

(19) **DANMARK**

(10) **DK/EP 3649260 T3**



Patent- og
Varemærkestyrelsen

(12) Oversættelse af
europæisk patentskrift

-
- (51) Int.Cl.: **C 12 Q 1/6806 (2018.01)** **C 12 Q 1/6883 (2018.01)** **C 12 Q 1/6886 (2018.01)**
- (45) Oversættelsen bekendtgjort den: **2022-08-08**
- (80) Dato for Den Europæiske Patentmyndigheds bekendtgørelse om meddelelse af patentet: **2022-05-11**
- (86) Europæisk ansøgning nr.: **18745511.8**
- (86) Europæisk indleveringsdag: **2018-07-06**
- (87) Den europæiske ansøgnings publiceringsdag: **2020-05-13**
- (86) International ansøgning nr.: **EP2018068441**
- (87) Internationalt publikationsnr.: **WO2019008172**
- (30) Prioritet: **2017-07-07 US 201762529779 P**
- (84) Designerede stater: **AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO RS SE SI SK SM TR**
- (73) Patenthaver: **NIPD GENETICS PUBLIC COMPANY LIMITED, Neas Engomis 31 , Engomi, Nicosia 2409, Cypern**
- (72) Opfinder: **KOUMBARIS, George, 101 Makariou III Street, Lithrodontas 2565, Cypern**
IOANNIDES, Marios, 37A Anastasiou Souroulla Strovolos, Nicosia 2416, Cypern
KYPRI, Elena, 4 Saphous Street, Flat 204 Strovolos, Nicosia 2007, Cypern
ACHILLEOS, Acilleas, 6 Ikarou St., Yermasoyia, Limassol 4045, Cypern
MINA, Petros, 133 Athalassas Avenue, Dasoupolis, Nicosia 2015, Cypern
ELIADES, Alexia, 26 Dionysiou Solomou, Flat 201, Aglantzia, Nicosia 2102, Cypern
LOIZIDES, Charalambos, 31 Axiou Street, Flat 202 Strovolos, Nicosia 2013, Cypern
PATSALIS, Philippos, 34 Gregoriou Xenopoulou Engomi, Nicosia 2402, Cypern
- (74) Fuldmægtig i Danmark: **CHAS. HUDE A/S, Langebrogade 1, 2. B2, 1411 København K, Danmark**
- (54) Benævnelse: **TARGET-BERIGET MULTIPLEKSET PARALLEL ANALYSE TIL VURDERING AF TUMORBIOMARKØRER**
- (56) Fremdragne publikationer:
EP-A1- 2 902 500
WO-A1-2012/092426
WO-A1-2014/130890
WO-A1-2016/189388
WO-A2-2008/027548
WO-A2-2016/024134
US-A1- 2008 194 414
US-A1- 2011 039 304
US-A1- 2011 160 076
US-A1- 2015 203 907
US-A1- 2016 068 889

Fortsættes ...

US-A1- 2017 051 355

ERIC J DUNCAVAGE ET AL: "Targeted next generation sequencing of clinically significant gene mutations and translocations in leukemia", MODERN PATHOLOGY, vol. 25, no. 6, 16 March 2012 (2012-03-16) , pages 795-804, XP055235397, GB ISSN: 0893-3952, DOI: 10.1038/modpathol.2012.29

XI LIN ET AL: "Applications of targeted gene capture and next-generation sequencing technologies in studies of human deafness and other genetic disabilities", HEARING RESEARCH, ELSEVIER SCIENCE PUBLISHERS, AMSTERDAM, NL, vol. 288, no. 1, 6 January 2012 (2012-01-06), pages 67-76, XP028519246, ISSN: 0378-5955, DOI: 10.1016/J.HEARES.2012.01.004 [retrieved on 2012-01-14]

STEPHAN BAU ET AL: "Targeted next-generation sequencing by specific capture of multiple genomic loci using low-volume microfluidic DNA arrays", ANALYTICAL AND BIOANALYTICAL CHEMISTRY, SPRINGER, BERLIN, DE, vol. 393, no. 1, 29 October 2008 (2008-10-29), pages 171-175, XP019652995, ISSN: 1618-2650

DESCRIPTION

Field of the Invention

[0001] The invention is in the field of biology, medicine and chemistry, more in particular in the field of molecular biology and more in particular in the field of molecular diagnostics.

Background of the Invention

[0002] The identification of tumor biomarkers has been an important advance in the detection, diagnosis and treatment of a wide variety of cancers. Various methods of detecting tumor biomarkers are known in the art; however, additional methods are still needed, in particular methods that allow for detection of tumor biomarkers non-invasively, such as in a plasma sample (liquid biopsy). The identification of hereditary (germline) mutations in patients with cancer or high risk individuals suspected of cancer-predisposing syndrome is a useful clinical tool that enables early medical intervention, prophylactic surgery and close monitoring. These germline mutations can be identified in an individual's healthy tissue (such as buccal swab or lymphocytes).

[0003] Next generation sequencing (NGS) technologies have been implemented in the development of non-invasive prenatal testing (NIPT). In 2008, two independent groups demonstrated that NIPT of trisomy 21 could be achieved using next generation massively parallel shotgun sequencing (MPSS) (Chiu, R. W. et al.(2008) Proc. Natl. Acad. Sci. USA 105:20458-20463; Fan, H.C. et al.(2008) Proc. Natl. Acad. Sci. USA 105:16266-162710). Large-scale clinical studies using NGS for NIPT have been described (Palomaki, G.E. et al. (2011) Genet. Med. 13:913-920; Ehrich, M. et al. (2011) Am. J. Obstet. Gynecol. 204:205e1-11; Chen, E.Z. et al. (2011) PLoS One 6:e21791; Sehnert, A.J. et al. (2011) Clin. Chem. 57:1042-1049; Palomaki, G.E. et al. (2012); Genet. Med. 14:296-305; Bianchi, D.W. et al. (2012) Obstet. Gynecol. 119:890-901; Zimmerman, B. et al. (2012) Prenat. Diagn. 32:1233-1241; Nicolaides, K.H. et al. (2013) Prenat. Diagn. 33:575-579; Sparks, A.B. et al. (2012) Prenat. Diagn. 32:3-9).

[0004] Initial NIPT approaches used massively parallel shotgun sequencing (MPSS) NGS methodologies (see e.g., US Patent No. 7,888,017; US Patent No. 8,008,018; US Patent No. 8,195,415; US Patent No. 8,296,076; US Patent No. 8,682,594; US Patent Publication 20110201507; US Patent Publication 20120270739). Thus, these approaches are whole genome-based. More recently, targeted-based NGS approaches for NIPT, in which only specific sequences of interest are sequenced, have been developed. For example, a targeted NIPT approach using TArget Capture Sequences (TACS) for identifying fetal chromosomal abnormalities using a maternal blood sample has been described (PCT Publication WO 2016/189388; US Patent Publication 2016/0340733; Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855.). Such targeted approaches require significantly less sequencing than the MPSS approaches, since sequencing is only performed on specific loci on the target sequence of interest rather than across the whole genome.

[0005] Additional methodologies for NGS-based approaches are still needed, in particular approaches that can target specific sequences of interest, such as for example tumor biomarkers, thereby greatly reducing the amount of sequencing needed as compared to whole genome-based approaches, as well as increasing the read-depth of regions of interest, thus enabling detection of low signal to noise ratio regions. In particular, additional methodologies are still needed that allow for genetic aberrations present in diminutive amounts in a sample to be reliably detected, such as for example in the early detection of cancer.

Summary of the Invention

[0006] This invention provides improved methods for enriching targeted genomic regions of interest to be analyzed by multiplexed parallel sequencing, wherein the enriched sequences are tumor biomarker sequences and the DNA sample used in the method is from a subject having or suspected of having a tumor. Accordingly, the methods allow for detection of tumor biomarkers in a variety of biological samples, including liquid samples, such as plasma samples (liquid biopsy), thereby providing non-invasive means for tumor detection and monitoring. The methods of the invention utilize a pool of TArget Capture Sequences (TACS) designed such that the sequences within the pool have features that optimize the efficiency, specificity and accuracy of genetic assessment of tumor biomarkers. The methods of the invention can be used, for example, in cancer diagnosis, cancer screening, cancer treatment regimen selection and/or cancer therapy monitoring.

[0007] Accordingly, in one aspect, the invention pertains to a method of detecting one or more tumor biomarkers in a DNA sample from a subject having or suspected of having a tumor, the method comprising:

1. (a) preparing a sequencing library from the DNA sample;
2. (b) hybridizing the sequencing library to a pool of double-stranded TArget Capture Sequences (TACS) that bind to one or more tumor biomarker sequences of interest, wherein: (i) each member sequence within the pool of TACS is between 150-260 base pairs in length, each member sequence having a 5' end and a 3' end; (ii) preferably and optionally each member sequence binds to the tumor biomarker sequence of interest at least 50 base pairs away, on both the 5' end and the 3' end, from regions harboring Copy Number Variations (CNVs), Segmental duplications or repetitive DNA elements; and (iii) the GC content of the pool of TACS is between 19% and 80%, as determined by calculating the GC content of each member within the pool of TACS; (iv) the pool of TACS comprises a plurality of TACS families each directed to a different tumor biomarker sequence of interest, wherein each TACS family comprises a plurality of member sequences, wherein each member sequence binds to the same tumor biomarker sequence of interest but has different start and/or stop positions with respect to a reference coordinate system for the tumor biomarker sequence of interest, optionally wherein the start and/or stop positions for the member sequences within a TACS family, with respect to a reference coordinate system for the tumor biomarker are staggered by 5 to 10 base pairs; (c) isolating members of the sequencing library that bind to the pool of TACS to obtain an enriched library; (d) amplifying and sequencing the enriched library; (e) aligning the enriched library to a reference genome thereby obtaining read-depth information and allelic counts; and (f) performing statistical analysis on the enriched library sequences, optionally utilizing only fragments of a specific size range, to thereby detect the tumor biomarker(s) in the DNA sample, wherein sequencing of the enriched library provides a read-depth for the genomic sequences of interest and read-depths for reference loci and the statistical analysis comprises applying an algorithm that tests sequentially the read-depth of the loci of from the genomic sequences of interest against the read-depth of the reference loci, the algorithm comprising steps for: (a) removal of inadequately sequenced loci, (b) GC-content bias alleviation, and (c) genetic status determination; and/or wherein sequencing of the enriched library provides the number and size of sequenced fragments for TACS-specific coordinates and the statistical analysis comprises applying an algorithm that tests sequentially the fragment-size proportion for the genomic sequence of interest against the fragment-size proportion of the reference loci, the algorithm comprising steps of: (a) removal of fragment-size outliers, (b) fragment-size proportion calculation, and (c) genetic status determination.

[0008] In one embodiment, the pool of TACS comprises a plurality of TACS families, wherein each member of a TACS family binds to the same tumor biomarker sequence of interest but with different start and/or stop positions on the sequence with respect to a reference coordinate system (i.e., binding of TACS family members to the target sequence is staggered) to thereby enrich for target sequences of interest, followed by massive parallel sequencing and statistical analysis of the enriched population. The use of families of TACS with the TACS pool that bind to each target sequence of interest, as compared to use of a single TACS within the TACS pool that binds to each target sequence of interest, significantly increases enrichment for the target sequences of interest, as evidenced by a greater than 50% average increase in read-depth for the family of TACS versus a single

TACS. Herein, the mutations detected or biomarkers detected may be due to somatic mutation or may be hereditary, i.e already present in the germ line.

[0009] Accordingly, in one embodiment, the pool of TACS comprises a plurality of TACS families directed to different tumor biomarker sequences of interest, wherein each TACS family comprises a plurality of member sequences, wherein each member sequence binds to the same tumor biomarker sequence of interest but has different start and/or stop positions with respect to a reference coordinate system for the genomic sequence of interest.

[0010] In certain embodiments, each TACS family comprises at least 3 member sequences or at least 5 member sequences. Alternative numbers of member sequences in each TACS family are described herein. In one embodiment, the pool of TACS comprises at least 50 different TACS families. Alternative numbers of different TACS families within the pool of TACS are described herein. In certain embodiments, the start and/or stop positions for the member sequences within a TACS family, with respect to a reference coordinate system for the genomic sequence of interest, are staggered by 5 to 10 base pairs.

[0011] In certain embodiments, the GC content of the pool of TACS is between 19% and 80% or is between 19% and 46%. Alternative % ranges for the GC content of the pool of TACS are described herein.

[0012] In one embodiment, the pool of TACS is fixed to a solid support. For example, in one embodiment, the TACS are biotinylated and are bound to streptavidin-coated magnetic beads.

[0013] In one embodiment, amplification of the enriched library is performed in the presence of blocking sequences that inhibit amplification of wild-type sequences.

[0014] In one embodiment, members of the sequencing library that bind to the pool of TACS are partially complementary to the TACS.

[0015] In one embodiment, the statistical analysis comprises a segmentation algorithm, for example, likelihood-based segmentation, segmentation using small overlapping windows, segmentation using parallel pairwise testing, and combinations thereof. In one embodiment, the statistical analysis comprises a score-based classification system. In one embodiment, sequencing of the enriched library provides a read-depth for the genomic sequences of interest and read-depths for reference loci and the statistical analysis comprises applying an algorithm that tests sequentially the read-depth of the loci of from the genomic sequences of interest against the read-depth of the reference loci, the algorithm comprising steps for: (a) removal of inadequately sequenced loci; (b) GC-content bias alleviation; and (c) genetic status determination. In one embodiment, GC-content bias is alleviated by grouping together loci of matching GC content. In one embodiment, sequencing of the enriched library provides the number and size of sequenced fragments for TACS-specific coordinates and the statistical analysis comprises applying an algorithm that tests sequentially the fragment-size proportion for the genomic sequence of interest against the fragment-size proportion of the reference loci, the algorithm comprising steps for: (a) removal of fragment-size outliers; (b) fragment-size proportion calculation; and (c) genetic status determination.

[0016] In one embodiment, the DNA sample comprises cell free tumor DNA (cftDNA). In various embodiments, the DNA sample is selected from a group comprising of a plasma sample, a urine sample, a sputum sample, a cerebrospinal fluid sample, an ascites sample and a pleural effusion sample from subject having or suspected of having a tumor. In one embodiment, the DNA sample is from a tissue sample from a subject having or suspected of having a tumor.

[0017] In one embodiment, the pool of TACS binds to a plurality of tumor biomarker sequences of interest selected from a group comprising ABL, AKT, AKT1, ALK, APC, AR, ARAF, ATM, BAP1, BARD1, BCL, BMPR1A, BRAF, BRCA, BRCA1, BRCA2, BRIP1, CDH1, CDKN, CHEK2, CTNNB1, DDB2, DDR2, DICER1, EGFR, EPCAM,

ErbB, ErcC, ESR1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FBXW7, FGFR, FLT, FLT3, FOXA1, FOXL2, GATA3, GNA11, GNAQ, GNAS, GREM1, HOX, HOXB13, HRAS, IDH1, JAK, JAK2, KEAP1, KIT, KRAS, MAP2Ks, MAP3Ks, MET, MLH1, MPL, MRE11A, MSH2, MSH6, MTOR, MUTYH, NBN, NPM1, NRAS, NTRK1, PALB2, PDGFRs, PI3Ks, PMS2, POLD1, POLE, POLH, PTEN, RAD50, RAD51C, RAD51D, RAF1, RB1, RET, RUNX1, SLX4, SMAD, SMAD4, SMARCA4, SPOP, STAT, STK11, TP53, VHL, XPA and XPC, and combinations thereof.

[0018] In another embodiment, the pool of TACS binds to a plurality of tumor biomarker sequences of interest selected from a group comprising , AKT1, ALK, APC, AR, ARAF, ATM, BAP1, BARD1, BMPR1A, BRAF, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A (p14ARF), CDKN2A (p16INK4a), CHEK2, CTNNB1, DDB2, DDR2, DICER1, EGFR, EPCAM, ERBB2, ERBB3, ERBB4, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ESR1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FBXW7, FGFR1, FGFR2, FLT3, FOXA1, FOXL2, GATA3, GNA11, GNAQ, GNAS, GREM1, HOXB13, IDH1, IDH2, JAK2, KEAP1, KIT, KRAS, MAP2K1, MAP3K1, MEN1, MET, MLH1, MPL, MRE11A, MSH2, MSH6, MTOR, MUTYH, MYC, MYCN, NBN, NPM1, NRAS, NTRK1, PALB2, PDGFRA, PIK3CA, PIK3CB, PMS2, POLD1, POLE, POLH, PTEN, RAD50, RAD51C, RAD51D, RAF1, RB1, RET, ROS1, RUNX1, SDHA, SDHAF2, SDHB, SDHC, SDHD, SLX4, SMAD4, SMARCA4, SPOP, STAT, STK11, TMRSS2, TP53, VHL, XPA, XPC and combinations thereof.

[0019] In one embodiment, the pool of TACS binds to a plurality of tumor biomarker sequences of interest selected from a group comprising EGFR_6240, KRAS_521, EGFR_6225, NRAS_578, NRAS_580, PIK3CA_763, EGFR_13553, EGFR_18430, BRAF_476, KIT_1314, NRAS_584, EGFR_12378, and combinations thereof.

[0020] In another embodiment, the pool of TACS binds to a plurality of tumor biomarker sequences of interest selected from a group comprising COSM6240 (EGFR_6240), COSM521 (KRAS_521), COSM6225 (EGFR_6225), COSM578 (NRAS_578), COSM580 (NRAS_580), COSM763 (PIK3CA_763), COSM13553 (EGFR_13553), COSM18430 (EGFR_18430), COSM476 (BRAF_476), COSM1314 (KIT_1314), COSM584 (NRAS_584), COSM12378 (EGFR_12378), and combinations thereof, wherein the identifiers refer to the COSMIC database ID number of the biomarker.

[0021] In one embodiment, the method further comprises making a diagnosis of the subject based on detection of at least one tumor biomarker sequence. In another embodiment, the method further comprises selecting a therapeutic regimen for the subject based on detection of at least one tumor biomarker sequence. In yet another embodiment, the method further comprises monitoring treatment efficacy of a therapeutic regimen in the subject based on detection of at least one tumor biomarker sequence.

Brief Description of the Figures

[0022] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

Figure 1 is a schematic diagram of multiplexed parallel analysis of targeted genomic regions for non-invasive prenatal testing using TArget Capture Sequences (TACS).

Figure 2 is a listing of exemplary chromosomal regions for amplifying TACS that bind to for example chromosomes 13, 18, 21 or X. A more extensive list is shown in Table 1 below.

Figure 3 is a schematic diagram of TACS-based enrichment of a sequence of interest (bold line) using a single TACS (left) versus TACS-based enrichment using a family of TACS (right).

Figures 4A-4B are graphs showing enrichment using families of TACS versus a single TACS, as illustrated by increase in the average read-depth. Figure 4A shows loci enriched using a family of TACS (red dots) as

compared to loci enriched using a single TACS (blue dots), with different target sequences shown on the x-axis and the fold change in read-depth shown on the y-axis. Figure 4B is a bar graph illustrating the average fold-increase in read-depth (54.7%) using a family of TACS (right) versus a single TACS (left).

Figure 5 shows bar graphs illustrating detection of known genetic mutations that are tumor biomarkers in certified reference material harboring the mutations. Two replicates of the reference material are shown. The line illustrates the expected minor allele frequency (MAF) for each of the assessed tumor loads. The bars (x-axis) illustrate the detected MAF (y-axis) for the indicated genetic mutations in the certified reference material.

Figure 6 shows bar graphs illustrating detection of tumor biomarkers in cancer patient samples. Results are shown for two patients, one harboring mutation PIK3CA E545K (top bars) and one harboring mutation TP53 K139 (bottom bars). Both tumor tissue samples ("Tissue Rep. 1" and "Tissue Rep. 2") and plasma samples ("Plasma") are shown. The y-axis shows % variant allele frequency (VAF) detected in the samples.

Figure 7 is a bar graph showing the observed pattern of somatic SNVs in breast cancer, as found in the COSMIC database. The x-axis shows a single base mutation observed in cancer in the context of its neighboring sequences. For example A[C>A]T describes the mutation of Cytosine (C) to Adenine (A) where the upstream sequence is Adenine and the downstream sequence is Thymine. The y-axis shows the frequency of occurrence of this mutation in breast cancer.

Figure 8 is a bar graph showing results of a simulations study where simulated sequencing data includes mutational motifs. The data were subjected to mutational motif detection. The bars indicate the average estimated frequency of the known mutational breast cancer motifs computed from a data set of 10000 simulations. Results illustrate that detection of mutational motifs is possible using the developed algorithm.

Figure 9 is a dot plot graph showing results of a fragments-based test for detecting increased numbers of smaller-size fragments in a mixed sample. An abnormal, aneuploid sample, with an estimated fetal fraction of 2.8%, was correctly detected using this method. The black dots are individual samples. The x-axis shows the sample index. The y-axis shows the score result of the fragments-size based method. A score result greater than the threshold shown by the grey line indicates a deviation from the expected size of fragments illustrating the presence of aneuploidy.

Figure 10 is a listing of exemplary chromosomal regions for amplifying TACS that bind to exemplary, non-limiting tumor biomarker genes.

Table 1 shows exemplary and preferred TACS positions.

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr1	11169250	11169491	0.434	MTOR	chr17	37880017	37880264	0.528	ERBB2
chr1	11169262	11169509	0.419	MTOR	chr17	37880031	37880255	0.524	ERBB2
chr1	11169280	11169519	0.400	MTOR	chr17	37880061	37880274	0.505	ERBB2
chr1	11169299	11169548	0.392	MTOR	chr17	37880069	37880274	0.500	ERBB2
chr1	11174376	11174632	0.541	MTOR	chr17	37880955	37881196	0.595	ERBB2
chr1	11174392	11174632	0.535	MTOR	chr17	37880969	37881216	0.589	ERBB2
chr1	11174392	11174691	0.527	MTOR	chr17	37880974	37881216	0.593	ERBB2
chr1	11174468	11174698	0.515	MTOR	chr17	37880983	37881227	0.592	ERBB2
chr1	11184541	11184796	0.504	MTOR	chr17	37881166	37881380	0.609	ERBB2
chr1	11184563	11184812	0.504	MTOR	chr17	37881201	37881450	0.584	ERBB2
chr1	11184564	11184816	0.502	MTOR	chr17	37881273	37881520	0.573	ERBB2
chr1	11187992	11188236	0.535	MTOR	chr17	37881304	37881521	0.573	ERBB2
chr1	11188010	11188249	0.521	MTOR	chr17	37881453	37881652	0.595	ERBB2
chr1	11188018	11188257	0.513	MTOR	chr17	37881465	37881668	0.598	ERBB2

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr1	11188029	11188274	0.492	MTOR	chr17	37881510	37881737	0.601	ERBB2
chr1	17345194	17345459	0.316	SDHB	chr17	37881598	37881798	0.632	ERBB2
chr1	17349096	17349342	0.543	SDHB	chr17	41196311	41196511	0.393	BRCA1
chr1	17350413	17350563	0.497	SDHB	chr17	41197220	41197464	0.429	BRCA1
chr1	17350566	17350779	0.430	SDHB	chr17	41197314	41197566	0.419	BRCA1
chr1	17354089	17354304	0.463	SDHB	chr17	41197571	41197819	0.550	BRCA1
chr1	17355058	17355208	0.417	SDHB	chr17	41199637	41199729	0.559	BRCA1
chr1	17359477	17359689	0.427	SDHB	chr17	41201055	41201304	0.476	BRCA1
chr1	17371214	17371394	0.470	SDHB	chr17	41202997	41203243	0.449	BRCA1
chr1	17380408	17380619	0.670	SDHB	chr17	41209041	41209195	0.445	BRCA1
chr1	43814917	43815186	0.633	MPL	chr17	41215338	41215577	0.433	BRCA1
chr1	45795001	45795250	0.536	MUTYH	chr17	41215806	41216045	0.375	BRCA1
chr1	45796024	45796223	0.530	MUTYH	chr17	41219623	41219726	0.337	BRCA1
chr1	45796871	45797092	0.536	MUTYH	chr17	41222828	41223088	0.402	BRCA1
chr1	45797060	45797289	0.648	MUTYH	chr17	41222835	41223088	0.406	BRCA1
chr1	45797289	45797529	0.635	MUTYH	chr17	41222885	41223141	0.444	BRCA1
chr1	45797602	45797802	0.577	MUTYH	chr17	41223090	41223269	0.494	BRCA1
chr1	45797819	45798019	0.622	MUTYH	chr17	41256181	41256358	0.315	BRCA1
chr1	45797986	45798270	0.593	MUTYH	chr17	41256830	41257034	0.376	BRCA1
chr1	45798204	45798404	0.602	MUTYH	chr17	41256884	41257140	0.339	BRCA1
chr1	45798364	45798564	0.547	MUTYH	chr17	41258410	41258681	0.324	BRCA1
chr1	45798532	45798732	0.557	MUTYH	chr17	41267598	41267807	0.371	BRCA1
chr1	45798672	45798872	0.567	MUTYH	chr17	41267602	41267807	0.369	BRCA1
chr1	45798867	45799097	0.628	MUTYH	chr17	41267603	41267794	0.354	BRCA1
chr1	45799150	45799357	0.582	MUTYH	chr17	41267603	41267834	0.371	BRCA1
chr1	45800062	45800304	0.539	MUTYH	chr17	41267630	41267779	0.353	BRCA1
chr1	115252133	115252352	0.445	NRAS	chr17	41267645	41267836	0.391	BRCA1
chr1	115252133	115252354	0.441	NRAS	chr17	41275961	41276197	0.312	BRCA1
chr1	115252138	115252350	0.446	NRAS	chr17	46805588	46805837	0.672	HOXB13
chr1	115252142	115252350	0.450	NRAS	chr17	47696239	47696485	0.453	SPOP
chr1	115256347	115256588	0.409	NRAS	chr17	47696300	47696545	0.455	SPOP
chr1	115256398	115256647	0.448	NRAS	chr17	47696324	47696565	0.442	SPOP
chr1	115256410	115256649	0.458	NRAS	chr17	47696359	47696607	0.422	SPOP
chr1	115256442	115256691	0.440	NRAS	chr17	47696424	47696669	0.415	SPOP
chr1	115256467	115256726	0.442	NRAS	chr17	47696450	47696669	0.405	SPOP
chr1	115256470	115256715	0.451	NRAS	chr17	47696450	47696689	0.413	SPOP
chr1	115258538	115258778	0.440	NRAS	chr17	47696486	47696715	0.387	SPOP
chr1	115258570	115258813	0.463	NRAS	chr17	56769976	56770175	0.590	RAD51C
chr1	115258607	115258846	0.492	NRAS	chr17	56772289	56772542	0.421	RAD51C
chr1	115258659	115258901	0.444	NRAS	chr17	56773994	56774243	0.404	RAD51C
chr1	156268500	156268651	0.454	VHLL	chr17	56780486	56780723	0.345	RAD51C

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr1	156269007	156269221	0.493	VHLL	chr17	56787247	56787446	0.365	RAD51C
chr1	156846129	156846362	0.641	NTRK1	chr17	56787285	56787460	0.341	RAD51C
chr1	156846129	156846377	0.643	NTRK1	chr17	56798102	56798172	0.352	RAD51C
chr1	156846130	156846362	0.639	NTRK1	chr17	56801331	56801553	0.390	RAD51C
chr1	156848889	156849132	0.611	NTRK1	chr17	56809830	56810049	0.382	RAD51C
chr1	156848911	156849153	0.617	NTRK1	chr17	56811478	56811716	0.385	RAD51C
chr1	156848921	156849168	0.613	NTRK1	chr17	59756779	59756979	0.313	BRIP1
chr1	156848925	156849168	0.611	NTRK1	chr17	59759726	59759955	0.252	BRIP1
chr1	161284168	161284376	0.598	SDHC	chr17	59760615	59760854	0.308	BRIP1
chr1	161293229	161293429	0.343	SDHC	chr17	59760809	59761044	0.335	BRIP1
chr1	161298181	161298414	0.436	SDHC	chr17	59761001	59761201	0.353	BRIP1
chr1	161333007	161333261	0.447	SDHC	chr17	59761265	59761494	0.413	BRIP1
chr1	161333275	161333550	0.391	SDHC	chr17	59761395	59761636	0.343	BRIP1
chr1	161333589	161333868	0.439	SDHC	chr17	59763229	59763449	0.357	BRIP1
chr1	161333890	161334157	0.392	SDHC	chr17	59763460	59763660	0.338	BRIP1
chr1	161334206	161334492	0.394	SDHC	chr17	59770816	59771046	0.307	BRIP1
chr1	162748235	162748450	0.440	DDR2	chr17	59793106	59793349	0.316	BRIP1
chr1	162748273	162748512	0.442	DDR2	chr17	59793137	59793367	0.338	BRIP1
chr1	162748316	162748557	0.450	DDR2	chr17	59820379	59820551	0.393	BRIP1
chr1	162748370	162748580	0.483	DDR2	chr17	59821796	59821945	0.373	BRIP1
chr10	8111358	8111588	0.506	GATA3	chr17	59853687	59853887	0.353	BRIP1
chr10	8111468	8111707	0.529	GATA3	chr17	59857537	59857737	0.333	BRIP1
chr10	8115737	8115986	0.572	GATA3	chr17	59858201	59858428	0.355	BRIP1
chr10	8115741	8115988	0.569	GATA3	chr17	59861553	59861773	0.326	BRIP1
chr10	8115783	8115988	0.612	GATA3	chr17	59870956	59871190	0.345	BRIP1
chr10	8115789	8115988	0.620	GATA3	chr17	59876405	59876605	0.388	BRIP1
chr10	43595933	43596179	0.623	RET	chr17	59876622	59876822	0.284	BRIP1
chr10	43597765	43598054	0.614	RET	chr17	59878569	59878769	0.413	BRIP1
chr10	43600476	43600682	0.686	RET	chr17	59878611	59878844	0.397	BRIP1
chr10	43601846	43602088	0.638	RET	chr17	59885818	59886038	0.439	BRIP1
chr10	43604444	43604706	0.620	RET	chr17	59886058	59886268	0.346	BRIP1
chr10	43606653	43606911	0.595	RET	chr17	59924485	59924714	0.348	BRIP1
chr10	43607465	43607728	0.659	RET	chr17	59926478	59926707	0.348	BRIP1
chr10	43608226	43608455	0.596	RET	chr17	59934381	59934581	0.383	BRIP1
chr10	43608980	43609217	0.626	RET	chr17	59937155	59937392	0.374	BRIP1
chr10	43609917	43610183	0.625	RET	chr17	59938714	59938914	0.333	BRIP1
chr10	43611943	43612187	0.522	RET	chr17	59940627	59940827	0.577	BRIP1
chr10	43613689	43613933	0.555	RET	chr17	59940844	59941054	0.592	BRIP1
chr10	43614921	43615150	0.687	RET	chr18	48556368	48556604	0.692	SMAD4
chr10	43615517	43615759	0.568	RET	chr18	48556368	48556608	0.689	SMAD4
chr10	43617287	43617531	0.457	RET	chr18	48556413	48556612	0.680	SMAD4

