	chr1:237060945-237067281	692.982	-6.250084	uc001hyi.4	chr1:237060945-237067281	
MTRF1L	613542	873.361	-5.774239	uc003gpl.4	chr6:153308400-153311029	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MITRN2L10	NA	483.947	-5.771478	uc002bvr.1	chrX:55207824-55208352	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MTX2	608555	954.446	-7.320755	uc002ukw.3	chr2:177202393-177202753	NA	NA	NA	uc001mqw.3	chr11:26580579-26582611	NA	NA	NA	NA	NA
MUC15	608566	NA	NA	NA	NA	NA	389.198	-8.549453	NA	NA	362.804	-5.933495	uc001sxx.1	chr11:1104264-1104417	
MUC2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MUCL1	610857	1378.95	-7.484818	uc001sgk.3	chr12:55252027-55252174	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MUL1	612037	NA	NA	NA	NA	NA	NA	NA	NA	NA	559.669	-6.261952	uc001bdl.4	chr1:20825941-20827182	
MURC	NA	389.119	-7.595946	uc004bba.3	chr9:103348734-103350173	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MUS81	606591	280.923	-6.049928	uc001ofv.4	chr11:65633524-65633914	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MUTYH	604933	NA	NA	NA	NA	NA	719	-7.380917	uc001cnf.3	chr1:45794914-45794977	NA	NA	NA	NA	NA
MVK	251170	586.893	-6.492262	uc001loy.4	chr12:110034383-110035071	NA	NA	NA	uc001cnf.3	chr1:45794914-45794977	NA	NA	NA	NA	NA
MXRA7	NA	NA	NA	NA	NA	NA	666.856	-7.585167	uc002jsk.1	chr17:74671809-74673669	346.21	-7.585167	uc002jsl.3	chr17:74675651-74676961	
MYB	189990	NA	NA	NA	NA	NA	NA	NA	NA	NA	651.201	-7.516773	uc003qfc.3	chr6:135539119-135540311	
MYBBP1A	604885	497.383	0.368133	uc002jya.4	chr17:4442191-4442709	NA	651.053	-3.161552	uc002jya.4	chr17:4442191-4442709	NA	NA	NA	NA	NA
MYCT1	NA	1304.83	-10.636237	uc003qpc.4	chr6:153043389-153045715	NA	NA	NA	NA	NA	1279.71	-9.509562	uc003qpc.4	chr6:153043389-153045715	
MYD88	602170	NA	NA	NA	NA	NA	NA	NA	NA	NA	244.154	-6.497243	uc011ajyl.2	chr3:38182644-38184512	
MYEF2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	451.598	-11.296831	uc001zmg.4	chr15:48431629-48435104	
MYF5	159990	357.21	-4.402231	uc001szg.2	chr12:81112831-81113447	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MYH3	160720	375.941	-6.907549	uc002gmq.2	chr17:10531843-10531969	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MYL1	160780	NA	NA	NA	NA	NA	NA	NA	NA	NA	239.239	-5.671791	uc002web.3	chr2:211154868-211155191	
MYL12A	NA	NA	NA	NA	NA	NA	732.759	-5.462073	uc002klr.3	chr18:3255917-3256234	NA	NA	NA	NA	NA
MYLIP	610082	493.276	-6.278528	uc003nbq.3	chr6:16146983-16148478	NA	801.184	-10.347252	uc003nbq.3	chr6:16146983-16148478	NA	NA	NA	NA	NA
MYLK3	612147	NA	NA	NA	NA	NA	847.911	-7.544139	uc002zeel.4	chr16:46736194-46741615	NA	NA	NA	NA	NA
MYLK4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	674.502	-5.441523	uc003mtx.4	chr6:2663863-2668133	
MYO1B	606537	NA	NA	NA	NA	NA	1290.44	-11.485266	uc002usq.2	chr2:192288687-192290115	1505.88	-12.488781	uc002usq.2	chr2:192288687-192290115	
MYO3B	610040	NA	NA	NA	NA	NA	422.462	-9.185753	uc002uga.3	chr2:171238638-171239276	NA	NA	NA	NA	NA
MYO9A	604875	NA	NA	NA	NA	NA	NA	NA	NA	NA	431.804	-9.607694	uc002atn.1	chr15:72181813-72185263	
MYOM2	603509	NA	NA	NA	NA	NA	451.193	-6.457045	uc003wpx.4	chr8:2092906-2093380	NA	NA	NA	NA	NA
MYOT	604103	NA	NA	NA	NA	NA	750.043	-9.755893	uc011cye.2	chr5:137223075-137223540	NA	NA	NA	NA	NA
MYOZ2	605602	NA	NA	NA	NA	NA	NA	NA	NA	NA	477.157	-7.359383	uc003icp.4	chr4:120107356-120108944	
MYZAP	614071	207.5	-4.692024	uc002ael.3	chr15:57976697-57977562	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
N6AMT2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1319.45	-11.709552	uc001uno.1	chr13:213303073-213303218	
NBEAP1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	428.368	-6.53265	uc010tze.1	chr15:20874797-20874834	
NBN	602687	NA	NA	NA	NA	NA	697.897	-7.547016	uc011lgb.1	chr8:90945564-90947823	695.686	-7.547016	uc003yel.1	chr8:90945564-90947809	
NCAM2	602040	915.155	-7.1916	uc002yld.2	chr21:22910279-22912517	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NCAPG2	608532	688.189	-9.129682	uc011kwc.1	chr7:158424003-158424357	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NCBP1	600469	742.559	-5.689753	uc004bxq.3	chr9:100433482-100436029	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NCF1	608512	NA	NA	NA	NA	NA	897.082	-4.745404	uc011kfh.1	chr7:74197565-74197975	740.643	-5.962718	uc011kfh.1	chr7:74197565-74197975	
NCF2	608515	NA	NA	NA	NA	NA	NA	NA	NA	NA	423.455	-4.978247	uc001lgl.4	chr1:183524697-183525252	
NCOA7	609752	274.779	-4.133205	uc003aag.3	chr6:126206494-126207312	NA	236.364	-5.953553	uc003qae.4	chr6:126249918-126253176	NA	NA	NA	NA	NA
NDE1	609449	NA	NA	NA	NA	NA	727.362	-7.905564	uc010uzy.2	chr16:15818109-15820208	NA	NA	NA	NA	NA

Table 1

[illegible]

Table 1

NID1	131390	NA	NA	NA	NA	207_408	-4.418834	uc009xgc.3	chr1:236139132-236141166	NA	NA	-5.137794	NA	chr14:5247947-52480887
NID2	605399	NA	NA	NA	NA	NA	NA	NA	NA	482_419	-5.137794	uc001wzp.3	NA	chr2:201768265-201768655
NIF3L	605778	1515.62	-8.28285	uc002uwl.2	chr2:201768402-201768655	NA	NA	NA	NA	232_813	-6.652392	uc002uwl.2	NA	NA
NIFK	611970	1043.04	-6.502793	uc002ink.3	chr2:122484521-122485299	829_152	-10.6482	uc002ink.3	chr2:122484521-122485299	NA	NA	NA	NA	NA
NIN	606864	256.08	-7.783399	uc001wyl.3	chr14:51186481-51190180	NA	NA	NA	NA	386_566	-7.45279	uc001wyl.3	NA	chr14:51186481-51190180
NINL	609580	NA	NA	NA	NA	549_439	-7.456744	uc002wuwl.1	chr20:25433338-25434086	342_355	-3.797401	uc002wuwl.1	NA	chr20:25433338-25434086
NIPAL2	NA	362.131	-7.769169	uc011lgw.1	chr8:99204387-99205205	NA	NA	NA	NA	NA	NA	NA	NA	NA
NIT1	604618	NA	NA	NA	NA	832_893	-5.039194	uc001fxw.3	chr1:161093946-161095235	NA	NA	NA	NA	NA
NKAIN2	609758	NA	NA	NA	NA	616_187	-5.165386	uc003pzn.1	chr6:124979626-124980104	NA	NA	NA	NA	NA
NKAIN4	612873	377.758	-4.055558	uc002yek.3	chr20:61872136-61872848	NA	NA	NA	NA	NA	NA	NA	NA	NA
NKAP	300766	NA	NA	NA	NA	1214_92	-6.978541	uc004esg.3	chrX:119059013-119059182	NA	NA	NA	NA	NA
NKRF	300440	289.183	-8.111559	uc004erq.3	chrX:118722300-118723314	NA	NA	NA	NA	NA	NA	NA	NA	NA
NKTR	161565	NA	NA	NA	NA	NA	NA	NA	NA	455_571	-10.632795	uc003clo.3	NA	chr3:42687468-42690233
NLN	611530	1354	-12.06769	uc003juc.3	chr5:65088780-65089459	NA	NA	NA	NA	NA	NA	NA	NA	NA
NLRP2	609364	483.161	-6.998254	uc021vbq.1	chr19:55512267-55512510	NA	NA	NA	NA	NA	NA	NA	NA	NA
NLRP8	609659	NA	NA	NA	NA	NA	NA	NA	NA	784_943	-7.9182	uc002qmh.3	NA	chr19:56499280-56499995
NMB	162340	NA	NA	NA	NA	NA	NA	NA	NA	575_047	-8.311893	uc002bkz.3	NA	chr15:85198360-85198604
NME5	603575	NA	NA	NA	NA	NA	NA	NA	NA	540_112	-7.264984	uc003lec.3	NA	chr5:137450861-137451369
NME7	613465	202.328	-6.379406	uc001lgw.1	chr1:169252460-169256454	NA	NA	NA	NA	NA	NA	NA	NA	NA
NME9	NA	NA	NA	NA	NA	NA	NA	NA	NA	334_142	-5.422168	uc003esg.3	NA	chr3:138020054-138020481
NMI	603525	1611.8	-15.733976	uc002bj.2	chr2:152133769-152135288	1497_24	-9.074067	uc002bj.2	chr2:152133769-152135288	458_955	-7.073818	uc010bxb.1	NA	chr2:152132068-152132259
NMRK2	608705	NA	NA	NA	NA	NA	NA	NA	NA	476_149	-4.926586	uc002lyz.4	NA	chr19:3942272-3942414
NMT1	160993	548.174	-7.265023	uc002hiz.3	chr17:43183008-43186382	NA	NA	NA	NA	NA	NA	NA	NA	NA
NMIU2	605108	282.172	-5.560655	uc003liw.2	chr5:151771102-151771751	NA	NA	NA	NA	NA	NA	NA	NA	NA
NOA1	614919	935.299	-9.757211	uc003hck.3	chr4:57829516-57829615	NA	NA	NA	NA	NA	NA	NA	NA	NA
NOC3L	610769	NA	NA	NA	NA	1076_97	-8.583747	uc001kq.1	chr10:96092989-96093933	NA	NA	NA	NA	NA
NOD1	605980	377.586	-4.231693	uc003lav.3	chr7:30464143-30465253	NA	NA	NA	NA	NA	NA	NA	NA	NA
NOD2	605956	NA	NA	NA	NA	297_952	-5.237521	uc002egm.1	chr16:50765731-50766987	NA	NA	NA	NA	NA
NOL4	603577	685.762	-5.289737	uc010xbs.2	chr18:31431064-31432805	NA	NA	NA	NA	NA	NA	NA	NA	NA
NOL8	611534	NA	NA	NA	NA	515_589	-8.229101	uc002bjw.1	chr9:95059640-95060117	NA	NA	NA	NA	NA
NOPI4	611526	NA	NA	NA	NA	441_727	-5.163575	uc003ggj.1	chr4:2939664-2939915	NA	NA	NA	NA	NA
NOS3	163729	589.319	-9.373703	uc011kuz.2	chr7:150700377-150701023	1725.64	-3.686087	uc003wlf.3	chr7:150711258-150711687	NA	NA	NA	NA	NA
NOSTRIN	607496	248.746	-7.808149	uc002uef.3	chr2:169721481-169721849	NA	NA	NA	NA	648_667	-7.940967	uc002uef.3	NA	chr2:169721481-169721849
NOTCH1	190198	675.846	-10.142011	uc004cia.1	chr9:139396889-139397370	NA	NA	NA	NA	576_953	-6.26778	uc004chz.3	NA	chr9:139388896-139390522
NOTCH2	600275	507.881	-4.552759	uc021osy.1	chr1:120492743-120493116	603_321	-6.582401	uc001tek.3	chr1:120454176-120457928	NA	NA	NA	NA	NA
NOTCH3	600276	NA	NA	NA	NA	NA	NA	NA	NA	565_96	-5.137274	uc002nan.3	NA	chr19:15270444-15271472
NOX1	300225	1158.35	-15.496887	uc004egj.3	chrX:100098313-100098940	NA	NA	NA	NA	426_554	-4.848856	uc004egj.3	NA	chrX:100098313-100098940
NOX5	606572	634.735	-8.098001	uc002arp.2	chr15:69349037-69349501	NA	NA	NA	NA	NA	NA	NA	NA	NA
NOXRED1	NA	980.401	-12.824805	uc001xtr.3	chr14:77860365-77860973	1032_1	-14.198376	uc001xtr.3	chr14:77860365-77860973	833_484	-15.632915	uc001xtr.3	NA	chr14:77860365-77860973
NPAS3	609430	254.242	-5.631028	uc001wrs.3	chr14:34270316-34273382	NA	NA	NA	NA	694_718	-6.724189	uc001wrs.3	NA	chr14:34270316-34273382
NPC1L1	608010	719.82	-6.551273	uc003lib.3	chr7:44552135-44553045	NA	NA	NA	NA	450_175	-4.530498	uc010wkt.2	NA	chr17:4569287-45700642
NPEPPS	606793	NA	NA	NA	NA	NA	NA	NA	NA	1209_16	-13.810218	uc003hgg.2	NA	chr4:73013530-73013918
NPFPR2	607449	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NPHS1	602716	407.701	-5.305648	uc002oby.3	chr19:36316274-36317415	NA	NA	NA	NA	NA	NA	NA	NA	NA
NPL	611412	NA	NA	NA	NA	NA	NA	NA	NA	397_946	-11.015261	uc010pnx.2	NA	chr1:182791259-182791334
NPM1	164040	470.122	-9.842239	uc003mbh.3	chr5:170833410-170833731	NA	NA	NA	NA	NA	NA	NA	NA	NA
NPPB	600295	NA	NA	NA	NA	852_976	-10.355564	uc001taj.3	chr1:11917521-11917711	NA	NA	NA	NA	NA
NPR3	108962	NA	NA	NA	NA	NA	NA	NA	NA	569_323	-6.054896	uc003jhw.2	NA	chr5:32786452-32791830
NQO1	125860	NA	NA	NA	NA	NA	NA	NA	NA	1051_2	-6.904812	uc002exp.3	NA	chr16:69743304-69744878

Table 1

NR0B2	604630	NA	NA	NA	NA	218.439	-4.98961	uc001bnf.3	chr1:27237975-27238335	NA	NA	NA	NA
NR1D2	602304	1546.02	-15.663207	uc003ccs.2	chr3:24018911-24022109	NA	NA	NA	NA	NA	NA	NA	NA
NR1H3	602423	249.665	-4.766255	uc009yil.2	chr11:47290248-47290584	700.573	-5.846009	uc009yil.2	chr11:47290248-47290584	NA	NA	NA	NA
NR1H4	603826	NA	NA	NA	NA	NA	NA	NA	NA	506.224	-6.571092	uc001thp.2	chr12:100957268-100957645
NR1I3	603881	349.011	-6.101502	uc021pbw.1	chr1:161199456-161199586	317.564	-3.9096	uc021pbw.1	chr1:161199456-161199586	NA	NA	NA	NA
NR2C2	601426	NA	NA	NA	NA	753.365	-11.669092	uc003bzi.3	chr3:15084516-15090780	NA	NA	NA	NA
NR2C2AP	608719	NA	NA	NA	NA	NA	NA	NA	NA	541.618	-5.742031	uc002nk.3	chr19:19312224-19312733
NR2F2	107773	700.642	-6.888181	uc002bip.3	chr15:96880852-96883492	NA	NA	NA	NA	NA	NA	NA	NA
NR5A2	604453	448.188	-5.046123	uc009wzh.3	chr1:200143339-200146550	NA	NA	NA	NA	NA	NA	NA	NA
NRCAM	601581	1257.77	-7.516446	uc003vra.3	chr7:107786071-107790354	NA	NA	NA	NA	519.992	-1.736759	uc003xip.3	chr8:32600287-32600770
NRG1	142445	677.651	-5.568273	uc022als.1	chr8:32621921-32622558	713.441	-3.864056	uc003xip.3	chr8:32600287-32600770	340.944	-6.15753	uc003lev.2	chr5:139226364-139227501
NRG2	603818	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NRG3	605533	NA	NA	NA	NA	402.629	-6.396274	uc001kca.2	chr10:84745362-84746935	532.386	-7.65789	uc002bbo.3	chr15:76234328-76235978
NRG4	610894	569.593	-10.791214	uc002bbo.3	chr15:76234328-76235978	NA	NA	NA	NA	NA	NA	NA	NA
NRIP1	602490	588.216	-5.947653	uc002yjk.2	chr21:163333556-16337036	NA	NA	NA	NA	NA	NA	NA	NA
NRK	300791	746.296	-11.270158	uc004emd.3	chrX:105199593-105202602	NA	NA	NA	NA	NA	NA	NA	NA
NRP1	602069	664.177	-10.425385	uc001lw.4	chr10:33466419-33469003	NA	NA	NA	NA	NA	NA	NA	NA
NRP2	602070	NA	NA	NA	NA	597.609	-5.151089	uc002mdc.3	chr19:5828185-5828335	755.525	-6.776111	uc002vat.3	chr2:206608304-206608422
NRTN	602018	NA	NA	NA	NA	2106.16	-18.648121	uc003mfq.3	chr5:176863092-176863332	NA	NA	NA	NA
NSD1	606681	434.03	-4.613158	uc003nft.4	chr5:176722461-176727214	NA	NA	NA	NA	NA	NA	NA	NA
NSG1	NA	740.887	-8.660488	uc011bvz.2	chr4:4419163-4420785	NA	NA	NA	NA	595.525	-4.944611	uc001hjm.3	chr1:212899495-212912028
NSL1	609174	NA	NA	NA	NA	663.154	-6.690391	uc001hjm.3	chr1:212899495-212912028	1207.61	-9.461411	uc001ffs.3	chr10:123716603-123716774
NSMCE4A	612987	NA	NA	NA	NA	447.329	-4.923393	uc001ffs.3	chr10:123716603-123716774	470.129	-5.92551	uc003jdt.3	chr5:6599352-6600038
NSUN2	610916	498.745	-4.774689	uc003jdt.3	chr5:6599352-6600038	NA	NA	NA	NA	NA	NA	NA	NA
NSUN3	NA	1086.59	-11.411576	uc003drl.1	chr3:93845335-93845630	NA	NA	NA	NA	604.447	-7.258824	uc003twm.3	chr7:72418832-72418922
NSUN5P2	NA	500.181	2.749109	uc003lwp.3	chr7:72418837-72419202	NA	NA	NA	NA	NA	NA	NA	NA
NSUN6	NA	723.448	-7.328372	uc010acp.1	chr10:18834264-18834861	NA	NA	NA	NA	552.83	-8.56521	uc003gwh.2	chr4:40776977-40777473
NSUN7	NA	237.155	-4.815741	uc003gvi.4	chr4:40810352-40812002	540.774	-6.814837	uc003gwh.2	chr4:40776977-40777473	643.165	-12.859234	uc010yju.2	chr2:18744137-18745061
NT5C1B	610526	NA	NA	NA	NA	NA	NA	NA	NA	760.324	-8.584455	uc001qmk.4	chr12:5604155-5604465
NTF3	162660	NA	NA	NA	NA	NA	NA	NA	NA	446.503	-5.525523	uc011mbs.1	chr9:132397595-132397879
NTMT1	613560	NA	NA	NA	NA	NA	NA	NA	NA	493.927	-6.036994	uc004anv.1	chr9:87425495-87430621
NTKX2	600456	NA	NA	NA	NA	NA	NA	NA	NA	361.676	-4.84583	uc002bmh.2	chr15:88419988-88420165
NTKX3	191316	460.142	-6.057215	uc002bmh.2	chr15:88419988-88420165	NA	NA	NA	NA	718.362	-5.354271	uc001tlj.1	chr12:106457125-106460579
NUAK1	608130	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUB1	607981	1507.83	-12.556695	uc003wjk.3	chr7:151074312-151075548	NA	NA	NA	NA	NA	NA	NA	NA
NUBPL	613621	NA	NA	NA	NA	1329.43	-9.756495	uc001wrk.4	chr14:32328387-32330429	NA	NA	NA	NA
NUCKS1	611912	NA	NA	NA	NA	407.823	-5.118065	uc001hdb.3	chr1:205681947-205687407	NA	NA	NA	NA
NUDCD1	606109	NA	NA	NA	NA	1538.01	-9.378541	uc003yna.3	chr8:110253148-110255237	NA	NA	NA	NA
NUDCD2	NA	NA	NA	NA	NA	939.876	-9.804752	uc003lze.3	chr5:162880586-162880972	NA	NA	NA	NA
NUDCD3	610296	NA	NA	NA	NA	NA	NA	NA	NA	494.612	-5.244314	uc003tkz.3	chr7:44421965-44425609
NUDT10	300527	NA	NA	NA	NA	NA	NA	NA	NA	439.22	-7.899343	uc004dph.3	chrX:51079092-51080377
NUDT13	609233	405.84	-4.408656	uc001lji.3	chr10:74890662-74891581	NA	NA	NA	NA	NA	NA	NA	NA
NUDT2	602852	480.314	-7.933249	uc003zub.3	chr9:34343439-34343711	NA	NA	NA	NA	NA	NA	NA	NA
NUDT21	604978	NA	NA	NA	NA	936.603	-7.900353	uc002eja.3	chr16:56463048-56466623	NA	NA	NA	NA
NUDT5	609230	NA	NA	NA	NA	605.879	-5.381491	uc001lji.3	NA	605.879	-5.381491	uc001lji.3	chr10:12209573-12209700
NUDT7	609231	314.772	-8.010681	uc010chd.3	chr16:777759512-77760697	676.584	-6.684518	uc002ffh.3	chr16:77759512-77760697	987.511	-14.649194	uc002ffh.3	chr16:77759512-77760697
NUFIP2	609356	NA	NA	NA	NA	502.702	-5.447309	uc002hdx.4	chr17:27582854-27591556	NA	NA	NA	NA
NUMA1	164009	2134.83	-12.017527	uc001orj.2	chr11:71719311-717174572	NA	NA	NA	NA	783.849	-6.070138	uc009ysy.2	chr11:7128045-7128597
NUMB	603728	758.416	-3.617743	uc010lhz.1	chr14:73741918-73743285	548.776	-6.521037	uc010lhz.1	chr14:73741918-73743285	NA	NA	NA	NA

Table 1

NUP107	607617	NA	NA	NA	NA	1424.28	-21.610159	uc001suf.3	chr12:69136243-69136473	NA	NA	NA	NA	NA	NA
NUP133	607613	1553.94	-8.409635	uc001hin.3	chr1:229577044-229577650	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUP160	607614	NA	NA	NA	NA	952.652	-5.214878	uc001ngm.3	chr11:47799670-47800656	1665.24	-11.304681	uc021aiu.1	chr11:47799670-47800562	NA	NA
NUP188	615587	NA	NA	NA	NA	NA	NA	NA	NA	477.089	-5.816282	uc004bwu.3	chr9:131765896-131766259	NA	NA
NUP205	614352	592.149	-6.040094	uc003vsw.3	chr7:135333305-135333499	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUP210P1	NA	1150.42	-6.745065	uc003oje.1	chr3:126390562-126390782	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUP214	114350	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUP35	608140	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUP37	609264	328.138	-6.492262	uc001ijc.3	chr12:102467973-102468131	NA	NA	NA	NA	734.139	-2.359867	uc001ijc.3	chr12:102467973-102468131	NA	NA
NUP62CL	NA	NA	NA	NA	NA	NA	NA	NA	NA	473.835	-5.733315	uc004ena.3	chrX:10636657-106367562	NA	NA
NUP65	170285	714.366	-6.376368	uc002jng.1	chr17:73231775-73231854	NA	NA	NA	NA	1035.28	-9.02277	uc002jng.1	chr17:73231775-73231854	NA	NA
NUP98	602552	1384.4	-14.14963	uc010vsv.2	chr17:5291837-5292090	950.895	-7.649286	uc010vsv.2	chr17:5291837-5292090	619.936	-9.973897	uc010vsv.2	chr17:5291837-5292090	NA	NA
NUP93	614351	2539.09	-19.565774	uc002eka.3	chr16:56878522-56878861	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NUPL1	NA	NA	NA	NA	NA	513.757	-6.855184	uc001uug.1	chr13:25905720-25910478	NA	NA	NA	NA	NA	NA
NUSAP1	612818	NA	NA	NA	NA	754.561	-7.345449	uc001znr.4	chr15:41672385-41673248	NA	NA	NA	NA	NA	NA
NVL	602426	NA	NA	NA	NA	464.075	-6.74485	uc001hok.3	chr1:224415036-224415327	NA	NA	NA	NA	NA	NA
NXF5	300319	NA	NA	NA	NA	NA	NA	NA	NA	959.488	-6.316019	uc011mrk.1	chrX:101087085-101087239	NA	NA
NXTF2	300320	NA	NA	NA	NA	NA	NA	NA	NA	408.487	-6.909668	uc004eoc.2	chrX:108785918-108787927	NA	NA
OARD1	614393	704.066	-3.023456	uc003opm.3	chr6:41034531-41035073	341.113	-5.962321	uc003opm.3	chr6:41034531-41035073	NA	NA	NA	NA	NA	NA
OAS1	164350	696.483	-7.377879	uc010syn.2	chr12:113354581-113354760	NA	NA	NA	NA	328.76	-6.255066	uc010syo.2	chr12:113354319-113354760	NA	NA
OAS3	603351	NA	NA	NA	NA	1277.61	-9.938905	uc001tue.3	chr12:113379732-113380100	NA	NA	NA	NA	NA	NA
OAT	613349	NA	NA	NA	NA	383.345	-4.988412	uc001lhp.3	chr10:126085872-126086510	NA	NA	NA	NA	NA	NA
OBFC1	613128	NA	NA	NA	NA	349.108	-6.181194	uc001kxl.3	chr10:105637318-105642441	NA	NA	NA	NA	NA	NA
OC90	601658	NA	NA	NA	NA	NA	NA	NA	NA	676.109	-7.533595	uc003yrg.2	chr8:133036467-133036727	NA	NA
OCEL1	NA	NA	NA	NA	NA	NA	NA	NA	NA	1164.14	-5.231913	uc002tfp.3	chr19:17339735-17340028	NA	NA
ODAM	614843	NA	NA	NA	NA	NA	NA	NA	NA	1007.34	-7.78942	uc003hfc.3	chr4:71069892-71070293	NA	NA
OGFR	606459	NA	NA	NA	NA	NA	NA	NA	NA	884.562	-7.795273	uc002vdj.3	chr20:61445002-61445352	NA	NA
OGN	602383	324.345	-5.641394	uc004asa.3	chr9:95146249-95147901	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OGT	300255	NA	NA	NA	NA	NA	NA	NA	NA	694.231	-5.756156	uc004eaa.2	chrX:70793645-70795747	NA	NA
OLFM4	614061	NA	NA	NA	NA	NA	NA	NA	NA	858.78	-8.959844	uc001vhl.3	chr13:53624907-53626196	NA	NA
OLFML1	NA	642.989	-4.473998	uc001mfl.3	chr11:7531420-7532606	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OLFML2B	NA	1425.58	-15.758764	uc001lgt.3	chr1:161952982-161953464	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OLFML3	610088	NA	NA	NA	NA	1807.66	-8.612216	uc001tear.1	chr11:114524392-114524875	NA	NA	NA	NA	NA	NA
OEFP	611689	292.533	-8.403957	uc003pgu.4	chr6:74078280-74078506	NA	NA	NA	NA	269.532	-3.513168	uc003pgu.4	chr6:74078280-74078506	NA	NA
OOSP2	NA	NA	NA	NA	NA	207.785	-4.690336	uc001nol.3	chr11:59814547-59815516	NA	NA	NA	NA	NA	NA
OPN4	606665	NA	NA	NA	NA	1004.95	-11.790599	uc009sxx.1	chr10:88423749-88423870	NA	NA	NA	NA	NA	NA
OPRK1	165196	NA	NA	NA	NA	NA	NA	NA	NA	575.588	-5.242228	uc022aup.1	chr8:54138276-54141856	NA	NA
OPRM1	600018	NA	NA	NA	NA	793.474	-5.345192	uc011efd.2	chr6:154439857-154440594	NA	NA	NA	NA	NA	NA
OR11A1	NA	NA	NA	NA	NA	NA	NA	NA	NA	248.177	-4.603861	uc003nmg.3	chr6:293933281-29394470	NA	NA
OR12D3	NA	NA	NA	NA	NA	1114.57	-10.821066	uc003nme.3	chr6:29341200-29342113	NA	NA	NA	NA	NA	NA
OR13A1	NA	NA	NA	NA	NA	1183.54	-4.462235	uc001jcc.1	chr10:45798102-45798883	NA	NA	NA	NA	NA	NA
OR2A9P	NA	NA	NA	NA	NA	NA	NA	NA	NA	879.573	-5.947149	uc003wei.2	chr7:143997399-143997598	NA	NA
OR2B3	NA	599.185	-6.516424	uc003njk.3	chr6:29053985-29054083	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OR2H1	NA	951.163	-9.567343	uc003nmf.3	chr6:29430498-29432099	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OR2J3	615016	578.636	-5.125223	uc011hhl.2	chr6_mcf_hap5:444969-445896	NA	NA	NA	NA	464.941	-4.967909	uc011hhl.2	chr6_mcf_hap5:444969-445896	NA	NA
OR4C12	NA	475.977	-4.213754	uc010ria.2	chr11:50003009-50003107	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OR51B5	NA	541.571	-6.948222	uc001maq.2	chr11:5363744-5363815	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
OR51D1	NA	NA	NA	NA	NA	NA	NA	NA	NA	562.699	-5.212676	uc010qyk.2	chr11:4661996-4662068	NA	NA
OR51E2	611288	NA	NA	NA	NA	NA	NA	NA	NA	1894.87	-16.090418	uc001lzk.2	chr11:4701401-4702978	NA	NA

Table 1

OR52K1	NA	NA	NA	NA	NA	501.996	-7.847095	uc001lza.2	chr11:4511076-4511138	NA	NA	NA	NA
OR7E12P	NA	NA	NA	NA	NA	1035.97	-7.679921	uc021lqcl.1	chr11:3411937-3412607	NA	NA	NA	NA
OR9Q1	NA	NA	NA	NA	NA	790.619	-9.979769	uc001nmj.3	chr11:57947850-57949038	NA	NA	NA	NA
ORC1	601902	NA	NA	NA	NA	590.481	-5.511061	uc001clt.3	chr1:52838501-52838852	NA	NA	NA	NA
ORC4	603056	NA	NA	NA	NA	NA	NA	NA	NA	395.832	-6.10338	uc002twj.3	chr2:148687966-148693078
ORC6	607213	361.918	-3.792813	uc010cbe.2	chr16:46729622-46730131	581.62	-5.39511	uc002eeg.1	chr16:46727099-46728576	NA	NA	NA	NA
ORMDL1	610073	771.925	-9.284996	uc002urb.4	chr2:190634993-190636492	NA	NA	NA	NA	NA	NA	NA	NA
ORMDL2	610074	NA	NA	NA	NA	NA	NA	NA	NA	717.502	-7.781309	uc001shw.1	chr12:56214180-56214959
OSBP2	606729	NA	NA	NA	NA	NA	NA	NA	NA	323.145	-5.2379	uc011ala.1	chr22:31302327-31303811
OSBPL10	606738	NA	NA	NA	NA	NA	NA	NA	NA	578.758	-6.291906	uc003ceui.1	chr3:31699403-31705510
OSBPL1A	606730	NA	NA	NA	NA	505.611	-6.06863	uc002lvd.3	chr18:21742011-21743142	377.46	-8.772797	uc002kvr.3	chr18:21771629-21776079
OSBPL2	606731	515.633	-6.797588	uc002cyk.1	chr20:60868944-60871269	NA	NA	NA	NA	1075.81	-12.015268	uc002cyk.1	chr20:60868944-60871269
OSBPL3	606732	242.951	-4.186842	uc003sxj.1	chr7:24873706-24873921	804.477	-5.736782	uc003sxf.3	chr7:24836164-24839801	NA	NA	NA	NA
OSGEPL1	NA	NA	NA	NA	NA	833.451	-9.161101	uc002uqz.1	chr2:190611386-190611894	769.968	-6.91387	uc002uqz.1	chr2:190611386-190611894
OSMR	601743	610.547	-5.021246	uc003jln.2	chr5:38933547-38935743	NA	NA	NA	NA	NA	NA	NA	NA
OTOF	603681	414.999	-4.230366	uc010yla.2	chr2:26680071-26680907	NA	NA	NA	NA	NA	NA	NA	NA
OTOG1	614925	NA	NA	NA	NA	NA	NA	NA	NA	1242.23	-8.982257	uc001zsd.3	chr12:80771829-80772870
OTOR	606067	NA	NA	NA	NA	246.678	-4.316653	uc002wpi.3	chr20:16731764-16732809	NA	NA	NA	NA
OTUD1	612022	1004.98	-9.711742	uc001lir.2	chr10:23729833-23731310	NA	NA	NA	NA	NA	NA	NA	NA
OTUD6B	612021	NA	NA	NA	NA	NA	NA	NA	NA	1661.75	-10.072529	uc003yeu.4	chr8:92097097-92099323
OTUD7A	612024	NA	NA	NA	NA	NA	NA	NA	NA	469.594	-5.562474	uc010baa.1	chr15:31850386-31851109
OTX1	600036	NA	NA	NA	NA	540.091	-5.756144	uc021vim.1	chr2:63283452-63284966	NA	NA	NA	NA
OVOL2	616441	644.599	-5.276431	uc002wql.1	chr20:18004796-18005279	211.626	-5.009895	uc002wql.1	chr20:18004796-18005279	291.288	-7.651077	uc002wql.1	chr20:18004796-18005279
OXAL1	601066	NA	NA	NA	NA	NA	NA	NA	NA	563.891	-6.739103	uc001wgn.2	chr14:23240768-23244098
OXCT1	601424	NA	NA	NA	NA	2221.41	-20.556358	uc011cpo.2	chr5:41730167-41731830	NA	NA	NA	NA
OXGR1	606922	NA	NA	NA	NA	NA	NA	NA	NA	904.151	-7.734293	uc001vmx.1	chr13:97637973-97638999
OXSR1	604046	NA	NA	NA	NA	955.056	-8.707562	uc010hha.1	chr3:38271952-38272184	596.474	-6.079549	uc010hha.1	chr3:38271952-38272184
P2RY1	601167	NA	NA	NA	NA	406.501	-6.97294	uc003ezq.3	chr3:152554694-152555843	NA	NA	NA	NA
P2RY10	300529	NA	NA	NA	NA	NA	NA	NA	NA	744.835	-6.075441	uc004ede.3	chrX:78217038-78217438
P2RY12	600515	459.342	-6.688892	uc011boa.2	chr3:151055236-151056023	NA	NA	NA	NA	NA	NA	NA	NA
P4HA1	176710	517.008	-9.569027	uc021plj.1	chr10:74766980-74767979	933.887	-8.58822	uc021plj.1	chr10:74766980-74767979	932.055	-7.483303	uc021plj.1	chr10:74766980-74767979
P4HA2	600608	NA	NA	NA	NA	801.578	-5.149202	uc003kwg.3	chr5:131528304-131528702	NA	NA	NA	NA
PABPC1L	NA	219.178	-4.841167	uc010ggv.1	chr20:435567767-43567962	NA	NA	NA	NA	813.556	-2.230357	uc010ggv.1	chr20:435567767-43567962
PABPC4L	NA	NA	NA	NA	NA	NA	NA	NA	NA	271.865	-6.127914	uc010loe.3	chr4:135117489-135121061
PABPC5	300407	NA	NA	NA	NA	835.341	-5.648522	uc004elig.3	chrX:90691726-90693583	NA	NA	NA	NA
PACRG	608427	333.476	-3.420584	uc003qua.3	chr6:163736020-163736524	263.223	-7.140932	uc003qua.3	chr6:163736020-163736524	NA	NA	NA	NA
PACRGL	NA	207.18	-4.351278	uc003gpz.3	chr4:20728965-20729980	627.538	-4.454362	uc003gpz.3	chr4:20728965-20729980	1012.47	-7.949803	uc003gpz.3	chr4:20728965-20729980
PAC32	610423	401.913	-7.538082	uc001yqs.2	chr14:105861010-105864484	620.586	-3.372642	uc001yqs.2	chr14:105861010-105864484	NA	NA	NA	NA
PADJ4	605347	NA	NA	NA	NA	NA	NA	NA	NA	439.615	-6.715664	uc001baj.2	chr1:17690251-17690495
PAFAH2	602344	594.317	-6.327632	uc001bid.4	chr1:26286258-26288479	NA	NA	NA	NA	NA	NA	NA	NA
PAGE5	NA	NA	NA	NA	NA	401.184	-5.668802	uc004duj.3	chrX:55250437-55250541	NA	NA	NA	NA
PAH	612349	NA	NA	NA	NA	NA	NA	NA	NA	284.367	-4.617248	uc001tq.1	chr12:103232104-103232952
PAK1IP1	607811	NA	NA	NA	NA	1345.98	-9.758406	uc003mzg.3	chr6:10709686-10709970	NA	NA	NA	NA
PAK2	605022	548.153	-5.264453	uc003fwy.4	chr3:196555277-196559518	NA	NA	NA	NA	269.032	-4.356527	uc003fwy.4	chr3:196555277-196559518
PAK6	608110	NA	NA	NA	NA	NA	NA	NA	NA	692.188	-4.8243	uc010bbl.3	chr15:40568296-40569688
PALM2	NA	529.829	-3.370613	uc004beg.3	chr9:112705706-112713756	489.416	-5.532302	uc004beg.3	chr9:112705706-112713756	554.146	-3.515224	uc004beg.3	chr9:112705706-112713756
PALMD	610182	1067.21	-10.364466	uc001dsg.3	chr1:100159619-100160097	NA	NA	NA	NA	NA	NA	NA	NA
PAMR1	NA	NA	NA	NA	NA	NA	NA	NA	NA	769.562	-8.539456	uc001mwf.3	chr11:35453376-35453903
PAN2	NA	NA	NA	NA	NA	926.009	-6.691851	uc001skw.3	chr12:56710007-56711392	NA	NA	NA	NA

Table 1

PAN3	NA	NA	NA	NA	692,323	-6,248,338	uc010ido.1	chr13:28846224-28846450	NA	NA	NA	NA	NA
PANK3	606161	633,955	-7,589,978	uc003tzz.2	NA	NA	NA	NA	694,513	-7,256,153	uc003tzz.2	NA	chr5:167982628-167984575
PANK4	606162	867,77	-8,935,503	uc001ajm.1	NA	NA	NA	NA	929,05	-7,462,958	uc001ajm.1	NA	chr1:2439975-2440285
PAPD4	614121	NA	NA	NA	NA	NA	NA	NA	468,523	-4,809,185	uc003hfr.2	NA	chr5:78981097-78982471
PAPD5	605540	NA	NA	NA	NA	NA	NA	NA	454,687	-5,213,643	uc002efr.3	NA	chr16:50263240-50269219
PAPSS2	603005	NA	NA	NA	450,749	-5,999,988	uc001kew.3	chr10:89505728-89507462	887,681	-14,360,217	uc001kew.3	NA	chr10:89505728-89507462
PAQR9	614580	NA	NA	NA	NA	NA	NA	NA	1654,34	-16,334,787	uc003evg.3	NA	chr3:142680074-142681044
PARD3B	NA	NA	NA	NA	NA	NA	NA	NA	451,828	-9,597,776	uc002vap.2	NA	chr2:206480538-206484886
PARD6A	607484	NA	NA	NA	815,795	-5,605,366	uc002eis.3	chr16:67696551-67696681	NA	NA	NA	NA	NA
PARK2	602544	261,093	-5,776,608	uc011egl.2	NA	NA	NA	NA	NA	NA	NA	NA	NA
PARL	607858	533,606	-10,429,358	uc003ind.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
PARP11	NA	643,692	-5,576,862	uc001gmh.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
PARP12	612481	NA	NA	NA	NA	NA	NA	NA	475,336	-4,181,136	uc003vvl.1	NA	chr7:139723549-139724359
PARP14	610028	1242,51	-10,457,936	uc003efr.4	NA	NA	NA	NA	NA	NA	NA	NA	NA
PARP3	607726	NA	NA	NA	NA	NA	NA	NA	403,847	-8,374,723	uc003dby.3	NA	chr3:51982497-51982883
PARP4	607519	NA	NA	NA	NA	NA	NA	NA	661,198	-5,079,902	uc001upl.3	NA	chr13:24995069-24995256
PARP6	NA	NA	NA	NA	NA	NA	NA	NA	568,847	-12,785,208	uc003jon.4	NA	chr5:50137903-50142356
PARP9	612065	NA	NA	NA	397,416	-5,973,242	uc003eff.4	chr3:122246760-122247210	1048,76	-8,300,11	uc003eff.2	NA	chr3:122250620-122254961
PARBP3	613687	642,365	-7,392,803	uc001lfr.3	NA	NA	NA	NA	202,305	-2,644,914	uc001lfr.3	NA	chr12:102542257-102542785
PARS2	612036	NA	NA	NA	NA	NA	NA	NA	894,02	-8,054,96	uc001oxy.3	NA	chr1:55222571-55223406
PASK	607505	NA	NA	NA	458,445	-7,313,594	uc010zpl.2	chr2:242045514-242045980	738,436	-5,445,168	uc010zpl.2	NA	chr2:242045514-242045980
PATE2	NA	494,224	-5,440,58	uc001lqu.3	492,23	-5,788,252	uc001lqu.3	chr11:125646028-125647276	1269,09	-10,344,437	uc001lqu.3	NA	chr11:125646028-125647276
PATE3	NA	NA	NA	NA	544,163	-6,188,894	uc009zbs.3	chr11:125660498-125661495	NA	NA	NA	NA	NA
PAX6	607108	NA	NA	NA	NA	NA	NA	NA	416,42	-6,869,805	uc001lmd.4	NA	chr11:31806340-31811481
PAXBP1	NA	611,603	-5,706,94	uc002yql.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
PAXIP1	608254	1256,66	-7,280,952	uc003wir.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
PBX4	608127	401,121	-5,755,988	uc002nmy.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
PBXIP1	NA	555,539	-5,706,663	uc001lfr.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
PCCA	232000	292,865	-6,532,82	uc001vao.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
PCDH10	608286	499,907	-3,593,354	uc003lgr.3	559,693	-10,263,184	uc003lgr.3	chr4:134073987-134074404	814,106	-11,051,495	uc003lgr.3	NA	chr4:134073987-134074404
PCDH11X	300246	NA	NA	NA	NA	NA	NA	NA	670,334	-7,876,405	uc004efj.1	NA	chrX:91134306-91134997
PCDH15	605514	675,172	-10,476,841	uc021pvy.1	565,855	-7,883,029	uc021pvy.1	chr10:55580860-55581617	773,289	-7,566,218	uc010qhq.2	NA	chr10:55562533-55566338
PCDH17	611760	377,017	-4,196,924	uc001vhn.1	NA	NA	NA	NA	867,604	-7,832,288	uc001vhn.1	NA	chr13:58299429-58303065
PCDH19	300460	NA	NA	NA	1247,65	-9,008,373	uc004efw.4	chrX:99548642-99551274	NA	NA	NA	NA	NA
PCDH9	603581	NA	NA	NA	601,513	-7,674,885	uc001vin.3	chr13:67798639-67799473	767,018	-5,125,811	uc001vin.3	NA	chr13:67798639-67799473
PCDHA1	606307	488,753	-8,222,83	uc003lgr.3	1061,96	-16,161,703	NA	NA	NA	NA	NA	NA	NA
PCDHAC1	606320	NA	NA	NA	NA	NA	NA	NA	344,025	-4,807,503	uc003lig.1	NA	chr5:140308935-140309385
PCDHB10	606336	NA	NA	NA	NA	NA	NA	NA	988,137	-9,469,104	uc003lik.3	NA	chr5:140574529-140575213
PCDHB11	606337	NA	NA	NA	1032,31	-7,242,553	uc003lly.3	chr5:140581742-140582618	1146,78	-12,713,468	uc003lly.3	NA	chr5:140581742-140582618
PCDHB14	606340	NA	NA	NA	1213,71	-11,325,538	uc003ljb.3	chr5:140605475-140605860	NA	NA	NA	NA	NA
PCDHB2	606328	NA	NA	NA	NA	NA	NA	NA	1639,48	-17,169,039	uc003lil.3	NA	chr5:140407672-140407694
PCDHB6	606332	788,112	-9,018,265	uc003lir.3	933,566	-9,613,379	uc003lir.3	chr5:140532224-140532868	NA	NA	NA	NA	NA
PCDHGA11	606298	NA	NA	NA	538,09	-8,247,88	uc003lko.1	chr5:140803309-140803653	NA	NA	NA	NA	NA
PCDHGA7	606294	297,856	-8,124,57	uc003ljl.1	1026,19	-8,486,555	uc003ljl.1	chr5:140764921-140765187	NA	NA	NA	NA	NA
PCDHGB7	606304	NA	NA	NA	418,526	-6,392,19	uc003lkm.3	chr5:140799854-140799996	1014,9	-10,757,509	uc003lkm.3	NA	chr5:140799854-140799996
PCF11	608876	NA	NA	NA	NA	NA	NA	NA	536,78	-8,415,092	uc001lox.4	NA	chr11:82895937-82896835
PCGF2	600346	NA	NA	NA	452,248	-6,464,928	uc002hqp.1	chr17:36890150-36891475	596,76	-4,639,559	uc002hqp.1	NA	chr17:36890150-36891475
PCIF1	NA	872,197	-9,683,287	uc002xql.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
PCK2	614095	NA	NA	NA	690,169	-8,520,481	uc001lws.3	chr14:24569515-24569770	NA	NA	NA	NA	NA

Table 1

PCLO	604918	1034.99	-14.206451	uc003uhx.2	chr7:82383321-82387890	NA	NA	NA	NA	chr6:150123516-150123667	1294.92	-12.455279	uc003uhx.2	chr7:82383321-82387890
PCMT1	176851	584.573	-5.996024	uc003qna.3	chr6:150123516-150123667	637.385	-6.893598	uc003qna.3	NA	chr6:150123516-150123667	NA	NA	NA	NA
PCNX	NA	NA	NA	NA	NA	624.877	-8.115316	uc001xnm.4	NA	chr14:71478209-71479537	NA	NA	NA	NA
PCNXL3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	460.85	-6.699406	uc001oey.2	chr11:65404450-65404910
PCNXL4	NA	NA	NA	NA	NA	445.943	-10.562603	uc001xer.4	NA	chr14:60600940-60601532	1259.82	-9.377136	uc001xer.4	chr14:60600940-60601532
PCOLCE	600270	NA	NA	NA	NA	NA	NA	NA	NA	NA	579.815	-7.028651	uc003uwo.3	chr7:100205727-100205798
PCP4L1	NA	NA	NA	NA	NA	567.089	-5.768709	uc001gad.3	NA	chr1:161254272-161255240	NA	NA	NA	NA
PCSK1	162150	1048.32	-10.274687	uc010jbl.2	chr5:95726040-95728704	NA	NA	NA	NA	NA	NA	NA	NA	NA
PCSK5	600488	NA	NA	NA	NA	NA	NA	NA	NA	NA	542.177	-7.811798	uc004akc.2	chr9:78973839-78977255
PCYTB	300948	582.087	-7.302437	uc004dbi.3	chrX:24576204-24580409	NA	NA	NA	NA	NA	NA	NA	NA	NA
PCYT2	602679	NA	NA	NA	NA	NA	NA	NA	NA	NA	900.207	-7.298237	uc002kce.2	chr17:79860777-79862708
PDC	171490	NA	NA	NA	NA	411.01	-4.987813	uc001grz.3	NA	chr1:186412698-186413110	1081.31	-16.69568	uc001grz.3	chr1:186412698-186413110
PDCD2	600866	1112.35	-0.785064	uc003qvx.3	chr6:170884660-170886646	NA	NA	NA	NA	NA	1312.77	-11.507561	uc003qvx.2	chr6:170887570-170887723
PDCD4	608610	NA	NA	NA	NA	NA	NA	NA	NA	NA	972.356	-9.350582	uc001leg.3	chr10:112657847-112659764
PDCD5	604583	1061.37	-6.421878	uc002nlm.3	chr19:33078207-33078358	NA	NA	NA	NA	NA	225.976	-5.017376	uc002ntl.3	chr19:33076946-33077449
PDE10A	610652	623.543	-6.382891	uc011legk.2	chr6:165740776-165746513	NA	NA	NA	NA	NA	534.829	-6.971976	uc011legk.2	chr6:165740776-165746513
PDE12	616519	877.9	-10.671512	uc003div.3	chr3:57545148-57546664	NA	NA	NA	NA	NA	424.846	-6.737641	uc003dlw.4	chr3:57545732-57547768
PDE1C	602987	208.923	-4.814194	uc003tem.2	chr7:31792632-31792997	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDE3B	602047	600.178	-13.980412	uc001nlm.2	chr11:14793588-14798209	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDE4C	600128	NA	NA	NA	NA	NA	NA	NA	NA	NA	200.471	-4.156455	uc002nlg.4	chr19:18318771-18321738
PDE4D	600129	496.29	-5.276431	uc003jrs.2	chr5:58264866-58270490	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDE5A	603310	NA	NA	NA	NA	1709.54	-17.043792	uc003dlf.3	NA	chr4:120415550-120419755	349.222	-7.834542	uc003df.3	chr4:120415550-120419755
PDE6B	180072	859.179	-4.263594	uc003gao.4	chr4:663897-664681	NA	NA	NA	NA	NA	1131.11	-9.234445	uc002vse.1	chr2:232597147-232597661
PDE6D	602676	632.005	-5.149074	uc002vse.1	chr2:232597147-232597661	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDE7A	171885	NA	NA	NA	NA	281.197	-8.368252	uc003xvp.3	NA	chr8:66626569-66631524	344.704	-5.612617	uc021stv.1	chr15:85681135-85682376
PDE8A	602972	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDGFB	190040	1433.7	-9.856361	uc003axe.3	chr22:39619685-39621318	NA	NA	NA	NA	NA	1170.84	-12.838491	uc003iph.2	chr4:157682763-157684241
PDGFC	608452	NA	NA	NA	NA	NA	NA	NA	NA	NA	691.075	-8.023667	uc003haa.3	chr4:55161440-55164412
PDGFRA	173490	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDH8	179060	1144.94	-6.086681	uc003dke.4	chr3:58413357-58413760	NA	NA	NA	NA	NA	721.089	-9.68529	uc001mvt.3	chr11:35016720-35017675
PDH9	608769	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDIA4	NA	NA	NA	NA	NA	780.513	-5.202882	uc003wff.2	NA	chr7:148700154-148700885	NA	NA	NA	NA
PDIA6	611099	313.681	-4.067054	uc002rau.3	chr2:10923517-10924383	NA	NA	NA	NA	NA	230.552	-3.291903	uc002rau.3	chr2:10923517-10924383
PDIK1L	610785	NA	NA	NA	NA	1051.13	-8.094871	uc010oew.2	NA	chr1:26449069-26452039	NA	NA	NA	NA
PDL1T	NA	544.418	-8.520297	uc002dht.1	chr16:20370492-20370640	NA	NA	NA	NA	NA	832.954	-5.092557	NA	NA
PDK1	602524	NA	NA	NA	NA	569.163	-6.980223	uc002uhs.3	NA	chr2:173460698-173463862	1243.19	-9.740104	uc002uhs.3	chr2:173460698-173463862
PDLIM4	603422	297.33	-5.294382	uc003kwn.3	chr5:131607923-131609147	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDLIM7	605903	584.754	-4.805341	uc003mha.1	chr5:176910395-176910644	231.747	-3.171367	uc003kwp.3	NA	chr5:131607789-131609147	NA	NA	NA	NA
PDPR	NA	707.093	-5.11112	uc002eyf.1	chr16:70190783-70195184	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDSSA	613200	NA	NA	NA	NA	NA	NA	NA	NA	NA	1349.71	-13.602491	uc003guv.4	chr4:39824483-39827104
PDSBB	605333	1130.1	-7.054615	uc001lun.3	chr13:33226202-33226715	NA	NA	NA	NA	NA	816.477	-8.080704	uc001lun.3	chr13:332262828-332265405
PDSB1	607429	868.32	-1.264631	uc001lsv.3	chr10:27035403-27035726	734.638	-4.814194	uc001lsv.3	NA	chr10:27035403-27035726	NA	NA	NA	NA
PDSB2	610564	338.293	-4.355081	uc011eak.1	chr6:107473761-107475822	NA	NA	NA	NA	NA	614.528	-7.88281	uc003prv.3	chr6:107585390-107585623
PDZD2	610697	768.778	-11.025304	uc003jhl.3	chr5:32108242-32111038	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDZD9	NA	450.98	-6.119854	uc002dka.2	chr16:21995186-21995587	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDZK1	603831	NA	NA	NA	NA	372.419	-5.418603	uc001tcqw.3	NA	chr1:47649261-47649642	498.675	-4.754342	uc001con.2	chr1:45763624-145764206
PDZK1IP1	607178	NA	NA	NA	NA	402.155	-6.323867	uc011bgl.1	NA	chr3:73431652-73432515	NA	NA	NA	NA
PZDRN3	609729	NA	NA	NA	NA	522.218	-8.162259	uc010skn.2	NA	chr12:41967693-41968392	NA	NA	NA	NA
PZDRN4	609730	NA	NA	NA	NA									