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr10	43619092	43619322	0.584	RET	chr18	48556414	48556616	0.675	SMAD4
chr10	43620303	43620509	0.551	RET	chr18	48573249	48573492	0.328	SMAD4
chr10	43623746	43624029	0.493	RET	chr18	48573500	48573738	0.364	SMAD4
chr10	43624152	43624439	0.490	RET	chr18	48575147	48575346	0.340	SMAD4
chr10	43624946	43625222	0.433	RET	chr18	48575524	48575724	0.294	SMAD4
chr10	50686414	50686655	0.368	ERCC6	chr18	48581203	48581433	0.455	SMAD4
chr10	88635669	88635923	0.333	BMPRI1A	chr18	48581249	48581498	0.428	SMAD4
chr10	88649829	88650073	0.384	BMPRI1A	chr18	48584399	48584599	0.443	SMAD4
chr10	88659444	88659644	0.368	BMPRI1A	chr18	48584673	48584893	0.439	SMAD4
chr10	88677042	88677242	0.388	BMPRI1A	chr18	48586106	48586306	0.308	SMAD4
chr10	89622844	89623045	0.594	KLLN	chr18	48591791	48592035	0.408	SMAD4
chr10	89624131	89624370	0.492	PTEN	chr18	48593378	48593608	0.407	SMAD4
chr10	89624178	89624422	0.465	PTEN	chr18	48602902	48603166	0.430	SMAD4
chr10	89624198	89624444	0.445	PTEN	chr18	48602922	48603132	0.445	SMAD4
chr10	89624214	89624463	0.436	PTEN	chr18	48603000	48603249	0.424	SMAD4
chr10	89685273	89685522	0.304	PTEN	chr18	48603132	48603332	0.289	SMAD4
chr10	89692746	89692946	0.398	PTEN	chr18	48604566	48604815	0.488	SMAD4
chr10	89692746	89692977	0.392	PTEN	chr18	48604617	48604861	0.490	SMAD4
chr10	89692746	89692999	0.402	PTEN	chr18	48604640	48604881	0.492	SMAD4
chr10	89692763	89693015	0.403	PTEN	chr18	48604711	48604957	0.421	SMAD4
chr10	89692787	89692999	0.413	PTEN	chr18	48605303	48605503	0.294	SMAD4
chr10	89711788	89712024	0.380	PTEN	chr18	48605551	48605798	0.351	SMAD4
chr10	89711798	89712045	0.367	PTEN	chr18	48605981	48606181	0.318	SMAD4
chr10	89711867	89712069	0.399	PTEN	chr18	48606203	48606477	0.349	SMAD4
chr10	89711880	89712129	0.348	PTEN	chr18	48606469	48606712	0.357	SMAD4
chr10	89717531	89717770	0.404	PTEN	chr18	48607311	48607586	0.326	SMAD4
chr10	89717558	89717802	0.408	PTEN	chr18	48607638	48607926	0.412	SMAD4
chr10	89717558	89717831	0.394	PTEN	chr18	48608009	48608208	0.375	SMAD4
chr10	89717571	89717820	0.400	PTEN	chr18	48608225	48608485	0.368	SMAD4
chr10	89717602	89717831	0.413	PTEN	chr18	48608754	48608904	0.450	SMAD4
chr10	89717603	89717769	0.455	PTEN	chr18	48609535	48609685	0.470	SMAD4
chr10	89717627	89717872	0.362	PTEN	chr18	48609670	48609869	0.355	SMAD4
chr10	89720757	89720967	0.336	PTEN	chr18	48610653	48610803	0.358	SMAD4
chr10	89720757	89721005	0.329	PTEN	chr18	48610833	48611078	0.488	SMAD4
chr10	89720767	89720968	0.337	PTEN	chr18	48611097	48611339	0.490	SMAD4
chr10	89720775	89721018	0.324	PTEN	chr18	48611405	48611605	0.353	SMAD4
chr10	89726371	89726571	0.289	PTEN	chr19	1206543	1206797	0.643	STK11
chr10	89726794	89727038	0.310	PTEN	chr19	1206613	1206843	0.558	STK11
chr10	89727021	89727240	0.282	PTEN	chr19	1206770	1207017	0.560	STK11
chr10	89727261	89727519	0.317	PTEN	chr19	1206962	1207206	0.596	STK11
chr10	89727756	89727916	0.404	PTEN	chr19	1218302	1218502	0.532	STK11

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr10	89727978	89728203	0.389	PTEN	chr19	1219161	1219399	0.653	STK11
chr10	89728310	89728512	0.389	PTEN	chr19	1220251	1220492	0.632	STK11
chr10	89729027	89729257	0.251	PTEN	chr19	1220276	1220492	0.636	STK11
chr10	89729816	89729967	0.336	PTEN	chr19	1220475	1220701	0.705	STK11
chr10	89730284	89730433	0.307	PTEN	chr19	1220502	1220701	0.715	STK11
chr10	89731453	89731610	0.329	PTEN	chr19	1220681	1220938	0.647	STK11
chr11	22644366	22644570	0.273	FANCF	chr19	1220681	1220941	0.648	STK11
chr11	22644511	22644731	0.344	FANCF	chr19	1221151	1221351	0.582	STK11
chr11	22644738	22644938	0.318	FANCF	chr19	1221821	1222071	0.685	STK11
chr11	22645645	22645808	0.348	FANCF	chr19	1222984	1223224	0.643	STK11
chr11	22645808	22646060	0.352	FANCF	chr19	1226453	1226708	0.715	STK11
chr11	22646058	22646268	0.322	FANCF	chr19	1226464	1226754	0.704	STK11
chr11	22646388	22646588	0.532	FANCF	chr19	1226465	1226707	0.716	STK11
chr11	22646657	22646927	0.598	FANCF	chr19	1228261	1228461	0.547	STK11
chr11	22646959	22647229	0.657	FANCF	chr19	3114798	3115046	0.683	GNA11
chr11	22647378	22647578	0.478	FANCF	chr19	3114798	3115049	0.683	GNA11
chr11	47236728	47236949	0.635	DDB2	chr19	3114839	3115040	0.688	GNA11
chr11	47237804	47238058	0.537	DDB2	chr19	3114841	3115040	0.685	GNA11
chr11	47238291	47238491	0.483	DDB2	chr19	3118772	3118996	0.622	GNA11
chr11	47254333	47254547	0.470	DDB2	chr19	3118795	3119044	0.620	GNA11
chr11	47256241	47256494	0.547	DDB2	chr19	3118818	3119047	0.613	GNA11
chr11	47256782	47257010	0.594	DDB2	chr19	3118863	3119109	0.636	GNA11
chr11	47259397	47259552	0.468	DDB2	chr19	10600276	10600491	0.588	KEAP1
chr11	47259555	47259796	0.492	DDB2	chr19	10600284	10600528	0.592	KEAP1
chr11	47260567	47260808	0.483	DDB2	chr19	10600284	10600532	0.594	KEAP1
chr11	61197603	61197830	0.588	SDHAF2	chr19	10602242	10602441	0.645	KEAP1
chr11	61205114	61205296	0.481	SDHAF2	chr19	10602423	10602671	0.691	KEAP1
chr11	61205433	61205588	0.404	SDHAF2	chr19	10602539	10602747	0.632	KEAP1
chr11	61213390	61213639	0.488	SDHAF2	chr19	10602539	10602753	0.628	KEAP1
chr11	61213676	61213931	0.508	SDHAF2	chr19	10602653	10602854	0.609	KEAP1
chr11	61213967	61214232	0.462	SDHAF2	chr19	10610056	10610289	0.585	KEAP1
chr11	64570946	64571196	0.478	MEN1	chr19	10610069	10610306	0.576	KEAP1
chr11	64571178	64571436	0.544	MEN1	chr19	10610081	10610306	0.580	KEAP1
chr11	64571465	64571704	0.546	MEN1	chr19	10610083	10610306	0.580	KEAP1
chr11	64571732	64571978	0.567	MEN1	chr19	11094768	11095038	0.697	SMARCA4
chr11	64572483	64572713	0.619	MEN1	chr19	11095950	11096150	0.592	SMARCA4
chr11	64573013	64573278	0.602	MEN1	chr19	11096820	11097078	0.625	SMARCA4
chr11	64573641	64573871	0.593	MEN1	chr19	11097475	11097685	0.645	SMARCA4
chr11	64574483	64574728	0.602	MEN1	chr19	11098265	11098553	0.706	SMARCA4
chr11	64575094	64575345	0.544	MEN1	chr19	11098298	11098538	0.726	SMARCA4
chr11	64575352	64575623	0.614	MEN1	chr19	11098376	11098606	0.732	SMARCA4

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr11	64577138	64577410	0.634	MEN1	chr19	11099901	11100111	0.607	SMARCA4
chr11	64577437	64577683	0.700	MEN1	chr19	11101757	11101957	0.612	SMARCA4
chr11	64577902	64578171	0.681	MEN1	chr19	11105466	11105666	0.522	SMARCA4
chr11	94150558	94150800	0.362	MRE11A	chr19	11106694	11106939	0.557	SMARCA4
chr11	94151042	94151242	0.373	MRE11A	chr19	11107143	11107352	0.476	SMARCA4
chr11	94151616	94151816	0.537	MRE11A	chr19	11113645	11113845	0.592	SMARCA4
chr11	94151903	94152103	0.343	MRE11A	chr19	11113855	11114055	0.493	SMARCA4
chr11	94152190	94152390	0.333	MRE11A	chr19	11118483	11118683	0.587	SMARCA4
chr11	94153182	94153395	0.308	MRE11A	chr19	11120977	11121177	0.557	SMARCA4
chr11	94168979	94169178	0.335	MRE11A	chr19	11123551	11123751	0.592	SMARCA4
chr11	94170337	94170576	0.300	MRE11A	chr19	11129571	11129781	0.555	SMARCA4
chr11	94178876	94179116	0.386	MRE11A	chr19	11130134	11130372	0.619	SMARCA4
chr11	94180384	94180615	0.500	MRE11A	chr19	11130167	11130367	0.612	SMARCA4
chr11	94189360	94189588	0.323	MRE11A	chr19	11130245	11130468	0.585	SMARCA4
chr11	94192639	94192838	0.370	MRE11A	chr19	11130248	11130473	0.584	SMARCA4
chr11	94193992	94194257	0.301	MRE11A	chr19	11132367	11132587	0.611	SMARCA4
chr11	94197223	94197451	0.349	MRE11A	chr19	11132607	11132807	0.622	SMARCA4
chr11	94200864	94201064	0.363	MRE11A	chr19	11134126	11134326	0.557	SMARCA4
chr11	94203635	94203874	0.404	MRE11A	chr19	11134905	11135105	0.617	SMARCA4
chr11	94204708	94204908	0.368	MRE11A	chr19	11135986	11136186	0.602	SMARCA4
chr11	94209357	94209557	0.348	MRE11A	chr19	11136874	11137104	0.610	SMARCA4
chr11	94211862	94212106	0.359	MRE11A	chr19	11138402	11138674	0.502	SMARCA4
chr11	94212728	94212928	0.378	MRE11A	chr19	11138598	11138818	0.597	SMARCA4
chr11	94219015	94219215	0.348	MRE11A	chr19	11141332	11141532	0.637	SMARCA4
chr11	94219225	94219425	0.264	MRE11A	chr19	11141549	11141749	0.627	SMARCA4
chr11	94223880	94224120	0.344	MRE11A	chr19	11143924	11144134	0.621	SMARCA4
chr11	94223898	94224142	0.327	MRE11A	chr19	11144041	11144262	0.617	SMARCA4
chr11	94225885	94226125	0.394	MRE11A	chr19	11144868	11145108	0.618	SMARCA4
chr11	108093593	108093813	0.615	ATM	chr19	11145552	11145823	0.654	SMARCA4
chr11	108093873	108094073	0.617	ATM	chr19	11151919	11152129	0.616	SMARCA4
chr11	108098331	108098581	0.335	ATM	chr19	11151919	11152189	0.627	SMARCA4
chr11	108098372	108098572	0.333	ATM	chr19	11152171	11152371	0.572	SMARCA4
chr11	108098382	108098631	0.316	ATM	chr19	11168890	11169140	0.625	SMARCA4
chr11	108098397	108098626	0.309	ATM	chr19	11169359	11169619	0.644	SMARCA4
chr11	108098399	108098628	0.304	ATM	chr19	11170610	11170850	0.668	SMARCA4
chr11	108099818	108100062	0.327	ATM	chr19	11172452	11172706	0.498	SMARCA4
chr11	108106395	108106596	0.356	ATM	chr19	11172557	11172757	0.423	SMARCA4
chr11	108114723	108115004	0.333	ATM	chr19	11172753	11172953	0.493	SMARCA4
chr11	108114777	108115004	0.329	ATM	chr19	45854611	45854870	0.581	ERCC2
chr11	108115492	108115736	0.351	ATM	chr19	45854917	45855123	0.589	ERCC2
chr11	108117690	108117930	0.324	ATM	chr19	45855406	45855649	0.656	ERCC2

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr11	108119692	108119907	0.343	ATM	chr19	45855711	45855931	0.611	ERCC2
chr11	108119737	108119952	0.361	ATM	chr19	45855908	45856123	0.611	ERCC2
chr11	108121367	108121602	0.377	ATM	chr19	45855910	45856123	0.612	ERCC2
chr11	108121609	108121764	0.359	ATM	chr19	45855914	45856123	0.610	ERCC2
chr11	108122506	108122706	0.363	ATM	chr19	45855948	45856167	0.609	ERCC2
chr11	108122716	108122936	0.317	ATM	chr19	45855959	45856169	0.607	ERCC2
chr11	108123498	108123718	0.321	ATM	chr19	45856222	45856442	0.652	ERCC2
chr11	108124529	108124729	0.393	ATM	chr19	45857893	45858113	0.597	ERCC2
chr11	108126954	108127154	0.363	ATM	chr19	45860528	45860730	0.635	ERCC2
chr11	108128041	108128241	0.294	ATM	chr19	45860797	45861007	0.635	ERCC2
chr11	108129523	108129756	0.316	ATM	chr19	45864772	45864905	0.575	ERCC2
chr11	108137908	108138102	0.374	ATM	chr19	45866937	45867137	0.706	ERCC2
chr11	108139112	108139322	0.374	ATM	chr19	45867119	45867343	0.724	ERCC2
chr11	108139329	108139529	0.338	ATM	chr19	45867124	45867373	0.716	ERCC2
chr11	108141794	108142040	0.324	ATM	chr19	45867329	45867584	0.684	ERCC2
chr11	108142019	108142263	0.359	ATM	chr19	45867491	45867711	0.656	ERCC2
chr11	108143141	108143341	0.323	ATM	chr19	45867506	45867746	0.660	ERCC2
chr11	108143328	108143577	0.336	ATM	chr19	45867566	45867806	0.618	ERCC2
chr11	108150264	108150498	0.328	ATM	chr19	45868096	45868344	0.635	ERCC2
chr11	108151721	108151951	0.364	ATM	chr19	45868149	45868349	0.637	ERCC2
chr11	108153427	108153675	0.285	ATM	chr19	45868154	45868396	0.626	ERCC2
chr11	108153471	108153632	0.284	ATM	chr19	45868287	45868486	0.600	ERCC2
chr11	108153471	108153677	0.275	ATM	chr19	45871786	45871991	0.524	ERCC2
chr11	108153505	108153680	0.267	ATM	chr19	45872064	45872264	0.582	ERCC2
chr11	108153510	108153680	0.269	ATM	chr19	45872211	45872411	0.562	ERCC2
chr11	108154843	108155094	0.282	ATM	chr19	45873397	45873585	0.661	ERCC2
chr11	108154858	108155070	0.291	ATM	chr19	45873421	45873651	0.675	ERCC2
chr11	108154954	108155155	0.396	ATM	chr19	45873436	45873665	0.687	ERCC2
chr11	108154962	108155211	0.388	ATM	chr19	45873632	45873861	0.700	ERCC2
chr11	108157899	108158161	0.354	ATM	chr19	45873636	45873901	0.684	ERCC2
chr11	108158376	108158580	0.337	ATM	chr19	45873726	45873936	0.645	ERCC2
chr11	108159642	108159842	0.343	ATM	chr19	45916987	45917191	0.571	ERCC1
chr11	108160273	108160473	0.299	ATM	chr19	45918047	45918240	0.619	ERCC1
chr11	108163344	108163589	0.378	ATM	chr19	45918047	45918243	0.619	ERCC1
chr11	108164044	108164225	0.324	ATM	chr19	45918048	45918243	0.622	ERCC1
chr11	108164078	108164281	0.314	ATM	chr19	45918053	45918243	0.628	ERCC1
chr11	108165595	108165795	0.358	ATM	chr19	45918060	45918235	0.625	ERCC1
chr11	108167798	108168039	0.269	ATM	chr19	45922222	45922436	0.567	ERCC1
chr11	108167811	108168065	0.267	ATM	chr19	45923506	45923678	0.607	ERCC1
chr11	108170423	108170622	0.380	ATM	chr19	45924445	45924632	0.638	ERCC1
chr11	108172321	108172561	0.340	ATM	chr19	45926611	45926815	0.615	ERCC1

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr11	108173513	108173723	0.351	ATM	chr19	50902097	50902336	0.650	POLD1
chr11	108173723	108173923	0.313	ATM	chr19	50902458	50902658	0.582	POLD1
chr11	108175366	108175566	0.398	ATM	chr19	50904960	50905171	0.656	POLD1
chr11	108178629	108178814	0.360	ATM	chr19	50905153	50905392	0.671	POLD1
chr11	108179595	108179834	0.375	ATM	chr19	50905436	50905665	0.683	POLD1
chr11	108180801	108181050	0.320	ATM	chr19	50905615	50905913	0.659	POLD1
chr11	108180821	108181050	0.322	ATM	chr19	50905899	50906137	0.665	POLD1
chr11	108180821	108181066	0.313	ATM	chr19	50906253	50906464	0.679	POLD1
chr11	108180871	108181071	0.333	ATM	chr19	50906723	50906971	0.622	POLD1
chr11	108183026	108183226	0.333	ATM	chr19	50906755	50906971	0.613	POLD1
chr11	108186520	108186768	0.357	ATM	chr19	50909485	50909773	0.640	POLD1
chr11	108186672	108186911	0.404	ATM	chr19	50910320	50910533	0.631	POLD1
chr11	108188080	108188262	0.399	ATM	chr19	50910334	50910578	0.629	POLD1
chr11	108190668	108190878	0.313	ATM	chr19	50910376	50910627	0.631	POLD1
chr11	108191937	108192186	0.392	ATM	chr19	50912042	50912281	0.617	POLD1
chr11	108195999	108196199	0.413	ATM	chr19	50912288	50912520	0.635	POLD1
chr11	108196116	108196316	0.388	ATM	chr19	50912795	50913010	0.667	POLD1
chr11	108196772	108196944	0.422	ATM	chr19	50916709	50916950	0.640	POLD1
chr11	108198304	108198504	0.398	ATM	chr19	50916970	50917221	0.623	POLD1
chr11	108199732	108199932	0.373	ATM	chr19	50917955	50918169	0.628	POLD1
chr11	108200863	108201105	0.374	ATM	chr19	50917960	50918169	0.624	POLD1
chr11	108201993	108202237	0.318	ATM	chr19	50918653	50918824	0.640	POLD1
chr11	108202461	108202678	0.330	ATM	chr19	50919033	50919269	0.692	POLD1
chr11	108202483	108202676	0.309	ATM	chr19	50919496	50919745	0.684	POLD1
chr11	108202496	108202676	0.298	ATM	chr19	50919683	50919957	0.691	POLD1
chr11	108202530	108202730	0.308	ATM	chr19	50919685	50919957	0.689	POLD1
chr11	108203403	108203613	0.336	ATM	chr19	50919770	50920048	0.699	POLD1
chr11	108203427	108203679	0.344	ATM	chr19	50919821	50920050	0.691	POLD1
chr11	108203480	108203724	0.339	ATM	chr19	50921104	50921313	0.576	POLD1
chr11	108203524	108203768	0.339	ATM	chr2	29443543	29443787	0.539	ALK
chr11	108203540	108203784	0.347	ATM	chr2	29443549	29443783	0.545	ALK
chr11	108204436	108204676	0.407	ATM	chr2	29443555	29443789	0.540	ALK
chr11	108205641	108205841	0.368	ATM	chr2	29443585	29443816	0.500	ALK
chr11	108206452	108206651	0.400	ATM	chr2	29445100	29445340	0.552	ALK
chr11	108213868	108214068	0.393	ATM	chr2	29445107	29445340	0.556	ALK
chr11	108216481	108216700	0.355	ATM	chr2	29445121	29445350	0.570	ALK
chr11	108217894	108218094	0.328	ATM	chr2	29445121	29445367	0.571	ALK
chr11	108224395	108224595	0.403	ATM	chr2	47600500	47600700	0.323	EPCAM
chr11	108225445	108225655	0.346	ATM	chr2	47600912	47601112	0.473	EPCAM
chr11	108235722	108235932	0.365	ATM	chr2	47601122	47601322	0.383	EPCAM
chr11	108235932	108236132	0.383	ATM	chr2	47602199	47602445	0.328	EPCAM

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr11	108235986	108236232	0.433	ATM	chr2	47604131	47604282	0.342	EPCAM
chr11	108236004	108236249	0.431	ATM	chr2	47605987	47606187	0.249	EPCAM
chr11	108236050	108236290	0.415	ATM	chr2	47606812	47606991	0.361	EPCAM
chr11	108236051	108236251	0.438	ATM	chr2	47612268	47612488	0.398	EPCAM
chr11	108236071	108236273	0.438	ATM	chr2	47613710	47613910	0.343	EPCAM
chr11	108238313	108238513	0.373	ATM	chr2	47630105	47630305	0.652	MSH2
chr11	111957513	111957759	0.591	SDHD	chr2	47630152	47630400	0.643	MSH2
chr11	111959529	111959746	0.486	SDHD	chr2	47630268	47630467	0.615	MSH2
chr11	111965449	111965740	0.414	SDHD	chr2	47630315	47630515	0.667	MSH2
chr11	111965464	111965754	0.416	SDHD	chr2	47630316	47630530	0.647	MSH2
chr12	25378488	25378688	0.353	KRAS	chr2	47630384	47630615	0.690	MSH2
chr12	25378503	25378751	0.341	KRAS	chr2	47630425	47630625	0.706	MSH2
chr12	25378546	25378778	0.352	KRAS	chr2	47635539	47635709	0.339	MSH2
chr12	25378554	25378783	0.348	KRAS	chr2	47637342	47637582	0.456	MSH2
chr12	25380153	25380359	0.411	KRAS	chr2	47637389	47637594	0.442	MSH2
chr12	25380166	25380337	0.407	KRAS	chr2	47639447	47639662	0.310	MSH2
chr12	25380167	25380326	0.406	KRAS	chr2	47641283	47641487	0.327	MSH2
chr12	25380167	25380359	0.420	KRAS	chr2	47643346	47643546	0.398	MSH2
chr12	25398080	25398329	0.360	KRAS	chr2	47656945	47657096	0.388	MSH2
chr12	25398145	25398394	0.348	KRAS	chr2	47672586	47672786	0.299	MSH2
chr12	25398153	25398397	0.351	KRAS	chr2	47690076	47690276	0.303	MSH2
chr12	25398159	25398408	0.356	KRAS	chr2	47693747	47693947	0.348	MSH2
chr12	25398186	25398433	0.347	KRAS	chr2	47698159	47698397	0.326	MSH2
chr12	56478765	56478994	0.552	ERBB3	chr2	47702121	47702341	0.394	MSH2
chr12	56478781	56479029	0.558	ERBB3	chr2	47702174	47702413	0.388	MSH2
chr12	56478784	56479029	0.561	ERBB3	chr2	47703453	47703653	0.428	MSH2
chr12	56478807	56479047	0.560	ERBB3	chr2	47703663	47703863	0.363	MSH2
chr12	56481533	56481774	0.541	ERBB3	chr2	47705399	47705630	0.397	MSH2
chr12	56481559	56481798	0.521	ERBB3	chr2	47707788	47708018	0.424	MSH2
chr12	56481594	56481833	0.546	ERBB3	chr2	47709903	47710113	0.327	MSH2
chr12	56481628	56481942	0.530	ERBB3	chr2	47710107	47710336	0.287	MSH2
chr12	56481740	56481979	0.517	ERBB3	chr2	48010393	48010592	0.725	MSH6
chr12	56481773	56482020	0.476	ERBB3	chr2	48010420	48010619	0.740	MSH6
chr12	56481807	56482048	0.467	ERBB3	chr2	48010573	48010824	0.690	MSH6
chr12	56482218	56482457	0.513	ERBB3	chr2	48010575	48010781	0.725	MSH6
chr12	56482252	56482491	0.496	ERBB3	chr2	48017953	48018200	0.419	MSH6
chr12	56482278	56482521	0.504	ERBB3	chr2	48018205	48018415	0.431	MSH6
chr12	56482331	56482580	0.528	ERBB3	chr2	48023040	48023272	0.455	MSH6
chr12	56486559	56486791	0.502	ERBB3	chr2	48023105	48023304	0.430	MSH6
chr12	56486561	56486791	0.502	ERBB3	chr2	48025749	48025949	0.428	MSH6
chr12	56486566	56486813	0.508	ERBB3	chr2	48025933	48026201	0.476	MSH6

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr12	56486569	56486818	0.508	ERBB3	chr2	48026177	48026376	0.460	MSH6
chr12	56490766	56491006	0.523	ERBB3	chr2	48026340	48026558	0.457	MSH6
chr12	56490766	56491013	0.520	ERBB3	chr2	48026511	48026711	0.458	MSH6
chr12	56490773	56491013	0.519	ERBB3	chr2	48026765	48026965	0.383	MSH6
chr12	56490777	56491011	0.523	ERBB3	chr2	48027019	48027219	0.438	MSH6
chr12	56491580	56491801	0.554	ERBB3	chr2	48027273	48027473	0.438	MSH6
chr12	56491592	56491801	0.557	ERBB3	chr2	48027527	48027727	0.398	MSH6
chr12	56491596	56491799	0.559	ERBB3	chr2	48027746	48028017	0.426	MSH6
chr12	56491596	56491801	0.558	ERBB3	chr2	48028124	48028364	0.415	MSH6
chr12	58141882	58142151	0.396	CDK4	chr2	48030536	48030736	0.433	MSH6
chr12	58142160	58142391	0.474	CDK4	chr2	48030729	48031008	0.371	MSH6
chr12	58142983	58143287	0.570	CDK4	chr2	48031952	48032152	0.443	MSH6
chr12	58142985	58143287	0.568	CDK4	chr2	48032026	48032237	0.420	MSH6
chr12	58144413	58144686	0.478	CDK4	chr2	48032772	48032971	0.315	MSH6
chr12	58144452	58144687	0.479	CDK4	chr2	48033358	48033554	0.365	MSH6
chr12	58144692	58144932	0.490	CDK4	chr2	48033416	48033655	0.367	MSH6
chr12	58144696	58144939	0.492	CDK4	chr2	48033581	48033782	0.401	MSH6
chr12	58144957	58145214	0.523	CDK4	chr2	48034024	48034264	0.307	MSH6
chr12	58145023	58145294	0.515	CDK4	chr2	58386432	58386632	0.333	FANCL
chr12	58145309	58145580	0.544	CDK4	chr2	58386777	58386929	0.307	FANCL
chr12	58145326	58145580	0.541	CDK4	chr2	58387189	58387389	0.338	FANCL
chr12	58145924	58146140	0.673	CDK4	chr2	58388496	58388732	0.346	FANCL
chr12	133200375	133200607	0.541	POLE	chr2	58389905	58390169	0.328	FANCL
chr12	133200794	133201005	0.604	POLE	chr2	58390005	58390214	0.352	FANCL
chr12	133200978	133201217	0.608	POLE	chr2	58390571	58390773	0.379	FANCL
chr12	133201185	133201425	0.610	POLE	chr2	58392779	58392979	0.398	FANCL
chr12	133201428	133201670	0.654	POLE	chr2	58431158	58431358	0.363	FANCL
chr12	133202187	133202429	0.621	POLE	chr2	58448972	58449172	0.323	FANCL
chr12	133202217	133202436	0.605	POLE	chr2	58453736	58453936	0.308	FANCL
chr12	133202217	133202437	0.606	POLE	chr2	58456824	58457044	0.285	FANCL
chr12	133202218	133202437	0.605	POLE	chr2	58459138	58459342	0.351	FANCL
chr12	133202355	133202555	0.622	POLE	chr2	58468279	58468479	0.592	FANCL
chr12	133202648	133202868	0.606	POLE	chr2	128014784	128015047	0.394	ERCC3
chr12	133208842	133209042	0.517	POLE	chr2	128015087	128015289	0.522	ERCC3
chr12	133209059	133209259	0.577	POLE	chr2	128016793	128017023	0.541	ERCC3
chr12	133209191	133209391	0.647	POLE	chr2	128018729	128018934	0.476	ERCC3
chr12	133210529	133210806	0.590	POLE	chr2	128028846	128029046	0.493	ERCC3
chr12	133212413	133212654	0.488	POLE	chr2	128030334	128030534	0.488	ERCC3
chr12	133214538	133214738	0.557	POLE	chr2	128036695	128036895	0.413	ERCC3
chr12	133215637	133215885	0.582	POLE	chr2	128037952	128038168	0.535	ERCC3
chr12	133218204	133218451	0.597	POLE	chr2	128044271	128044501	0.580	ERCC3

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr12	133218707	133218953	0.579	POLE	chr2	128044494	128044693	0.500	ERCC3
chr12	133219069	133219298	0.574	POLE	chr2	128046183	128046383	0.502	ERCC3
chr12	133219399	133219599	0.617	POLE	chr2	128046840	128047040	0.468	ERCC3
chr12	133219778	133220012	0.591	POLE	chr2	128047177	128047377	0.522	ERCC3
chr12	133219996	133220226	0.606	POLE	chr2	128047669	128047869	0.448	ERCC3
chr12	133220308	133220545	0.571	POLE	chr2	128050206	128050419	0.514	ERCC3
chr12	133225529	133225773	0.612	POLE	chr2	128051102	128051343	0.566	ERCC3
chr12	133225887	133226117	0.645	POLE	chr2	128051633	128051852	0.655	ERCC3
chr12	133226161	133226408	0.613	POLE	chr2	128051746	128051946	0.577	ERCC3
chr12	133233672	133233909	0.550	POLE	chr2	209112977	209113230	0.394	IDH1
chr12	133233774	133234003	0.557	POLE	chr2	209113091	209113340	0.444	IDH1
chr12	133234350	133234550	0.458	POLE	chr2	212288833	212289075	0.366	ERBB4
chr12	133235953	133236173	0.534	POLE	chr2	212288836	212289075	0.367	ERBB4
chr12	133237539	133237827	0.543	POLE	chr2	212288849	212289089	0.378	ERBB4
chr12	133237547	133237781	0.519	POLE	chr2	212288867	212289111	0.376	ERBB4
chr12	133238036	133238236	0.468	POLE	chr2	212483732	212483976	0.327	ERBB4
chr12	133240495	133240681	0.545	POLE	chr2	212483745	212483975	0.338	ERBB4
chr12	133241011	133241211	0.587	POLE	chr2	212483745	212483989	0.343	ERBB4
chr12	133241805	133242034	0.600	POLE	chr2	212483745	212483992	0.347	ERBB4
chr12	133244016	133244246	0.563	POLE	chr2	212529983	212530215	0.468	ERBB4
chr12	133244860	133245070	0.578	POLE	chr2	212529983	212530219	0.468	ERBB4
chr12	133245148	133245397	0.616	POLE	chr2	212530006	212530255	0.444	ERBB4
chr12	133245378	133245623	0.537	POLE	chr2	212530049	212530293	0.420	ERBB4
chr12	133248734	133248981	0.556	POLE	chr2	212587102	212587341	0.379	ERBB4
chr12	133249169	133249404	0.568	POLE	chr2	212587102	212587342	0.378	ERBB4
chr12	133249662	133249902	0.539	POLE	chr2	212587104	212587343	0.379	ERBB4
chr12	133250240	133250445	0.549	POLE	chr2	215591713	215591913	0.348	BARD1
chr12	133250282	133250482	0.517	POLE	chr2	215592049	215592249	0.313	BARD1
chr12	133251897	133252126	0.600	POLE	chr2	215592385	215592585	0.318	BARD1
chr12	133252231	133252480	0.512	POLE	chr2	215592721	215592921	0.284	BARD1
chr12	133252591	133252826	0.470	POLE	chr2	215593393	215593593	0.458	BARD1
chr12	133253058	133253290	0.502	POLE	chr2	215593464	215593712	0.482	BARD1
chr12	133253869	133254099	0.429	POLE	chr2	215595070	215595319	0.348	BARD1
chr12	133254080	133254312	0.502	POLE	chr2	215609774	215610018	0.331	BARD1
chr12	133256057	133256299	0.494	POLE	chr2	215610357	215610557	0.368	BARD1
chr12	133256546	133256806	0.441	POLE	chr2	215617201	215617402	0.322	BARD1
chr12	133256751	133257006	0.469	POLE	chr2	215617244	215617478	0.315	BARD1
chr12	133257134	133257364	0.429	POLE	chr2	215632137	215632347	0.398	BARD1
chr12	133257609	133257851	0.523	POLE	chr2	215632347	215632547	0.299	BARD1
chr13	28592527	28592791	0.434	FLT3	chr2	215633841	215634041	0.348	BARD1
chr13	32889625	32889857	0.631	BRCA2	chr2	215645283	215645483	0.418	BARD1

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr13	32889901	32890111	0.583	BRCA2	chr2	215645568	215645768	0.398	BARD1
chr13	32890514	32890741	0.346	BRCA2	chr2	215645789	215646022	0.385	BARD1
chr13	32893139	32893383	0.339	BRCA2	chr2	215645997	215646196	0.405	BARD1
chr13	32900135	32900368	0.252	BRCA2	chr2	215646018	215646167	0.413	BARD1
chr13	32900239	32900484	0.305	BRCA2	chr2	215656994	215657164	0.421	BARD1
chr13	32900514	32900762	0.373	BRCA2	chr2	215661815	215662059	0.355	BARD1
chr13	32903445	32903674	0.278	BRCA2	chr2	215674040	215674299	0.662	BARD1
chr13	32904938	32905182	0.343	BRCA2	chr2	215674057	215674299	0.671	BARD1
chr13	32905002	32905201	0.315	BRCA2	chr2	215674060	215674299	0.675	BARD1
chr13	32905048	32905165	0.339	BRCA2	chr2	215674115	215674321	0.681	BARD1
chr13	32905048	32905168	0.347	BRCA2	chr20	57484302	57484538	0.439	GNAS
chr13	32905048	32905170	0.341	BRCA2	chr21	36252718	36252963	0.427	RUNX1
chr13	32905049	32905165	0.342	BRCA2	chr21	36252753	36253001	0.454	RUNX1
chr13	32906224	32906468	0.302	BRCA2	chr21	36252796	36253037	0.471	RUNX1
chr13	32906406	32906650	0.310	BRCA2	chr21	36252819	36253063	0.469	RUNX1
chr13	32906408	32906628	0.317	BRCA2	chr22	29092793	29093014	0.383	CHEK2
chr13	32906426	32906673	0.306	BRCA2	chr22	29095766	29095985	0.468	CHEK2
chr13	32906464	32906663	0.305	BRCA2	chr22	29099378	29099614	0.354	CHEK2
chr13	32906520	32906768	0.317	BRCA2	chr22	29105946	29106126	0.243	CHEK2
chr13	32906575	32906818	0.361	BRCA2	chr22	29105988	29106140	0.288	CHEK2
chr13	32906606	32906846	0.378	BRCA2	chr22	29107796	29107996	0.373	CHEK2
chr13	32906668	32906912	0.388	BRCA2	chr22	29115374	29115613	0.292	CHEK2
chr13	32906748	32906987	0.388	BRCA2	chr22	29120968	29121207	0.358	CHEK2
chr13	32906815	32907062	0.363	BRCA2	chr22	29121185	29121429	0.376	CHEK2
chr13	32906856	32907103	0.367	BRCA2	chr22	29130538	29130762	0.556	CHEK2
chr13	32906893	32907106	0.383	BRCA2	chr22	29130552	29130805	0.508	CHEK2
chr13	32906938	32907183	0.378	BRCA2	chr22	29137634	29137834	0.547	CHEK2
chr13	32907059	32907264	0.374	BRCA2	chr3	10070202	10070402	0.383	FANCD2
chr13	32907059	32907307	0.378	BRCA2	chr3	10074431	10074641	0.303	FANCD2
chr13	32907288	32907533	0.350	BRCA2	chr3	10076444	10076673	0.430	FANCD2
chr13	32910416	32910655	0.354	BRCA2	chr3	10076732	10076932	0.323	FANCD2
chr13	32910596	32910835	0.388	BRCA2	chr3	10077981	10078130	0.313	FANCD2
chr13	32910778	32911027	0.340	BRCA2	chr3	10080961	10081110	0.367	FANCD2
chr13	32910967	32911215	0.317	BRCA2	chr3	10081391	10081592	0.510	FANCD2
chr13	32910988	32911187	0.335	BRCA2	chr3	10083255	10083471	0.433	FANCD2
chr13	32911008	32911252	0.331	BRCA2	chr3	10116194	10116415	0.405	FANCD2
chr13	32911035	32911252	0.321	BRCA2	chr3	10119764	10119916	0.523	FANCD2
chr13	32911045	32911295	0.331	BRCA2	chr3	10122693	10122903	0.422	FANCD2
chr13	32911167	32911415	0.341	BRCA2	chr3	10122903	10123103	0.378	FANCD2
chr13	32911340	32911588	0.333	BRCA2	chr3	10123144	10123344	0.358	FANCD2
chr13	32911594	32911838	0.322	BRCA2	chr3	10127494	10127703	0.433	FANCD2

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr13	32911841	32912085	0.384	BRCA2	chr3	10128659	10128873	0.414	FANCD2
chr13	32912080	32912319	0.342	BRCA2	chr3	10130055	10130255	0.448	FANCD2
chr13	32912267	32912511	0.265	BRCA2	chr3	10130418	10130618	0.398	FANCD2
chr13	32912502	32912746	0.331	BRCA2	chr3	10131860	10132052	0.461	FANCD2
chr13	32912749	32912986	0.307	BRCA2	chr3	10133776	10133976	0.418	FANCD2
chr13	32912979	32913218	0.404	BRCA2	chr3	10134833	10135033	0.448	FANCD2
chr13	32913217	32913460	0.336	BRCA2	chr3	10135971	10136220	0.484	FANCD2
chr13	32913444	32913691	0.323	BRCA2	chr3	10136796	10137016	0.425	FANCD2
chr13	32913682	32913927	0.321	BRCA2	chr3	10137928	10138128	0.398	FANCD2
chr13	32913944	32914192	0.329	BRCA2	chr3	10140403	10140603	0.448	FANCD2
chr13	32914208	32914455	0.347	BRCA2	chr3	10140685	10140895	0.322	FANCD2
chr13	32914462	32914709	0.343	BRCA2	chr3	10183302	10183451	0.653	VHL
chr13	32914691	32914936	0.329	BRCA2	chr3	10183681	10183874	0.706	VHL
chr13	32914776	32915021	0.333	BRCA2	chr3	10188234	10188438	0.390	VHL
chr13	32914895	32915115	0.326	BRCA2	chr3	10191445	10191700	0.484	VHL
chr13	32914896	32915115	0.327	BRCA2	chr3	10191721	10191932	0.392	VHL
chr13	32914906	32915155	0.328	BRCA2	chr3	10192245	10192450	0.350	VHL
chr13	32915087	32915334	0.355	BRCA2	chr3	12645599	12645838	0.504	RAF1
chr13	32915144	32915384	0.357	BRCA2	chr3	12645599	12645843	0.502	RAF1
chr13	32918540	32918787	0.258	BRCA2	chr3	12645599	12645844	0.500	RAF1
chr13	32920834	32921033	0.295	BRCA2	chr3	12645603	12645844	0.504	RAF1
chr13	32928970	32929189	0.345	BRCA2	chr3	14186692	14186898	0.319	XPC
chr13	32928972	32929201	0.357	BRCA2	chr3	14186863	14187104	0.521	XPC
chr13	32928992	32929236	0.351	BRCA2	chr3	14187085	14187334	0.532	XPC
chr13	32928996	32929196	0.358	BRCA2	chr3	14187312	14187552	0.589	XPC
chr13	32928996	32929208	0.357	BRCA2	chr3	14187523	14187722	0.570	XPC
chr13	32929176	32929423	0.339	BRCA2	chr3	14188679	14188879	0.552	XPC
chr13	32929177	32929426	0.344	BRCA2	chr3	14189299	14189509	0.583	XPC
chr13	32929220	32929467	0.323	BRCA2	chr3	14189991	14190191	0.597	XPC
chr13	32929274	32929479	0.335	BRCA2	chr3	14190286	14190496	0.578	XPC
chr13	32929297	32929498	0.322	BRCA2	chr3	14193741	14194025	0.596	XPC
chr13	32930589	32930789	0.448	BRCA2	chr3	14197850	14198050	0.483	XPC
chr13	32931650	32931879	0.257	BRCA2	chr3	14199573	14199852	0.543	XPC
chr13	32931817	32932017	0.318	BRCA2	chr3	14199862	14200062	0.582	XPC
chr13	32932034	32932234	0.313	BRCA2	chr3	14200146	14200394	0.522	XPC
chr13	32936641	32936885	0.384	BRCA2	chr3	14206322	14206487	0.434	XPC
chr13	32937319	32937563	0.384	BRCA2	chr3	14206933	14207089	0.522	XPC
chr13	32937529	32937773	0.376	BRCA2	chr3	14208699	14208911	0.474	XPC
chr13	32944444	32944688	0.359	BRCA2	chr3	14209663	14209863	0.517	XPC
chr13	32945080	32945249	0.359	BRCA2	chr3	14211839	14212049	0.384	XPC
chr13	32950820	32951019	0.440	BRCA2	chr3	14214355	14214600	0.476	XPC

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr13	32953333	32953533	0.348	BRCA2	chr3	14220004	14220204	0.682	XPC
chr13	32953442	32953686	0.363	BRCA2	chr3	37034589	37034809	0.570	EPM2AIP1
chr13	32953840	32954084	0.327	BRCA2	chr3	37034790	37035063	0.544	EPM2AIP1
chr13	32954054	32954299	0.346	BRCA2	chr3	37035069	37035306	0.622	MLH1
chr13	32954054	32954300	0.344	BRCA2	chr3	37038000	37038200	0.368	MLH1
chr13	32968741	32968971	0.359	BRCA2	chr3	37042434	37042645	0.354	MLH1
chr13	32968820	32969069	0.384	BRCA2	chr3	37045773	37045973	0.418	MLH1
chr13	32970989	32971236	0.379	BRCA2	chr3	37048411	37048645	0.353	MLH1
chr13	32971106	32971335	0.348	BRCA2	chr3	37050230	37050436	0.377	MLH1
chr13	32972257	32972489	0.373	BRCA2	chr3	37053207	37053427	0.335	MLH1
chr13	32972463	32972703	0.390	BRCA2	chr3	37053528	37053730	0.340	MLH1
chr13	32972600	32972845	0.378	BRCA2	chr3	37055893	37056093	0.373	MLH1
chr13	32972664	32972864	0.418	BRCA2	chr3	37058865	37059114	0.424	MLH1
chr13	32972671	32972922	0.397	BRCA2	chr3	37061804	37062039	0.542	MLH1
chr13	32972708	32972954	0.389	BRCA2	chr3	37067171	37067392	0.500	MLH1
chr13	32973392	32973641	0.336	BRCA2	chr3	37067236	37067492	0.514	MLH1
chr13	32973613	32973807	0.267	BRCA2	chr3	37070194	37070394	0.408	MLH1
chr13	48916668	48916868	0.318	RB1	chr3	37070355	37070605	0.462	MLH1
chr13	48919151	48919351	0.284	RB1	chr3	37081625	37081777	0.438	MLH1
chr13	48921945	48922145	0.308	RB1	chr3	37083681	37083889	0.354	MLH1
chr13	48923001	48923221	0.258	RB1	chr3	37088877	37089113	0.468	MLH1
chr13	48936897	48937117	0.330	RB1	chr3	37088933	37089152	0.473	MLH1
chr13	48939068	48939268	0.318	RB1	chr3	37089899	37090099	0.468	MLH1
chr13	48941560	48941760	0.318	RB1	chr3	37090327	37090527	0.428	MLH1
chr13	48947429	48947629	0.323	RB1	chr3	37091892	37092087	0.480	MLH1
chr13	48951017	48951237	0.348	RB1	chr3	37091894	37092142	0.466	MLH1
chr13	48954364	48954564	0.328	RB1	chr3	41265974	41266223	0.464	CTNNB1
chr13	48955326	48955526	0.303	RB1	chr3	41266013	41266252	0.488	CTNNB1
chr13	48955536	48955736	0.338	RB1	chr3	41266021	41266268	0.476	CTNNB1
chr13	49027033	49027233	0.333	RB1	chr3	41266036	41266265	0.474	CTNNB1
chr13	49030212	49030472	0.364	RB1	chr3	52435062	52435320	0.583	BAP1
chr13	49033792	49033992	0.428	RB1	chr3	52435350	52435631	0.543	BAP1
chr13	49037854	49038084	0.299	RB1	chr3	52435934	52436211	0.561	BAP1
chr13	49039190	49039390	0.378	RB1	chr3	52436217	52436465	0.647	BAP1
chr13	49039267	49039467	0.383	RB1	chr3	52436552	52436790	0.552	BAP1
chr13	49047356	49047616	0.287	RB1	chr3	52436807	52437063	0.572	BAP1
chr13	49050783	49050983	0.373	RB1	chr3	52437127	52437370	0.574	BAP1
chr13	49051484	49051724	0.299	RB1	chr3	52437447	52437693	0.599	BAP1
chr13	49054133	49054333	0.413	RB1	chr3	52437754	52437978	0.556	BAP1
chr13	49054700	49054910	0.251	RB1	chr3	52438443	52438682	0.575	BAP1
chr13	49055078	49055278	0.323	RB1	chr3	52439130	52439357	0.583	BAP1

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr13	49055456	49055656	0.343	RB1	chr3	52439752	52440014	0.544	BAP1
chr13	49055834	49056034	0.254	RB1	chr3	52440273	52440505	0.618	BAP1
chr13	103498123	103498440	0.629	ERCC5	chr3	52440695	52440946	0.552	BAP1
chr13	103498155	103498432	0.640	ERCC5	chr3	52441181	52441475	0.576	BAP1
chr13	103498190	103498390	0.642	ERCC5	chr3	52441983	52442230	0.532	BAP1
chr13	103498192	103498440	0.631	ERCC5	chr3	52442460	52442693	0.500	BAP1
chr13	103498192	103498453	0.626	ERCC5	chr3	52443505	52443740	0.602	BAP1
chr13	103498470	103498701	0.608	ERCC5	chr3	138374171	138374400	0.400	PIK3CB
chr13	103498494	103498713	0.618	ERCC5	chr3	138374183	138374428	0.386	PIK3CB
chr13	103498494	103498717	0.621	ERCC5	chr3	138374197	138374427	0.398	PIK3CB
chr13	103498574	103498757	0.641	ERCC5	chr3	138374204	138374443	0.408	PIK3CB
chr13	103504312	103504529	0.349	ERCC5	chr3	138409848	138410087	0.375	PIK3CB
chr13	103504364	103504578	0.372	ERCC5	chr3	138409848	138410097	0.380	PIK3CB
chr13	103506028	103506230	0.409	ERCC5	chr3	138409872	138410116	0.380	PIK3CB
chr13	103506526	103506726	0.463	ERCC5	chr3	138409872	138410118	0.385	PIK3CB
chr13	103508374	103508544	0.275	ERCC5	chr3	138417690	138417920	0.390	PIK3CB
chr13	103510603	103510803	0.393	ERCC5	chr3	138417690	138417924	0.383	PIK3CB
chr13	103513836	103514056	0.407	ERCC5	chr3	138417696	138417915	0.391	PIK3CB
chr13	103514321	103514572	0.433	ERCC5	chr3	138417697	138417916	0.395	PIK3CB
chr13	103514574	103514792	0.534	ERCC5	chr3	138665132	138665361	0.600	FOXL2
chr13	103514801	103515020	0.482	ERCC5	chr3	138665147	138665396	0.600	FOXL2
chr13	103515021	103515221	0.428	ERCC5	chr3	138665151	138665396	0.602	FOXL2
chr13	103515235	103515435	0.433	ERCC5	chr3	138665170	138665409	0.613	FOXL2
chr13	103517984	103518184	0.478	ERCC5	chr3	178916725	178916970	0.362	PIK3CA
chr13	103518194	103518404	0.412	ERCC5	chr3	178916766	178917010	0.351	PIK3CA
chr13	103518516	103518726	0.370	ERCC5	chr3	178916782	178917028	0.356	PIK3CA
chr13	103519057	103519257	0.368	ERCC5	chr3	178916822	178917068	0.336	PIK3CA
chr13	103520541	103520748	0.370	ERCC5	chr3	178917417	178917566	0.320	PIK3CA
chr13	103524493	103524693	0.413	ERCC5	chr3	178917417	178917618	0.347	PIK3CA
chr13	103524585	103524802	0.445	ERCC5	chr3	178917420	178917590	0.345	PIK3CA
chr13	103525496	103525696	0.368	ERCC5	chr3	178917420	178917604	0.351	PIK3CA
chr13	103527656	103527856	0.408	ERCC5	chr3	178921331	178921578	0.367	PIK3CA
chr13	103527863	103528063	0.408	ERCC5	chr3	178921339	178921585	0.372	PIK3CA
chr13	103528070	103528300	0.437	ERCC5	chr3	178921347	178921596	0.368	PIK3CA
chr14	38060515	38060750	0.589	FOXA1	chr3	178921364	178921608	0.351	PIK3CA
chr14	38060564	38060810	0.591	FOXA1	chr3	178927888	178928114	0.339	PIK3CA
chr14	38060574	38060818	0.592	FOXA1	chr3	178927898	178928114	0.346	PIK3CA
chr14	38060586	38060833	0.601	FOXA1	chr3	178927910	178928144	0.323	PIK3CA
chr14	45605103	45605333	0.558	FANCM	chr3	178927974	178928182	0.354	PIK3CA
chr14	45605305	45605553	0.610	FANCM	chr3	178935873	178936102	0.313	PIK3CA
chr14	45605573	45605799	0.511	FANCM	chr3	178935930	178936133	0.353	PIK3CA

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr14	45606233	45606433	0.398	FANCM	chr3	178935944	178936197	0.335	PIK3CA
chr14	45618024	45618224	0.363	FANCM	chr3	178935995	178936197	0.365	PIK3CA
chr14	45620541	45620741	0.333	FANCM	chr3	178936030	178936279	0.320	PIK3CA
chr14	45623034	45623234	0.348	FANCM	chr3	178951914	178952159	0.382	PIK3CA
chr14	45628297	45628497	0.408	FANCM	chr3	178951915	178952140	0.385	PIK3CA
chr14	45633510	45633710	0.373	FANCM	chr3	178951921	178952140	0.386	PIK3CA
chr14	45633720	45633920	0.383	FANCM	chr3	178951921	178952159	0.381	PIK3CA
chr14	45636166	45636386	0.376	FANCM	chr3	178951948	178952109	0.389	PIK3CA
chr14	45639788	45640013	0.341	FANCM	chr3	178952004	178952152	0.389	PIK3CA
chr14	45642242	45642442	0.403	FANCM	chr3	178952010	178952109	0.390	PIK3CA
chr14	45644281	45644486	0.340	FANCM	chr3	178952109	178952152	0.386	PIK3CA
chr14	45644653	45644863	0.313	FANCM	chr4	55151865	55152127	0.513	PDGFRA
chr14	45644862	45645099	0.382	FANCM	chr4	55593487	55593733	0.389	KIT
chr14	45645143	45645342	0.350	FANCM	chr4	55593505	55593749	0.400	KIT
chr14	45645413	45645613	0.378	FANCM	chr4	55593514	55593765	0.397	KIT
chr14	45645666	45645955	0.331	FANCM	chr4	55593530	55593778	0.390	KIT
chr14	45645983	45646183	0.303	FANCM	chr4	55594116	55594365	0.416	KIT
chr14	45650718	45650970	0.332	FANCM	chr4	55594125	55594365	0.411	KIT
chr14	45650772	45650971	0.320	FANCM	chr4	55594139	55594380	0.401	KIT
chr14	45652886	45653086	0.338	FANCM	chr4	55594139	55594385	0.401	KIT
chr14	45654389	45654589	0.303	FANCM	chr4	55599168	55599408	0.365	KIT
chr14	45656912	45657134	0.269	FANCM	chr4	55599173	55599417	0.367	KIT
chr14	45658004	45658204	0.333	FANCM	chr4	55599207	55599435	0.384	KIT
chr14	45658183	45658427	0.371	FANCM	chr4	55602645	55602892	0.423	KIT
chr14	45658417	45658644	0.368	FANCM	chr4	55602657	55602888	0.422	KIT
chr14	45665608	45665811	0.348	FANCM	chr4	55602657	55602892	0.424	KIT
chr14	45667934	45668145	0.358	FANCM	chr4	153244069	153244316	0.464	FBXW7
chr14	45668983	45669204	0.320	FANCM	chr4	153244075	153244315	0.465	FBXW7
chr14	45669474	45669678	0.346	FANCM	chr4	153244085	153244324	0.454	FBXW7
chr14	95557315	95557515	0.313	DICER1	chr4	153244106	153244353	0.427	FBXW7
chr14	95557526	95557726	0.463	DICER1	chr4	153245291	153245531	0.398	FBXW7
chr14	95559982	95560182	0.542	DICER1	chr4	153245297	153245541	0.400	FBXW7
chr14	95560204	95560434	0.494	DICER1	chr4	153245312	153245560	0.406	FBXW7
chr14	95560444	95560644	0.398	DICER1	chr4	153245328	153245572	0.396	FBXW7
chr14	95562161	95562361	0.368	DICER1	chr4	153247109	153247353	0.433	FBXW7
chr14	95562361	95562592	0.530	DICER1	chr4	153247122	153247369	0.448	FBXW7
chr14	95562601	95562801	0.438	DICER1	chr4	153247150	153247399	0.456	FBXW7
chr14	95562666	95562891	0.398	DICER1	chr4	153249264	153249512	0.414	FBXW7
chr14	95566129	95566335	0.406	DICER1	chr4	153249285	153249525	0.419	FBXW7
chr14	95569682	95569882	0.468	DICER1	chr4	153249290	153249529	0.417	FBXW7
chr14	95569994	95570194	0.403	DICER1	chr4	153249303	153249551	0.414	FBXW7

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr14	95570228	95570428	0.418	DICER1	chr4	153250763	153251006	0.340	FBXW7
chr14	95571340	95571540	0.488	DICER1	chr4	153250791	153251017	0.348	FBXW7
chr14	95571974	95572174	0.348	DICER1	chr4	153250791	153251031	0.349	FBXW7
chr14	95572314	95572514	0.428	DICER1	chr4	153250808	153251047	0.342	FBXW7
chr14	95572524	95572764	0.249	DICER1	chr4	153251774	153252018	0.380	FBXW7
chr14	95573959	95574159	0.338	DICER1	chr4	153251789	153252028	0.388	FBXW7
chr14	95574168	95574368	0.348	DICER1	chr4	153251792	153252040	0.382	FBXW7
chr14	95574657	95574857	0.443	DICER1	chr4	153251832	153252071	0.379	FBXW7
chr14	95577599	95577799	0.433	DICER1	chr4	153258843	153259092	0.356	FBXW7
chr14	95578391	95578591	0.358	DICER1	chr4	153258850	153259097	0.355	FBXW7
chr14	95579340	95579540	0.358	DICER1	chr4	153258888	153259137	0.344	FBXW7
chr14	95581926	95582126	0.433	DICER1	chr4	153258953	153259199	0.368	FBXW7
chr14	95582756	95582956	0.358	DICER1	chr4	153268077	153268219	0.517	FBXW7
chr14	95582966	95583166	0.348	DICER1	chr4	153268078	153268219	0.514	FBXW7
chr14	95583900	95584100	0.378	DICER1	chr4	153268079	153268219	0.518	FBXW7
chr14	95590532	95590732	0.358	DICER1	chr5	56161075	56161306	0.328	MAP3K1
chr14	95590767	95590967	0.393	DICER1	chr5	56161096	56161325	0.330	MAP3K1
chr14	95592822	95593064	0.305	DICER1	chr5	56161113	56161321	0.349	MAP3K1
chr14	95595734	95595934	0.358	DICER1	chr5	56161178	56161386	0.321	MAP3K1
chr14	95596337	95596537	0.343	DICER1	chr5	56161545	56161787	0.346	MAP3K1
chr14	95598778	95598978	0.383	DICER1	chr5	56161548	56161797	0.348	MAP3K1
chr14	95598988	95599188	0.308	DICER1	chr5	56161563	56161807	0.355	MAP3K1
chr14	95599591	95599801	0.436	DICER1	chr5	56161577	56161806	0.365	MAP3K1
chr14	95623722	95623973	0.750	DICER1	chr5	56180437	56180676	0.363	MAP3K1
chr14	105246388	105246637	0.596	AKT1	chr5	56180457	56180659	0.389	MAP3K1
chr14	105246483	105246730	0.617	AKT1	chr5	56180502	56180707	0.369	MAP3K1
chr14	105246501	105246707	0.633	AKT1	chr5	56181614	56181861	0.335	MAP3K1
chr14	105246501	105246745	0.633	AKT1	chr5	56181627	56181876	0.332	MAP3K1
chr15	32968921	32969121	0.303	GREM1	chr5	56181632	56181871	0.338	MAP3K1
chr15	32976883	32977083	0.393	GREM1	chr5	56181648	56181887	0.346	MAP3K1
chr15	32984845	32985055	0.469	GREM1	chr5	56183135	56183374	0.429	MAP3K1
chr15	32988826	32989036	0.370	SCG5	chr5	56183138	56183347	0.429	MAP3K1
chr15	33000769	33000969	0.512	GREM1	chr5	56183138	56183361	0.429	MAP3K1
chr15	33022952	33023162	0.654	GREM1	chr5	56183176	56183375	0.455	MAP3K1
chr15	33022952	33023205	0.638	GREM1	chr5	112043137	112043364	0.649	APC
chr15	33023018	33023279	0.626	GREM1	chr5	112043137	112043365	0.651	APC
chr15	33023148	33023435	0.521	GREM1	chr5	112043186	112043431	0.663	APC
chr15	33023151	33023435	0.519	GREM1	chr5	112043190	112043431	0.661	APC
chr15	33023205	33023450	0.504	GREM1	chr5	112043201	112043471	0.672	APC
chr15	33023686	33023886	0.517	GREM1	chr5	112043206	112043428	0.668	APC
chr15	33024084	33024294	0.464	GREM1	chr5	112073451	112073699	0.639	APC

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr15	33024482	33024682	0.398	GREM1	chr5	112073948	112074148	0.488	APC
chr15	33026472	33026672	0.299	GREM1	chr5	112090491	112090691	0.373	APC
chr15	66727327	66727566	0.546	MAP2K1	chr5	112102006	112102208	0.330	APC
chr15	66727339	66727587	0.550	MAP2K1	chr5	112102893	112103093	0.433	APC
chr15	66727339	66727588	0.548	MAP2K1	chr5	112111368	112111578	0.289	APC
chr15	66727359	66727598	0.542	MAP2K1	chr5	112116375	112116639	0.340	APC
chr15	66729024	66729277	0.496	MAP2K1	chr5	112128134	112128341	0.332	APC
chr15	66729065	66729264	0.515	MAP2K1	chr5	112128152	112128420	0.309	APC
chr15	66774016	66774220	0.527	MAP2K1	chr5	112136780	112137014	0.404	APC
chr15	66774016	66774260	0.510	MAP2K1	chr5	112151086	112151286	0.368	APC
chr15	66774048	66774260	0.516	MAP2K1	chr5	112154610	112154859	0.424	APC
chr15	66774052	66774260	0.517	MAP2K1	chr5	112154826	112155071	0.504	APC
chr15	66777305	66777541	0.591	MAP2K1	chr5	112157485	112157695	0.341	APC
chr15	66777336	66777568	0.597	MAP2K1	chr5	112162781	112162991	0.379	APC
chr15	66777336	66777570	0.600	MAP2K1	chr5	112163441	112163655	0.288	APC
chr15	66777338	66777568	0.597	MAP2K1	chr5	112163452	112163681	0.309	APC
chr15	89787224	89787484	0.651	FANCI	chr5	112164471	112164655	0.319	APC
chr15	89790756	89790956	0.368	FANCI	chr5	112170600	112170800	0.393	APC
chr15	89801818	89802048	0.403	FANCI	chr5	112170810	112171010	0.289	APC
chr15	89803854	89804054	0.403	FANCI	chr5	112173249	112173449	0.383	APC
chr15	89804662	89804884	0.372	FANCI	chr5	112173471	112173712	0.405	APC
chr15	89804949	89805159	0.365	FANCI	chr5	112173688	112173932	0.404	APC
chr15	89806635	89806874	0.371	FANCI	chr5	112173840	112174071	0.466	APC
chr15	89807040	89807240	0.403	FANCI	chr5	112174070	112174313	0.361	APC
chr15	89807671	89807891	0.344	FANCI	chr5	112174297	112174537	0.353	APC
chr15	89811673	89811922	0.364	FANCI	chr5	112174544	112174783	0.392	APC
chr15	89817473	89817702	0.370	FANCI	chr5	112174788	112175027	0.400	APC
chr15	89819937	89820137	0.418	FANCI	chr5	112174985	112175185	0.378	APC
chr15	89821824	89822080	0.358	FANCI	chr5	112175164	112175405	0.459	APC
chr15	89824311	89824511	0.333	FANCI	chr5	112175413	112175652	0.471	APC
chr15	89824830	89825066	0.359	FANCI	chr5	112175519	112175768	0.460	APC
chr15	89828191	89828429	0.439	FANCI	chr5	112175523	112175780	0.461	APC
chr15	89833373	89833592	0.368	FANCI	chr5	112175853	112176053	0.333	APC
chr15	89834739	89834949	0.365	FANCI	chr5	112175867	112176116	0.380	APC
chr15	89835684	89835936	0.336	FANCI	chr5	112175900	112176040	0.326	APC
chr15	89836099	89836321	0.327	FANCI	chr5	112176145	112176391	0.449	APC
chr15	89837021	89837221	0.358	FANCI	chr5	112176384	112176633	0.412	APC
chr15	89838207	89838356	0.480	FANCI	chr5	112176631	112176875	0.322	APC
chr15	89843116	89843345	0.417	FANCI	chr5	112176860	112177104	0.396	APC
chr15	89843449	89843649	0.403	FANCI	chr5	112176995	112177234	0.400	APC
chr15	89844490	89844700	0.455	FANCI	chr5	112177404	112177650	0.385	APC