Table 1

PEAK1	614248	829.457	-4.534261	uc002bcn.2	chr15:77447542-77450812	NA	NA	NA	NA	NA	NA	307.931	-5.859153	uc021sqv.1	chr15:77400498-77406497
PEAR1	610278	NA	NA	NA	NA	311.496	-4.008825	uc001fclj.1	NA	chr1:156884591-156886226	NA	NA	NA	NA	NA
PEB10	604591	NA	NA	NA	NA	715.174	-4.682318	uc010szcc.1	NA	chr12:118582752-118583387	NA	NA	NA	NA	NA
PEG10	609810	NA	NA	NA	NA	NA	NA	NA	NA	NA	729.099	-7.822272	uc003uno.3	chr7:94294995-94299006	NA
PER2	603426	634.171	-0.951344	uc002vyc.3	chr2:239152679-239155015	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PET117	614771	1712.38	-16.748124	uc021wba.1	chr20:18123002-18123812	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PEX1	602136	748.097	-8.969383	uc003uly.3	chr7:92116337-92116770	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PEX13	601789	793.139	-7.143347	uc002sau.4	chr2:61275906-61279125	746.19	-6.329673	uc002sau.4	NA	chr2:61275906-61279125	NA	NA	NA	NA	NA
PEX3	603164	1201.46	-1.258677	uc011edk.1	chr6:143793481-143793620	NA	NA	NA	NA	NA	599.008	-5.772396	uc003qjl.3	chr6:143810364-143811751	NA
PEX7	601757	NA	NA	NA	NA	NA	NA	NA	NA	NA	632.878	-6.732259	uc003qhd.3	chr6:137234665-137235072	NA
PFDN2	613466	NA	NA	NA	NA	387.502	-5.01218	uc001fxu.3	NA	chr1:161070346-161070472	1221.06	-7.257112	uc001fxu.3	chr1:161070346-161070472	NA
PFDM4	604898	1021.35	-12.702964	uc002xkw.3	chr20:52835690-52836492	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PFKM	610681	NA	NA	NA	NA	NA	NA	NA	NA	NA	279.248	-5.83137	uc001rra.2	chr12:48539492-48540187	NA
PFN2	176590	NA	NA	NA	NA	778.72	-4.492359	uc003exu.1	NA	chr3:149682691-149683953	NA	NA	NA	NA	NA
PGAP1	611655	NA	NA	NA	NA	NA	NA	NA	NA	NA	500.835	-8.089105	uc010fsi.3	chr2:197697728-197705957	NA
PGBD1	NA	NA	NA	NA	NA	231.344	-12.74781	uc003inky.3	NA	chr6:28270062-28270326	NA	NA	NA	NA	NA
PGD	172200	627.522	-5.370967	uc001arc.3	chr1:10479807-10480201	NA	NA	NA	NA	NA	601.058	-5.720853	uc001arc.3	chr1:10479807-10480201	NA
PGK1	311800	NA	NA	NA	NA	384.66	-5.31166	uc004eczc.4	NA	chrX:77381328-77382324	NA	NA	NA	NA	NA
PGM3	172100	574.557	-9.793614	uc003plw.3	chr6:83874593-83879016	1544.97	-2.988636	uc003plu.2	NA	chr6:83874593-83878952	480.632	-0.969448	uc003plu.2	chr6:83874593-83878952	NA
PGR	607311	973.049	-13.015832	uc001pgg.2	chr11:100900355-10090846	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRMC1	300435	620.246	-6.830253	uc004erb.3	chrX:118377218-118378429	567.642	-9.808776	uc004erb.3	NA	chrX:118377218-118378429	1076.48	-10.781495	uc004erb.3	chrX:118377218-118378429	NA
PHACTR1	608723	675.953	-4.597364	uc003nag.2	chr6:13273156-13276355	729.814	-6.279615	uc003nah.2	NA	chr6:13287311-13288075	486.62	-5.192605	uc003nah.3	chr6:12934125-12935069	NA
PHACTR4	608726	1554.13	-6.132852	uc001bpu.3	chr1:28793288-28793725	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PHB	176705	442.829	-5.625484	uc002lhx.1	chr17:47481420-47482353	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PHF1	602881	NA	NA	NA	NA	521.631	-6.641573	uc003oei.3	NA	chr6:33383652-33384230	NA	NA	NA	NA	NA
PHF10	613069	NA	NA	NA	NA	878.355	-7.522051	uc011etia.1	NA	chr6:170107132-170110310	NA	NA	NA	NA	NA
PHF12	NA	363.255	-4.821629	uc010wbb.1	chr17:27323271-273233200	NA	NA	NA	NA	NA	214.275	-6.175775	uc010wbb.1	chr17:27323271-273233200	NA
PHF13	NA	697.758	-5.552244	uc001aob.4	chr1:6681698-6684093	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PHF14	NA	1153.44	-6.791433	uc003sry.2	chr7:11142126-11147376	806.405	-5.877645	uc003sry.2	NA	chr7:11142126-11147376	NA	NA	NA	NA	NA
PHF2	604351	NA	NA	NA	NA	1505.3	-25.528641	uc004aub.3	NA	chr9:96439959-96441869	1177.64	-11.466611	uc004aub.3	chr9:96439959-96441869	NA
PHF21A	603325	970.016	-11.868892	uc001mcb.4	chr11:45950870-45955518	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PHF6	300414	NA	NA	NA	NA	794.356	-5.493047	uc004exh.3	NA	chrX:133548253-133548321	219.756	-7.720945	uc004exh.3	chrX:133549253-133549321	NA
PHF8	300560	379.28	-5.885366	uc004dsi.3	chrX:53963113-53965590	222.825	-9.968539	uc004dsx.3	NA	chrX:53969048-53969796	NA	NA	NA	NA	NA
PHKG2	172471	NA	NA	NA	NA	NA	NA	NA	NA	NA	236.779	-4.357947	uc021tgo.1	chr16:30771482-30772497	NA
PHLDA1	605335	NA	NA	NA	NA	NA	NA	NA	NA	NA	766.318	-9.127107	uc001xuu.3	chr12:76419227-76423872	NA
PHLDB1	612834	NA	NA	NA	NA	203.858	-4.587647	uc001plr.2	NA	chr11:118527534-118528748	NA	NA	NA	NA	NA
PHLDB3	NA	333.675	-4.36515	uc010eil.3	chr19:43979255-43979561	378.916	-6.167544	uc010eil.3	NA	chr19:43979255-43979561	679.976	-6.038933	uc002owo.3	chr19:44000184-44001254	NA
PHLP2	611066	NA	NA	NA	NA	NA	NA	NA	NA	NA	1037.13	-7.022437	uc002fay.1	chr16:71711377-71712653	NA
PHOX2B	603851	NA	NA	NA	NA	NA	NA	NA	NA	NA	975.225	-5.480359	uc003gwf.4	chr4:41746099-41747823	NA
PHITF1	604950	868.403	-11.733697	uc001edo.1	chr1:114243899-114248454	NA	NA	NA	NA	NA	324.633	-3.939015	uc001edn.3	chr1:114246447-114246678	NA
PHYH	602026	NA	NA	NA	NA	202.417	-4.150326	uc001ime.3	NA	chr10:13319796-13320300	NA	NA	NA	NA	NA
PHYHPL	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	431.396	-4.536699	uc001jkk.4	chr10:61005332-61007534	NA
PHYKPL	614683	NA	NA	NA	NA	502.737	-5.005975	uc003mjld.1	NA	chr5:177637969-177638921	NA	NA	NA	NA	NA
PI15	607076	NA	NA	NA	NA	1372.93	-10.981316	uc003yal.3	NA	chr8:75761489-75767264	581.8	-9.912882	uc003yal.3	chr8:75761489-75767264	NA
PI4K2B	612101	NA	NA	NA	NA	243.415	-8.194586	uc011bxs.2	NA	chr4:25278810-25280831	NA	NA	NA	NA	NA
PI4K4	600286	NA	NA	NA	NA	NA	NA	NA	NA	NA	731.953	-8.395262	uc010sq.2	chr22:2115770-21157867	NA
PIA3Z	603567	439.522	-6.338471	uc002lck.3	chr18:44390023-44392395	560.806	-7.049207	uc002lcl.3	NA	chr18:44395673-44396339	1443.22	-2.985424	uc002lck.3	chr18:44390023-44392395	NA
PIA5A	605989	NA	NA	NA	NA	NA	NA	NA	NA	NA	463.45	-4.649074	uc002lpg.3	chr19:4037874-4038067	NA
PIBF1	607532	319.976	-5.68271	uc001vjc.3	chr13:73590058-73590591	NA	NA	NA	NA	NA	370.121	-5.58409	uc001vjb.3	chr13:73547862-73548389	NA

Table 1

PIEZ02	613629	469.376	-6.993796	uc002kq.3	chr18:10670244-10671523	852.17	-6.216005	uc002kq.3	chr18:10670244-10671523	NA	NA	NA	NA	NA	NA
PiFO	614234	731.029	-3.653042	uc001eaw.2	chr1:111893950-111895639	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr1:111893950-111895639
PiGA	311770	NA	NA	NA	NA	NA	NA	NA	NA	208.118	-5.369073	uc010neu.3	NA	NA	chrX:15337573-15339627
PiGF	600153	1159.4	-8.571925	uc002rvc.3	chr2:46808413-46808730	1249.99	-5.512043	uc002rvc.3	chr2:46808413-46808730	NA	NA	NA	NA	NA	NA
PiGG	NA	1067.56	-8.422388	uc011buw.2	chr4:515555-516632	296.732	-5.069151	uc011buw.2	chr4:515555-516632	506.47	-4.991984	uc003gam.3	NA	NA	chr4:515502-516632
PiGK	605087	NA	NA	NA	NA	NA	NA	NA	NA	336.937	-7.222813	uc001dhk.3	NA	NA	chr1:77554667-77558058
PiGN	606097	NA	NA	NA	NA	900.707	-10.069057	uc021iub.1	chr18:59711458-59713088	NA	NA	NA	NA	NA	NA
PiGP	605938	NA	NA	NA	NA	661.024	-8.407417	uc002yvw.1	chr21:38437664-38437881	NA	NA	NA	NA	NA	NA
PiGQ	605754	NA	NA	NA	NA	292.163	2.111161	uc010bgw.3	chr16:633036-634136	NA	NA	NA	NA	NA	NA
PiGU	608528	856.094	-6.207949	uc010zui.2	chr20:33148346-33148783	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PiGW	610275	938.791	-7.644802	uc002hmy.1	chr17:34894466-34895150	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PIH1D1	611480	409.429	-5.101542	uc002pns.2	chr19:49949550-49949638	1131.82	-9.299662	uc010yaq.2	chr19:49952349-49952468	1610.42	-5.61701	uc002pns.2	NA	NA	chr19:49949550-49949638
PIH1D2	NA	366.931	-9.810662	uc009yyl.3	chr11:111934734-111934891	618.265	-2.749135	uc009yyl.3	chr11:111934734-111934891	431.086	-4.86249	uc001pmp.4	NA	NA	chr11:111938523-111938594
PIK3AP1	607942	850.098	-4.935659	uc001kmo.3	chr10:98353069-98355333	NA	NA	NA	NA	543.3	-6.519618	uc001kmo.3	NA	NA	chr10:98353069-98355333
PIK3C2A	603601	969.808	-3.62142	uc009ygu.1	chr11:17099277-17099412	1235.19	-6.572311	uc009ygu.1	chr11:17099277-17099412	NA	NA	NA	NA	NA	NA
PIK3CA	171834	NA	NA	NA	NA	269.408	-4.710082	uc003jfk.3	chr3:178952153-178952497	NA	NA	NA	NA	NA	NA
PIK3CD	602839	NA	NA	NA	NA	NA	NA	NA	NA	822.471	-8.478028	uc001aqb.4	NA	NA	chr1:9787105-9789172
PIK3R3	606076	833.106	-6.315417	uc010olv.2	chr1:46505812-46509344	1066.56	-9.087541	uc010olv.2	chr1:46505812-46509344	847.558	-5.131431	uc010olv.2	NA	NA	chr1:46505812-46509344
PIK3R4	602610	797.961	-8.443188	uc003enj.3	chr3:130397778-130398158	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PILR4	605341	435.64	-4.2571	uc011kjo.2	chr7:99997557-99997716	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PIM2	300295	777.631	-8.529398	uc004dlb.3	chrX:48770459-48771407	376.064	-4.641796	uc004dlb.3	chrX:48770459-48771407	NA	NA	NA	NA	NA	NA
PIN4	300252	NA	NA	NA	NA	NA	NA	NA	NA	255.212	-11.282868	uc004eam.3	NA	NA	chrX:71417377-71418194
PINK1	608309	NA	NA	NA	NA	NA	NA	NA	NA	652.791	-9.061417	uc001bdm.3	NA	NA	chr1:20977185-20978004
PIP4K2A	603140	NA	NA	NA	NA	NA	NA	NA	NA	493.868	-4.706335	uc003wcf.1	NA	NA	chr7:142836736-142836834
PIP5K1A	603275	559.854	-8.918435	uc010pcv.2	chr1:151220424-151222007	720.654	-6.125561	uc001exl.3	NA	667.946	-7.72586	uc010qcu.2	NA	NA	chr10:22823766-22826129
PIP5K1P1	NA	NA	NA	NA	NA	231.277	-4.443856	uc003mxx.4	chr6:79883309-7990577	NA	NA	NA	NA	NA	NA
PIWIL4	610315	496.911	-6.697477	uc001pia.3	chr11:94354159-94354587	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PKD1P1	NA	266.987	-2.93942	NA	NA	669.682	-6.941304	uc002dew.4	chr16:16443949-16444465	NA	NA	NA	NA	NA	NA
PKD2	173910	NA	NA	NA	NA	823.115	-9.284738	uc003hre.3	chr4:88996847-88998931	NA	NA	NA	NA	NA	NA
PKDCC	614150	NA	NA	NA	NA	559.335	-4.363961	uc002rsg.3	chr2:42284829-42285668	NA	NA	NA	NA	NA	NA
PKH01	606702	NA	NA	NA	NA	NA	NA	NA	NA	501.477	-5.478561	uc003pah.1	NA	NA	chr6:51480145-51483878
PKIB	606914	NA	NA	NA	NA	NA	NA	NA	NA	863.824	-8.218676	uc003pyz.3	NA	NA	chr6:123046341-123047518
PKNOX1	602100	NA	NA	NA	NA	NA	NA	NA	NA	1143.86	-12.406823	uc002zcg.1	NA	NA	chr21:44450212-44453688
PKP1	601975	NA	NA	NA	NA	NA	NA	NA	NA	901.024	-5.987639	uc001agwd.3	NA	NA	chr1:201299202-201302121
PKP2	602861	NA	NA	NA	NA	777.074	-6.974659	uc001rlj.4	chr12:32943680-32945357	715.561	-7.275091	uc001rlj.4	NA	NA	chr12:32943680-32945357
PKP4	604276	545.072	-4.261875	uc002tzv.3	chr2:159537190-159537940	350.876	-1.060779	uc002tzv.3	chr2:159537190-159537940	266.661	-4.406856	uc002tzv.3	NA	NA	chr2:159537190-159537940
PLA1A	607460	462.624	-4.539498	uc003ecu.3	chr3:119348316-119348658	506.903	-6.426749	uc003ecu.3	chr3:119348316-119348658	NA	NA	NA	NA	NA	NA
PLA2G16	613867	356.074	-6.144294	uc001nht.2	chr11:63341944-63342416	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PLA2G4A	600522	NA	NA	NA	NA	NA	NA	NA	NA	748.476	-13.440079	uc001gsc.3	NA	NA	chr1:186957641-186958113
PLA2G4D	612864	598.955	-5.076075	uc001zox.3	chr15:42359881-42360912	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PLA2G4E	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PLA2G5	601192	637.733	-6.002068	uc001box.3	chr1:20417186-20418394	NA	NA	NA	NA	424.404	-4.377904	uc010udc.2	NA	NA	chr15:42273780-42275951
PLA2G7	601690	1268.93	-8.765556	uc011dwd.1	chr6:46677401-46678263	812.188	-15.84813	uc010jzf.3	chr6:46672053-46672296	925.403	-8.10754	uc011dwd.1	NA	NA	chr6:46677401-46678263
PLAC1	300296	NA	NA	NA	NA	1463.1	-6.237881	uc004exo.1	chrX:13369873-133700073	NA	NA	NA	NA	NA	NA
PLAC8	607515	338.968	-7.637076	uc003hoe.3	chr4:84011211-84012124	263.037	-4.120206	uc003inv.3	chr5:145463876-145463994	NA	NA	NA	NA	NA	NA
PLAC8L1	NA	NA	NA	NA	NA	224.44	-2.799258	uc001jwa.3	chr10:75676324-75677258	NA	NA	NA	NA	NA	NA
PLAU	191840	884.113	-10.776448	uc001jwa.3	chr10:75676324-75677258	1749.27	-20.956607	uc002rmc.3	chr2:28816921-28818926	NA	NA	NA	NA	NA	NA
PLB1	610179	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

PLCB2	604114	NA	NA	NA	NA	210.782	-5.654323	uc001zle.4	chr15:40592870-40593792	NA	NA	NA	NA
PLCB3	600230	NA	NA	NA	NA	465.957	-4.539498	uc009ypg.2	chr11:64035029-64036924	NA	NA	NA	NA
PLCB4	600810	478.844	-1.6349	uc010gbx.3	chr20:9459637-9461462	477.292	-5.871015	uc010gbx.3	chr20:9459637-9461462	NA	NA	NA	NA
PLCL1	600597	NA	NA	NA	NA	891.395	-10.57252	uc002uuv.4	chr2:199011687-199014608	NA	NA	NA	NA
PLD1	602382	1001.1	-7.575397	uc003fhs.3	chr3:171318195-171320867	NA	NA	NA	NA	NA	NA	NA	NA
PLD5	NA	1187.88	-6.914249	uc001hzi.4	chr1:242251689-242253155	652.426	-5.731036	uc001hzi.4	chr1:242251689-242253155	NA	NA	NA	NA
PLD6	614960	309.365	-4.344823	uc002gqz.3	chr17:17104309-17106080	NA	NA	NA	NA	NA	NA	NA	NA
PLEKHA5	607770	314.53	-5.749776	uc001rdz.4	chr12:19353263-19354937	NA	NA	NA	NA	NA	NA	NA	NA
PLEKH81	607651	NA	NA	NA	NA	NA	NA	NA	NA	482.49	-5.04009	uc001oua.3	chr11:73372648-73373864
PLEKH01	NA	NA	NA	NA	NA	NA	NA	NA	NA	540.858	2.064394	uc001xli.2	chr14:69967028-69970407
PLEKH36	611743	NA	NA	NA	NA	511.944	-8.977533	uc003qny.1	chr6:151162033-151164799	NA	NA	NA	NA
PLEKHH1	NA	633.374	-6.929407	uc001xjl.1	chr14:68053953-68056255	528.819	-7.606735	uc001qnr.3	chr12:6437312-6437672	NA	NA	NA	NA
PLEKHH2	612723	286.014	-4.410744	uc002rtf.3	chr2:43968199-43968500	270.452	-5.473154	uc010lss.1	chr14:68054024-68056255	NA	NA	NA	NA
PLEKHJ1	NA	NA	NA	NA	NA	873.878	-6.014774	uc002tts.3	chr2:43937805-43939522	NA	NA	NA	NA
PLEKHM2	609613	594.545	-6.608819	uc010obo.2	chr1:16060430-16061264	1228.79	-12.934199	uc002lwf.1	chr19:2233155-2233838	NA	NA	NA	NA
PLEKHO1	608335	NA	NA	NA	NA	951.321	-6.257365	uc001tts.3	chr1:150131719-150131825	NA	NA	NA	NA
PLEKHS1	NA	NA	NA	NA	NA	362.35	-5.399189	uc001lar.2	chr10:115540362-115542192	NA	NA	NA	NA
PLG	173350	NA	NA	NA	NA	665.088	-11.790675	uc021zhr.1	chr6:161132228-161132904	NA	NA	NA	NA
PLIN5	613248	NA	NA	NA	NA	NA	NA	NA	NA	1737.22	-23.160515	uc002mas.3	chr19:4522544-4523539
PLK2	607023	947.906	-9.584497	uc003jrn.3	chr5:57749810-57750409	NA	NA	NA	NA	NA	NA	NA	NA
PLK4	605031	NA	NA	NA	NA	NA	NA	NA	NA	325.882	-7.774605	uc003fo.3	chr4:128819697-128820377
PLRD2	601865	NA	NA	NA	NA	NA	NA	NA	NA	912.902	-5.223977	uc003evq.1	chr3:145787228-145788503
PLRG1	605961	NA	NA	NA	NA	1068.06	-8.572879	uc003iny.3	chr4:155456149-155457836	639.613	-5.265555	uc003iny.3	chr4:155456149-155457836
PLSCR1	604170	NA	NA	NA	NA	NA	NA	NA	NA	816.02	-4.848651	uc003ewa.2	chr3:146245733-146246325
PLSCR4	607612	1078.32	-5.143917	uc010huy.3	chr3:145910124-145912197	NA	NA	NA	NA	NA	NA	NA	NA
PLSCR6	NA	1170.69	-9.845634	uc010hvb.3	chr3:146294395-146294512	NA	NA	NA	NA	NA	NA	NA	NA
PMAIP1	604959	NA	NA	NA	NA	893.608	-7.57558	uc002lts.2	chr18:57569986-57571538	NA	NA	NA	NA
PMCH	176795	517.535	-8.703149	uc001tjj.3	chr12:102590237-102590429	NA	NA	NA	NA	NA	NA	NA	NA
PMPCA	613036	NA	NA	NA	NA	NA	NA	NA	NA	375.578	-4.523741	uc011mdy.1	chr9:139310985-139311356
PMPCB	603131	1022.97	-9.390863	uc010liu.1	chr7:102949573-102949706	510.651	-6.838519	uc011kll.1	chr7:102969500-102969958	NA	NA	NA	NA
PMS2LP5	NA	NA	NA	NA	NA	NA	NA	NA	NA	462.341	-5.703427	uc011xb.1	chr7:6777303-6777567
PMS2P5	NA	NA	NA	NA	NA	452.938	-9.376961	uc003ubli.2	chr7:74321780-74322330	NA	NA	NA	NA
PNCK	300680	NA	NA	NA	NA	NA	NA	NA	NA	1056.52	-8.817601	uc010nuh.2	chrX:152936533-152937576
PNISR	616653	208.308	-4.863108	uc003pps.2	chr6:99859451-99860189	315.484	-4.630178	uc003ppo.4	chr6:99847841-99848415	NA	NA	NA	NA
PNP	164050	NA	NA	NA	NA	206.733	-3.512989	uc010alhn.3	chr14:20942792-20943322	317.124	-5.583529	uc001vxo.4	chr14:20944761-20946165
POC1B	614784	NA	NA	NA	NA	NA	NA	NA	NA	616.515	-6.695257	uc001tba.3	chr12:89813498-89814929
POF1B	300603	NA	NA	NA	NA	1665.67	-7.220709	uc004eer.2	chrX:84532395-84534426	1547.27	-11.949237	uc004eer.2	chrX:84532395-84534426
POFUT1	607491	600.626	-10.651106	uc002wko.3	chr20:30804854-30805726	NA	NA	NA	NA	NA	NA	NA	NA
POFUT2	610249	446.2	-5.93492	uc002zhd.3	chr21:46683843-46687365	NA	NA	NA	NA	418.163	-6.061661	uc011afq.1	chr21:46704937-46705314
POGLUT1	615618	NA	NA	NA	NA	656.802	-7.707613	uc003ecm.3	chr3:119211286-119213554	NA	NA	NA	NA
POGZ	614787	473.186	-7.513237	uc001eyg.2	chr1:15139679-151400284	NA	NA	NA	NA	NA	NA	NA	NA
POLA2	NA	398.914	-5.819525	uc009yql.1	chr11:65047131-65047491	NA	NA	NA	NA	NA	NA	NA	NA
POLB	174760	468.763	-9.583439	uc003kaz.2	chr8:42229176-42229331	914.222	-8.420926	uc003kaz.2	chr8:42229176-42229331	NA	NA	NA	NA
POLDIP2	611519	NA	NA	NA	NA	824.555	-8.908061	uc002haz.3	chr17:26673659-26675142	NA	NA	NA	NA
POLG	174763	502.139	-5.770486	uc002bnr.4	chr15:89859536-89859981	NA	NA	NA	NA	NA	NA	NA	NA
POLG2	604983	866.449	-8.484058	uc010deg.2	chr17:62481711-62481820	1087.11	-12.984047	uc010deg.2	chr17:62481711-62481820	872.348	-10.775339	uc021ubq.1	chr17:62473902-62473939
POLH	603968	NA	NA	NA	NA	NA	NA	NA	NA	1129.85	-9.441735	uc010ju.2	chr6:43582295-43582458
POLI	605252	642.02	-6.274411	uc002ljj.4	chr18:51820838-51824604	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

POLR1B	602000	NA	NA	NA	NA	NA	447.076	-8.419309	uc002lhw.2	chr2:113333307-113334727	NA	NA	NA	1229.88	-14.482919	NA	chr9:37503200-37503693
POLR1E	NA	NA	NA	NA	NA	NA	1876.39	-17.898689	uc003hcl.1	chr4:57897155-57897334	NA	NA	NA	NA	NA	NA	NA
POLR2B	180661	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	664.806	-8.986666	NA	chr22:38363773-38365319
POLR2F	604414	221.768	-5.622688	uc003aul.3	chr22:38363723-38365319	NA	NA	NA	NA	NA	NA	NA	NA	623.087	-6.278528	NA	chr11:62533980-62534187
POLR2G	602013	1297.06	-9.726277	uc001nva.3	chr11:62533980-62534187	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
POLR2J2	609881	1043.01	-8.031869	uc010ljl.2	chr7:102277195-102277971	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
POLR2K	606033	659.743	-6.52391	uc003yjf.3	chr8:101165545-101166230	510.104	-7.628874	uc003yjf.3	uc003yjf.3	chr8:101165545-101166230	NA	NA	NA	NA	NA	NA	NA
POLR3GL	NA	NA	NA	NA	NA	1062.23	-15.078463	uc001tenp.1	uc010lam.1	chr1:145456236-145456636	NA	NA	NA	NA	NA	NA	NA
POM121	615753	1160.55	-3.937003	uc010lam.1	chr7:72419010-72421979	822.058	-5.326524	uc010lam.1	uc010lam.1	chr7:72419010-72421979	1191.66	-10.471916	uc010lam.1	NA	NA	NA	chr7:72419010-72421979
POMIP	613386	NA	NA	NA	NA	795.082	-13.288406	uc001luf.3	uc001luf.3	chr13:29252240-29253093	NA	NA	NA	NA	NA	NA	NA
PON3	602720	970.789	-9.060639	uc003unt.3	chr7:94898184-94899284	431.955	-5.933048	uc001lkl.2	uc001lkl.2	chr7:948992794-94993170	NA	NA	NA	NA	NA	NA	NA
POP5	609992	NA	NA	NA	NA	317.267	-5.922878	uc001lys.3	uc001lys.3	chr12:121016848-121017120	NA	NA	NA	NA	NA	NA	NA
PORCN	300651	NA	NA	NA	NA	501.795	-6.062114	uc004djr.1	NA	chrX:48378865-48379202	NA	NA	NA	NA	NA	NA	NA
POU1F1	173110	NA	NA	NA	NA	NA	NA	NA	NA	NA	759.443	-8.45257	uc003daq.1	NA	NA	NA	chr3:87308783-87309043
POU3F2	600494	NA	NA	NA	NA	296.308	-5.4862	uc003ppe.3	uc003ppe.3	chr6:99284082-99286666	NA	NA	NA	NA	NA	NA	NA
POU4F2	113725	NA	NA	NA	NA	701.264	-4.20991	uc003ikv.3	uc003ikv.3	chr4:147561961-147563623	NA	NA	NA	NA	NA	NA	NA
POU6F2	609062	446.248	-4.277697	uc010kxo.3	chr7:39413106-39413307	1336.87	-9.755068	uc001jgv.1	uc001jgv.1	chr10:71962596-71962910	NA	NA	NA	NA	NA	NA	NA
PPA1	179030	NA	NA	NA	NA	NA	NA	NA	NA	NA	500.443	-6.590136	uc003hxl.3	NA	NA	NA	chr4:106290234-106290881
PPA2	609988	NA	NA	NA	NA	NA	NA	NA	NA	NA	301.173	-5.200789	uc001oyl.2	NA	NA	NA	chr1:56960419-56962222
PPAP2B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PPAPDC1B	NA	NA	NA	NA	NA	656.258	-5.469545	uc003xlg.4	uc003xlg.4	chr8:38122258-38122450	NA	NA	NA	NA	NA	NA	NA
PPARG	601487	693.626	-7.33651	uc003bwr.3	chr3:12475645-12475855	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PPCDC	609854	NA	NA	NA	NA	278.639	-4.127464	uc002axo.3	uc002axo.3	chr15:75341577-75343067	NA	NA	NA	NA	NA	NA	NA
PPEF2	602256	523.669	-5.490739	uc003hix.3	chr4:76781026-76781819	398.708	-7.627851	uc003hix.3	uc003hix.3	chr4:76781026-76781819	NA	NA	NA	NA	NA	NA	NA
PPF1A2	603143	NA	NA	NA	NA	843.424	-9.319295	uc010sue.2	uc010sue.2	chr12:81652880-81653144	NA	NA	NA	NA	NA	NA	NA
PPFBP1	603141	NA	NA	NA	NA	716.285	-7.508159	uc001rltz.2	uc001rltz.2	chr12:27800818-27800900	NA	NA	NA	NA	NA	NA	NA
PPIAL4E	608608	NA	NA	NA	NA	544.896	-4.739693	uc010paz.2	uc010paz.2	chr1:148644581-148644795	251.647	-4.558076	uc010paz.2	NA	NA	NA	chr1:148644581-148644795
PPIAP30	NA	NA	NA	NA	NA	487.757	-4.60718	uc010qca.1	uc010qca.1	chr10:15196721-15196797	NA	NA	NA	NA	NA	NA	NA
PPIB	123841	NA	NA	NA	NA	NA	NA	NA	NA	NA	452.163	-5.514129	uc010bgx.1	NA	NA	NA	chr15:64451473-64452261
PPIC	123842	NA	NA	NA	NA	1681.43	-3.615525	uc003klh.3	uc003klh.3	chr5:122359078-122359569	471.724	-5.573441	uc011cwp.1	NA	NA	NA	chr5:122364188-122364831
PPID	601753	873.291	-7.854077	uc003lqc.3	chr4:159630279-159630887	NA	NA	NA	NA	NA	334.306	-7.092339	uc003lqc.3	NA	NA	NA	chr4:159630279-159630887
PPIG	606093	NA	NA	NA	NA	NA	NA	NA	NA	NA	1594.8	-6.645383	uc002lwx.3	NA	NA	NA	chr2:170494034-170494254
PPIH	606095	NA	NA	NA	NA	NA	NA	NA	NA	NA	521.063	-11.11152	uc009vwl.2	NA	NA	NA	chr1:43133091-43133568
PPM1A	606108	NA	NA	NA	NA	NA	NA	NA	NA	NA	643.807	-7.34583	uc001xex.4	NA	NA	NA	chr14:60752483-60755272
PPM1B	603770	NA	NA	NA	NA	296.507	-8.733805	uc002thu.3	uc002thu.3	chr2:44457141-44458611	783.723	-8.905991	uc002rtt.3	NA	NA	NA	chr2:44457858-44458611
PPM1N	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	367.656	-5.666301	uc002pce.3	NA	NA	NA	chr19:46005344-46005764
PPP1CB	600590	NA	NA	NA	NA	470.445	-6.047224	uc010ymj.2	uc010ymj.2	chr2:29022170-29025806	NA	NA	NA	NA	NA	NA	NA
PPP1CC	176914	998.924	-7.830697	uc001tru.3	chr12:111157613-111158880	485.983	-4.588473	uc001tru.3	uc001tru.3	chr12:111157613-111158880	379.001	-2.314566	uc001tru.3	NA	NA	NA	chr12:111157613-111158880
PPP1R11	606670	NA	NA	NA	NA	NA	NA	NA	NA	NA	1200.73	-7.824314	uc003rep.3	NA	NA	NA	chr6:30037084-30038108
PPP1R12C	613245	NA	NA	NA	NA	NA	NA	NA	NA	NA	417.57	-5.702283	uc010fys.2	NA	NA	NA	chr19:55602281-55602839
PPP1R14A	608153	839.492	-7.499396	uc002ohq.3	chr19:38741877-38741957	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PPP1R14C	613242	NA	NA	NA	NA	NA	NA	NA	NA	NA	375.653	-4.184393	uc003gnt.3	NA	NA	NA	chr6:150569957-150571528
PPP1R15A	611048	NA	NA	NA	NA	1103.73	-7.539785	uc002pkv.4	uc002pkv.4	chr19:49379231-49379319	NA	NA	NA	NA	NA	NA	NA
PPP1R15B	613257	NA	NA	NA	NA	NA	NA	NA	NA	NA	751.391	-7.435796	uc001hav.4	NA	NA	NA	chr1:204372492-204375219
PPP1R1A	613246	NA	NA	NA	NA	NA	NA	NA	NA	NA	686.872	-7.352737	uc001lsg.2	NA	NA	NA	chr12:54973024-54974170
PPP1R1B	604399	NA	NA	NA	NA	NA	NA	NA	NA	NA	416.697	-4.782596	uc002hrt.3	NA	NA	NA	chr17:37797119-37792878
PPP1R2	601792	633.978	-16.676052	uc003fup.3	chr3:195241221-195243693	NA	NA	NA	NA	NA	651.952	-4.406856	uc003fup.3	NA	NA	NA	chr3:195241221-195243693
PPP1R26	614056	227.484	-6.066031	uc004cfr.1	chr9:138379987-138380739	232.984	-4.447864	uc004cfr.1	uc004cfr.1	chr9:138379987-138380739	817.79	-6.733842	uc004cfr.1	NA	NA	NA	chr9:138379987-138380739
PPP1R2P3	NA	821.29	-10.310598	uc003lwl.1	chr5:156278192-156279539	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

PPP1R2P9	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	643.785	-7.824973	uc004dfv.3	chrX:42636617-42636721
PPP1R35	NA	775.722	-9.059802	uc003uuy.1	chr7:100032912-100032982	NA	NA	NA	NA	NA	NA	NA	NA	NA
PPP1R3D	603326	NA	NA	NA	NA	1256.95	-8.296879	uc002ybb.3	chr20:58511887-58514086	NA	NA	NA	NA	NA
PPP1R7	602877	NA	NA	NA	NA	NA	NA	NA	NA	280.464	-4.670793	uc002wat.1	chr2:242122239-242122439	NA
PPP2CA	176915	NA	NA	NA	NA	401.543	-6.750479	uc003kze.3	chr5:133532148-133533462	NA	NA	NA	NA	NA
PPP2CB	176916	NA	NA	NA	NA	NA	NA	NA	NA	348.844	-7.741803	uc003xik.3	chr8:30643126-30643750	NA
PPP2R1B	603113	NA	NA	NA	NA	NA	NA	NA	NA	236.984	-5.714804	uc001pk.1	chr11:111608605-111612319	NA
PPP2R2D	613992	288.886	-6.142211	uc001lkr.3	chr10:133769468-133770053	NA	NA	NA	NA	NA	NA	NA	NA	NA
PPP2R3C	615902	NA	NA	NA	NA	NA	NA	NA	NA	550.598	-6.313376	uc010amn.1	chr14:35567869-35568431	NA
PPP2R4	600756	NA	NA	NA	NA	NA	NA	NA	NA	201.967	-6.325484	uc004bxl.2	chr9:131909744-131911225	NA
PPP2R5A	601643	460.842	-7.965048	uc001hjb.3	chr1:212534113-212535205	333.884	-6.153444	uc001hjb.3	chr1:212534113-212535205	NA	NA	NA	NA	NA
PPP3CA	114105	997.15	-10.681226	uc003hvs.2	chr4:101944587-101947021	1193.95	-10.619017	uc003hvs.2	chr4:101944587-101947021	NA	NA	NA	NA	NA
PPP3CB	114106	827.771	-5.965954	uc010qkj.2	chr10:75196563-75197999	NA	NA	NA	NA	NA	NA	NA	NA	NA
PPP3CC	114107	NA	NA	NA	NA	1243.78	-7.360191	uc003xbs.3	chr8:22398316-22398657	NA	NA	NA	NA	NA
PPP3R1	601302	202.632	-4.082962	uc002sei.1	chr2:68405989-68408094	402.076	-4.244388	uc002sei.1	chr2:68405989-68408094	NA	NA	NA	NA	NA
PPP4R2	613822	NA	NA	NA	NA	740.175	-11.155499	uc003dph.1	chr3:73114874-73115011	NA	NA	NA	NA	NA
PPP6R2	610877	NA	NA	NA	NA	826.329	-2.349148	uc003bky.2	chr22:50882663-50883518	826.314	-6.670711	uc003bkz.2	chr22:50882677-50883518	NA
PPRC1	NA	NA	NA	NA	NA	609.519	-6.03315	uc001kum.3	chr10:103909787-103910090	395.266	-3.020272	uc001kum.3	chr10:103909787-103910090	NA
PQBP1	300463	NA	NA	NA	NA	552.836	-5.948957	uc004dlj.1	chrX:48759893-48760367	NA	NA	NA	NA	NA
PQLC1	NA	NA	NA	NA	NA	NA	NA	NA	NA	373.45	-7.305904	uc010xfm.1	chr18:77662420-77664121	NA
PQLC2L	NA	1121.83	-9.894497	uc003fbo.3	chr3:157296123-157296680	233.897	-4.070743	uc003fbo.3	chr3:157296123-157296680	NA	NA	NA	NA	NA
PRADC1	NA	678.679	-5.7815	uc002siy.3	chr2:73455134-73455581	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRAMEF1	NA	1387.94	-13.241679	uc001auj.2	chr1:12856146-12856777	213.607	-2.502641	uc001auj.2	chr1:12856146-12856777	NA	NA	NA	NA	NA
PRAMEF12	NA	616.587	-7.280617	uc001aul.3	chr1:12837743-12838048	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRAMEF20	NA	256.344	-4.418053	uc009vny.1	chr1:13526874-13526943	NA	NA	NA	NA	985.487	-3.982038	uc009vny.1	chr1:13526874-13526943	NA
PRAMEF5	NA	NA	NA	NA	NA	329.938	-5.898029	uc001auu.1	chr1:13368734-13369057	259.67	-5.03943	uc001auu.1	chr1:13368734-13369057	NA
PRAMEF8	NA	766.477	-5.070669	uc001aup.3	chr1:12980234-12980568	NA	NA	NA	NA	680.226	-7.454099	uc001aup.3	chr1:12980234-12980568	NA
PRAMEF9	NA	NA	NA	NA	NA	342.999	-4.224731	uc001auw.1	chr1:13427860-13428191	NA	NA	NA	NA	NA
PRCP	176785	1082.54	-9.633736	uc001ozr.3	chr11:82535409-82535947	1428.18	-13.449655	uc001ozr.3	chr11:82535409-82535947	NA	NA	NA	NA	NA
PRDM1	603423	521.307	-5.212678	uc003prd.2	chr6:106555362-106557814	418.965	-7.283789	uc003prd.2	chr6:106555362-106557814	NA	NA	NA	NA	NA
PRDM10	NA	NA	NA	NA	NA	NA	NA	NA	NA	252.248	-5.093698	uc001dfj.3	chr11:129769601-129772207	NA
PRDM13	NA	548.061	-5.52181	uc003pqg.1	chr6:100062636-100063454	NA	NA	NA	NA	495.819	-5.867576	uc003pqg.1	chr6:100062636-100063454	NA
PRDM15	NA	NA	NA	NA	NA	NA	NA	NA	NA	462.395	-6.833814	uc002yzo.3	chr21:43218385-43221399	NA
PRDX4	300927	547.556	-5.170307	uc004dam.3	chrX:23704453-23704514	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRELID2	NA	934.445	-11.875292	uc003hno.1	chr5:145138582-145140088	NA	NA	NA	NA	981.893	-11.183492	uc003hno.1	chr5:145138582-145140088	NA
PREPL	609557	NA	NA	NA	NA	NA	NA	NA	NA	516.127	-6.958248	uc002rug.3	chr2:44544748-44548494	NA
PRIM2	176636	927.196	-5.490174	uc003pdv.1	chr6:57190862-57191161	658.205	-7.028892	uc003pdv.3	chr6:57512703-57512788	282.404	-4.578215	uc003pdv.1	chr6:57190862-57191161	NA
PRIMA1	613851	NA	NA	NA	NA	387.932	-5.101985	uc001ybw.1	chr14:94184644-94187789	NA	NA	NA	NA	NA
PRIMPOL	615421	227.145	-7.481932	uc003liw.2	chr4:185615934-185616112	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKAA1	602739	444.15	-3.123422	uc003jmb.3	chr5:40759481-40762879	851.324	-6.572413	uc003jmb.3	chr5:40759481-40762879	NA	NA	NA	NA	NA
PRKAA2	600497	1052.34	-5.304457	uc001cyk.4	chr1:57173387-57181008	231.326	-7.040073	uc001cyk.4	chr1:57173387-57181008	NA	NA	NA	NA	NA
PRKAB2	602741	351.258	-4.151407	uc001epe.3	chr1:146626685-146631143	1375.11	-8.72506	uc009wif.1	chr1:146633093-146633248	NA	NA	NA	NA	NA
PRKACA	601639	1039.16	-8.187108	uc002myb.3	chr19:14202507-14203923	1067.45	-1.769593	uc002myb.3	chr19:14202507-14203923	NA	NA	NA	NA	NA
PRKACB	176892	NA	NA	NA	NA	NA	NA	NA	NA	231.107	-4.597109	uc001dlj.3	chr1:84700989-84704181	NA
PRKACG	176893	1082.75	-9.850744	uc004agy.3	chr9:71627449-71627952	600.584	-6.219539	uc004agy.3	chr9:71627449-71627952	NA	NA	NA	NA	NA
PRKARB	176911	NA	NA	NA	NA	208.692	-5.59229	uc003slu.2	chr7:588834-590066	NA	NA	NA	NA	NA
PRKCB	176970	NA	NA	NA	NA	NA	NA	NA	NA	638.011	-6.791426	uc002dme.3	chr16:24226138-24231932	NA
PRKCZ	176982	NA	NA	NA	NA	NA	NA	NA	NA	425.548	-6.582401	uc009vib.3	chr1:2087536-2088167	NA
PRKD3	607077	1227.42	-8.435821	uc002rqf.1	chr2:37494711-37496698	NA	NA	NA	NA	543.909	-4.74564	uc002rqf.1	chr2:37494711-37496698	NA

Table 1

PRKDC	600899	NA	NA	NA	NA	692,004	-6,02719	uc003xql.3	chr8:48685669-48686733	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKG1	176894	1270.96	-7,124208	uc001ljm.3	chr10:54053661-54058110	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKGA	603424	654.975	-6.420746	uc002umc.3	chr2:179296141-179296823	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKRIP1	NA	510.496	-4,789046	uc003uzh.2	chr7:102065559-102067129	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKRIR	607374	NA	NA	NA	NA	620,335	-6,706162	uc001toxh.1	chr11:76061004-76061907	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRKX	300083	NA	NA	NA	NA	237,423	-7,296506	uc010nde.3	chrX:3522384-3526986	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRL	176760	NA	NA	NA	NA	738,589	-7,126055	uc003ndo.3	chr6:22287473-22287630	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRLHR	600895	305.178	-4,590193	uc001ldp.1	chr10:120352916-120353643	NA	NA	NA	NA	575,74	-8,229101	uc001ldp.1	chr10:120352916-120353643	NA	NA	NA	NA	NA	NA
PRMT2	601961	680.167	-4,650683	uc002jw.3	chr21:48078837-48080068	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRMT3	603190	NA	NA	NA	NA	644,578	-9,073898	uc001mqb.3	chr11:20529960-20530879	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRMT4	176640	NA	NA	NA	NA	896,068	-10,343675	uc002wkl.1	chr20:4680629-4682233	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PROM1	604365	593.708	-7,141342	uc003goo.2	chr4:15969849-15970991	NA	NA	NA	NA	741,01	-5,089498	uc003goo.2	chr4:15969849-15970991	NA	NA	NA	NA	NA	NA
PROM2	NA	NA	NA	NA	NA	581,937	-10,611033	uc002suh.2	chr2:95954972-95957055	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PROS1	176880	508.807	-7,65441	uc010hoo.3	chr3:93591881-93593088	NA	NA	NA	NA	1561,58	-9,79659	uc010hoo.3	chr3:93591881-93593088	NA	NA	NA	NA	NA	NA
PROSER3	NA	NA	NA	NA	NA	NA	NA	NA	NA	1484,7	-10,413012	uc021usz.1	chr19:36259448-36260077	NA	NA	NA	NA	NA	NA
PRPF18	604993	NA	NA	NA	NA	NA	NA	NA	NA	633,934	-7,889927	uc001imp.3	chr10:13672341-13672868	NA	NA	NA	NA	NA	NA
PRPF38A	NA	NA	NA	NA	NA	432,619	-5,708473	uc001ctv.4	chr1:52882363-52883992	2134,38	-14,226575	uc001ctv.4	chr1:52882363-52883992	NA	NA	NA	NA	NA	NA
PRPF39	614907	1196.34	-8,548215	uc001wvy.4	chr14:45584117-45584804	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRPF8	607300	615.088	-6,450075	uc002fte.3	chr17:1553923-1554095	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRPS2	311860	NA	NA	NA	NA	NA	NA	NA	NA	954,167	-5,078181	uc004ova.3	chrX:12840916-12842346	NA	NA	NA	NA	NA	NA
PRR14	NA	1298.36	-9,874897	uc002dy.3	chr16:30667633-30667734	685,632	-7,169206	uc002dy.3	chr16:30667633-30667734	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRR14L	NA	1647,72	-12,951215	uc003alp.4	chr22:32077334-32081512	1646,21	-2,465276	uc003alp.4	chr22:32077334-32081512	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRR16	615931	NA	NA	NA	NA	NA	NA	NA	NA	1013,56	-14,814108	uc003ksp.3	chr5:120022405-120022964	NA	NA	NA	NA	NA	NA
PRR23A	NA	NA	NA	NA	NA	NA	NA	NA	NA	488,808	-5,276431	uc011bms.2	chr3:138722804-138724309	NA	NA	NA	NA	NA	NA
PRR23B	NA	NA	NA	NA	NA	NA	NA	NA	NA	348,47	-5,324471	uc003esy.1	chr3:13873873-138738705	NA	NA	NA	NA	NA	NA
PRR23C	NA	711,16	-7,999624	uc011bmt.1	chr3:138760944-138762673	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRR26	NA	NA	NA	NA	NA	NA	NA	NA	NA	474,752	-5,044074	uc001ifr.3	chr10:708903-711109	NA	NA	NA	NA	NA	NA
PRR27	NA	NA	NA	NA	NA	NA	NA	NA	NA	470,326	-9,784376	uc003hfa.4	chr4:71028412-71032326	NA	NA	NA	NA	NA	NA
PRR3	NA	493,769	-4,890177	uc003nql.2	chr6:30530273-30532473	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRR32	NA	473,456	-8,68197	uc010nra.3	chrX:125955519-125955768	NA	NA	NA	NA	717,227	-3,771981	uc010nra.3	chrX:125955519-125955768	NA	NA	NA	NA	NA	NA
PRR34	NA	780,67	-6,100478	uc003bgq.1	chr22:46446339-46447706	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRR9	NA	NA	NA	NA	NA	521,659	-7,316097	uc021ozw.1	chr1:153190972-153191783	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRRC1	NA	1443,46	-7,643477	uc003kuj.4	chr5:126883743-126887834	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRRG1	300935	1637,02	-9,643232	uc022bul.1	chrX:37300122-37301477	NA	NA	NA	NA	415,644	-5,477706	uc022agt.1	chrX:150869506-150870063	NA	NA	NA	NA	NA	NA
PRRG3	300685	NA	NA	NA	NA	NA	NA	NA	NA	310,457	-3,945671	uc003nzu.3	chr6:32116140-32116489	NA	NA	NA	NA	NA	NA
PRRT1	NA	NA	NA	NA	NA	1126,71	-4,780384	uc003nzs.3	chr6:32116140-32116998	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRRT2	614386	578,343	-4,048622	uc002due.4	chr16:29825960-29827202	NA	NA	NA	NA	598,608	-9,68033	uc002cry.1	chr16:2902728-2903093	NA	NA	NA	NA	NA	NA
PRSS22	609343	NA	NA	NA	NA	NA	NA	NA	NA	1547,05	-15,845934	uc010fts.1	chr11:86519838-86520169	NA	NA	NA	NA	NA	NA
PRSS23	NA	492,913	-5,607231	uc010fts.1	chr11:86519838-86520169	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRSS35	NA	NA	NA	NA	NA	248,079	-8,39324	uc003piz.3	chr6:84234403-84235421	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRSS42	NA	NA	NA	NA	NA	393,69	-7,07113	uc003cqi.3	chr3:46871894-46871954	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRSS45	NA	393,444	-4,350072	uc010hij.3	chr3:46783581-46783839	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRSS55	615144	NA	NA	NA	NA	473,422	-4,859588	uc022art.1	chr8:10411543-10411676	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRTG	613261	NA	NA	NA	NA	755,806	-9,052608	uc011lisk.2	chr9:79226292-79229485	253,616	-4,894043	uc002adg.3	chr15:55903739-55912209	NA	NA	NA	NA	NA	NA
PRUNE2	610691	NA	NA	NA	NA	590,453	-3,924998	uc002onq.3	chr19:40899671-40899872	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PRX	605725	NA	NA	NA	NA	276,587	-4,393927	uc001jsm.3	chr10:73576055-73577197	343,447	-4,631893	uc002onq.3	chr19:40899671-40899872	NA	NA	NA	NA	NA	NA
PSAP	176801	NA	NA	NA	NA	NA	NA	NA	NA	663,027	-6,941757	uc001jsm.3	chr10:73576055-73577197	NA	NA	NA	NA	NA	NA
PSD3	614440	510,399	-8,67216	uc003wyx.4	chr8:18384813-18393252	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
PSEN2	600759	575,096	-9,09846	uc009veo.1	chr1:227083281-227083804	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

PSG11	176401	NA	NA	NA	NA	499.226	-7.759387	NA	NA	chr19:4325794-43226242	NA	212.223	-4.213259	uc002ovp.1	chr19:43511809-43512262	
PSG3	176392	NA	NA	NA	NA	322.983	-6.990292	uc002oue.3	NA	NA	NA	246.861	-4.486051	NA	NA	
PSG9	176398	275.409	-5.296089	chr19:43761312-43762108	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PSMA1	602854	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	388.29	-14.081733	uc001mlk.3	chr11:14526422-14526737	
PSMA2	176842	NA	NA	NA	NA	534.915	-7.582176	uc0001xdj.2	NA	chr14:58738614-58738727	NA	1286.11	-12.635253	uc003thz.1	chr7:42957686-42961452	
PSMA3	176843	NA	NA	NA	NA	763.384	-7.228475	uc0002bdu.4	NA	chr15:78841287-78841563	644.559	-9.173064	uc002bdu.4	chr15:78841287-78841563		
PSMA4	176846	NA	NA	NA	NA	NA	NA	NA	NA	NA	912.351	-9.230074	uc001dxn.3	chr1:109941653-109944634		
PSMA5	176844	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PSMA6	602855	257.156	-4.915418	uc0001lwd.3	chr14:35786513-35786682	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PSMB1	602017	1063.58	-9.550596	uc0003qxr.3	chr6:170844204-170844307	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PSMB2	602175	NA	NA	NA	NA	1093.51	-7.113083	uc0001bzd.2	chr1:36035413-36040299	1165.1	-6.010468	uc001bzd.2	chr1:36035413-36040299			
PSMB3	602176	581.496	-4.937854	uc0002hqr.3	chr17:36920421-36920478	NA	NA	NA	NA	NA	257.794	-3.444616	uc0002hqr.3	chr17:36920421-36920478		
PSMB4	602177	426.102	-5.345978	uc010pda.2	chr1:151373075-151373603	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PSMB5	603006	788.485	-7.900773	uc0001wii.3	chr14:23495060-23495297	994.85	-9.890269	uc0001wii.3	chr14:23495060-23495297	NA	NA	NA	NA	NA	NA	
PSMB9	177045	NA	NA	NA	NA	328.886	-3.3351	uc0111daj.2	chr6:32826348-32826899	515.541	-5.459571	uc003sga.3	chr6:32827310-32827628			
PSMC6	602708	1049	-10.965282	uc010lqv.2	chr14:53176326-53177053	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PSMD10	300880	1134.59	-4.454212	uc0004enp.2	chrX:107327435-107328203	1048.78	-10.411734	uc0004enp.2	chrX:107327435-107328203	434.701	-3.713154	uc0004enp.2	chrX:107327435-107328203			
PSMD12	604450	NA	NA	NA	NA	NA	NA	NA	NA	NA	322.935	-5.521405	uc010det.1	chr17:65341728-65341856		
PSMG2	609702	NA	NA	NA	NA	377.856	-12.926561	uc0002krg.3	chr18:12725531-12725739	646.405	-6.986496	uc0002kri.2	chr18:12724640-12725658			
PSPC1	612408	NA	NA	NA	NA	2456	-12.767525	uc021fgr.1	chr13:20277009-20277314	NA	NA	NA	NA	NA	NA	
PSPH	172480	1309.82	-6.103682	uc0003rth.3	chr7:56078744-56079454	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTAR1	NA	NA	NA	NA	NA	1140.4	-12.08511	uc0004ahj.4	chr9:72324438-72333257	NA	NA	NA	NA	NA	NA	
PTCD2	615484	NA	NA	NA	NA	792.594	-5.233079	uc011csf.1	chr5:71654255-71654650	NA	NA	NA	NA	NA	NA	
PTCHD1	300828	565.775	-8.019903	uc010mfu.2	chrX:23398443-23399551	NA	NA	NA	NA	NA	744.267	-5.30746	uc010jxx.1	chr6:42892123-42892552		
PTCRA	606817	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTF1A	607194	301.967	-6.411047	uc0001fip.3	chr10:23482836-23483181	NA	NA	NA	NA	NA	549.438	-4.28105	uc0001dfg.1	chr1:71318036-71318542		
PTGER3	176806	461.369	-4.535372	uc0001dfg.1	chr1:71318036-71318542	NA	NA	NA	NA	NA	431.505	-6.309721	uc0003jiz.3	chr5:40692481-40693837		
PTGER4	601586	NA	NA	NA	NA	NA	NA	NA	NA	NA	626.027	-9.660505	uc0001slu.4	chr12:57057125-57058262		
PTGES3	607061	NA	NA	NA	NA	NA	NA	NA	NA	NA	1308.9	-13.197962	uc0001xow.3	chr14:74350881-74352168		
PTGR2	608642	NA	NA	NA	NA	866.647	-9.366878	uc0001gsb.3	chr1:186640944-186643484	NA	NA	NA	NA	NA	NA	
PTGS2	600262	NA	NA	NA	NA	289.505	-4.09858	uc0001mlb.3	chr11:13513601-13513951	NA	NA	NA	NA	NA	NA	
PTH	168450	NA	NA	NA	NA	319.813	-8.352434	uc0102jb.2	chr2:209358385-209359231	1028.45	-5.971116	uc0102jb.2	chr2:209358385-209359231			
PTH2R	601469	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTN	162095	1286.22	-9.774317	uc0003vtq.2	chr7:136912092-136912766	NA	NA	NA	NA	NA	590.556	-5.089477	uc0003pek.3	chr6:64290080-64293489		
PTP4A1	601585	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTPDC1	NA	1037.44	-11.609441	uc0004auf.2	chr9:96870227-96872138	NA	NA	NA	NA	NA	228.382	-4.798654	uc0001ttw.1	chr12:112924438-112924727		
PTPN11	176876	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTPN2	176887	515.343	-6.466919	uc0002knp.3	chr18:12792301-12794276	NA	NA	NA	NA	NA	561.863	-6.877569	uc0001eds.3	chr1:114356433-114357526		
PTPN22	600716	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTPRA	176884	652.951	-7.355988	uc0002whj.3	chr20:3018780-3019315	NA	NA	NA	NA	NA	349.307	-4.813704	uc0003zkr.3	chr9:8314246-8317873		
PTPRD	601598	898.324	-7.931225	uc0003zkr.3	chr9:8314246-8317873	1017.28	-5.094383	uc0003zkt.1	chr9:8528152-8528424	NA	NA	NA	NA	NA	NA	
PTPRE	600926	NA	NA	NA	NA	891.603	-3.792211	uc0001lkb.3	chr10:129881171-129884164	NA	NA	NA	NA	NA	NA	
PTPRF	179590	452.329	-2.57137	uc0001lqj.4	chr1:44044957-44045736	NA	NA	NA	NA	NA	721.348	-4.388217	uc0001cjq.4	chr1:44044957-44045736		
PTPRJ	600925	671.736	-8.589169	uc0001ngp.4	chr11:48188915-48192394	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
PTPRK	602545	NA	NA	NA	NA	NA	NA	NA	NA	NA	679.577	-7.727752	uc0003qbl.1	chr6:128321132-128321416		
PTPRN2	601698	NA	NA	NA	NA	652.677	-9.07873	uc0001kwa.2	chr7:157331750-157333407	NA	NA	NA	NA	NA	NA	
PTPRR	602853	NA	NA	NA	NA	NA	NA	NA	NA	NA	337.849	-4.551348	uc010xtr.1	chr12:71054720-71054981		
PTPRS	601576	NA	NA	NA	NA	418.011	-5.048321	uc0002mbu.1	chr19:5158506-5159109	513.651	-5.767386	uc010xin.2	chr19:5205519-5206784			
PTRF	603198	NA	NA	NA	NA	NA	NA	NA	NA	NA	229.095	-4.015238	uc010wgi.2	chr17:40554467-40556704		