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr15	89846965	89847165	0.388	FANCI	chr5	112177589	112177789	0.408	APC
chr15	89848390	89848629	0.479	FANCI	chr5	112177796	112178080	0.389	APC
chr15	89848727	89848927	0.478	FANCI	chr5	112178130	112178379	0.456	APC
chr15	89849176	89849396	0.439	FANCI	chr5	112178293	112178573	0.391	APC
chr15	89850578	89850778	0.403	FANCI	chr5	112178510	112178755	0.407	APC
chr15	89850795	89850995	0.438	FANCI	chr5	112178763	112179036	0.449	APC
chr15	89857735	89857935	0.398	FANCI	chr5	112179030	112179324	0.380	APC
chr15	89858460	89858694	0.498	FANCI	chr5	112179325	112179525	0.423	APC
chr15	89859420	89859663	0.430	FANCI	chr5	112179582	112179827	0.472	APC
chr15	89859773	89859973	0.517	FANCI	chr5	112180193	112180393	0.338	APC
chr15	89859992	89860192	0.443	FANCI	chr5	112181061	112181261	0.398	APC
chr15	89860258	89860477	0.359	FANCI	chr5	112181929	112182129	0.313	APC
chr15	90631785	90632007	0.570	IDH2	chr5	131892606	131892857	0.718	RAD50
chr15	90631814	90632043	0.548	IDH2	chr5	131892983	131893197	0.474	RAD50
chr15	90631843	90632054	0.519	IDH2	chr5	131892984	131893223	0.463	RAD50
chr16	3631168	3631388	0.443	SLX4	chr5	131893020	131893223	0.466	RAD50
chr16	3632424	3632665	0.645	SLX4	chr5	131893049	131893292	0.492	RAD50
chr16	3632693	3632893	0.597	SLX4	chr5	131894808	131895037	0.252	RAD50
chr16	3633083	3633283	0.582	SLX4	chr5	131911382	131911618	0.376	RAD50
chr16	3633339	3633565	0.590	SLX4	chr5	131915004	131915223	0.382	RAD50
chr16	3634696	3634896	0.502	SLX4	chr5	131915567	131915717	0.364	RAD50
chr16	3639002	3639202	0.617	SLX4	chr5	131923251	131923500	0.312	RAD50
chr16	3639197	3639423	0.652	SLX4	chr5	131923517	131923757	0.328	RAD50
chr16	3639505	3639754	0.632	SLX4	chr5	131924402	131924651	0.364	RAD50
chr16	3639692	3639932	0.639	SLX4	chr5	131925323	131925552	0.343	RAD50
chr16	3639911	3640159	0.530	SLX4	chr5	131926850	131927094	0.363	RAD50
chr16	3640185	3640409	0.498	SLX4	chr5	131927570	131927750	0.354	RAD50
chr16	3640478	3640721	0.607	SLX4	chr5	131930491	131930738	0.323	RAD50
chr16	3640760	3641047	0.660	SLX4	chr5	131931278	131931508	0.442	RAD50
chr16	3641072	3641272	0.468	SLX4	chr5	131939061	131939291	0.377	RAD50
chr16	3642628	3642858	0.597	SLX4	chr5	131939553	131939789	0.350	RAD50
chr16	3644537	3644773	0.608	SLX4	chr5	131940409	131940654	0.346	RAD50
chr16	3645495	3645705	0.673	SLX4	chr5	131944351	131944557	0.261	RAD50
chr16	3646003	3646244	0.698	SLX4	chr5	131944387	131944597	0.251	RAD50
chr16	3646031	3646244	0.720	SLX4	chr5	131944873	131945090	0.271	RAD50
chr16	3646124	3646405	0.699	SLX4	chr5	131951603	131951803	0.323	RAD50
chr16	3646149	3646391	0.712	SLX4	chr5	131951820	131952020	0.294	RAD50
chr16	3646157	3646403	0.704	SLX4	chr5	131953730	131953966	0.333	RAD50
chr16	3647312	3647583	0.610	SLX4	chr5	131972864	131973090	0.454	RAD50
chr16	3647601	3647800	0.540	SLX4	chr5	131973728	131973957	0.443	RAD50
chr16	3647864	3648074	0.578	SLX4	chr5	131976168	131976417	0.520	RAD50

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr16	3650971	3651251	0.530	SLX4	chr5	131977815	131978052	0.378	RAD50
chr16	3652058	3652258	0.557	SLX4	chr5	131978075	131978308	0.372	RAD50
chr16	3656390	3656622	0.506	SLX4	chr5	131978265	131978518	0.417	RAD50
chr16	3656642	3656842	0.443	SLX4	chr5	131978882	131979101	0.486	RAD50
chr16	3658480	3658725	0.528	SLX4	chr5	170837389	170837646	0.318	NPM1
chr16	3658510	3658671	0.562	SLX4	chr5	170837423	170837672	0.316	NPM1
chr16	3658784	3659014	0.455	SLX4	chr6	35419950	35420204	0.710	FANCE
chr16	3659560	3659760	0.438	SLX4	chr6	35420484	35420712	0.677	FANCE
chr16	14013935	14014175	0.651	ERCC4	chr6	35423523	35423753	0.610	FANCE
chr16	14013966	14014166	0.662	ERCC4	chr6	35423747	35423980	0.568	FANCE
chr16	14013970	14014170	0.662	ERCC4	chr6	35423937	35424160	0.500	FANCE
chr16	14013971	14014170	0.665	ERCC4	chr6	35425325	35425579	0.541	FANCE
chr16	14015823	14016023	0.373	ERCC4	chr6	35425576	35425862	0.516	FANCE
chr16	14016033	14016243	0.355	ERCC4	chr6	35425990	35426190	0.602	FANCE
chr16	14020466	14020710	0.351	ERCC4	chr6	35427014	35427214	0.443	FANCE
chr16	14021912	14022151	0.338	ERCC4	chr6	35427343	35427543	0.552	FANCE
chr16	14024532	14024732	0.373	ERCC4	chr6	35428293	35428492	0.560	FANCE
chr16	14025949	14026157	0.344	ERCC4	chr6	35433986	35434203	0.550	FANCE
chr16	14027949	14028149	0.348	ERCC4	chr6	35434173	35434385	0.493	FANCE
chr16	14028984	14029224	0.415	ERCC4	chr6	43544117	43544321	0.459	POLH
chr16	14029445	14029685	0.452	ERCC4	chr6	43550014	43550163	0.420	POLH
chr16	14031514	14031714	0.373	ERCC4	chr6	43550754	43550953	0.415	POLH
chr16	14038575	14038734	0.494	ERCC4	chr6	43554978	43555223	0.476	POLH
chr16	14041470	14041670	0.468	ERCC4	chr6	43565476	43565625	0.467	POLH
chr16	14041655	14041919	0.509	ERCC4	chr6	43568621	43568821	0.448	POLH
chr16	14041900	14042126	0.498	ERCC4	chr6	43571533	43571733	0.423	POLH
chr16	14042120	14042369	0.404	ERCC4	chr6	43572382	43572582	0.433	POLH
chr16	14042584	14042854	0.424	ERCC4	chr6	43572829	43573058	0.374	POLH
chr16	14042844	14043078	0.336	ERCC4	chr6	43578220	43578420	0.507	POLH
chr16	14042902	14043146	0.347	ERCC4	chr6	43581333	43581514	0.407	POLH
chr16	14043430	14043679	0.284	ERCC4	chr6	43581613	43581843	0.433	POLH
chr16	14044214	14044436	0.332	ERCC4	chr6	43581852	43582085	0.517	POLH
chr16	14045149	14045380	0.276	ERCC4	chr6	43582072	43582231	0.475	POLH
chr16	14045389	14045634	0.427	ERCC4	chr6	43587356	43587593	0.361	POLH
chr16	14045727	14045927	0.328	ERCC4	chr6	43587578	43587778	0.393	POLH
chr16	14046154	14046384	0.303	ERCC4	chr6	43587842	43588084	0.444	POLH
chr16	23614570	23614827	0.310	PALB2	chr6	152265305	152265551	0.555	ESR1
chr16	23614836	23615076	0.407	PALB2	chr6	152265322	152265569	0.556	ESR1
chr16	23619110	23619349	0.479	PALB2	chr6	152265335	152265582	0.548	ESR1
chr16	23625213	23625413	0.398	PALB2	chr6	152265349	152265597	0.562	ESR1
chr16	23632741	23632891	0.391	PALB2	chr6	152332663	152332910	0.444	ESR1

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr16	23634215	23634415	0.393	PALB2	chr6	152332707	152332937	0.463	ESR1
chr16	23635260	23635465	0.374	PALB2	chr6	152332732	152332961	0.483	ESR1
chr16	23637513	23637713	0.458	PALB2	chr6	152415449	152415694	0.553	ESR1
chr16	23640440	23640682	0.370	PALB2	chr6	152415449	152415729	0.555	ESR1
chr16	23640927	23641175	0.470	PALB2	chr6	152415452	152415694	0.556	ESR1
chr16	23641292	23641502	0.431	PALB2	chr6	152415469	152415763	0.542	ESR1
chr16	23641570	23641813	0.385	PALB2	chr6	152419792	152420036	0.576	ESR1
chr16	23646217	23646416	0.470	PALB2	chr6	152419822	152420047	0.575	ESR1
chr16	23646250	23646449	0.460	PALB2	chr6	152419877	152420111	0.591	ESR1
chr16	23646427	23646636	0.390	PALB2	chr7	6029374	6029583	0.367	PMS2
chr16	23646623	23646823	0.403	PALB2	chr7	6035119	6035348	0.387	PMS2
chr16	23646780	23647008	0.345	PALB2	chr7	6036912	6037112	0.378	PMS2
chr16	23646984	23647228	0.400	PALB2	chr7	6038718	6039008	0.430	PMS2
chr16	23647144	23647434	0.385	PALB2	chr7	55241468	55241710	0.564	EGFR
chr16	23647358	23647558	0.483	PALB2	chr7	55241542	55241789	0.565	EGFR
chr16	23647369	23647610	0.467	PALB2	chr7	55241576	55241746	0.526	EGFR
chr16	23649127	23649357	0.355	PALB2	chr7	55241613	55241853	0.531	EGFR
chr16	23649265	23649465	0.358	PALB2	chr7	55242269	55242500	0.509	EGFR
chr16	23652430	23652650	0.692	PALB2	chr7	55242271	55242505	0.506	EGFR
chr16	23652647	23652887	0.647	PALB2	chr7	55242272	55242520	0.506	EGFR
chr16	68772169	68772389	0.679	CDH1	chr7	55242280	55242532	0.506	EGFR
chr16	68835529	68835729	0.463	CDH1	chr7	55242319	55242558	0.496	EGFR
chr16	68835564	68835767	0.485	CDH1	chr7	55242332	55242584	0.490	EGFR
chr16	68842243	68842453	0.469	CDH1	chr7	55248852	55249080	0.585	EGFR
chr16	68842518	68842718	0.423	CDH1	chr7	55248896	55249120	0.622	EGFR
chr16	68844017	68844227	0.512	CDH1	chr7	55248933	55249182	0.600	EGFR
chr16	68845519	68845719	0.483	CDH1	chr7	55248937	55249187	0.598	EGFR
chr16	68845706	68845945	0.517	CDH1	chr7	55248961	55249208	0.597	EGFR
chr16	68845947	68846147	0.502	CDH1	chr7	55259335	55259571	0.523	EGFR
chr16	68846157	68846377	0.416	CDH1	chr7	55259337	55259586	0.532	EGFR
chr16	68847216	68847450	0.477	CDH1	chr7	55259356	55259602	0.534	EGFR
chr16	68849385	68849585	0.488	CDH1	chr7	55259368	55259570	0.537	EGFR
chr16	68849423	68849649	0.529	CDH1	chr7	55259391	55259640	0.544	EGFR
chr16	68853169	68853348	0.522	CDH1	chr7	116411722	116411963	0.417	MET
chr16	68855861	68856061	0.453	CDH1	chr7	116411832	116412076	0.424	MET
chr16	68856071	68856271	0.488	CDH1	chr7	116411854	116412102	0.410	MET
chr16	68856802	68857067	0.560	CDH1	chr7	116411942	116412183	0.347	MET
chr16	68857287	68857494	0.481	CDH1	chr7	140453006	140453257	0.381	BRAF
chr16	68862023	68862255	0.511	CDH1	chr7	140453042	140453283	0.364	BRAF
chr16	68863473	68863683	0.488	CDH1	chr7	140453060	140453259	0.385	BRAF
chr16	68867121	68867366	0.488	CDH1	chr7	140453085	140453319	0.336	BRAF

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr16	68867369	68867599	0.476	CDH1	chr7	140453086	140453335	0.340	BRAF
chr16	89804046	89804215	0.553	FANCA	chr7	140453105	140453353	0.329	BRAF
chr16	89804303	89804513	0.592	FANCA	chr7	140481224	140481471	0.355	BRAF
chr16	89804648	89804858	0.635	FANCA	chr7	140481234	140481475	0.360	BRAF
chr16	89804928	89805172	0.596	FANCA	chr7	140481251	140481496	0.358	BRAF
chr16	89805241	89805441	0.498	FANCA	chr7	140481263	140481507	0.363	BRAF
chr16	89805462	89805662	0.612	FANCA	chr8	90947700	90947947	0.319	NBN
chr16	89805672	89805892	0.548	FANCA	chr8	90949123	90949343	0.326	NBN
chr16	89806299	89806509	0.502	FANCA	chr8	90955446	90955690	0.351	NBN
chr16	89807188	89807437	0.364	FANCA	chr8	90958290	90958510	0.321	NBN
chr16	89809197	89809432	0.542	FANCA	chr8	90959971	90960119	0.329	NBN
chr16	89811314	89811494	0.646	FANCA	chr8	90965407	90965703	0.347	NBN
chr16	89812889	89813109	0.557	FANCA	chr8	90965709	90965960	0.333	NBN
chr16	89813161	89813385	0.551	FANCA	chr8	90967522	90967722	0.388	NBN
chr16	89814966	89815166	0.587	FANCA	chr8	90967762	90967962	0.299	NBN
chr16	89816227	89816392	0.608	FANCA	chr8	90970951	90971177	0.414	NBN
chr16	89818546	89818699	0.416	FANCA	chr8	90976592	90976816	0.324	NBN
chr16	89825033	89825256	0.563	FANCA	chr8	90976592	90976817	0.323	NBN
chr16	89825068	89825276	0.545	FANCA	chr8	90982598	90982805	0.385	NBN
chr16	89828413	89828604	0.396	FANCA	chr8	90983304	90983514	0.308	NBN
chr16	89831297	89831493	0.533	FANCA	chr8	90990344	90990544	0.318	NBN
chr16	89833531	89833695	0.358	FANCA	chr8	90992886	90993086	0.323	NBN
chr16	89836321	89836521	0.617	FANCA	chr8	90993103	90993303	0.284	NBN
chr16	89836550	89836790	0.598	FANCA	chr8	90993522	90993742	0.321	NBN
chr16	89836823	89837062	0.604	FANCA	chr8	90994780	90995004	0.347	NBN
chr16	89836842	89837075	0.615	FANCA	chr8	90996593	90996859	0.678	NBN
chr16	89836876	89837138	0.635	FANCA	chr9	5073651	5073873	0.354	JAK2
chr16	89836882	89837082	0.627	FANCA	chr9	21968200	21968432	0.545	CDKN2A
chr16	89836894	89837156	0.627	FANCA	chr9	21970919	21971216	0.721	CDKN2A
chr16	89838040	89838261	0.514	FANCA	chr9	21970920	21971216	0.721	CDKN2A
chr16	89839593	89839838	0.573	FANCA	chr9	21973486	21973718	0.365	CDKN2A
chr16	89842062	89842262	0.498	FANCA	chr9	21974363	21974602	0.500	CDKN2A
chr16	89845140	89845350	0.483	FANCA	chr9	21994083	21994336	0.654	CDKN2A
chr16	89845256	89845456	0.527	FANCA	chr9	21994085	21994334	0.656	CDKN2A
chr16	89846317	89846557	0.498	FANCA	chr9	35073773	35074045	0.432	FANCG
chr16	89849141	89849341	0.502	FANCA	chr9	35074052	35074258	0.517	FANCG
chr16	89849323	89849591	0.554	FANCA	chr9	35074248	35074484	0.565	FANCG
chr16	89857774	89858016	0.560	FANCA	chr9	35074847	35075072	0.535	FANCG
chr16	89858250	89858450	0.567	FANCA	chr9	35075125	35075335	0.493	FANCG
chr16	89858752	89858951	0.555	FANCA	chr9	35075354	35075564	0.531	FANCG
chr16	89862215	89862425	0.512	FANCA	chr9	35075451	35075651	0.562	FANCG

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr16	89865452	89865652	0.532	FANCA	chr9	35075668	35075868	0.587	FANCG
chr16	89865648	89865886	0.498	FANCA	chr9	35075897	35076097	0.557	FANCG
chr16	89865874	89866074	0.408	FANCA	chr9	35076388	35076632	0.494	FANCG
chr16	89869678	89869909	0.461	FANCA	chr9	35076699	35076959	0.529	FANCG
chr16	89871619	89871819	0.522	FANCA	chr9	35076908	35077108	0.537	FANCG
chr16	89874567	89874718	0.375	FANCA	chr9	35077204	35077404	0.517	FANCG
chr16	89877021	89877274	0.382	FANCA	chr9	35078145	35078385	0.593	FANCG
chr16	89877278	89877525	0.520	FANCA	chr9	35078512	35078712	0.522	FANCG
chr16	89880876	89881036	0.342	FANCA	chr9	35079068	35079268	0.587	FANCG
chr16	89882268	89882508	0.564	FANCA	chr9	35079437	35079667	0.671	FANCG
chr17	7572710	7572941	0.547	TP53	chr9	35079767	35079970	0.667	FANCG
chr17	7572841	7573094	0.524	TP53	chr9	35079828	35080069	0.702	FANCG
chr17	7573785	7574015	0.571	TP53	chr9	35079839	35080069	0.706	FANCG
chr17	7573785	7574050	0.583	TP53	chr9	35079923	35080159	0.667	FANCG
chr17	7573803	7574050	0.593	TP53	chr9	80336120	80336372	0.478	GNAQ
chr17	7573811	7574017	0.580	TP53	chr9	80336121	80336372	0.476	GNAQ
chr17	7576734	7576934	0.468	TP53	chr9	80336223	80336472	0.500	GNAQ
chr17	7576933	7577155	0.552	TP53	chr9	80336253	80336500	0.484	GNAQ
chr17	7576951	7577151	0.557	TP53	chr9	80336259	80336500	0.483	GNAQ
chr17	7576970	7577197	0.548	TP53	chr9	80409367	80409598	0.353	GNAQ
chr17	7576998	7577191	0.552	TP53	chr9	80409379	80409628	0.352	GNAQ
chr17	7576998	7577241	0.529	TP53	chr9	97863312	97863512	0.572	FANCC
chr17	7576998	7577242	0.531	TP53	chr9	97863840	97864111	0.548	FANCC
chr17	7577014	7577263	0.532	TP53	chr9	97869338	97869594	0.595	FANCC
chr17	7577304	7577572	0.565	TP53	chr9	97872619	97872829	0.308	FANCC
chr17	7577329	7577570	0.574	TP53	chr9	97872955	97873165	0.398	FANCC
chr17	7577329	7577576	0.569	TP53	chr9	97873179	97873409	0.494	FANCC
chr17	7577346	7577570	0.596	TP53	chr9	97873711	97873957	0.587	FANCC
chr17	7577346	7577576	0.589	TP53	chr9	97876827	97877027	0.517	FANCC
chr17	7577371	7577620	0.564	TP53	chr9	97879613	97879852	0.404	FANCC
chr17	7577398	7577598	0.572	TP53	chr9	97887262	97887462	0.403	FANCC
chr17	7578196	7578426	0.563	TP53	chr9	97888682	97888882	0.423	FANCC
chr17	7578263	7578502	0.629	TP53	chr9	97897551	97897761	0.417	FANCC
chr17	7578283	7578494	0.637	TP53	chr9	97897761	97897961	0.313	FANCC
chr17	7578298	7578566	0.617	TP53	chr9	97912208	97912455	0.456	FANCC
chr17	7578299	7578502	0.642	TP53	chr9	97933298	97933498	0.363	FANCC
chr17	7578363	7578562	0.615	TP53	chr9	97934219	97934419	0.333	FANCC
chr17	7578363	7578598	0.597	TP53	chr9	98002823	98003043	0.321	FANCC
chr17	7579266	7579515	0.624	TP53	chr9	98009694	98009940	0.328	FANCC
chr17	7579311	7579460	0.620	TP53	chr9	98011375	98011575	0.418	FANCC
chr17	7579326	7579526	0.627	TP53	chr9	98011585	98011785	0.433	FANCC

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr17	7579332	7579550	0.616	TP53	chr9	98079868	98080148	0.669	FANCC
chr17	7579817	7579987	0.556	TP53	chr9	100437190	100437390	0.428	XPA
chr17	7590681	7590919	0.573	TP53	chr9	100437359	100437558	0.475	XPA
chr17	33426833	33427064	0.474	RAD51D	chr9	100437525	100437765	0.299	XPA
chr17	33427044	33427283	0.500	RAD51D	chr9	100437793	100437993	0.383	XPA
chr17	33427269	33427513	0.437	RAD51D	chr9	100444474	100444677	0.397	XPA
chr17	33427477	33427725	0.518	RAD51D	chr9	100447108	100447308	0.348	XPA
chr17	33427706	33427935	0.504	RAD51D	chr9	100449321	100449540	0.309	XPA
chr17	33427916	33428162	0.498	RAD51D	chr9	100451744	100451944	0.323	XPA
chr17	33428100	33428345	0.577	RAD51D	chr9	100455831	100456031	0.328	XPA
chr17	33430196	33430419	0.567	RAD51D	chr9	100459275	100459499	0.720	XPA
chr17	33430401	33430620	0.573	RAD51D	chr9	100459396	100459601	0.728	XPA
chr17	33433344	33433506	0.564	RAD51D	chr9	100459482	100459691	0.724	XPA
chr17	33433897	33434133	0.489	RAD51D	chr9	100459482	100459695	0.720	XPA
chr17	33434295	33434532	0.500	RAD51D	chr9	100459482	100459721	0.721	XPA
chr17	33445499	33445672	0.586	RAD51D	chrX	14861796	14861980	0.416	FANCB
chr17	33446550	33446780	0.662	RAD51D	chrX	14861961	14862165	0.322	FANCB
chr17	37868175	37868423	0.606	ERBB2	chrX	14862588	14862788	0.368	FANCB
chr17	37868177	37868424	0.605	ERBB2	chrX	14862805	14863005	0.294	FANCB
chr17	37868184	37868432	0.614	ERBB2	chrX	14862977	14863177	0.358	FANCB
chr17	37868192	37868432	0.622	ERBB2	chrX	14863227	14863447	0.403	FANCB
chr17	41226314	41226567	0.433	BRCA1	chrX	14868691	14868896	0.306	FANCB
chr17	41228463	41228682	0.368	BRCA1	chrX	14871130	14871330	0.313	FANCB
chr17	41231290	41231560	0.432	BRCA1	chrX	14875743	14875993	0.307	FANCB
chr17	41234185	41234455	0.435	BRCA1	chrX	14877225	14877425	0.313	FANCB
chr17	41234392	41234631	0.438	BRCA1	chrX	14877435	14877635	0.274	FANCB
chr17	41242906	41243146	0.444	BRCA1	chrX	14882681	14882881	0.393	FANCB
chr17	41243450	41243690	0.411	BRCA1	chrX	14882885	14883085	0.328	FANCB
chr17	41243675	41243921	0.397	BRCA1	chrX	14883089	14883289	0.383	FANCB
chr17	41243914	41244153	0.433	BRCA1	chrX	14883275	14883501	0.291	FANCB
chr17	41244048	41244300	0.368	BRCA1	chrX	14883493	14883735	0.350	FANCB
chr17	41244075	41244265	0.366	BRCA1	chrX	14887070	14887270	0.323	FANCB
chr17	41244473	41244712	0.371	BRCA1	chrX	14890941	14891170	0.578	FANCB
chr17	41244534	41244778	0.376	BRCA1	chrX	47426013	47426262	0.636	ARAF
chr17	41244766	41245013	0.387	BRCA1	chrX	47426015	47426263	0.635	ARAF
chr17	41245011	41245240	0.409	BRCA1	chrX	47426016	47426262	0.640	ARAF
chr17	41245209	41245462	0.374	BRCA1	chrX	47426063	47426266	0.627	ARAF
chr17	41245347	41245586	0.404	BRCA1	chrX	66765925	66766173	0.635	AR
chr17	41245598	41245827	0.370	BRCA1	chrX	66765934	66766173	0.638	AR
chr17	41245825	41246064	0.375	BRCA1	chrX	66766002	66766226	0.671	AR
chr17	41246061	41246310	0.376	BRCA1	chrX	66766013	66766226	0.682	AR

Chr.	Start	Stop	GC	Gene	Chr.	Start	Stop	GC	Gene
chr17	41246304	41246553	0.416	BRCA1	chrX	66931238	66931486	0.522	AR
chr17	41246534	41246786	0.423	BRCA1	chrX	66931245	66931461	0.525	AR
chr17	41246546	41246786	0.427	BRCA1	chrX	66931245	66931492	0.524	AR
chr17	41246595	41246842	0.419	BRCA1	chrX	66931246	66931484	0.523	AR
chr17	41246643	41246890	0.403	BRCA1	chrX	66937264	66937498	0.536	AR
chr17	41246709	41246956	0.379	BRCA1	chrX	66937327	66937559	0.532	AR
chr17	41246794	41247027	0.338	BRCA1	chrX	66937327	66937576	0.524	AR
chr17	41247801	41248006	0.403	BRCA1	chrX	66943491	66943695	0.468	AR
chr17	41249211	41249311	0.356	BRCA1	chrX	66943494	66943696	0.473	AR
chr17	41251673	41251893	0.380	BRCA1	chrX	66943515	66943684	0.476	AR
chr17	41251732	41251945	0.397	BRCA1	chrX	66943534	66943689	0.474	AR

Detailed Description

[0023] The invention pertains to a method for analyzing tumor biomarker sequences that involves hybridization-based enrichment of selected target regions across the human genome in a multiplexed panel assay, followed by quantification, coupled with a novel bioinformatics and mathematical analysis pipeline. An overview of the method is shown schematically in Figure 1.

[0024] In-solution hybridization enrichment has been used in the past to enrich specific regions of interest prior to sequencing (see e.g., Meyer, M and Kirchner, M. (2010) Cold Spring Harb. Protoc. 2010(6):pdbprot5448; Liao, G.J. et al. (2012) PLoS One 7:e38154; Maricic, T. et al. (2010) PLoS One 5:e14004; Tewhey, R. et al.(2009) Genome Biol. 10:R116; Tsangaras, K. et al. (2014) PLoS One 9:e109101; PCT Publication WO 2016/189388; US Patent Publication 2016/0340733; Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855). However, for the methods of the invention, the target sequences (referred to as TArget Capture Sequences, or TACS) used to enrich for specific regions of interest have been optimized for maximum efficiency, specificity and accuracy and, furthermore, in certain embodiments are used in families of TACS, comprising a plurality of members that bind to the same tumor biomarker sequence but with differing start and/or stop positions, such that enrichment of the tumor biomarker sequences of interest is significantly improved compared to use of a single TACS binding to the genomic sequence. An example of a configuration of such families of TACS is illustrated schematically in Figure 3, showing that the different start and/or stop positions of the members of the TACS family when bound to the genomic sequence of interest results in a staggered binding pattern for the family members.

[0025] The use of families of TACS with the TACS pool that bind to each target sequence of interest, as compared to use of a single TACS within the TACS pool that binds to each target sequence of interest, significantly increases enrichment for the target sequences of interest, as evidenced by a greater than 50% average increase in read-depth for the family of TACS versus a single TACS. Comparison of use of a family of TACS versus a single TACS, and the significantly improved read-depth that was observed, is described in detail in Example 5.

Tumor Biomarker Detection

[0026] The methods and kits of the disclosure are used in the analysis of tumor biomarkers in biological samples. As described in detail in Examples 6-9, the methods of the invention can be used for the detection of large panels of tumor biomarkers at tumor loads as low as 0.1% and can detect tumor biomarkers in both tumor tissue

and in liquid biopsy samples from tumor patients. Accordingly, in one aspect, the invention pertains to a method of detecting one or more tumor biomarkers in a DNA sample from a subject having or suspected of having a tumor, the method comprising:

1. (a) preparing a sequencing library from the DNA sample;(b) hybridizing the sequencing library to a pool of double-stranded TArget Capture Sequences (TACS) that bind to one or more tumor biomarker sequences of interest, wherein:(i) each member sequence within the pool of TACS is between 150-260 base pairs in length, each member sequence having a 5' end and a 3' end;(ii) preferably and optionally each member sequence binds to the tumor biomarker sequence of interest at least 50 base pairs away, on both the 5' end and the 3' end, from regions harboring Copy Number Variations (CNVs), Segmental duplications or repetitive DNA elements; and(iii) the GC content of the pool of TACS is between 19% and 80%, as determined by calculating the GC content of each member within the pool of TACS; (iv) the pool of TACS comprises a plurality of TACS families each directed to a different tumor biomarker sequence of interest, wherein each TACS family comprises a plurality of member sequences, wherein each member sequence binds to the same tumor biomarker sequence of interest but has different start and/or stop positions with respect to a reference coordinate system for the tumor biomarker sequence of interest, optionally wherein the start and/or stop positions for the member sequences within a TACS family, with respect to a reference coordinate system for the tumor biomarker are staggered by 5 to 10 base pairs;(c) isolating members of the sequencing library that bind to the pool of TACS to obtain an enriched library;(d) amplifying and sequencing the enriched library;(e) aligning the enriched library to a reference genome thereby obtaining read-depth information and allelic counts; and(f) performing statistical analysis on the enriched library sequences, optionally utilizing only fragments of a specific size range, to thereby detect the tumor biomarker(s) in the DNA sample, wherein sequencing of the enriched library provides a read-depth for the genomic sequences of interest and read-depths for reference loci and the statistical analysis comprises applying an algorithm that tests sequentially the read-depth of the loci of from the genomic sequences of interest against the read-depth of the reference loci, the algorithm comprising steps for:(a) removal of inadequately sequenced loci,(b) GC-content bias alleviation, and(c) genetic status determination; and/or wherein sequencing of the enriched library provides the number and size of sequenced fragments for TACS-specific coordinates and the statistical analysis comprises applying an algorithm that tests sequentially the fragment-size proportion for the genomic sequence of interest against the fragment-size proportion of the reference loci, the algorithm comprising steps of:(a) removal of fragment-size outliers,(b) fragment-size proportion calculation, and(c) genetic status determination.

[0027] In one embodiment, the pool of TACS comprises a plurality of TACS families, wherein each member of a TACS family binds to the same tumor biomarker sequence of interest but with different start and/or stop positions on the sequence with respect to a reference coordinate system (i.e., binding of TACS family members to the target sequence is staggered) to thereby enrich for target sequences of interest, followed by massive parallel sequencing and statistical analysis of the enriched population. Typically, the reference coordinate system that is used for analyzing human genomic DNA is the human reference genome built hg19, which is publically available in the art, although other versions may be used. Alternatively, the reference coordinate system can be an artificially created genome based on built hg19 that contains only the genomic sequences of interest. Exemplary non-limiting examples of start/stop positions for TACS that bind to chromosome 13, 18, 21, X or Y are shown in Figure 2. Exemplary non-limiting examples of start/stop positions for TACS that bind to NRAS on chromosome 1, PI3KCA on chromosome 3, EGFR on chromosome 7 or KRAS on chromosome 12 (as non-limiting examples of tumor biomarkers) are shown in Figure 10.

[0028] The TACS-enrichment based method of the disclosure can be used in the detection of a wide variety of genetic abnormalities. In one embodiment, the genetic abnormality is a chromosomal aneuploidy (such as a trisomy, a partial trisomy or a monosomy). In other embodiments, the genomic abnormality is a structural abnormality, including but not limited to copy number changes including microdeletions and microduplications, insertions, translocations, inversions and small-size mutations including point mutations and mutational

signatures. In another embodiment, the genetic abnormality is a chromosomal mosaicism.

[0029] Further aspects and features of the methods of the disclosure are described in the subsections below.

Target Capture Sequence Design

[0030] As used herein, the term "Target Capture Sequences" or "TACS" refers to short DNA sequences that are complementary to the region(s) of interest on a genomic sequence(s) of interest (e.g., chromosome(s) of interest) and which are used as "bait" to capture and enrich the region of interest from a large library of sequences, such as a whole genomic sequencing library prepared from a biological sample. In addition to the features of the families of TACS described above (e.g., staggered binding to the genomic sequence of interest), a pool of TACS is used for enrichment wherein the sequences within the pool have been optimized with regard to: (i) the length of the sequences; (ii) the distribution of the TACS across the region(s) of interest; and (iii) the GC content of the TACS. The number of sequences within the TACS pool (pool size) has also been optimized.

[0031] It has been discovered that TACS having a length of 150-260 base pairs are optimal to maximize enrichment efficiency. In various other embodiments, each sequence within the pool of TACS is between 150-260 base pairs or 200-260 base pairs in length. In preferred embodiments, the length of the TACS within the pool is 250 base pairs or is 260 base pairs.

[0032] The distribution of the TACS across each region or chromosome of interest has been optimized to avoid, if applicable, high copy repeats, low copy repeats and copy number variants, while at the same time also being able to target informative single nucleotide polymorphisms (SNPs) in order to enable both aneuploidy, or structural copy number change detection, and fraction of interest estimation. Accordingly, each sequence within the TACS pool is designed such that the 5' end and the 3' end are each at least 50 base pairs away from regions in the genome that are known to harbor one or more of the following genomic elements: Copy Number Variations (CNVs), Segmental duplications and/or repetitive DNA elements (such as transposable elements or tandem repeat areas). In various other embodiments, each sequence within the TACS pool is designed such that the 5' end and the 3' end are each at least 50, 100, 150, 200, 250, 300, 400 or 500 base pairs away from regions in the genome that are known to harbor one or more of the aforementioned elements.

[0033] The term "Copy Number Variations" is a term of art that refers to a form of structural variation in the human genome in which there can be alterations in the DNA of the genome in different individuals that can result in a fewer or greater than normal number of a section(s) of the genome in certain individuals. CNVs correspond to relatively large regions of the genome that may be deleted (e.g., a section that normally is A-B-C-D can be A-B-D) or may be duplicated (e.g., a section that normally is A-B-C-D can be A-B-C-C-D). CNVs account for roughly 13% of the human genome, with each variation ranging in size from about 1 kilobase to several megabases in size.

[0034] The term "Segmental duplications" (also known as "low-copy repeats") is also a term of art that refers to blocks of DNA that range from about 1 to 400 kilobases in length that occur at more than one site within the genome and typically share a high level (greater than 90%) of sequence identity. Segmental duplications are reviewed in, for example, Eichler. E.E. (2001) Trends Genet. 17:661-669.

[0035] The term "repetitive DNA elements" (also known as "repeat DNA" or "repeated DNA") is also a term of art that refers to patterns of DNA that occur in multiple copies throughout the genome. The term "repetitive DNA element" encompasses terminal repeats, tandem repeats and interspersed repeats, including transposable elements. Repetitive DNA elements in NGS is discussed further in, for example, Todd, J. et al. (2012) Nature Reviews Genet. 13:36-46.

[0036] The TACS are designed with specific GC content characteristics in order to minimize data GC bias and to

allow a custom and innovative data analysis pipeline. It has been determined that TACS with a GC content of 19-80% achieve optimal enrichment and perform best with cell free DNA. Within the pool of TACS, different sequences can have different % GC content, although to be selected for inclusion with the pool, the % GC content of each sequence is chosen as between 19-80%, as determined by calculating the GC content of each member within each family of TACS. That is, every member within each family of TACS has a % GC content within the given percentage range (e.g., between 19-80% GC content).

[0037] In some instances, the pool of TACS (i.e., each member within each family of TACS) may be chosen so as to define a different % GC content range, deemed to be more suitable for the assessment of specific genetic abnormalities. Non-limiting examples of various % GC content ranges, can be between 19% and 80%, or between 19% and 79%, or between 19% and 78%, or between 19% and 77%, or between 19% and 76%, or between 19% and 75%, or between 19% and 74%, or between 19% and 73%, or between 19% and 72%, or between 19% and 71%, or between 19% and 70%, or between 19% and 69%, or between 19% and 68%, or between 19% and 67%, or between 19% and 66%, or between 19% and 65%, or between 19% and 64%, or between 19% and 63%, or between 19% and 62%, or between 19% and 61%, or between 19% and 60%, or between 19% and 59%, or between 19% and 58%, or between 19% and 57%, or between 19% and 56%, or between 19% and 55%, or between 19% and 54%, or between 19% and 53%, or between 19% and 52%, or between 19% and 51%, or between 19% and 50%, or between 19% and 49%, or between 19% and 48%, or between 19% and 47%, or between 19% and 46%, or between 19% and 45%, or between 19% and 44%, or between 19% and 43%, or between 19% and 42%, or between 19% and 41%, or between 19% and 40%.

[0038] As described in further detail below with respect to one embodiment of the data analysis, following amplification and sequencing of the enriched sequences, the test loci and reference loci can then be "matched" or grouped together according to their % GC content (e.g., test loci with a % GC content of 40% is matched with reference loci with a % GC content of 40%). It is appreciated that the % GC content matching procedure may allow slight variation in the allowed matched % GC range. A non-limiting instance, and with reference to the previously described example in text, a test locus with % GC content of 40% could be matched with reference loci of % GC ranging from 39-41%, thereby encompassing the test locus % GC within a suitable range.

[0039] To prepare a pool of TACS having the optimized criteria set forth above with respect to size, placement within the human genome and % GC content, both manual and computerized analysis methods known in the art can be applied to the analysis of the human reference genome. In one embodiment, a semi-automatic method is implemented where regions are firstly manually designed based on the human reference genome build 19 (hg19) ensuring that, if applicable, the aforementioned repetitive regions are avoided and subsequently are curated for GC-content using software that computes the % GC-content of each region based on its coordinates on the human reference genome build 19 (hg19). In another embodiment, custom-built software is used to analyses the human reference genome in order to identify suitable TACS regions that fulfill certain criteria, such as but not limited to, % GC content, proximity to repetitive regions and/or proximity to other TACS.

[0040] The number of TACS in the pool has been carefully examined and adjusted to achieve the best balance between result robustness and assay cost/throughput. The pool typically contains at least 800 or more TACS, but can include more, such as 1500 or more TACS, 2000 or more TACS or 2500 or more TACS or 3500 or more TACS or 5000 or more TACS. It has been found that an optimal number of TACS in the pool is 5000. It will be appreciated by the ordinarily skilled artisan that a slight variation in pool size typically can be used without altering the results (e.g., the addition or removal of a small number of TACS); accordingly, the number sizes of the pool given herein are to be considered "about" or "approximate", allowing for some slight variation (e.g., 1-5%) in size. Thus, for example, a pool size of "1600 sequences" is intended to refer to "about 1600 sequences" or "approximately 1600 sequences", such that, for example, 1590 or 1610 sequences is also encompassed.

[0041] In view of the foregoing, in another aspect, the invention provides a method for preparing a pool of TACS for use in the method of the invention for detecting risk of a chromosomal and/or other genetic abnormality, wherein the method for preparing the pool of TACS comprises: selecting regions in one or more chromosomes of

interest having the criteria set forth above (e.g., at least 50 base pairs away on either end from the aforementioned repetitive sequences and a GC content of between 19% and 80%, as determined by calculating the GC content of each member within each family of TACS), preparing primers that amplify sequences that hybridize to the selected regions, and amplifying the sequences, wherein each sequence is 100-500 base pairs in length.

[0042] For use in the methods of the disclosure, the pool of TACS typically is fixed to a solid support, such as beads (such as magnetic beads) or a column. In one embodiment, the pool of TACS are labeled with biotin and are bound to magnetic beads coated with a biotin-binding substance, such as streptavidin or avidin, to thereby fix the pool of TACS to a solid support. Other suitable binding systems for fixing the pool of TACS to a solid support (such as beads or column) are known to the skilled artisan and readily available in the art. When magnetic beads are used as the solid support, sequences that bind to the TACS affixed to the beads can be separated magnetically from those sequences that do not bind to the TACS.

Families of TACS

[0043] In one embodiment, the pool of TACS comprises a plurality of TACS families directed to different tumor biomarker sequences of interest. Each TACS family comprises a plurality of members that bind to the same tumor biomarker sequence of interest but having different start and/or stop positions with respect to a reference coordinate system for the genomic sequence of interest. Typically, the reference coordinate system that is used for analyzing human genomic DNA is the human reference genome built hg19, which is publically available in the art, but other coordinate systems may also be used. Alternatively, the reference coordinate system can be an artificially created genome based on publically available coordinate systems, such as for example built hg19 of the human genome, that contains only the genomic sequences of interest. Exemplary non-limiting examples of start/stop positions for TACS that bind to chromosome 13, 18, 21, X or Y are shown in Figure 2.

[0044] Each TACS family comprises at least 2 members that bind to the same genomic sequence of interest. In various embodiments, each TACS family comprises at least 2 member sequences, or at least 3 member sequences, or at least 4 member sequences, or at least 5 member sequences, or at least 6 member sequences, or at least 7 member sequences, or at least 8 member sequence, or at least 9 member sequences, or at least 10 member sequences. In various embodiments, each TACS family comprises 2 member sequences, or 3 member sequences, or 4 member sequences, or 5 member sequences, or 6 member sequences, or 7 member sequences, or 8 member sequences, or 9 member sequences, or 10 member sequences. In various embodiments, the plurality of TACS families comprises different families having different numbers of member sequences. For example, a pool of TACS can comprise one TACS family that comprises 3 member sequences, another TACS family that comprises 4 member sequences, and yet another TACS family that comprises 5 member sequences, and the like. In one embodiment, a TACS family comprises 3-5 member sequences. In another embodiment, the TACS family comprises 4 member sequences.

[0045] The pool of TACS comprises a plurality of TACS families. Thus, a pool of TACS comprises at least 2 TACS families. In various embodiments, a pool of TACS comprises at least 3 different TACS families, or at least 5 different TACS families, or at least 10 different TACS families, or at least 50 different TACS families, or at least 100 different TACS families, or at least 500 different TACS families, or at least 1000 different TACS families, or at least 2000 TACS families, or at least 4000 TACS families, or at least 5000 TACS families.

[0046] Each member within a family of TACS binds to the same genomic region of interest but with different start and/or stop positions, with respect to a reference coordinate system for the genomic sequence of interest, such that the binding pattern of the members of the TACS family is staggered (for example see Figure 3). In various embodiments, the start and/or stop positions are staggered by 5-10 base pairs. In one embodiment, the start and/or stop positions are staggered by 5 base pairs. In another embodiment, the start and/or stop positions are staggered by 10 base pairs.

Sample Collection and Preparation

[0047] The methods of the invention can be used with a variety of biological samples. Essentially any biological sample containing DNA, and in particular cell-free DNA (cfDNA), can be used as the sample in the methods, allowing for genetic analysis of the DNA therein. For example, a peripheral whole blood sample can be obtained from a subject and plasma can be obtained from the whole blood sample by standard methods. Total cell free DNA can then be extracted from the sample using standard techniques, non-limiting examples of which include a Qiasymphony protocol (Qiagen) suitable for cell free DNA isolation or any other manual or automated extraction method suitable for cell free DNA isolation.

[0048] For tumor biomarker detection, the sample is a biological sample obtained from a patient having or suspected of having a tumor. In one embodiment, the DNA sample comprises cell free tumor DNA (cftDNA). In one embodiment, the oncology sample is a sample of tissue (e.g., from a tumor biopsy). In another embodiment, the sample is a patient's urine, sputum, ascites, cerebrospinal fluid or pleural effusion. In another embodiment, the oncology sample is a patient plasma sample, prepared from patient peripheral blood. Thus, the sample can be a liquid biopsy sample that is obtained non-invasively from a patient's blood sample, thereby potentially allowing for early detection of cancer prior to development of a detectable or palpable tumor, or can be from a tissue that has or is suspected of having cancer. In another embodiment, the oncology sample is a patient's healthy tissue such as buffy coat, prepared from patient peripheral blood, or buccal swab or healthy tissue adjacent to the tumor or another source of healthy cells. Thus, the healthy cells can provide a source of DNA that allows for detection of germline mutations and comparison with tumor DNA.

[0049] For the biological sample preparation, typically cells are lysed and DNA is extracted using standard techniques known in the art, a non-limiting example of which is the Qiagen DNeasy Blood and Tissue protocol. In another embodiment, cell free DNA is isolated from plasma using standard techniques, a non-limiting example of which is the Qiasymphony (Qiagen) protocol.

[0050] Following isolation, the cell free DNA of the sample is used for sequencing library construction to make the sample compatible with a downstream sequencing technology, such as Next Generation Sequencing. Typically this involves ligation of adapters onto the ends of the cell free DNA fragments, followed by amplification. Sequencing library preparation kits are commercially available. A non-limiting exemplary protocol for sequencing library preparation is described in detail in Example 1. In another embodiment, nuclear DNA (a non-limiting example of which is DNA extracted from tissue of buffy coat) is fragmented using standard techniques. A non-limiting example of DNA fragmentation is sonication. Fragmented nuclear DNA is then subjected to the same downstream procedures for cell free DNA described in this paragraph.

Enrichment by TACS Hybridization

[0051] The region(s) of interest on the chromosome(s) of interest (e.g., tumor biomarker sequences) is enriched by hybridizing the pool of TACS to the sequencing library, followed by isolation of those sequences within the sequencing library that bind to the TACS. To facilitate isolation of the desired, enriched sequences, typically the TACS sequences are modified in such a way that sequences that hybridize to the TACS can be separated from sequences that do not hybridize to the TACS. Typically, this is achieved by fixing the TACS to a solid support. This allows for physical separation of those sequences that bind the TACS from those sequences that do not bind the TACS. For example, each sequence within the pool of TACS can be labeled with biotin and the pool can then be bound to beads coated with a biotin-binding substance, such as streptavidin or avidin. In a preferred embodiment, the TACS are labeled with biotin and bound to streptavidin-coated magnetic beads. The ordinarily skilled artisan will appreciate, however, that other affinity binding systems are known in the art and can be used instead of biotin-streptavidin/avidin. For example, an antibody-based system can be used in which the TACS are

labeled with an antigen and then bound to antibody-coated beads. Moreover, the TACS can incorporate on one end a sequence tag and can be bound to a solid support via a complementary sequence on the solid support that hybridizes to the sequence tag. Furthermore in addition to magnetic beads, other types of solid supports can be used, such as polymer beads and the like.

[0052] In certain embodiments, the members of the sequencing library that bind to the pool of TACS are fully complementary to the TACS. In other embodiments, the members of the sequencing library that bind to the pool of TACS are partially complementary to the TACS. For example, in certain circumstances it may be desirable to utilize and analyze data that are from DNA fragments that are products of the enrichment process but that do not necessarily belong to the genomic regions of interest (i.e. such DNA fragments could bind to the TACS because of part homologies (partial complementarity) with the TACS and when sequenced would produce very low coverage throughout the genome in non-TACS coordinates).

[0053] Following enrichment of the sequence(s) of interest using the TACS, thereby forming an enriched library, the members of the enriched library are eluted from the solid support and are amplified and sequenced using standard methods known in the art. Next Generation Sequencing is typically used, although other sequencing technologies can also be employed, which provides very accurate counting in addition to sequence information. To detect genetic abnormalities, such as but not limited to, aneuploidies or structural copy number changes requires very accurate counting and NGS is a type of technology that enables very accurate counting. Accordingly, for the detection of genetic abnormalities, such as but not limited to, aneuploidies or structural copy number changes, other accurate counting methods, such as digital PCR and microarrays can also be used instead of NGS. Non-limiting exemplary protocols for amplification and sequencing of the enriched library are described in detail in Example 3.

Data Analysis

[0054] The information obtained from the sequencing of the enriched library can be analyzed using an innovative biomathematical/biostatistical data analysis pipeline. Details of an exemplary analysis using this pipeline are described in depth in Example 4, and in further detail below. Alternative data analysis approaches for different purposes are also provided herein. For example, data analysis approaches for analyzing oncology samples are described in detail in Example 6-9 and in the oncology section below.

[0055] The analysis pipeline described in Example 4 exploits the characteristics of the TACS, and the high-efficiency of the target capture enables efficient detection of aneuploidies or structural copy number changes, as well as other types of genetic abnormalities. In the analysis, first the sample's sequenced DNA fragments are aligned to the human reference genome. QC metrics are used to inspect the aligned sample's properties and decide whether the sample is suitable to undergo classification. These QC metrics can include, but are not limited to, analysis of the enrichment patterns of the loci of interest, such as for example the overall sequencing depth of the sample, the on-target sequencing output of the sample, TACS performance, GC bias expectation, fraction of interest quantification. For determining the risk of a chromosomal abnormality in the DNA of the sample, an innovative algorithm is applied. The steps of the algorithm include, but are not limited to, removal of inadequately sequenced loci, read-depth and fragment-size information extraction at TACS-specific coordinates, genetic (GC-content) bias alleviation and ploidy status classification.

[0056] Ploidy status determination can be achieved using one or more statistical methods, non-limiting examples of which include a t-test method, a bootstrap method, a permutation test and/or a binomial test of proportions and/or segmentation-based methods and/or combinations thereof. It will be appreciated by the ordinarily skilled artisan that the selection and application of tests to be included in ploidy status determination is based on the number of data points available. As such, the suitability of each test is determined by various factors such as, but not limited to, the number of TACS utilized and the respective application for GC bias alleviation, if applicable. Thus, the aforementioned methods are to be taken as examples of the types of statistical analysis that may be

employed and are not the only methods suitable for the determination of ploidy status. Typically, the statistical method results in a score value for the mixed sample and risk of the chromosomal abnormality in the DNA is detected when the score value for the mixed sample is above a reference threshold value.

[0057] In particular, one aspect of the statistical analysis involves quantifying and alleviating GC-content bias. In addition to the challenge of detecting small signal changes in DNA in the mixed sample, and/or other components of DNA of interest part of a mixed sample (for example, but not limited to, additional or less genetic material from certain chromosomal regions), the sequencing process itself introduces certain biases that can obscure signal detection. One such bias is the preferential sequencing/amplification of genetic regions based on their GC-content. As such, certain detection methods, such as but not limited to, read-depth based methods, need to account for such bias when examining sequencing data. Thus, the bias in the data needs to be quantified and, subsequently, suitable methods are applied to account for it such that genetic context dependencies cannot affect any statistical methods that may be used to quantify genetic abnormality risk.

[0058] For example, one method of quantifying the GC-content bias is to use a locally weighted scatterplot smoothing (LOESS) technique on the sequencing data. Each targeted locus may be defined by its sequencing read-depth output and its' GC-content. A line of best fit through these two variables, for a large set of loci, provides an estimate of the expected sequencing read-depth given the GC-content. Once this GC-bias quantification step is completed, the next step is to use this information to account for possible biases in the data. One method is to normalize the read-depth of all loci by their expected read-depth (based on each locus' GC-content). In principle, this unlinks the read-depth data from their genetic context and makes all data comparable. As such, data that are retrieved from different GC-content regions, such as for example, but not limited, to different chromosomes, can now be used in subsequent statistical tests for detection of any abnormalities. Thus, using the LOESS procedure, the GC bias is unlinked from the data prior to statistical testing. In one embodiment, the statistical analysis of the enriched library sequences comprises alleviating GC bias using a LOESS procedure.

[0059] In an alternative embodiment, the GC-content bias is quantified and alleviated by grouping together loci of similar (matching) GC-content. Thus, conceptually this method for alleviating GC-content bias comprises of three steps, as follows:

1. 1) identification and calculation of GC-content in the TACS;
2. 2) alleviation/accounting of GC-content bias using various matching/grouping procedures of the TACS; and
3. 3) calculation of risk of any genetic abnormalities that may be present in the fetus utilizing statistical and mathematical methods on datasets produced from step 2.

[0060] For the t-test method, the dataset is split into two groups; the test loci and the reference loci. For each group, subsets of groups are created where loci are categorized according to their GC-content as illustrated in a non-limiting example in the sample Table 1 below:

Table 1

GC	Reference loci read-depth	Test loci read-depth
40%	$x_1^{40}, x_2^{40}, \dots, x_{nx40}^{40}$	$y_1^{40}, y_2^{40}, \dots, y_{ny40}^{40}$
41%	$x_1^{41}, x_2^{41}, \dots, x_{nx41}^{41}$	$y_1^{41}, y_2^{41}, \dots, y_{ny41}^{41}$
42%	$x_1^{42}, x_2^{42}, \dots, x_{nx42}^{42}$	$y_1^{42}, y_2^{42}, \dots, y_{ny42}^{42}$
...	...	...

[0061] It is appreciated by the ordinarily skilled artisan that subgroup creation may involve encompassing a range of appropriate GC-content and/or a subset of loci that are defined by a given GC-content and/or GC-content range. Accordingly, the % GC content given in the non-limiting example of Table 1 are to be considered "about" or "approximate", allowing for some slight variation (e.g., 1-2%). Thus, for example, a % GC content of "40%" is intended to refer to "about 40%" or "approximately 40%", such that, for example, "39%-41%" GC-content loci may also be encompassed if deemed appropriate.

[0062] Hence, when referring to a particular GC-content it is understood that the reference and test loci subgroups may comprise of any number of loci related to a particular % GC content and/or range.

[0063] Subsequently, for each GC-content subgroup, a representative read-depth is calculated. A number of methods may be utilized to choose this such as, but not limited to, the mean, median or mode of each set. Thus, two vectors of representative read-depth are created where one corresponds to the reference loci and the other to the test loci (e.g., X_m , Y_m). In one embodiment, the two vectors may be tested against each other to identify significant differences in read-depth. In another embodiment, the difference of the two vectors may be used to assess if there are significant discrepancies between the test and reference loci. The sample is attributed the score of the test.

[0064] For statistical analysis using a bootstrap approach, the dataset is split into two groups, the test loci and the reference loci. The GC-content of each locus is then calculated. Then the following procedure is performed: A random locus is selected from the reference loci; its read-depth and GC-content are recorded. Subsequently, a random locus from the test loci is selected, with the only condition being that its' GC-content is similar to that of the reference locus. Its read-depth is recorded. It is appreciated by the ordinarily skilled artisan that GC-content similarity may encompass a range of suitable GC-content. As such, referral to a specific % GC content may be considered as "approximate" or "proximal" or "within a suitable range" (e.g., 1%-2%) encompassing the specific % GC content under investigation. Thus, a reference-test locus pair of similar GC-content is created. The difference of the reference-test pair is recorded, say E_1 . The loci are then replaced to their respective groups. This process is repeated until a bootstrap sample of the same size as the number of test TACS present is created. A representative read-depth of the bootstrap sample is estimated, say E_{μ} , and recorded. A number of methods may be utilized to do so, such as but not limited to, the mean, mode or median value of the vector, and/or multiples thereof.

[0065] The process described above is repeated as many times as necessary and a distribution of E_{μ} is created. The sample is then attributed a score that corresponds to a percentile of this distribution.

[0066] For statistical analysis using a permutation test, the dataset is sorted firstly into two groups, the test-loci and the reference loci. For each group, subsets of groups are created, where loci are categorized according to their GC-content similarity (see columns 2 and 3 of the non-limiting sample Table 2 below). The number of loci present in each test subgroup is also recorded. The loci of the test group are utilized to calculate an estimate of the test-group's read-depth, say Y_{obs} . A representative number from each GC-content subgroup may be selected to do so. Any number of methods may be used to provide a read-depth estimate, such as but not limited to, the mean, median or mode of the chosen loci.

Table 2

GC	Reference loci read-	Test loci read-depth	test loci	Merging of loci
40%	$x_1^{40}, x_2^{40}, \dots, x_{nx40}^{40}$	$y_1^{40}, y_2^{40}, \dots, y_{ny40}^{40}$	ny40	$x_1^{40}, \dots, x_{nx40}^{40}, y_1^{40}, \dots, y_{ny40}^{40}$
41%	$x_1^{41}, x_2^{41}, \dots, x_{nx41}^{41}$	$y_1^{41}, y_2^{41}, \dots, y_{ny41}^{41}$	ny41	$x_1^{41}, \dots, x_{nx41}^{41}, y_1^{41}, \dots, y_{ny41}^{41}$
42%	$x_1^{42}, x_2^{42}, \dots, x_{nx42}^{42}$	$y_1^{42}, y_2^{42}, \dots, y_{ny42}^{42}$	ny42	$x_1^{42}, \dots, x_{nx42}^{42}, y_1^{42}, \dots, y_{ny42}^{42}$

GC	Reference loci read-	Test loci read-depth	test loci	Merging of loci
...	...	...	...	...

[0067] A distribution to test Yobs is then built utilizing loci irrespective of their test or reference status as follows. The test and reference loci of each GC-content subgroup (see last column of sample Table 2) are combined to allow for calculation of a new read-depth estimate. From each merged subgroup a number of loci are chosen at random, where this number is upper-bounded by the number of test-loci utilized in the original calculation of Yobs (e.g., for GC content 40%, and in the context of the non-limiting sample Table 2, this number of loci may be in the range [1,ny40]). The new read-depth estimate is calculated from all the chosen loci. The procedure is iterated as many times as necessary in order to build a distribution of observed means. A sample is then attributed a score that corresponds to the position of Yobs in this distribution using a suitable transformation that accounts for the moments of the built distribution. As with the already described methods, it is appreciated that slight variation in % GC content is allowed (e.g., 1%-2%), if deemed appropriate. Hence, reference to a specific GC-content could be taken as "about" or "approximate", so that for example when referring to a 40% GC-content, loci that are "approximately" or "about" 40% (e.g., 39%-41%) may be utilized in the method.

[0068] For statistical analysis using a binomial test of proportions, fragment-sizes aligned to TACS-specific genomic coordinates are used. There is evidence from the literature that specific types of cancer can be characterized by and/or associated with fragments in the plasma having a smaller size than the expected size of fragments originating from healthy tissues (Jiang et al, (2015), Proceedings of the National Academy of Sciences, 112(11), ppE1317-E1325). The same hypothesis holds true for fragments originating from the placenta/fetus. Specifically, it has been shown that fragments of cell free genetic material originating from the placenta tend to be smaller in length when compared to other cell free genetic material (Chan, K.C. (2004) Clin. Chem. 50:88-92). Hence, the statistic of interest is whether the proportion of small-size fragments aligned to a TACS-specific test-region deviates significantly from what is expected when comparing it to the respective proportion of other TACS-specific reference-regions, as this would indicate fetal genetic abnormalities.

[0069] Thus, fragment-sizes are assigned into two groups. Sizes related to the test loci are assigned to one group and fragment-sizes related to the reference loci are assigned to the other group. Subsequently, in each group, fragment sizes are distributed into two subgroups, whereby small-size fragments are assigned into one subgroup and all remaining fragments are designated to the remaining subgroup. The last step computes the proportion of small-sized fragments in each group and uses these quantities in a binomial test of proportions. The score of the test is attributed to the sample under investigation.

[0070] The final result of a sample may be given by combining one or more scores derived from the different statistical methods, non-limiting examples of which are given in Example 4.

[0071] For statistical analysis using segmentation methods, the read-depth and sequence composition of non-overlapping genomic regions of interest of fixed-size is obtained. On the obtained dataset, GC-content read-depth bias alleviation may be performed, but is not limited to, using a local polynomial fitting method in order to estimate the expected read-depth of regions based on their GC content. The expected value, dependent on GC-content, is then used to normalize regions using suitable methods known to those skilled in the art. The normalized dataset is subsequently processed using one or more segmentation-based classification routines. To do so the algorithms process consecutive data points to detect the presence of read-depth deviations which manifest in the form of a "jump/drop" from their surrounding data points. Depending on the segmentation routine used, data points are given a score which is used towards assigning membership into segments of similar performing read-depths. For example, consecutive data points with score values within a suitable range may be classified as one segment, whereas consecutive data points with score values which exceed the set thresholds may be assigned to a different segment.

Oncology Uses

[0072] In various embodiments, the TACS-based enrichment method of the disclosure can be used for a variety of purposes in the oncology field. As described in detail in Examples 6-9, the method allows for detection of tumor biomarkers (including cancer related-germline mutations) in biological samples. The method can be applied to the analysis of essentially any known tumor biomarker. An extensive catalogue of known cancer-associated mutations is known in the art, referred to as COSMIC (Catalogue of Somatic Mutations in Cancer), described in, for example, Forbes, S.A. et al. (2016) *Curr. Protocol Hum. Genetic* 91:10.11.1-10.11.37; Forbes, S.A. et al. (2017) *Nucl. Acids Res.* 45:D777-D783; and Prior et al. (2012) *Cancer Res.* 72:2457-2467. The COSMIC database is publically available at www.cancer.sanger.ac.uk. The database includes oncogenes that have been associated with cancers, any of which can be analyzed using the method of the disclosure. In addition to the COSMIC catalogue, other compilations of tumor biomarker mutations have been described in the art, non limiting examples of which include the ENCODE Project, which describes mutations in the regulatory sites of oncogenes (see e.g., Shar, N.A. et al. (2016) *Mol. Canc.* 15:76) and ClinVar, a National Center for Biotechnology Information (NCBI) database for genomic variations associated with human health. The ClinVar database is publicly available at www.ncbi.nlm.nih.gov/clinvar.

[0073] The methods of the invention can be used to simultaneously analyze a large panel of tumor biomarkers in a single biological sample. For example, in various embodiments, the pool of TACS used in the method detects at least 5, or at least 10, or at least 15, or at least 20, or at least 25, or at least 30, or at least 35, or at least 40, or at least 45 or at least 50 different tumor biomarkers.

[0074] For detection of tumor biomarkers, TACS are designed based on the design criteria described herein and the known sequences of tumor biomarker genes and genetic mutations therein associated with cancer. In one embodiment, a plurality of TACS families used in the method bind to a plurality of tumor biomarker sequences of interest selected from the group comprising of ABL, AKT, AKT1, ALK, APC, AR, ARAF, ATM, BAP1, BARD1, BCL, BMPR1A, BRAF, BRCA, BRCA1, BRCA2, BRIP1, CDH1, CDKN, CHEK2, CTNNB1, DDB2, DDR2, DICER1, EGFR, EPCAM, ErbB, ErcC, ESR1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FBXW7, FGFR, FLT, FLT3, FOXA1, FOXL2, GATA3, GNA11, GNAQ, GNAS, GREM1, HOX, HOXB13, HRAS, IDH1, JAK, JAK2, KEAP1, KIT, KRAS, MAP2Ks, MAP3Ks, MET, MLH1, MPL, MRE11A, MSH2, MSH6, MTOR, MUTYH, NBN, NPM1, NRAS, NTRK1, PALB2, PDGFRs, PI3KCs, PMS2, POLD1, POLE, POLH, PTEN, RAD50, RAD51C, RAD51D, RAF1, RB1, RET, RUNX1, SLX4, SMAD, SMAD4, SMARCA4, SPOP, STAT, STK11, TP53, VHL, XPA and XPC, and combinations thereof.

[0075] In one embodiment, the plurality of TACS families used in the method bind to a plurality of tumor biomarker sequences of interest selected from the group consisting of, but not limited to, EGFR_6240, KRAS_521, EGFR_6225, NRAS_578, NRAS_580, PIK3CA_763, EGFR_13553, EGFR_18430, BRAF_476, KIT_1314, NRAS_584, EGFR_12378, and combinations thereof.

[0076] Representative, exemplary and non-limiting examples of chromosomal start and stop positions for amplifying TACS that bind to exemplary, non-limiting tumor biomarker genes are shown in Figure 10, for NRAS on chromosome 1, for PI3KCA on chromosome 3, for EGFR on chromosome 7 and for KRAS on chromosome 12. Alternative suitable chromosomal start and stop positions, for these oncogenes and/or for other oncogenes, for amplifying TACS are readily identifiable by one of ordinary skill in the art based on the teachings herein.