Table 1

PTRH1	NA	NA	NA	NA	NA	288,632	-5,071,129	uc004bro.3	chr9:130476227-130476378	740,228	-1,159,269	uc004bro.3	chr9:130476227-130476378
PUS10	612787	208,452	-3,828,765	uc010fci.3	chr2:61167548-61169529	1400	-21,349,705	uc010fci.3	chr2:61167548-61169529	NA	NA	NA	NA
PUS3	616283	NA	NA	NA	NA	NA	NA	NA	NA	380,664	-5,845,215	uc001rev.2	chr11:125763380-125763679
PUS7	616261	NA	NA	NA	NA	939,689	-13,134,619	uc010jli.3	chr7:105096960-105098236	NA	NA	NA	NA
PVRIG	NA	NA	NA	NA	NA	NA	NA	NA	NA	200,894	-4,323,446	uc003uec.2	chr7:99818875-99819111
PVRL3	607147	682,441	-9,526,082	uc003dxu.2	chr3:110912227-110913016	NA	NA	NA	NA	NA	NA	NA	NA
PWP2	601475	NA	NA	NA	NA	NA	NA	NA	NA	835,86	-9,873,087	uc002zeb.3	chr21:45550654-45551063
PXMP2	NA	NA	NA	NA	NA	NA	NA	NA	NA	545,602	-5,545,275	uc001ukt.3	chr12:133281274-133281577
PXT1	NA	671,788	-7,007,601	uc003omd.2	chr6:36358329-36359546	NA	NA	NA	NA	NA	NA	NA	NA
PXYLP1	NA	NA	NA	NA	NA	NA	NA	NA	NA	368,773	-5,693,356	uc003etr.3	chr3:141012048-141013486
PYCARD	606838	NA	NA	NA	NA	NA	NA	NA	NA	1163,57	-11,976,28	uc002ebm.3	chr16:31212807-31212905
PYGL	613741	741,577	-7,244,696	uc001wyu.3	chr14:51371935-51372109	NA	NA	NA	NA	1620,61	-9,626,832	uc001wyu.3	chr14:51371935-51372109
PYROXD2	NA	NA	NA	NA	NA	NA	NA	NA	NA	220,033	-4,424,258	uc010qpe.2	chr10:100154759-100154948
PZP	176420	500,401	-1,338,685	uc001qvl.3	chr12:9301436-9301567	787,293	-2,601,649	uc001qvl.3	chr12:9301436-9301567	1832,25	-3,320,483	uc001qvl.3	chr12:9301436-9301567
QDPR	612676	NA	NA	NA	NA	NA	NA	NA	NA	830,768	-6,996,416	uc003gpd.3	chr4:17488016-17488753
QRICH1	NA	1168,95	-11,902,126	uc010hka.3	chr3:49067142-49067884	788,841	-8,853,02	uc010hka.3	chr3:49067142-49067884	NA	NA	NA	NA
QSER1	NA	NA	NA	NA	NA	NA	NA	NA	NA	337,217	-8,540,432	uc001mtv.3	chr11:32998021-33001814
R3HCC1	NA	NA	NA	NA	NA	270,906	-6,066,948	uc003xdf.3	chr8:23153611-23153792	NA	NA	NA	NA
RAB10	612672	485,587	-4,048,622	uc002rgv.3	chr2:26357891-26360323	NA	NA	NA	NA	NA	NA	NA	NA
RAB11FIP2	608599	NA	NA	NA	NA	1177,41	-9,540,304	uc001ldi.2	chr10:119764427-119768508	NA	NA	NA	NA
RAB14	612673	NA	NA	NA	NA	240,707	-5,610,86	uc004bhc.3	chr9:123940415-123943673	NA	NA	NA	NA
RAB25	612942	586,088	-4,231,258	uc001fnc.3	chr1:156040079-156040295	NA	NA	NA	NA	NA	NA	NA	NA
RAB28	612994	979,411	-11,941,848	uc003gmt.2	chr4:13369347-13370274	NA	NA	NA	NA	482,096	-4,742,365	uc003gmt.2	chr4:13369347-13370274
RAB29	603949	NA	NA	NA	NA	485,353	-6,523,898	uc001hde.4	chr1:205737114-205739469	419,121	-6,805,075	uc001hde.4	chr1:205737114-205739469
RAB32	612906	NA	NA	NA	NA	670,995	-8,732,021	uc003qln.1	chr6:146875742-146876086	NA	NA	NA	NA
RAB33A	300333	NA	NA	NA	NA	264,009	-5,204,762	uc004evl.3	chrX:129318715-129318844	NA	NA	NA	NA
RAB33B	605950	619,82	-9,849,871	uc003lhw.3	chr4:140394281-140397069	NA	NA	NA	NA	NA	NA	NA	NA
RAB38	606281	NA	NA	NA	NA	768,714	-7,189,877	uc001pcj.2	chr11:87846415-87847155	NA	NA	NA	NA
RAB3C	612829	NA	NA	NA	NA	535,044	-8,963,511	uc003jrp.3	chr5:58147179-58147406	839,769	-5,925,835	uc003jrp.3	chr5:58147179-58147406
RAB3GAP1	602536	NA	NA	NA	NA	NA	NA	NA	NA	372,793	-4,530,498	uc002tuj.3	chr2:135926352-135928279
RAB3GAP2	609275	NA	NA	NA	NA	510,41	-6,523,898	uc010pum.1	chr1:220382749-220383720	NA	NA	NA	NA
RAB6B	615852	876,21	-4,342,808	uc003epy.3	chr3:133543080-133547631	NA	NA	NA	NA	NA	NA	NA	NA
RAB6C	612909	1735,93	-16,591,35	uc002lpx.1	chr2:130738454-130740311	803,332	-4,941,699	uc002lpx.1	chr2:130738454-130740311	NA	NA	NA	NA
RAB9A	300284	NA	NA	NA	NA	NA	NA	NA	NA	431,328	-5,280,409	uc004cvm.3	chrX:13727472-13727944
RABEP1	603616	NA	NA	NA	NA	1291,81	-7,876,476	uc002gbi.3	chr17:5239828-5239985	NA	NA	NA	NA
RABGAP1L	609238	924,512	-2,6387	uc001giw.3	chr1:174517194-174517699	296,683	-4,630,178	uc001giw.3	chr1:174514090-174515050	310,248	-2,893,792	uc001giw.3	chr1:174927043-174927327
RABIF	603417	434,7	-6,365,482	uc001gyi.3	chr1:202847410-202850105	NA	NA	NA	NA	NA	NA	NA	NA
RABL2A	605412	378,984	-5,521,81	uc002khn.4	chr2:114399707-114400975	491,225	-5,970,035	uc002khn.4	chr2:114400767-114400975	1181,34	-13,232,776	uc002khn.4	chr2:114400767-114400975
RABL3	NA	NA	NA	NA	NA	368,387	-6,034,115	uc003edix.3	chr3:120405528-120408669	NA	NA	NA	NA
RAC1	602048	NA	NA	NA	NA	799,744	-6,136,854	uc003spw.3	chr7:6442078-6443598	NA	NA	NA	NA
RAC3	602050	303,231	-7,784,229	uc002kdf.3	chr17:79991706-79992080	NA	NA	NA	NA	NA	NA	NA	NA
RACGAP1	604980	NA	NA	NA	NA	1363,54	-8,093,843	uc001rvs.2	chr12:50382945-50384050	NA	NA	NA	NA
RAD1	603153	NA	NA	NA	NA	2201,25	-19,377,118	uc003jliw.3	chr5:34905366-34908869	NA	NA	NA	NA
RAD17	603139	NA	NA	NA	NA	698,803	-7,177,67	uc003jwg.3	chr5:68710120-68710630	NA	NA	NA	NA
RAD51AP1	603070	NA	NA	NA	NA	1188	-7,120,424	uc001qmu.3	chr12:4668160-4669213	800,858	-8,471,614	uc001qmu.3	chr12:4668160-4669213
RAD52	600392	637,551	-9,163,282	uc001qis.1	chr12:1021255-1022556	NA	NA	NA	NA	NA	NA	NA	NA
RAE1	603343	NA	NA	NA	NA	1053,31	-7,969,055	uc010gis.1	chr20:55950152-55950408	NA	NA	NA	NA
RAET1E	609243	NA	NA	NA	NA	283,971	-6,156,827	uc003qni.3	chr6:150204511-150205623	NA	NA	NA	NA
RAG2	179616	NA	NA	NA	NA	1581,46	-13,407,261	uc001mwv.4	chr11:36613493-36614134	327,484	-4,026,644	uc001mwv.4	chr11:36613493-36614134

Table 1

RA141	606586	423.548	-8.479352	uc003jir.3	chr5:34830871-34832717	992.399	-6.706005	uc003jir.3	chr5:34830871-34832717	NA	NA	NA	NA
RALA	179550	NA	NA	NA	NA	1128.92	-13.514866	uc003lnd.3	chr7:39745845-39747723	NA	NA	NA	NA
RALBP1	605801	NA	NA	NA	NA	279.387	-4.01076	uc002kob.3	chr18:9535936-9538106	NA	NA	NA	NA
RALGAP1	608864	1041.83	-7.78228	uc001wli.3	chr14:36007556-36008896	NA	NA	NA	NA	NA	NA	NA	NA
RALGAP2	NA	NA	NA	NA	NA	236.983	-4.038807	uc002wry.3	chr20:20370272-20373742	NA	NA	NA	NA
RALGAPB	NA	NA	NA	NA	NA	NA	NA	NA	NA	591.834	-6.166166	uc002ja.1	chr20:37175094-37176749
RALGPS2	NA	208.373	-5.450553	uc001gly.1	chr1:178848132-178848923	NA	NA	NA	NA	624.746	-7.770538	uc001gly.1	chr1:178848132-178848923
RALYL	614648	263.509	-5.239969	uc003ycq.4	chr8:85833147-85834078	NA	NA	NA	NA	NA	NA	NA	NA
RANBP1	601180	1328.77	-11.441149	uc011ahl.1	chr22:20113136-20113711	1368.56	-7.888697	NA	NA	971.615	-6.621777	uc011ahl.1	chr22:20113136-20113711
RANBP7	606141	572.173	-3.064965	uc003maw.3	chr5:170336803-170338342	995.043	-5.357335	uc003maw.3	chr5:170336803-170338342	235.415	-8.544508	uc003maw.3	chr5:170336803-170338342
RANBP9	603854	338.53	-4.792728	uc003nba.3	chr6:13621730-13622593	489.043	-9.27527	uc003nba.3	chr6:13621730-13622593	NA	NA	NA	NA
RAP1B	179530	394.081	-7.230876	uc010sie.2	chr12:69050968-69051493	NA	NA	NA	NA	NA	NA	NA	NA
RAP2A	179540	NA	NA	NA	NA	NA	NA	NA	NA	507.34	-7.242086	uc001vnd.3	chr13:98116697-98120252
RAP2B	179541	496.544	-7.548112	uc003ezr.3	chr3:152881035-152886263	NA	NA	NA	NA	NA	NA	NA	NA
RAPGEF3	606057	483.012	-3.916108	uc001rqa.3	chr7:22157908-22162023	387.764	-4.709328	uc001rqa.3	chr7:22157908-22162023	NA	NA	NA	NA
RAPGEF5	609527	942.179	-8.265161	uc003svg.3	chr7:22157908-22162023	NA	NA	NA	NA	NA	NA	NA	NA
RAPGEF6	610499	238.938	-8.140971	uc010jdk.3	chr5:130799308-130799729	1417.73	-13.566523	uc003kvm.2	chr5:130799308-130799729	NA	NA	NA	NA
RAPH1	609035	970.304	-10.602931	uc002val.3	chr2:204306357-204309572	NA	NA	NA	NA	286.641	-8.692233	uc002vad.3	chr2:204298539-204304159
RARB	180220	NA	NA	NA	NA	NA	NA	NA	NA	344.487	-6.075257	uc011awl.2	chr3:25638108-25639422
RASA2	601589	494.762	-4.542236	uc011bnc.1	chr3:141305720-141306804	NA	NA	NA	NA	NA	NA	NA	NA
RASAL3	616561	NA	NA	NA	NA	368.69	-4.201256	uc002nbe.2	chr19:15562438-15562805	NA	NA	NA	NA
RASGEF1B	614532	NA	NA	NA	NA	700.32	-7.511695	uc003hmk.3	chr4:82372047-82377609	NA	NA	NA	NA
RASSF5	607020	NA	NA	NA	NA	973.848	-1.249445	uc001hec.1	chr1:206758082-206762606	633.17	-7.067342	uc001hec.1	chr1:206758082-206762606
RASSF9	610383	NA	NA	NA	NA	734.605	-8.436583	uc001faf.1	chr12:86198331-86198479	NA	NA	NA	NA
RAVER1	609950	1194.39	-10.155889	uc002mmz.3	chr19:10426889-10428149	NA	NA	NA	NA	NA	NA	NA	NA
RB1	614041	NA	NA	NA	NA	517.074	-6.819136	uc001vcb.3	chr13:49054208-49056026	NA	NA	NA	NA
RBBP4	602923	NA	NA	NA	NA	359.039	-5.316018	uc001bvr.3	chr1:33145307-33151812	735.557	-8.251079	uc001bvr.3	chr1:33145307-33151812
RBBP5	600697	214.025	-7.200108	uc010prd.2	chr1:205055270-205057914	379.804	-6.707422	uc010prd.2	chr1:205055270-205057914	NA	NA	NA	NA
RBBP7	300825	NA	NA	NA	NA	1235.45	-7.803934	uc004cxs.2	chrX:16862775-16863157	NA	NA	NA	NA
RBBP9	602908	NA	NA	NA	NA	207.624	-5.332478	uc002wty.3	chr20:18467188-18470407	NA	NA	NA	NA
RBF1	591.153	7.288123	-7.288123	uc002lms.3	chr18:77806156-77810652	NA	NA	NA	NA	216.828	-3.544881	uc002lms.3	chr18:77806156-77810652
RBKS	611132	212.049	-5.827729	uc010yng.2	chr2:28032166-28032846	NA	NA	NA	NA	NA	NA	NA	NA
RBMT10	300080	NA	NA	NA	NA	NA	NA	NA	NA	430.701	-5.343295	uc004dhf.3	chrX:47045999-47046214
RBMT12	607179	NA	NA	NA	NA	NA	NA	NA	NA	442.533	-12.548489	uc002xdq.3	chr20:34236847-34240445
RBMT12B	NA	NA	NA	NA	NA	1157.74	-9.01972	uc003yfr.3	chr8:94743731-94745632	NA	NA	NA	NA
RBMT14	612409	739.718	-5.041005	uc001oil.3	chr11:66394140-66397397	NA	NA	NA	NA	NA	NA	NA	NA
RBMT20	613171	NA	NA	NA	NA	NA	NA	NA	NA	870.367	-7.567188	uc001kzf.2	chr10:112595737-112599227
RBMT22	612430	NA	NA	NA	NA	295.39	-6.281993	uc003lnt.3	chr5:150070352-150071312	337.039	-7.862267	uc003lnt.3	chr5:150070352-150071312
RBMT24	680.826	NA	-3.340406	uc003nby.4	chr6:17291987-17294099	NA	NA	NA	NA	515.78	-5.921955	uc011div.2	chr6:17292364-17294099
RBMT3	300027	NA	NA	NA	NA	NA	NA	NA	NA	232.103	-6.420261	uc004dhf.2	chrX:48435853-48439553
RBMT33	NA	762.281	-5.548884	uc010lqk.1	chr7:155567736-155574179	NA	NA	NA	NA	NA	NA	NA	NA
RBMT34	NA	1616.29	-7.047109	uc001hwn.3	chr1:235294498-235295027	771.05	-5.964326	uc001hwn.3	chr1:235294498-235295027	NA	NA	NA	NA
RBMT38	612428	NA	NA	NA	NA	353.633	-4.520683	uc010zji.2	chr20:55982903-55984386	NA	NA	NA	NA
RBMT39	604739	NA	NA	NA	NA	NA	NA	NA	NA	748.356	-6.69328	uc002xdz.3	chr20:34291531-34292402
RBMT4	602571	NA	NA	NA	NA	549.352	-7.536437	uc010rpj.2	chr11:66433437-66435858	NA	NA	NA	NA
RBMT41	NA	674.145	-5.486222	uc004emz.3	chrX:106309533-106310756	446.37	-7.156665	uc004emny.2	chrX:106305118-106308983	NA	NA	NA	NA
RBMT48	NA	640.063	-4.514284	uc003ulz.3	chr7:92166252-92166823	NA	NA	NA	NA	NA	NA	NA	NA
RBMT6	606886	1119.11	-7.424622	uc003cyc.3	chr3:50114587-50114885	1570.93	-13.68876	NA	NA	987.571	-8.557262	uc003cyc.3	chr3:50114587-50114685
RBMT7	612413	714.307	-7.497925	uc001pov.3	chr11:114278530-114279635	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

RBMB6A	605313	NA	NA	NA	NA	806.597	-7.502817	uc001ent.2	chr1:145509212-145513535	NA	NA	NA	NA
RBMS1	602310	NA	NA	NA	NA	595.931	-6.796921	uc002ubi.4	chr2:161128662-161131275	NA	NA	NA	NA
RBMX	300199	NA	NA	NA	NA	663.112	-7.961674	uc004fad.1	chrX:135954427-135957218	NA	NA	NA	NA
RBMX2	NA	NA	NA	NA	NA	496.261	-5.902194	uc004devt.3	chrX:129546823-129547317	NA	NA	NA	NA
RBMY1B	NA	NA	NA	NA	NA	NA	NA	NA	NA	1767.71	-12.633257	uc004fu0.4	chrY:23687395-23687672
RBP1	180260	NA	NA	NA	NA	660.631	-10.800286	uc011bmny.2	chr3:139245247-139246148	NA	NA	NA	NA
RBPJ	147183	NA	NA	NA	NA	659.736	-6.91876	uc011bxt.2	chr4:26431733-26432079	NA	NA	NA	NA
RBPJL	616104	NA	NA	NA	NA	NA	NA	NA	NA	473.188	-4.702568	uc002xns.3	chr20:43945600-43946464
RBPMS2	NA	NA	NA	NA	NA	NA	NA	NA	NA	513.185	-8.812308	uc002anq.3	chr15:65032095-65033199
RBX1	603814	NA	NA	NA	NA	593.644	-9.108675	uc003azrk.3	chr22:41368493-41369019	NA	NA	NA	NA
RC3H2	615231	NA	NA	NA	NA	580.844	-5.698038	uc004bne.4	chr9:125616024-125616152	NA	NA	NA	NA
RCAN2	604876	480.407	-6.423466	uc003oyb.2	chr6:46188467-46190877	NA	NA	NA	NA	NA	NA	NA	NA
RCL1	611405	NA	NA	NA	NA	411.828	-5.341638	uc003zls.2	chr9:4860276-4861064	NA	NA	NA	NA
RCN1	602735	NA	NA	NA	NA	NA	NA	NA	NA	346.196	-9.037077	uc021qfp.1	chr11:32126019-32127272
RCOR3	NA	383.826	-7.3276	uc001hie.3	chr1:211486337-211486655	333.019	-4.179919	uc001hie.3	chr1:211486337-211486655	NA	NA	NA	NA
RCSD1	610579	NA	NA	NA	NA	NA	NA	NA	NA	495.996	-5.807569	uc001igem.3	chr1:167673934-167675486
RDH10	607599	NA	NA	NA	NA	537.051	-7.889299	uc003xzi.3	chr8:74235272-74237520	1020.15	-6.960205	uc003xzi.3	chr8:74235272-74237520
RDH11	607849	NA	NA	NA	NA	NA	NA	NA	NA	990.092	-8.362002	uc001xjv.4	chr14:68143519-68145037
RDH16	NA	NA	NA	NA	NA	934.489	-7.622858	uc001smli.4	chr12:57345216-57345812	NA	NA	NA	NA
RDM1	612896	NA	NA	NA	NA	NA	NA	NA	NA	1742.3	-13.260051	uc002Hkg.4	chr17:34245085-34245345
RDX	179410	762.904	-7.640571	uc001pls.3	chr11:110100166-110102593	833.87	-5.256722	uc009xyy.3	chr11:110066286-110068890	NA	NA	NA	NA
RECQL5	603781	NA	NA	NA	NA	301.009	-4.764601	uc002jcl.4	chr17:73622925-73623501	742.583	-4.497177	uc002jot.4	chr17:73622925-73623501
REEP1	609139	NA	NA	NA	NA	NA	NA	NA	NA	334.982	-4.049061	uc002srh.4	chr2:86441120-86444222
REG3A	167805	NA	NA	NA	NA	NA	NA	NA	NA	344.667	-5.036692	uc002sod.2	chr2:79384132-79384351
REG4	609846	1084.84	-5.137012	uc001eif.3	chr1:120336641-120337240	NA	NA	NA	NA	NA	NA	NA	NA
RELA	164014	NA	NA	NA	NA	384.897	-4.829984	uc001afe.2	chr11:65421072-65423057	NA	NA	NA	NA
RELL2	611213	NA	NA	NA	NA	NA	NA	NA	NA	483.207	-5.801316	uc003ilh.3	chr5:141020238-141020631
RELN	600514	NA	NA	NA	NA	508.466	-4.773767	uc010li.3	chr7:10312231-103113258	NA	NA	NA	NA
REP15	610848	510.709	-7.671178	uc001rig.1	chr12:27850207-27850566	NA	NA	NA	NA	NA	NA	NA	NA
REPIN1	NA	NA	NA	NA	NA	770.049	-7.070446	uc003whnd.2	chr7:150070035-150071133	NA	NA	NA	NA
REPS1	614825	NA	NA	NA	NA	NA	NA	NA	NA	634.614	-11.799067	uc003dig.4	chr6:139225620-139226200
RESE	605226	782.156	-8.265219	uc001apd.3	chr1:8412464-8415146	NA	NA	NA	NA	497.632	-7.123806	uc001apd.3	chr1:8412464-8415146
RERGL	NA	NA	NA	NA	NA	848.769	-16.515193	uc001rdq.3	chr12:18233803-18234124	NA	NA	NA	NA
RET	164761	NA	NA	NA	NA	989.985	-5.931364	uc001jak.1	chr10:43622203-43622952	NA	NA	NA	NA
REV1	606134	1265.05	-14.231679	uc002iac.3	chr2:100016938-100017703	NA	NA	NA	NA	NA	NA	NA	NA
REX01	609614	1292.71	-16.915306	uc010dsq.3	chr19:1815245-1816064	1296.76	-14.725383	uc010dsq.3	chr19:1815245-1816064	1009.94	-9.22389	uc010dgs.1	chr19:1815542-1815678
RF03	604005	918.039	-2.529366	uc010ted.1	chr13:34409394-34410019	1633.09	-8.71789	uc001uuz.3	chr13:34410433-34411644	636.543	-3.93454	uc001uuz.3	chr13:34410433-34411644
RF04	102577	732.76	-7.659927	uc003fzr.3	chr3:186507682-186507757	NA	NA	NA	NA	NA	NA	NA	NA
RFK	613010	NA	NA	NA	NA	1629.29	-22.203425	uc004akd.2	chr9:79000433-79002314	667.31	-7.647025	uc004akd.2	chr9:79000433-79002314
RFPL2	605969	NA	NA	NA	NA	NA	NA	NA	NA	1010.99	-5.280024	uc003ame.3	chr22:32586422-32586758
RFPL3	605970	2110.52	-13.613852	uc010gwn.3	chr22:32756820-32757148	NA	NA	NA	NA	NA	NA	NA	NA
RFT1	611908	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
RFWD2	608067	NA	NA	NA	NA	505.743	-7.236318	uc009www.2	chr1:175913967-175914288	NA	NA	NA	NA
RFX4	603958	NA	NA	NA	NA	761.14	-11.810153	uc001tlr.3	chr12:107155248-107156582	NA	NA	NA	NA
RFX5	601863	779.092	-8.953047	uc001exv.1	chr1:151313116-151314661	330.399	-4.956776	uc001exv.1	chr1:151313116-151314661	NA	NA	NA	NA
RFX6	612659	1210.38	-8.953702	uc003pxm.3	chr6:117252670-117253326	NA	NA	NA	NA	NA	NA	NA	NA
RFX7	612660	NA	NA	NA	NA	570.314	-8.329597	uc010bln.3	chr15:56382731-56385542	NA	NA	NA	NA
RFXAP	601861	611.42	-6.246403	uc001uvu.1	chr13:37401891-37403740	NA	NA	NA	NA	1481.05	-13.293995	uc001uvu.1	chr13:37401891-37403740
RGL4	612214	525.11	-6.142766	uc002zro.3	chr22:24041301-24041363	565.967	-5.407299	uc002zrn.3	chr22:24041071-24041363	884.654	-7.046384	uc002zrx.3	chr22:24041156-24041363

Table 1

RGMB1	612687	1064.84	-10.101658	uc003knc.3	chr5:98129458-98132198	913.246	-8.841809	uc003knc.3	chr5:98129458-98132198	1031.88	-13.577719	uc003kmb.2	chr5:98115847-98116889
RGPD1	612704	NA	NA	NA	NA	1402.86	-9.015155	uc010lcv.3	chr2:87239671-87241099	NA	NA	NA	NA
RGPD4	612707	NA	NA	NA	NA	920.055	-6.870155	uc010ywk.2	chr2:108507188-108509000	477.774	-4.252805	uc010ywk.2	chr2:108507188-108509000
RGSI1	600323	937.972	-8.800242	uc010pou.1	chr1:192547582-192548085	NA	NA	NA	NA	NA	NA	NA	NA
RGSI10	602856	NA	NA	NA	NA	NA	NA	NA	NA	570.781	-7.362308	uc001lee.3	chr10:121259339-121259624
RGSI12	602512	364.498	-3.872909	uc003ggx.1	chr4:3344790-3344916	786.327	-6.681777	uc010lcs.1	chr4:3419418-3419984	1097.08	-5.819383	uc010lcs.1	chr4:3430071-3430325
RGSI18	607192	1176.63	-11.464826	uc001psg.3	chr1:192153685-192154945	NA	NA	NA	NA	NA	NA	NA	NA
RGSI2	600861	539.972	-4.731056	uc001gsl.3	chr1:192780727-192781407	NA	NA	NA	NA	NA	NA	NA	NA
RGSI20	607193	522.94	-9.592224	uc003xrp.3	chr8:54871019-54871863	NA	NA	NA	NA	NA	NA	NA	NA
RHBDL2	608962	NA	NA	NA	NA	1778.35	-15.523203	uc010lcn.1	chr1:39351479-39352290	NA	NA	NA	NA
RHBDL3	NA	630.04	-7.174341	uc002hhe.1	chr17:30648249-30651680	213.565	-4.45596	uc002hhe.1	chr17:30648249-30651680	NA	NA	NA	NA
RHO	180380	697.092	-7.042919	uc003emil.3	chr3:129252562-129254187	NA	NA	NA	NA	NA	NA	NA	NA
RHOBTB3	607353	207.865	-7.679003	uc003kl.3	chr5:95067876-95068453	984.613	-5.945958	uc003kl.3	chr5:95067876-95068453	507.307	-9.104608	uc003kl.1	chr5:95091519-95091797
RHOE	NA	NA	NA	NA	NA	280.799	-6.726374	uc001ubd.4	chr12:122218393-122218735	NA	NA	NA	NA
RHOT1	613888	725.98	-4.52644	uc002hgv.3	chr17:30535333-30536757	NA	NA	NA	NA	678.506	-11.387724	uc002hgv.3	chr17:30535333-30536757
RIC3	610509	411.224	-8.969225	uc001mgf.4	chr11:8161208-8161477	NA	NA	NA	NA	NA	NA	NA	NA
RIC8B	609147	421.308	1.043569	uc001llw.3	chr12:107264758-107265251	NA	NA	NA	NA	316.244	-2.442181	uc001llw.3	chr12:107279794-107283094
RICTOR	609022	1019.59	-9.44363	uc003jlo.2	chr5:38938022-38942405	863.742	-9.727569	uc003jlo.2	chr5:38938022-38942405	NA	NA	NA	NA
RIF1	608952	655.48	-5.992434	uc002lcn.3	chr2:152331586-152333860	NA	NA	NA	NA	NA	NA	NA	NA
RIMKLB	614054	NA	NA	NA	NA	NA	NA	NA	NA	627.11	-5.585072	uc001lqux.2	chr12:8926381-8929787
RIMS2	606630	877.763	-7.893051	uc003ykt.3	chr8:104987739-104988481	NA	NA	NA	NA	NA	NA	NA	NA
RINT1	610089	NA	NA	NA	NA	246.391	-6.992598	uc003vda.1	chr7:105207759-105208124	620.002	-5.839065	uc003vda.1	chr7:105207759-105208124
RIOK1	NA	288.4	-4.355113	uc003mxn.3	chr6:7417675-7418270	766.861	-8.583916	uc003mxn.3	chr6:7417675-7418270	NA	NA	NA	NA
RIOK2	NA	NA	NA	NA	NA	1115.7	-3.213421	uc003kmz.3	chr5:96496571-96498764	857.957	-7.927737	uc003kmz.3	chr5:96496571-96498764
RIOK3	603579	NA	NA	NA	NA	445.841	-7.893837	uc002kui.4	chr18:21061244-21063099	NA	NA	NA	NA
RIPK2	603455	1831.63	-13.894201	uc003yee.3	chr8:90802645-90803292	NA	NA	NA	NA	539.817	-6.660883	uc003yee.3	chr8:90802645-90803292
RIPK4	605706	NA	NA	NA	NA	417.755	-4.926379	uc002yzn.1	chr21:43159529-43160997	430.599	-5.654323	uc002yzn.1	chr21:43159529-43160997
RIPPL1	609892	NA	NA	NA	NA	687.399	-5.491844	uc010gnd.3	chr21:38390599-38391958	NA	NA	NA	NA
RLF	180610	NA	NA	NA	NA	NA	NA	NA	NA	452.541	-5.905764	uc001cfc.4	chr1:40706120-40706593
RMND1	614917	NA	NA	NA	NA	554.907	-8.203878	uc003qoj.3	chr6:151757370-151757566	NA	NA	NA	NA
RND3	602924	317.088	-5.723566	uc010zlv.2	chr2:151325757-151326505	213.982	-3.09917	uc002kxe.3	chr2:151324707-151326500	NA	NA	NA	NA
RNF10	615998	757.776	-6.568832	uc001typ.4	chr12:121014470-121015397	930.284	-12.190837	uc001typ.4	chr12:121014470-121015397	NA	NA	NA	NA
RNF121	NA	NA	NA	NA	NA	1448.03	-10.967688	uc009yst.3	chr11:71707241-71708643	NA	NA	NA	NA
RNF14	605675	415.534	-5.170137	uc003lly.3	chr5:141367356-141369856	NA	NA	NA	NA	NA	NA	NA	NA
RNF141	616641	NA	NA	NA	NA	473.616	-6.265867	uc001mis.1	chr11:10533225-10536462	NA	NA	NA	NA
RNF144A	NA	NA	NA	NA	NA	490.442	-4.679879	uc002qys.3	chr2:7179892-7184309	NA	NA	NA	NA
RNF145	NA	236.137	-4.387198	uc011ddv.2	chr5:158584417-158585677	NA	NA	NA	NA	NA	NA	NA	NA
RNF149	NA	NA	NA	NA	NA	NA	NA	NA	NA	495.621	-6.021172	uc002taz.2	chr2:101892063-101893699
RNF168	612688	476.404	-8.671134	uc003lwd.3	chr3:196195657-196198689	NA	NA	NA	NA	NA	NA	NA	NA
RNF170	614649	492.566	-5.859185	uc011lxx.2	chr8:42704780-42705933	NA	NA	NA	NA	NA	NA	NA	NA
RNF175	NA	774.894	-11.078049	uc003int.3	chr4:154631312-154631520	NA	NA	NA	NA	547.697	-6.399226	uc003int.3	chr4:154631312-154631520
RNF183	NA	NA	NA	NA	NA	NA	NA	NA	NA	1510.46	-12.412116	uc004hgz.3	chr9:116059373-116059885
RNF185	NA	NA	NA	NA	NA	722.478	-4.952018	uc003akb.3	chr22:31600573-31603005	NA	NA	NA	NA
RNF187	613754	468.223	-8.115257	uc001thb.3	chr1:228681587-228683889	NA	NA	NA	NA	NA	NA	NA	NA
RNF19B	610872	NA	NA	NA	NA	NA	NA	NA	NA	986.583	-8.386903	uc010oho.2	chr1:33402050-33402406
RNF207	NA	698.237	-8.324887	uc001amf.1	chr1:6267983-6268366	NA	NA	NA	NA	NA	NA	NA	NA
RNF212	612041	NA	NA	NA	NA	263.264	-6.773869	uc003gci.3	chr4:1065266-1066803	654.996	-3.457817	uc003gci.3	chr4:1065266-1066661
RNF219	615906	558.464	-7.133526	uc001vkw.1	chr13:79188421-79189714	NA	NA	NA	NA	NA	NA	NA	NA
RNF24	612489	NA	NA	NA	NA	NA	NA	NA	NA	660.131	-7.761294	uc002whh.2	chr20:3912069-3914709

Table 1

RNF31	612487	435.423	-5.675879	uc001wml.1	chr14:24629783-24630547	NA	NA	NA	NA	507.104	-7.167761	uc001wml.1	chr14:24629783-24630547
RNF38	612488	NA	NA	NA	NA	NA	NA	NA	NA	1273.22	-12.629689	uc003zzh.3	chr9:36336399-36339748
RNF39	607524	NA	NA	NA	NA	420.996	-7.229661	uc003npd.3	chr6:30038043-30038887	NA	NA	NA	NA
RNF40	607700	NA	NA	NA	NA	942.027	-7.317469	uc010vic.1	chr16:30783611-30784104	NA	NA	NA	NA
RNF41	NA	NA	NA	NA	NA	NA	NA	NA	NA	581.52	-8.0057	uc021qyz.1	chr12:56596288-56600230
RNF5P1	NA	1367.67	-12.798826	uc003xly.3	chr8:39457693-39458238	NA	NA	NA	NA	1032.19	-5.410062	uc003xly.3	chr8:38457693-38458238
RNF6	604242	NA	NA	NA	NA	547.508	-6.014946	uc001uqo.3	chr13:26786905-26787960	NA	NA	NA	NA
RNLS	609360	1066.88	-13.215476	uc010qms.1	chr10:89892057-89892287	NA	NA	NA	NA	681.597	-18.696989	uc010qms.1	chr10:89892057-89892287
RNPC3	NA	843.2	-3.62816	uc010oul.1	chr1:104095896-104096306	NA	NA	NA	NA	1684.74	-6.806305	uc010oul.1	chr1:104095896-104096306
ROB03	608630	454.34	-4.826271	uc010saq.2	chr11:124747716-124748306	NA	NA	NA	NA	NA	NA	NA	NA
ROR1	602336	625.422	-5.537733	uc001dbi.4	chr1:64608342-64609052	NA	NA	NA	NA	NA	NA	NA	NA
RP1	603937	NA	NA	NA	NA	845.425	-8.128276	uc003xsd.1	chr8:55542914-55543394	NA	NA	NA	NA
RP1L1	608581	NA	NA	NA	NA	899.695	-6.328448	uc003wic.3	chr8:10463860-10464404	NA	NA	NA	NA
RPAP2	611476	NA	NA	NA	NA	1236.01	-8.378721	uc001ldt.2	chr1:92852569-92853732	NA	NA	NA	NA
RPE65	180069	NA	NA	NA	NA	587.041	-4.963536	uc001dei.1	chr1:68894507-68895458	318.414	-3.828765	uc001dei.1	chr1:68894507-68895458
RPGR	312610	1241.28	-8.844338	uc004deb.3	chrX:38128423-38128878	NA	NA	NA	NA	1214.01	-1.604151	uc004deb.3	chrX:38128423-38128878
RPGRIPL1	610937	NA	NA	NA	NA	NA	NA	NA	NA	934.353	-9.298945	uc002eho.4	chr16:53633818-53635987
RPL10	312173	NA	NA	NA	NA	979.39	-5.410864	uc004fko.2	chrX:153629365-153630680	NA	NA	NA	NA
RPL13	113703	NA	NA	NA	NA	924.008	-0.351779	uc002fmm.2	chr16:89629451-89633237	NA	NA	NA	NA
RPL19	180466	855.395	-7.638152	uc002hmq.1	chr17:37360902-37360980	NA	NA	NA	NA	NA	NA	NA	NA
RPL22L1	NA	479.601	-4.313187	uc003fnc.4	chr3:170582665-170584168	NA	NA	NA	NA	NA	NA	NA	NA
RPL23AP3	NA	806.158	-8.322818	uc010yat.1	chr2:54756876-54756978	NA	NA	NA	NA	504.054	-8.395207	NA	NA
RPL27A	603637	496.175	-8.527996	uc001mgs.4	chr11:8707354-8711419	NA	NA	NA	NA	NA	NA	NA	NA
RPL3	604163	NA	NA	NA	NA	NA	NA	NA	NA	224.702	-6.837667	uc003axh.3	chr22:39708887-39708944
RPL34	NA	NA	NA	NA	NA	NA	NA	NA	NA	374.859	-7.773146	uc003hyz.3	chr4:10955177-109551639
RPL35A	180468	542.111	-5.730053	uc003fyr.3	chr3:197682645-197682721	NA	NA	NA	NA	NA	NA	NA	NA
RPL37	604181	NA	NA	NA	NA	NA	NA	NA	NA	715.523	-13.025816	uc003jme.1	chr5:40831430-40832605
RPL39L	607547	414.509	-5.958674	uc003fre.1	chr3:186838741-186838932	1509.37	-17.470803	uc003fre.1	chr3:186838741-186838932	NA	NA	NA	NA
RPL4	180479	NA	NA	NA	NA	NA	NA	NA	NA	448.635	-9.750265	uc010ujq.2	chr15:66793346-66793704
RPL41	613315	433.943	-6.437403	uc001sln.3	chr12:56511309-56511616	NA	NA	NA	NA	NA	NA	NA	NA
RPL5	603634	NA	NA	NA	NA	NA	NA	NA	NA	604.405	-11.91061	uc001doz.3	chr1:93307423-93307481
RPL7	604166	831.644	-10.184897	uc003zqg.3	chr8:74202874-74202940	NA	NA	NA	NA	NA	NA	NA	NA
RPL7L1	NA	NA	NA	NA	NA	668.086	-9.304783	uc003oss.2	chr6:42854898-42855668	820.468	-5.426185	uc003csq.1	chr6:42854203-42854731
RPS21	180477	NA	NA	NA	NA	NA	NA	NA	NA	436.778	-6.838519	uc002ycr.3	chr20:60963523-60963576
RPS24	602412	NA	NA	NA	NA	558.105	-4.201959	uc001jzp.3	chr10:79800373-79800473	NA	NA	NA	NA
RPS27L	612055	NA	NA	NA	NA	467.441	-6.141367	uc002aly.3	chr15:63445539-63446230	NA	NA	NA	NA
RPS28	603685	867.325	-6.264164	uc002mjn.3	chr19:8387156-8387280	NA	NA	NA	NA	593.221	-7.557419	uc002mjn.3	chr19:8387156-8387280
RPS4X	312760	NA	NA	NA	NA	687.394	-5.697381	uc004ear.3	chrX:71492453-71492520	NA	NA	NA	NA
RPS6KA5	603607	1149.15	-7.878725	uc001xyt.3	chr14:91360319-91360750	NA	NA	NA	NA	NA	NA	NA	NA
RPS6KA6	300303	NA	NA	NA	NA	563.763	-5.510348	uc004eej.2	chrX:83313354-83319284	NA	NA	NA	NA
RPS6KC1	NA	NA	NA	NA	NA	676.487	-7.647649	uc001hkd.3	chr1:213445978-213446808	NA	NA	NA	NA
RPTOR	607130	266.911	-5.924138	uc002jys.3	chr17:78797028-78797422	NA	NA	NA	NA	NA	NA	NA	NA
RRAGA	612194	938.389	-12.466179	uc003znj.3	chr9:19050600-19051021	651.13	-7.768666	uc003znj.3	chr9:19050600-19051021	NA	NA	NA	NA
RRAS2	600098	446.211	-4.701466	uc021qec.1	chr11:14299466-14300882	533.477	-5.021064	uc021qec.1	chr11:14299466-14300882	NA	NA	NA	NA
RRN3P1	NA	NA	NA	NA	NA	312.436	-6.806895	uc010vbl.1	chr16:21807951-21808402	NA	NA	NA	NA
RRP15	611193	1309.46	-12.648148	uc001hij.3	chr1:218504434-218511325	NA	NA	NA	NA	NA	NA	NA	NA
RSBN1	615858	406.924	-7.648909	uc001edq.3	chr1:114304454-114308601	NA	NA	NA	NA	422.669	-3.615692	uc001edq.3	chr1:114304454-114308601
RSF1	608522	1265.01	-10.897865	uc001oym.3	chr11:77377274-77377961	NA	NA	NA	NA	NA	NA	NA	NA
RSL24D1	613262	NA	NA	NA	NA	955.686	-8.082955	uc002aen.3	chr15:55473512-55474349	NA	NA	NA	NA

Table 1

RSPH14	605663	NA	NA	NA	NA	278.26	-6.26861	uc010g1v.1	chr22:23475723-23476087	NA	NA	NA	NA
RSPH4A	612647	NA	NA	NA	NA	296.078	-4.894743	uc003pxe.2	chr6:116953605-116954148	NA	NA	NA	NA
RSP02	610575	717.903	-8.889672	uc003ymq.3	chr8:108911544-108913302	NA	NA	NA	NA	NA	NA	NA	NA
RSU1	179555	NA	NA	NA	NA	697.779	-4.627778	uc001iok.3	chr10:16632617-16635392	NA	NA	NA	NA
RTKN	602288	804.111	-5.912374	uc010flb.1	chr2:74658749-74659404	NA	NA	NA	NA	NA	NA	NA	NA
RTN3	604249	NA	NA	NA	NA	NA	NA	NA	NA	882.556	-7.125377	uc001nmx.3	chr11:63525674-63527363
RTN4RL1	610461	NA	NA	NA	NA	490.726	-6.418714	uc002fip.3	chr17:1837971-1839789	NA	NA	NA	NA
RTF4	609350	NA	NA	NA	NA	433.203	-5.382524	uc003frm.3	chr3:187089162-187089369	NA	NA	NA	NA
RTTN	610436	NA	NA	NA	NA	957.02	-10.813389	uc010tdqp.2	chr18:67671043-67671386	NA	NA	NA	NA
RUFY2	610328	489.684	-6.953858	uc001jpe.1	chr10:70153521-70153716	NA	NA	NA	NA	NA	NA	NA	NA
RUNC3B	NA	479.587	-7.640984	uc003ujb.3	chr7:87459346-87461613	462.956	-7.394517	uc003ujb.3	chr7:87459346-87461613	NA	NA	NA	NA
RUNK1	151385	299.247	-7.804626	uc010gmw.1	chr21:36205258-36206416	735.542	-2.010638	uc002yul.1	chr21:36169710-36170351	NA	NA	NA	NA
RUNK1T1	133435	NA	NA	NA	NA	NA	NA	NA	NA	602.431	-6.003529	uc010man.2	chr8:92957195-92972469
RUNK2	600211	NA	NA	NA	NA	NA	NA	NA	NA	602.809	-11.20612	uc010dvw.2	chr6:45515043-45518819
RUSC1	NA	NA	NA	NA	NA	227.402	-5.369505	uc001fkj.2	chr1:155300363-155300909	NA	NA	NA	NA
RWDD3	615875	972.633	-10.408398	uc009wdu.3	chr1:95712427-95712781	609.454	-3.093908	uc001drl.4	chr1:95712312-95712781	NA	NA	NA	NA
RWDD4	NA	1000.12	-14.884815	uc003lvt.1	chr4:184560789-184562588	NA	NA	NA	NA	NA	NA	NA	NA
RXFP1	606654	255.694	-4.215035	uc010lqj.2	chr4:159567496-159567833	NA	NA	NA	NA	NA	NA	NA	NA
RXFP2	606655	281.312	-4.603758	uc001uti.3	chr13:32376543-32377009	NA	NA	NA	NA	NA	NA	NA	NA
S100A11	603114	NA	NA	NA	NA	397.012	-6.040094	uc001ezn.3	chr1:152004982-152005137	NA	NA	NA	NA
S100A6	114110	NA	NA	NA	NA	NA	NA	NA	NA	553.916	-8.322051	uc001fbw.1	chr1:153507076-153507171
S100B	176990	NA	NA	NA	NA	769.586	-5.304445	uc002zju.1	chr21:48018531-48019275	NA	NA	NA	NA
SA41	104750	NA	NA	NA	NA	NA	NA	NA	NA	326.225	-4.129361	uc021qem.1	chr11:18291403-18291523
SA42	104751	NA	NA	NA	NA	NA	NA	NA	NA	333.692	-4.129361	uc009yhj.3	chr11:18259780-18261494
SAFB	602895	506.846	-7.134092	uc010xqj.2	chr19:55648069-5648303	NA	NA	NA	NA	NA	NA	NA	NA
SAFB2	608066	1288.88	-9.542092	uc002mcd.3	chr19:5587010-5587253	257.54	-7.202482	uc002mcd.3	chr19:5587010-5587253	NA	NA	NA	NA
SALL4	607343	NA	NA	NA	NA	NA	NA	NA	NA	737.856	-8.228353	uc002xwh.4	chr20:50400593-50400803
SAMDA4	610747	NA	NA	NA	NA	397.244	-7.243906	uc001xba.3	chr14:55169328-55170589	780.22	-3.77979	uc001xba.3	chr14:55169328-55170589
SAMD4B	NA	290.195	-4.956984	uc002olb.3	chr19:39874168-39875537	NA	NA	NA	NA	1479.77	-12.764074	uc002olb.3	chr19:39874168-39875537
SAMD8	611575	NA	NA	NA	NA	967.269	-11.914279	uc001jwx.2	chr10:76936451-76941881	NA	NA	NA	NA
SAMD9	610456	NA	NA	NA	NA	501.709	-5.264453	uc003umf.3	chr7:92728826-92730640	NA	NA	NA	NA
SAMD9L	611170	NA	NA	NA	NA	NA	NA	NA	NA	1613.06	-13.828282	uc003umh.1	chr7:92759368-92760529
SAMHD1	606754	NA	NA	NA	NA	NA	NA	NA	NA	575.593	-6.40661	uc002xgh.2	chr20:35520227-35521334
SAP130	609697	230.469	-5.654323	uc002lbn.2	chr2:128698791-128699579	NA	NA	NA	NA	NA	NA	NA	NA
SAP18	602949	NA	NA	NA	NA	489.555	-6.859768	uc001uns.3	chr13:21721482-21723224	1389.82	-10.887166	uc001uns.3	chr13:21721482-21723224
SAP30	603378	NA	NA	NA	NA	2271.44	-17.27085	uc003ltd.3	chr4:174298479-174298683	2705.02	-24.748406	uc003ltd.3	chr4:174298479-174298683
SART1A	607691	NA	NA	NA	NA	939.591	-6.330928	uc010qlh.2	chr10:71909961-71912231	NA	NA	NA	NA
SARNP	610049	NA	NA	NA	NA	1468.93	-7.945461	uc001isht.3	chr12:56151054-56151295	NA	NA	NA	NA
SARS2	612804	NA	NA	NA	NA	302.622	-6.327632	uc002zjz.2	chr19:39405904-39406245	NA	NA	NA	NA
SASH3	300441	NA	NA	NA	NA	NA	NA	NA	NA	340.061	-7.175152	uc004eui.3	chrX:128927909-128929176
SAS36	609321	NA	NA	NA	NA	815.881	-8.8021	uc001dsu.3	chr1:100549102-100550883	745.959	-6.683051	uc001dsu.3	chr1:100549102-100550883
SATB1	602075	433.28	-5.015775	uc003cbi.3	chr3:18389133-18390661	NA	NA	NA	NA	NA	NA	NA	NA
SATL1	NA	NA	NA	NA	NA	585.363	-8.971367	uc004een.3	chrX:84347292-84347544	589.82	-5.742459	uc004een.3	chrX:84347292-84347544
SAYSD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	700.989	-7.707613	uc003ook.1	chr6:39071840-39073207
SBD5	607444	NA	NA	NA	NA	NA	NA	NA	NA	359.206	-6.155634	uc003tvm.1	chr7:66452690-66453357
SBF2	607697	NA	NA	NA	NA	1136.12	-6.310896	uc001mic.2	chr11:9800214-9801964	NA	NA	NA	NA
SBSN	609969	205.619	-5.592734	uc002bad.2	chr19:36014269-36014411	NA	NA	NA	NA	NA	NA	NA	NA
SCAF11	603668	260.211	-5.948058	uc001row.3	chr12:46312914-46315830	NA	NA	NA	NA	NA	NA	NA	NA
SCAF4	616023	NA	NA	NA	NA	NA	NA	NA	NA	1295.1	-4.252365	uc002ydp.2	chr21:33043313-33043711

Table 1

SCAMP1	606911	1038.86	-7.993159	uc003kl1.3	chr5:77771492-77776562	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SCAR3	602728	326.555	-4.642283	uc003xga.1	chr8:2752869-27530537	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SCGB1D1	615060	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr11:61960901-61961009
SCGB1D2	615061	832.199	-8.676733	uc001mtb.3	chr11:62012172-62012280	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SCGB2A1	604398	NA	NA	NA	NA	834.715	-6.541795	uc001nta.2	chr11:61981243-61981411	NA	NA	NA	NA	NA	NA	NA	NA
SCGB2A2	605562	773.169	-4.429267	uc001ntc.3	chr11:62040468-62040628	651.361	-8.931535	uc001ntc.3	chr11:62040468-62040628	NA	NA	NA	NA	NA	NA	NA	NA
SCGN	609202	NA	NA	NA	NA	979.603	-7.897464	uc003nfb.3	chr6:25701564-25702008	NA	NA	NA	NA	NA	NA	NA	NA
SCIN	613416	529.48	-5.499084	uc003ssn.4	chr7:12692341-12693228	920.089	-5.654323	uc003ssn.4	chr7:12692341-12693228	NA	NA	NA	NA	NA	NA	NA	NA
SLC11	611399	NA	NA	NA	NA	439.161	-2.962916	uc003igr.2	chr4:129957750-129959175	684.658	-8.739428	uc003ign.2	chr4:129805152-129805631	NA	NA	NA	NA
SLCML4	NA	NA	NA	NA	NA	280.599	-5.725473	uc003pry.4	chr6:108023364-108026403	NA	NA	NA	NA	NA	NA	NA	NA
SCN11A	604385	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr3:38890776-38891963
SCN11A	182389	242.022	-4.605035	uc010fpk.3	chr2:166845670-166847754	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SCN2A	182390	NA	NA	NA	NA	333.66	-8.450202	uc002udc.3	chr2:166246335-166248820	NA	NA	NA	NA	NA	NA	NA	NA
SCN3A	182391	NA	NA	NA	NA	515.934	-9.616292	uc010zoy.2	chr2:165944030-165946659	NA	NA	NA	NA	NA	NA	NA	NA
SCN7A	182392	494.228	-7.154231	uc002udu.2	chr2:167260083-167262089	767.319	-5.619645	uc002udu.2	chr2:167260083-167262089	NA	NA	NA	NA	NA	NA	NA	NA
SCN8A	600702	1508.64	-8.486448	uc001ryv.2	chr12:52159830-52160035	NA	NA	NA	NA	452.384	-5.622688	uc001ryv.2	chr12:52159830-52160035	NA	NA	NA	NA
SCN9A	603415	515.497	-7.444738	uc010fpl.3	chr2:167051697-167055181	490.713	-5.90296	uc010fpl.3	chr2:167051697-167055181	NA	NA	NA	NA	NA	NA	NA	NA
SCNM1	608095	NA	NA	NA	NA	NA	NA	NA	NA	355.378	-5.340497	uc010pks.2	chr1:1511139982-151140384	NA	NA	NA	NA
SOOC	NA	741.443	-6.311104	uc003lib.2	chr4:141302259-141303710	919.481	-7.195297	uc003lib.2	chr4:141302259-141303710	NA	NA	NA	NA	NA	NA	NA	NA
SCR2	184755	NA	NA	NA	NA	218.143	-10.376985	uc001cur.2	chr1:53516377-53517289	NA	NA	NA	NA	NA	NA	NA	NA
SCRG1	603163	379.222	-6.423129	uc003lie.3	chr4:174309299-174309491	836.077	-10.454743	uc003lie.3	chr4:174309299-174309491	NA	NA	NA	NA	NA	NA	NA	NA
SCRIB	607733	541.592	-5.644961	uc003yzn.1	chr8:144873090-144873332	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SDC2	142460	NA	NA	NA	NA	NA	NA	NA	NA	807.021	-9.294949	uc003yhw.1	chr8:97621177-97624037	NA	NA	NA	NA
SDE2	NA	NA	NA	NA	NA	NA	NA	NA	NA	820.368	-10.554356	uc001hpu.4	chr1:226170403-226173002	NA	NA	NA	NA
SDF2	602934	785.827	-8.187108	uc010cvs.2	chr17:26987506-26988143	1227.81	-7.297103	uc002hbv.3	chr17:26975374-26976006	614.734	-5.447398	uc010cvs.2	chr17:26987506-26988143	NA	NA	NA	NA
SDF2L1	607551	NA	NA	NA	NA	NA	NA	NA	NA	377.428	-4.319356	uc002zvf.3	chr22:21998465-21998588	NA	NA	NA	NA
SDF4	614282	NA	NA	NA	NA	876.14	-14.265693	uc001adh.4	chr1:1152288-1152891	NA	NA	NA	NA	NA	NA	NA	NA
SDHAF2	613019	851.759	-5.82507	uc001mtt.3	chr11:61213544-61214239	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SDHAF4	NA	422.82	-5.061724	uc003plq.1	chr6:71298428-71298606	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SDHAP1	NA	NA	NA	NA	NA	NA	NA	NA	NA	602.964	-5.831581	uc003fyv.3	chr3:195568976-1955690205	NA	NA	NA	NA
SDHAP2	NA	NA	NA	NA	NA	288.2	-5.84104	uc003iou.4	chr3:195398067-195398654	NA	NA	NA	NA	NA	NA	NA	NA
SDHC	602413	422.111	-5.438701	uc001gai.3	chr1:161332331-161334535	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SDR9C7	609769	NA	NA	NA	NA	NA	NA	NA	NA	881.137	-8.075916	uc010sqw.2	chr12:57316938-57317616	NA	NA	NA	NA
SEC11C	NA	1069.48	-9.152644	uc010dpo.1	chr18:56819922-56820593	NA	NA	NA	NA	1786.53	-10.96981	uc010dpo.1	chr18:56819922-56820593	NA	NA	NA	NA
SEC13	600152	NA	NA	NA	NA	NA	NA	NA	NA	254.896	-6.53282	uc003bvl.3	chr3:10342615-10342944	NA	NA	NA	NA
SEC14L2	607558	NA	NA	NA	NA	NA	NA	NA	NA	596.112	-7.12631	uc003ahq.3	chr22:30812491-30812964	NA	NA	NA	NA
SEC14L3	612824	NA	NA	NA	NA	NA	NA	NA	NA	582.29	-5.681859	uc003ahy.3	chr22:30855216-30856007	NA	NA	NA	NA
SEC24C	607185	NA	NA	NA	NA	614.619	-5.382207	uc009xrt.2	chr10:75528974-75529233	NA	NA	NA	NA	NA	NA	NA	NA
SEC24D	607186	NA	NA	NA	NA	1392.9	-12.020158	uc003ick.2	chr4:119650283-119652434	NA	NA	NA	NA	NA	NA	NA	NA
SEC31B	610258	NA	NA	NA	NA	903.366	-4.089837	uc001krg.1	chr10:102254602-102255102	309.526	-3.740945	uc001krg.1	chr10:102254602-102255102	NA	NA	NA	NA
SEC81A1	609213	1224.41	-11.296715	uc003ekb.3	chr3:127788506-127790526	NA	NA	NA	NA	536.257	-8.656397	uc003ekb.3	chr3:127788506-127790526	NA	NA	NA	NA
SEC81A2	NA	NA	NA	NA	NA	NA	NA	NA	NA	753.101	-6.103947	uc001ile.2	chr10:12206454-12207403	NA	NA	NA	NA
SEC61B	609214	NA	NA	NA	NA	NA	NA	NA	NA	394.535	-4.884743	uc004azh.3	chr9:101992707-101992901	NA	NA	NA	NA
SEC63	608648	NA	NA	NA	NA	NA	NA	NA	NA	767.584	-7.000931	uc003psb.4	chr6:108188960-108192907	NA	NA	NA	NA
SECISBP2	607693	NA	NA	NA	NA	338.937	-9.43777	uc004aqj.1	chr9:91973740-91974561	1605.42	-9.467912	uc004aqj.1	chr9:91973740-91974561	NA	NA	NA	NA
SECISBP2L	615756	451.064	-4.379546	uc001zxd.2	chr15:49280835-49284440	NA	NA	NA	NA	1850.66	-12.458836	uc001zxd.2	chr15:49280835-49284440	NA	NA	NA	NA
SEH1L	609263	1596.55	-14.571067	uc002kqr.3	chr18:12987057-12987536	748.786	-6.141995	uc002krr.3	chr18:12985252-12987536	NA	NA	NA	NA	NA	NA	NA	NA
SEL1L3	NA	NA	NA	NA	NA	NA	NA	NA	NA	429.118	-8.85119	uc003gru.4	chr4:25749049-25750046	NA	NA	NA	NA
SELP	173610	728.346	-9.641103	uc001ggh.3	chr1:169558088-169558803	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