[0077] In one embodiment of the method, following sequencing of the library preparation and enrichment for the sequences of interest through TACS hybridization, the subsequent step of amplifying the enriched library is performed in the presence of blocking sequences that inhibit amplification of wild-type sequences. Thus, amplification is biased toward amplification of the mutant tumor biomarker sequences.

[0078] The pool of TACS and families of TACS used in the method of detecting tumor biomarkers can include any of the design features described herein with respect to the design of the TACS. For example, in various

embodiments, each TACS family comprises at least 2, at least 3, at least 4 or at least 5 different member sequences. In one embodiment, each TACS family comprises 4 different member sequences. In various embodiments, the start and/or stop positions for the member sequences within a TACS family, with respect to a reference coordinate system for the genomic sequence of interest, are staggered by at least 5 base pairs, or at least 10 base pairs, or by 5-10 base pairs. In various embodiments, the pool of TACS comprises at least 5, or at least 10 or at least 50 or at least 100 different TACS families, or more.

[0079] Suitable statistical analysis approaches for use with oncology samples and detection of tumor biomarkers are described further in Examples 6-9.

[0080] The method for detecting tumor biomarkers can be used in a variety of different clinical circumstances in the oncology field. For example, the method can be used for making an initial cancer diagnosis in a subject suspected of having cancer. Accordingly in one embodiment, the method further comprises making a diagnosis of the subject based on detection of at least one tumor biomarker sequence.

[0081] Additionally, the method can be used to select an appropriate treatment regimen for a patient diagnosed with cancer, wherein the treatment regimen is designed to be effective against a tumor having the tumor biomarkers detected in the patient's tumor (i.e., known in the art as personalized medicine). Accordingly, in another embodiment, the method further comprises selecting a therapeutic regimen for the subject based on detection of at least one tumor biomarker sequence.

[0082] Still further, the method can be used to monitor the efficacy of a therapeutic regimen, wherein changes in tumor biomarker detection are used as an indicator of treatment efficacy. Accordingly, in another embodiment, the method further comprises monitoring treatment efficacy of a therapeutic regimen in the subject based on detection of at least one tumor biomarker sequence.

[0083] Moreover, the method can be used to detect relapse and minimal residual disease (MRD), wherein detection of at least one tumor biomarker are used as an indicator of remaining tumor cells in a patient after treatment or tumor recurrence. Accordingly in another embodiment, the method further informs of MRD and disease relapse.

[0084] Also, the method can be used to detect cancer-related germline (hereditary) mutations in patients with cancer or individuals suspected of a cancer pre-disposing syndrome wherein detection of at least one germline mutation is used as an indicator for having a cancer pre-disposing syndrome. Accordingly, in another embodiment, the method further comprises diagnosing a patient or an individual with a hereditary cancer pre-disposing syndrome that can inform the clinician to allow for early medical intervention, treatment selection and close monitoring.

Fragment-Based Analysis

[0085] In another aspect, the invention pertains to fragment based analysis of samples, described further in Example 9. There is evidence from the literature that specific types of cancer can be characterized by and/or associated with fragments in the plasma having a smaller size than the expected size of fragments originating from healthy tissues (Jiang et al, (2015), Proceedings of the National Academy of Sciences, 112(11), ppE1317-E1325). The same hypothesis holds true for fragments originating from the placenta/fetus. Specifically, placenta derived fragments are generally of smaller size when compared to fragments originating from maternal tissues/cells. Accordingly, a fragment size-based test was developed and assessed, demonstrating its ability to identify samples harboring chromosomal abnormalities.

[0086] Thus, the fragments-based detection may be used to detect abnormalities in mixed samples with low signal-to-noise ratio (e.g., as is the case in detection of cancer).

[0087] Accordingly, in one embodiment, a fragments-based test is utilized to detect the presence of somatic copy number aberrations in a sample from a patient suspected of having cancer. For example, a binomial test of proportions, as described Example 4 and Example 9, can be used for the detection of increased presence of nucleic acid material originating from non-healthy tissue (e.g., tumor tissue) based on fragment size. In particular, under the null hypothesis that the distribution of fragment sizes originating from both healthy and cancerous cells is the same, a binomial test for proportions (as described in Example 4 and Example 9) using continuity correction can be utilized to quantify any evidence against it.

EXAMPLES

[0088] The present invention is further illustrated by the following examples, which should not be construed as further limiting.

Example 1: Sample Collection and Library Preparation

[0089] The general methodology for the TACS-based multiplexed parallel analysis approach for genetic assessment is shown schematically in Figure 1. In this example, methods for collecting and processing a maternal plasma sample (containing maternal and fetal DNA), followed by sequencing library preparation for use in the methodology of Figure 1 are described. The DNA sample and library preparation described herein can similarly be used with DNA samples from tumors for tumor biomarker detection (see Example 6-9).

Sample collection

[0090] Plasma samples were obtained anonymously from pregnant women after the 10th week of gestation. Protocols used for collecting samples for our study were approved by the Cyprus National Bioethics Committee, and informed consent was obtained from all participants.

Sample extraction

[0091] Cell Free DNA was extracted from 2-4ml plasma from each individual using a manual or automated extraction method suitable for cell free DNA isolation such as for example, but not limited to, Qiasymphony protocol suitable for cell free fetal DNA isolation (Qiagen) (Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855).

Sequencing library preparation

[0092] Extracted DNA from maternal plasma samples was used for sequencing library construction. Standard library preparation methods were used with the following modifications. A negative control extraction library was prepared separately to monitor any contamination introduced during the experiment. During this step, 5' and 3' overhangs were filled-in, by adding 12 units of T4 polymerase (NEB) while 5' phosphates were attached using 40 units of T4 polynucleotide kinase (NEB) in a 100µl reaction and subsequent incubation at 25°C for 15 minutes and then 12° C for 15 minutes. Reaction products were purified using the MinElute kit (Qiagen). Subsequently, adaptors P5 and P7 (see adaptor preparation) were ligated at 1:10 dilution to both fill-in reaction with 16 units of Bst polymerase (NEB) in a 40 µl reaction with subsequent incubation at 65°C for 25 minutes and then 12°C for 20 minutes. Products were purified using the MinElute kit (Qiagen). Library amplification was performed using a

Fusion polymerase (Herculase II Fusion DNA polymerase (Agilent Technologies) or Pfuusion High Fidelity Polymerase (NEB)) in 50 µl reactions and with the following cycling conditions, 95°C for 3 minutes; followed by 10 cycles at 95°C for 30 seconds, 60°C for 30 seconds, 72°C for 30 seconds and finally 72°C for 3 minutes (Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855). The final library products were purified using the MinElute Purification Kit (Qiagen) and measured by spectrophotometry.

Adaptor preparation

[0093] Hybridization mixtures for adaptor P5 and P7 were prepared separately and incubated for 10 seconds at 95° C followed by a ramp from 95° C to 12° C at a rate of 0.1° C /second. P5 and P7 reactions were combined to obtain a ready-to-use adapter mix (100 µM of each adaptor). Hybridization mixtures were prepared as follows: P5 reaction mixture contained adaptor P5_F (500 µM) at a final concentration of 200 µM, adaptor P5+P7_R (500 µM) at a final concentration of 200 µM with 1X oligo hybridization buffer. In addition, P7 reaction mixture contained adaptor P7_F (500 µM) at a final concentration of 200 µM, adaptor P5+P7_R(500 µM) at a final concentration of 200 µM with 1X oligo hybridization buffer (Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855.). Sequences were as follows, wherein * = a phosphorothioate bond (PTO) (Integrated DNA Technologies):

adaptor P5_F:

A*C*A*C*TCTTTCCTACACGACGCTCTTCCG*A*T*C*T (SEQ ID NO: XX)

adaptor P7_F:

G*T*G*A*CTGGAGTTCAGACGTGTGCTCTTCCG*A*T*C*T (SEQ ID NO: YY),

adaptor_P5+P7_R:

A*G*A*T*CGGAA*G*A*G*C (SEQ ID NO: ZZ).

Example 2: TArget Capture Sequences (TACS) Design and Preparation

[0094] This example describes preparation of custom TACS for the detection of whole or partial chromosomal abnormalities for chromosomes 13, 18, 21, X, Y or any other chromosome, as well as other genetic abnormalities, such as but not limited to, microdeletion/microduplication syndromes, translocations, inversions, insertions, and other point or small size mutations. The genomic target-loci used for TACS design were selected based on their GC content and their distance from repetitive elements (minimum 50 bp away). TACS size can be variable. In one embodiment of the method the TACS range from 100-500 bp in size and are generated through a PCR-based approach as described below. The TACS were prepared by simplex polymerase chain reaction using standard Taq polymerase, primers designed to amplify the target-loci, and normal DNA used as template. The chromosomal regions used to design primers to amplify suitable loci on chromosomes 13, 18, 21 and X, to thereby prepare the pool of TACS for analysis of chromosomes 13, 18, 21 and X, are shown in Figure 2.

[0095] All custom TACS were generated using the following cycling conditions: 95°C for 3 minutes; 40 cycles at 95°C for 15 seconds, 60°C for 15 seconds, 72°C for 12 seconds; and 72°C for 12 seconds, followed by verification via agarose gel electrophoresis and purification using standard PCR clean up kits such as the Qiaquick PCR Purification Kit (Qiagen) or the NucleoSpin 96 PCR clean-up (Mackerey Nagel) or the Agencourt AMPure XP for PCR Purification (Beckman Coulter). Concentration was measured by Nanodrop (Thermo Scientific).

Example 3: TACS Hybridization and Amplification

[0096] This example describes the steps schematically illustrated in Figure 1 of target capture by hybridization using TACS, followed by quantitation of captured sequences by Next Generation Sequencing (NGS).

TACS Biotinylation

[0097] TACS were prepared for hybridization, as previously described (Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855), starting with blunt ending with the Quick Blunting Kit (NEB) and incubation at room temperature for 30 minutes. Reaction products were subsequently purified using the MinElute kit (Qiagen) and were ligated with a biotin adaptor using the Quick Ligation Kit (NEB) in a 40µl reaction at RT for 15 minutes. The reaction products were purified with the MinElute kit (Qiagen) and were denatured into single stranded DNA prior to immobilization on streptavidin coated magnetic beads (Invitrogen).

TACS Hybridization

[0098] Amplified libraries were mixed with blocking oligos (Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855) (200 µM), 5µg of Cot-1 DNA (Invitrogen), 50 µg of Salmon Sperm DNA (Invitrogen), Agilent hybridization buffer 2×, Agilent blocking agent 10X, and were heated at 95°C for 3 minutes to denature the DNA strands. Denaturation was followed by 30 minute incubation at 37°C to block repetitive elements and adaptor sequences. The resulting mixture was then added to the biotinylated TACS. All samples were incubated in a rotating incubator for 12- 48 hours at 66°C. After incubation, the beads were washed as described previously and DNA was eluted by heating (Koumbaris, G. et al. (2016) Clinical chemistry, 62(6), pp.848-855). Eluted products were amplified using outer-bound adaptor primers. Enriched amplified products were pooled equimolarly and sequenced on a suitable platform.

[0099] If appropriate, amplification may be biased toward amplification of specific/desired sequences. In one embodiment of the method, this is performed when amplification is performed in the presence of sequences that hybridize to the undesired sequence of interest, and as such block the action of the polymerase enzyme during the process. Hence, the action of the amplification enzyme is directed toward the sequence of interest during the process.

Example 4: Bioinformatics Sample Analysis

[0100] This example describes representative statistical analysis approaches for use in the methodology illustrated in Figure 1 ("analysis pipeline" in Figure 1).

Human Genome Alignment

[0101] For each sample, the bioinformatic pipeline routine described below was applied in order to align the sample's sequenced DNA fragments to the human reference genome. Targeted paired-end read fragments obtained from NGS results were processed to remove adaptor sequences and poor quality reads (Q-score<25) using the cutadapt software (Martin, M. et al. (2011) EMB.netJournal 17.1). The quality of the raw and/or processed reads as well as any descriptive statistics which aid in the assessment of quality check of the sample's sequencing output were obtained using the FastQC software (Babraham Institute (2015) FastQC) and/or other custom-built software. Processed reads which were at least 25 bases long were aligned to the human reference genome built hg19 (UCSC Genome Bioinformatics) using the Burrows-Wheel Alignment algorithm (Li, H. and

Durbin, R. (2009) *Bioinformatics* 25:1754-1760) but other algorithms known to those skilled in the art may be used as well. If relevant, duplicate reads were removed post-alignment. Where applicable, sequencing output pertaining to the same sample but processed on separate sequencing lanes, was merged to a single sequencing output file. The removal of duplicates and merging procedures were performed using the Picard tools software suite (Broad Institute (2015) Picard) and/or the Sambamba tools software suite (Tarasov, Artem, et al. "Sambamba: fast processing of NGS alignment formats." *Bioinformatics* 31.12 (2015): 2032-2034.). A realignment procedure, using tools known to those in the art, may also be performed.

[0102] The above software analysis resulted in a final aligned version of a sequenced sample against the human reference genome and all subsequent steps were based on this aligned version. Information in terms of Short Nucleotide Polymorphisms (SNPs) at loci of interest was obtained using bcftools from the SAMtools software suite (Li, H. et al. (2009) *Bioinformatics* 25:2078-2079) and/or other software known to those skilled in the art. The read-depth per base, at loci of interest, was obtained using the mpileup option of the SAMtools software suite, from here on referred to as the mpileup file. Information pertaining to the size of the aligned fragments was obtained using the view option of the SAMtools software suite, from here on referred to as the fragment-sizes file and/or other software known to those skilled in the art.

[0103] The mpileup file and the fragment-sizes file were processed using custom-build application programming interfaces (APIs) written in the Python and R programming languages (Python Software Foundation (2015) *Python*; The R Foundation (2015) *The R Project for Statistical Computing*). The APIs were used to determine the ploidy state of chromosomes of interest, and/or other genetic abnormalities in regions of interest across the human genome, using a series of steps (collectively henceforth referred to as the "algorithm") and to also collect further descriptive statistics to be used as quality check metrics, such as but not limited to fetal fraction and/or fraction of interest quantification (collectively henceforth referred to as the "QC metrics"). The APIs can also be used for the assessment of genetic abnormalities from data generated when applying the described method in cases of multiple gestation pregnancies, as well as other genetic abnormalities such as, but not limited to, microdeletions, microduplications, copy number variations, translocations, inversions, insertions, point mutations and mutational signatures.

QC Metrics

[0104] QC metrics were used to inspect an aligned sample's properties and decide whether the sample was suitable to undergo classification. These metrics were, but are not limited to:

1. (a) The enrichment of a sample. The patterns of enrichment are indicative of whether a sample has had adequate enrichment across loci of interest in a particular sequencing experiment (herein referred to as a "run"). To assess this, various metrics are assessed, non-limiting examples of which are:
 1. (i) overall sample on-target read depth,
 2. (ii) sample on-target sequencing output with respect to total mapped reads,
 3. (iii) individual TACS performance in terms of achieved read-depth,
 4. (iv) kurtosis and skewness of individual TACS enrichment,
 5. (v) kurtosis and skewness moments that arise from all TACS,
 6. (vi) fragment size distribution,
 7. (vii) percentage of duplication,
 8. (viii) percentage of paired reads and,
 9. (ix) percentage of aligned reads,
 if applicable.

The above checks are also taken into consideration with regards to GC-bias enrichment. Samples that fail to meet one or more of the criteria given above are flagged for further inspection, prior to classification.

2. (b) A sample's fetal fraction or fraction of interest. Samples with an estimated fetal fraction, or fraction of interest, that is below a specific threshold are not classified. Furthermore, if applicable the fraction of

interest may be calculated using more than one method and concordance of results between estimation methods may be used as an additional QC prior to classification.

The Algorithm

[0105] The algorithm is a collection of data processing, mathematical and statistical model routines arranged as a series of steps. The algorithm's steps aim in deciding the relative ploidy state of a chromosome of interest with respect to all other chromosomes of the sequenced sample and is used for the detection of whole or partial chromosomal abnormalities for chromosomes 13, 18, 21, X, Y or any other chromosome, as well as other genetic abnormalities such as, but not limited to, microdeletion/microduplication syndromes and other point or small size mutations. As such the algorithm can be used, but is not limited to, the detection of whole or partial chromosomal abnormalities for chromosomes 13, 18, 21, X,Y or any other chromosome, as well as other genetic abnormalities such as, but not limited to, microdeletions, microduplications, copy number variations, translocations, inversions, insertions, point mutations and other mutational signatures. The algorithm carries out, but is not limited to, two types of assessments, one pertaining to the read-depth information of each sample and the other to the distribution of fragment-sizes, across TACS-specific regions. One or more statistical tests may be associated with each type of assessment, non-limiting examples of which are given in the statistical methods described herein.

[0106] In the case of read-depth associated tests, the algorithm compares sequentially the read-depth of loci from each chromosome of interest (herein referred to as the test chromosome) against the read-depth of all other loci (herein referred to as the reference loci) to classify its ploidy state. For each sample, these steps were, but are not limited to:

1. (a) Removal of inadequately sequenced loci. The read-depth of each locus was retrieved. Loci that have not achieved a minimum number of reads, were considered as inadequately enriched and were removed prior to subsequent steps.
2. (b) Genetic (GC-content) bias alleviation. The sequencing procedure may introduce discrepancies in read-depth across the loci of interest depending on their GC content. To account for such bias, a novel sequence-matching approach that increases both sensitivity and specificity to detect chromosomal aneuploidies was employed. The GC content of each locus on the test chromosome was identified and similar genetic loci were grouped together to form genetically matched groups. The procedure was repeated for the reference loci. Then, genetically matched groups from the test chromosome were conditionally paired with their genetically matched group counterparts on the reference chromosome(s). The groups may have any number of members. The conditionally matched groups were then used to assess the ploidy status of test chromosomes.
3. (c) Genetic abnormality determination. Ploidy status determination, or other genetic abnormalities of interest such as but not limited to microdeletions, microduplications, copy number variations, translocations, inversions, insertions, point mutations and other mutational signatures was achieved using a single statistical method and/or a weighted score approach on the result from the following, but not limited to, statistical methods:

Statistical Method 1: The differences in read-depth of the conditionally paired groups were tested for statistical significance using the t-test formula:

$$t = \frac{\bar{x} - \mu}{s/\sqrt{n}}$$

where t is the result of the t-test, $\bar{x}$ is the average of the differences of the conditionally paired groups, μ is the expected read-depth and is set to a value that represents insignificant read-depth differences between the two groups, s the standard deviation of the differences of the conditionally paired groups and n the length of the vector of the conditionally paired differences. The magnitude of the t-score was then used to

identify evidence, if any, against the null hypothesis of same ploidy between reference and test chromosomes. Specifically, $t \geq c_1$ (where c_1 is a predefined threshold belonging to the set of all positive numbers) shows evidence against the null hypothesis of no difference.

Statistical Method 2: Bivariate nonparametric bootstrap. The bootstrap method depends on the relationship between the random variables X (read-depth of reference loci) and Y (read-depth of test loci). Here, the read depth of baits on the reference group (random variable denoted by X) were treated as the independent covariate. The first step of the iterative procedure involved random sampling with replacement (bootstrapping) of the read-depths of loci on the reference chromosomes, i.e. $(x_1, g_1), \dots, (x_n, g_n)$, where the parameter g is known and denotes the GC-content of the chosen bait. Then, for each randomly selected reference bait (x_i, g_i) , a corresponding read depth was generated for a genetically matched locus i.e., $(y_1, g_1), \dots, (y_n, g_n)$. Thus, the bivariate data $(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)$ was arrived at, which was conditionally matched on their GC-content (parameter g_i). The differences between the read depths of the genetically matched bootstrapped values x_i and y_i were used to compute the statistic of interest in each iteration. In one embodiment this statistical measure can be but is not limited to the mode mean or median of the recorded differences, and/or multiples thereof. The procedure was repeated as necessary to build up the distribution of the statistic of interest from these differences. The sample was assigned a score that corresponds to a specific percentile of the built distribution (e.g. 5th percentile). Under the null hypothesis the ploidy between chromosomes in the reference and test groups is not different. As such, samples whose score for a particular chromosome, was greater than a predefined threshold, say c_2 , were classified as statistically unlikely to have the same ploidy. Other statistical measures may be employed.

Statistical Method 3: Stratified permutation test. The statistic of interest is the read-depth estimate of the test chromosome, denoted by $\hat{Y}_{obs}$, which is calculated using all loci of the test chromosome's genetically matched groups as follows:

$$\hat{Y}_{obs} = \frac{\sum_{j=1}^T \sum_{i=1}^{N_j} y_{ij}}{\sum_{j=1}^T N_j}$$

where y_{ij} is the read-depth of locus i part of the genetically matched group j (i.e., loci belonging to a specific group based on their GC-content), N_j is the number of test loci part of the genetically matched group j and T the number of genetically matched groups.

Subsequently, a null distribution to test $\hat{Y}_{obs}$ was built. To do so, for each group j , the test and reference loci were combined (exchangeability under the null hypothesis), and each group j was sampled randomly up to N_j times without replacement (stratified permutation). This created a vector of values, say y_i , and from this the vector's average value, say $\hat{y}_i$, was calculated. The procedure was repeated as necessary to build the null distribution. Finally $\hat{Y}_{obs}$, was studentised against the null distribution using the formula:

$$Z_{Y_{obs}} = \frac{\hat{Y}_{obs} - \bar{\hat{y}}}{\sigma_{\hat{y}}}$$

where $\bar{\hat{y}}$ and $\sigma_{\hat{y}}$ are the first and square root of the second moment of all permuted $\hat{y}_i$ statistic values. Samples whose $Z_{Y_{obs}}$ was greater than a predefined threshold, say c_3 , were statistically less likely to have the same ploidy in the reference and test groups.

In the case of fragment-size associated tests, the algorithm computes the proportion of small-size fragments found in test-loci and compares it with the respective proportion in reference-loci as described in Statistical Method 4 below.

Statistical Method 4: Fragment Size Proportions. For each sample the number and size of fragments aligned onto the human reference genome at the corresponding TACS coordinates, is extracted. The data is subsequently filtered so as to remove fragment-sizes considered statistical outliers using the median outlier detection method. Specifically, outliers are defined as those fragments whose size is above or below the thresholds, F_{thr} , set by equation:

$$F_{thr} = F_{median} \pm (X \times IQR)$$

where F_{median} is the median fragment-size of all fragments of a sample, X is a variable that can take

values from the set of R^+ , and IQR is the interquartile range of fragment sizes. Thereafter, a binomial test of proportions is carried out to test for supporting evidence against the null hypothesis, H_0 , where this is defined as:

H_0 : The proportion of small fragments of the test-region is not different from the proportion of small-fragments of the reference region.

[0107] In various embodiments of the invention, small fragments are defined as those fragments whose size is less than or equal to a subset of Z^+ , that is upper-bounded by 160bp. If the set of all TACS are defined as T , then the test region can be any proper subset S which defines the region under investigation, and the reference region is the relative complement of S in T . For example, in one embodiment of the invention, the set S is defined by all TACS-captured sequences of chromosome 21 and thus the reference set is defined by all TACS-captured fragments on the reference chromosomes, and/or other reference loci

[0108] The alternative hypothesis, H_1 , is defined as:

H_1 : The proportion of small fragments of the test-region is not equal to the proportion of test fragments of the reference region.

[0109] As such, and taking into account continuity correction, the following score is computed (Brown et. al, Harrel):

$$W_{test} = (\hat{p} - p_{ref}) / \sqrt{\frac{\hat{p}(1-\hat{p})}{N_{test}}}$$

where

$$\hat{p} = \frac{(\hat{F} + 0.5)}{(N_{test} + 1)}$$

$$p_{ref} = \frac{(F_{ref} + 0.5)}{(N_{ref} + 1)}$$

[0110] $\hat{F}$ is the number of small-size fragments on the test-region, F_{ref} the number of small size fragments on the reference region, N_{test} the number of all fragments on the test region and N_{ref} the number of all fragments on the reference region.

[0111] For each sample, the algorithm tests sequentially the proportion of fragment sizes of regions under investigation (for example, but not limited to, chromosome 21, chromosome 18, chromosome 13 or other (sub)chromosomal regions of interest) against reference regions; those not under investigation at the time of testing. For each sample a score is assigned for each test. Scores above a set-threshold, say c_4 , provide evidence against the null hypothesis.

[0112] Weighted Score method 1: In one embodiment of the method, a weighted score was attributed to each sample s , computed as a weighted sum of all statistical methods using the formula:

$$V_s(R, F) = z_1 \max\{R_s, F_s\} + (1 - z_1) \min\{R_s, F_s\}$$

where R_s is the run-specific corrected score arising from a weighted contribution of each read-depth related statistical method for sample s and is defined as:

$$R_s = \frac{(\sum_i w_i S_{is} - \hat{R}_r)}{\sigma_r}$$

and $\hat{R}_r$ is the run-specific median value calculated from the vector of all unadjusted read-depth related weighted scores that arise from a single sequencing run, and σ_r is a multiple of the standard deviation of R scores calculated from a reference set of 100 euploid samples. The terms $\max\{R_s, F_s\}$ and $\min\{R_s, F_s\}$ denote the maximum and minimum values of the bracketed set, respectively.

[0113] F_s is the run-specific corrected score arising from the fragment-size related statistical method and is defined as:

$$F_s = \frac{(W_{test} - \hat{R}_f)}{\sigma_f}$$

where W_{test} is as defined earlier, $\hat{R}_f$ is the run specific median calculated from the vector of all unadjusted fragment-related statistical scores that arise from a single sequencing run, and σ_f is a multiple of the standard deviation of F scores calculated from a reference set of 100 euploid samples.

[0114] A unique classification score of less than a predefined value indicates that there is no evidence from the observed data that a sample has a significant risk of aneuploidy.

[0115] Weighted Score method 2: In another embodiment of the method, the weighted score arising from the statistical methods described above was used to assign each sample a unique genetic abnormality risk score using the formula:

$$R(t, c) = \sum_{j=0}^{j=N} w_j \frac{t_j}{c_j}$$

where R is the weighted score result, w_j the weight assigned to method j, t_j the observed score resulting from method j, and c_j the threshold of method j.

[0116] A unique classification score of less than a predefined value indicates that there is no evidence from the observed data that a sample has a significant risk of aneuploidy.

[0117] Since all read depths from baits in the reference group were assumed to be generated from the same population, and in order to have a universal threshold, run-specific adjustments were also employed to alleviate run-specific biases.

[0118] The aforementioned method(s), are also suitable for the detection of other genetic abnormalities, such as but not limited to, subchromosomal abnormalities. A non-limiting example is the contiguous partial loss of chromosomal material leading to a state of microdeletion, or the contiguous partial gain of chromosomal material leading to a state of microduplication. A known genetic locus subject to both such abnormalities is 7q11.23. In one embodiment of statistical method 1, synthetic plasma samples of 5%, 10% and 20% fetal material were tested for increased risk of microdeletion and/or microduplication states for the genetic locus 7q11.23.

[0119] For point mutations various binomial tests are carried out that take into consideration the fetal fraction estimate of the sample, f, the read-depth of the minor allele, r, and the total read-depth of the sequenced base, n. Two frequent, yet non-limiting examples involve assessment of the risk when the genetic abnormality is a recessive point mutation or a dominant point mutation.

[0120] In the non-limiting example of a recessive point mutation the null hypothesis tested is that both the mother and the fetus are heterozygous (minor allele frequency is 0.5) against the alternative in which the fetus is homozygous (minor allele frequency is 0.5-f/2). A small p-value from the corresponding likelihood ratio test would indicate evidence against the null. In the non-limiting example of a dominant point mutation the null hypothesis tested is that the mother and fetus are homozygous at the given position against the alternative in which only the fetus is heterozygous for the given position. A small p-value from the corresponding likelihood ratio test would indicate evidence against the null.

[0121] In addition to the above, fetal sex determination methods were also developed, with non-limiting examples given below. In one embodiment of the invention, fetal sex was assigned to a sample using a Poisson test using the formula:

$$Pr(r_y \leq k) = e^{-\lambda} \sum_{i=0}^{i=k} \frac{\lambda^i}{i!}$$

where

$$\lambda = \frac{fB\mu}{2}$$

and f is the fetal fraction estimate of the sample, B is the number of target sequences on chromosome Y, μ is the read-depth of the sample and k is the sum of reads obtained from all targets B . The null hypothesis of the Poisson test was that the sample is male. A value of $\Pr(r_y)$ less than a threshold c_y was considered as enough evidence to reject the null hypothesis, i.e. the sample is not male. If any of the terms for computing $\Pr(r_y)$ were unavailable, then the sample's sex was classified as NA (not available).

[0122] In another embodiment of the invention, fetal sex was assigned using the average read-depth of target sequences on chromosome Y. If the average read-depth of the target-sequences was over a predefined threshold, where such threshold may be defined using other sample-specific characteristics such as read-depth and fetal-fraction estimate, the fetal sex was classified as male. If the average read-depth was below such threshold then the sample was classified as female.

Fetal Fraction Estimation/Fraction of Interest Estimation

[0123] Several methods have been developed to estimate fetal fraction that can be applied to singleton and/or to multiple gestation pregnancies. As such, and dependent on the type of pregnancy, the fetal fraction estimate can be obtained from either method or as a weighted estimate from a subset and/or all developed methods. Some non-limiting examples are given below.

[0124] In one embodiment, a machine learning technique has been developed based on Bayesian inference to compute the posterior distribution of fetal DNA fraction using allelic counts at heterozygous loci in maternal plasma of singleton pregnancies. Three possible informative combinations of maternal/fetal genotypes were utilized within the model to identify those fetal DNA fraction values that get most of the support from the observed data.

[0125] Let f denote the fetal DNA fraction. If the mother is heterozygous at a given genomic locus, the fetal genotype can be either heterozygous or homozygous resulting in expected minor allele frequencies at 0.5 and $0.5-f/2$, respectively. If the mother is homozygous and the fetus is heterozygous then the expected minor allele frequency will be $f/2$. A Markov chain Monte Carlo method (a Metropolis-Hastings algorithm) (The R Foundation (2015) *The R Project for Statistical Computing*) was used with either a non-informative or an informative prior (i.e. incorporate additional information such as gestational age, maternal weight etc.) to obtain a sequence of random samples from the posterior probability distribution of fetal DNA fraction that is based on a finite mixture model.

[0126] In another embodiment, the fetal fraction estimate is computed only from the fetus-specific minor allele frequency (MAF) cluster, i.e. the cluster formed when the mother is homozygous and the fetus is heterozygous for a given genomic locus. It is assumed that the mean value of the fetal fraction estimate is normally distributed as $N(2\bar{x}, \sigma_{\bar{x}})$, where $\bar{x}$ is the mean of the fetus-specific MAF, and $\sigma_{\bar{x}}$ is the standard deviation of the fetus-specific MAF. The fetal fraction estimate is then obtained from percentiles of the computed distribution, $N(2\bar{x}, \sigma_{\bar{x}})$.

[0127] For multiple gestation pregnancies, non-limiting examples of which include monozygotic and dizygotic twin pregnancies, triplet pregnancies and various egg and/or sperm donor cases, the fetal fraction can be estimated using information obtained from heterozygous genetic loci whose MAF value is less than a threshold, say M_{thresh} , and derived from potential fetus-specific SNPs. The ordinarily skilled artisan will appreciate that fetus specific SNPs can originate from any fetus, or from any possible combination of the fetuses or from all the fetuses of the gestation. As such, an algorithm that estimates the fetal fraction of the fetus with the smallest contribution to the total fetal content, by taking into account the combinatorial contribution of each fetus to the MAF values that define fetus-specific SNPs, and also allows for inhomogeneous contribution of fetal material to

the total fetal content of plasma derived material has been developed. To this effect, a two-step approach is employed by the algorithm.