SEMA3C	602645	NA	NA	NA	NA	NA	NA	NA	NA	NA	649,806	-8,761,978	uc003uhj.3	chr7:80371854-80374209
SEMA3D	609907	NA	NA	NA	NA	NA	NA	NA	NA	NA	281,405	-12,174,579	uc010lee.1	chr7:84679673-84680042
SEMA3E	608166	336,312	-4,657,47	uc0022agy.1	chr7:82993222-82996901	NA	NA	NA	NA	NA	NA	NA	NA	NA
SEMA3F	601124	NA	NA	NA	NA	597,779	-9,205,546	uc003cyl.3	chr3:50225549-50228508	NA	NA	NA	NA	NA
SEMA4D	601866	789,156	-8,246,932	uc004aqo.1	chr9:91992152-91993618	NA	NA	NA	NA	NA	NA	NA	NA	NA
SEMA5A	609297	626,249	-5,469,355	uc003jek.2	chr5:9035138-9043008	NA	NA	NA	NA	NA	NA	NA	NA	NA
SEMA6D	609295	693,342	-6,278,528	uc001zvw.3	chr15:48063983-48066420	1313,13	-8,393,848	uc001zvw.3	chr15:48063983-48066420	483,811	-5,001,191	uc001zvw.3	chr15:48063983-48066420	
SEN2P	608261	NA	NA	NA	NA	772,698	-3,887,156	uc003pid.4	chr6:76425311-76427994	NA	NA	NA	NA	NA
SEN6P	605003	800,539	-7,440,186	uc003pid.4	chr6:76425311-76427994	573,566	-6,433,821	uc001imh.3	chr10:13359438-13361141	601,978	-7,126,631	uc009yje.3	chr10:13370879-13371676	
SEPHS1	609092	NA	NA	NA	NA	601,306	-7,155,03	uc003qrb.2	chr6:158530536-158532397	803,473	-8,198,251	uc003qrb.2	chr6:158530536-158532397	
SERAC1	614725	NA	NA	NA	NA	555,921	-4,263,594	uc010bdq.3	chr15:44086171-44088287	NA	NA	NA	NA	NA
SERF2	605054	NA	NA	NA	NA	650,549	-4,899,992	uc002xmf.1	chr20:43127901-43128936	NA	NA	NA	NA	NA
SERINC3	607165	NA	NA	NA	NA	876,033	-6,359,74	uc002jlc.3	chr18:61264598-61266433	NA	NA	NA	NA	NA
SERP1NB13	604445	NA	NA	NA	NA	280,055	-3,887,937	uc002lly.2	chr18:61160458-61160928	NA	NA	NA	NA	NA
SERP1NB2	173390	NA	NA	NA	NA	NA	NA	NA	NA	NA	696,87	-6,458,15	uc002jlo.3	chr18:61570540-61571124
SERP1NB5	154790	NA	NA	NA	NA	NA	NA	NA	NA	587,759	-4,285,699	uc002liz.4	chr18:61170956-61172318	
SERP1NB6	173321	250,62	-6,491,485	uc003muk.3	chr6:2948393-2948531	NA	NA	NA	NA	NA	NA	NA	NA	NA
SERP1NB8	601697	810,375	-6,562,87	uc002jll.3	chr18:61653501-61653887	323,247	-5,450,701	uc002jll.3	chr18:61654513-61656608	NA	NA	NA	NA	NA
SERPINC1	107300	1245,42	-9,427,397	NA	NA	NA	NA	NA	NA	660,993	-6,797,235	uc001igt.3	chr1:173872942-173873026	
SERPIND1	142360	705,767	-9,136,318	uc002ztb.1	chr22:21141355-21142008	NA	NA	NA	NA	NA	NA	NA	NA	NA
SERPINE2	177010	623,912	-6,582,679	uc010zlr.1	chr2:224839765-224840583	883,844	-12,559,109	uc010zlr.1	chr2:224839765-224840583	NA	NA	NA	NA	NA
SERTAD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	611,878	-6,278,893	uc002ont.4	chr19:40928409-40928742	
SERTAD2	NA	800,745	-7,653,805	uc002sde.2	chr2:64858755-64863060	NA	NA	NA	NA	NA	NA	NA	NA	NA
SERTAD4	NA	NA	NA	NA	NA	793,308	-8,443,861	uc001lhy.3	chr1:210415683-210416440	NA	NA	NA	NA	NA
SESNA3	607768	NA	NA	NA	NA	NA	NA	NA	NA	1522	-11,900,284	uc001pfl.3	chr11:94917299-94917554	
SETD2	612778	NA	NA	NA	NA	NA	NA	NA	NA	579,26	-7,087,816	uc003cqr.3	chr3:47057898-47058582	
SETD5	615743	NA	NA	NA	NA	1367,87	-12,046,49	uc003brw.1	chr3:9487069-9487648	NA	NA	NA	NA	NA
SETD8	NA	NA	NA	NA	NA	NA	NA	NA	NA	484,319	-6,886,394	uc001uew.3	chr12:123892251-123893900	
SETD9	NA	763,127	-1,397,767	uc003jpx.3	chr5:56212730-56213165	477,989	-4,701,703	uc003jpx.3	chr5:56212730-56213165	NA	NA	NA	NA	NA
SETD81	604396	NA	NA	NA	NA	579,839	-9,348,083	uc001evu.2	chr1:150936841-150937220	NA	NA	NA	NA	NA
SF1	601516	392,432	-5,572,536	uc010rmm.2	chr11:64532076-64532925	NA	NA	NA	NA	NA	NA	NA	NA	NA
SF3B1	605590	1359,02	-9,524,901	uc002uug.3	chr2:198283521-198285101	627,815	-6,054,904	uc002uue.3	chr2:198256698-198257026	736,029	-12,896,702	uc002uue.3	chr2:198256698-198257026	
SF3B2	605591	NA	NA	NA	NA	NA	NA	NA	NA	814,998	-4,795,31	uc001lgy.1	chr11:65836217-65836382	
SF3B4	605593	373,98	-10,105,238	uc001elt.2	chr1:149895209-149895433	503,484	-5,159,143	uc001elt.2	chr1:149895209-149895433	NA	NA	NA	NA	NA
SF3B6	607835	509,997	-4,532,328	uc002rev.3	chr2:24290454-24290631	NA	NA	NA	NA	606,839	-9,143,665	uc002rev.3	chr2:24290454-24290631	
SFMBT1	607319	NA	NA	NA	NA	NA	NA	NA	NA	330,766	-5,101,268	uc010hmr.3	chr3:52937583-52939151	
SFMBT2	615392	NA	NA	NA	NA	447,589	-4,818,843	uc009xio.2	chr10:7200586-7205731	NA	NA	NA	NA	NA
SFPQ	605199	NA	NA	NA	NA	NA	NA	NA	NA	882,996	-13,619,774	uc001bys.3	chr1:35649201-35650056	
SFTA3	NA	590,003	-7,395,705	uc001wtr.3	chr14:36942494-36943062	NA	NA	NA	NA	295,409	-5,842,809	uc001wtr.3	chr14:36942494-36943062	
SFXN2	615570	NA	NA	NA	NA	NA	NA	NA	NA	361,03	-9,773,869	uc001kwb.2	chr10:104497520-104498946	
SGCA	600119	315,865	-4,767,099	uc010wmh.1	chr17:48246712-48246775	NA	NA	NA	NA	NA	NA	NA	NA	NA
SGCB	600900	NA	NA	NA	NA	NA	NA	NA	NA	1689,28	-13,293,778	uc003gzi.2	chr4:52886861-52890122	
SGCD	601411	NA	NA	NA	NA	1368,06	-9,025,634	uc003lwb.3	chr5:156184788-156185070	NA	NA	NA	NA	NA
SGCE	604149	1874,49	-15,099,137	uc003unn.2	chr7:94214536-94214776	NA	NA	NA	NA	582,452	-5,022,438	uc003unn.2	chr7:94214536-94214776	
SGK494	NA	NA	NA	NA	NA	1176,12	-11,038,011	uc010crq.2	chr17:26934982-26937495	NA	NA	NA	NA	NA
SGMS2	611574	NA	NA	NA	NA	714,577	-10,133,666	uc003hyt.4	chr4:108831710-108836204	NA	NA	NA	NA	NA
SGOL1	609168	950,38	-9,597,608	uc003cca.3	chr3:20209936-20212195	NA	NA	NA	NA	NA	NA	NA	NA	NA
SGOL2	612425	751,965	-10,886,799	uc002uvv.4	chr2:201434657-201434865	723,959	-10,886,799	uc002uvv.4	chr2:201434657-201434865	207,623	-5,634,665	NA	NA	NA
SGPP1	612826	NA	NA	NA	NA	375,252	-5,801,316	uc001xgi.3	chr14:64150935-64152822	NA	NA	NA	NA	NA

Table 1

SGTB1	NA	NA	NA	NA	NA	1057.5	-6.901791	uc003jud.3	chr5:64961755-64966072	NA	NA	NA	NA	NA	NA	NA
SH2B1	608937	NA	NA	NA	NA	395.2	-4.595556	uc002dri.3	chr16:28885142-28885534	NA	NA	NA	NA	NA	NA	NA
SH2D1A	300460	493.422	-6.148191	uc004euf.4	chrX:123505242-123507010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SH2D4B	NA	1415.05	-7.757434	uc001kck.1	chr10:82403836-82406316	NA	NA	NA	NA	1067.96	-11.206231	uc001kcm.1	chr10:82403842-82406316	NA	NA	NA
SH3D19	608674	766.566	-7.425515	uc003imb.2	chr4:152041433-152043242	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SH3GL3	603362	760.819	-11.257689	uc002bju.3	chr15:84287040-84287493	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SH3GLB1	609287	NA	NA	NA	NA	NA	NA	NA	NA	813.311	-6.666573	uc001dlw.3	chr1:87208919-97213867	NA	NA	NA
SH3GLB2	609288	NA	NA	NA	NA	334.691	-5.473382	uc004bvw.3	chr9:131770313-131770962	NA	NA	NA	NA	NA	NA	NA
SH3PXD2B	613293	NA	NA	NA	NA	232.499	-5.521473	uc003mbr.3	chr5:171760503-171765372	NA	NA	NA	NA	NA	NA	NA
SH3RF2	613377	517.458	-4.02524	uc003int.3	chr5:145442265-145442879	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SH3YL1	NA	NA	NA	NA	NA	648.222	-5.154952	uc002qvv.3	chr2:218136-218810	NA	NA	NA	NA	NA	NA	NA
SHCBP1L	NA	NA	NA	NA	NA	618.755	-6.321233	uc001lpu.3	chr1:182869000-182869117	NA	NA	NA	NA	NA	NA	NA
SHF	NA	NA	NA	NA	NA	NA	NA	NA	NA	891.748	-1.561477	uc010uen.2	chr15:45459412-45460144	NA	NA	NA
SHFM1	601285	706.993	-8.185853	uc010lfn.1	chr7:96302237-96303071	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SHISA5	607290	NA	NA	NA	NA	576.137	-6.661343	uc011bbk.1	chr3:48509197-48510269	NA	NA	NA	NA	NA	NA	NA
SHPRH	608048	NA	NA	NA	NA	575.48	-2.570248	uc003qle.3	chr6:146205945-146207563	899.281	-9.597785	uc003qli.1	chr6:146239553-146240468	NA	NA	NA
SHQ1	613663	NA	NA	NA	NA	1069.51	-8.828643	uc001vap.3	chr13:46354416-46357517	697.418	-5.705785	uc003dpl.3	chr3:72798428-72799434	NA	NA	NA
SHROOM4	300579	NA	NA	NA	NA	499.516	-6.379406	uc003eak.3	chr3:113346556-113348422	NA	NA	NA	NA	NA	NA	NA
SI	609845	925.204	-8.019863	uc003lei.3	chr3:164696686-164697149	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIAB	610079	NA	NA	NA	NA	231.371	-5.506555	uc001pqh.1	chr11:17068783-17068161	NA	NA	NA	NA	NA	NA	NA
SIAB2	602213	1168.81	-9.342077	uc003eyi.3	chr3:150458910-150459927	NA	NA	NA	NA	1190.56	-7.505937	uc001ppw.3	chr11:116714118-116716345	NA	NA	NA
SIAB3	615609	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIDT1	606816	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIDT2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIGLEC17P	NA	392.403	-4.522166	uc002pyv.4	chr19:51676233-51676780	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIK3	614776	NA	NA	NA	NA	696.355	-8.011673	uc002bak.4	chr15:75711551-75714882	NA	NA	NA	NA	NA	NA	NA
SIN3A	607776	801.032	-6.918983	uc002bak.4	chr15:75711551-75714882	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIN3B	607777	777.251	-7.606245	uc002new.3	chr19:16965077-16966543	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIRP2	NA	NA	NA	NA	NA	NA	NA	NA	NA	358.631	-5.098168	uc002wfg.2	chr20:1455236-1456811	NA	NA	NA
SIRPD	NA	397.527	-5.460339	uc002wfl.3	chr20:1514897-1515070	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIRT1	604479	471.516	-6.838519	uc001jnd.3	chr10:69676351-69678147	380.143	-8.523816	uc001jnd.3	chr10:69676351-69678147	NA	NA	NA	NA	NA	NA	NA
SIRT5	604483	NA	NA	NA	NA	NA	NA	NA	NA	280.832	-5.248158	uc003max.3	chr6:13612098-13615390	NA	NA	NA
SIRT6	606211	1363.49	-9.616177	uc002lzo.3	chr19:4174106-4174613	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SIVA1	605567	NA	NA	NA	NA	782.14	-8.2104	uc001yph.3	chr14:105225823-105225996	867.307	-5.718441	uc001yph.3	chr14:105225823-105225996	NA	NA	NA
SIX4	606342	637.517	-4.602671	uc001xlc.3	chr14:61176256-61180124	707.516	-4.798624	uc001xlc.3	chr14:61176256-61180124	NA	NA	NA	NA	NA	NA	NA
SKAP2	605215	235.258	-6.317373	uc011jzl.2	chr7:26706688-26709275	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SKIDA1	NA	827.514	-8.056853	uc009kld.3	chr10:21802409-21804024	365.826	-8.72643	uc009kld.3	chr10:21802409-21804024	NA	NA	NA	NA	NA	NA	NA
SKL	165340	828.136	-11.169164	uc003lgu.3	chr3:170110206-170114637	801.806	-6.537313	uc003kic.2	chr5:36182134-36184142	788.168	-10.28636	uc003lgu.3	chr3:170110206-170114637	NA	NA	NA
SKP2	601436	NA	NA	NA	NA	997.643	-10.477445	uc003gdi.1	chr4:1694527-1695323	816.921	-7.538222	uc003gdi.1	chr4:1694527-1695323	NA	NA	NA
SLBP	602422	NA	NA	NA	NA	NA	NA	NA	NA	504.636	-7.895007	uc001kxr.2	chr14:70242552-70242998	NA	NA	NA
SLC10A1	182396	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC10A3	312090	767.422	-7.344369	uc004lfp.3	chrX:153715650-153715845	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC10A4	NA	569.79	-8.374872	uc003gyc.2	chr4:48490957-48491541	606.223	-6.645311	uc003klt.3	chr4:147362820-147363889	NA	NA	NA	NA	NA	NA	NA
SLC10A7	611459	1078.18	-10.273109	uc003klr.2	chr4:147175137-147177642	995.316	-11.49697	uc001rxg.2	chr12:51379775-51382107	NA	NA	NA	NA	NA	NA	NA
SLC11A2	600523	280.552	-8.050774	uc001rxd.4	chr12:51373566-51375586	321.097	-4.666856	uc003vkm.3	chr7:122753588-122755571	NA	NA	NA	NA	NA	NA	NA
SLC13A1	606193	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC15A1	600544	614.982	-7.700839	uc001vno.3	chr13:99336055-99336977	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC15A3	610408	463.932	-3.012948	uc001nqn.2	chr11:60704555-60704690	NA	NA	NA	NA	375.219	-11.550179	uc001nqn.2	chr11:60704555-60704690	NA	NA	NA
SLC15A5	NA	NA	NA	NA	NA	759.956	-9.618592	uc021qys.1	chr12:16341419-16342801	NA	NA	NA	NA	NA	NA	NA

Table 1

SLC16A10	607550	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	812.009	-7.518199	uc003pus.3		chr6:111543439-1111544606
SLC16A12	611910	1813.5	-11.922528	uc001lgl.3	chr10:91190051-91192820	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC16A3	603877	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC16A6	603880	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	733.883	-4.229249	uc002jlg.2		chr17:66263167-66265236
SLC16A9	614242	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	710.109	-6.616615	uc010qlg.1		chr10:61410522-61412529
SLC17A2	611049	1228.96	-3.629431	uc001ldkb.2	chr6:25912984-25913544	NA	NA	NA	NA	NA	NA	782.505	-10.064784	uc011dkc.2		chr6:25912984-25913671
SLC17A3	611034	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1046.6	-13.156793	uc003nfl.4		chr6:25845328-25845526
SLC17A4	604216	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC17A5	604322	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	579.678	-8.641121	uc010kak.3		chr6:74303102-74304799
SLC17A6	607563	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	921.682	-6.634812	uc001mqk.3		chr11:22399287-22401046
SLC19A2	603941	436.323	-7.69805	uc001ggc.4	chr1:169433149-169435086	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC1A3	600111	358.874	-7.059048	uc0021xkn.1	chr5:36608724-36609399	885.755	-7.723163	uc021xkn.1	chr5:36608724-36609399	NA	NA	NA	NA	NA	NA	NA
SLC1A5	109190	513.297	-5.463256	uc001oxyh.2	chr19:47278140-47278766	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC20A1	137570	360.876	-6.278528	uc002tlb.3	chr2:113420603-113421400	NA	NA	NA	NA	NA	NA	524.001	-7.564059	uc002tlb.3		chr2:113420603-113421400
SLC22A11	607097	429.004	-6.808122	uc001oath.1	chr11:64333117-64334171	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC22A15	608275	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC22A17	611461	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1026.67	-8.040848	uc010akl.1		chr14:23817836-23818376
SLC22A18AS	603240	208.266	-4.413404	NA	NA	NA	NA	NA	NA	NA	NA	210.386	-5.311726	uc001llw.4		chr11:2909327-2909409
SLC22A2	602608	461.627	-5.162856	uc003qth.2	chr6:160670198-160671523	NA	NA	NA	NA	NA	NA	935.742	-6.286131	uc003qth.2		chr6:160670198-160671523
SLC22A20	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	490.475	-6.482192	uc021qlg.1		chr11:64993168-64993511
SLC22A5	603377	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC22A7	604995	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1764.51	-4.989747	uc003ous.3		chr6:43272017-43272218
SLC23A2	603791	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC23A3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1067.48	-11.382537	uc010fwb.3		chr2:220026181-220026630
SLC24A1	603617	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC24A4	609840	2050.62	-20.777665	uc010auj.3	chr14:925959820-925967825	NA	NA	NA	NA	NA	NA	344.123	-5.031061	uc010auj.3		chr14:925959820-925967825
SLC24A5	609802	472.265	-4.084102	uc001zwd.3	chr15:48414302-48416873	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC25A13	603859	610.033	-7.312252	uc003uof.4	chr7:95749532-95750502	333.213	-5.027257	uc003uof.4	chr7:95749532-95750502	NA	NA	NA	NA	NA	NA	NA
SLC25A16	139080	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	520.743	-5.408945	uc001poi.3		chr10:70242090-70243188
SLC25A2	608157	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	572.895	-6.428508	uc003jff.3		chr5:140682196-140682526
SLC25A21	607571	477.741	-7.896688	uc021rsf.1	chr14:37147126-37147688	874.035	-9.947714	uc021rsf.1	chr14:37147126-37147688	NA	NA	NA	NA	NA	NA	NA
SLC25A22	609302	573.275	-5.024157	uc001lhi.3	chr11:790475-791914	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC25A29	615064	1226.22	-12.795013	uc010lwx.2	chr14:100757453-100758492	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC25A38	610819	1411.43	-5.836883	uc003qjp.2	chr3:39438012-39438819	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC25A42	610823	390.036	-5.786139	uc010xqn.1	chr19:19217199-19217743	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC25A43	300641	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	568.845	-7.506828	uc004erd.3		chrX:118587029-118588437
SLC25A5	300150	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC26A11	610117	620.782	-10.033834	uc002jyb.2	chr17:78226516-78227308	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC26A4	605646	367.528	-6.69921	uc003vcp.3	chr17:1073555892-107358252	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC26A5	604943	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	501.578	-6.238269	uc003vbu.2		chr7:102993177-102993336
SLC26A7	608479	534.627	-4.116085	uc003yex.3	chr6:92407326-92410378	NA	NA	NA	NA	NA	NA	242.45	-4.64793	uc003yex.3		chr8:92407326-92410378
SLC28A1	606207	876.695	-5.654323	uc002bif.3	chr15:85438676-85439268	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC28A2	606208	656.498	-8.554999	uc001zva.2	chr15:45567712-45568132	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC28A3	608269	470.297	-4.787594	uc010mpz.3	chr9:86890765-868993132	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC29A1	602193	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC2A4	138190	839.712	-5.832316	uc002qjp.3	chr17:7189949-7191367	NA	NA	NA	NA	NA	NA	767.785	-5.88215	uc011dvp.1		chr6:44197861-44198218
SLC2A5	138230	617.919	-2.441959	uc010nzy.2	chr1:9097005-9097644	NA	NA	NA	NA	NA	NA	454.918	-5.63302	uc010nzy.2		chr1:9097005-9097644
SLC2A9	606142	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLC30A1	609521	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	750.301	-10.73908	uc001hic.1		chr1:211748381-211748729

Table 1

	SLC30A4	602095	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr9:116022754-116026772	uc001zvj.3	-4.37522	379.872					chr15:45774680-45777360
	SLC30A8	611145	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		uc010mc.3	-9.735854	1024.05					chr8:118184921-118188953
	SLC31A1	603085	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA			NA	NA					NA
	SLC31A2	603088	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		uc004bga.3	-4.053285	332.591					chr9:115925198-115926422
	SLC35D3	612519	819.866	-5.954949	uc003qhe.3	chr6:137245835-137246776	495.042	-11.252378	uc003qhe.3	chr6:137245835-137246776	259.32	-5.154149	uc003qhe.3	chr6:137445835-137446776		NA	NA	NA					chr6:137445835-137446776
	SLC35E1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		uc002nem.1	-4.691898	NA				NA	
	SLC35F1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		uc003ppx.4	-8.448609	NA				NA	
	SLC35F5	NA	445.873	-5.300225	uc002lku.1	chr2:114471933-114472772	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC35G1	NA	1092.74	-7.692895	uc001kij.2	chr10:95661248-95662491	1124.68	-10.009294	uc001kij.2	chr10:95661248-95662491	NA	NA	NA	NA		uc001kij.2	NA	NA	NA	NA	NA	NA	NA
	SLC35G2	NA	344.847	-8.529233	uc003gef.4	chr3:136574542-136574734	1407.86	-16.961189	uc003gef.4	chr3:136574542-136574734	NA	NA	NA	NA		uc003gef.4	NA	NA	NA	NA	NA	NA	NA
	SLC36A2	608331	1281.59	-3.572473	uc003lly.3	chr5:150694539-150696377	693.029	-7.358289	uc003lly.3	chr5:150694539-150696377	1093.2	-7.873186	uc003lly.3	chr5:150694539-150696377		NA	NA	NA	NA	NA	NA	NA	chr5:150694539-150696377
	SLC36A3	608332	565.089	-7.942201	uc003llv.2	chr5:150656926-150656953	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC36A4	613760	NA	NA	NA	NA	512.91	-4.785205	uc001pdm.3	chr11:92880850-92881702	1222.92	-6.513519	uc001qbn.3	chr11:124958031-124960412		NA	NA	NA	NA	NA	NA	NA	chr11:124958031-124960412
	SLC37A2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC37A3	NA	590.049	-8.144378	uc003avo.3	chr7:140033552-140035211	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC38A1	608490	333.015	-6.327632	uc009akj.1	chr12:46389508-46389909	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC38A10	616525	907.276	-11.74543	uc002kab.3	chr17:79224671-79225014	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC38A11	616526	1870.96	-13.73534	uc002ucc.2	chr2:165754709-165754946	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC38A4	608065	635.513	-4.482586	uc001tpi.2	chr12:47158544-47160483	506.918	-7.790842	uc001tpi.2	chr12:47158544-47160483	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC38A6	616518	NA	NA	NA	NA	351.734	-4.471718	uc001xig.2	chr14:61519148-61519703	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC39A11	616508	NA	NA	NA	NA	NA	NA	NA	NA	1360.62	-8.194136	uc002jja.3	chr17:70642085-70643722		NA	NA	NA	NA	NA	NA	NA	NA
	SLC39A12	608734	967.088	-14.324873	uc001ipn.2	chr10:18331763-18332221	NA	NA	NA	NA	750.021	-10.489348	uc001ipn.2	chr10:18331763-18332221		NA	NA	NA	NA	NA	NA	NA	NA
	SLC39A14	608736	NA	NA	NA	NA	1615.95	-10.465388	uc003xpbp.4	chr8:22277212-22280249	1538.23	-11.215104	uc003xpbp.4	chr8:22277212-22280249		NA	NA	NA	NA	NA	NA	NA	NA
	SLC39A8	608732	NA	NA	NA	NA	513.519	-5.668802	uc011ceo.1	chr4:103172198-103174578	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC3A2	158070	919.782	-8.568334	uc001nwc.3	chr11:62856166-62866355	NA	NA	NA	NA	1172.58	-11.021755	uc002upp.4	chr2:190425316-190426603		NA	NA	NA	NA	NA	NA	NA	NA
	SLC40A1	604653	762.312	-7.503075	uc002upp.4	chr2:190425316-190426603	NA	NA	NA	NA	469.406	-5.710395	uc001nkk.3	chr11:57252004-57252568		NA	NA	NA	NA	NA	NA	NA	NA
	SLC43A1	603733	NA	NA	NA	NA	NA	NA	NA	NA	1583.59	-10.150444	uc001dgr.2	chr1:75667816-75669411		NA	NA	NA	NA	NA	NA	NA	NA
	SLC44A5	NA	NA	NA	NA	NA	NA	NA	NA	NA	632.321	-5.804303	uc003jif.4	chr5:33951511-33951756		NA	NA	NA	NA	NA	NA	NA	NA
	SLC45A2	606202	625.058	-7.386931	uc003jie.3	chr5:33945972-33947252	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC45A3	605097	493.228	-4.84295	uc001lha.1	chr1:205626981-205628361	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC41A10	605556	NA	NA	NA	NA	NA	NA	NA	NA	1219.75	-9.161436	uc002ubx.4	chr2:1628395689-162841786		NA	NA	NA	NA	NA	NA	NA	NA
	SLC41A11	610206	NA	NA	NA	NA	NA	NA	NA	NA	1430.89	-8.279836	uc002wlg.3	chr20:3208063-3208432		NA	NA	NA	NA	NA	NA	NA	NA
	SLC5A1	182380	378.772	-4.712636	uc003amc.3	chr22:32506201-32509011	NA	NA	NA	NA	804.265	-4.813803	uc003amc.3	chr22:32506201-32509011		NA	NA	NA	NA	NA	NA	NA	NA
	SLC6A16	607972	NA	NA	NA	NA	529.33	-4.193113	uc002pmz.3	chr19:49792892-49793379	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC6A2	163970	NA	NA	NA	NA	354.516	-4.466028	uc002eif.3	chr16:55736259-55737700	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC6A20	605616	NA	NA	NA	NA	729.378	-5.863761	uc003caw.3	chr3:45796941-45800469	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC6A5	604159	1361.73	-8.507564	uc001mqi.3	chr11:20676415-20676610	587.384	-6.021172	uc001mqi.3	chr11:20676415-20676610	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC7A10	607959	NA	NA	NA	NA	1346.43	-10.11949	uc002nul.2	chr19:33699570-33699796	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA
	SLC7A2	601872	NA	NA	NA	NA	NA	NA	NA	NA	793.263	-9.400311	uc011kvc.2	chr8:17422656-17428077		NA	NA	NA	NA	NA	NA	NA	NA
	SLC7A4	603752	NA	NA	NA	NA	NA	NA	NA	NA	882.033	-5.146117	uc002ud.3	chr22:21383007-21383343		NA	NA	NA	NA	NA	NA	NA	NA
	SLC7A8	604235	NA	NA	NA	NA	NA	NA	NA	NA	413.218	-6.003216	uc001wiw.3	chr14:23594504-23596385		NA	NA	NA	NA	NA	NA	NA	NA
	SLC8A1	182305	NA	NA	NA	NA	637.729	-7.672779	uc002rx.3	chr2:40339286-40342392	982.729	-12.925295	uc002rx.3	chr2:40339286-40342392		NA	NA	NA	NA	NA	NA	NA	NA
	SLC9A4	600531	NA	NA	NA	NA	1040.63	-12.942616	uc002lhz.4	chr2:103149148-103150431	248.088	-6.69725	uc002lhz.4	chr2:103149148-103150431		NA	NA	NA	NA	NA	NA	NA	NA
	SLC9B1	611527	NA	NA	NA	NA	NA	NA	NA	NA	989.871	-10.607229	uc003hww.3	chr4:1038222085-103822273		NA	NA	NA	NA	NA	NA	NA	NA
	SLC9C1	612738	NA	NA	NA	NA	NA	NA	NA	NA	441.632	-5.354181	uc011bhu.2	chr3:111859752-111860118		NA	NA	NA	NA	NA	NA	NA	NA
	SLOC1A2	602883	431.733	-5.536743	uc010sio.2	chr12:21417534-21422481	1391.19	-10.304464	uc010sio.2	chr12:21417534-21422481	257.213	-12.83682	uc001ret.3	chr12:21427849-21428222		NA	NA	NA	NA	NA	NA	NA	NA
	SLOC3A1	612435	NA	NA	NA	NA	NA	NA	NA	NA	412.403	-6.806471	uc002bqz.2	chr15:92703636-92709137		NA	NA	NA	NA	NA	NA	NA	NA
	SLOC4C1	609013	656.762	-9.227442	uc003kmm.3	chr5:101569692-101572561	NA	NA	NA	NA	821.741	-5.000387	uc002bqz.2	chr15:92703636-92709137		NA	NA	NA	NA	NA	NA	NA	NA
	SLFN11	614953	538.634	-6.188126	uc002jig.4	chr17:33677329-33679374	NA	NA	NA	NA	NA	NA	NA	NA		NA	NA	NA	NA	NA	NA	NA	NA

Table 1

SLFN12	614955	1001.33	-14.759082	uc002hjl.4	chr17:33738081-33738356	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLFN14	614958	258.049	-4.024696	uc010ctu.1	chr17:33875144-33875257	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLFN5	614952	836.648	-6.642239	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr17:33586727-33586839
SLIT2	603746	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr4:20620633-20620788
SLITRK2	300561	NA	NA	NA	NA	324.306	-6.715158	uc004fcd.3	chrX:144906482-144907360	NA	NA	NA	NA	NA	NA	NA	NA
SLITRK3	609679	700.878	-8.157872	uc003fej.4	chr3:164904508-164905684	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr3:164904508-164905684
SLK	616563	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr10:105785479-105787342
SLMAP	602701	693.203	-11.016308	uc003djd.1	chr3:57913116-57914894	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLP	107285	956.435	-9.66316	uc002xnm.1	chr20:43880879-43881055	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SLX1A	615822	667.35	-6.159967	uc002dsx.3	chr16:29469446-29469545	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMAD4	600993	1175.69	-13.669574	uc010xdp.2	chr18:48604838-48611411	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMAD5	603110	1329.21	-12.253239	uc003ljl.1	chr5:135513169-135518422	879.937	-10.738188	uc003ljl.1	chr5:135513169-135518422	NA	NA	NA	NA	NA	NA	NA	NA
SMARCA1	300012	NA	NA	NA	NA	407.84	-6.152469	uc004leun.4	chrX:128580478-128581278	336.483	-6.688818	uc004leun.4	NA	NA	NA	NA	chrX:128580478-128581278
SMARCA2	600014	532.215	-5.538332	uc003zht.3	chr9:2192740-2193623	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMARCA5	603375	502.401	-8.785072	uc003jlg.3	chr4:144474338-144478642	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMARCD1	612761	NA	NA	NA	NA	914.553	-8.737093	uc003hnb.4	chr4:95210686-95212443	NA	NA	NA	NA	NA	NA	NA	NA
SMARCD2	601735	NA	NA	NA	NA	723.961	-6.393706	uc001rvx.4	chr12:50492784-50494494	NA	NA	NA	NA	NA	NA	NA	NA
SMARCD3	601736	NA	NA	NA	NA	483.672	-4.580312	uc010wpt.1	chr17:61909441-61910297	NA	NA	NA	NA	NA	NA	NA	NA
SMARCE1	603111	NA	NA	NA	NA	1985.39	-10.812725	uc002huu.2	chr17:38783976-38785036	NA	NA	NA	NA	NA	NA	NA	NA
SMC2	605576	NA	NA	NA	NA	835.54	-6.871384	uc004bbv.3	chr9:106901597-106903700	NA	NA	NA	NA	NA	NA	NA	NA
SMC3	606062	NA	NA	NA	NA	NA	NA	NA	NA	1169.01	-9.22734	uc001lze.3	chr10:112364061-112364392	NA	NA	NA	NA
SMC5	609386	NA	NA	NA	NA	NA	NA	NA	NA	627.183	-6.132507	uc004ahr.2	chr9:72967248-72969789	NA	NA	NA	NA
SMC6	609387	NA	NA	NA	NA	NA	NA	NA	NA	550.001	-5.409413	uc002rcn.3	chr2:17845079-17846765	NA	NA	NA	NA
SMCO1	NA	NA	NA	NA	NA	1000.83	-9.241189	uc003fwr.3	chr3:196233750-196234757	NA	NA	NA	NA	NA	NA	NA	NA
SMCO3	NA	864.734	-9.49666	uc001rck.1	chr12:14957584-14958936	754.215	-9.700225	uc001rck.1	chr12:14957584-14958936	NA	NA	NA	NA	NA	NA	NA	NA
SMCO4	609477	NA	NA	NA	NA	284.853	-4.940173	uc001pds.4	chr11:93211639-93212175	NA	NA	NA	NA	NA	NA	NA	NA
SMCP	601148	NA	NA	NA	NA	NA	NA	NA	NA	741.973	-7.112372	uc001fat.3	chr1:152857250-152857523	NA	NA	NA	NA
SMEK1	NA	NA	NA	NA	NA	1361.66	-11.284748	uc001xzm.3	chr14:91923956-91925102	NA	NA	NA	NA	NA	NA	NA	NA
SMC8	613175	1161.43	-10.375812	uc002kik.3	chr17:57292364-57292611	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMG9	613176	502.679	-10.493111	uc002oxj.2	chr19:44235301-44235747	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMIM12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMIM13	NA	NA	NA	NA	NA	716.901	-4.239128	uc011dio.2	chr6:11134836-11138969	NA	NA	NA	NA	NA	NA	NA	NA
SMIM14	NA	NA	NA	NA	NA	855.152	-8.603154	uc003guo.3	chr4:39552546-39553745	NA	NA	NA	NA	NA	NA	NA	NA
SMIM15	NA	NA	NA	NA	NA	495.016	-5.78456	uc010fwr.1	chr5:60453536-60455773	NA	NA	NA	NA	NA	NA	NA	NA
SMNDC1	603519	1124.34	-12.109985	uc001kzc.4	chr10:112052798-112053907	951.788	-4.9999	uc001kzc.4	chr10:112052798-112053907	NA	NA	NA	NA	NA	NA	NA	NA
SMPDL3B	NA	572.614	-5.457567	uc001bpg.3	chr1:28285350-28285663	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SMTN	602127	NA	NA	NA	NA	368.923	-5.482789	uc003ajlk.2	chr22:31500302-31500610	NA	NA	NA	NA	NA	NA	NA	NA
SMU1	NA	NA	NA	NA	NA	NA	NA	NA	NA	854.689	-6.366339	uc003sf.1	chr9:33041850-33047290	NA	NA	NA	NA
SMUJ1	607753	432.422	-2.289898	uc001sff.2	chr12:54574142-54575879	NA	NA	NA	NA	564.091	-6.269116	uc001fff.2	chr12:54574142-54575879	NA	NA	NA	NA
SMYD1	606846	NA	NA	NA	NA	1254.13	-9.802419	uc002ssq.2	chr2:88411639-88412896	NA	NA	NA	NA	NA	NA	NA	NA
SMYD3	608783	NA	NA	NA	NA	NA	NA	NA	NA	1264.76	-12.311109	uc001ljl.3	chr1:245912642-245912864	NA	NA	NA	NA
SMYD4	NA	858.305	-5.809248	uc002flm.4	chr17:1682829-1684579	NA	NA	NA	NA	1799.1	-11.909435	uc002flm.4	chr17:1682829-1684579	NA	NA	NA	NA
SNCA	163890	NA	NA	NA	NA	NA	NA	NA	NA	1442.54	-9.011522	uc003hso.3	chr4:90645250-90647778	NA	NA	NA	NA
SNED1	616634	NA	NA	NA	NA	504.204	-5.745131	uc002wal.3	chr2:242011617-242015020	NA	NA	NA	NA	NA	NA	NA	NA
SNK	603032	NA	NA	NA	NA	NA	NA	NA	NA	600.425	-5.163575	uc002bhf.3	chr16:11770193-11773015	NA	NA	NA	NA
SNRK	612760	283.77	-6.898301	uc003cms.4	chr3:43390050-43392634	597.651	-6.943247	uc003cms.4	chr3:43390050-43392634	NA	NA	NA	NA	NA	NA	NA	NA
SNRNP70	180740	888.648	-9.198827	uc002pmk.3	chr19:49611701-49611870	888.279	-9.198827	uc002pmk.3	chr19:49611701-49611870	NA	NA	NA	NA	NA	NA	NA	NA
SNRPB	182282	NA	NA	NA	NA	292.961	-0.221107	uc010gan.3	chr20:2446882-2447903	553.907	-7.435828	uc002wfr.1	chr20:2442281-2442401	NA	NA	NA	NA
SNRPB2	603520	NA	NA	NA	NA	NA	NA	NA	NA	631.838	-12.533528	uc002wph.2	chr20:16721651-16722417	NA	NA	NA	NA

Table 1

	SNRPC:	603522	NA	NA	NA	NA	663.963	-6.998157	uc003qjl.2	chr6:34741348-34741634	NA	NA	NA	NA	NA	NA	NA	NA
	SNRPD1:	601063	1291.6	-13.884622	uc002ktj.1	chr18:19209100-19210208	NA	NA	NA	NA	408.648	-12.154357	uc002ktj.1	NA	NA	NA	NA	NA
	SNRPF:	603541	1000.96	-9.209761	uc001tej.3	chr12:96259850-96260238	1055.3	-7.053791	uc001fej.3	chr12:96259850-96260238	400.949	-5.579401	uc001tej.3	NA	NA	NA	NA	NA
	SNW1:	603055	NA	NA	NA	NA	531.877	-6.611368	uc010vtn.1	chr14:78184296-78184405	537.679	-6.611368	uc001vuf.3	NA	NA	NA	NA	NA
	SNX1:	601272	713.149	-6.352225	uc002amv.3	chr15:64429818-64436433	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SNX10:	614780	NA	NA	NA	NA	NA	NA	NA	NA	363.912	-7.367387	uc003sxx.3	NA	NA	NA	NA	NA
	SNX13:	606589	492.854	-9.957658	uc003slw.1	chr7:17832486-17836441	NA	NA	NA	NA	422.513	-2.932451	uc010hub.3	NA	NA	NA	NA	NA
	SNX20:	613281	NA	NA	NA	NA	1401.88	-13.019967	uc002egi.3	chr16:50700211-50701925	1546.23	-10.070407	uc002egi.3	NA	NA	NA	NA	NA
	SNX25:	NA	NA	NA	NA	NA	465.42	-8.023953	uc003ikx.3	chr4:186284620-186285120	NA	NA	NA	NA	NA	NA	NA	NA
	SNX5:	605937	NA	NA	NA	NA	NA	NA	NA	NA	553.066	-7.419147	uc010rrt.1	NA	NA	NA	NA	NA
	SNX6:	606098	1179.44	-10.573606	uc001wse.1	chr14:35030618-35032327	893.814	-5.476563	uc001wse.1	chr14:35030618-35032327	NA	NA	NA	NA	NA	NA	NA	NA
	SNX7:	614904	NA	NA	NA	NA	383.099	-5.465924	uc001dsa.3	chr1:99225688-99226056	NA	NA	NA	NA	NA	NA	NA	NA
	SOAT1:	102642	794.622	-5.314795	uc001gmil.3	chr1:179322777-179327814	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SOC51:	603597	NA	NA	NA	NA	NA	NA	NA	NA	422.224	-6.209258	uc002aar.1	NA	NA	NA	NA	NA
	SOD1:	147450	NA	NA	NA	NA	568.069	-6.993796	uc002ypa.3	chr21:33040892-33041243	NA	NA	NA	NA	NA	NA	NA	NA
	SOHLH1:	610224	1217.38	-10.425149	uc004cgl.3	chr9:138585255-138586191	637.307	-2.613077	uc010nbe.3	chr9:138585255-138585442	NA	NA	NA	NA	NA	NA	NA	NA
	SON:	182465	NA	NA	NA	NA	NA	NA	NA	NA	274.434	-13.767928	uc002ysb.1	NA	NA	NA	NA	NA
	SORBS1:	605264	NA	NA	NA	NA	490.626	-6.817215	uc001kkk.3	chr10:97071530-97074815	1055.02	-7.285255	uc001kkk.3	NA	NA	NA	NA	NA
	SORBS2:	616349	579.232	-6.712493	uc011cky.1	chr4:186547820-186547968	NA	NA	NA	NA	211.964	-5.55084	uc011cku.2	NA	NA	NA	NA	NA
	SORBS3:	610795	NA	NA	NA	NA	NA	NA	NA	NA	216.691	-4.264527	uc003xbv.3	NA	NA	NA	NA	NA
	SORCS3:	606285	538.158	-4.416637	uc001kyt.1	chr10:107023133-107024993	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SOST:	605740	NA	NA	NA	NA	526.261	-7.230777	uc002lec.1	chr17:41831098-41832709	NA	NA	NA	NA	NA	NA	NA	NA
	SOWAHC:	NA	242.596	-3.026875	uc002tfb.3	chr2:110373645-110376564	NA	NA	NA	NA	506.292	-6.379406	uc002tfb.3	NA	NA	NA	NA	NA
	SOX13:	604748	NA	NA	NA	NA	487.242	-2.327148	uc001lhal.3	chr1:204086883-204088974	330.485	-5.202928	uc001hal.3	NA	NA	NA	NA	NA
	SOX17:	610928	NA	NA	NA	NA	855.522	-14.204228	uc003xsb.4	chr8:55372556-55373456	NA	NA	NA	NA	NA	NA	NA	NA
	SOX18:	601618	503.059	-9.876274	uc002yls.3	chr20:62679079-62679518	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SOX21:	604974	NA	NA	NA	NA	297.277	-6.453732	uc001vma.3	chr13:95361879-95363472	NA	NA	NA	NA	NA	NA	NA	NA
	SOX9:	608160	1574.13	-17.117795	uc002jiw.3	chr17:70120529-70122560	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SP100:	604585	1289.55	0.899627	uc002vqq.2	chr2:231334828-231335250	NA	NA	NA	NA	613.616	-6.323353	uc002vqq.2	NA	NA	NA	NA	NA
	SP140L:	NA	NA	NA	NA	NA	NA	NA	NA	NA	691.626	-6.957186	uc010fkm.1	NA	NA	NA	NA	NA
	SP3:	601804	869.83	-14.202541	uc002ule.3	chr2:174771187-174774668	NA	NA	NA	NA	815.642	-11.697071	uc002ule.3	NA	NA	NA	NA	NA
	SPACA3:	612749	NA	NA	NA	NA	541.874	-6.636273	uc002hhs.1	chr17:31324797-31324892	NA	NA	NA	NA	NA	NA	NA	NA
	SPACA5:	300593	1029.65	-10.229265	NA	NA	729.536	-7.538841	uc004dlu.3	chrX:47869043-47869128	NA	NA	NA	NA	NA	NA	NA	NA
	SPAG17:	616554	NA	NA	NA	NA	NA	NA	NA	NA	505.858	-5.507895	uc001ehk.2	NA	NA	NA	NA	NA
	SPAG5:	615562	NA	NA	NA	NA	234.033	-4.782118	uc002hbg.3	chr17:26904583-26904716	NA	NA	NA	NA	NA	NA	NA	NA
	SPAG6:	605730	NA	NA	NA	NA	423.166	-1.202299	uc001lri.3	chr10:22705618-22706539	538.301	-8.382127	uc009xkh.3	NA	NA	NA	NA	NA
	SPAG8:	605731	890.511	-5.254453	uc003zyg.3	chr9:35809807-35809934	NA	NA	NA	NA	592.82	-6.327632	NA	NA	NA	NA	NA	NA
	SPAG9:	605430	NA	NA	NA	NA	478.312	-5.659283	uc002lta.3	chr17:49039535-49043632	687.185	-2.002605	uc002lta.3	NA	NA	NA	NA	NA
	SPAM1:	600930	NA	NA	NA	NA	NA	NA	NA	NA	339.049	-7.073237	uc003vle.3	NA	NA	NA	NA	NA
	SPARCL1:	606041	NA	NA	NA	NA	NA	NA	NA	NA	954.019	-8.603204	uc011cdc.2	NA	NA	NA	NA	NA
	SPATA12:	609869	843.373	-11.07683	uc003dij.1	chr3:57108296-57109460	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SPATA13:	613324	565.733	-1.553179	uc001upg.2	chr13:24876912-24881212	401.022	-6.033792	uc001lupi.1	chr13:24874700-24876597	454.2	-1.892292	uc001upg.2	NA	NA	NA	NA	NA
	SPATA21:	NA	713.179	-4.617924	uc001ayn.3	chr1:16725138-16725259	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SPATA22:	NA	NA	NA	NA	NA	NA	NA	NA	NA	509.641	-5.926885	uc002fvm.3	NA	NA	NA	NA	NA
	SPATA24:	NA	358.95	-5.601384	NA	NA	606.274	-5.454961	uc003lem.2	chr5:138737190-138737261	355.188	-3.864088	uc003lem.2	NA	NA	NA	NA	NA
	SPATA31D5P:	NA	215.651	-5.142823	uc001lsl.2	chr9:84531193-84534842	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SPATA45:	NA	505.487	-5.187592	uc001lbg.3	chr1:213003485-213003583	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	SPATA6L:	NA	NA	NA	NA	NA	325.157	-5.178956	uc003zim.3	chr9:4625655-4629089	575.645	-6.264313	uc011lly.2	NA	NA	NA	NA	NA
	SPATA9:	608039	NA	NA	NA	NA	NA	NA	NA	NA	432.002	-7.624494	uc003lji.1	NA	NA	NA	NA	NA

Table 1

SPATS1	NA	NA	NA	NA	981.96	-5.59685	uc021yzz.1	chr6:44344801-44344904	NA	NA	NA	NA	NA
SPC25	609395	NA	NA	NA	1149.44	-24.471959	uc002uel.3	chr2:169727401-169727940	NA	NA	NA	NA	NA
SPCS1	610358	260.833	-4.231693	chr3:52741829-52742197	533.106	-7.44409	uc01lbei.2	chr3:52741829-52742197	NA	NA	NA	NA	NA
SPCS2	NA	923.471	-6.053154	chr11:74688089-74690076	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPCS3	NA	1837.67	-27.374743	chr4:177249482-177253396	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPDL1	616401	300.513	-10.391336	chr5:169031212-169031781	NA	NA	NA	NA	428.659	-3.854858	uc010lji.3	chr5:169028829-169029025	NA
SPEF2	610172	603.709	-8.351957	chr5:35670351-35671676	795.907	-1.038239	uc003jln.4	chr5:35709232-35710951	1643.89	-0.768195	uc003jin.1	chr5:35670351-35671676	NA
SPERT	NA	476.474	-6.042993	uc001van.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPG11	610844	1765.19	-22.540734	uc010uel.2	NA	NA	NA	NA	1239.33	-7.515399	uc010bdw.3	chr15:44854894-44855318	NA
SPHG20	607111	NA	NA	NA	234.561	-2.923473	uc010len.2	chr13:36875775-36878501	383.064	-6.517393	uc010ten.2	chr13:36875775-36878501	NA
SPHK1	603730	NA	NA	NA	899.972	-4.112876	uc002jlf.1	chr17:74383668-74383941	NA	NA	NA	NA	NA
SP11	165170	NA	NA	NA	639.364	-9.461244	uc009yjp.1	chr11:47379732-47380149	NA	NA	NA	NA	NA
SPIC	612568	NA	NA	NA	NA	NA	NA	NA	668.265	-7.802478	uc001tid.3	chr12:101880550-101880775	NA
SPICE1	613447	865.231	-6.066186	uc003eag.4	512.221	-4.853026	uc003eah.1	chr3:113167682-113169105	315.829	-3.216705	uc003eah.1	chr3:113167682-113169105	NA
SPIDR	615384	NA	NA	NA	NA	NA	NA	NA	403.964	-5.124578	uc003xqd.3	chr8:48648013-48648563	NA
SPIN4	NA	NA	NA	NA	900.111	-10.304266	uc004dvl.3	chrX:62567107-62569948	NA	NA	NA	NA	NA
SPINK13	615205	NA	NA	NA	815.174	-8.001947	uc003ipc.3	chr5:147665612-147665773	220.442	-3.126082	uc003ipc.3	chr5:147665612-147665773	NA
SPINK5	605010	NA	NA	NA	379.353	-2.594932	uc003lox.2	chr5:147516555-147516925	1254.9	-10.746705	uc003low.2	chr5:147504413-147504503	NA
SPINK6	615868	NA	NA	NA	1486.13	-7.914863	uc003ipa.3	chr5:147594514-147594700	NA	NA	NA	NA	NA
SPINK9	613511	NA	NA	NA	NA	NA	NA	NA	248.578	-6.870792	uc003ipe.1	chr5:147719276-147719412	NA
SPIRE1	608216	NA	NA	NA	1156.46	-5.954216	uc010wzw.2	chr18:12446511-12449636	NA	NA	NA	NA	NA
SPNSZ	612584	NA	NA	NA	NA	NA	NA	NA	271.715	-4.93645	uc002fxk.2	chr17:4440748-4443228	NA
SPO11	605114	NA	NA	NA	400.773	-5.03142	uc002xye.3	chr20:55918517-55919049	NA	NA	NA	NA	NA
SPOCH3	607989	820.38	-11.383772	uc021xul.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPON1	604989	NA	NA	NA	NA	NA	NA	NA	572.782	-8.004886	uc001mle.3	chr11:14287234-14289679	NA
SPP2	602637	231.849	-5.182534	uc002vvk.1	NA	NA	NA	NA	1171.96	-8.017187	uc002vvk.1	chr2:234985489-234985776	NA
SPPL2A	608238	NA	NA	NA	628.072	-8.90362	uc001zyv.3	chr15:50999737-50999986	NA	NA	NA	NA	NA
SPPL3	608240	NA	NA	NA	NA	NA	NA	NA	1431.04	-10.939804	uc001zrc.3	chr12:121200313-121202801	NA
SPR	182125	364.117	-4.828377	uc002sik.2	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPRR4	616363	NA	NA	NA	NA	NA	NA	NA	680.48	-8.471494	uc001fav.1	chr1:152944607-152945069	NA
SPRY2	602466	NA	NA	NA	687.388	-9.534851	uc001vli.3	chr13:80910112-80910892	472.103	-9.308535	uc001vli.3	chr13:80910112-80910892	NA
SPRYD3	NA	NA	NA	NA	NA	NA	NA	NA	369.366	-4.282406	uc001btt.2	chr12:53458100-53459615	NA
SPRYD4	NA	NA	NA	NA	NA	NA	NA	NA	1096.87	-5.894511	uc010sqo.1	chr12:56863362-56863623	NA
SPRYD7	607866	1511.29	-15.432984	uc001vdl.2	NA	NA	NA	NA	1204.16	-10.480485	uc001vdl.2	chr13:50486842-50489198	NA
SPTBN1	182790	830.261	-9.019285	uc002rxu.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPTBN2	604985	NA	NA	NA	434.344	-6.191224	uc001ojc.1	chr11:66452723-66453864	NA	NA	NA	NA	NA
SPTBN4	606214	225.748	-8.520059	uc002omx.3	NA	NA	NA	NA	291.213	-2.645011	uc010egy.1	chr19:41060737-41061208	NA
SPTLC3	611120	NA	NA	NA	NA	NA	NA	NA	581.814	-6.994388	uc002woc.3	chr20:13030004-13030816	NA
SPTSSB	610412	1226.74	-11.837198	uc003fec.3	NA	NA	NA	NA	425.683	-4.853266	uc003fec.3	chr3:161062580-161063880	NA
SPTYD1	NA	NA	NA	NA	NA	NA	NA	NA	1057.89	-5.287116	uc010rdi.1	chr11:18633712-18633856	NA
SPX	NA	864.408	-7.476042	uc001fia.1	NA	NA	NA	NA	1135.32	-8.377746	NA	NA	NA
SOSTM1	601530	NA	NA	NA	NA	NA	NA	NA	779.686	-9.3016	uc011dgr.2	chr5:179263594-179265077	NA
SRBD1	NA	388.979	-6.375699	uc010yoc.2	NA	NA	NA	NA	NA	NA	NA	NA	NA
SRC	190090	NA	NA	NA	NA	NA	NA	NA	863.712	-6.09356	uc002xgx.3	chr20:36031783-36033821	NA
SRCIN1	610786	NA	NA	NA	302.731	-4.756481	uc002hqf.1	chr17:36697519-36699365	NA	NA	NA	NA	NA
SRF	600589	934.356	-6.010926	uc003oui.3	NA	NA	NA	NA	NA	NA	NA	NA	NA
SRGAP2	606524	NA	NA	NA	NA	NA	NA	NA	253.21	-5.490174	uc001hdy.3	chr1:206634766-206637783	NA
SRGAP3	606525	NA	NA	NA	563.742	-7.234438	uc003brj.1	chr3:9075115-9079742	NA	NA	NA	NA	NA
SRGN	177040	NA	NA	NA	NA	NA	NA	NA	541.629	-8.642394	uc001poz.3	chr10:70863877-70864567	NA

Table 1

SRI	182520	1246.41	-5.72651	uc003ujr.1	chr7:87834432-87835792	NA	NA	NA	NA	NA	NA	NA	841.11	-7.137879	NA	NA	chr16:4239375-4242153
SRP	604992	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	240.802	-3.373497	uc003vzv.4	NA	chr5:112203101-112204089
SRP19	182175	NA	NA	NA	NA	591.577	-7.665719	uc003kqc.3	chr5:112203235-112204089	NA	NA	NA	730.57	-9.569327	uc003kqb.2	NA	chr4:57368028-57369847
SRP72	602122	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	uc003hvv.3	NA	NA
SRPX	300187	NA	NA	NA	NA	476.457	-6.305272	uc004ddy.2	chrX:38000588-38008963	NA	NA	NA	NA	NA	NA	NA	NA
SRRD	602254	NA	NA	NA	NA	225.86	-6.044834	uc003acp.4	chr22:26887639-26887904	NA	NA	NA	NA	NA	NA	NA	NA
SRRM1	605975	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	655.437	-9.660024	uc001bjm.3	NA	chr1:24998778-24999772
SRRT	614469	559.343	-5.576236	uc003uwv.2	chr7:100486171-100486285	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SRSF1	600812	NA	NA	NA	NA	775.066	-7.691442	uc002wv.3	chr17:56078280-56082766	NA	NA	NA	656.991	-11.148425	uc002lvj.3	NA	chr17:56078280-56083107
SRSF11	602010	1747.54	-7.031443	uc009wbi.3	chr1:70694967-70695717	NA	NA	NA	NA	NA	NA	NA	841.592	-9.925747	uc001des.3	NA	chr1:70716489-70717701
SRSF5	600914	1367.24	-8.168521	uc001xll.3	chr14:70238179-70238722	NA	NA	NA	NA	NA	NA	NA	1012.87	-9.167801	uc021vuj.1	NA	chr14:70236279-70236553
SRSF6	601944	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	569.071	-4.178595	uc002xki.3	NA	chr20:42089704-42092244
SRSF7	600572	658.583	-9.678988	uc002rqz.3	chr2:38970741-38972274	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SS18L1	606472	676.217	-5.158266	uc002yeb.3	chr20:60754265-60757566	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SSC4D	607639	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	208.938	-5.911657	uc003ufa.3	NA	chr7:76018646-76019332
SSF42	118990	1075.98	-6.180949	uc010zfm.1	chr2:182757392-182759422	NA	NA	NA	NA	NA	NA	NA	532.419	-6.544587	uc010zfm.1	NA	chr2:182757392-182759422
SSH2	606779	482.336	-7.471751	uc002heq.3	chr17:28000930-28001122	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SSMEM1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	431.753	-6.151653	uc003vpp.3	NA	chr7:129856311-129856684
SSR3	606213	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	274.413	-6.870155	uc003fau.3	NA	chr3:156257929-156260991
SSRP1	604328	559.305	-4.294962	uc001njt.3	chr11:57093459-57093880	NA	NA	NA	NA	NA	NA	NA	1005.49	-7.739203	uc001njt.3	NA	chr11:57093459-57093880
SSU72	NA	460.439	-6.681802	uc001agd.3	chr1:1477053-1477445	NA	NA	NA	NA	NA	NA	NA	882.012	-0.352972	uc001agd.3	NA	chr1:1477053-1477445
SSX2IP	608690	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	829.896	-4.199744	uc001dhf.3	NA	chr2:85109390-85113115
ST14	606797	NA	NA	NA	NA	541.95	-9.748608	uc010sca.1	chr11:130066604-130066689	NA	NA	NA	NA	NA	NA	NA	NA
STGAL2	608472	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	203.522	-6.04655	uc002tdq.3	NA	chr2:107418056-107423133
ST8SIA2	602546	584.274	-9.212801	uc002bra.3	chr15:93007616-93011958	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ST8SIA4	602547	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1620.63	-8.344025	uc003knk.3	NA	chr5:100142639-100147550
ST8SIA5	607162	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1203.06	-7.081312	uc002lci.1	NA	chr18:44259081-44260004
STAG1	604358	314.965	-4.445701	uc003era.1	chr3:136055999-136057095	NA	NA	NA	NA	NA	NA	NA	299.9	-4.731915	uc003era.1	NA	chr3:136055999-136057095
STAG3	608489	537.362	-5.703427	uc003uix.1	chr7:99811639-99812010	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STAM	601899	538.899	-6.411042	uc001lpl.2	chr10:17756780-17758821	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STAM2	606244	1006.18	-5.703558	uc002lyc.4	chr2:152973315-152977087	559.157	-6.60004	uc002lyc.4	chr2:152973315-152977087	NA	NA	NA	NA	NA	NA	NA	NA
STARD13	609866	NA	NA	NA	NA	528.738	-6.796975	uc021ria.1	chr13:33691685-33692187	209.503	-4.414655	uc001uuu.3	NA	NA	NA	NA	chr13:3367272-33679729
STARD3NL	611759	258.856	-5.310095	uc003lfr.3	chr7:38269524-38270272	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STARD4	607049	NA	NA	NA	NA	242.84	-6.129348	uc003kph.1	chr5:110834022-110835583	337.207	-7.422482	uc003kpl.2	NA	NA	NA	NA	chr5:110835944-110836616
STARD7	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	587.126	-6.579027	uc002svl.3	NA	chr2:96850603-96852467
STAT1	600555	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1256.43	-4.915878	uc021vue.1	NA	chr2:191833762-191835428
STAT2	600556	NA	NA	NA	NA	699.775	-3.322284	uc001slb.3	chr12:56735392-56737172	836.53	-5.502189	uc001slb.3	NA	NA	NA	NA	chr12:56735392-56737172
STAT4	600558	845.126	-13.230902	uc002uso.2	chr2:191898652-191897678	893.437	-8.74047	uc002usm.2	chr2:191894302-191894565	1180.5	-3.608431	uc002uso.2	NA	NA	NA	NA	chr2:191896852-191897678
STAT5B	604260	1184.21	-12.483906	uc002hzh.3	chr17:40351195-40353755	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STC1	601185	557.513	-6.208496	uc003xdw.1	chr8:23699434-23702282	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STC2	603665	690.729	-4.235682	uc003mcn.1	chr5:172741726-172744849	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STEAP1	604415	289.652	-14.053589	NA	NA	1594.23	-18.156936	uc010lem.3	chr7:99791408-99791565	331.495	-4.006339	uc003ujz.3	NA	NA	NA	NA	chr7:99861939-99866992
STEAP2	605094	NA	NA	NA	NA	761.288	-4.264527	uc003ujz.3	chr7:89861939-89866992	764.529	-4.069949	uc002tlp.3	NA	NA	NA	NA	chr2:120020915-120023227
STEAP3	609671	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
STK17B	604727	NA	NA	NA	NA	572.166	-9.133948	uc002ulk.3	chr2:196998307-197002170	NA	NA	NA	NA	NA	NA	NA	NA
STK19	604977	948.393	-8.569052	uc003nyl.3	chr6:31948827-31949223	NA	NA	NA	NA	NA	NA	NA	477.369	-5.793653	uc003nyf.3	NA	chr6:31948827-31949223
STK24	604984	293.317	-5.321444	uc001vnm.1	chr13:99102455-99105426	1676.33	-12.429815	uc001vnm.1	chr13:99102455-99105426	NA	NA	NA	NA	NA	NA	NA	NA
STK26	300547	647.935	-4.348404	uc004ewk.1	chrX:131208188-131209971	883.645	-8.170298	uc004ewk.1	chrX:131208188-131209971	NA	NA	NA	NA	NA	NA	NA	NA
STK31	605790	391.221	-5.616137	uc003swv.1	chr7:23943871-23944365	909.807	-7.422209	uc003swv.1	chr7:23943871-23944365	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

STK32A	NA	714.241	-6.051403	uc003lom.2	chr5:146754827-146755479	357.161	-3.62337	uc003lol.4	chr5:146728287-146728392	200.158	-6.004877	uc003lol.4	chr5:146728287-146728392
STK32C	NA	235.692	-3.430123	uc009ybd.1	chr10:134038659-134038878	NA	NA	NA	NA	596.008	-5.386896	uc009ybd.1	chr10:134038659-134038878
STK35	609370	NA	NA	NA	NA	1699.34	-12.096032	uc010zpu.2	chr20:2124543-2129198	1168.57	-10.093986	uc002wfw.4	chr20:2124430-2129198
STK36	607652	818.096	-4.49311	uc002vlu.3	chr2:219566733-219567440	NA	NA	NA	NA	563.637	-5.888658	uc002vlu.3	chr2:219566733-219567440
STK38	606964	NA	NA	NA	NA	601.14	-5.722554	uc003omrg.3	chr6:36461669-36463560	NA	NA	NA	NA
STMN1	151442	209.049	-4.439937	uc001lhz.3	chr1:26228607-26227506	NA	NA	NA	NA	NA	NA	NA	NA
STMN4	NA	897.767	-7.943527	uc011lai.2	chr8:27093814-27094422	NA	NA	NA	NA	NA	NA	NA	NA
STMND1	NA	NA	NA	NA	NA	1397	-12.449978	uc021ymc.1	chr6:17131113-17131603	NA	NA	NA	NA
STOML2	608292	1502.11	-10.015998	NA	NA	NA	NA	NA	NA	772.95	-10.130422	uc003zwl.3	chr9:35099889-35100031
STOML3	608327	508.621	-6.075611	uc001luwx.3	chr13:39540062-39540961	NA	NA	NA	NA	569.154	-4.46022	uc001luwx.3	chr13:39540062-39540961
STOX1	609397	NA	NA	NA	NA	512.281	-2.051256	uc001jqz.3	chr10:70652493-70652816	373.888	-5.407401	uc001jqz.3	chr10:70652493-70652816
STOX2	NA	326.077	-1.345168	uc003lvz.1	chr4:184938438-184938875	NA	NA	NA	NA	1034.8	-6.267608	uc003lvz.1	chr4:184938438-184938875
STPG1	615826	662.112	-9.108675	uc010oej.2	chr1:24683489-24684661	NA	NA	NA	NA	NA	NA	NA	NA
STRADA	608626	290.449	-5.103201	uc002lhm.3	chr17:61780192-61780958	NA	NA	NA	NA	NA	NA	NA	NA
STRN1	614765	NA	NA	NA	NA	414.952	-4.138054	uc002rpn.3	chr2:37064841-37076598	NA	NA	NA	NA
STRN3	614766	487.609	-12.384805	uc001wqu.2	chr14:31363005-31364616	NA	NA	NA	NA	NA	NA	NA	NA
STT3A	601134	905.847	-3.945138	uc009zbm.2	chr11:125479523-125479793	NA	NA	NA	NA	589.887	-8.499585	uc001qcd.2	chr11:125490706-125491280
STX18	606046	285.618	-4.694269	uc003gic.3	chr4:4420696-4421760	NA	NA	NA	NA	NA	NA	NA	NA
STX1A	186590	NA	NA	NA	NA	NA	NA	NA	NA	1527.72	-14.544135	uc003tyy.3	chr7:73113535-73114801
STX3	600876	619.733	-5.366505	uc001nog.3	chr11:59568328-59573355	NA	NA	NA	NA	NA	NA	NA	NA
STX5	603189	NA	NA	NA	NA	NA	NA	NA	NA	1589.08	-25.854653	uc001mwh.3	chr11:62574332-62574940
STXBP5	604586	NA	NA	NA	NA	571.411	-7.297077	uc003qlz.3	chr6:147705892-147711612	NA	NA	NA	NA
STXBP6	607958	NA	NA	NA	NA	367.538	-6.327632	uc001wpt.3	chr14:25281306-25281914	NA	NA	NA	NA
SUB1	600503	1553.78	-16.177929	uc003jhs.2	chr5:32601191-32604185	NA	NA	NA	NA	NA	NA	NA	NA
SUCLA2	603921	NA	NA	NA	NA	1303.15	-19.348472	uc010lgb.2	chr13:48516791-48517505	NA	NA	NA	NA
SUCO	NA	NA	NA	NA	NA	NA	NA	NA	NA	1011.02	-5.972094	uc010pmm.1	chr1:172571963-172572423
SUDS3	608250	NA	NA	NA	NA	1197.16	-9.223827	uc001twz.3	chr12:118852239-118855840	1282.9	-14.402776	uc001twz.3	chr12:118852239-118855840
SUGCT	609187	NA	NA	NA	NA	360.247	-7.304372	uc003thm.2	chr7:40900079-40900366	NA	NA	NA	NA
SUGP2	607993	NA	NA	NA	NA	245.838	-8.496098	uc002nkk.2	chr19:19101697-19101958	1146.2	-5.369502	uc002nkk.2	chr19:19101697-19101958
SULT1A4	615819	NA	NA	NA	NA	NA	NA	NA	NA	524.797	-5.274785	uc010vdp.2	chr16:29474888-29475661
SULT1E1	600043	942.633	-6.888518	uc003heo.3	chr4:70706930-70707711	1283.51	-10.252111	uc003heo.3	chr4:70706930-70707711	NA	NA	NA	NA
SULT2A1	125263	NA	NA	NA	NA	1538.62	-13.504115	uc002phr.2	chr19:48373723-48374711	NA	NA	NA	NA
SULT6B1	NA	NA	NA	NA	NA	244.992	-4.507734	uc002rpu.3	chr2:37394963-37395077	682.209	-7.65441	uc002rpu.3	chr2:37394963-37395077
SUMO1	601912	1115.36	-11.31308	uc002uyz.1	chr2:203070903-203071975	353.979	-4.941899	uc002uyz.1	chr2:203070903-203071975	735.484	-9.015469	uc002uyz.1	chr2:203070903-203071975
SUMO3	602231	534.338	-4.498862	uc002zfr.1	chr21:46225532-46226865	NA	NA	NA	NA	NA	NA	NA	NA
SUN1	607723	589.152	-8.217307	uc021tzy.1	chr7:883274-8833509	843.609	-6.362308	uc021tzy.1	chr7:883274-8833509	1188.66	-12.617362	uc003sje.1	chr7:889327-890404
SUN3	NA	NA	NA	NA	NA	318.241	-4.833538	uc010kyq.3	chr7:48026746-48026926	NA	NA	NA	NA
SUOX	606887	NA	NA	NA	NA	NA	NA	NA	NA	715.025	-6.729523	uc009zoh.3	chr12:5639619-56396838
SUPT20H	613417	637.668	-6.726369	uc001luwd.3	chr13:37583451-37583845	1363.44	-1.582399	uc001luwd.3	chr13:37583451-37583845	1362.49	-16.032758	uc001luwe.3	chr13:37583451-37583808
SUPV3L1	605122	675.813	-7.185091	uc001lpe.1	chr10:70968792-70968849	1096.54	-13.264115	NA	NA	NA	NA	NA	NA
SUSD5	NA	NA	NA	NA	NA	NA	NA	NA	NA	1074.77	-7.447648	uc003dfo.1	chr3:33191537-33194233
SUV39H2	606503	NA	NA	NA	NA	632.508	-8.631463	uc001ing.3	chr10:14944512-14946304	NA	NA	NA	NA
SUV420H1	NA	NA	NA	NA	NA	250.335	-5.196714	uc001ono.1	chr11:67933186-67934440	NA	NA	NA	NA
SV2A	185860	571.658	-6.777748	uc001eth.2	chr1:149877024-149877427	NA	NA	NA	NA	NA	NA	NA	NA
SVEP1	611691	NA	NA	NA	NA	1188.24	-5.458538	uc010mly.3	chr9:113127529-113128818	640.844	-7.586458	uc010mty.3	chr9:113127529-113128818
SVIL	604126	999.623	-12.399563	uc010qdw.1	chr10:29746277-29747175	NA	NA	NA	NA	NA	NA	NA	NA
SVOP1	611700	NA	NA	NA	NA	865.302	-8.510422	uc003vue.3	chr7:138279030-138279354	NA	NA	NA	NA
SWAP70	604762	567.632	-7.268639	uc001mhv.3	chr11:9762013-9763487	NA	NA	NA	NA	NA	NA	NA	NA
SWSAP1	614536	NA	NA	NA	NA	734.199	-5.998646	uc002mrq.1	chr19:11486693-11487627	NA	NA	NA	NA

Table 1

SWT11	NA	1030.25	-14.717634	uc001lgr.4	chr1:185259936-185260913	NA	NA	NA	NA	NA	1101.52	-11.023731	NA	NA	chr8:110586405-110587134
SYBU	611568	505.324	-8.808789	uc0003ynh.4	chr8:110586405-110587134	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYCE1	611486	332.859	-4.934889	uc001lhm.2	chr10:135367404-135367793	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYCP1	602162	926.38	-10.64099	uc001leq.3	chr1:115537641-115537990	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYCP2	604105	1334.32	-5.135784	uc002yaz.3	chr20:58438618-58439365	671.987	-9.989008	uc10lgu.1	chr20:58474860-58475108	NA	NA	NA	NA	NA	NA
SYDE2	NA	NA	NA	NA	NA	NA	NA	NA	NA	930.817	-12.652767	uc009wcm.3	chr1:85623356-85624432	NA	NA
SYF2	607090	1319.59	-12.567114	uc010ooo.1	chr1:25553284-25553928	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYMPK	602388	513.572	-8.477677	uc002pdo.1	chr19:46322171-46324357	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYNJ2	609410	1152.88	-13.182496	uc003qqx.2	chr6:158517397-158520207	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYNP02	NA	NA	NA	NA	NA	680.523	-0.693219	uc003icm.4	chr4:119953213-119959669	356.46	-4.976344	uc010na.3	chr4:119958345-119959669	NA	NA
SYNPR	NA	249.021	-5.529019	uc003dlp.3	chr3:63601158-63602597	517.543	-6.331813	uc003dlp.3	chr3:63601158-63602597	NA	NA	NA	NA	NA	NA
SYNRG	607291	NA	NA	NA	NA	371.963	-4.377383	uc002hoa.3	chr17:35874900-35879042	788.165	-9.246318	uc002hof.3	chr17:35900753-35902065	NA	NA
SYPL2	NA	NA	NA	NA	NA	1047.13	-7.595238	uc001dkp.3	chr1:110022171-110024764	NA	NA	NA	NA	NA	NA
SYT1	185605	NA	NA	NA	NA	NA	NA	NA	NA	353.633	-5.928584	uc001sys.3	chr12:79842905-79845788	NA	NA
SYT16	610950	NA	NA	NA	NA	914.702	-9.640186	uc001xlu.1	chr14:62567426-62568427	NA	NA	NA	NA	NA	NA
SYT2	600104	NA	NA	NA	NA	NA	NA	NA	NA	1006.24	-8.049553	uc001lgye.3	chr1:202559725-202565884	NA	NA
SYT4	600103	NA	NA	NA	NA	1449.72	-12.865505	uc002law.3	chr18:40847857-40850305	NA	NA	NA	NA	NA	NA
SYT6	607718	NA	NA	NA	NA	931.476	-4.783196	uc001eeu.3	chr1:114631914-114634632	NA	NA	NA	NA	NA	NA
SYTL4	300723	610.159	-6.540885	uc004egg.4	chrX:99939710-99943302	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SYTL5	NA	685.23	-4.191906	uc004ddu.3	chrX:37985984-37988073	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAB1	602615	NA	NA	NA	NA	371.825	-5.838255	uc003axr.3	chr22:39826228-39827887	NA	NA	NA	NA	NA	NA
TAC1	162320	NA	NA	NA	NA	443.457	-5.440098	uc003uop.4	chr7:97369233-97369784	586.085	-4.957228	uc003uop.4	chr7:97369233-97369784	NA	NA
TACC3	605303	1319.32	-11.124323	uc003gdo.3	chr4:1746741-1746905	NA	NA	NA	NA	602.241	-6.139999	uc010lbz.3	chr4:1739718-1740077	NA	NA
TADA2A	602276	NA	NA	NA	NA	643.464	-9.226754	uc002hml.3	chr17:35837088-35837226	NA	NA	NA	NA	NA	NA
TAF1	313650	445.757	-0.227644	uc004dzt.4	chrX:70683897-70685855	NA	NA	NA	NA	983.358	-8.998031	uc004dzt.4	chrX:70683897-70685855	NA	NA
TAF12	600773	NA	NA	NA	NA	NA	NA	NA	NA	1258.8	-9.320778	uc001lqx.3	chr1:28929609-28930050	NA	NA
TAF13	600774	NA	NA	NA	NA	NA	NA	NA	NA	743.015	-10.435717	uc001dwm.1	chr1:109606998-109607144	NA	NA
TAF1B	604904	917.874	-9.513878	uc010exc.2	chr2:10053443-10053714	NA	NA	NA	NA	416.751	-5.778962	uc010exc.2	chr2:10053443-10053714	NA	NA
TAF4	601796	374.117	-7.497794	uc002ybs.3	chr20:60549854-60551223	638.926	-4.265719	uc002ybs.3	chr20:60549854-60551223	NA	NA	NA	NA	NA	NA
TAF4B	601689	434.947	-5.244409	uc002kvl.4	chr18:23969977-23971650	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAF5L	NA	NA	NA	NA	NA	397.954	-7.686045	uc001lht.3	chr1:229728866-229730043	NA	NA	NA	NA	NA	NA
TAF7	600573	277.373	-4.576565	uc003lgl.3	chr5:140698057-140698561	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAF7L	300314	905.057	-8.768204	uc004eha.3	chrX:100523241-100524180	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAF9	600822	NA	NA	NA	NA	690.346	-14.446521	uc003jwc.1	chr5:68660570-68660769	819.014	-14.289625	uc003jwa.3	chr5:68647553-68647887	NA	NA
TALD01	602063	1022.91	-5.717111	uc001lpz.3	chr11:764846-765024	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAMM41	614948	638.633	-4.397041	uc003bwh.3	chr3:11831919-11831978	1184.55	-8.903991	uc011tao.1	chr3:11848768-11848884	422.785	-7.06065	uc002uag.3	chr2:160087524-160089170	NA	NA
TANC1	611397	1089.92	-14.358168	uc002uag.3	chr2:160087524-160089170	NA	NA	NA	NA	471.993	-3.122276	uc011ahg.1	chr22:20052088-20053447	NA	NA
TANGO2	NA	NA	NA	NA	NA	464.875	-6.845506	uc002zre.2	chr22:20041283-20043764	NA	NA	NA	NA	NA	NA
TANGO6	NA	890.336	-9.333679	uc002ewh.3	chr16:68901135-68901883	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TANK	603893	605.954	-6.868704	uc002ubq.1	chr2:162061338-162061490	NA	NA	NA	NA	677.857	-8.390802	uc002heb.1	chr17:27838026-27842015	NA	NA
TAOK1	610266	NA	NA	NA	NA	604.47	-6.759758	uc002heb.1	chr17:27838026-27842015	NA	NA	NA	NA	NA	NA
TAOK3	NA	NA	NA	NA	NA	576.451	-4.663648	uc001ttw.3	chr12:118587606-118588801	NA	NA	NA	NA	NA	NA
TAP1	170260	NA	NA	NA	NA	387.3	-5.745131	uc011dql.2	chr6:32812986-32813355	546.418	-4.428412	uc011dql.2	chr6:32812986-32813355	NA	NA
TAP2	170261	435.294	-3.866571	uc003occ.3	chr6:32793187-32796682	NA	NA	NA	NA	336.032	-8.063926	uc003ocb.1	chr6:32789610-32790065	NA	NA
TAPBP	601962	NA	NA	NA	NA	NA	NA	NA	NA	527.289	-4.906838	uc003odk.2	chr6:33267472-33269536	NA	NA
TARBP1	605052	695.436	-4.312845	uc001hwd.3	chr1:234527059-234527322	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TARDBP	605078	714.576	-5.806374	uc001art.3	chr1:11082712-11085549	NA	NA	NA	NA	464.386	-9.981928	uc001art.3	chr1:11082712-11085549	NA	NA
TARP	NA	261.245	-4.37522	uc022aby.1	chr7:38279181-38279624	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TARSL2	NA	674.061	-7.48428	NA	NA	NA	NA	NA	NA	224.93	-6.733621	uc002btl.3	chr15:102193955-102194933	NA	NA

Table 1

TAS2R20	613962	615519	-7.661829	uc001qzm.2	chr12:11148561-11149544	NA	NA	NA	uc003vwr.1	chr7:141491062-141491166	NA	NA	NA	NA
TAS2R5	605062	NA	NA	NA	NA	600.833	-4.200766	NA	NA	chr7:141491062-141491166	NA	NA	NA	NA
TASP1	608270	467.592	-5.644081	uc002vot.3	chr20:13370036-13371006	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAZ	300394	754.465	-5.032023	uc004fkx.3	chrX:153649344-153650063	614.296	-3.166743	NA	uc004fkx.3	chrX:153649344-153650063	NA	NA	NA	NA
TBC1D15	612662	552.744	-4.949832	uc001swu.3	chr12:72316985-72320629	827.856	-5.446609	NA	uc001swu.3	chr12:72316985-72320629	325.816	-3.987032	uc001swu.3	chr12:72316985-72320629
TBC1D22A	NA	NA	NA	NA	NA	337.161	-5.666301	NA	uc003bib.3	chr22:47569270-47571342	NA	NA	NA	NA
TBC1D22B	NA	NA	NA	NA	NA	431.305	-7.580244	NA	uc003omn.3	chr6:37298949-37300746	NA	NA	NA	NA
TBC1D2B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	386.076	-4.075074	uc002bcy.4	chr15:78287327-78290501
TBC1D3	607741	669.02	-9.140311	uc002hoo.2	chr17:36294601-36295098	769.959	-0.014241	NA	uc002hoo.2	chr17:36294601-36295098	NA	NA	NA	NA
TBC1D30	615077	NA	NA	NA	NA	900.303	-22.796976	NA	uc001tsh.2	chr12:65269569-65274798	NA	NA	NA	NA
TBC1D31	NA	NA	NA	NA	NA	799.115	-8.702229	NA	uc003ypo.1	chr8:124113266-124113325	NA	NA	NA	NA
TBC1D5	615740	475.143	-8.115435	uc010heu.3	chr3:17198654-17202454	NA	NA	NA	NA	NA	NA	NA	NA	NA
TBC1D7	612655	653.57	-7.122441	uc003naj.3	chr6:13266774-13268067	343.821	-4.714545	NA	uc003naj.3	chr6:13266774-13268067	NA	NA	NA	NA
TBC1D9	NA	590.541	-6.915958	uc010loj.3	chr4:141541936-141543348	988.716	-7.929471	NA	uc010loj.3	chr4:141541936-141543348	637.53	-6.883852	uc010loj.3	chr4:141541936-141543348
TBCA	610058	NA	NA	NA	NA	669.365	-4.894416	NA	uc003kth.1	chr5:76986995-76987242	604.158	-6.10436	uc003kth.1	chr5:76986995-76987242
TBCB	601303	898.882	-10.904862	uc002odg.1	chr19:36616685-36616849	NA	NA	NA	NA	NA	NA	NA	NA	NA
TBCC	602971	1545.17	-7.465973	uc003osl.3	chr6:42712234-42712770	NA	NA	NA	NA	NA	1219.28	-11.2432	uc003osl.3	chr6:42712234-42712770
TBCE	604934	NA	NA	NA	NA	823.282	-7.955397	NA	uc001hwz.1	chr1:235612078-235612280	NA	NA	NA	NA
TBP	600075	1272.98	-12.556877	uc003qxt.3	chr6:170881354-170881958	747.772	-6.666109	NA	uc003qxt.3	chr6:170881354-170881958	557.218	-7.004682	uc003qxt.3	chr6:170881354-170881958
TBPL2	608964	NA	NA	NA	NA	552.042	-6.702338	NA	uc001xby.3	chr14:55880930-55881096	NA	NA	NA	NA
TBRG1	610614	NA	NA	NA	NA	642.636	-12.373415	NA	uc001tqaj.4	chr11:124502135-124505822	NA	NA	NA	NA
TBX1	602054	285.319	-6.619927	uc002zqb.3	chr22:19766931-19767068	NA	NA	NA	NA	NA	NA	NA	NA	NA
TBX22	300307	NA	NA	NA	NA	284.692	-5.418754	NA	uc004edi.1	chrX:79286611-79287268	NA	NA	NA	NA
TBX3	601621	NA	NA	NA	NA	353.491	-4.861494	NA	uc010syw.1	chr12:115117761-115118608	NA	NA	NA	NA
TCAM	NA	NA	NA	NA	NA	594.711	-6.550765	NA	uc003cnb.4	chr3:443398757-44401294	NA	NA	NA	NA
TCEAL1	300237	1339.45	-10.692594	uc004eks.3	chrX:102885325-102885876	NA	NA	NA	NA	NA	1174.53	-12.12478	uc004eks.3	chrX:102885325-102885876
TCEAL2	NA	407.954	-4.933537	uc004eip.3	chrX:101382487-101382684	NA	NA	NA	NA	NA	954.348	-9.647427	uc004eip.3	chrX:101382487-101382684
TCEAL4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	943.825	-9.73005	uc004ekl.3	chrX:102842252-102842655
TCEAL7	300771	1373.1	-11.174553	uc004ekc.2	chrX:102586635-102587251	NA	NA	NA	NA	NA	NA	NA	NA	NA
TCEB1	600788	NA	NA	NA	NA	NA	NA	NA	NA	NA	413.53	-5.5702	uc022awv.1	chr8:74857373-74858864
TOERG1	605409	NA	NA	NA	NA	514.596	-5.733898	NA	uc003leb.3	chr5:145890206-145891069	NA	NA	NA	NA
TOF24	NA	1586.68	-14.105595	uc022avi.1	chr8:67858736-67860285	NA	NA	NA	NA	NA	NA	NA	NA	NA
TCF7L1	604652	788.666	-5.388776	uc002soy.3	chr2:85536586-85537511	NA	NA	NA	NA	NA	NA	NA	NA	NA
TOFL5	604745	NA	NA	NA	NA	367.226	-7.351356	NA	uc002ydc.3	chr20:61472467-61473326	NA	NA	NA	NA
TCL1B	603769	319.376	-3.676631	uc001yfa.3	chr14:96157659-96158965	322.924	-3.115225	NA	uc001yfa.3	chr14:96157659-96158965	801.36	-7.459216	uc001yfa.3	chr14:96157659-96158965
TCP1	186980	NA	NA	NA	NA	1557.68	-12.617483	NA	uc003qsr.3	chr6:160199530-160200076	NA	NA	NA	NA
TCPI0	187020	NA	NA	NA	NA	NA	NA	NA	NA	NA	631.072	-9.881305	uc003qvw.3	chr6:167787380-167789973
TCPI0L	603865	1178.78	-12.784408	uc002ypw.4	chr21:33947151-33949083	NA	NA	NA	NA	NA	NA	NA	NA	NA
TCPI11	186982	NA	NA	NA	NA	328.137	-5.591052	NA	uc003ojz.1	chr6:35085849-35086045	NA	NA	NA	NA
TCPI11L1	NA	712.032	-5.053127	uc001mud.3	chr11:33094223-33095109	NA	NA	NA	NA	NA	NA	NA	NA	NA
TCTA	600690	996.254	-10.483305	uc003cww.4	chr3:49452296-49453909	NA	NA	NA	NA	NA	NA	NA	NA	NA
TCTN3	613847	880.835	-10.926835	uc001kib.4	chr10:97423153-97423823	NA	NA	NA	NA	NA	NA	NA	NA	NA
TDG	601423	344.594	-4.718874	uc001lkg.3	chr12:104380869-104382656	NA	NA	NA	NA	NA	NA	NA	NA	NA
TDP1	607198	NA	NA	NA	NA	NA	NA	NA	NA	NA	222.149	-7.293817	uc010atn.3	chr14:90509414-90511108
TDP2	605764	NA	NA	NA	NA	NA	NA	NA	NA	NA	823.61	-8.527362	uc003nej.3	chr6:24650205-24651015
TDRD1	605796	722.864	-8.998752	uc001lbg.1	chr10:115991277-115992063	NA	NA	NA	NA	NA	NA	NA	NA	NA
TDRD10	NA	547.489	-7.397976	uc001lfd.3	chr1:154520187-154520623	NA	NA	NA	NA	NA	NA	NA	NA	NA
TDRD9	NA	NA	NA	NA	NA	735.973	-8.220191	NA	uc001yom.4	chr14:104518420-104519004	NA	NA	NA	NA
TDRKH	609501	901.219	-8.115406	uc009wnb.1	chr1:151744041-151744462	367.979	-3.085372	NA	uc001eyy.2	chr1:151742583-151743038	628.452	-4.221173	uc009wnb.1	chr1:151744041-151744462

Table 1

TEAD1	189967	596.256	-13.238792	uc021qdk.1	chr11:12958770-12966284	NA	NA	NA	NA	NA	NA	439.372	-14.086679	uc021qdk.1	chr11:12958770-12966284
TEC	600583	687.467	-7.550431	uc003gxyz.3	chr4:48137800-48139432	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TEDDM1	NA	623.469	-10.60106	uc001gpe.3	chr1:182367252-182368798	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TEFM	616422	1692.23	-12.766101	uc002hfu.2	chr17:29226001-29226186	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TENN3	610083	1176.2	-13.044868	uc003ive.1	chr4:183676417-183676506	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TENN4	610084	448.024	-5.59229	uc001ozk.4	chr11:78364328-78369102	1028.95	-2.887993	uc001ozk.4	chr11:78364328-78369102	NA	NA	NA	NA	NA	NA
TER1	600951	NA	NA	NA	NA	861.305	-7.780448	uc003xzd.2	chr8:73958373-73959987	NA	NA	NA	NA	NA	NA
TES	606085	NA	NA	NA	NA	389.861	-5.651652	uc011kmx.2	chr7:115889405-115890086	NA	NA	NA	NA	NA	NA
TET1	607790	NA	NA	NA	NA	1244.77	-10.884352	uc001jpk.4	chr10:70451572-70454239	NA	NA	NA	NA	NA	NA
TET2	612839	458.611	-4.80488	uc021xqk.1	chr4:106158598-106163928	NA	NA	NA	NA	NA	NA	765.489	-5.825271	uc021xqk.1	chr4:106158598-106163928
TEX10	NA	569.217	-8.671513	uc011hvf.2	chr9:103064357-103064472	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TEX14	605792	1470.93	-10.504005	uc002hwr.2	chr17:56634038-56634371	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TEX15	605795	NA	NA	NA	NA	1105.41	-10.311931	uc003xll.3	chr8:30689080-30690801	NA	NA	NA	NA	NA	NA
TEX19	615647	208.876	-7.305838	uc002keq.3	chr17:80320522-80321652	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TEX26	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	809.819	-9.871849	uc001luf.3	chr13:31549045-31549153
TEX28	300092	438.835	-6.511622	uc004fke.3	chrX:153498930-153499079	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TEX36	NA	NA	NA	NA	NA	708.67	-10.318708	uc001lik.4	chr10:127344263-127344468	NA	NA	NA	NA	NA	NA
TEX39	NA	491.5	-8.426228	uc002adp.3	chr15:56737869-56738072	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TFAP2D	610161	NA	NA	NA	NA	216.236	-8.525509	uc003paf.3	chr6:50740578-50740746	NA	NA	1108.49	-15.435091	uc003paf.3	chr6:50740578-50740746
TFAP4	600743	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	916.086	-9.6515	uc010uug.2	chr16:4307187-4308055
TFB1M	607033	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	481.834	-6.901953	uc003oql.4	chr6:155577264-155578969
TFB2M	607055	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	809.417	-5.516638	uc001lbn.3	chr1:246703863-246704332
TFDP1	189902	478.726	-4.288233	uc010ikd.2	chr13:114294583-114295788	554.017	-5.850123	uc010ikd.2	chr13:114294583-114295788	NA	NA	NA	NA	NA	NA
TFDP2	602160	NA	NA	NA	NA	674.747	-7.035547	uc003euk.4	chr3:141663270-141671354	NA	NA	NA	NA	NA	NA
TFEB	600744	NA	NA	NA	NA	1230	-6.432874	uc003boqv.1	chr6:41654267-41654827	NA	NA	NA	NA	NA	NA
TFEC	604732	1263.23	-10.829664	uc003vhm.2	chr7:115580006-115581928	1030.28	-9.361933	uc003vhl.4	chr7:115580006-115581928	1730.22	-14.328992	uc003vhm.2	uc003vhm.2	uc003vhm.2	chr7:115575202-115580604
TFE2	182590	NA	NA	NA	NA	848.27	-8.568182	uc002zaw.3	chr21:43766467-43766641	NA	NA	NA	NA	NA	NA
TFPI	152310	905.004	-7.692655	uc002upy.3	chr2:188328958-188331662	927.842	-10.995082	uc002uqa.2	chr2:188343305-188343402	NA	NA	NA	NA	NA	NA
TFRC	190010	NA	NA	NA	NA	495.327	-6.555534	uc003lvz.4	chr3:195776155-195778812	NA	NA	NA	NA	NA	NA
TGDS	616146	NA	NA	NA	NA	222.445	-2.239237	uc001vlw.3	chr13:95226308-95227035	1243.66	-7.9318	uc001vlw.3	uc001vlw.3	uc001vlw.3	chr13:95226308-95227035
TGF82	190220	531.832	-7.076974	uc001hll.3	chr1:218578882-218585206	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TGFBR1	190181	NA	NA	NA	NA	1210.04	-9.105145	uc004azc.3	chr9:101911588-101916473	NA	NA	NA	NA	NA	NA
TGM6	613900	NA	NA	NA	NA	382.636	-8.791568	uc010gal.1	chr20:2413181-2413399	267.909	-1.937402	uc010gal.1	uc010gal.1	uc010gal.1	chr20:2413181-2413399
TGOLN2	603062	1031.48	-8.76258	uc002soz.3	chr2:85545141-85549858	593.72	-4.10407	uc021vjw.1	chr2:85545141-85549787	611.141	-5.413715	uc002soz.3	uc002soz.3	uc002soz.3	chr2:85545141-85549858
THADA	611800	483.911	-6.201144	uc010far.3	chr2:43457975-43458086	NA	NA	NA	NA	NA	NA	228.782	-4.873454	uc002sz.3	chr2:43570148-43571217
THAP1	609520	483.596	-8.209774	uc003xpl.3	chr8:42691817-42693388	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
THAP2	612531	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	498.38	-5.223571	uc001swq.3	chr12:72070889-72074428
THAP6	612535	658.397	-9.807312	uc010lis.1	chr4:76447117-76447792	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
THBS2	188061	NA	NA	NA	NA	690.015	-4.254192	uc003qwl.3	chr6:169615875-169617916	NA	NA	NA	NA	NA	NA
THBS3	188062	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	557.7	-5.804303	uc009wql.1	chr1:155174361-155174589
THG1L	NA	592.869	-5.851657	uc003kdl.3	chr5:157166491-157166772	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
THNSL1	611260	NA	NA	NA	NA	728.168	-4.896404	uc001isi.4	chr10:25314385-25315593	829.021	-4.694072	uc004etu.3	uc004etu.3	uc004etu.3	chrX:122734412-122735189
THOC2	300395	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	482.515	-7.797255	NA	NA
THRB	190160	687.067	-3.80782	uc003ccx.4	chr3:24158645-24164374	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
THSD1	NA	510.89	-9.172291	uc001vgo.3	chr13:52951303-52951545	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
THSD7B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	404.907	-5.959122	uc002bvb.3	chr2:138169466-138169604
THUMP01	616662	583.519	-7.513854	uc010vaz.2	chr16:20744989-20748201	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
THYN1	613739	1733.97	-1.401795	uc001qht.3	chr11:134118718-134118331	NA	NA	NA	NA	NA	NA	1140	-7.867199	uc001qht.3	chr11:134118173-134118331
TIA1	603518	NA	NA	NA	NA	631.597	-16.666589	uc010yql.2	chr2:70456092-70456345	NA	NA	NA	NA	NA	NA

Table 1

TIAM1	600687	NA	NA	NA	NA	447,548	-5,666,313	uc011adk.1	chr21:32490736-32493155	NA	NA	NA	NA
TIAM2	604709	860,157	-11,746,629	uc003qqb.3	chr6:155578256-155578857	NA	NA	NA	NA	NA	NA	NA	NA
TICAM2	608321	404,651	-5,346,843	uc003krc.3	chr5:114914339-114916245	283,904	-4,163,164	uc003krc.3	chr5:114914339-114916245	NA	NA	NA	NA
TICRR	613298	372,823	-5,920,453	uc002boe.3	chr15:90170318-90171253	NA	NA	NA	NA	NA	NA	NA	NA
TIGD2	612973	NA	NA	NA	NA	NA	NA	NA	NA	394,662	-6,093,462	uc003hsk.3	chr4:90035704-90036052
TIGIT	612859	1367,03	-15,868,414	uc003ebg.2	chr3:114026979-114029135	NA	NA	NA	NA	227,139	-6,968,486	uc003cbg.2	chr3:114026979-114029135
TIIM113	607383	392,741	-7,744,807	uc002lrv.1	chr19:2425622-2428945	NA	NA	NA	NA	NA	NA	NA	NA
TIIM21	615180	NA	NA	NA	NA	357,089	-5,634,665	uc010dqr.1	chr18:71825716-71826204	NA	NA	NA	NA
TIPIN	610716	NA	NA	NA	NA	929,267	-6,121,934	uc010ujn.1	chr15:66629008-66629295	NA	NA	NA	NA
TIPRL	611807	493,494	-5,448,758	uc001gfr.3	chr1:168161467-168161633	NA	NA	NA	NA	NA	NA	NA	NA
TJAF1	612658	833,057	-4,325,646	uc010jqv.2	chr6:43470410-43471246	NA	NA	NA	NA	NA	NA	NA	NA
TKT	606781	NA	NA	NA	NA	221,47	-4,706,069	uc003dgp.2	chr3:53259653-53259771	NA	NA	NA	NA
TKTL2	NA	432,285	-8,810,967	uc003kqp.4	chr4:164392247-164393005	NA	NA	NA	NA	NA	NA	NA	NA
TL4	605132	1388,96	-12,671	uc004alc.3	chr9:82340060-82341656	NA	NA	NA	NA	NA	NA	NA	NA
TLK1	608438	1130,42	-8,666,513	uc010zdn.1	chr2:171847333-171850289	NA	NA	NA	NA	547,086	-6,286,079	uc010zdn.1	chr2:171847333-171850289
TLL2	606743	NA	NA	NA	NA	636,476	-8,360,967	uc001kml.2	chr10:98124363-98127844	NA	NA	NA	NA
TLR2	603028	1200,7	-13,825,418	uc003lnt.3	chr4:154626415-154627242	NA	NA	NA	NA	NA	NA	NA	NA
TLR5	603031	717,777	-6,509,887	uc001lrv.2	chr1:223282748-223283796	NA	NA	NA	NA	NA	NA	NA	NA
TLR7	300365	1088,56	-4,608,894	uc004cvc.3	chrX:12906778-12908480	NA	NA	NA	NA	NA	NA	NA	NA
TLX1NB	612734	NA	NA	NA	NA	NA	NA	NA	NA	1101,99	-5,745,913	uc001ksv.3	chr10:102849078-102849293
TM2D1	610080	1160,4	-6,079,941	uc001czz.1	chr1:62146719-62147022	NA	NA	NA	NA	NA	NA	NA	NA
TM4SF1	191155	NA	NA	NA	NA	869,068	-7,091,895	uc003exb.1	chr3:149086805-149087652	NA	NA	NA	NA
TM6SF1	606562	1268,25	-2,458,108	uc002bjp.3	chr15:83805425-83806111	973,446	-7,076,929	uc002bjp.3	chr15:83805425-83806111	NA	NA	NA	NA
TM7SF3	605181	NA	NA	NA	NA	1170,77	-10,245,499	uc010sji.2	chr12:27124506-27126997	NA	NA	NA	NA
TM9SF1	NA	658,879	-5,355,261	uc001wnb.1	chr14:24657925-24658620	NA	NA	NA	NA	1077,46	-8,917,969	uc001kmm.4	chr10:98277867-98282019
TM9SF3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMA7	615808	NA	NA	NA	NA	528,65	-8,359,05	uc003cte.1	chr3:48485291-48485537	NA	NA	NA	NA
TMBIM1	610364	488,337	-5,425,105	uc002vho.1	chr2:219138917-219140197	NA	NA	NA	NA	NA	NA	NA	NA
TMC1	606706	NA	NA	NA	NA	696,856	-8,799,212	uc004alz.1	chr9:75450890-75451267	NA	NA	NA	NA
TMC2	606707	565,913	-4,025,987	uc002wgl.1	chr20:2621998-2622430	NA	NA	NA	NA	NA	NA	NA	NA
TMC8	605829	NA	NA	NA	NA	784,351	-0,176,723	uc002jur.1	chr17:76135254-76135809	689,736	-7,761,294	uc002jur.1	chr17:76135254-76135809
TMCC3	NA	NA	NA	NA	NA	503,704	-3,641,512	uc001ldi.2	chr12:94960900-94965210	477,169	-6,926,266	uc001ldi.2	chr12:94960900-94965210
TMCO2	NA	526,993	-6,366,614	uc001cfe.2	chr1:40717267-40717365	NA	NA	NA	NA	NA	NA	NA	NA
TMCO5A	NA	NA	NA	NA	NA	501,855	-7,494,36	uc001zlv.1	chr15:38258845-38258925	NA	NA	NA	NA
TMED2	NA	NA	NA	NA	NA	NA	NA	NA	NA	781,878	-9,257,712	uc001ufg.3	chr12:124081277-124082688
TMED4	612038	1012,06	-8,004,054	uc003lli.3	chr7:44618762-44619077	NA	NA	NA	NA	NA	NA	NA	NA
TMED8	NA	457,833	-4,189,219	uc001xin.1	chr14:77807201-77808113	NA	NA	NA	NA	NA	NA	NA	NA
TMEFF2	605734	NA	NA	NA	NA	488,918	-6,609,527	uc002utc.3	chr2:192814747-192815036	897,438	-10,391,133	uc002utc.3	chr2:192814747-192815036
TMEM101	NA	NA	NA	NA	NA	1045,68	-10,304,082	uc002lew.3	chr17:42088556-42089295	NA	NA	NA	NA
TMEM105	NA	NA	NA	NA	NA	855,335	-8,995,33	uc002kad.2	chr17:79285072-79287450	NA	NA	NA	NA
TMEM107	616183	NA	NA	NA	NA	481,421	-4,895,187	uc002gkg.4	chr17:8076297-8077520	NA	NA	NA	NA
TMEM108	NA	437,739	-5,865,353	uc003eph.3	chr3:133114831-133116619	566,418	-2,202,582	uc003eph.3	chr3:133114831-133116619	NA	NA	NA	NA
TMEM11	NA	NA	NA	NA	NA	NA	NA	NA	NA	880,844	-10,074,558	uc002gyp.2	chr17:21101263-21101636
TMEM116	NA	592,3	-6,278,528	uc001ttc.2	chr12:112369087-112369424	NA	NA	NA	NA	NA	NA	NA	NA
TMEM117	NA	317,504	-7,770,1546	uc009zkc.3	chr12:44781848-44783541	NA	NA	NA	NA	NA	NA	NA	NA
TMEM120B	616551	1314,94	-16,021,353	uc009zxi.3	chr12:122213515-122219874	NA	NA	NA	NA	NA	NA	NA	NA
TMEM123	606356	222,445	-7,108,724	uc001phia.3	chr11:102267056-102269597	NA	NA	NA	NA	NA	NA	NA	NA
TMEM125	NA	NA	NA	NA	NA	413,847	-4,355,081	uc001cfr.3	chr1:43739054-43739673	NA	NA	NA	NA
TMEM132B	NA	454,151	0,492,528	uc001uhe.1	chr12:126139257-126143589	1222,97	-10,251,192	uc001uhe.1	chr12:126139257-126143589	764,842	-0,489,188	uc001uhe.1	chr12:126139257-126143589

Table 1

TMEM143	NA	413.47	-5.736782	uc002pik.1	chr19:48835616-48836475	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM147	613585	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM14A	NA	NA	NA	NA	NA	601.518	-5.698418	uc003pax.3	chr6:52550848-52551385	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM14E	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM150B	NA	NA	NA	NA	NA	686.056	-4.71784	uc002qki.3	chr19:55830828-55831328	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM155	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM158	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM159	611304	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM164	NA	689.148	-6.030082	uc004eon.2	chrX:109416680-109421016	571.577	-4.357673	uc004eon.2	chrX:109416680-109421016	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM168	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM169	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM171	NA	NA	NA	NA	NA	1615.78	-11.463203	uc003kcm.2	chr5:72427558-72427644	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM174	614909	NA	NA	NA	NA	327.889	-7.399936	uc010lzc.3	chr5:72469993-72470970	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM175	616660	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM176A	610334	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM177	NA	NA	NA	NA	NA	847.926	-5.601168	uc002imc.1	chr2:120439366-120439694	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM178B	NA	NA	NA	NA	NA	774.632	-13.614865	uc003vwg.2	chr7:141170587-141180179	666.026	-11.140634	uc003vwg.2	chr7:141170587-141180179	NA	NA	NA	NA	NA	NA
TMEM179B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM18	613220	667.346	-4.4795	uc002qwi.3	chr2:667973-669579	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM180	NA	NA	NA	NA	NA	683.412	-7.79789	uc001kvi.3	chr10:104235742-104236802	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM181	613209	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM182	NA	NA	NA	NA	NA	485.3	-4.849623	uc002lcc.4	chr2:103431428-103434138	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM184C	613937	426.581	-5.709059	uc003lla.4	chr4:148555586-148556672	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM186	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM191B	NA	546.772	-4.663012	NA	NA	605.509	-5.96895	uc021twlv.1	chr22:20380327-20380440	355.677	-4.499573	uc002cze.3	chr4:148555586-148556672	NA	NA	NA	NA	NA	NA
TMEM192	NA	NA	NA	NA	NA	558.189	-4.572998	uc003lqz.4	chr4:165997230-166000809	NA	NA	NA	chr16:8889037-88899808	NA	NA	NA	NA	NA	NA
TMEM194A	NA	1128.14	-15.822401	uc001smx.3	chr12:57449426-57453661	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM200A	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM209	NA	720.959	-9.263397	uc003ypn.2	chr7:129804555-129806290	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM213	NA	208.559	-6.889125	uc010lla.3	chr7:138487815-138490769	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM216	613277	NA	NA	NA	NA	478.464	-7.003611	uc010hj.2	chr11:61165749-61166335	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM220	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM225	NA	936.987	-13.172931	uc001pzi.3	chr11:123753633-123753844	2059.28	-10.615101	uc001pzi.3	chr11:123753633-123753844	250.121	-9.707727	uc002pmx.3	chr17:10616639-10618769	NA	NA	NA	NA	NA	NA
TMEM229A	NA	628.775	-6.002181	uc011kob.2	chr7:123670970-123671914	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM237	614423	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM246	NA	683.528	-9.880758	uc004bbm.3	chr9:104237608-104238162	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM255A	NA	NA	NA	NA	NA	1449.98	-11.382324	uc004eso.4	chrX:119392505-119394724	903.052	-7.44691	uc004eso.4	chrX:119392505-119394724	NA	NA	NA	NA	NA	NA
TMEM258	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM26	NA	795.373	-7.664509	uc001jlo.2	chr10:63166401-63170079	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM260	NA	1059.25	-10.808132	uc010aol.1	chr14:57082750-57082982	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM261	NA	1543.27	-6.282512	uc003zki.3	chr9:7796491-7798435	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM27	300631	NA	NA	NA	NA	1128.1	-8.144942	uc004exc.2	chrX:15645441-15646093	269.722	-11.1395	uc022bdl.1	chr9:7796491-7798572	NA	NA	NA	NA	NA	NA
TMEM30A	611028	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM35	NA	NA	NA	NA	NA	1068.72	-9.040564	uc004egw.3	chrX:100349946-100351355	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM37	NA	NA	NA	NA	NA	339.989	-4.129568	uc002tlv.3	chr2:120195017-120196096	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM39B	NA	773.644	-8.056818	uc010ogu.1	chr1:32566302-32566804	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TMEM41A	NA	NA	NA	NA	NA	353.352	-3.796348	uc003fpi.2	chr3:185207389-185209324	392.038	-4.75833	uc003fpi.2	chr3:185207389-185209324	NA	NA	NA	NA	NA	NA
TMEM41B	NA	NA	NA	NA	NA	986.227	-3.273391	uc001mln.2	chr11:9302201-9304970	740.342	-13.323604	uc001mhm.3	chr11:9302201-9302588	NA	NA	NA	NA	NA	NA
TMEM45A	NA	NA	NA	NA	NA	922.415	-10.474646	uc003dlz.1	chr3:100295863-100296285	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