[0128] In one embodiment of the algorithm, the multiple gestation pregnancy under consideration is a dizygotic twin pregnancy. As a first step, the algorithmic implementation of the model utilizes all informative SNPs and allows for inhomogeneous fetal contribution that can be explained with a fold-difference in fetal fraction estimates of a set threshold, say cf . Specifically, if $f1$ and $f2$ represent the fetal fractions of fetus one and fetus two, and $f1 \leq f2$, then the assumption is that $f2 \leq cf \cdot f1$, with cf being a positive real number greater than or equal to 1. Under this assumption, the observed data D , defined as counts of the alternate and reference alleles at informative SNP loci, are believed to be generated from a mixture distribution of three Binomials (defined by parameters, $f1/2$, $f2/2$ and $(f1+f2)/2$), with the posterior distribution $p(f1, f2 | D)$ being proportional to the observational model which can be written as $p(f1 | f2, D) \cdot p(f2 | D)$. The posterior distribution $p(f1, f2 | D)$ is sampled with an MCMC Metropolis-Hastings algorithm using a uniform prior. The empirical quantile approach is performed on the generated data array to infer the fetal fractions.

[0129] As a second step, the algorithm runs a model-based clustering algorithm (Finite Gaussian mixture modeling fitted via EM algorithm; R-package: mclust) to identify whether there exists a separate outlier SNP cluster which is believed to be centered around $f1/2$. Existence of such a cluster with a mean invalidating the $cf \geq f2/f1$ assumption, leads to estimation of $f1$ using only SNPs part of the identified cluster.

[0130] The methods described above are suited to the determination of the fraction of any component of interest part of a mixed sample. As such, the methods are not to be understood as applicable only to the application of fetal fraction estimation and can be applied to the estimation of any component of interest part of a mixed sample, as outlined in Example 6.

Example 5: Target Enrichment Using Families of TACS

[0131] In this example, a family of TACS, containing a plurality of members that all bind to the same target sequence of interest, was used for enrichment, compared to use of a single TACS binding to a target sequence of interest. Each member of the family of TACS bound to the same target sequence of interest but had different start/stop coordinates with respect to a reference coordinate system for that target sequence (e.g., the human reference genome, built hg19). Thus, when aligned to the target sequence, the family of TACS exhibit a staggered binding pattern, as illustrated in Figure 3. Typically, the members of a TACS family were staggered approximately 5-10 base pairs.

[0132] A family of TACS containing four members (i.e., four sequences that bound to the same target sequence but having different start and/or stop positions such that the binding of the members to the target sequence was staggered) was prepared. Single TACS hybridization was also prepared as a control. The TACS were fixed to a solid support by labelling with biotin and binding to magnetic beads coated with a biotin-binding substance (e.g., streptavidin or avidin) as described in Example 3. The family of TACS and single TACS were then hybridized to a sequence library, bound sequences were eluted and amplified, and these enriched amplified products were then pooled equimolarly and sequenced on a suitable sequencing platform, as described in Example 3.

[0133] The enriched sequences from the family of TACS sample and the single TACS sample were analyzed for read-depth. The results are shown in Figures 4A and 4B. As shown in Figure 4A, target sequences of interest enriched using the family of four TACS (red dots) exhibited a fold-change in read-depth when compared to control sequences that were subjected to enrichment using only a single TACS (blue dots). Fold-change was assessed by normalizing the read-depth of each locus by the average read-depth of a sample, wherein the average read-depth was calculated from all loci enriched with a single TACS. As shown in Figure 4B, an overall 54.7% average increase in read-depth was observed using the family of four TACS.

[0134] This example demonstrates that use of a family of TACS, as compared to a single TACS, results in significantly improved enrichment of a target sequence of interest resulting in significantly improved read-depth of that sequence.

Example 6: Tumor Biomarker Detection in Reference Material

[0135] In this example, the TACS methodology, illustrated in Figure 1, was used for the detection of tumor biomarkers in certified reference material known to harbor particular genetic mutations that are tumor biomarkers. For detection of the tumor biomarker sequences of interest, families of TACS, as described in Example 5, were used.

[0136] A sample of certified reference material harboring known tumor-associated genetic mutations was commercially obtained and samples were prepared to simulate tumor loads of 0.1%, 1.0% and 5.0%.

[0137] The samples were subjected to the TACS methodology illustrated in Figure 1 using families of TACS that bound to the following tumor-associated genetic mutations: EGFR_6240, KRAS_521, EGFR 6225, NRAS 578, NRAS 580, PIK3CA 763, EGFR 13553, EGFR 18430.

[0138] Following amplification and sequence of the TACS-enriched products, data analysis was performed as follows. Sequencing products were processed to remove adaptor sequences and poor quality reads. Reads whose length was at least 25 bases long post adaptor-removal were aligned to either:

1. (a) the human reference genome built hg19, or
2. (b) an artificially created genome based on built hg19 which contains only sequences of interest.

[0139] If relevant, duplicate reads were removed post-alignment. Where applicable, sequencing output pertaining to the same sample but processed on separate sequencing lanes was merged to a single sequencing output file. Local realignment of the data, using tools known in the art, may also be performed. The above software analysis provided a final aligned version of a sequenced sample against the reference genome, defined here as the final BAM file, where information can be extracted from it in terms of Short Nucleotide Polymorphisms (SNPs), Single Nucleotide Variants (SNVs) and other genetic variations with respect to a reference sequence at loci of interest, read-depth per base and the size of aligned fragments. Various available tools known to those skilled in the art, such as but not limited to bcftools, which is part of the samtools software suite, or varDict can be used to collect SNP information from the final BAM file. Such information concerns the sequence and number of times each variant is present in a sequenced sample was detected and was used to

1. (a) infer the presence of a genetic mutation, and
2. (b) to estimate the tumor load using the fetal-fraction estimation/fraction of interest estimation method described in Example 4.

[0140] In addition to the detection of the genetic mutation, statistical confidence was ascribed to a detected mutation using the estimated tumor load of the sample and the read-depth of each of the detected variants at a given position using binomial statistics. More than one test may be employed from which one can compute the probability of obtaining the sequenced information, or obtain a 95% confidence interval which describes a range of possible read-depths for the genetic mutation, or whether the obtained proportion of reads which can be ascribed to the genetic mutation is consistent with what would be expected at the given tumor load. A suitable binomial test of proportions is described in Example 4 (in the context of classification of chromosomal abnormalities).

[0141] The results are shown in Figure 5. The line illustrates the expected minor allele frequency (MAF) for each percent (%) tumor load. The bars (x-axis) illustrate the detected MAF (y-axis) for each sample for the indicated genetic mutations. Two technical replicates are shown for the reference material.

[0142] The data demonstrates that the TACS methodology successfully detected the tumor-associated genetic mutations EGFR_6240, KRAS_521, EGFR_6225, NRAS_578, NRAS_580, PIK3CA_763, EGFR_13553 and EGFR_18430 at the expected tumor loads of 1.0% and 5.0%. Mutations EGFR_6240, NRAS_578, PIK3CA_763, EGFR_13553 and EFGR_18430 were also successfully detected at 0.1% tumor load.

[0143] Accordingly, this example demonstrates the successful detection of a large panel of different tumor biomarkers using the TACS methodology at tumor loads as low as 0.1%.

Example 7: Tumor Biomarker Detection in Patient Samples

[0144] In this example, the TACS methodology, illustrated in Figure 1, was used for the detection of tumor biomarkers in tumor tissue and blood plasma samples from untreated cancer patients with confirmed diagnosis. For detection of the tumor biomarker sequences of interest, families of TACS, as described in Example 5, were used.

[0145] Matched pairs of peripheral blood and tumor tissue samples from untreated cancer patients were used to further validate the performance of the TACS methodology for tumor biomarker detection for a patient harboring mutation PIK3CA E545K (Patient 1) and for a patient harboring mutation TP53 K139 (Patient 2). The results are shown in Figure 6.

[0146] As shown in Figure 6, application of the TACS methodology to a tissue sample obtained from Patient 1 harboring mutation PIK3CA E545K (top bars) provided a variant allele frequency (VAF) percentage (i.e., the percentage that the genetic mutation is present instead of the normal allele) of ~62%. Plasma obtained from peripheral blood of Patient 1 was processed according to the method described in Example 1 and provided a 6.05 % VAF. Similarly, application of the TACS methodology to samples obtained from Patient 2 harboring mutation TP53 K139 (bottom bars) provided a VAF of ~60% for tumor tissue and a VAF of 4.88 % for plasma obtained from a peripheral blood sample.

[0147] Accordingly, this example demonstrates the successful detection of tumor biomarkers in cancer patient samples, in both tumor tissue samples and plasma samples, thereby demonstrating the suitability of the TACS methodology for tissue biopsy and for non-invasive tumor biomarker detection using liquid biopsy.

Example 8: Detection of Mutational Profiles

[0148] Given the ability of the TACS methodology illustrated in Figure 1 to detect a number of somatic single nucleotide variations (SNVs), these can be examined in the context of motifs, also referred to as mutational profiles. Most somatic mutations in tumors can be considered as passengers and may not be associated with pathogenesis if examined individually. Nonetheless, examining the profile of detected mutations as a whole can be useful in determining and/or detecting a pathogenesis-associated mutational profile. Various algorithms have been developed to decompose known mutational motifs operative in many cancer types. Alternatively, other metrics utilizing specific characteristics such as the type of mutations detected in the context of their neighboring bases can be utilized to this effect. The developed algorithms can infer the most likely scenario(s) that explain the observed data. Decomposition of the number and types of known mutational patterns/signatures that have, most likely, generated the observed mutational profile has been achieved using, but not limited to, the Lawson-Hanson non-negative least squares algorithm.

[0149] Figure 7 shows the observed pattern of somatic SNVs for breast cancer using data downloaded from the COSMIC database. The x-axis shows a single base mutation observed in cancer in the context of its neighboring sequences. For example A[C>A]T describes the mutation of Cytosine (C) to Adenine (A) where the upstream sequence is Adenine and the downstream sequence is Thymine. The y-axis shows the frequency of occurrence of this mutation in breast cancer.

[0150] Figure 8 illustrates the results of a simulations study where mutational profiles were randomly generated by sampling a subset of SNVs each time, from data available in the COSMIC database, thereby simulating individuals. The simulated data were then subjected to the decomposition algorithms described above in order to detect the likely underlying mutational motifs. The bars indicate the average estimated frequency of the known mutational breast signatures computed from a data set of 10000 simulations. The developed algorithm shows evidence of detection of the mutational profiles, thereby demonstrating that detection of mutational profiles, or motifs, is possible using the developed algorithms.

Example 9: Fragment Size Based Tests

[0151] There is evidence from the literature that specific types of cancer can be characterized by and/or associated with fragments in the plasma having a smaller size than the expected size of fragments originating from healthy tissues (Jiang et al, (2015), Proceedings of the National Academy of Sciences, 112(11), ppE1317-E1325). Thus, a fragments-size based test can be utilized to detect the presence of somatic copy number variations in individuals suspected of having cancer. To this effect, a binomial test of proportions, as described Example 4, can be used for the detection of increased presence of nucleic acid material originating from non-healthy tissue (e.g., tumor tissue) based on fragment size. In particular, under the null hypothesis that the distribution of fragment sizes originating from both healthy and non-healthy cells (for example, but not limited to cancerous cells) is the same, a binomial test for proportions (as described in Example 4) using continuity correction can be utilized to quantify any evidence against it.

[0152] The same hypothesis holds true for fragments originating from the placenta/fetus. Specifically, placenta derived fragments are generally of smaller size when compared to fragments originating from maternal tissues/cells. Accordingly, assessment of the fragment size-based test was performed using maternal plasma samples (i.e., mixed samples where cell free DNA is of maternal and fetal origin). The size of fragments that have aligned to TACS-enriched regions can be obtained from the aligned data. Subsequently, the proportion of fragments under a specific threshold from a test region is compared respective proportion of fragments from a reference region for evidence against the null hypothesis H_0 ,

[0153] H_0 : The proportion of small fragments of the test-region is not different from the proportion of small-fragments of the reference region.

[0154] Figure 9 shows results when applying the fragment sizes method to the mixed sample containing maternal and fetal DNA. The black dots are individual samples. The x-axis shows the sample index. The y-axis shows the score result of the fragments-based method. A score result greater than the one indicated by the threshold, illustrated as a grey line, indicates a deviation from the expected size of fragments illustrating the presence of aneuploidy. The results demonstrate that an aneuploid sample, having an estimated fetal fraction equal to 2.8%, was correctly identified, illustrating that fragments-based detection may be used to detect abnormalities in mixed samples with low signal-to-noise ratio (e.g., as is the case in detection of cancer).

[0155] Accordingly, this example demonstrates the successful ability of the fragments-based detection method in detecting genetic abnormalities in mixed samples with low signal-to-noise ratios, thereby demonstrating the suitability of the fragments-based test for analysis of either cancer samples for oncology purposes or maternal samples for NIPT.

[0156] Since small-sized fragments are associated with fragments from non-healthy tissues (Jiang et al, (2015), Proceedings of the National Academy of Sciences, 112(11), ppE1317-E1325) they can also be leveraged for the detection of small-sized mutations, such as point mutations and mutational signatures. For example, one may only use small-sized fragments in Variant Allele Frequency estimation as described in examples 6-9, thereby increasing the signal-to-noise ratio.

Example 10: Use of the method for tissue biopsies

[0157] Five FFPE samples from Breast carcinoma and 13 tissue samples (fresh/frozen and FFPE) from lung adenocarcinoma were subjected to the method and the mutational status was successfully detected. The data are presented below.

Breast Carcinoma:

[0158]

Type of specimen	Patient ID	Gene	CDS mutation	AA change	COSMIC ID	MAF%
FFPE	BCa1	TP53	c.569delC	p.190fs*57	COSM100030	17.39
		TP53	c.559+25G>A	intronic	COSM45841	22.22
FFPE	BCa2	PIK3CA	c.1624G>A	p.E542K	COSM760	32.15
		FLT3	c.2501G>A	p.R834Q	COSM28047	2.01
FFPE	BCa3	ALK	c.3515+18C>T	intronic	COSM28496	49.43
FFPE	BCa4	AKT1	c.49G>A	p.E17K	COSM33765	42.86
FFPE	BCa5	PIK3CA	c.1633G>A	E545K	COSM763	62.79
		PTEN	c.1-9C>G	intronic	COSM5915	26.19

		TP53	c.415A>T	p.K139*	COSM44678	60.63
--	--	------	----------	---------	-----------	-------

Lung adenocarcinoma:

[0159]

Type of specimen	Sample ID	COSMIC ID	NIPD method	Independent method
Fresh/frozen	LCA1	COSM459	0.0245	0.0261
		COSM527	0.036	0.0378
Fresh/frozen	LCA2	COSM763	0.1427	0.1558
Fresh/frozen	LCA3	COSM522	0.3815	0.3492
Fresh/frozen	LCA4	COSM521	0.106	0.0923
Fresh/frozen	LCA6	COSM3675521	0.1387	0.1026
Fresh/frozen	LCA13	MET	0.0126	Not covered

Fresh/frozen	LCA15	c.3028+1G>T	0.1352	Not covered
Fresh/frozen	LCA15	COSM27887	0.1352	Not covered
		COSM521	0.2871	0.3185
Fresh/frozen	LCA21	COSM763	0.2798	0.3128
FFPE	LCA36	COSM6224	0.2431	0.1847
FFPE	LCA40	COSM6225	0.08	0.1148
FFPE	LCA45	COSM6223	0.2098	0.2456
FFPE	LCA47	COSM12370	0.6295	0.5719
FFPE	LCA48	COSM522	0.2649	0.4032

[0160] For the lung cancer data, results were compared with data obtained for the same tissue samples with an independent method. For the genomic regions covered by both methods we observed 100% concordance.

SEQUENCE LISTING

[0161]