TMEM50A	605348	NA	NA	NA	NA	NA	NA	NA	NA	746.744	-6.515125	uc001bke.3	chr1:25687197-25688852
TMEM56	NA	474.644	-6.774212	uc021oqe.1	chr1:95657425-95663161	NA	NA	NA	NA	NA	NA	NA	NA
TMEM60	NA	NA	NA	NA	NA	NA	NA	NA	NA	804.216	-7.761775	uc003ugn.3	chr7:77423045-77423288
TMEM64	NA	NA	NA	NA	NA	NA	NA	NA	NA	482.158	-8.431918	uc003yen.2	chr8:91634223-91637898
TMEM67	609884	449.25	-9.077709	uc010mav.3	chr8:94770816-94771695	NA	NA	NA	NA	467.531	-1.798714	uc010mau.3	chr8:94768131-94769330
TMEM68	NA	602.125	-7.899208	uc003xsi.1	chr8:56673332-56675110	1789.57	-14.558953	uc003xsi.1	chr8:56673332-56675110	NA	NA	NA	NA
TMEM70	612418	663.873	-7.601725	uc003yab.3	chr8:74893857-74895018	659.457	-4.533754	uc003yab.3	chr8:74893857-74895018	NA	NA	NA	NA
TMEM71	NA	355.883	-5.993919	uc003ylim.2	chr8:133722192-133723212	NA	NA	NA	NA	NA	NA	NA	NA
TMEM87A	NA	1195.79	-6.152799	uc010bcu.1	chr15:42525077-42525395	333.414	-22.55068	uc021sfr.1	chr15:42502726-42503905	1029.92	-8.571662	uc010bcu.1	chr15:42525077-42525395
TMEM87B	NA	NA	NA	NA	NA	509.147	-6.107475	NA	NA	1134.51	-4.70973	uc010knc.2	chr2:112838912-112839095
TMEM95	NA	NA	NA	NA	NA	477.464	-4.621829	uc002ggf.1	chr17:7259952-7260538	NA	NA	NA	NA
TMEM98	615949	NA	NA	NA	NA	NA	NA	NA	NA	847.582	-5.106554	uc002hqd.3	chr17:31268012-31268667
TMEM99	NA	NA	NA	NA	NA	NA	NA	NA	NA	660.229	-10.633992	uc021bxc.1	chr17:38991546-38992526
TMIGD1	NA	592.872	-10.974731	uc010csh.1	chr17:28643366-28643708	NA	NA	NA	NA	592.931	-6.238248	uc002hfa.1	chr17:28643366-28643704
TMOD3	605112	NA	NA	NA	NA	NA	NA	NA	NA	1385.21	-16.262564	uc002abn.3	chr15:52201008-52204331
TMPO	188380	799.909	-8.876389	uc001tff.3	chr12:98941637-98944157	1107.48	-6.012344	uc001tff.2	chr12:98928121-98929412	NA	NA	NA	NA
TMPRSS11B	NA	479.536	-3.899403	uc003hdw.4	chr4:69092371-69093628	1779.73	-17.195853	uc003hdw.4	chr4:69092371-69093628	NA	NA	NA	NA
TMPRSS11E	610398	NA	NA	NA	NA	619.46	-6.136667	uc003hdz.4	chr4:69362523-69363322	980.192	-11.421012	uc003hdz.4	chr4:69362523-69363322
TMPRSS11F	NA	NA	NA	NA	NA	NA	NA	NA	NA	1111.37	-8.022727	uc003hdt.1	chr4:68918916-68919626
TMPRSS12	NA	429.331	-8.644107	uc001rwx.4	chr12:51281297-51281663	1639.27	-4.993075	uc001rwx.4	chr12:51281297-51281663	1532.01	-10.273483	uc001rwy.3	chr12:51279340-51281663
TMPRSS13	610050	586.508	-9.023535	uc001prs.2	chr11:117771356-117772953	NA	NA	NA	NA	472.991	-1.948539	uc021qrc.1	chr11:117773757-117774151
TMPRSS2	602060	NA	NA	NA	NA	NA	NA	NA	NA	493.879	-9.110815	uc010gor.3	chr21:42836478-42838068
TMPRSS7	NA	275.578	-3.562982	uc010hqb.2	chr3:111799932-111800116	698.68	-9.427889	uc010hqb.2	chr3:111799932-111800116	NA	NA	NA	NA
TMSB15B	NA	NA	NA	NA	NA	NA	NA	NA	NA	955.093	-7.700446	uc010noz.3	chrX:103220150-103220563
TMSB4X	300159	NA	NA	NA	NA	805.988	-8.086966	uc004cvf.3	chrX:12994931-12995346	705.071	-9.013701	uc004cvf.3	chrX:12994931-12995346
TMSB4Y	400017	1436.28	-8.297621	uc004ftb.3	chrY:15817140-15817902	1222.93	-11.994557	uc004ftb.3	chrY:15817140-15817902	1233.11	-13.096152	uc004ftb.3	chrY:15817140-15817902
TMTC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	906.802	-10.316319	uc001tau.3	chr12:88589427-88593664
TMTC4	NA	662.829	-7.898314	uc001vot.3	chr13:101256090-101257247	NA	NA	NA	NA	NA	NA	NA	NA
TMX1	610527	NA	NA	NA	NA	NA	NA	NA	NA	870.055	-8.678989	uc010tqr.1	chr14:51712037-51712569
TMX3	616102	NA	NA	NA	NA	1029.27	-7.844863	uc010xia.1	chr18:66358251-66358493	696.428	-6.411855	uc002tkf.3	chr18:66340925-66344169
TNFAIP6	600410	NA	NA	NA	NA	NA	NA	NA	NA	1640.07	-18.191771	uc002tkk.3	chr2:152236048-152236562
TNFAIP8L1	615869	551.449	-7.003759	uc002max.3	chr19:4652443-4655580	NA	NA	NA	NA	NA	NA	NA	NA
TNFAIP8L2	612112	NA	NA	NA	NA	NA	NA	NA	NA	757.339	-5.038288	uc001ewx.2	chr1:151131729-151132225
TNFAIP8L3	616438	759.897	-6.472095	uc001zyt.3	chr15:51348798-51350077	NA	NA	NA	NA	NA	NA	NA	NA
TNFRSF10B	603612	NA	NA	NA	NA	NA	NA	NA	NA	574.589	-5.622688	uc003xss.1	chr8:22877648-22880183
TNFRSF19	606122	NA	NA	NA	NA	NA	NA	NA	NA	297.468	-8.32921	uc001uot.3	chr13:24247520-24250244
TNFRSF1A	191190	NA	NA	NA	NA	504.185	-4.032327	uc001qnt.3	chr12:6437923-6438477	838.509	-10.377469	uc010afa.2	chr12:6440406-6441053
TNFRSF25	603366	291.745	-5.52181	uc001ana.3	chr1:6521214-6521493	NA	NA	NA	NA	NA	NA	NA	NA
TNFSF11	602642	1106.6	-9.170385	uc001luy.2	chr13:43181055-43182149	NA	NA	NA	NA	821.427	-7.029483	uc001luy.2	chr13:43181055-43182149
TNFK	610005	NA	NA	NA	NA	NA	NA	NA	NA	914.407	-7.927842	uc003ffg.2	chr3:170780292-170781669
TNIP3	608019	344.868	-5.390137	uc010lmg.3	chr4:122052564-122053785	NA	NA	NA	NA	NA	NA	NA	NA
TNKS	603303	NA	NA	NA	NA	738.686	-6.73257	uc003wss.3	chr8:9634247-9639856	NA	NA	NA	NA
TNMD	300459	NA	NA	NA	NA	758.974	-5.172724	uc004efy.4	chrX:99854715-99854882	NA	NA	NA	NA
TNNC2	191039	527.545	-7.456744	uc002xpr.3	chr20:44451855-44451986	NA	NA	NA	NA	NA	NA	NA	NA
TNP2	190232	NA	NA	NA	NA	718.897	-6.240289	uc002das.3	chr16:11361714-11361852	NA	NA	NA	NA
TNP02	603002	496.416	-9.425499	uc002mnp.3	chr19:12810008-12812057	NA	NA	NA	NA	NA	NA	NA	NA
TNR	601995	1275.76	-0.956325	uc001gkp.1	chr1:175291935-175292492	969.952	-2.820077	uc001gkp.1	chr1:175291935-175292492	684.101	-5.005171	uc001gkp.1	chr1:175291935-175292492
TNRC6A	610739	NA	NA	NA	NA	NA	NA	NA	NA	849.426	-8.166125	uc010vcc.1	chr16:24807339-24807689
TNS4	608385	NA	NA	NA	NA	NA	NA	NA	NA	758.971	-8.876956	uc002huu.4	chr17:38632080-38633839

Table 1

TOE1	613931	NA	NA	NA	NA	300.532	-5.889622	uc009vqx.3	chr1:45809375-45809650	NA	NA	-7.457879	NA	NA	chr17:52993287-52994810
TOM1L1	604701	NA	NA	NA	NA	886.512	-12.700055	uc003awe.3	chr22:39079847-39080766	NA	NA	NA	NA	NA	NA
TOMM22	607046	NA	NA	NA	NA	1630.18	-10.185609	uc010ggd.1	chr20:39658405-39659162	NA	NA	NA	NA	NA	NA
TOP1	126420	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-5.285353	237.273	NA	chr17:38544773-38545770
TOP2A	126430	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	-6.52083	574.9	NA	chr3:44373504-44373590
TOPAZ1	614412	1190.23	-13.061134	uc003cna.4	chr3:44373504-44373590	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TOR1A	605204	273.169	-8.149276	uc004byn.3	chr9:132583655-132584709	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TOX4	614032	NA	NA	NA	NA	661.237	-6.918115	uc001tway.3	chr14:21963556-21964371	NA	NA	NA	NA	NA	NA
TP53	191170	NA	NA	NA	NA	264.548	-5.571166	uc002gig.1	chr17:7565097-7565256	NA	NA	NA	NA	NA	NA
TP53BP1	605230	672.06	-9.815919	uc001zrp.3	chr15:43699412-43699580	862.545	-9.220502	uc001zrp.3	chr15:43699412-43699580	NA	NA	NA	NA	NA	NA
TP53I13	606185	NA	NA	NA	NA	1778.76	-12.475656	uc003yhg.3	chr8:95938200-95942706	330.666	-4.406856	uc002hee.3	NA	NA	chr17:27899943-27900175
TP53TG3D	NA	392.993	-7.388735	uc021lgy.1	chr16:32268725-32267243	NA	NA	NA	NA	1560.76	-12.452769	uc003yhh.3	NA	NA	chr8:95938200-95942956
TP63	603273	341.89	-7.775176	uc003fny.2	chr3:189612292-189615068	NA	NA	NA	NA	1417.67	-20.820805	uc003frx.2	NA	NA	chr3:189597968-189599284
TPCNP1	609666	NA	NA	NA	NA	520.748	-4.940266	uc001luw.3	chr12:113733882-113736389	568.219	-3.877711	uc010syf.1	NA	NA	chr12:113726131-113726652
TPD52	604068	696.155	-8.207528	uc003ybr.1	chr8:80947105-80950350	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TPD52L3	NA	375.838	-2.563724	uc003zyv.3	chr9:6330214-6330918	420.84	-10.710551	uc003zyw.3	chr9:6329019-6330918	NA	NA	NA	NA	NA	NA
TPH2	607478	NA	NA	NA	NA	971.52	-10.669275	uc009zrw.1	chr12:72425476-72426221	NA	NA	NA	NA	NA	NA
TPP2	190470	NA	NA	NA	NA	493.983	-7.285751	uc001vpi.4	chr13:103330667-103331523	NA	NA	NA	NA	NA	NA
TPPP	608773	427.24	-6.358679	uc003lbg.4	chr5:659977-665216	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TPST1	603125	NA	NA	NA	NA	NA	NA	NA	NA	515.282	-4.048634	uc003luw.3	NA	NA	chr7:65824882-65825438
TPT1	600763	554.107	-5.627623	uc001luz.1	chr13:45911304-45911520	546.677	-5.474717	uc010fp.1	chr13:45914161-45914486	1015.86	-6.957147	uc001luz.1	NA	NA	chr13:45911304-45911520
TRA2A	602718	NA	NA	NA	NA	NA	NA	NA	NA	1293.49	-12.32654	uc003swi.3	NA	NA	chr7:23544401-23545177
TRA2D	602719	NA	NA	NA	NA	NA	NA	NA	NA	1104.92	-9.550851	uc003fpv.3	NA	NA	chr3:185632358-185635502
TRA2B	603500	NA	NA	NA	NA	NA	NA	NA	NA	638.663	-5.163575	uc002erh.1	NA	NA	chr16:67188089-67188551
TRAF6	602355	NA	NA	NA	NA	NA	NA	NA	NA	624.075	-4.938577	uc001mwa.2	NA	NA	chr11:36505317-36511387
TRAFD1	613197	301.126	-4.227005	uc009zwb.2	chr12:112579058-112579295	243.398	-3.91827	uc009zwb.2	chr12:112579058-112579295	NA	NA	NA	NA	NA	NA
TRAIP	605958	873.075	-6.754905	uc011bcx.2	chr3:49880578-49881197	NA	NA	NA	NA	882.504	-10.392995	uc003oxs.1	NA	NA	chr3:49866028-49866535
TRAPPC10	602103	NA	NA	NA	NA	674.017	-8.97631	uc002zdz.3	chr21:45479387-45480110	483.027	-7.291957	uc002zdz.3	NA	NA	chr21:45479387-45480110
TRAPPC11	614138	NA	NA	NA	NA	238.406	-4.345266	uc003lvx.3	chr4:184633798-184634747	236.358	-4.93645	uc003lvw.3	NA	NA	chr4:184633776-184634747
TRAPPC4	610971	402.786	-5.080165	uc010ryo.2	chr11:18894110-118894385	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRAPPC8	614136	621.519	-6.761596	uc021luj.1	chr18:29453538-29454394	672.77	-9.045454	uc002kxb.4	chr18:29409136-29410717	1367.29	-9.652444	uc002kxb.4	NA	NA	chr18:29409136-29410717
TRDMT1	602478	747.162	-3.903894	uc010qcc.1	chr10:17193582-17194039	1071.48	-12.277707	uc001lop.3	chr10:17184982-17191038	702.567	-3.435211	uc010qcc.1	NA	NA	chr10:17193582-17194039
TRDN	603283	NA	NA	NA	NA	1643.61	-11.786563	uc010kem.2	chr6:123537484-123539745	203.61	-5.283375	uc003pzk.2	NA	NA	chr6:123670620-123673669
TREH	275360	NA	NA	NA	NA	NA	NA	NA	NA	539.289	-6.095685	uc009ak.3	NA	NA	chr11:118531675-118531864
TRERF1	610322	NA	NA	NA	NA	NA	NA	NA	NA	576.574	-6.616015	uc011duq.1	NA	NA	chr6:42192669-42196082
TRIM10	605701	NA	NA	NA	NA	515.698	-11.649932	uc003nnp.2	chr6:30119723-30121464	NA	NA	NA	NA	NA	NA
TRIM13	605661	961.443	-6.135689	uc001vdp.1	chr13:50587301-50592603	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIM14	606556	458.788	-5.143853	uc004ayd.2	chr9:100831569-100831969	750.812	-6.749504	uc004ayd.2	chr9:100831569-100831969	224.367	-7.284515	uc004ayd.2	NA	NA	chr9:100831569-100831969
TRIM17	606123	NA	NA	NA	NA	811.851	-9.750894	uc001hsu.3	chr11:228595636-228595901	654.203	-4.877984	uc001hsu.3	NA	NA	chr1:228595636-228595901
TRIM22	606559	NA	NA	NA	NA	757.054	-8.840709	uc001mbr.3	chr11:5730879-5732093	NA	NA	NA	NA	NA	NA
TRIM23	601747	398.3	-6.832996	uc003lwr.3	chr5:64885507-64886129	NA	NA	NA	NA	342.052	-6.832996	uc003lwr.3	NA	NA	chr5:64885507-64886129
TRIM24	603406	NA	NA	NA	NA	1807.83	-10.721894	uc003vub.3	chr7:138269697-138270332	NA	NA	NA	NA	NA	chr7:138269697-138270332
TRIM27	602165	NA	NA	NA	NA	917.189	-9.765031	uc003nlf.3	chr6:28870779-28871846	NA	NA	NA	NA	NA	NA
TRIM34	605684	NA	NA	NA	NA	514.568	-12.843755	uc001mbj.3	chr11:5662460-5662526	NA	NA	NA	NA	NA	NA
TRIM36	609317	215.367	-5.313716	uc003kqv.3	chr5:114513236-114513446	NA	NA	NA	NA	1476.84	-2.696473	uc011cwc.2	NA	NA	chr5:114460459-114462199
TRIM37	605073	NA	NA	NA	NA	1417.66	-8.365379	uc002lwx.4	chr17:57075561-57076737	NA	NA	NA	NA	NA	NA
TRIM39	605700	NA	NA	NA	NA	864.495	-9.505817	uc003npz.3	chr6:30310037-30311506	NA	NA	NA	NA	NA	NA
TRIM41	610530	774.786	-10.450423	uc003mnd.2	chr5:180662380-180662808	551.038	-9.775034	uc003mnc.2	chr5:180667867-180662803	NA	NA	NA	NA	NA	NA

Table 1

TRIM42	NA	NA	NA	NA	NA	775.635	-11.153637	uc003elo.2	chr3:140419817-140419992	NA	NA	NA	NA
TRIM43	NA	963.729	-6.398594	uc002suv.3	chr2:96265322-96265469	NA	NA	NA	NA	NA	NA	NA	NA
TRIM48	NA	329.312	-6.689596	uc010rid.2	chr11:55037913-55038595	NA	NA	NA	NA	NA	NA	NA	NA
TRIM49D2	NA	NA	NA	NA	NA	223.206	-6.16423	uc009yvv.3	chr11:89666054-89666229	NA	NA	NA	NA
TRIM5	608487	1074.13	-5.131939	uc001mbm.2	chr11:56844425-5686038	437.463	-5.120926	uc001mbm.2	chr11:56844425-5686038	212.458	-12.695463	uc001mbm.2	chr11:5684425-5686038
TRIM51	NA	NA	NA	NA	NA	680.133	-4.609693	uc010rp.2	chr11:55659109-55659284	NA	NA	NA	NA
TRIM53AP	NA	524.042	-7.365576	uc010rv.2	chr11:89583463-89584136	NA	NA	NA	NA	NA	NA	NA	NA
TRIM59	616148	NA	NA	NA	NA	492.289	-8.079707	uc003fdm.3	chr3:160153291-160155759	NA	NA	NA	NA
TRIM6	607564	NA	NA	NA	NA	NA	NA	NA	NA	1581.94	-15.393373	uc001mbc.2	chr11:5632573-5634188
TRIM60	NA	411.1	-5.201677	uc003lqv.1	chr4:165962641-165962896	454.493	-7.464625	uc003lqv.1	chr4:165962641-165962896	NA	NA	NA	NA
TRIM61	NA	NA	NA	NA	NA	NA	NA	NA	NA	352.054	-7.91159	uc003lqv.3	chr4:165875598-165875920
TRIM64	NA	460.586	-4.294814	uc010ry.2	chr11:89707058-89707240	NA	NA	NA	NA	NA	NA	NA	NA
TRIM66	612000	NA	NA	NA	NA	NA	NA	NA	NA	780.284	-9.509643	uc010rbo.2	chr11:8633594-8639490
TRIM7	609315	593.03	-8.248656	uc003mma.2	chr5:180630120-180630496	NA	NA	NA	NA	292.398	-8.792952	uc003mma.2	chr5:180630120-180630496
TRIM71	NA	931.461	-6.665593	uc003cff.3	chr3:32933304-32933771	NA	NA	NA	NA	NA	NA	NA	NA
TRIM74	612550	435.383	-4.74985	uc010ldc.3	chr7:75039889-75040279	NA	NA	NA	NA	NA	NA	NA	NA
TRIML2	NA	NA	NA	NA	NA	NA	NA	NA	NA	290.145	-5.715404	uc011clf.1	chr4:189019783-189020143
TRIO	601893	583.959	-2.350896	uc003jff.3	chr5:14508532-14509458	NA	NA	NA	NA	1123.88	-4.608103	uc003jff.3	chr5:14508532-14509458
TRIP12	604506	NA	NA	NA	NA	943.149	-13.437842	uc010kxh.1	chr2:230672035-230672324	NA	NA	NA	NA
TRIP13	604507	NA	NA	NA	NA	337.048	-4.406856	uc010lte.2	chr5:908581-909047	NA	NA	NA	NA
TRIP4	604501	1114.71	-8.600685	uc002anm.3	chr15:64747264-64747502	1233.81	-5.775136	uc002anm.3	chr15:64747264-64747502	NA	NA	NA	NA
TRMT112	NA	881.424	-9.311554	uc001nzt.3	chr11:64084165-64084332	NA	NA	NA	NA	756.989	-8.610542	uc001nzt.3	chr11:64084165-64084332
TRMT13	NA	NA	NA	NA	NA	NA	NA	NA	NA	628.442	-8.171769	uc001dsv.3	chr1:100614377-100616054
TRMT1L	611673	NA	NA	NA	NA	NA	NA	NA	NA	652.976	-10.237446	uc001grf.4	chr1:185087218-185089150
TRMT2B	NA	NA	NA	NA	NA	543.935	-5.244314	uc004egs.3	chrX:100264334-100265696	NA	NA	NA	NA
TRMT5	611023	NA	NA	NA	NA	789.348	-5.907535	uc001xlf.4	chr14:61438167-61441826	NA	NA	NA	NA
TRNP1	NA	NA	NA	NA	NA	384.57	-4.693168	uc001bnj.4	chr1:27326338-27327377	NA	NA	NA	NA
TROVE2	600063	689.811	-3.262306	uc001gsw.3	chr1:193060816-193060906	NA	NA	NA	NA	549.553	-5.412565	uc001gss.3	chr1:193053862-193055115
TRPC3	602345	1279.58	-7.302085	uc010lnr.2	chr4:122800183-122800890	NA	NA	NA	NA	NA	NA	NA	NA
TRPC5OS	NA	1737.46	-19.984186	uc022ccr.1	chrX:111145414-111147213	NA	NA	NA	NA	NA	NA	NA	NA
TRPC6	603652	762.794	-6.566346	uc001pgk.4	chr11:101322295-101323685	NA	NA	NA	NA	NA	NA	NA	NA
TRPM1	603576	NA	NA	NA	NA	NA	NA	NA	NA	776.813	-7.694955	uc010axy.3	chr15:31293264-31294024
TRPM3	608961	225.878	-3.91827	uc004ahu.3	chr9:73149966-73150868	1271.98	-11.595986	uc010mor.3	chr9:73253709-73253960	1156.25	-0.854312	uc004ahu.3	chr9:73149966-73150868
TRPM7	605692	NA	NA	NA	NA	933.923	-10.573458	uc001zyr.3	chr15:50849352-50853874	NA	NA	NA	NA
TRPV2	606676	1184.1	-6.606848	uc002gpy.3	chr17:16340204-16340317	332.684	-3.467294	NA	NA	223.475	-4.855477	uc003wbwv.1	chr7:142568960-142569459
TRPV6	606680	NA	NA	NA	NA	NA	NA	NA	NA	649.131	-5.429239	uc004cca.2	chr9:135766735-135771621
TSC1	605284	315.151	-4.027565	uc011mer.2	chr9:135771468-135771845	NA	NA	NA	NA	NA	NA	NA	NA
TSEN15	608756	854.684	-6.640712	uc001gqt.4	chr1:184041982-184043344	NA	NA	NA	NA	906.146	-4.344078	uc003bwr.3	chr3:12574221-12574820
TSEN2	608753	NA	NA	NA	NA	NA	NA	NA	NA	756.644	-8.575433	uc002sag.4	chr2:99613724-99614659
TSGA10	607166	NA	NA	NA	NA	NA	NA	NA	NA	727.561	-4.291694	uc001wvc.3	chr14:81575026-81575294
TSHZ3	614119	1055.34	-8.146966	uc002nsy.4	chr19:31765851-31767452	NA	NA	NA	NA	NA	NA	NA	NA
TSLP	607003	686.94	-11.011081	uc003kpb.2	chr5:110411773-110413722	415.476	-3.152673	uc003kpb.2	chr5:110411773-110413722	NA	NA	NA	NA
TSN	600575	NA	NA	NA	NA	666.139	-4.292288	uc002tnl.3	chr2:122522944-12252428	NA	NA	NA	NA
TSPAN12	613138	1025.3	-8.598114	uc010lkj.3	chr7:120427374-120428645	NA	NA	NA	NA	NA	NA	NA	NA
TSPAN19	NA	432.87	-6.084067	uc009nsj.3	chr12:85408094-85408265	NA	NA	NA	NA	NA	NA	NA	NA
TSPAN3	613134	NA	NA	NA	NA	NA	NA	NA	NA	448.317	-5.386896	uc002bcj.3	chr15:77336360-77339176
TSPAN31	181035	NA	NA	NA	NA	NA	NA	NA	NA	1495.59	-11.100844	uc001spt.3	chr12:58141074-58142026
TSPYL1	604714	NA	NA	NA	NA	685.094	-5.940568	uc003pwp.4	chr6:116596022-116599679	NA	NA	NA	NA

Table 1

TSPYL5	614721	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1603.31	-9.224588	uc003hyh.3	chr8:98285714-98288818
TSR2	300945	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	655.974	-4.928807	uc004dte.3	chrX:54477084-54471731
TSSK2	610710	NA	NA	NA	NA	258.396	-6.174009	uc002zow.2	chr22:19119990-19120136	NA	NA	NA	NA	NA	NA
TTBK2	611695	NA	NA	NA	NA	1378.06	-10.726805	uc001zup.3	chr15:43069116-43069200	NA	NA	328.233	-13.670088	uc001zqp.2	chr15:43036542-43037992
TTC13	NA	298.684	-6.441019	uc001huf.4	chr1:231041987-231042650	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TTC16	NA	625.072	-6.003195	uc004brq.1	chr9:130493685-130493879	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TTC17	NA	NA	NA	NA	NA	381.514	-4.047834	uc001mxl.3	chr11:43515455-43516483	966.47	-5.298098	uc001mxl.3	chr11:43515455-43516483	NA	NA
TTC23	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	828.896	-9.262755	uc002buz.2	chr15:99695569-99696319	NA
TTC25	NA	NA	NA	NA	NA	419.197	-8.036526	uc002hyj.4	chr17:40117502-40117668	NA	NA	NA	NA	NA	NA
TTC26	NA	294.704	-2.012221	uc003vuq.2	chr7:138845793-138846089	NA	NA	NA	NA	NA	632.235	-6.454627	uc003vuq.2	chr7:138845793-138846089	NA
TTC30B	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	686.574	-7.878972	uc002ujn.3	chr2:178414881-178415493	NA
TTC33	NA	NA	NA	NA	NA	583.211	-6.693676	uc003jma.3	chr5:40711678-40716246	NA	NA	NA	NA	NA	NA
TTC37	614589	NA	NA	NA	NA	NA	NA	NA	NA	NA	532.519	-5.299933	uc003klb.3	chr5:94799599-94800310	NA
TTCh	608132	NA	NA	NA	NA	1072.99	-9.628535	uc001xxi.3	chr14:89343755-89344335	NA	NA	NA	NA	NA	NA
TTF2	604718	NA	NA	NA	NA	NA	NA	NA	NA	NA	1148.5	-11.075655	uc001legx.1	chr1:117624698-117624997	NA
TTK	604092	NA	NA	NA	NA	1371.03	-9.810581	uc003plb.4	chr6:80751920-80752244	NA	NA	NA	NA	NA	NA
TTL12	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	211.727	-5.060917	uc003bdp.3	chr22:43562628-43564165	NA
TTL5	612268	225.83	-1.80743	uc001xrw.2	chr14:76175592-76176742	1525.47	-2.510657	uc001xrv.3	chr14:76150004-76151340	436.768	-4.078126	uc001xrv.3	chr14:76150004-76151340	NA	NA
TTL6	610849	NA	NA	NA	NA	301.441	-7.958981	uc002lob.3	chr17:46839593-46840335	NA	NA	NA	NA	NA	NA
TTL7	NA	524.009	-7.312862	uc001djc.3	chr1:84335057-84335644	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TTPAL	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	779.025	-7.667123	uc010grg.1	chr20:43118183-43123244	NA
TTYH1	605784	1113.89	-9.301509	uc010vey.2	chr19:54947268-54947351	NA	NA	NA	NA	NA	837.483	-4.067544	uc002dfq.3	chr19:54947513-54947899	NA
TTYH2	608855	NA	NA	NA	NA	NA	NA	NA	NA	NA	541.09	-5.877645	uc002jkc.3	chr17:72256349-72258157	NA
TUBA1B	602530	NA	NA	NA	NA	200.919	-4.081744	uc001rhl.3	chr12:49521567-49521740	NA	NA	NA	NA	NA	NA
TUBA1C	NA	1410.36	-9.893629	uc010smh.1	chr12:49667011-49667113	657.398	-10.331473	NA	NA	NA	965.779	-7.825848	uc010smh.1	chr12:49667011-49667113	NA
TUBA3C	602528	NA	NA	NA	NA	277.354	-6.567511	uc009zzj.3	chr13:19747910-19748002	NA	NA	NA	NA	NA	NA
TUBA8	605742	570.191	-5.154781	uc002zrv.2	chr22:18613904-18614498	NA	NA	NA	NA	NA	1182.96	-9.516766	uc011lkh.2	chr6_qbl_hap6:1985106-1986127	NA
TUBB	191130	820.878	-5.099143	uc003mrl.3	chr6:30692175-30693195	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TUBB2A	615101	NA	NA	NA	NA	646.075	-7.27408	uc003mnb.3	chr6:3153902-3154096	NA	NA	NA	NA	NA	NA
TUBD1	607344	NA	NA	NA	NA	603.151	-6.437236	uc002ikw.2	chr17:57936841-57937682	NA	NA	NA	NA	NA	NA
TUBE1	607345	1519.04	-9.113577	uc003pvq.3	chr6:112391860-112392614	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TUBG2	605785	522.368	-4.540313	uc010wgr.2	chr17:40818819-40819024	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TUBGCP5	608147	820.972	-12.389103	uc001yuq.2	chr15:22872547-22872783	NA	NA	NA	NA	NA	1213.4	-20.867193	uc001yuq.2	chr15:22872547-22872783	NA
TUBGCP6	610053	1069.26	-6.698238	uc003bkd.1	chr22:50661416-50662565	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TULP4	NA	NA	NA	NA	NA	687.26	-4.281175	uc003qrg.3	chr6:158927633-158932856	NA	NA	NA	NA	NA	NA
TUSC3	601385	624.951	-5.419743	NA	NA	1529.45	-11.993518	uc003www.3	chr8:15621728-15624158	NA	NA	NA	NA	NA	NA
TYP23B	NA	568.25	-5.671865	uc002gum.2	chr17:18708881-18710026	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TWF1	610932	NA	NA	NA	NA	928.76	-14.391641	uc001rab.3	chr12:44187526-44189387	NA	NA	NA	NA	NA	NA
TWSO1	605049	NA	NA	NA	NA	603.815	-11.306238	uc002knz.3	chr18:9399526-9402418	NA	NA	NA	NA	NA	NA
TXK	600058	601.247	-7.679564	uc011bzj.2	chr4:48068410-48069653	904.925	-3.711218	uc011bzj.2	chr4:48068410-48069653	960.609	-8.785107	uc011bzj.2	chr4:48068410-48069653	NA	NA
TXLNG	300677	NA	NA	NA	NA	751.541	-7.514511	uc004cxq.2	chrX:16859890-16862642	NA	NA	NA	NA	NA	NA
TXNDC17	NA	NA	NA	NA	NA	222.522	-7.484942	uc002gdf.4	chr17:6546340-6547861	NA	NA	NA	NA	NA	NA
TXNDC9	612564	685.941	-12.361999	uc010yvp.1	chr2:99923088-99923235	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TXNIP	606599	684.52	-4.712368	uc001enn.4	chr1:145441219-145442628	1565.19	-7.135645	uc001enn.4	chr1:145441219-145442628	784.279	-6.790833	uc001enn.4	chr1:145441219-145442628	NA	NA
TXNL1	603049	235.614	-5.921003	uc002lgs.3	chr18:54270053-54270257	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TXNL4A	611595	NA	NA	NA	NA	NA	NA	NA	NA	NA	318.035	-5.958945	uc002lhp.3	chr18:77732867-77733684	NA
TXNRD1	601112	796.094	-9.058965	uc001tkm.1	chr12:104651881-104653174	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TXNRD3	606235	NA	NA	NA	NA	NA	NA	NA	NA	NA	332.235	-4.792627	uc003ejd.2	chr3:126325895-126326753	NA
TYK2	178441	NA	NA	NA	NA	657.301	-8.060459	uc002mod.2	chr19:10468061-10468139	NA	NA	NA	NA	NA	NA

Table 1

TYMS1	188350	NA	NA	NA	NA	chr18:649620-649964	NA	418,752	-4,571,352	uc010dka.1	chr18:672998-673499	NA	NA	NA	NA	NA
TYMSOS1	NA	336,996	-5,539,277	uc002kkr.3	uc002kkr.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
TYR1P1	115501	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	375,384	-4,098,234	uc003kvr.4	chr9:12709183-12710266	NA
TYW51	NA	421,41	-7,485,64	uc002juvl.3	uc002juvl.3	chr2:200806806-200812994	NA	NA	NA	NA	NA	637,007	-13,430,128	uc002uvi.4	chr2:200793634-200797789	NA
U2AF1	191317	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	726,957	-6,873,462	uc002zcy.1	chr21:44513066-44513211	NA
UACA1	612516	2242,38	-11,986,929	uc002asq.3	uc002asq.3	chr15:70946893-70949394	NA	NA	NA	NA	NA	1300,16	-8,235,658	uc002asq.3	chr15:70946893-70949394	NA
UAP1	602862	1189,67	-9,090,898	uc001gce.4	uc001gce.4	chr1:162569154-162569633	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBA2	613295	411,381	-6,382,872	uc002nvk.3	uc002nvk.3	chr19:34960127-34960798	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBA3	603172	630,874	-7,272,483	uc003dno.3	uc003dno.3	chr3:69103881-69104587	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBA5	610552	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	661,474	-6,991,999	uc010htr.3	chr3:132395371-132396944	NA
UBA6	611361	654,394	-10,172,307	uc003hdi.3	uc003hdi.3	chr4:68527381-68527840	828,355	-4,585,563	uc003hdg.4	chr4:68481479-68484714	584,669	-5,981,199	uc003hdg.4	chr4:68481479-68484714	NA	NA
UBAP1	609787	406,883	-4,319,956	uc010mka.2	uc010mka.2	chr9:34250884-34251097	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBAP2	NA	1444,89	-8,277,195	uc011lbg.1	uc011lbg.1	chr9:33927795-33927878	578,986	-5,919,444	uc011lbg.1	chr9:33927795-33927878	1151,01	-8,541,654	uc003ttn.1	chr9:33921691-33922501	NA	NA
UBAP2L	616472	378,682	-7,042,752	uc009wot.3	uc009wot.3	chr1:154235629-154235980	607,289	-1,898,382	uc009wot.3	chr1:154235629-154235980	333,202	0,125,152	uc009wot.3	chr1:154235629-154235980	NA	NA
UBASH3B	609201	290,804	-5,744,894	uc001pyl.4	uc001pyl.4	chr11:122680595-122685187	NA	NA	NA	NA	NA	750,233	-6,315,939	uc001pyl.4	chr11:122680595-122685187	NA
UBB1	191339	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	810,235	-6,861,926	uc010vwe.1	chr17:16285912-16286053	NA
UBC1	191340	332,81	-4,738,296	uc001tgs.4	uc001tgs.4	chr12:125396192-125396259	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBD1	606050	NA	NA	NA	NA	NA	356,69	-5,587,808	uc003nmo.3	chr6:29523389-29523656	554,464	-5,131,939	uc003nmo.3	chr6:29523389-29523656	NA	NA
UBE2A	312180	NA	NA	NA	NA	NA	1318,94	-11,429,864	uc004erl.3	chrX:118717219-118718379	NA	NA	NA	NA	NA	NA
UBE2C	605574	525,482	-8,586,587	uc002xpl.3	uc002xpl.3	chr20:444445407-444445596	524,952	-3,599,807	uc002xpl.3	chr20:444445407-444445596	NA	NA	NA	NA	NA	NA
UBE2D1	602961	NA	NA	NA	NA	NA	547,942	-4,216,01	uc001jke.2	chr10:80128526-60130513	NA	NA	NA	NA	NA	NA
UBE2D3	602963	1321,48	-10,537,612	uc003hwl.3	uc003hwl.3	chr4:103717133-103718617	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBE2E1	602916	NA	NA	NA	NA	NA	214,967	-5,324,836	uc003cch.3	chr3:23932098-23933131	1076,42	-1,848,533	uc003cch.3	chr3:23932098-23933131	NA	NA
UBE2E2	602163	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	571,497	-4,093,154	uc003crg.2	chr3:23631323-23632296	NA
UBE2G1	601569	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	431,723	-4,811,342	uc002fks.3	chr17:4172512-4175811	NA
UBE2H1	601082	NA	NA	NA	NA	NA	528,308	-7,776,855	uc022aln.1	chr7:129470573-129474776	317,84	-2,773,247	uc022aln.1	chr7:129470573-129474776	NA	NA
UBE2I	601661	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	508,297	-4,031,028	uc002clc.2	chr16:1374795-1377019	NA
UBE2N	603679	947,653	-9,723,963	uc001tep.3	uc001tep.3	chr12:93802088-93803814	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBE2NL	NA	910,377	-6,785,665	uc004fca.3	uc004fca.3	chrX:142967665-142968357	400,59	-3,726,964	uc004fca.3	chrX:142967665-142968357	NA	NA	NA	NA	NA	NA
UBE2Q1	NA	213,278	-6,507,027	uc001fff.1	uc001fff.1	chr1:154521051-154522913	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBE2T1	610538	NA	NA	NA	NA	NA	564,248	-5,745,131	uc001dbn.1	chr1:64709817-64710027	1087,25	-12,512,426	uc001gxx.4	chr1:202300785-202300962	NA	NA
UBE2U	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBE3A	601623	603,43	-9,631,106	uc001zar.3	uc001zar.3	chr15:25582396-25584283	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBE3C	614454	545,499	-8,367,664	uc003wnf.2	uc003wnf.2	chr7:156981656-156981988	317,969	-4,858,109	uc003wnf.2	chr7:156981656-156981988	NA	NA	NA	NA	NA	NA
UBE3D	612495	277,205	-9,748,534	uc003pjp.2	uc003pjp.2	chr6:83602186-83602740	1070,33	-12,347,438	uc003pjp.3	chr6:83728901-83728687	556,045	-4,407,357	uc003pjp.2	chr6:83602186-83602740	NA	NA
UBLCP1	609867	576,823	-8,209,628	uc003kqj.2	uc003kqj.2	chr5:158711940-158713048	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBN1	609771	644,022	-6,559,835	uc010uxw.2	uc010uxw.2	chr16:4930134-4932363	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBN2	613841	538,16	-8,596,946	uc003vuv.3	uc003vuv.3	chr7:138960898-138962460	NA	NA	NA	NA	NA	244,636	-6,895,978	uc011kqr.2	chr7:138982583-138992982	NA
UBQLN1	605046	653,118	-5,771,348	uc004amv.3	uc004amv.3	chr9:86274878-86276701	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBQLN2	300264	NA	NA	NA	NA	NA	357,282	-4,231,094	uc004dlus.3	chrX:56592182-56593443	NA	NA	NA	NA	NA	NA
UBQLN3	605473	555,669	-5,432,485	uc001may.1	uc001may.1	chr11:5528530-5528820	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBR2	609134	472,076	-4,681,19	uc011dur.2	uc011dur.2	chr6:42658912-42661243	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBR3	613831	942,951	-8,900,266	uc010zdl.2	uc010zdl.2	chr2:170938354-170940639	1541,73	-12,546,746	uc010zdl.2	chr2:170938354-170940639	NA	NA	NA	NA	NA	NA
UBR4	609890	NA	NA	NA	NA	NA	660,861	-5,445,086	uc001bbf.3	chr1:19401000-19401325	460,73	-5,739,793	uc001bbf.3	chr1:19401000-19401325	NA	NA
UBR5	608413	1168,52	-10,731,402	uc003yqj.3	uc003yqj.3	chr8:103264502-103266529	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBTD2	610174	1234,72	-5,334,442	uc003mbp.1	uc003mbp.1	chr5:171636650-171638833	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UBXN1	616378	NA	NA	NA	NA	NA	919,626	-11,021,188	uc010rmf.2	chr11:62445390-62445689	850,913	-2,263,788	uc001nuj.3	chr11:62443972-62444189	NA	NA
UBXN4	611216	NA	NA	NA	NA	NA	1067,78	-15,097,854	uc002tur.3	chr2:136540458-136542633	NA	NA	NA	NA	NA	NA
UBXN8	602155	NA	NA	NA	NA	NA	202,895	-4,242,932	uc003xii.3	chr8:30623911-30624520	NA	NA	NA	NA	NA	NA

Table 1

UCHL5	610667	253.258	-7.646475	uc001gsm.3	chr1:192981496-192985480	394.718	-1.306594	uc001gsm.3	chr1:192981496-192985480	NA	NA	NA	NA	NA	chr1:165877061-165880855
UCK2	609329	NA	NA	NA	NA	NA	NA	NA	NA	NA	-5.787604	uc001gdp.3	NA	NA	NA
UFD1L	601754	396.643	-7.437874	uc002zpo.2	chr22:19437464-19438262	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UFL1	613372	NA	NA	NA	NA	NA	NA	NA	NA	NA	801.196	uc003por.3	NA	NA	chr6:97001380-97003151
UFM1	610553	NA	NA	NA	NA	585.171	-6.218525	uc001uwu.3	chr13:38934916-38937143	NA	NA	NA	NA	NA	NA
UFSF2	611482	466.272	-5.070744	uc003kx.2	chr4:186320694-186321545	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UGDH	603370	1278.04	-18.059957	uc003guk.2	chr4:39500375-39501762	NA	NA	NA	NA	978.756	-12.853361	uc003guk.2	NA	NA	chr4:39500375-39501762
UGT2	605898	NA	NA	NA	NA	554.068	-9.470427	uc001vms.3	chr13:96453836-96454043	801.143	-12.647975	uc001vmv.3	NA	NA	chr13:96637163-96637503
UGT2A2	NA	NA	NA	NA	NA	NA	NA	NA	NA	661.057	-6.115824	uc010lfs.3	NA	NA	chr4:70454135-70455089
UGT8	601291	492.359	-7.769474	uc003lfs.2	chr4:115597445-115598202	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UHMK1	608849	NA	NA	NA	NA	488.087	-5.800977	uc009wu.2	chr1:1624922205-162499419	432.805	-4.912083	uc001igcd.3	NA	NA	chr1:162492341-162499419
UHRF1	607990	NA	NA	NA	NA	NA	NA	NA	NA	730.403	-7.136125	uc002mbo.3	NA	NA	chr19:4960815-4962165
UHRF2	615211	463.081	-8.256508	uc003zjy.3	chr9:6506180-6507051	1175.6	-11.638468	uc003zjy.3	chr9:6506180-6507051	1077.28	-4.736012	uc003zjy.3	NA	NA	chr9:6506180-6507051
ULK4	NA	639.014	-11.284347	uc003ckw.2	chr3:41830949-41831146	815.736	-12.87016	uc003ckw.2	chr3:41830949-41831146	NA	NA	NA	NA	NA	NA
UMAD1	NA	NA	NA	NA	NA	NA	NA	NA	NA	1670.05	-13.107885	uc011jxf.2	NA	NA	chr7:7917170-7918851
UNC13C	614568	NA	NA	NA	NA	NA	NA	NA	NA	471.289	-7.603686	uc021smr.1	NA	NA	chr15:54919312-54920806
UNC45A	611219	388.547	-5.141351	uc002bqi.3	chr15:91496947-91497323	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UNC45B	611220	324.401	-5.70809	uc002hja.3	chr17:33513579-33516364	1439.01	-8.008879	uc002hja.3	chr17:33513579-33516364	NA	NA	NA	NA	NA	NA
UNC5A	607869	636.117	-4.775867	uc003mex.1	chr5:176297556-176299002	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UNC5C	603610	374.26	-6.33888	uc003htq.3	chr4:96137194-96137270	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UNC5D	616466	NA	NA	NA	NA	290.263	-6.600572	uc003xjr.2	chr8:35648082-35652181	NA	NA	NA	NA	NA	NA
UNC79	NA	NA	NA	NA	NA	987.954	-12.303545	uc001ybs.1	chr14:94173251-94173689	365.333	-4.15702	uc001ybs.1	NA	NA	chr14:94173251-94173689
UNC80	612636	1144.06	-5.346047	uc002vdk.2	chr2:210832366-210835038	242.235	-4.430497	uc002vdj.1	chr2:210659544-210661271	658.825	-6.21985	uc002vdj.1	NA	NA	chr2:210659544-210661271
UNKL	NA	600.783	-6.567511	uc002ctq.3	chr16:1448306-1448842	NA	NA	NA	NA	523.383	-4.684457	uc009xyz.2	NA	NA	chr10:11993896-11994035
UPF2	605529	NA	NA	NA	NA	2297.77	-15.009323	uc001lfs.3	chr10:11962021-11963296	NA	NA	NA	NA	NA	NA
UPK1A	611557	1043.4	-7.363395	uc002oaw.3	chr19:36168922-36169367	NA	NA	NA	NA	1278.99	-16.547362	uc002tzo.3	NA	NA	chr2:158991403-158992666
UPP2	NA	NA	NA	NA	NA	NA	NA	NA	NA	952.763	-4.944037	uc004ecb.2	NA	NA	chrX:74523347-74524732
UPRT	300656	NA	NA	NA	NA	NA	NA	NA	NA	327.023	-14.238029	uc002djk.3	NA	NA	chr16:21994493-21994668
UQCRC2	191329	935.779	-14.377456	uc002djp.1	chr16:21987569-21988268	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UQCRF51	191327	486.173	-4.420234	uc002nsd.2	chr19:29698167-29698454	NA	NA	uc001cpp.3	chr1:46782257-46782447	NA	NA	NA	NA	NA	NA
UQCRH1	613844	1582.99	-13.819643	uc001cpp.3	chr1:46782257-46782447	478.424	-6.733621	uc009vol.1	chr1:16133657-16133868	NA	NA	NA	NA	NA	NA
UQCRH2	NA	789.825	-11.669218	uc009vol.1	chr1:16133657-16133868	NA	NA	uc002tql.3	chr16:90106169-90106780	630.01	-2.676877	uc002tql.3	NA	NA	NA
URAHF	615805	NA	NA	NA	NA	411.292	-8.505054	uc003liu.3	chr7:43915501-43916265	NA	NA	NA	NA	NA	chr16:90106169-90106780
URGCP	610337	NA	NA	NA	NA	289.767	-4.489315	NA	NA	1498.63	-11.224585	uc001hku.1	NA	NA	chr1:215796236-215799122
USH2A	608400	NA	NA	NA	NA	NA	NA	uc001kww.2	chr10:105148809-105148923	NA	NA	NA	NA	NA	NA
USMG5	615204	304.196	-5.710224	uc001kww.2	chr10:105148809-105148923	559.492	-7.408863	uc003hlu.3	chr4:76734449-76735366	NA	NA	NA	NA	NA	NA
USO1	603344	NA	NA	NA	NA	974.905	-5.868698	NA	NA	NA	NA	NA	NA	NA	NA
USP1	603478	729.905	-9.503031	uc001daj.2	chr1:62916653-62917475	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP12	NA	NA	NA	NA	NA	NA	NA	NA	NA	847.277	-5.851042	uc001luy.3	NA	NA	chr13:27640287-27643419
USP13	603591	1108.98	-9.180637	uc003fkf.3	chr3:179501930-179507189	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP15	604731	533.303	-7.251536	uc010ssk.2	chr12:62698559-62698804	587.007	-6.491781	uc001sra.3	chr12:62728972-62730474	248.725	-4.187755	uc001sra.3	NA	NA	chr12:62728972-62730474
USP16	604735	NA	NA	NA	NA	571.437	-4.592422	uc002ymw.3	chr21:30426509-30426807	NA	NA	NA	NA	NA	NA
USP25	604736	NA	NA	NA	NA	NA	NA	NA	NA	400.718	-6.07264	uc002yjj.1	NA	NA	chr21:17250795-17252377
USP28	610748	690.89	-4.965312	uc001pog.3	chr11:113668597-113669961	812.323	-3.34239	uc001pog.3	chr11:113668597-113669961	NA	NA	NA	NA	NA	NA
USP29	609546	NA	NA	NA	NA	589.293	-8.355632	uc002qny.3	chr19:57642813-57643293	NA	NA	NA	NA	NA	NA
USP31	NA	1191.63	-7.083002	uc002dlk.3	chr16:23072728-23079366	NA	NA	NA	NA	810.188	-9.077913	uc002dlk.3	NA	NA	chr16:23077278-23079366
USP33	615146	1391.24	-6.415754	uc001dhs.3	chr1:78161674-78163159	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP34	615295	1089.38	-12.508196	uc002sbf.3	chr2:61453925-61454197	1220.99	-7.657131	uc002sbf.3	chr2:61453925-61454197	1423.17	-8.800875	uc002sbf.3	NA	NA	chr2:61414590-61415236
USP37	NA	359.991	-6.660353	uc002vie.2	chr2:219314974-219319652	414.803	-3.46084	uc002vie.2	chr2:219314974-219319652	NA	NA	NA	NA	NA	NA

Table 1

USP4:	603486	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	802,523	-13,155,983	uc003cwp.2	chr3:49314577-49315725
USP40:	610570	555.81	-5,565,904	uc002vuo.1	chr2:234401310-234402020	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP43:	NA	NA	NA	NA	NA	708,382	-4,559,373	uc002gma.4	chr17:9632308-9633003	NA	NA	NA	NA	NA	NA
USP44:	610993	NA	NA	NA	NA	519,745	-5,243,149	uc009zie.3	chr12:95910888-95911929	514,374	-7,787,187	uc009ite.3	chr12:95910888-95911929	NA	NA
USP45:	NA	NA	NA	NA	NA	NA	NA	NA	NA	1054,95	-6,897,281	uc003ppw.2	chr6:99880184-99883591	NA	NA
USP46:	612849	455.713	-4,486,431	uc011bzs.2	chr4:53457127-53463907	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP48:	NA	NA	NA	NA	NA	1208,81	-8,375,458	uc001bfi.3	chr1:22054339-22055054	588,894	-5,594,467	uc001bfi.3	chr1:22054339-22055054	NA	NA
USP49:	NA	786,626	-8,732,385	uc003ori.3	chr6:41765383-41766414	NA	NA	NA	NA	596,893	-8,157,872	uc003ori.3	chr6:41765383-41766414	NA	NA
USP53:	NA	1724.9	-14,759,936	uc003iclr.4	chr4:120214367-120216673	NA	NA	NA	NA	445,275	-5,850,203	uc010qkk.2	chr10:75257296-75258386	NA	NA
USP54:	NA	269,63	-2,903,609	uc010qkk.2	chr10:75257296-75258386	NA	NA	NA	NA	1558,97	-11,038,804	uc001lks.1	chr10:11502509-11504439	NA	NA
USP6NL	605405	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP9Y	400005	1255.26	-8,139,452	uc004fst.1	chrY:14971342-14972768	NA	NA	NA	NA	532,057	-6,817,215	uc002lts.3	chr17:49375143-49375292	NA	NA
USPL1	NA	NA	NA	NA	NA	968,632	-17,009,666	uc001luc.2	chr13:31233494-31233686	NA	NA	NA	NA	NA	NA
UTP14A:	300508	529,401	-5,388,806	uc004euz.3	chrX:129063585-129063738	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UTP18:	612816	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UTP20:	612822	786,722	-6,630,549	uc009ztl.1	chr12:101684685-101685205	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UTP23:	NA	NA	NA	NA	NA	887,183	-6,838,519	uc003yoc.3	chr8:117784082-117786921	NA	NA	NA	NA	NA	NA
UTP3:	611614	NA	NA	NA	NA	NA	NA	NA	NA	512,123	-6,366,387	uc003hfo.3	chr4:71555835-71556268	NA	NA
UTP6:	NA	NA	NA	NA	NA	574.7	-8,525,416	uc002hgg.3	chr17:30190190-30190377	NA	NA	NA	NA	NA	NA
UTRN:	128240	779,139	-4,714,799	uc003qkt.3	chr6:145172134-145174170	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
UTS2B:	NA	NA	NA	NA	NA	NA	NA	NA	NA	620,175	-4,154,171	uc003fsu.3	chr3:190984944-190986204	NA	NA
UTY:	400009	NA	NA	NA	NA	230,003	-3,272,38	uc004fsy.3	chrY:15409389-15409582	518,199	-7,268,639	uc022cni.1	chrY:15434948-15435228	NA	NA
UVSSA:	614632	1568.6	-10,073,427	uc003gde.4	chr4:1379750-1381837	NA	NA	NA	NA	233,115	-5,852,098	uc003gde.4	chr4:1379750-1381837	NA	NA
UXS1:	609749	213,232	-3,097,356	uc010ywh.2	chr2:106717107-106717456	813,924	-4,848,651	uc002tlk.3	chr2:106709759-106710481	1132,16	-8,768,342	uc002cdk.3	chr2:106709759-106710481	NA	NA
VAMP3:	603657	512,698	-8,742,986	uc001baol.3	chr1:7839706-7841492	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VAMP7:	300053	NA	NA	NA	NA	1224,23	-8,073,351	uc004fmr.3	chrX:155171616-155173433	NA	NA	NA	NA	NA	NA
VANGL1:	610132	307,012	-6,859,971	uc001etv.1	chr1:116234001-116240845	459,18	-5,878,843	uc001etv.1	chr1:116234001-116240845	NA	NA	NA	NA	NA	NA
VANGL2:	600533	979,897	-8,039,917	uc001fwb.2	chr1:160395169-160398468	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VAPA:	605703	789,041	-7,963,787	uc002kaj.3	chr18:9954209-9960018	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VAPB:	605704	NA	NA	NA	NA	1365,32	-16,904,204	uc002zza.3	chr20:57019292-57026156	735,573	-6,605,864	uc002zxd.2	chr20:57019222-57026156	NA	NA
VARS2:	612802	NA	NA	NA	NA	278,136	-6,832,622	uc003nsc.2	chr6:3089988-30894235	NA	NA	NA	NA	NA	NA
VASH2:	610471	519,257	-5,669,945	uc001hju.2	chr1:213140469-213142572	532,946	-6,894,293	uc001hju.3	chr1:213161927-213164927	538,288	-4,484,882	uc001hju.2	chr1:213140469-213142572	NA	NA
VAX1:	604294	NA	NA	NA	NA	1334,58	-18,087,359	uc001ldb.1	chr10:118888032-118891719	NA	NA	NA	NA	NA	NA
VCPKMT:	615260	NA	NA	NA	NA	NA	NA	NA	NA	268,599	-5,458,538	uc001wxo.1	chr14:50573350-50576416	NA	NA
VCX2:	300532	341,927	-7,595,584	uc004csb.3	chrX:8137985-8138072	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VDAC2:	193245	NA	NA	NA	NA	341,254	-4,308,621	uc021plp.1	chr10:76990748-76991207	NA	NA	NA	NA	NA	NA
VEGFC:	601528	1408,07	-7,791,75	uc003lius.1	chr4:177604691-177605076	208,649	-6,688,754	uc003lius.1	chr4:177604691-177605076	NA	NA	NA	NA	NA	NA
VENTX:	607158	515,33	-7,171,605	uc010quy.1	chr10:135053811-135055433	1206,36	-7,545,518	uc010quy.1	chr10:135053811-135055433	NA	NA	NA	NA	NA	NA
VEPH1:	609594	NA	NA	NA	NA	255,682	-5,825,682	uc021xgk.1	chr3:157177410-157177710	577,425	-6,445,244	uc003fbj.2	chr3:156977532-156978922	NA	NA
VHL:	608537	NA	NA	NA	NA	NA	NA	NA	NA	504,013	-5,245,893	uc003bvc.3	chr3:10191650-10195354	NA	NA
VILL:	NA	528,767	-6,182,147	uc003chj.3	chr3:38048547-38048676	NA	NA	NA	NA	685,581	-1,060,779	uc010hgu.3	chr3:38043427-38043971	NA	NA
VIMP:	607918	NA	NA	NA	NA	463,211	-5,554,474	uc021xsv.1	chr15:101812390-101812975	814,952	-7,175,158	uc021xsv.1	chr15:101811214-101811850	NA	NA
VKORC1:	608547	NA	NA	NA	NA	1596,47	-13,179,805	uc002eas.3	chr16:31102175-31102454	NA	NA	NA	NA	NA	NA
VKORC1L1:	608838	1112,84	-8,018,322	uc003lul.3	chr7:65419288-65419800	NA	NA	NA	NA	1379,59	-20,054,154	uc003tul.3	chr7:65419288-65419800	NA	NA
VNA21:	300913	414,329	-5,772,85	uc004feu.3	chrX:150573531-150577836	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VNI1R1:	605234	710,654	-8,666,665	uc002qps.2	chr19:57966542-57966792	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VNN1:	603570	595,981	-6,743,194	uc003qdo.3	chr6:133001997-133004278	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
VNN2:	603571	956,147	-7,251,903	uc003qds.3	chr6:133065009-133065438	743,98	-6,501,921	uc003qds.3	chr6:133065009-133065438	NA	NA	NA	NA	NA	NA
VPS13A:	605978	1311,19	-10,617,67	uc004akq.4	chr9:79999600-80000106	849,695	-1,445,958	uc004akp.4	chr9:79997216-79997921	664,015	-9,455,562	uc004akq.4	chr9:79999600-80000106	NA	NA

Table 1

VPS13D	608877	NA	NA	NA	NA	1139.89	-10.064773	uc001atlv.3	chr1:12569079-12572098	NA	NA	NA	NA
VPS16	608550	NA	NA	NA	NA	325.689	-5.135784	uc002whe.3	chr20:2847221-2847378	NA	NA	NA	NA
VPS29	606932	864.424	-9.948315	uc001ltqx.3	chr12:110929330-110929809	974.283	-6.335621	uc001ltqx.3	chr12:110929330-110929809	NA	NA	NA	NA
VPS37A	609927	NA	NA	NA	NA	696.862	-8.98045	uc003wvj.3	chr8:17152496-17155633	NA	NA	NA	NA
VPS37B	610037	NA	NA	NA	NA	NA	NA	NA	NA	232.958	-5.560655	uc001udl.3	chr12:123349875-123351662
VPS39	612188	971.15	-6.767124	uc001zpb.3	chr15:42450898-42452951	NA	NA	NA	NA	NA	NA	NA	NA
VPS45	610035	806.59	-8.947284	uc001elp.3	chr1:150116975-150117505	404.723	-6.909188	uc010pbs.2	chr1:150117100-150117505	731.951	-3.188108	uc001etp.3	chr1:150116975-150117505
VPS4B	609983	NA	NA	NA	NA	1628.51	-2.977678	uc002lik.3	chr18:61056425-61058207	478.978	-4.973335	uc002lix.3	chr18:61056425-61058207
VP58	NA	NA	NA	NA	NA	1168.86	-7.427853	uc003pb.1	chr3:184769814-184770402	NA	NA	NA	NA
VRK1	602168	588.794	-7.207068	uc001yft.3	chr14:97347546-97347951	1219.6	-12.388429	uc001yft.3	chr14:97347546-97347951	NA	NA	NA	NA
VSIG1	300620	377.351	-7.454226	uc004eno.3	chrX:107320612-107322414	NA	NA	NA	NA	589.318	-12.264342	NA	NA
VSTM1	NA	NA	NA	NA	NA	672.198	-7.095617	uc002qgw.4	chr19:54544080-54544214	NA	NA	NA	NA
VSTM2A	NA	591.119	-6.829362	uc010kzf.3	chr7:54636779-54636948	NA	NA	NA	NA	701.598	-5.662022	uc002ape.4	chr15:65871096-65871745
VSTM4	NA	345.169	-5.858718	uc001jhh.2	chr10:50310217-50311786	NA	NA	NA	NA	NA	NA	NA	NA
VWA8	NA	405.322	-4.546767	uc001uyj.3	chr13:42140961-42142332	NA	NA	NA	NA	NA	NA	NA	NA
VWA9	NA	1744.36	-13.373683	uc010ujc.2	chr15:65891715-65892081	NA	NA	NA	NA	NA	NA	NA	NA
WARS	191050	741.733	-6.952775	uc010lwz.1	chr14:100820530-100820779	NA	NA	NA	NA	NA	NA	NA	NA
WARS2	604733	606.849	-5.497864	uc010oxf.2	chr1:119573839-119575533	NA	NA	NA	NA	232.651	-7.949099	uc010oxf.2	chr1:119573839-119575533
WASF1	605035	488.294	-4.616519	uc003plv.1	chr6:110421022-110421724	NA	NA	NA	NA	NA	NA	NA	NA
WASF2	605875	434.962	-1.335796	uc001bol.2	chr1:27730734-27734682	226.977	-5.789662	uc001bof.2	chr1:27730734-27734682	NA	NA	NA	NA
WASF3	605068	874.525	-8.857904	uc001uqv.3	chr13:27259983-27263082	NA	NA	NA	NA	NA	NA	NA	NA
WASL	605056	879.472	-11.180351	uc003vlf.3	chr7:123321997-123324572	879.019	-11.594764	uc003vfk.3	chr7:123321997-123324572	NA	NA	NA	NA
WBP4	604981	760.649	-5.058893	uc001luxl.3	chr13:411657051-411658139	NA	NA	NA	NA	256.716	-5.763649	uc001luxt.3	chr13:41657051-41658139
WBP5	NA	NA	NA	NA	NA	NA	NA	NA	NA	1017.74	-8.049021	uc004ekd.3	chrX:102612928-102613397
WBSOR16	NA	NA	NA	NA	NA	499.838	-6.222642	uc010lca.3	chr7:74456283-74457139	NA	NA	NA	NA
WBSOR22	615733	226.473	-0.629678	uc003tyt.3	chr7:73112217-73112551	765.506	-6.056652	uc003tyl.3	chr7:73112217-73112551	279.412	-1.905319	uc003tyt.3	chr7:73112217-73112551
WDFY2	610418	703.261	-12.409781	uc010ads.1	chr13:52325633-52325801	NA	NA	NA	NA	710.214	-11.264004	uc001vfp.3	chr13:52333906-52336171
WDHD1	608126	NA	NA	NA	NA	NA	NA	NA	NA	1661.93	-7.733782	uc010aom.2	chr14:55405656-55408207
WDPCP	613580	NA	NA	NA	NA	NA	NA	NA	NA	639.444	-8.289262	uc002sci.2	chr2:63595958-63596586
WDR11	606417	NA	NA	NA	NA	424.59	-5.929628	uc021pzt.1	chr10:122668226-122669038	NA	NA	NA	NA
WDR13	300512	NA	NA	NA	NA	NA	NA	NA	NA	453.715	-6.677427	uc004dkj.2	chrX:48463421-48463582
WDR17	609005	NA	NA	NA	NA	NA	NA	NA	NA	1564.61	-7.868223	uc003luj.3	chr4:177100731-177103979
WDR19	608151	658.304	-6.304242	NA	NA	262.731	-4.096046	uc003gtu.1	chr4:39226504-39226653	879.903	-9.761341	uc003grv.3	chr4:39287107-39287430
WDR25	NA	NA	NA	NA	NA	NA	NA	NA	NA	524.48	-5.320044	uc010avx.3	chr14:100996379-100996640
WDR26	NA	NA	NA	NA	NA	828.942	-5.46163	uc001hnp.4	chr1:224572845-224577536	NA	NA	NA	NA
WDR3	604737	NA	NA	NA	NA	725.552	-5.150329	uc010bxv.1	chr1:118502071-118503049	811.605	-8.042688	uc010bxv.1	chr1:118502071-118503049
WDR34	613363	NA	NA	NA	NA	NA	NA	NA	NA	433.308	-4.487595	uc004bvq.1	chr9:131395940-131396022
WDR35	613602	284.798	-5.248158	uc002rdh.3	chr2:20110029-20111362	NA	NA	NA	NA	318.778	-9.26074	uc002rdh.3	chr2:20110029-20113362
WDR44	NA	448.152	-6.531276	uc004eqn.3	chrX:117582951-117583923	858.856	-5.531028	uc010nqi.3	chrX:117582951-117583923	244.289	-3.556469	uc010nqi.3	chrX:117582975-117583923
WDR61	609540	NA	NA	NA	NA	1539.62	-5.560655	uc002bdn.3	chr15:78575578-78575773	545.882	-6.838519	uc002bdn.3	chr15:78575578-78575773
WDR63	NA	459.914	-4.686362	uc001dkt.3	chr1:85598682-85598821	NA	NA	NA	NA	539.185	-5.733898	uc001dkt.3	chr1:85598682-85598821
WDR64	NA	NA	NA	NA	NA	NA	NA	NA	NA	314.392	-4.763226	uc001hag.2	chr1:241964518-241965434
WDR66	NA	985.825	-10.278746	uc009zxx.3	chr12:122441671-122441832	NA	NA	NA	NA	NA	NA	NA	NA
WDR70	NA	671.959	-5.073113	uc010lva.1	chr5:37697757-37698009	668.657	-7.515247	uc010lva.1	chr5:37697757-37698009	NA	NA	NA	NA
WDR75	NA	543.236	-7.495303	uc002uql.1	chr2:190340144-190340264	590.163	-8.586587	uc002uql.1	chr2:190340144-190340264	NA	NA	NA	NA
WDR78	NA	1418.41	-12.627953	uc009waw.3	chr1:67278572-67279812	NA	NA	NA	NA	NA	NA	NA	NA
WDR82	611059	NA	NA	NA	NA	794.574	-4.740904	uc003ddk.2	chr3:52288438-52291505	761.704	-7.062322	uc003ddk.2	chr3:52288438-52291505
WDR83OS	NA	617.55	-6.019465	uc002nud.2	chr19:12778881-12779172	NA	NA	NA	NA	NA	NA	NA	NA
WDSUB1	NA	NA	NA	NA	NA	921.457	-14.508126	uc002uej.4	chr2:160092304-160092543	NA	NA	NA	NA

Table 1

WDYHV1	NA	NA	NA	NA	1173.29	-8.830245	uc003yqn.1	chr8:124453656-124454260	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WEE2	614084	NA	NA	NA	NA	NA	NA	NA	267.609	-7.916905	uc003vwn.2	chr7:141430121-141431071						
WDFC11	NA	NA	NA	NA	469.982	-4.008825	uc002xpa.3	chr20:444277202-44277357	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WHSC1	602952	1638.44	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WIPF1	602357	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WIPF2	609692	NA	NA	NA	NA	NA	NA	NA	493.779	-7.268639	uc010fqt.1	chr2:175425498-175426828						
WIP2	609225	797.72	-9.068449	uc003snr.3	NA	NA	NA	NA	450.785	-4.690899	uc010cww.1	chr17:38417066-38417249						
WLS	611514	426.688	-4.408963	uc001dee.3	1811.04	-0.249394	uc001dee.3	chr1:68564142-68564314	741.68	-7.282005	uc003mz.3	chr7:5256903-5258662						
WNK1	605232	NA	NA	NA	NA	NA	NA	NA	412.736	-8.183116	uc001dee.3	chr1:68564142-68564314						
WNK2	606249	NA	NA	NA	NA	NA	NA	NA	1145.36	-6.754803	uc001qin.3	chr12:936458-936665						
WNK249	NA	NA	NA	NA	NA	NA	NA	NA	731.936	-7.427786	uc004atj.3	chr9:96082675-96082854						
WNIT16	606267	NA	NA	NA	220.295	-4.519577	uc003yiv.3	chr7:120979400-120981158	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WNIT5A	164975	NA	NA	NA	875.91	-8.038902	uc003dhn.3	chr3:55499743-55504119	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WNIT5B	606361	335.654	-6.708782	uc009zdz.3	NA	NA	NA	NA	507.349	-7.114783	uc009zdz.3	chr12:1755419-1756378						
WRN	604611	NA	NA	NA	626.069	-7.19844	uc003xio.4	chr8:31030619-31031277	1029.28	-7.228198	uc003xio.4	chr8:31030619-31031277						
WSB1	610091	313.262	-4.099179	uc010crl.1	569.474	-9.552608	uc010vzy.1	chr17:25633942-25634452	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WSB2	NA	NA	NA	NA	657.726	-4.418834	uc010sza.1	chr12:118470492-118472000	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WWC2	NA	623.434	-4.346268	uc010lrx.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
WWC3	NA	NA	NA	NA	1313.03	-11.504309	uc004csx.4	chrX:10109542-10112518	395.846	-7.716406	uc004csx.4	chrX:10109542-10112518						
WWP1	602307	298.432	-6.449343	uc010mai.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XCL1	600250	NA	NA	NA	414.855	-5.022438	uc001lgo.2	chr1:16850459-168551315	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XDH	607633	NA	NA	NA	773.658	-6.294807	uc002mv.1	chr2:31557188-31558823	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XK	314850	NA	NA	NA	1011.66	-8.641637	uc004ddq.3	chrX:37587716-37591383	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XKR9	NA	NA	NA	NA	952.716	-12.411752	uc003xyq.3	chr8:71646660-71648177	2018.6	-19.38421	uc003xyq.3	chr8:71646660-71648177						
XKRX	300684	235.64	-4.36345	uc004egn.2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XKRY2	NA	NA	NA	NA	NA	NA	NA	NA	350.789	-4.344921	uc004ftn.3	chrY:20298352-20298915						
XPNEP1	602443	451.261	-4.52644	uc010qra.1	448.491	-3.423992	uc001kyp.2	chr10:111624524-111624941	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XPNEP3	613553	NA	NA	NA	1547.85	-11.449672	uc003azf.2	chr22:41257622-41258785	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XPO1	602559	NA	NA	NA	818.025	-6.606604	uc002sbh.3	chr2:61705069-61705954	664.368	-4.492278	uc002sbh.3	chr2:61705069-61705954						
XPO5	607845	NA	NA	NA	200.822	-3.548652	uc003ovp.3	chr6:43490068-43491605	469.284	-5.622688	uc003ovp.3	chr6:43490068-43491605						
XPO7	606140	932.221	-5.532586	uc003xaa.4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XPR1	605237	NA	NA	NA	NA	NA	NA	NA	662.869	-5.769086	uc001gol.3	chr1:180853203-180859415						
XRCC4	194363	NA	NA	NA	NA	NA	NA	NA	648.984	-6.162584	uc003kia.1	chr5:82606648-82606888						
XRCC5	194364	NA	NA	NA	611.556	-5.918196	uc002vfy.3	chr2:217069926-217071016	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
XRN2	608851	NA	NA	NA	NA	NA	NA	NA	867.188	-7.022875	uc002wsf.1	chr20:21369977-21370463						
YAE1D1	NA	381.847	-4.31136	uc003lhc.4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YAF2	607534	NA	NA	NA	258.092	-6.046885	uc001rmv.3	chr12:42550907-42554390	528.908	-5.129908	uc001rmv.3	chr12:42550907-42554390						
YES1	164880	NA	NA	NA	NA	NA	NA	NA	481.777	-5.685331	uc002kky.3	chr18:721592-724423						
YIF1A	611484	828.002	-9.919865	uc009yrc.3	NA	NA	NA	NA	1055.12	-10.816531	uc009yrc.3	chr11:66054683-66054973						
YIF1B	NA	NA	NA	NA	NA	NA	NA	NA	1009.94	-6.853972	uc002oia.2	chr19:38794200-38796128						
YIPF1	NA	898.803	-8.082015	uc001cvu.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YIPF6	NA	886.279	-6.904818	uc004dwz.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YIPF7	NA	NA	NA	NA	853.127	-6.866834	uc021xnx.1	chr4:44624354-44624430	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YLP1M1	NA	NA	NA	NA	1257.88	-8.897863	uc001xoj.4	chr14:75302478-75304013	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YME1L1	607472	NA	NA	NA	987.743	-6.926434	uc001lil.3	chr10:27399040-27400905	915.366	-13.982702	uc001lil.3	chr10:27399040-27400905						
YPEL3	609724	498.484	-6.136366	uc002dwl.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YPEL5	609726	769.47	-4.950524	uc002mz.4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YRDC	612276	NA	NA	NA	NA	NA	NA	NA	620.503	-6.986578	uc001cca.1	chr1:38268614-38269596						
YTHDC1	NA	978.994	-10.343749	uc003hdx.3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YTHDC2	616530	243.641	-6.37698	uc010jee.2	1047.41	-4.855266	uc010jee.2	chr5:112891836-112892057	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

YWHAG	605356	NA	NA	NA	NA	521,012	-6,644,434	uc011kgj.1	chr7:75956108-75958893	484,962	-2,884,215	uc011kgj.1	chr7:75956108-75958893
YWHAAQ	609009	NA	NA	NA	NA	313,525	-5,770,733	uc002qzx.3	chr2:9724106-9725414	NA	NA	NA	NA
YWHAAZ	601288	NA	NA	NA	NA	NA	NA	NA	NA	547,406	-6,530,626	uc011lhc.1	chr8:101930804-101932920
ZADH2	NA	433,451	-7,392,319	uc010dqy.3	chr18:72909278-72913370	NA	NA	NA	NA	NA	NA	NA	NA
ZAK	NA	NA	NA	NA	NA	485,848	-5,718,206	uc002juh.3	chr2:174086259-174091873	254,922	-5,853,795	uc002uhx.3	chr2:174074652-174077527
ZAN	602372	NA	NA	NA	NA	NA	NA	NA	NA	499,366	-6,914,249	uc003uwj.3	chr7:100395355-100395419
ZBBX	NA	NA	NA	NA	NA	843,827	-8,634,713	uc003lep.3	chr3:166958077-166959580	NA	NA	NA	NA
ZBED2	615246	NA	NA	NA	NA	NA	NA	NA	NA	790,671	-7,128,74	uc003dxy.3	chr3:111311747-1113112391
ZBTB11	NA	NA	NA	NA	NA	NA	NA	NA	NA	984,82	-17,101,509	uc003dxf.2	chr3:101389457-101390719
ZBTB14	602126	NA	NA	NA	NA	NA	NA	NA	NA	661,793	-8,077,312	uc002kmd.3	chr18:5289018-5290856
ZBTB24	614064	NA	NA	NA	NA	742,599	-10,125,248	NA	NA	778,196	-8,325,525	uc003pm.3	chr6:109802152-109802227
ZBTB26	NA	1228,66	-16,046,607	uc004bnj.3	chr9:12680378-125680887	NA	NA	NA	NA	NA	NA	NA	NA
ZBTB41	NA	507,029	-4,6895	uc001glx.1	chr1:197122814-197128488	NA	NA	NA	NA	292,775	-6,016,288	uc001gtx.1	chr1:197122814-197128488
ZBTB44	NA	NA	NA	NA	NA	1263,78	-8,682,794	uc001qgb.4	chr11:130096574-130104157	NA	NA	NA	NA
ZBTB7A	605878	1226,15	-13,344,107	uc002lzh.3	chr19:4045216-4047749	NA	NA	NA	NA	NA	NA	NA	NA
ZBTB8OS	615891	NA	NA	NA	NA	729,908	-9,328,028	uc001bvp.3	chr1:33087307-33087462	NA	NA	NA	NA
ZC3H12B	300889	643,934	-7,230,777	uc010nko.3	chrX:64723090-64727767	NA	NA	NA	NA	NA	NA	NA	NA
ZC3H12C	615001	NA	NA	NA	NA	NA	NA	NA	NA	739,11	-4,421,335	uc010wc.2	chr11:110036463-110042566
ZC3H13	616453	660,647	-6,525,005	uc001vaq.2	chr13:46529805-46531261	1345,18	-10,260,147	uc001vaq.2	chr13:46529805-46531261	712,08	-7,456,926	uc001vaq.2	chr13:46529805-46531261
ZC3H18	NA	NA	NA	NA	NA	801,933	-12,760,48	uc002lky.3	chr16:88697708-88698372	NA	NA	NA	NA
ZC3HAV1L	NA	NA	NA	NA	NA	587,306	-7,716,744	uc003vum.1	chr7:138710452-138711289	NA	NA	NA	NA
ZC4H2	300897	NA	NA	NA	NA	454,485	-6,072,48	uc011mow.2	chrX:64135682-64137643	297,599	-5,539,277	uc004dvy.3	chrX:64135682-64137662
ZCCHC11	613692	670,961	-6,859,61	uc001ctx.2	chr1:52888948-52889606	738,754	-6,074,677	uc001ctud.3	chr1:52890466-52981514	883,08	-12,286,837	uc001ctx.2	chr1:52888948-52889606
ZCCHC6	613467	610,159	-2,732,229	uc004aov.3	chr9:88952242-88952327	651,77	-4,462,441	uc004aow.3	chr9:88954735-88954919	642,126	-6,730,075	uc010mqc.3	chr9:88902648-88903591
ZCCHC7	NA	1618,44	-17,320,409	uc003zqz.3	chr9:37357266-37358145	NA	NA	NA	NA	1450,74	-9,351,069	uc003zqz.3	chr9:37357266-37358145
ZCCHC9	NA	NA	NA	NA	NA	NA	NA	NA	NA	922,403	-8,137,362	uc003khi.3	chr5:80608482-80608965
ZCRB1	610750	NA	NA	NA	NA	525,223	-6,327,632	uc001rmz.3	chr12:42705688-42706868	NA	NA	NA	NA
ZCWPW1	NA	1192,83	-7,962,833	uc011kqz.2	chr7:99998495-99998636	NA	NA	NA	NA	NA	NA	NA	NA
ZCWPW2	NA	NA	NA	NA	NA	976,158	-12,056,495	uc003ceh.3	chr3:28566180-28566632	NA	NA	NA	NA
ZDHHC20	NA	638,162	-7,889,04	uc001uoa.2	chr13:21946710-21950786	597,145	-4,682,281	uc001uoa.2	chr13:21946710-21950786	NA	NA	NA	NA
ZDHHC22	NA	NA	NA	NA	NA	NA	NA	NA	NA	1172,49	-8,681,427	uc010asp.3	chr14:77597613-77600025
ZDHHC9	300646	NA	NA	NA	NA	NA	NA	NA	NA	495,086	-5,296,089	uc004cuv.3	chrX:128937264-128940345
ZEB2	605802	NA	NA	NA	NA	431,362	-1,582,171	uc002lvu.3	chr2:145141942-145147017	795,778	-8,139,896	uc002lvu.3	chr2:145141942-145147017
ZFAND1	NA	NA	NA	NA	NA	778,122	-7,316,599	uc003ycj.2	chr8:82613566-82614929	NA	NA	NA	NA
ZFAND3	607455	NA	NA	NA	NA	NA	NA	NA	NA	582,631	-6,491,781	uc003onx.3	chr6:38120166-38122399
ZFAND4	NA	685,107	-4,144,118	uc001jcl.4	chr10:46111039-46111883	1090,26	-8,967,023	uc001jcl.4	chr10:46111039-46111883	560,158	-4,888,933	uc001jcl.4	chr10:46111039-46111883
ZFAND5	604761	NA	NA	NA	NA	506,463	-6,093,796	uc010mox.1	chr9:74966341-74970868	NA	NA	NA	NA
ZFAT	610931	539,819	-4,698,753	uc003yur.3	chr8:135609787-135612576	NA	NA	NA	NA	NA	NA	NA	NA
ZFC3H1	NA	987,13	-9,397,22	uc001swp.3	chr12:72050124-72050638	489,903	-7,878,051	uc001swo.2	chr12:72003379-72004207	NA	NA	NA	NA
ZFP3	194480	NA	NA	NA	NA	491,383	-8,878,373	uc002gag.3	chr17:49963309-4999669	NA	NA	NA	NA
ZFP82	NA	1027,32	-12,912,387	uc002ody.1	chr19:36882861-36883642	NA	NA	NA	NA	NA	NA	NA	NA
ZFPL1	NA	NA	NA	NA	NA	NA	NA	NA	NA	443,438	-8,779,604	uc009yqa.3	chr11:64852791-64853485
ZFPM2	603693	NA	NA	NA	NA	402,417	-6,147,08	uc003ymd.3	chr8:106815767-106816767	NA	NA	NA	NA
ZFY	490000	766,595	-7,090,805	uc011nan.2	chrY:2848035-2850547	NA	NA	NA	NA	NA	NA	NA	NA
ZFYVE16	608880	NA	NA	NA	NA	685,659	-5,501,843	uc010jak.2	chr5:79735863-79736195	NA	NA	NA	NA
ZFYVE26	612012	NA	NA	NA	NA	1105,65	-10,764,442	uc010lla.2	chr14:68262950-68264344	NA	NA	NA	NA
ZG1BB	NA	NA	NA	NA	NA	632,376	-8,886,318	uc002cru.3	chr16:2882161-2882285	626,27	-6,399,892	uc002cru.3	chr16:2882161-2882285
ZGRF1	NA	NA	NA	NA	NA	NA	NA	NA	NA	764,698	-15,072,476	uc003lat.3	chr4:113460489-113460702
ZHX3	609598	583,538	-9,700,302	uc010ggg.1	chr20:39807089-39813841	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

ZIC3	300265	953.047	-5.856546	uc004fak.3	chrX:136652230-136654259	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZIC5	NA	602.862	-8.845695	uc001vom.1	chr13:100615275-100617630	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZIM2	NA	NA	NA	NA	NA	839.086	-8.975825	uc010yq.1	chr19:57285923-57286055	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZKSCAN4	611643	324.949	-5.641394	uc003nks.1	chr6:28212490-28212893	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZMAT2	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZMAT3	606452	NA	NA	NA	NA	287.32	-5.59229	uc003jlg.3	chr3:178735011-178742804	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZMYM2	602221	NA	NA	NA	NA	930.963	-5.655263	uc001umq.3	chr13:20593825-20594095	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZMYM3	300061	500.48	-4.551348	uc004dzh.2	chrX:70459474-70460765	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZMYM4	613568	485.495	-9.485016	uc001byl.3	chr1:35885279-35887545	847.952	-7.942883	uc001byl.3	chr1:35885279-35887545	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZMYM5	616443	324.125	-8.371301	uc001umn.3	chr13:20411593-20411684	923.429	-8.125019	uc001umn.1	chr13:20397624-20398616	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF107	603989	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF114	603996	499.022	-7.459915	uc002pil.1	chr19:48790136-48790863	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF124	194631	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF131	604073	680.761	-7.344369	uc003jnn.3	chr5:43123421-43125133	1364.16	-8.958102	uc003jnl.4	chr5:43175236-43175823	623.194	-8.564484	uc001icj.1	chr1:247319203-247319867	NA	NA	NA	NA	NA	NA
ZNF135	604077	NA	NA	NA	NA	677.984	-8.007047	uc021vcl.1	chr19:58574990-58575304	977.95	-7.300275	uc003pnj.4	chr5:43175236-43175823	NA	NA	NA	NA	NA	NA
ZNF141	194648	567.769	-3.591434	uc003fzz.2	chr4:352215-352339	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF160	600398	NA	NA	NA	NA	1851.16	-12.879768	uc002qaq.4	chr19:53569867-53571329	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF169	603404	NA	NA	NA	NA	309.74	-5.072083	uc004aam.1	chr9:97063653-97065291	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF174	603900	1880.58	-13.033241	uc002cva.2	chr16:3454774-3454994	466.75	-7.300275	uc002cvc.3	chr16:3458920-3459364	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF180	606740	573.511	-5.983265	uc002ozh.4	chr19:44979859-44980618	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF181	606741	NA	NA	NA	NA	805.004	-9.78771	uc002nvu.3	chr19:35233003-35233774	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF184	602277	NA	NA	NA	NA	254.3	-6.497481	uc003njij.3	chr6:27418521-27419081	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF197	NA	NA	NA	NA	NA	484.765	-6.315821	uc003cmn.3	chr3:44688018-44689963	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF207	603428	476.035	-10.75427	uc002hhir.4	chr17:30696779-30697468	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF217	602967	NA	NA	NA	NA	286.393	-5.575122	uc002xwq.4	chr20:52183610-52185803	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF221	NA	NA	NA	NA	NA	513.735	-8.011947	uc002oxx.2	chr19:44471509-44471752	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF223	NA	2297.12	-19.080374	uc002oyf.1	chr19:44571431-44572142	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF225	NA	795.06	-10.33946	uc002oyj.1	chr19:44636889-44637255	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF230	NA	1508.97	-12.952782	uc002oyb.1	chr19:44515617-44518072	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF233	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF235	604749	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF236	604760	NA	NA	NA	NA	562.225	-6.27991	uc002lmi.3	chr18:74680296-74682682	1176.44	-11.630075	uc002oyv.2	chr19:44778827-44779470	NA	NA	NA	NA	NA	NA
ZNF239	601069	889.147	-9.453945	uc001jaw.4	chr10:44051793-44052150	NA	NA	NA	NA	597.724	-8.126585	uc010ejl.3	chr19:44740263-44740868	NA	NA	NA	NA	NA	NA
ZNF24	194534	207.201	-4.484937	uc002kyl.2	chr18:32912178-32917195	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF264	604668	425.032	-5.802614	uc002qob.3	chr19:57724350-57734214	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF271P	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF277	605465	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF28	NA	NA	NA	NA	NA	514.707	-8.676004	uc002qac.3	chr19:53300661-53302940	485.794	-8.628321	uc002kyp.4	chr18:32887861-32890730	NA	NA	NA	NA	NA	NA
ZNF284	NA	2902.11	-25.619176	uc002oyg.1	chr19:44591414-44591623	NA	NA	NA	NA	1173.19	-7.185867	uc003vgc.3	chr7:111927134-111929008	NA	NA	NA	NA	NA	NA
ZNF286A	NA	NA	NA	NA	NA	NA	NA	NA	NA	237.442	-6.317802	uc002wc.1	chr22:22838772-22842091	NA	NA	NA	NA	NA	NA
ZNF287	NA	1377.38	-10.767865	uc021trd.1	chr17:16453631-16455169	282.746	-0.442396	uc002goz.4	chr17:15620605-15622454	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF292	616213	849.562	-6.880458	uc003pil.1	chr6:87932553-87933654	NA	NA	NA	NA	1167.78	-11.747416	uc021trd.1	chr17:16453631-16455169	NA	NA	NA	NA	NA	NA
ZNF304	613840	800.755	-10.758471	uc010slw.3	chr19:57869218-57871265	NA	NA	NA	NA	563.846	-6.079686	uc003pil.1	chr6:87932553-87933654	NA	NA	NA	NA	NA	NA
ZNF311	NA	NA	NA	NA	NA	1447.59	-7.293132	uc011dlk.1	chr6:28962594-28962777	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF322	610847	NA	NA	NA	NA	NA	NA	NA	NA	709	-10.527689	uc011dlk.1	chr6:28962594-28962777	NA	NA	NA	NA	NA	NA
ZNF326	614601	NA	NA	NA	NA	214.197	-7.499971	uc001dnq.2	chr1:90493261-90494094	353.758	-7.773393	uc003nil.4	chr6:26634611-26637572	NA	NA	NA	NA	NA	NA
ZNF330	609550	NA	NA	NA	NA	1367.22	-7.680346	uc003liq.4	chr4:142155144-142155850	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF331	606043	NA	NA	NA	NA	539.136	-7.048793	uc002qbx.1	chr19:54081207-54083523	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 1

ZNF3411	NA	NA	NA	NA	NA	687.229	-5.080246	uc002wzx.3	chr20:32379324-32380075	NA	NA	NA	NA	NA	NA	NA
ZNF3501	605422	NA	NA	NA	NA	413.215	-7.45784	uc003mjl.3	chr5:178311293-178311424	NA	NA	NA	NA	NA	NA	chr19:52467593-52468106
ZNF354B1	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF354C1	NA	435.239	-4.752623	uc003njl.3	chr5:178507099-178507691	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF3671	610160	NA	NA	NA	NA	234.956	-7.191689	uc004awf.3	chr9:99148225-99150518	NA	NA	NA	NA	NA	NA	NA
ZNF3941	NA	NA	NA	NA	NA	1244.95	-12.856537	uc003uqs.3	chr7:99090854-99091151	NA	NA	NA	NA	NA	NA	NA
ZNF3951	609494	736.594	-5.150466	uc003xgq.3	chr8:28203102-28206235	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF3971	609601	681.349	-8.982616	uc002kyl.3	chr18:32823326-32824064	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF3981	NA	747.101	-10.990159	uc011kul.2	chr7:148876894-148880118	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	chr7:148876894-148880118
ZNF4281	NA	NA	NA	NA	NA	707.212	-10.093828	uc002oxa.3	chr19:444111376-44111768	NA	NA	NA	NA	NA	NA	NA
ZNF4381	NA	NA	NA	NA	NA	492.352	-5.903432	uc001ivn.3	chr10:31133565-31133889	600.104	-6.104688	uc001vln.3	NA	NA	NA	chr10:31133565-31133889
ZNF4411	194542	NA	NA	NA	NA	562.649	-7.972789	uc010dys.3	chr19:12382625-12383221	NA	NA	NA	NA	NA	NA	NA
ZNF4421	NA	NA	NA	NA	NA	245.753	-5.92491	uc002mtr.1	chr19:12460185-12460514	NA	NA	NA	NA	NA	NA	NA
ZNF4451	NA	NA	NA	NA	NA	NA	NA	NA	NA	509.591	-7.343588	uc011azv.1	NA	NA	NA	chr3:44481262-44488066
ZNF4491	300627	278.625	-5.372219	uc004eyr.4	chrX:134481539-134482942	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF4601	604755	NA	NA	NA	NA	NA	NA	NA	NA	278.274	-5.530242	uc010ygv.1	NA	NA	NA	chr19:57803599-57805436
ZNF4611	608640	1598.84	-10.922821	uc002oem.3	chr19:37128283-37129554	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF4741	NA	NA	NA	NA	NA	502.786	-5.296089	uc003ksv.3	chr5:121488781-121489266	NA	NA	NA	NA	NA	NA	NA
ZNF4831	NA	604.741	-3.134538	uc004big.2	chr9:114338695-114340124	613.137	-6.103943	uc004bfr.2	chr9:114305451-114306712	304.293	-2.614778	uc010nud.1	NA	NA	NA	chr9:114290213-114290300
ZNF4851	NA	NA	NA	NA	NA	NA	NA	NA	NA	764.051	-8.3963	uc010qfc.2	NA	NA	NA	chr10:44112818-44113352
ZNF4911	837.229	NA	-9.713999	uc002nso.1	chr19:11918083-11919306	NA	NA	NA	NA	765.404	-4.904265	uc002nso.1	NA	NA	NA	chr19:11918083-11919306
ZNF4931	NA	NA	NA	NA	NA	562.367	-4.742618	uc002npu.3	chr19:21590331-21591601	242.563	-4.619047	uc002npu.3	NA	NA	NA	chr19:21590331-21591601
ZNF4961	613911	NA	NA	NA	NA	551.808	-5.811104	uc009xgv.3	chr1:247463622-247463820	NA	NA	NA	NA	NA	NA	NA
ZNF5071	NA	NA	NA	NA	NA	NA	NA	NA	NA	698.924	-6.947905	uc002htc.2	NA	NA	NA	chr19:32847690-32850707
ZNF5111	NA	689.902	-6.972852	uc001lml.1	chr10:135125455-135126666	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF518A1	NA	441.054	-7.495805	uc001kbp.3	chr10:97920531-97923517	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF518B1	NA	NA	NA	NA	NA	NA	NA	NA	NA	494.048	-4.385552	uc003gmn.3	NA	NA	NA	chr4:10441504-10444727
ZNF5211	610974	NA	NA	NA	NA	535.88	-8.334623	uc002kxk.2	chr18:22641888-22642675	NA	NA	NA	NA	NA	NA	NA
ZNF5271	NA	NA	NA	NA	NA	NA	NA	NA	NA	611.415	-4.3871	uc002age.3	NA	NA	NA	chr19:37875889-37876545
ZNF5291	NA	354.128	-6.566834	uc002oeg.4	chr19:37034517-37037767	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5301	NA	NA	NA	NA	NA	772.434	-6.079823	uc002qpk.2	chr19:58118694-58119637	894.788	-8.501527	uc002qpk.2	NA	NA	NA	chr19:58118694-58119637
ZNF5361	NA	NA	NA	NA	NA	NA	NA	NA	NA	1458.33	-15.052646	uc002nsu.1	NA	NA	NA	chr19:31048072-31048965
ZNF5501	NA	663.971	-7.188694	uc002qpe.1	chr19:58057825-58058342	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5541	NA	NA	NA	NA	NA	NA	NA	NA	NA	322.552	-6.844844	uc002lwl.2	NA	NA	NA	chr19:2834851-2836733
ZNF5591	NA	1101.65	-11.206608	uc002mld.3	chr19:9452146-9454519	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5621	NA	364.796	-5.037515	uc002mlk.3	chr19:9759338-9763624	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5641	NA	NA	NA	NA	NA	NA	NA	NA	NA	909.799	-5.687784	uc002mtt.3	NA	NA	NA	chr19:12636184-12637259
ZNF5711	NA	NA	NA	NA	NA	NA	NA	NA	NA	702.033	-8.219443	uc002ogr.1	NA	NA	NA	chr19:38045684-38046770
ZNF5721	NA	NA	NA	NA	NA	462.621	-5.428603	uc003yrr.3	chr8:125990101-125991630	906.162	-6.915777	uc003yrr.3	NA	NA	NA	chr8:125990101-125991630
ZNF5821	615600	NA	NA	NA	NA	948.327	-9.069843	uc002qmqz.1	chr19:56894648-56895231	NA	NA	NA	NA	NA	NA	NA
ZNF5891	NA	258.55	-4.667519	uc011bbg.2	chr3:48327804-48329115	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5921	613624	NA	NA	NA	NA	NA	NA	NA	NA	222.614	-4.64615	uc002bld.3	NA	NA	NA	chr15:85345635-85349663
ZNF5951	NA	NA	NA	NA	NA	NA	NA	NA	NA	594.465	-10.571519	uc003fzv.1	NA	NA	NA	chr4:87315-88099
ZNF5961	NA	686.268	-6.508722	uc003wol.3	chr8:196363-197339	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5971	614685	1158.22	-10.11781	uc002cvd.3	chr16:3486110-3486423	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF5991	NA	NA	NA	NA	NA	NA	NA	NA	NA	1173.62	-12.119387	uc010edm.2	NA	NA	NA	chr19:35248979-35249938
ZNF6051	NA	NA	NA	NA	NA	NA	NA	NA	NA	257.849	-4.91507	uc001ulh.3	NA	NA	NA	chr12:133498019-133501958
ZNF6061	613905	382.077	-5.948923	uc002qpw.3	chr19:58488441-58489668	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF6141	NA	535.299	-11.392896	uc002pyl.4	chr19:52516018-52516389	552.71	-6.28192	uc002pyl.4	chr19:52516018-52516389	NA	NA	NA	NA	NA	NA	NA

Table 1

ZNF619:	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	505.576	-8.711761	uc003ekj.3	chr3:40529733-40531728
ZNF626:	NA	399.517	-5.128135	uc002npd.1	chr19:20827509-20828201	NA	NA	NA	NA	NA	648.349	-7.14498	uc002npd.1	chr19:20827509-20828201
ZNF630:	300819	NA	NA	NA	NA	403.018	-7.171605	uc004div.4	chrX:47917567-47917856	NA	NA	NA	NA	NA
ZNF638:	614349	708.105	-9.13175	uc010fec.2	chr2:71622404-71622817	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF644:	614159	NA	NA	NA	NA	570.803	-11.790652	uc001goz.3	chr1:182023705-182025438	NA	NA	NA	NA	NA
ZNF648:	NA	NA	NA	NA	NA	495.69	-6.162537	uc002iov.4	chr17:47366568-47375774	NA	NA	NA	NA	NA
ZNF652:	613907	NA	NA	NA	NA	632.064	-9.271647	uc003urc.3	chr7:99161683-99162328	NA	NA	NA	NA	NA
ZNF655:	NA	NA	NA	NA	NA	734.849	-9.393264	uc003cmi.2	chr3:42956847-42960825	NA	NA	NA	NA	NA
ZNF662:	NA	NA	NA	NA	NA	483.181	-4.350072	uc010cag.2	chr16:31072164-31072388	489.398	-3.664751	uc010cag.2	chr16:31072164-31072388	
ZNF668:	NA	NA	NA	NA	NA	702.689	-10.412303	uc001lcl.2	chr1:247197940-247200750	NA	NA	NA	NA	NA
ZNF670:	NA	NA	NA	NA	NA	NA	NA	NA	NA	1668.61	-28.856056	uc004dgr.3	chrX:46357160-46359277	
ZNF674:	300573	NA	NA	NA	NA	NA	NA	NA	NA	823.215	-8.555345	uc002nrl.3	chr19:23835708-23836027	
ZNF675:	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF680:	NA	NA	NA	NA	NA	1316.04	-11.917273	uc003lta.2	chr7:63980255-63981538	NA	NA	NA	NA	NA
ZNF687:	610568	569.982	-4.749762	uc001exq.3	chr1:15126386-151264381	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF7:	194531	NA	NA	NA	NA	1393.42	-4.894253	uc003zeh.2	chr8:146071564-146072894	426.765	-6.043343	uc003zeh.2	chr8:146071564-146072894	
ZNF705D:	NA	208.736	-5.701588	uc003wva.3	chr8:11970668-11973025	235.049	-7.472382	uc003wva.3	chr8:11970668-11973025	NA	NA	NA	NA	NA
ZNF708:	NA	288.798	-5.46298	uc002npq.1	chr19:21473963-21476075	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF709:	NA	833.003	-7.531268	uc002mtv.4	chr19:12571998-12574809	685.05	-7.942586	uc002mtv.4	chr19:12571998-12574809	NA	NA	NA	NA	NA
ZNF736:	NA	460.532	-5.671791	uc011kdo.2	chr7:63809526-63810017	NA	NA	NA	NA	516.485	-5.560655	uc011kdo.2	chr7:63809526-63810017	
ZNF738:	NA	1586.07	-14.983602	uc002nps.4	chr19:21560286-21571384	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF749:	NA	NA	NA	NA	NA	788.462	-7.594226	uc002qqq.2	chr19:57956864-57957191	NA	NA	NA	NA	NA
ZNF770:	NA	NA	NA	NA	NA	518.253	-9.124667	uc001ziw.3	chr15:35270542-35273559	NA	NA	NA	NA	NA
ZNF772:	NA	NA	NA	NA	NA	211.455	-7.473411	uc002qol.3	chr19:57980954-57984641	NA	NA	NA	NA	NA
ZNF773:	NA	NA	NA	NA	NA	209.51	-4.791537	uc002qox.3	chr19:58018793-58019510	NA	NA	NA	NA	NA
ZNF774:	NA	1228.49	-5.646419	uc002bpk.4	chr15:90904516-90904715	NA	NA	NA	NA	657.773	-7.981874	uc002bpk.4	chr15:90904516-90904715	
ZNF780A:	NA	NA	NA	NA	NA	NA	NA	NA	NA	330.853	-12.142169	uc002omw.4	chr19:40575059-40578556	
ZNF788:	NA	217.904	-5.711274	uc002mtc.1	chr19:12208899-12210475	NA	NA	NA	NA	572.226	-3.509843	uc002mtc.3	chr19:12224211-12225494	
ZNF789:	NA	NA	NA	NA	NA	416.155	-5.522748	uc003uqq.1	chr7:99085112-99085217	771.982	-9.939626	uc003uqp.3	chr7:99079824-99079948	
ZNF799:	NA	NA	NA	NA	NA	939.96	-9.224523	uc002mls.4	chr19:12490003-12491154	431.649	-9.402634	uc010dyt.3	chr19:12500828-12501279	
ZNF80:	194553	904.756	-7.650566	uc010hqo.3	chr3:113953480-113955099	NA	NA	NA	NA	679.504	-5.914253	uc010hqo.3	chr3:113953480-113955099	
ZNF833P:	NA	NA	NA	NA	NA	702.564	-9.749107	uc021upi.1	chr19:11796898-11797384	NA	NA	NA	NA	NA
ZNF84:	NA	NA	NA	NA	NA	NA	NA	NA	NA	1086.64	-11.177794	uc001ulm.4	chr12:133635519-133639885	
ZNF841:	NA	1141.18	-10.872431	uc002pyl.1	chr19:52567719-52568359	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNF92:	603974	NA	NA	NA	NA	NA	NA	NA	NA	486.676	-5.545064	uc003ttz.3	chr7:64864789-64865998	
ZNF93:	603975	NA	NA	NA	NA	NA	NA	NA	NA	1286.2	-12.019108	uc002nom.3	chr19:20042963-20043806	
ZNFHT3:	604500	NA	NA	NA	NA	NA	NA	NA	NA	562.089	-8.363934	uc010cus.1	chr17:34848794-34848953	
ZNFHT6:	NA	692.253	-7.368537	uc001dlh.3	chr1:86115106-86119740	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZNRF3:	612062	333.4	-4.014158	uc003aeg.3	chr22:29449611-29453476	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZP4:	613514	NA	NA	NA	NA	533.237	-5.591052	uc001hym.3	chr1:238041164-238041682	300.738	-2.93942	uc001hym.3	chr1:238041164-238041682	
ZPBIP:	608498	NA	NA	NA	NA	343.667	-8.108816	uc003iou.3	chr7:49977024-49977123	1066.8	-3.484454	uc003tou.3	chr7:49977024-49977123	
ZPB22:	608499	NA	NA	NA	NA	579.343	-6.149369	uc002hte.3	chr17:38033063-38034149	NA	NA	NA	NA	NA
ZPLD1:	615915	NA	NA	NA	NA	NA	NA	NA	NA	694.332	-9.212451	uc003dvs.1	chr3:102196463-102198685	
ZPR1:	603901	NA	NA	NA	NA	NA	NA	NA	NA	424.147	-4.925141	uc001ppp.3	chr11:116649276-116649640	
ZSCAN20:	611315	NA	NA	NA	NA	207.115	-5.206264	uc001bxj.4	chr1:33961077-33961995	434.091	-1.153455	uc001bxj.4	chr1:33961077-33961995	
ZSCAN21:	601261	698.442	-12.368239	uc003usn.1	chr7:99662275-99662661	NA	NA	NA	NA	NA	NA	NA	NA	NA
ZSCAN31:	610794	NA	NA	NA	NA	NA	NA	NA	NA	947.644	-8.76849	uc003nla.3	chr6:28292515-28293942	
ZSCAN32:	NA	NA	NA	NA	NA	NA	NA	NA	NA	569.021	-5.464605	uc002cux.4	chr16:3432085-3432851	
ZSCAN4:	613419	823.336	-10.726047	uc002apu.3	chr19:58190274-58190520	NA	NA	NA	NA	865.474	-8.886073	uc002apu.3	chr19:58190274-58190520	

Table 1

ZSCAN9	602246	NA	NA	NA	NA	NA	NA	NA	NA	638.979	-7.069345	uc003nkg.2	chr6:28200957-28201264
ZSWIM7	614535	NA	NA	NA	NA	NA	NA	NA	NA	406.085	-5.834956	uc002gpe.3	chr17:35879875-15881227
ZW10	603954	NA	NA	NA	NA	586.789	-7.229224	NA	NA	NA	NA	NA	NA
ZXDB	300236	881.262	-10.926491	uc004hvd.3	chrX:57620894-57623910	481.464	-3.699241	uc004dvd.3	chrX:57620894-57623910	1396.79	-11.874533	uc004dvd.3	chrX:57620894-57623910
ZZEF1	NA	NA	NA	NA	NA	335.879	-4.621829	uc002lxe.3	chr17:3907739-3910183	1115.99	-2.984226	uc002lxe.3	chr17:3907739-3910183

Table 4

Frame 1			Frame 2			Frame 3						
MM Number	TANGO	PASTA	UCSC Transcript ID	Hq19 Location	TANGO	PASTA	UCSC Transcript ID	Hq19 Location	TANGO	PASTA	UCSC Transcript ID	Hq19 Location
603452	NA	NA	NA	NA	NA	814.821	NA	NA	NA	-6.711982	uc002mc1.2	chr22:2200774488-2200774659
164690	239.103	-3.707258	uc001gm1.3	chr11:79053983-17906398	239.705	-6.350043	uc009hwa.3	chr11:79079716-179079939	NA	NA	NA	NA
603418	NA	NA	NA	NA	339.705	-5.292472	uc009hwa.3	chr11:19629202-19630718	NA	NA	NA	NA
611223	NA	NA	NA	NA	1108.45	-10.380057	uc001lab.2	chr12:45669021-245668550	NA	NA	NA	NA
NA	NA	NA	NA	NA	415.007	-0.327008	uc004aya.3	chr9:100777714-100778274	NA	NA	NA	NA
600040	1110.13	-6.56831	uc002ph1.1	chr19:49464495-49464519	677.648	-6.681534	uc002ph1.3	chr19:494644894-49465055	NA	NA	NA	NA
606557	699.926	-2.465276	uc002ab1.3	chr2:60678302-60679709	NA	NA	NA	NA	699.15	-9.206331	uc002ab1.3	chr2:60678302-60679709
151430	664.489	-1.553062	uc002bk1.1	chr18:60790579-60795857	NA	NA	NA	NA	NA	NA	NA	NA
151410	NA	NA	NA	NA	416.91	-4.886939	uc001ep1.3	chr1:147096761-147098015	NA	NA	NA	NA
603832	NA	NA	NA	NA	208.345	-4.748612	uc001ep1.3	NA	NA	-5.00011	uc002wv1.3	chr22:2365770-236602274
602452	380.956	-6.294105	uc002gl2.1	chr22:111418445-111419154	NA	NA	uc001ep1.3	NA	NA	NA	NA	NA
60491	422.435	-4.526567	uc002hy1.3	chr17:92383947-92394220	992.771	-5.67275	uc003dwa.3	chr3:105377109-105377813	NA	NA	NA	NA
158105	NA	NA	NA	NA	890.205	-11.527604	uc001qmo.3	chr12:4409176-4414522	NA	NA	NA	chr3:105377109-105377813
123833	621.915	-6.99868	uc002rm1.3	chr19:93014685-93015215	NA	NA	NA	NA	896.409	-7.285364	uc001qmo.3	chr12:4409176-4414522
602668	NA	NA	NA	NA	560.794	-8.852866	uc001qdb1.4	chr11:12526713-125830636	NA	NA	NA	chr3:44414449-44418161
608707	NA	NA	NA	NA	606.546	-6.696259	uc009hwa.3	chr10:95287911-95288849	NA	NA	NA	NA
610000	NA	NA	NA	NA	NA	NA	NA	NA	454.913	-5.439775	uc001on1.3	chr11:67820326-67821454
119491	491.187	-6.89372	uc001hp1.3	chr12:40072535-240072717	NA	NA	NA	NA	NA	NA	NA	NA
119496	692.539	-8.42437	uc001hh1.1	chr15:94356519-94357267	NA	NA	NA	NA	NA	NA	NA	NA
164762	303.225	-5.60408	uc002rf1.2	chr22:21904134-21308037	787.286	-6.122336	uc002fsl.3	chr17:13246467-1326806	NA	NA	NA	NA
164770	NA	NA	NA	NA	278.288	-7.858606	uc002rf1.2	chr22:21904134-21308037	308.904	-9.22987	uc002rf1.2	chr22:21904134-21308037
164765	449.089	-6.181621	uc001op1.3	chr11:70282515-70282690	NA	NA	NA	NA	688.995	-7.060869	uc001lhw1.2	chr5:14945667-149456695
108390	NA	NA	NA	NA	1714.88	-10.599976	uc001op1.4	chr11:70281269-70282690	546.925	-11.59448	uc001lhw1.2	chr11:70282515-70282690
603905	NA	NA	NA	NA	NA	NA	NA	NA	1322.6	-11.844586	uc001op1.2	chr15:75013061-75013091
600326	1099.42	-6.227878	uc001pie1.2	chr11:118619473-118622806	NA	NA	NA	NA	376.579	-8.960392	uc003h1.1	chr3:18260559-18262881
300239	1687.5	-12.053467	uc004cn1.3	chr1:13651215-13651694	NA	NA	NA	NA	NA	NA	NA	NA
600051	1288.32	-13.627571	uc001sp1.3	chr1:15819895-51823371	NA	NA	NA	NA	495.428	-9.285163	uc004cn1.3	chr1:13651215-13651694
600543	637.759	-7.258569	uc002reg1.1	chr22:22400442-212248399	NA	NA	NA	NA	NA	NA	NA	NA
600541	937.692	-8.075469	uc0021zw1.1	chr7:13946055-13946137	1074.2	-5.289375	uc021z1.1	chr7:13980856-139815490	NA	NA	NA	NA
60457	904.1	-7.115195	uc001qpm1.2	chr11:70052580-70053508	NA	NA	NA	NA	NA	NA	NA	NA
600558	861.158	-7.06114	uc003wnc1.1	chr8:16850394-16850590	NA	NA	NA	NA	NA	NA	NA	NA
603392	492.159	-4.682318	uc002ex1.3	chr2:105377283-105377739	1149.08	-10.823681	uc002ex1.3	NA	NA	NA	NA	NA
137070	522.526	-7.680538	uc001hw1.2	chr16:31194165-31194671	NA	NA	NA	chr2:105377283-105377739	1317.91	-7.489084	uc002ex1.1	chr2:105388004-105389846
60898	1427.08	-15.72479	uc003df1.3	chr5:162918171-162918853	257.017	-4.07378	uc001su1.1	chr12:6608695-6609277	688.695	-4.840621	uc001hw1.2	chr16:31194165-31194671
190020	351.497	-4.164841	uc001hw1.2	chr11:532242-532725	1778.49	-29.870699	uc003df1.3	chr5:162918171-162918853	NA	NA	NA	NA
147576	1792.14	-13.227448	uc003hw1.4	chr4:185308976-185308911	NA	NA	NA	chr4:185308976-185308911	NA	NA	NA	NA
601800	NA	NA	NA	NA	1609.34	-10.44092	uc003hw1.4	chr6:601816-402697	496.077	-5.244314	uc001jnc1.2	chr6:401816-402697
60235	682.472	-5.10203	uc004df1.2	chr5:110247135-110248031	753.367	-6.69249	uc003hw1.2	chr9:110247133-110248031	NA	NA	NA	NA
130070	372.819	-4.225845	uc001rg1.1	chr12:2558360-255836245	582.265	-4.46887	uc004df1.2	chr5:110247133-110248031	NA	NA	NA	NA
600699	927.675	-10.702852	uc001hw1.2	chr12:96711462-29671679	NA	NA	NA	chr9:110247133-110248031	NA	NA	NA	NA
177075	1281.56	-13.87832	uc002fm1.3	chr16:7627745-7628356	767.442	-7.210776	uc001hwa.2	chr12:96711462-29671679	NA	NA	NA	NA
601158	NA	NA	NA	NA	698.904	-9.996509	uc001lg1.3	chr10:4964299-49643183	NA	NA	NA	NA
162180	NA	NA	NA	NA	NA	NA	NA	chr10:4964299-49643183	365.428	-5.789976	uc003qz1.3	chr6:169328966-169329107
31030	NA	NA	NA	NA	316.908	-4.583797	uc001mh1.2	chr1:136663930-136664601	NA	NA	NA	NA
30087	NA	NA	NA	NA	815.102	-7.648517	uc004ex1.3	chr1:119746120-119755016	964.019	-9.739943	uc004ex1.3	chr1:119746120-119755016
604705	NA	NA	NA	NA	1140.46	-10.994985	uc002zh1.1	chr2:112786442-112786945	NA	NA	NA	NA
60402	1055.4	-14.709356	uc003bw1.3	chr3:158322992-158324249	NA	NA	NA	NA	NA	NA	NA	NA
604884	964.857	-7.940541	uc001lew1.3	chr1:151039974-151040873	NA	NA	NA	NA	NA	NA	NA	NA
159558	1121.3	-14.78143	uc001lhw1.1	chr9:2084968-20846440	NA	NA	NA	NA	NA	NA	NA	NA
159559	447.909	-6.204244	uc021jl1.1	chr5:168370616-168377700	NA	NA	NA	NA	NA	NA	NA	NA
120520	558.147	-4.926569	uc0010hw1.1	chr3:154898249-154901518	NA	NA	NA	NA	751.938	-7.985108	uc021jl1.1	chr6:168370616-168377700
300116	NA	NA	NA	NA	786.117	-4.124339	uc004fm1.2	chr1:15492309-15493674	NA	NA	NA	NA
189990	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
16409	2134.83	-12.017527	uc001on1.2	chr11:7113911-7114572	NA	NA	NA	NA	651.201	-7.516773	uc003hc1.3	chr6:13553919-135540311
14350	NA	NA	NA	NA	NA	NA	NA	NA	783.849	-6.070138	uc009hw1.2	chr11:71728045-71728857
607484	NA	NA	NA	NA	815.795	-5.605366	uc002ex1.3	chr16:67696551-67696681	352.165	-6.258106	uc001mf1.3	chr9:134070758-134071045
130040	1433.7	-9.856561	uc003aw1.3	chr22:3961985-39621318	NA	NA	NA	NA	NA	NA	NA	NA
174900	NA	NA	NA	NA	269.408	-4.710082	uc003hp1.3	chr3:178952153-178952497	691.075	-6.02967	uc003hwa.3	chr4:551640-55164412
174894	NA	NA	NA	NA	693.608	-7.5758	uc002ic1.2	chr18:5769986-5751538	NA	NA	NA	NA
604959	NA	NA	NA	NA	401.549	-6.750479	uc003ec1.3	chr5:139393744-1393939462	NA	NA	NA	NA
176915	NA	NA	NA	NA	NA	NA	NA	NA	590.556	-5.089477	uc003pek1.3	chr6:64230080-64230849
176876	NA	NA	NA	NA	NA	NA	NA	NA	228.362	-4.796654	uc001cw1.1	chr12:11392438-113924777
179550	NA	NA	NA	NA	1128.92	-13.514866	uc003hd1.3	chr7:39745845-39747729	NA	NA	NA	NA
602908	NA	NA	NA	NA	207.624	-5.332478	uc002wq1.3	chr20:18467186-18470407	232.103	-6.420261	uc004dk1.2	chr7:48458563-48459593
300027	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 4

RET	Oncogene	164761	NA	NA	NA	598.985	-5.991364	uc001jak.1	chr10:43622205-43622952	NA	NA	NA	NA	NA
RRS2	Other	600861	539.972	-4.731056	uc001gsl.3	NA	NA	NA	chr1:19278077-192781407	NA	NA	NA	NA	NA
RRAS2	Other	600998	446.211	-4.701466	uc021gac.1	NA	NA	NA	chr11:14299466-14300882	NA	NA	NA	NA	NA
RSU1	Other	179555	NA	NA	NA	697.779	-4.677778	uc001lok.3	chr10:16638617-16639392	NA	NA	NA	NA	NA
RUNX1	Other	151385	299.247	-7.804626	uc010gmw.1	NA	NA	NA	chr21:36169710-36170351	NA	NA	NA	NA	NA
RUNX2	Oncogene	133435	NA	NA	NA	735.542	-2.010638	uc002yyl.1	NA	602.431	-6.093529	uc010mam.2	chr8:392657195-92977469	NA
S100A11	Other	600211	NA	NA	NA	NA	NA	NA	NA	602.809	-11.20612	uc011dhw.2	chr6:45515043-45518819	NA
SALL4	Oncogene	607343	NA	NA	NA	397.012	-6.040094	uc001umt.3	chr1:157004982-157005137	NA	NA	NA	NA	NA
SEMA3E	Other	605166	336.312	-4.65747	uc022abg.1	NA	NA	NA	chr7:82959322-82959601	NA	NA	NA	chr20:50400588-50400803	NA
SERTAD1	Oncogene	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SERTAD2	Other	NA	800.745	-7.653805	uc002zde.2	NA	NA	NA	NA	NA	NA	NA	chr19:40928409-40928742	NA
SETD81	Oncogene	604396	NA	NA	NA	579.839	-9.348083	uc001evu.2	chr1:150936841-150937220	NA	NA	NA	NA	NA
SKP2	Oncogene	165340	828.136	-11.169164	uc003fgu.3	NA	NA	NA	chr5:586182134-36184142	NA	NA	NA	chr8:170110206-170114637	NA
SLC6A4	Other	607793	NA	NA	NA	801.806	-6.57913	uc003ikc.2	NA	785.168	-10.78636	uc003fgu.3	NA	NA
SPHL1	Oncogene	607930	NA	NA	NA	899.972	-4.112876	uc002jrl.1	chr17:74883668-74883941	NA	NA	NA	NA	NA
SPY1	Oncogene	165170	NA	NA	NA	639.564	-9.461244	uc003ypl.1	chr11:47379752-47380149	NA	NA	NA	NA	NA
SPC	Oncogene	190890	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
SPY19	Other	182175	NA	NA	NA	597.577	-7.665719	uc003qec.3	chr5:112092925-11204089	NA	NA	NA	chr20:96931788-36039621	NA
TRAC3	Other	605303	1319.32	-11.124323	uc003gdo.3	NA	NA	NA	chr4:1746741-1746805	NA	NA	NA	chr5:11209103-11204089	NA
TCL18	Other	300934	754.465	-5.092023	uc004flc.3	614.296	-3.166743	uc004flc.3	chrX:153449344-153650063	NA	NA	NA	NA	NA
TEAD1	Oncogene	607669	919.376	-3.676631	uc001yfa.3	322.924	-3.115225	uc001yfa.3	chrX:153449344-153650063	NA	NA	NA	chr14:96157659-96158965	NA
TEC	Oncogene	189967	596.256	-13.238792	uc021gde.1	NA	NA	NA	chr14:96157659-96158965	NA	NA	NA	chr11:12958770-12966284	NA
TEC	Oncogene	600583	687.467	-7.550431	uc003gpc.3	NA	NA	NA	chr4:48137800-48139432	NA	NA	NA	NA	NA
TFDP2	Other	602160	NA	NA	NA	674.747	-7.095547	uc003nuh.4	chr5:141669270-141671354	NA	NA	NA	NA	NA
TIAM1	Other	190160	687.067	-3.80782	uc003ccz.4	NA	NA	NA	NA	NA	NA	NA	NA	NA
TIAM1	Other	600687	NA	NA	NA	447.548	-5.666313	uc011adk.1	chr21:32490736-32499155	NA	NA	NA	NA	NA
TRIO	Oncogene	600698	696.155	-8.207528	uc003yfr.1	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIO	Oncogene	601899	583.959	-2.350896	uc003jfr.3	NA	NA	NA	chr5:80947105-80950350	NA	NA	NA	chr5:14508332-14509458	NA
USP4	Oncogene	605486	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
USP4	Oncogene	602952	1638.44	-14.749706	uc003gdx.3	NA	NA	NA	chr4:1920596-1920896	NA	NA	NA	NA	NA
WHS1	Oncogene	164880	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YES1	Oncogene	602967	NA	NA	NA	286.393	-5.575122	uc002xwh.4	chr20:52183610-52185803	NA	NA	NA	NA	NA
ZNFX17	Oncogene	602967	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Table 5

GENE	OMIM #	NM #	CAE reading frame	Cancer	gRNA Sequence	PAM	Exon
ABL2	164690	NM_007314	1 and 2	Glioblastoma Melanoma Pancreatic Thyroid	AAATCAGTGATGTGGTGCAG (SEQ ID NO: 1) TGTACAGGAAATCAGTGATG (SEQ ID NO: 2)	AGG TGG	12
BCL9	609004	NM_004326	2	Breast Thyroid	ATGTCCATGCAGGGCATGAT (SEQ ID NO: 3) GGGATCATGATGTTCTGTG (SEQ ID NO: 4)	GGG GGG	10
BIRC5	603352	NM_001168	2	Thyroid	CATCGAGCAGCTGGCTGCCA (SEQ ID NO: 5) CGGCCAGAGGCCTCAATCCA (SEQ ID NO: 6) CAGCTGGCTGCCATGGATTG (SEQ ID NO: 7)	TGG TGG AGG	5
CCNE1	123837	NM_001238	1	Breast Carcinoid Cervical Colorectal Endometrial Glioblastoma Stomach	AGCGGTAAGAAGCAGAGCAG (SEQ ID NO: 8) TAAGAAGCAGAGCAGCGGGC (SEQ ID NO: 9)	CGG CGG	12
CEP55	610000	NM_018131	2	Carcinoid Endometrial Liver	TCGCGATCTGCTTGTCCATG (SEQ ID NO: 10) ACTTTGAACAGTATTCCACA (SEQ ID NO: 11)	TGG TGG	9
CSF1R	164770	NM_005211	3	Melanoma Pancreatic	AACAACTATCAGTTCTGCTG (SEQ ID NO: 12)	AGG	22
FUS	137070	NM_004960	1 and 3	Breast Cervical Colorectal Glioblastoma Melanoma Pancreatic	TGAGCACAGACAGGATCGCA (SEQ ID NO: 13) ACAGACAGGATCGCAGGGAG (SEQ ID NO: 14)	GGG AGG	15
IRF2	147576	NM_002199	1 and 2	Breast Glioblastoma	AGGCTTAACAGCTCTTGACG (SEQ ID NO: 15) GGCTTAACAGCTCTTGACGC (SEQ ID NO: 16) GAAACATCGGATATCACCC (SEQ ID NO: 17)	CGG GGG AGG	9
MYB	189990	NM_005375	3	Breast Carcinoid Glioblastoma Melanoma Liver Pancreatic Thyroid Ovarian	ACGTGAATGCATTCTCAGCC (SEQ ID NO: 18) TGCATTCTCAGCCCGGACGC (SEQ ID NO: 19) TGTCTCATGACCAGCGTC (SEQ ID NO: 20)	CGG TGG CGG	16
NUMA1	164009	NM_006185	1 and 3	Breast Glioblastoma Melanoma Pancreatic	CTTTCAGGCAAAGCACTAAA (SEQ ID NO: 21) TCTTTCAGGCAAAGCACTAA (SEQ ID NO: 22) CTGAAAGAGACACAGTCACA (SEQ ID NO: 23)	GGG AGG TGG	25
SALL4	607343	NM_020436	3	Testicular	ACAAGATTGCGGTCAGCTAA (SEQ ID NO: 24)	GGG	4
SEMA3E	608166	NM_012431	1	Breast Pancreatic Liver	CACACGCTGGACTCCTGATG (SEQ ID NO: 25) CCGCTGCCAGGCACACGC (SEQ ID NO: 26) CAGGAGTCCAGCGTGTGCTC (SEQ ID NO: 27) CTGAGCATTACCGCTGCC (SEQ ID NO: 28)	GGG TGG GGG AGG	17
SERTAD2	N/A	NM_014755	1	Breast Glioblastoma Pancreatic	CACATCATGGAGGTGCTTGT (SEQ ID NO: 29) AGAGCTGGACCACATCATGG (SEQ ID NO: 30)	TGG AGG	2
SPHK1	603730	NM_182965	2	Glioblastoma Melanoma Liver	GGTCATAAGGGCTCTTCTGG (SEQ ID NO: 31) GCGCGGCCAGGGGTCATAA (SEQ ID NO: 32)	CGG GGG	8
TACC3	605303	NM_006342	1 and 3	Breast Carcinoid Lung Pancreatic Prostate	TGGACAGCTTGTGGGAAGCG (SEQ ID NO: 33) TCACTGCCTGGACAGCTTGT (SEQ ID NO: 34) TCGCTTCCACAAGCTGTCC (SEQ ID NO: 35)	AGG GGG AGG	6
TIAM1	600687	NM_003253	2	Breast Colorectal Lymphoma	CTCAGTGTTCAGTTTCCTGG (SEQ ID NO: 36) TCAGTGTTCAGTTTCCTGGA (SEQ ID NO: 37) CAGTGTTCAGTTTCCTGGAG (SEQ ID NO: 38)	AGG GGG GGG	29
CTTN	164765	NM_005231	1, 2 and 3	Breast Colorectal Lung Ovarian Pancreatic Skin Thyroid Stomach	GCAGCTCCACATAGTTGGCT (SEQ ID NO: 39) GCTCTCCAGCCAACTATG (SEQ ID NO: 40) CTATGTGGAGCTGCGGCAGT (SEQ ID NO: 41) TATGTGGAGCTGCGGCAGTA (SEQ ID NO: 42)	GGG TGG AGG GGG	17

Table 6

GENE	Tumor Associated Genes	MIM Number	TANGO	PASTA	UCSC Transcript ID	Hg19 Location	TANGO	PASTA	UCSC Transcript ID	Hg19 Location	TANGO	PASTA	UCSC Transcript ID	Hg19 Location
BAX	Other	60040	1110.13	-2.45276 uc002pif.1	chr19:49464355-49464519	677.648	-6.681534 uc002pif.3	NA	NA	chr19:49464894-49465055	NA	NA	NA	NA
BCL11A	Oncogene	60657	699.926	-2.45276 uc002pif.3	chr2:60678302-60679709	NA	NA	NA	NA	NA	699.15	-9.206531 uc002ab.3	NA	chr2:60678302-60679709
BCL2	Oncogene	151430	664.489	-1.553062 uc002pif.1	chr18:60790579-60795857	NA	NA	NA	NA	NA	NA	NA	NA	NA
BUB1	Other	602452	380.956	-6.294105 uc002pif.2	chr2:111418445-111419154	NA	NA	NA	NA	NA	NA	NA	NA	NA
CCL2	Other	158105	422.435	-4.526567 uc002pif.3	chr17:32583847-32584220	NA	NA	NA	NA	NA	NA	NA	NA	NA
CNIE1	Oncogene	123837	621.915	-6.998668 uc002pif.3	chr19:30314685-30315215	NA	NA	NA	NA	NA	NA	NA	NA	NA
CHRM5	Other	118494	431.187	-6.899372 uc001hpf.3	chr1:24007252-24007277	NA	NA	NA	NA	NA	NA	NA	NA	NA
CHRM5	Other	118496	632.539	-8.422437 uc001hpf.1	chr1:34356518-34357287	NA	NA	NA	NA	NA	NA	NA	NA	NA
CKL1	Oncogene	602007	303.225	-5.60498 uc002pif.2	chr22:21304134-21308037	279.288	-7.858606 uc002pif.2	NA	NA	chr22:21304134-21308037	308.904	-3.22987 uc002pif.2	NA	chr22:21304134-21308037
DDX6	Other	60326	1099.482	-6.181622 uc001pif.3	chr11:18618473-18622806	1714.88	-10.593976 uc001pif.4	NA	NA	chr11:18618473-18622806	546.925	-1.59443 uc001pif.3	NA	chr11:18618473-18622806
EGF6	Other	300239	1697.5	-12.053467 uc004cvi.3	chrX:13651215-13651694	NA	NA	NA	NA	NA	NA	NA	NA	NA
EPB5	Other	600551	1288.32	-13.627571 uc001esp.3	chr1:51819935-51822371	NA	NA	NA	NA	NA	NA	NA	NA	NA
ERBB4	Oncogene	600543	613.759	-7.258569 uc002pif.1	chr2:212240442-212248339	NA	NA	NA	NA	NA	NA	NA	NA	NA
ETV1	Oncogene	600541	937.692	-3.075469 uc002pif.2	chr7:13946055-13946137	1074.2	-5.283375 uc002pif.1	NA	NA	chr7:13946055-13946137	NA	NA	NA	NA
FADD	Other	602457	904.1	-7.115195 uc001pif.2	chr11:70052580-70053508	NA	NA	NA	NA	NA	NA	NA	NA	NA
FGF20	Oncogene	605558	861.158	-7.06114 uc003wxe.1	chr8:16850334-16850580	1149.03	-10.829891 uc002pif.3	NA	NA	chr8:16850334-16850580	NA	NA	NA	NA
FLH2	Other	602633	492.159	-4.682318 uc002pif.3	chr2:105977283-105977739	NA	NA	NA	NA	chr2:105977283-105977739	1317.91	-7.48904 uc002pif.1	NA	chr2:105977283-105977739
HIMR	Oncogene	600936	1427.08	-15.74279 uc003pif.3	chr5:162918171-162918953	1778.43	-23.870699 uc003pif.3	NA	NA	chr5:162918171-162918953	NA	NA	NA	NA
HIRAS	Oncogene	190020	351.437	-4.164841 uc010pif.2	chr11:532242-532755	NA	NA	NA	NA	NA	NA	NA	NA	NA
KLF4	Oncogene	602253	682.472	-5.102033 uc004pif.2	chr9:110247133-110248031	582.265	-4.488817 uc004pif.2	NA	NA	chr9:110247133-110248031	NA	NA	NA	NA
KRAS	Oncogene	190070	372.819	-4.225845 uc001pif.1	chr12:55358180-55362845	NA	NA	NA	NA	NA	NA	NA	NA	NA
LGALS8	Other	606099	927.675	-10.702852 uc001hpf.2	chr1:236711462-236716279	767.442	-7.210276 uc001hpf.2	NA	NA	chr1:236711462-236716279	NA	NA	NA	NA
MAF	Oncogene	177075	1281.56	-13.878332 uc002pif.3	chr16:79627745-79628356	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLF1	Oncogene	601402	1055.4	-14.703598 uc003pif.3	chr3:158322992-158324249	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLL1	Oncogene	604684	964.857	-7.940541 uc001pif.3	chr1:151039974-151040973	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLL1	Oncogene	159558	1321.3	-14.728143 uc011hpf.1	chr9:20344968-20346440	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLL1	Oncogene	159559	447.903	-6.204244 uc011hpf.1	chr6:168370616-168372700	NA	NA	NA	NA	NA	NA	NA	NA	NA
MLL1	Oncogene	120520	558.147	-4.926569 uc010hpf.1	chr3:154898249-154901518	NA	NA	NA	NA	NA	NA	NA	NA	NA
PDGFB	Oncogene	190040	1433.7	-9.856361 uc003pif.3	chr22:39619685-39621318	NA	NA	NA	NA	NA	NA	NA	NA	NA
RG52	Other	600861	539.972	-4.731056 uc001pif.3	chr1:192780727-192781407	NA	NA	NA	NA	NA	NA	NA	NA	NA
RRAS2	Other	600098	446.211	-4.701466 uc021pif.1	chr11:14299466-14300882	533.477	-5.021064 uc021pif.1	NA	NA	chr11:14299466-14300882	NA	NA	NA	NA
RUN1	Other	151385	299.247	-7.804628 uc010pif.1	chr21:36205258-36206416	735.542	-2.010638 uc002pif.1	NA	NA	chr21:36205258-36206416	NA	NA	NA	NA
SENNAE	Other	608166	336.312	-4.65747 uc022pif.1	chr7:7993222-79936901	NA	NA	NA	NA	NA	NA	NA	NA	NA
SKL	Oncogene	165340	828.136	-11.169164 uc003pif.3	chr3:170110206-170114637	NA	NA	NA	NA	NA	NA	NA	NA	NA
TAC3	Other	605303	1319.32	-11.124323 uc003pif.3	chr4:1746741-1746905	NA	NA	NA	NA	NA	NA	NA	NA	NA
TCL1B	Oncogene	603769	319.376	-3.676631 uc001pif.3	chrX:153649344-153650063	614.296	-3.166743 uc004pif.3	NA	NA	chrX:153649344-153650063	NA	NA	NA	NA
TEAD1	Oncogene	189967	596.256	-13.238792 uc021pif.1	chr14:96157659-96158965	322.924	-3.115225 uc001pif.3	NA	NA	chr14:96157659-96158965	801.36	-7.459216 uc001pif.3	NA	chr14:96157659-96158965
TRC	Oncogene	600883	687.467	-7.550331 uc003pif.3	chr11:12958770-12966284	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRH8	Oncogene	100160	687.067	-3.80782 uc003pif.4	chr3:24158645-24164374	NA	NA	NA	NA	NA	NA	NA	NA	NA
TP52	Oncogene	604068	696.155	-8.207528 uc003pif.1	chr8:80947105-80950350	NA	NA	NA	NA	NA	NA	NA	NA	NA
TRIO	Oncogene	601893	583.959	-2.350896 uc003pif.3	chr5:14508532-14509458	NA	NA	NA	NA	NA	NA	NA	NA	NA
WHSC1	Oncogene	602952	1638.44	-14.749306 uc003pif.3	chr4:1920396-1920896	NA	NA	NA	NA	NA	NA	NA	NA	NA

WHAT IS CLAIMED IS:

1. A method of treating a mammalian subject to inhibit growth of neoplastic cells comprising:
administering to the subject a composition that comprises an agent selected from the group consisting of:
 - a. an agent that comprises an amyloidogenic peptide;
 - b. an agent that comprises a nucleotide sequence that encodes the amyloidogenic peptide; and
 - c. an agent that induces expression of an endogenous nucleotide sequence that encodes the amyloidogenic peptide;wherein the amyloidogenic peptide is either:
 - (i) a Cryptic Amyloidogenic Element ("CAE") encoded by nucleic acid in a 3'-untranslated region ("3'-UTR") of a gene in the neoplastic cell; or
 - (ii) comprises an amino acid sequence at least 70% identical to the CAE and retains the property of amyloidogenic aggregation.
2. Use of a composition that comprises an agent to inhibit growth of neoplastic cells in a mammalian subject, wherein the agent is selected from the group consisting of:
 - a. an agent that comprises an amyloidogenic peptide;
 - b. an agent that comprises a nucleotide sequence that encodes the amyloidogenic peptide; and
 - c. an agent that induces expression of an endogenous nucleotide sequence that encodes the amyloidogenic peptide;wherein the amyloidogenic peptide is either:
 - (i) a Cryptic Amyloidogenic Element ("CAE") encoded by nucleic acid in a 3'-untranslated region ("3'-UTR") of a gene in the neoplastic cell; or
 - (ii) comprises an amino acid sequence at least 70% identical to the CAE and retains the property of amyloidogenic aggregation.
3. Use of a composition that comprises an agent for the manufacture of a medicament to inhibit growth of neoplastic cells in a mammalian subject, wherein the agent is selected from the group consisting of:
 - a. an agent that comprises an amyloidogenic peptide;
 - b. an agent that comprises a nucleotide sequence that encodes the amyloidogenic peptide; and
 - c. an agent that induces expression of an endogenous nucleotide sequence that encodes the amyloidogenic peptide;wherein the amyloidogenic peptide is either:

- (i) a Cryptic Amyloidogenic Element (“CAE”) encoded by nucleic acid in a 3'-untranslated region (“3'-UTR”) of a gene in the neoplastic cell; or
- (ii) comprises an amino acid sequence at least 70% identical to the CAE and retains the property of amyloidogenic aggregation.

4. The method or use according to any one of claims 1-3, wherein the agent is administered in an amount effective to kill neoplastic cells in the subject.

5. The method or use according to any one of claims 1-4, wherein the mammalian subject is human.

6. The method or use according to any one of claims 1-5, wherein the neoplastic cells are malignant.

7. The method or use according to any one of claims 1-6, wherein the neoplastic cells are from a cancer of neurogenic origin or a glia-derived tumor.

8. The method or use according to claim 7, wherein the cancer is selected from the group consisting of neuroblastomas, central neurocytomas, and retinoblastomas.

9. The method or use according to any one of claims 6-8, wherein the amyloidogenic peptide is encoded by the 3'-UTR of an NEFH or NEFL gene.

10. The method or use according to any one of claims 1-9, wherein the CAE is located in a gene that is highly expressed in the neoplastic cells.

11. The method or use according to any one of claims 1-10, further comprising:
screening the neoplastic cells to identify one or more genes that are highly expressed therein;
and

selecting, as the amyloidogenic peptide, a peptide that is encoded by a CAE that is located in the 3'-UTR of one of the highly expressed genes.

12. The method or use according to claim 11, wherein the screening of the neoplastic cells comprises measuring protein and/or mRNA in a sample of the neoplastic cells.

13. The method or use according to claim 11, wherein the screening of the neoplastic cells comprises:

pathological examination to characterize the neoplastic cells; and
identifying genes that are highly expressed in a database of gene expression data for the neoplastic cell type or for healthy cells of the type from which the neoplastic cells arose.

14. The method or use according to any one of claims 11-13, wherein the selecting of the amyloidogenic peptide comprises analyzing the 3'-UTR of the genes identified as highly expressed and selecting a gene having a 3'-UTR containing an open reading frame that encodes a peptide with amyloidogenic properties.

15. The method or use according to any one of claims 11-13, wherein the selecting of the amyloidogenic peptide comprises selected a gene from Table 1 that is among the genes identified as highly expressed.

16. The method or use according to any one of claims 1-15, wherein the CAE is present in the 3'-UTR of a gene set forth in Table 1.

17. The method or use according to any one of claims 1-15, wherein the CAE is in the 3'-UTR of gene is selected from the group consisting of APOA2, ATXN2, B2M, FGB, FUS, IAPP, LYZ, NOTCH3, PRNP, RHO, SAA1, SNCA, NEFH, NEFL, BSCL2, MAPT, and TTR.

18. The method or use according to any one of claims 1-15, wherein the CAE is in the 3'-UTR of a gene is selected from *NEFH*, *NEFL*, and *FUS*.

19. The method or use according to claim 18, wherein the amyloidogenic peptide comprises the amino acid sequence QFSLFLSL.

20. The method or use according to any one of claims 1-15, wherein the amyloidogenic peptide comprises an amino acid sequence at least 70% identical to the sequence SSRIRVTQFSLFLSLCKKKLLR and retains the property of amyloidogenic aggregation.

21. The method or use according to any one of claims 1-20, wherein the agent comprises a nucleotide sequence that encodes the amyloidogenic peptide.

22. The method or use according to claim 21, wherein the agent comprises cDNA or mRNA encoding the amyloidogenic peptide.

23. The method or use according to claim 21 or 22, wherein the agent further comprises a promoter operatively linked to the nucleotide sequence that encodes the amyloidogenic peptide.

24. The method or use according to claim 23, wherein the promoter is a tissue-selective promoter that promotes expression of genes in the neoplastic cells.

25. The method or use according to any one of claims 21-24, wherein the agent comprises a vector that comprises the nucleotide sequence that encodes the amyloidogenic peptide.

26. The method or use according to any one of claims 21-25, wherein the amyloidogenic peptide comprises an amino acid sequence at least 70% identical to the amino acid sequence of the CAE and retains the property of amyloidogenic aggregation.

27. The method or use according to any one of claims 1-20, wherein the amyloidogenic peptide comprises the CAE, and the agent causes expression of an endogenous nucleotide sequence that encodes the CAE.

28. The method or use according to claim 27, wherein the agent causes expression by causing translation of mRNA beyond the regular stop codon of the gene.

29. The method or use according to claim 28, wherein the agent comprises an aminoglycoside antibiotic that induces translational read-through.

30. The method or use according to claim 27, wherein the agent induces expression of the amyloidogenic peptide by modifying chromosomal DNA of the neoplastic cells to create a modified gene that includes the CAE in-frame with the start codon, uninterrupted by a stop codon.

31. The method or use according to claim 30, wherein the agent comprises a CRISPR Cas9 protein and one or more guide RNA molecules to introduce a site-specific modification of the chromosomal DNA to create a modified gene that includes the CAE in-frame with the start codon, uninterrupted by a stop codon.

32. The method or use according to claim 27, wherein the agent comprises a zinc finger nuclease or a transcription activator-like effector nuclease (TALEN) to introduce a site-specific modification of the chromosomal DNA to create a modified gene that includes the CAE in-frame with the start codon, uninterrupted by a stop codon.

33. The method or use according to any one of claims 30-32, wherein the chromosomal DNA is modified by eliminating the regular stop codon of the gene.

34. The method or use according to any one of claims 30-32, wherein the chromosomal DNA is modified by changing the reading frame of the gene such that the CAE is in-frame with the start codon free of interruption by a stop codon.

35. The method or use according to any one of claims 1-34, wherein the agent is locally administered to a tumor that comprises the neoplastic cells.

36. The method or use according to claim 35 or 36, wherein the tumor is in the eye or brain and the agent is administered intracranially or intravitreally.

37. A polynucleotide comprising a nucleotide sequence that encodes an amyloidogenic peptide fused in-frame with an expression control sequence to promote expression of the amyloidogenic peptide in mammalian cells,

wherein the amyloidogenic peptide is either:

(i) a Cryptic Amyloidogenic Element ("CAE") encoded by nucleic acid in a 3'-untranslated region ("3'-UTR") of a gene in the neoplastic cell; or

(ii) comprises an amino acid sequence at least 80% identical to the CAE and retains the property of amyloidogenic aggregation.

38. The polynucleotide according to claim 37, wherein the CAE is present in the 3'-UTR of a gene set forth in Table 1.

39. The polynucleotide according to claim 37, wherein the CAE is in the 3'-UTR of gene is selected from the group consisting of APOA2, ATXN2, B2M, FGB, FUS, IAPP, LYZ, NOTCH3, PRNP, RHO, SAA1, SNCA, NEFH, NEFL, BSCL2, MAPT, and TTR.

40. The method or use according to claim 37, wherein the CAE is in the 3'-UTR of a gene is selected from NEFH, NEFL, and FUS.

41. An expression vector comprising the polynucleotide according to any one of claims 37 – 40.

42. The expression vector according to claim 41, wherein the vector comprises a viral vector.

43. The expression vector according to claim 41 selected from the group consisting of a retroviral, adenoviral, adeno-associated viral (AAV), and herpes simplex viral vector.

44. A composition that comprises the polynucleotide or vector according to any one of claims 37 – 43 and a pharmaceutically acceptable carrier.

45. A polynucleotide comprising a nucleotide sequence of a crRNA sequence operably linked to a tracrRNA sequence, wherein the crRNA sequence targets a 3' end of a gene set forth in Table 1.

46. The polynucleotide according to claim 45 that is a chimeric guide RNA, said chimeric guide RNA including a tetraloop sequence positioned between the tracrRNA sequence and the crRNA sequence.

47. The polynucleotide according to any one of claims 45 – 47, wherein the crRNA sequence includes a nucleotide targeting sequence that is 17-20 nucleotides in length.

48. The polynucleotide according to claim 47, wherein the nucleotide targeting sequence comprises 17-20 nucleotides from a sequence set forth in any of SEQ ID NO. 1-42.

49. A polynucleotide comprising:

(a) a nucleotide sequence of a crRNA sequence, said crRNA sequence including:

(i) a nucleotide targeting sequence of 17-20 nucleotides that hybridizes to a 3' end ("target site") of a gene set forth in Table 1, and

(ii) a nucleotide sequence that hybridizes to a tracrRNA recognized by a Cas9 protein, wherein (i) is disposed 5' relative to (ii) and

wherein the targeting sequence targets a site inclusive or upstream of, and within 100 nucleotides of, the wild type stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence for said Cas9 protein; or

(b) a nucleotide sequence encoding (a).

50. A polynucleotide comprising:

(a) a nucleotide sequence of a CRISPR guide RNA including, from 5' to 3':

(i) a nucleotide targeting sequence of 17-20 nucleotides that hybridizes to a 3' end ("target site") of a gene set forth in Table 1,

(ii) a tetraloop sequence, and

(iii) a nucleotide sequence of a tracrRNA recognized by a Cas9 protein,

wherein the targeting sequence targets a site inclusive or upstream of, and within 100 nucleotides of, the wild type stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence for said Cas9 protein; or

(b) a nucleotide sequence encoding (a).

51. The polynucleotide according to any one of claims 45-50, wherein the crRNA sequence targets a 3' end of a gene set forth in Table 3 or Table 4.

52. The polynucleotide according to any one of claims 45-50, wherein the gene is selected from the group consisting of APOA2, ATXN2, B2M, FGB, FUS, IAPP, LYZ, NOTCH3, PRNP, RHO, SAA1, SNCA, NEFH, NEFL, BSCL2, MAPT, and TTR.

53. The polynucleotide according to any one of claims 45-50, wherein the gene is selected from NEFH, NEFL, and FUS.

54. The polynucleotide according to any one of claims 45-53, wherein the crRNA sequence targets a site upstream of, and within 100 nucleotides of, the natural stop codon of the gene, said site being immediately upstream of a protospacer adjacent motif (PAM) sequence for a Cas9 protein.

55. A vector comprising the polynucleotide according to any one of claims 45-54.

56. The vector according to claim 55, further comprising a nucleotide sequence that encodes a Cas9 polypeptide that complexes with the tracrRNA sequence and that cleaves upstream of the PAM sequence.

57. A vector comprising a nucleotide sequence that encodes the polynucleotide according to any one of claims 45-54.

58. An expression vector according to claim 57, wherein the nucleotide sequence that encodes the polynucleotide is operably linked to an expression control sequence to promote expression of the polynucleotide as RNA in a human cell.

59. The expression vector according to claim 58, wherein the human cell is a neoplastic cell having one or more genes that is highly expressed compared to a normal cell of the same cell type, and wherein the expression control sequence comprises a promoter of one of the genes that is highly expressed.

60. The expression vector according to claim 58, wherein the expression control sequence comprises a constitutive promoter .

61. The expression vector according to claim 58, wherein the expression control sequence comprises a promoter selected from the group consisting of U6, CMV, EF1 α , or CMV.

62. The expression vector according to any one of claims 58 – 61, further including a promoter sequence operably linked to a nucleotide sequence encoding a Cas9 nuclease that complexes with tracrRNA that comprises the tracrRNA sequence, and that cleaves upstream of the PAM sequence.

63. The expression vector according to claim 62, wherein the expression control sequence for the Cas9 nuclease further comprises a nuclear localization sequence (NLS).

64. The expression vector according to claim 62 or 63, wherein the Cas9 nuclease is selected from the group consisting of *Streptococcus pyogenes*, *Listeria innocua*, *Staphylococcus aureus*, *Streptococcus thermophiles*, and synthetic variants derived therefrom.

65. The expression vector according to any one of claims 62– 63, wherein the nucleotide sequence encoding the Cas9 nuclease is a codon-optimized sequence derived from *Streptococcus pyogenes*, *Listeria innocua*, *Staphylococcus aureus*, or *Streptococcus thermophiles*.

66. The expression vector according to any one of claims 62 -65, wherein the expression vector further includes a nucleotide sequence encoding a DNA repair template operably connected to a promoter.

67. The expression vector according to claim 66, wherein the DNA repair template includes a sequence to introduce a missense or frameshift mutation at point of cleavage by the Cas9 via homology-directed repair (HDR), and includes segments flanking said sequence that are homologous to the predicted site of Cas9 cleavage.

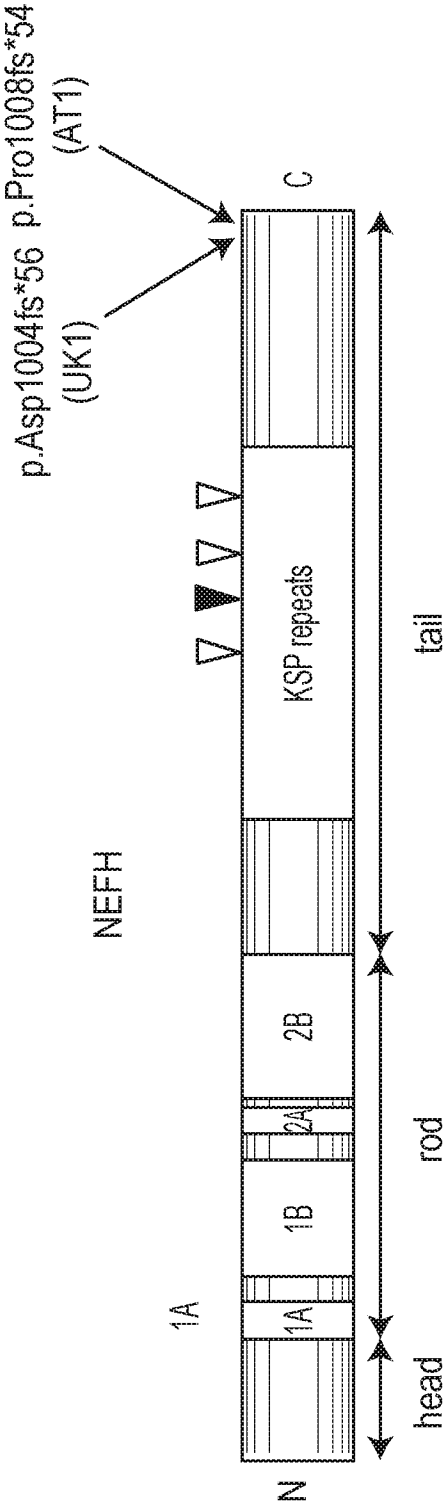
68. The expression vector according to claim 67, wherein the DNA repair template includes sequence to introduce a missense mutation in a stop codon of the gene, or a frameshift mutation in the coding sequence of the gene.

69. The vector according to any one of claims 55-68, selected from the group consisting of a retroviral, adenoviral, adeno-associated viral (AAV), and herpes simplex viral vector.

70. A lipid nanoparticle comprising or containing a polynucleotide according to any one of claims 45-54, or a vector according to any one of claims 55-69.

71. A composition comprising a polynucleotide or vector according to any one of claims 45-69, or a nanoparticle according to claim 70, and a pharmaceutically acceptable carrier.

72. The method or use according to any one of claims 1-20, 27-28, 30-31, 33-36, wherein the agent comprises a polynucleotide, vector, nanoparticle, or composition according to any one of claims 45-70.



▽ Coding KSP deletions in ALS
▼ Coding KSP insertions in ALS

FIGURE 1

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FIGURE 2A

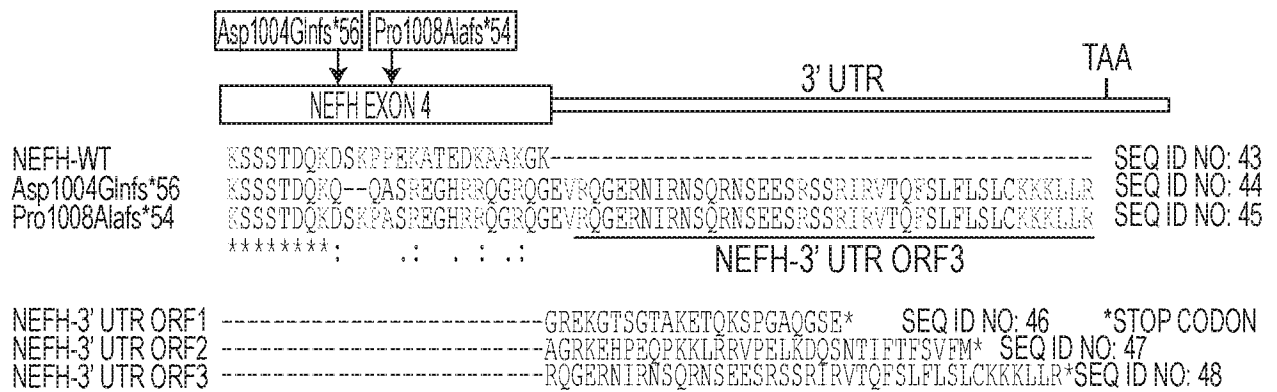


FIGURE 2B

NEFH-3' UTR ORF3	
Agg. Predictor	RQGERNIRNSQRNSEESRSSRIRVTQFSLEFLSLCKKKLLR SEQ ID NO: 48
TANGO	*****
AGGRESCAN	*****
FoldAmyloid	*****
PASTA 2.0	*****

* Consensus sequence

FIGURE 2C

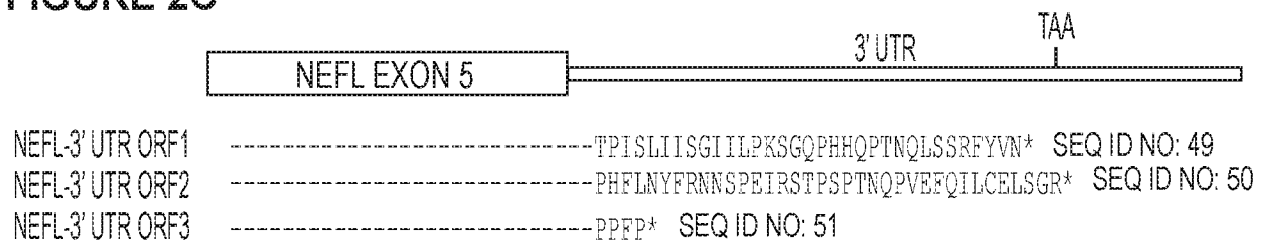


FIGURE 2D

NEFL 3'UTR ORF1	
Agg. Predictor	TPISLIISGIILPKSGQPHHPTNQLSSRFYVN SEQ ID NO: 49
TANGO	*****
AGGRESCAN	*****
FoldAmyloid	*****
PASTA 2.0	*****

* Consensus sequence

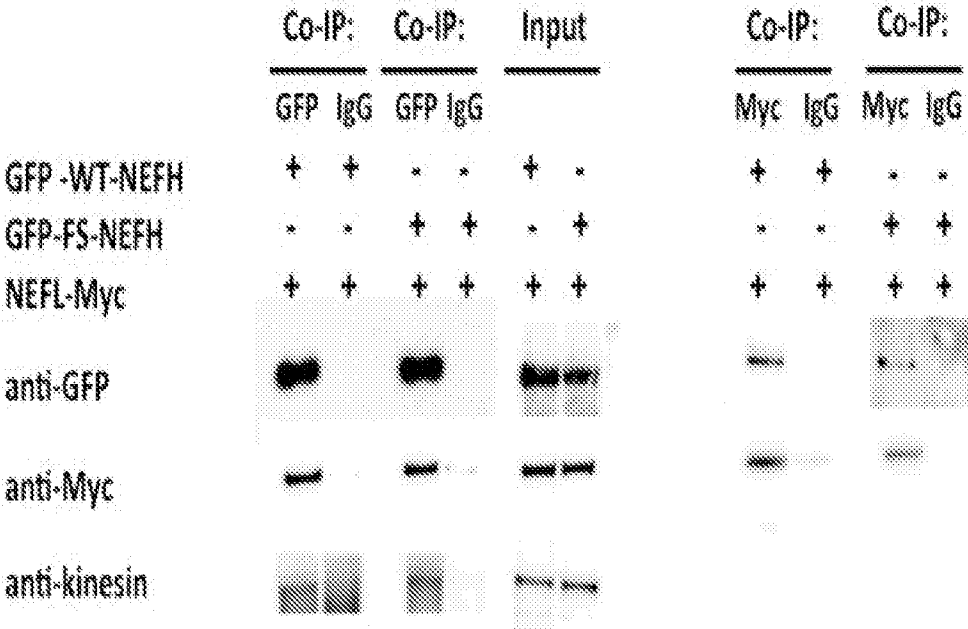
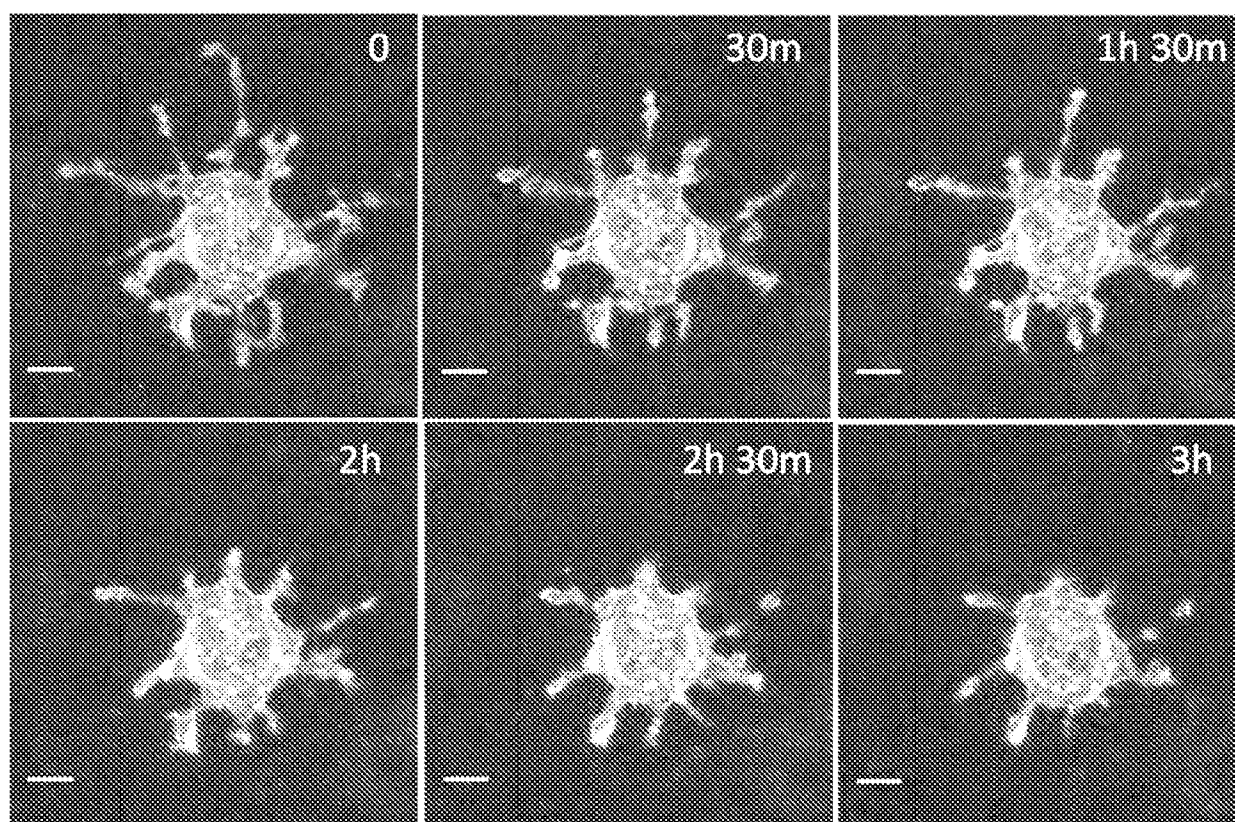


FIGURE 3

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**FIGURE 4**

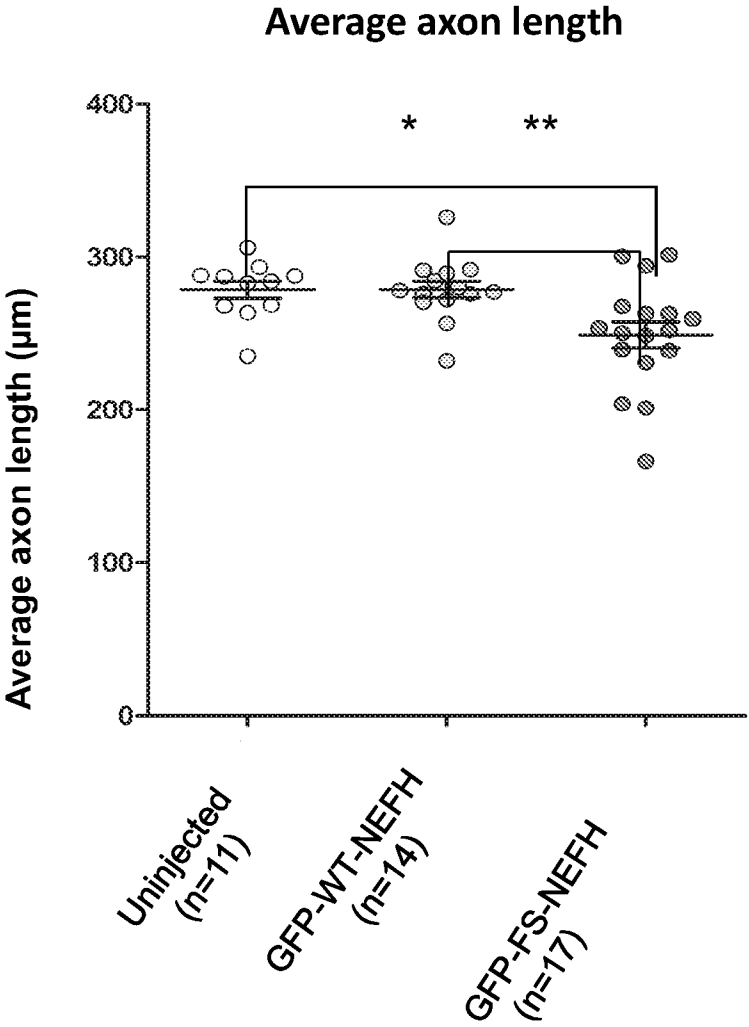


FIGURE 5

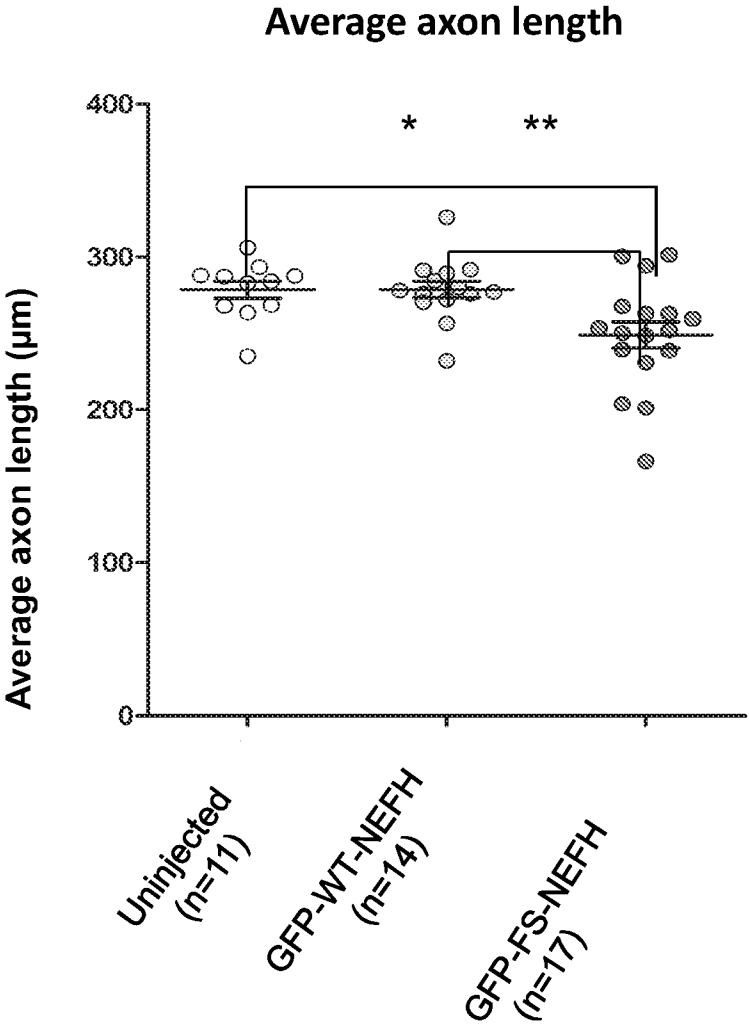


FIGURE 5

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 17/23901

A. CLASSIFICATION OF SUBJECT MATTER
 IPC(8) - C07K 14/00, A61P 35/00 (2017.01)
 CPC - C07K 14/4711, A61K 39/0007, A61K 9/0019

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

See Search History Document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

See Search History Document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History Document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 2012/0316117 A1 (LIANG et al.) 13 December 2012 (13.12.2012) para [0041]-[0043]	1-4
Y	Rebelo et al. A novel protein aggregation mechanism triggered by translation of cryptic amyloidogenic elements in the 3' UTR of neurofilament genes. The American Society of Human Genetics 2015 Meeting abstracts (presented 8 October 2015) pg 49, Abstract #102, http://www.ashg.org/2015meeting/pdf/57715_Platform.pdf , abstract	1-4

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

25 July 2017

Date of mailing of the international search report

28 AUG 2017

Name and mailing address of the ISA/US

Mail Stop PCT, Attn: ISA/US, Commissioner for Patents

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 17/23901

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 5-36, 44, 51-72
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

----- see extra sheet -----

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-4

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 17/23901

Continuation of Box No. III, Observations where unity of invention is lacking:

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I: Claims 1-4, directed to a method or use of an amyloidogenic peptide, Cryptic Amyloidogenic Element, or expression of a nucleic acid encoding said peptide to inhibit growth of neoplastic cells in a mammalian subject.

Group II: Claims 37-43, directed to a composition comprising a nucleotide sequence that encodes a cryptic amyloidogenic peptide fused in-frame with a control sequence to promote expression in mammalian cells,

Group III: Claims 45-50, directed to a polynucleotide comprising a crRNA linked to a tracrRNA sequence, wherein the crRNA sequence targets a 3' end of a gene.

The inventions listed as Groups I through III do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Special Technical Features

Groups II and III do not require a method or use of an amyloidogenic peptide or nucleic acid expressing said peptide for administering to a mammalian subject to inhibit growth of neoplastic cells, as required by group I.

Groups I and III do not require a composition comprising a polynucleotide that encodes an amyloidogenic peptide fused in-frame with an expression control sequence to promote expression of the amyloidogenic peptide, as required by group II.

Group I and II do not require a polynucleotide comprising a crRNA linked to a tracrRNA sequence, wherein the crRNA sequence targets a 3' end of a gene as required by group III.

Common Technical Features

The common technical feature shared by Groups I-III is a 3' end of gene. The common technical feature shared by Groups I and II is an amyloidogenic peptide (as a peptide or a nucleic acid, e.g. an expression vector) derived from a Cryptic Amyloidogenic Element encoded by nucleic acid in a 3' - untranslated region ("3' -UTR") of a gene in a disease cell. However, this shared technical feature does not represent a contribution over prior art, because the shared technical feature is made obvious by the meeting abstract entitled "A novel protein aggregation mechanism triggered by translation of cryptic amyloidogenic elements in the 3' UTR of neurofilament genes." by Rebelo et al. (The American Society of Human Genetics 2015 Meeting abstracts (presented 8 October 2015) pg 49, Abstract #102, retrieved on 07 June 2017, from http://www.ashg.org/2015meeting/pdf/57715_Platform.pdfAs) (abstract "We describe a novel mechanism for intracellular toxic aggregates induced by an unusual mutational event in axonal neuropathy families. We identified families with Charcot-Marie-Tooth disease type 2 (CMT2) carrying frameshift mutations in the neurofilament heavy gene (NEFH) leading to stop-loss and extended translation of 40 amino acids in the 3' UTR. In silico aggregation prediction analysis combined with experimental results demonstrated that the terminal 20 residues in the alternative protein is amyloidogenic and critical for the formation of aggregates. Expression of the mutant NEFH in neuro-2a cells resulted in prominent abnormal protein aggregates, leading to disruption of the neurofilament network, altered cell morphology and abnormal mitochondrial distribution. ... We also identified a similar aggregation induced mechanism triggered by translation of a cryptic amyloidogenic element present in the 3'UTR of the neurofilament light (NEFL), also known to cause aggregation in CMT and other diseases.").

As the technical feature was known in the art at the time of the invention, this cannot be considered a special technical feature that would otherwise unify the groups.

Groups I through III therefore lack unity under PCT Rule 13 because they do not share a same or corresponding special technical feature.