<110> NIPD Genetics

<120> TARGET-ENRICHED MULTIPLEXED PARALLEL ANALYSIS FOR ASSESSMENT OF TUMOR BIOMARKERS

<130> B281-0008WO1

<160> 2550

<170> PatentIn version 3.5

<210> 1

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1

tcttctcggt caagatgccg 20

<210> 2

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2

aaattacatg caaggctacc ac 22

<210> 3

<211> 21

<212> DNA

<213> Homo sapiens

<400> 3

acaggaagaa aggggagta c 21

<210> 4

<211> 20

<212> DNA

<213> Homo sapiens

<400> 4

ttcaggttgt gtgatgtgc 20

<210> 5

<211> 20

<212> DNA

<213> Homo sapiens

<400> 5

taagcagagg tttgttgcc 20

<210> 6

<211> 20

<212> DNA

<213> Homo sapiens

<400> 6

gtgaagtatt tgctgccacc 20

<210> 7

<211> 20

<212> DNA

<213> Homo sapiens

<400> 7

atggtcattct caacagcaca 20

<210> 8

<211> 20

<212> DNA

<213> Homo sapiens

<400> 8

tccactgacg ttgagattcg 20

<210> 9

<211> 20

<212> DNA

<213> Homo sapiens

<400> 9

cgaacctctt tgaccttta 20

<210> 10

<211> 22

<212> DNA

<213> Homo sapiens

<400> 10

gttatgttga taggggaagc tt 22

<210> 11
<211> 20
<212> DNA
<213> Homo sapiens

<400> 11
aagccctcta ctccatctgt 20

<210> 12
<211> 20
<212> DNA
<213> Homo sapiens

<400> 12
tcagaactcg tcagtggaag 20

<210> 13
<211> 19
<212> DNA
<213> Homo sapiens

<400> 13
gaagggccag acagcttat 19

<210> 14
<211> 21
<212> DNA
<213> Homo sapiens

<400> 14
atttgcttg ttttgtccc t 21

<210> 15
<211> 21
<212> DNA
<213> Homo sapiens

<400> 15
gatcattgct ttgttgac c 21

<210> 16
<211> 21
<212> DNA
<213> Homo sapiens

<400> 16
aggagaggaa aaatcttgac c 21

<210> 17
<211> 20
<212> DNA
<213> Homo sapiens

<400> 17
ctgcctgcag ccattattgt 20

<210> 18

<211> 22
<212> DNA
<213> Homo sapiens

<400> 18
ccttggggta tgttgttat gt 22

<210> 19
<211> 22
<212> DNA
<213> Homo sapiens

<400> 19
acttttctg tatcagtcac gg 22

<210> 20
<211> 20
<212> DNA
<213> Homo sapiens

<400> 20
ctgctttgt ggttcctt 20

<210> 21
<211> 20
<212> DNA
<213> Homo sapiens

<400> 21
ccagttcctg ttttctgcc 20

<210> 22
<211> 21
<212> DNA
<213> Homo sapiens

<400> 22
gccttactg atcctactt c 21

<210> 23
<211> 21
<212> DNA
<213> Homo sapiens

<400> 23
ggatatggg taggttttg t 21

<210> 24
<211> 20
<212> DNA
<213> Homo sapiens

<400> 24
actcatagaa ctggggctt 20

<210> 25
<211> 20

<212> DNA

<213> Homo sapiens

<400> 25

ctttgtaggt cctccagaga 20

<210> 26

<211> 20

<212> DNA

<213> Homo sapiens

<400> 26

cctgtttca gtgggtgaa 20

<210> 27

<211> 20

<212> DNA

<213> Homo sapiens

<400> 27

ccacgttgta ccttccatg 20

<210> 28

<211> 21

<212> DNA

<213> Homo sapiens

<400> 28

gagattcaaa acagtgggtg c 21

<210> 29

<211> 19

<212> DNA

<213> Homo sapiens

<400> 29

acaacactgt cctgggtt 19

<210> 30

<211> 20

<212> DNA

<213> Homo sapiens

<400> 30

taaatgtcct gtgtgctcg 20

<210> 31

<211> 20

<212> DNA

<213> Homo sapiens

<400> 31

gacaggacac atggagagag 20

<210> 32

<211> 21

<212> DNA

<213> Homo sapiens

<400> 32

aactgatggt gattgcatg t 21

<210> 33

<211> 20

<212> DNA

<213> Homo sapiens

<400> 33

ggcttctgga aacatcttgc 20

<210> 34

<211> 21

<212> DNA

<213> Homo sapiens

<400> 34

caatagaagt agggggtgag g 21

<210> 35

<211> 20

<212> DNA

<213> Homo sapiens

<400> 35

agctgggatg ggtgtttat 20

<210> 36

<211> 20

<212> DNA

<213> Homo sapiens

<400> 36

gccagttgtc agaagaatcc 20

<210> 37

<211> 20

<212> DNA

<213> Homo sapiens

<400> 37

caactgcatt ccaaacagc 20

<210> 38

<211> 21

<212> DNA

<213> Homo sapiens

<400> 38

gaagggaaac agtgagaaag a 21

<210> 39

<211> 20

<212> DNA

<213> Homo sapiens

<400> 39

tcaagcgccg taagtatgta 20

<210> 40

<211> 20

<212> DNA

<213> Homo sapiens

<400> 40

taaccataac atccagggca 20

<210> 41

<211> 20

<212> DNA

<213> Homo sapiens

<400> 41

ttgtaagctg gcacactgaa 20

<210> 42

<211> 20

<212> DNA

<213> Homo sapiens

<400> 42

ttaagaaagt gccgtgttgc 20

<210> 43

<211> 20

<212> DNA

<213> Homo sapiens

<400> 43

atgggtccat gaagagaagc 20

<210> 44

<211> 20

<212> DNA

<213> Homo sapiens

<400> 44

agttgtttcc agtactgcca 20

<210> 45

<211> 20

<212> DNA

<213> Homo sapiens

<400> 45

gtatgcttc aagtgcgcc 20

<210> 46

<211> 21

<212> DNA

<213> Homo sapiens

<400> 46

gaagacaatg caatgaggtg t 21

<210> 47

<211> 20

<212> DNA

<213> Homo sapiens

<400> 47

agacccaatg agaacaggaa 20

<210> 48

<211> 20

<212> DNA

<213> Homo sapiens

<400> 48

tgatggagga agtgtgaagc 20

<210> 49

<211> 20

<212> DNA

<213> Homo sapiens

<400> 49

tggcttttct gtagttggg 20

<210> 50

<211> 20

<212> DNA

<213> Homo sapiens

<400> 50

agcagcaaga gttgagaaga 20

<210> 51

<211> 21

<212> DNA

<213> Homo sapiens

<400> 51

ggctttgaaa aatcaccatg g 21

<210> 52

<211> 20

<212> DNA

<213> Homo sapiens

<400> 52

agaggttcc atcgttgcta 20

<210> 53

<211> 20

<212> DNA

<213> Homo sapiens

<400> 53

aacagcccca aacttcctac 20

<210> 54

<211> 20

<212> DNA

<213> Homo sapiens

<400> 54

atcactgcc acaagccatt 20

<210> 55

<211> 20

<212> DNA

<213> Homo sapiens

<400> 55

tgagttgtgg gggataaagg 20

<210> 56

<211> 20

<212> DNA

<213> Homo sapiens

<400> 56

tctgggcact ttccttatga 20

<210> 57

<211> 20

<212> DNA

<213> Homo sapiens

<400> 57

gcagtttga ggggagaaga 20

<210> 58

<211> 19

<212> DNA

<213> Homo sapiens

<400> 58

ttcatgatgc cacctctc 19

<210> 59

<211> 20

<212> DNA

<213> Homo sapiens

<400> 59

gccc aaatac ccctcagta 20

<210> 60

<211> 20

<212> DNA

<213> Homo sapiens

<400> 60

gcacctcaat cccgtacaat 20

<210> 61

<211> 20
<212> DNA
<213> Homo sapiens

<400> 61
gcgttttaag cagctgtgta 20

<210> 62
<211> 20
<212> DNA
<213> Homo sapiens

<400> 62
tctccagatc gaaacagcat 20

<210> 63
<211> 20
<212> DNA
<213> Homo sapiens

<400> 63
tcattcaaag ccaagatgcc 20

<210> 64
<211> 20
<212> DNA
<213> Homo sapiens

<400> 64
acacgctaca tagacactgg 20

<210> 65
<211> 20
<212> DNA
<213> Homo sapiens

<400> 65
caatcgaggt cacattcacc 20

<210> 66
<211> 21
<212> DNA
<213> Homo sapiens

<400> 66
tgacacgctg aagaaaatag c 21

<210> 67
<211> 20
<212> DNA
<213> Homo sapiens

<400> 67
ggaggggaatg gcagaagtaa 20

<210> 68
<211> 21

<212> DNA

<213> Homo sapiens

<400> 68

ggattttcag agcagagggt g 21

<210> 69

<211> 20

<212> DNA

<213> Homo sapiens

<400> 69

aagagttgcc tgtacccttc 20

<210> 70

<211> 19

<212> DNA

<213> Homo sapiens

<400> 70

gtctctttac tgggagcgt 19

<210> 71

<211> 20

<212> DNA

<213> Homo sapiens

<400> 71

acattgcccc tgacaacata 20

<210> 72

<211> 19

<212> DNA

<213> Homo sapiens

<400> 72

tcattatctg aggagccgg 19

<210> 73

<211> 21

<212> DNA

<213> Homo sapiens

<400> 73

ggctccataa tcttctgcaa t 21

<210> 74

<211> 20

<212> DNA

<213> Homo sapiens

<400> 74

cgtacatctg atttgtgggt 20

<210> 75

<211> 21

<212> DNA

<213> Homo sapiens

<400> 75

tgccactgat gatacaaaag c 21

<210> 76

<211> 20

<212> DNA

<213> Homo sapiens

<400> 76

gaaacgtgtg gtgtcctcta 20

<210> 77

<211> 20

<212> DNA

<213> Homo sapiens

<400> 77

agtgtttggg gctctatcag 20

<210> 78

<211> 20

<212> DNA

<213> Homo sapiens

<400> 78

ctttcccttt tgagtctctgc 20

<210> 79

<211> 20

<212> DNA

<213> Homo sapiens

<400> 79

tctcgcttac cttgctacat 20

<210> 80

<211> 20

<212> DNA

<213> Homo sapiens

<400> 80

aaagcgggaa ttggaacttt 20

<210> 81

<211> 20

<212> DNA

<213> Homo sapiens

<400> 81

ggggaacatt ggggaagagat 20

<210> 82

<211> 20

<212> DNA

<213> Homo sapiens

<400> 82

tctaccagct acaaacccat 20

<210> 83

<211> 20

<212> DNA

<213> Homo sapiens

<400> 83

tcagccaata cccatagcag 20

<210> 84

<211> 20

<212> DNA

<213> Homo sapiens

<400> 84

aatcagagga agatgggtcg 20

<210> 85

<211> 20

<212> DNA

<213> Homo sapiens

<400> 85

gagaactcca ccctgtcttt 20

<210> 86

<211> 20

<212> DNA

<213> Homo sapiens

<400> 86

gggagtgtgt gaatgtgtct 20

<210> 87

<211> 21

<212> DNA

<213> Homo sapiens

<400> 87

aagctttaca tcatggcact g 21

<210> 88

<211> 20

<212> DNA

<213> Homo sapiens

<400> 88

aaaggtccat aggctcacat 20

<210> 89

<211> 20

<212> DNA

<213> Homo sapiens

<400> 89

ttgaccaatg ccattaagcc 20

<210> 90

<211> 21

<212> DNA

<213> Homo sapiens

<400> 90

accagggaaa tgtagcttc t 21

<210> 91

<211> 21

<212> DNA

<213> Homo sapiens

<400> 91

tgctctgta tggttggagt t 21

<210> 92

<211> 20

<212> DNA

<213> Homo sapiens

<400> 92

gaagcggcag taattcagga 20

<210> 93

<211> 20

<212> DNA

<213> Homo sapiens

<400> 93

aactgtgtcc taagcagtga 20

<210> 94

<211> 20

<212> DNA

<213> Homo sapiens

<400> 94

gtcacctcca gagcttcat 20

<210> 95

<211> 21

<212> DNA

<213> Homo sapiens

<400> 95

gaacaatgca acctgagaac t 21

<210> 96

<211> 21

<212> DNA

<213> Homo sapiens

<400> 96

tgattgtcct ctaccatgca t 21

<210> 97

<211> 21

<212> DNA

<213> Homo sapiens

<400> 97

aggcttgaaa caccacctt a 21

<210> 98

<211> 20

<212> DNA

<213> Homo sapiens

<400> 98

ttgatttgtt ggggtgttg 20

<210> 99

<211> 20

<212> DNA

<213> Homo sapiens

<400> 99

tgccaatctg aggttttcc 20

<210> 100

<211> 20

<212> DNA

<213> Homo sapiens

<400> 100

actctgcttt agggcttctg 20

<210> 101

<211> 20

<212> DNA

<213> Homo sapiens

<400> 101

gcagaaaagc tccaaacaa 20

<210> 102

<211> 20

<212> DNA

<213> Homo sapiens

<400> 102

gaaaagaggt ggagaggag 20

<210> 103

<211> 20

<212> DNA

<213> Homo sapiens

<400> 103

aggaccctt tgctgattc 20

<210> 104

<211> 20
<212> DNA
<213> Homo sapiens

<400> 104
ctggcccaag tgcatacata 20

<210> 105
<211> 20
<212> DNA
<213> Homo sapiens

<400> 105
aaccagagag acacctgac 20

<210> 106
<211> 20
<212> DNA
<213> Homo sapiens

<400> 106
tcctccctat ctctgtgac 20

<210> 107
<211> 20
<212> DNA
<213> Homo sapiens

<400> 107
actctgccag aaaagcctac 20

<210> 108
<211> 20
<212> DNA
<213> Homo sapiens

<400> 108
cctttgtctt gaagcctct 20

<210> 109
<211> 20
<212> DNA
<213> Homo sapiens

<400> 109
ttgactgagc agagtagagc 20

<210> 110
<211> 22
<212> DNA
<213> Homo sapiens

<400> 110
ttctacctac aagcaaagag ag 22

<210> 111
<211> 21

<212> DNA

<213> Homo sapiens

<400> 111

tcaccaacag aggatcaaac t 21

<210> 112

<211> 20

<212> DNA

<213> Homo sapiens

<400> 112

ccgagggata acatacagct 20

<210> 113

<211> 20

<212> DNA

<213> Homo sapiens

<400> 113

cactagtcac agaagcaggt 20

<210> 114

<211> 20

<212> DNA

<213> Homo sapiens

<400> 114

gtagaaaccc cgagacaact 20

<210> 115

<211> 20

<212> DNA

<213> Homo sapiens

<400> 115

caatttgctg ttcagaggct 20

<210> 116

<211> 20

<212> DNA

<213> Homo sapiens

<400> 116

tcatgatgtg gcttagtggg 20

<210> 117

<211> 20

<212> DNA

<213> Homo sapiens

<400> 117

tacaccaca tgcatacaca 20

<210> 118

<211> 19

<212> DNA

<213> Homo sapiens

<400> 118

gaagtgtgca tgggagagt 19

<210> 119

<211> 21

<212> DNA

<213> Homo sapiens

<400> 119

tttgggtggc tctatgttag g 21

<210> 120

<211> 20

<212> DNA

<213> Homo sapiens

<400> 120

ctccttgact catttccgt 20

<210> 121

<211> 20

<212> DNA

<213> Homo sapiens

<400> 121

agagtaccac tgccaagaaa 20

<210> 122

<211> 20

<212> DNA

<213> Homo sapiens

<400> 122

ctgctagtct gtcaggagag 20

<210> 123

<211> 20

<212> DNA

<213> Homo sapiens

<400> 123

gggcagcagt ataaacatcc 20

<210> 124

<211> 20

<212> DNA

<213> Homo sapiens

<400> 124

gacattccct tccattgagc 20

<210> 125

<211> 20

<212> DNA

<213> Homo sapiens

<400> 125

ttcctggtaa atgtgctggt 20

<210> 126

<211> 20

<212> DNA

<213> Homo sapiens

<400> 126

ggccagattt gcagtgattt 20

<210> 127

<211> 21

<212> DNA

<213> Homo sapiens

<400> 127

agaatcaaca acaatggcag g 21

<210> 128

<211> 21

<212> DNA

<213> Homo sapiens

<400> 128

ctctgaggaa agctttagg a 21

<210> 129

<211> 20

<212> DNA

<213> Homo sapiens

<400> 129

aggttttcgt tctgcttcag 20

<210> 130

<211> 19

<212> DNA

<213> Homo sapiens

<400> 130

cgggtcagtg attctagct 19

<210> 131

<211> 20

<212> DNA

<213> Homo sapiens

<400> 131

gtcactatgg aatgggggtt 20

<210> 132

<211> 20

<212> DNA

<213> Homo sapiens

<400> 132

gcttcttccc cgcaatatga 20

<210> 133

<211> 20

<212> DNA

<213> Homo sapiens

<400> 133

cggttcagag tcaatgccta 20

<210> 134

<211> 21

<212> DNA

<213> Homo sapiens

<400> 134

taccaacaac gccagagaaa t 21

<210> 135

<211> 20

<212> DNA

<213> Homo sapiens

<400> 135

agagggaag tgcaaggaat 20

<210> 136

<211> 20

<212> DNA

<213> Homo sapiens

<400> 136

gttttcagc acactgtccc 20

<210> 137

<211> 20

<212> DNA

<213> Homo sapiens

<400> 137

accacattac tcacaaccct 20

<210> 138

<211> 20

<212> DNA

<213> Homo sapiens

<400> 138

aagcccttt catctccaca 20

<210> 139

<211> 20

<212> DNA

<213> Homo sapiens

<400> 139

ccagagctga gacaactact 20

<210> 140
<211> 20
<212> DNA
<213> Homo sapiens

<400> 140
gaagcaattc ctcacaccac 20

<210> 141
<211> 20
<212> DNA
<213> Homo sapiens

<400> 141
ttcagtcaga atgaggagcc 20

<210> 142
<211> 20
<212> DNA
<213> Homo sapiens

<400> 142
ctcctctccc ctctgatttt 20

<210> 143
<211> 21
<212> DNA
<213> Homo sapiens

<400> 143
ttttaagcg acagtcacac g 21

<210> 144
<211> 20
<212> DNA
<213> Homo sapiens

<400> 144
tcctctgcct tctacccttt 20

<210> 145
<211> 20
<212> DNA
<213> Homo sapiens

<400> 145
tgtgtgcct ttgttctgg 20

<210> 146
<211> 22
<212> DNA
<213> Homo sapiens

<400> 146
ttaggaggtg aggctggaaa aa 22

<210> 147

<211> 21
<212> DNA
<213> Homo sapiens

<400> 147
ctgtcagcaa ttcaggtca g 21

<210> 148
<211> 20
<212> DNA
<213> Homo sapiens

<400> 148
agacaaaggc ttcacggaac 20

<210> 149
<211> 20
<212> DNA
<213> Homo sapiens

<400> 149
ttcctctgtg tcttgaaggt 20

<210> 150
<211> 20
<212> DNA
<213> Homo sapiens

<400> 150
atcaatgcag gtgagtgta 20

<210> 151
<211> 20
<212> DNA
<213> Homo sapiens

<400> 151
cactccacat aagcctcaga 20

<210> 152
<211> 20
<212> DNA
<213> Homo sapiens

<400> 152
aggatgtagt tgggtgagga 20

<210> 153
<211> 20
<212> DNA
<213> Homo sapiens

<400> 153
cagtcatcac ggggagatac 20

<210> 154
<211> 20

<212> DNA

<213> Homo sapiens

<400> 154

gacagatatt tgtgcagggt 20

<210> 155

<211> 20

<212> DNA

<213> Homo sapiens

<400> 155

tcttagccct taccttcct 20

<210> 156

<211> 20

<212> DNA

<213> Homo sapiens

<400> 156

agcctgaatg tcactgatca 20

<210> 157

<211> 19

<212> DNA

<213> Homo sapiens

<400> 157

actcatcact tctggctgc 19

<210> 158

<211> 20

<212> DNA

<213> Homo sapiens

<400> 158

tcttggttt cctgccctat 20

<210> 159

<211> 20

<212> DNA

<213> Homo sapiens

<400> 159

ttgctgtgga tgagaatgga 20

<210> 160

<211> 20

<212> DNA

<213> Homo sapiens

<400> 160

tgagggcaga aagaaacaga 20

<210> 161

<211> 20

<212> DNA

<213> Homo sapiens

<400> 161

ggggtcacac atcactttc 20

<210> 162

<211> 20

<212> DNA

<213> Homo sapiens

<400> 162

atagggtcac aatccactgc 20

<210> 163

<211> 20

<212> DNA

<213> Homo sapiens

<400> 163

atattgagcc ccgcatgtta 20

<210> 164

<211> 20

<212> DNA

<213> Homo sapiens

<400> 164

ggttcagga gaaagaacat 20

<210> 165

<211> 20

<212> DNA

<213> Homo sapiens

<400> 165

tgccatgtaa ttgccaagat 20

<210> 166

<211> 19

<212> DNA

<213> Homo sapiens

<400> 166

cctgttctcc atccctctg 19

<210> 167

<211> 21

<212> DNA

<213> Homo sapiens

<400> 167

tcacaaacta cccaacacct a 21

<210> 168

<211> 21

<212> DNA

<213> Homo sapiens

<400> 168
cagaattagt tggggagctg t 21

<210> 169
<211> 20
<212> DNA
<213> Homo sapiens

<400> 169
gccatctcct gaaatagtc 20

<210> 170
<211> 20
<212> DNA
<213> Homo sapiens

<400> 170
gcaagtgttc ccatctagaa 20

<210> 171
<211> 20
<212> DNA
<213> Homo sapiens

<400> 171
attgataccc ctctcccag 20

<210> 172
<211> 19
<212> DNA
<213> Homo sapiens

<400> 172
aagtaagctg tctcctggc 19

<210> 173
<211> 20
<212> DNA
<213> Homo sapiens

<400> 173
aggtgggtg gcatgaagaa 20

<210> 174
<211> 20
<212> DNA
<213> Homo sapiens

<400> 174
agcagagttt caagacaagc 20

<210> 175
<211> 20
<212> DNA
<213> Homo sapiens

<400> 175

ttttacacag caggcctctt 20

<210> 176

<211> 21

<212> DNA

<213> Homo sapiens

<400> 176

gcaactccaa attatcaggg c 21

<210> 177

<211> 20

<212> DNA

<213> Homo sapiens

<400> 177

cagcaccttc ccttagcaaa 20

<210> 178

<211> 20

<212> DNA

<213> Homo sapiens

<400> 178

cttggtgtct tgtagccctg 20

<210> 179

<211> 20

<212> DNA

<213> Homo sapiens

<400> 179

cacagatata gacgtccaca 20

<210> 180

<211> 21

<212> DNA

<213> Homo sapiens

<400> 180

agctcagcaa ttaaacagtc c 21

<210> 181

<211> 20

<212> DNA

<213> Homo sapiens

<400> 181

tggtgagagt gccagagatg 20

<210> 182

<211> 20

<212> DNA

<213> Homo sapiens

<400> 182

cttcacctt ctgccaatga 20

<210> 183
<211> 20
<212> DNA
<213> Homo sapiens

<400> 183
ttctgacatt tgcaagcacc 20

<210> 184
<211> 20
<212> DNA
<213> Homo sapiens

<400> 184
ctgttgctag ttcttgggc 20

<210> 185
<211> 19
<212> DNA
<213> Homo sapiens

<400> 185
ttttccagtc ccagcacat 19

<210> 186
<211> 21
<212> DNA
<213> Homo sapiens

<400> 186
tctctctctt cctgaaacag c 21

<210> 187
<211> 21
<212> DNA
<213> Homo sapiens

<400> 187
aacctctgct ttgttagtg a 21

<210> 188
<211> 20
<212> DNA
<213> Homo sapiens

<400> 188
gagagaatgc aaggttcagc 20

<210> 189
<211> 20
<212> DNA
<213> Homo sapiens

<400> 189
tacagcatca aagaggaagc 20

<210> 190

<211> 20
<212> DNA
<213> Homo sapiens

<400> 190
gaggggatga ggggaaaaag 20

<210> 191
<211> 20
<212> DNA
<213> Homo sapiens

<400> 191
catgacctct gacggatctg 20

<210> 192
<211> 19
<212> DNA
<213> Homo sapiens

<400> 192
aggcaatgag gtcaaggac 19

<210> 193
<211> 20
<212> DNA
<213> Homo sapiens

<400> 193
atgatggccc caacttcttc 20

<210> 194
<211> 20
<212> DNA
<213> Homo sapiens

<400> 194
ttctagacac tgaggagca 20

<210> 195
<211> 20
<212> DNA
<213> Homo sapiens

<400> 195
aacgctacac ttacgagct 20

<210> 196
<211> 20
<212> DNA
<213> Homo sapiens

<400> 196
tcaacactac ctgccaatca 20

<210> 197
<211> 19

<212> DNA

<213> Homo sapiens

<400> 197

tgccgacaca aaagaatgc 19

<210> 198

<211> 19

<212> DNA

<213> Homo sapiens

<400> 198

aaagtgttcc tccctgctg 19

<210> 199

<211> 20

<212> DNA

<213> Homo sapiens

<400> 199

aggagcaaaa tagtctggct 20

<210> 200

<211> 21

<212> DNA

<213> Homo sapiens

<400> 200

accactcttg aatcattgca g 21

<210> 201

<211> 21

<212> DNA

<213> Homo sapiens

<400> 201

ccagccaatt ttctcttcc c 21

<210> 202

<211> 20

<212> DNA

<213> Homo sapiens

<400> 202

actgtcccta ctgccaattt 20

<210> 203

<211> 21

<212> DNA

<213> Homo sapiens

<400> 203

atctggttg aactgcca c 21

<210> 204

<211> 20

<212> DNA

<213> Homo sapiens

<400> 204

cactctgaat agctctcccc 20

<210> 205

<211> 20

<212> DNA

<213> Homo sapiens

<400> 205

ttatccggga cagtttcagg 20

<210> 206

<211> 20

<212> DNA

<213> Homo sapiens

<400> 206

gaatcttttg gccacactg 20

<210> 207

<211> 20

<212> DNA

<213> Homo sapiens

<400> 207

gtcagacaca ctagctggt 20

<210> 208

<211> 20

<212> DNA

<213> Homo sapiens

<400> 208

acacatttca ccttcaccct 20

<210> 209

<211> 20

<212> DNA

<213> Homo sapiens

<400> 209

gcactaatcc aggggcttaa 20

<210> 210

<211> 20

<212> DNA

<213> Homo sapiens

<400> 210

ccccttacca ccactctac 20

<210> 211

<211> 20

<212> DNA

<213> Homo sapiens

<400> 211

ttcagatccc ttaagcacgc 20

<210> 212

<211> 20

<212> DNA

<213> Homo sapiens

<400> 212

acctaaggcc tcaaattcca 20

<210> 213

<211> 20

<212> DNA

<213> Homo sapiens

<400> 213

cagaccacgg gcataagaaa 20

<210> 214

<211> 20

<212> DNA

<213> Homo sapiens

<400> 214

tggaatgtgt gatttgaga 20

<210> 215

<211> 19

<212> DNA

<213> Homo sapiens

<400> 215

ctggctgtct tctgggaaa 19

<210> 216

<211> 21

<212> DNA

<213> Homo sapiens

<400> 216

caagcagaac tgagaagagt c 21

<210> 217

<211> 20

<212> DNA

<213> Homo sapiens

<400> 217

agtggaacga ggattgtgt 20

<210> 218

<211> 20

<212> DNA

<213> Homo sapiens

<400> 218

ctcccatctg aaactgctga 20

<210> 219

<211> 19

<212> DNA

<213> Homo sapiens

<400> 219

acatcacaac caccctgac 19

<210> 220

<211> 20

<212> DNA

<213> Homo sapiens

<400> 220

gtgttgacct gatttgccaa 20

<210> 221

<211> 20

<212> DNA

<213> Homo sapiens

<400> 221

gaacaaagag gaacagagcc 20

<210> 222

<211> 20

<212> DNA

<213> Homo sapiens

<400> 222

ttcatgattc cagggtcctc 20

<210> 223

<211> 22

<212> DNA

<213> Homo sapiens

<400> 223

ggacggattt agtgtacatt gg 22

<210> 224

<211> 20

<212> DNA

<213> Homo sapiens

<400> 224

tttcctcca acaccacaga 20

<210> 225

<211> 20

<212> DNA

<213> Homo sapiens

<400> 225

tccttagggt tctgcgaaat 20

<210> 226
<211> 20
<212> DNA
<213> Homo sapiens

<400> 226
ggaaactccc tgccttctac 20

<210> 227
<211> 20
<212> DNA
<213> Homo sapiens

<400> 227
tcttccaaac accaggtcta 20

<210> 228
<211> 19
<212> DNA
<213> Homo sapiens

<400> 228
actcaatgga aggaagggc 19

<210> 229
<211> 20
<212> DNA
<213> Homo sapiens

<400> 229
aaggacttgt gctgtattgc 20

<210> 230
<211> 20
<212> DNA
<213> Homo sapiens

<400> 230
gacgggagcc agtattctac 20

<210> 231
<211> 20
<212> DNA
<213> Homo sapiens

<400> 231
gggattgaga gcttggttct 20

<210> 232
<211> 20
<212> DNA
<213> Homo sapiens

<400> 232
ctccccacca agatgttcaa 20

<210> 233

<211> 20
<212> DNA
<213> Homo sapiens

<400> 233
gttttgggtc atgcagtgtt 20

<210> 234
<211> 20
<212> DNA
<213> Homo sapiens

<400> 234
gacaaaaaca ctgtccagac 20

<210> 235
<211> 20
<212> DNA
<213> Homo sapiens

<400> 235
aaccatggct ttgcaagtac 20

<210> 236
<211> 20
<212> DNA
<213> Homo sapiens

<400> 236
ggaaccctct gctattttgc 20

<210> 237
<211> 20
<212> DNA
<213> Homo sapiens

<400> 237
tactccttgt gtgaaccct 20

<210> 238
<211> 20
<212> DNA
<213> Homo sapiens

<400> 238
acctttaccc cataccatcc 20

<210> 239
<211> 20
<212> DNA
<213> Homo sapiens

<400> 239
cattcctttg gttggtgtcc 20

<210> 240
<211> 20

<212> DNA

<213> Homo sapiens

<400> 240

ctaattgggcc tgtgttcct 20

<210> 241

<211> 20

<212> DNA

<213> Homo sapiens

<400> 241

caacctacct gcccatagtt 20

<210> 242

<211> 20

<212> DNA

<213> Homo sapiens

<400> 242

cgtagcaaatt tatggcgagg 20

<210> 243

<211> 20

<212> DNA

<213> Homo sapiens

<400> 243

ggtcagaagg gaaagggttc 20

<210> 244

<211> 20

<212> DNA

<213> Homo sapiens

<400> 244

ccagattaaa acgtgggtgcc 20

<210> 245

<211> 20

<212> DNA

<213> Homo sapiens

<400> 245

cccacaacta taggtcgcat 20

<210> 246

<211> 21

<212> DNA

<213> Homo sapiens

<400> 246

agttgtcca ttgtaccag c 21

<210> 247

<211> 19

<212> DNA

<213> Homo sapiens

<400> 247

ttggctgcac ttgagtca 19

<210> 248

<211> 20

<212> DNA

<213> Homo sapiens

<400> 248

cagatggccc attgtaaca 20

<210> 249

<211> 19

<212> DNA

<213> Homo sapiens

<400> 249

tattgaggtt cccgtgctg 19

<210> 250

<211> 20

<212> DNA

<213> Homo sapiens

<400> 250

agaatgtgaa gtggctccat 20

<210> 251

<211> 20

<212> DNA

<213> Homo sapiens

<400> 251

tttgggttg tgtgtgtg 20

<210> 252

<211> 20

<212> DNA

<213> Homo sapiens

<400> 252

aggaatctct ctctgccaag 20

<210> 253

<211> 20

<212> DNA

<213> Homo sapiens

<400> 253

tctcaaggc aggtcatagg 20

<210> 254

<211> 21

<212> DNA

<213> Homo sapiens

<400> 254
gaaacctaag acgtccact g 21

<210> 255
<211> 20
<212> DNA
<213> Homo sapiens

<400> 255
gagtgaaggg attggagcaa 20

<210> 256
<211> 20
<212> DNA
<213> Homo sapiens

<400> 256
atgtctcagg ctaggtgttc 20

<210> 257
<211> 20
<212> DNA
<213> Homo sapiens

<400> 257
aactcacao agcccagtta 20

<210> 258
<211> 20
<212> DNA
<213> Homo sapiens

<400> 258
gtgcagactc atgttatggc 20

<210> 259
<211> 20
<212> DNA
<213> Homo sapiens

<400> 259
aggatctcaa agcaccacag 20

<210> 260
<211> 20
<212> DNA
<213> Homo sapiens

<400> 260
aacgggaaga gggaaacttt 20

<210> 261
<211> 20
<212> DNA
<213> Homo sapiens

<400> 261

atgttcaaca gagtcaggct 20

<210> 262

<211> 20

<212> DNA

<213> Homo sapiens

<400> 262

cagtaacagt ccagggtctt 20

<210> 263

<211> 20

<212> DNA

<213> Homo sapiens

<400> 263

agtcctgggag cctagaatca 20

<210> 264

<211> 22

<212> DNA

<213> Homo sapiens

<400> 264

cattgtagtt tcaggacacc aa 22

<210> 265

<211> 20

<212> DNA

<213> Homo sapiens

<400> 265

accacagaat gacttcagc 20

<210> 266

<211> 20

<212> DNA

<213> Homo sapiens

<400> 266

tttcacgtgt aacaggagca 20

<210> 267

<211> 20

<212> DNA

<213> Homo sapiens

<400> 267

tgctacaggg aaaatggtct 20

<210> 268

<211> 20

<212> DNA

<213> Homo sapiens

<400> 268

tccactgctt agttgcctt 20

<210> 269

<211> 20

<212> DNA

<213> Homo sapiens

<400> 269

acaggtgggg agaaaaggta 20

<210> 270

<211> 20

<212> DNA

<213> Homo sapiens

<400> 270

ctgccactac tacacagcta 20

<210> 271

<211> 20

<212> DNA

<213> Homo sapiens

<400> 271

atgggtctct ggaatgcatg 20

<210> 272

<211> 20

<212> DNA

<213> Homo sapiens

<400> 272

agttctccac agcacatcat 20

<210> 273

<211> 20

<212> DNA

<213> Homo sapiens

<400> 273

tcttcatct cagctctgca 20

<210> 274

<211> 20

<212> DNA

<213> Homo sapiens

<400> 274

ccgaacagta tttgagggg 20

<210> 275

<211> 20

<212> DNA

<213> Homo sapiens

<400> 275

tttggctgtt tcctgttcc 20

<210> 276

<211> 20
<212> DNA
<213> Homo sapiens

<400> 276
acctaacttg cctgtcctt 20

<210> 277
<211> 20
<212> DNA
<213> Homo sapiens

<400> 277
acaggagaac aagcagcata 20

<210> 278
<211> 21
<212> DNA
<213> Homo sapiens

<400> 278
cagcctagta tatgggaacg t 21

<210> 279
<211> 23
<212> DNA
<213> Homo sapiens

<400> 279
acccatatgt agtatcgctc ttg 23

<210> 280
<211> 21
<212> DNA
<213> Homo sapiens

<400> 280
tatgggtttt tctgctccac t 21

<210> 281
<211> 20
<212> DNA
<213> Homo sapiens

<400> 281
aaatgtgagg gagatcgctc 20

<210> 282
<211> 19
<212> DNA
<213> Homo sapiens

<400> 282
gcaggaccct tcagcatta 19

<210> 283
<211> 20

<212> DNA

<213> Homo sapiens

<400> 283

gactggatga tgcaaagggtg 20

<210> 284

<211> 20

<212> DNA

<213> Homo sapiens

<400> 284

aacatttgca ggggatcaa 20

<210> 285

<211> 20

<212> DNA

<213> Homo sapiens

<400> 285

aaagatgcct ccttgtgtct 20

<210> 286

<211> 20

<212> DNA

<213> Homo sapiens

<400> 286

aagtatatctg cccagggaaa 20

<210> 287

<211> 20

<212> DNA

<213> Homo sapiens

<400> 287

tcctggctag ttttgctgaa 20

<210> 288

<211> 20

<212> DNA

<213> Homo sapiens

<400> 288

ctccttgctt gcctttacac 20

<210> 289

<211> 20

<212> DNA

<213> Homo sapiens

<400> 289

agccttaatt ccccatgcat 20

<210> 290

<211> 20

<212> DNA

<213> Homo sapiens

<400> 290

ttttctgtg gagtgggct 20

<210> 291

<211> 20

<212> DNA

<213> Homo sapiens

<400> 291

aaagagtcaa ccatgcactg 20

<210> 292

<211> 20

<212> DNA

<213> Homo sapiens

<400> 292

ggtgaagcag cctgaataaa 20

<210> 293

<211> 19

<212> DNA

<213> Homo sapiens

<400> 293

tcttgtacc aagctgcca 19

<210> 294

<211> 20

<212> DNA

<213> Homo sapiens

<400> 294

gcttctactt tccctccag 20

<210> 295

<211> 20

<212> DNA

<213> Homo sapiens

<400> 295

agaaaagcca acctctctt 20

<210> 296

<211> 20

<212> DNA

<213> Homo sapiens

<400> 296

ccagggtact aaaaggggac 20

<210> 297

<211> 20

<212> DNA

<213> Homo sapiens

<400> 297

ttgtgggtca atgtcaacac 20

<210> 298

<211> 20

<212> DNA

<213> Homo sapiens

<400> 298

agaaaagggtg gaggaaggga 20

<210> 299

<211> 21

<212> DNA

<213> Homo sapiens

<400> 299

ggagttgtt acaggtggac t 21

<210> 300

<211> 21

<212> DNA

<213> Homo sapiens

<400> 300

tagcttcaa ttcacaggtc a 21

<210> 301

<211> 20

<212> DNA

<213> Homo sapiens

<400> 301

ttaaatgcgc caagtccta 20

<210> 302

<211> 20

<212> DNA

<213> Homo sapiens

<400> 302

atttcctggg tcaagctct 20

<210> 303

<211> 20

<212> DNA

<213> Homo sapiens

<400> 303

cttgaccag gaatgtcta 20

<210> 304

<211> 20

<212> DNA

<213> Homo sapiens

<400> 304

aggcagtcag atccacctat 20

<210> 305

<211> 20

<212> DNA

<213> Homo sapiens

<400> 305

aaaattgcct gctgtttgga 20

<210> 306

<211> 20

<212> DNA

<213> Homo sapiens

<400> 306

gcacatcat gaaacctcct 20

<210> 307

<211> 20

<212> DNA

<213> Homo sapiens

<400> 307

ataggccagt ctcaggtaga 20

<210> 308

<211> 20

<212> DNA

<213> Homo sapiens

<400> 308

agattgcagc ctacccaaag 20

<210> 309

<211> 20

<212> DNA

<213> Homo sapiens

<400> 309

ttgactgaag tgttcaggt 20

<210> 310

<211> 20

<212> DNA

<213> Homo sapiens

<400> 310

gcttcttca accatccacc 20

<210> 311

<211> 20

<212> DNA

<213> Homo sapiens

<400> 311

gcagcactca actattccac 20

<210> 312
<211> 20
<212> DNA
<213> Homo sapiens

<400> 312
caggagttat ggcaccagtg 20

<210> 313
<211> 20
<212> DNA
<213> Homo sapiens

<400> 313
gagagtgtgg aggcagaaaa 20

<210> 314
<211> 20
<212> DNA
<213> Homo sapiens

<400> 314
gccaactta tttccagct 20

<210> 315
<211> 21
<212> DNA
<213> Homo sapiens

<400> 315
tcaagcccct tagattgaac a 21

<210> 316
<211> 20
<212> DNA
<213> Homo sapiens

<400> 316
gctgggcatg tagaactcaa 20

<210> 317
<211> 20
<212> DNA
<213> Homo sapiens

<400> 317
gggaaattgt caagggttt 20

<210> 318
<211> 21
<212> DNA
<213> Homo sapiens

<400> 318
cttagttgct gttgtgcttc t 21

<210> 319

<211> 20
<212> DNA
<213> Homo sapiens

<400> 319
agttgtagct gtatctgggt 20

<210> 320
<211> 20
<212> DNA
<213> Homo sapiens

<400> 320
agctgagtca tgttaaggc 20

<210> 321
<211> 21
<212> DNA
<213> Homo sapiens

<400> 321
caattcagac ttgcccaaa c 21

<210> 322
<211> 21
<212> DNA
<213> Homo sapiens

<400> 322
caatcattcc cacagttcca a 21

<210> 323
<211> 20
<212> DNA
<213> Homo sapiens

<400> 323
ctgtgatggt ccattcaagg 20

<210> 324
<211> 20
<212> DNA
<213> Homo sapiens

<400> 324
tagctggaaa ttgcaaggag 20

<210> 325
<211> 19
<212> DNA
<213> Homo sapiens

<400> 325
tctgttcacc tgagccttt 19

<210> 326
<211> 20

<212> DNA

<213> Homo sapiens

<400> 326

taacttggac tgtgaaccca 20

<210> 327

<211> 20

<212> DNA

<213> Homo sapiens

<400> 327

cgcaacagga tgaaggaaat 20

<210> 328

<211> 20

<212> DNA

<213> Homo sapiens

<400> 328

gactcacact ctgaaagcct 20

<210> 329

<211> 21

<212> DNA

<213> Homo sapiens

<400> 329

aatttaggta gcactgacct c 21

<210> 330

<211> 20

<212> DNA

<213> Homo sapiens

<400> 330

ctggggaatt aggaagcaga 20

<210> 331

<211> 19

<212> DNA

<213> Homo sapiens

<400> 331

atgacaaggc tggctcatc 19

<210> 332

<211> 20

<212> DNA

<213> Homo sapiens

<400> 332

ttagtttgg catgtggtgg 20

<210> 333

<211> 20

<212> DNA

<213> Homo sapiens

<400> 333

tggtgagga gtgtcttt 20

<210> 334

<211> 20

<212> DNA

<213> Homo sapiens

<400> 334

tcattgggg agtcattcac 20

<210> 335

<211> 20

<212> DNA

<213> Homo sapiens

<400> 335

gaagtgtgt gatgagggtg 20

<210> 336

<211> 20

<212> DNA

<213> Homo sapiens

<400> 336

aagtaggcc ctgtaagca 20

<210> 337

<211> 20

<212> DNA

<213> Homo sapiens

<400> 337

tgttggtcgg agtcagaaat 20

<210> 338

<211> 20

<212> DNA

<213> Homo sapiens

<400> 338

gtaaaagagg ttgggatgcc 20

<210> 339

<211> 20

<212> DNA

<213> Homo sapiens

<400> 339

cgttgacat ggatcatacc 20

<210> 340

<211> 22

<212> DNA

<213> Homo sapiens

<400> 340
tcacaacaag ggaaatagcc ta 22

<210> 341
<211> 20
<212> DNA
<213> Homo sapiens

<400> 341
tagtcaggta aacaacgcct 20

<210> 342
<211> 21
<212> DNA
<213> Homo sapiens

<400> 342
tctgtttctt gttggctga g 21

<210> 343
<211> 20
<212> DNA
<213> Homo sapiens

<400> 343
acataggtca cacaagggt 20

<210> 344
<211> 20
<212> DNA
<213> Homo sapiens

<400> 344
gtgtgacact ttctgcctt 20

<210> 345
<211> 21
<212> DNA
<213> Homo sapiens

<400> 345
ctggaaatag aaggccttg c 21

<210> 346
<211> 20
<212> DNA
<213> Homo sapiens

<400> 346
tcttggtctg ggaataagcc 20

<210> 347
<211> 20
<212> DNA
<213> Homo sapiens

<400> 347

tgcccctatg aacaacagaa 20

<210> 348

<211> 20

<212> DNA

<213> Homo sapiens

<400> 348

tgaacgtctt gcttaccac 20

<210> 349

<211> 19

<212> DNA

<213> Homo sapiens

<400> 349

gaaggaaggc agaggtaa 19

<210> 350

<211> 20

<212> DNA

<213> Homo sapiens

<400> 350

ctccacaaa gtctgcaac 20

<210> 351

<211> 20

<212> DNA

<213> Homo sapiens

<400> 351

atgtgaacca ttgaggga 20

<210> 352

<211> 20

<212> DNA

<213> Homo sapiens

<400> 352

aagagaaact accctggaa 20

<210> 353

<211> 20

<212> DNA

<213> Homo sapiens

<400> 353

gcatgtagtt cagtcaggc 20

<210> 354

<211> 20

<212> DNA

<213> Homo sapiens

<400> 354

atgaaatga atggggtgcg 20

<210> 355
<211> 20
<212> DNA
<213> Homo sapiens

<400> 355
ttttggcagt gatgacctg 20

<210> 356
<211> 20
<212> DNA
<213> Homo sapiens

<400> 356
ttcttggctt ttctgacct 20

<210> 357
<211> 21
<212> DNA
<213> Homo sapiens

<400> 357
ttgagaaaga cccaacaga a 21

<210> 358
<211> 22
<212> DNA
<213> Homo sapiens

<400> 358
gaaaataaca cagtagggat gc 22

<210> 359
<211> 20
<212> DNA
<213> Homo sapiens

<400> 359
gaatggagag gcagtttca 20

<210> 360
<211> 20
<212> DNA
<213> Homo sapiens

<400> 360
caccccttct ctgttttgca 20

<210> 361
<211> 21
<212> DNA
<213> Homo sapiens

<400> 361
agaagaaact tgcagtgttg g 21

<210> 362

<211> 21
<212> DNA
<213> Homo sapiens

<400> 362
tgcagcatta ttctttctgg g 21

<210> 363
<211> 21
<212> DNA
<213> Homo sapiens

<400> 363
acacacatat tagggaacag c 21

<210> 364
<211> 20
<212> DNA
<213> Homo sapiens

<400> 364
gagtgtaggt gcttgggtat 20

<210> 365
<211> 20
<212> DNA
<213> Homo sapiens

<400> 365
ccttagaatc ctagcgctt 20

<210> 366
<211> 20
<212> DNA
<213> Homo sapiens

<400> 366
tcatgaggtt gccagtgtt 20

<210> 367
<211> 20
<212> DNA
<213> Homo sapiens

<400> 367
ccccatacat catcacatgc 20

<210> 368
<211> 20
<212> DNA
<213> Homo sapiens

<400> 368
gggtaatgct ttctgggga 20

<210> 369
<211> 20

<212> DNA

<213> Homo sapiens

<400> 369

agttgagaag ggaaggcaag 20

<210> 370

<211> 21

<212> DNA

<213> Homo sapiens

<400> 370

ctctggtgg cttattttg a 21

<210> 371

<211> 22

<212> DNA

<213> Homo sapiens

<400> 371

tctggatttt ggctactcat ga 22

<210> 372

<211> 20

<212> DNA

<213> Homo sapiens

<400> 372

gtagtctctcc ttgcccttc 20

<210> 373

<211> 20

<212> DNA

<213> Homo sapiens

<400> 373

gacatgcaca gatcgaaacc 20

<210> 374

<211> 20

<212> DNA

<213> Homo sapiens

<400> 374

cgcatttgac aacagggatc 20

<210> 375

<211> 20

<212> DNA

<213> Homo sapiens

<400> 375

aagccacctg ttctctca 20

<210> 376

<211> 20

<212> DNA

<213> Homo sapiens

<400> 376

attccaacca ttccgacacc 20

<210> 377

<211> 20

<212> DNA

<213> Homo sapiens

<400> 377

aaagaaaatg gtgaacgtgc 20

<210> 378

<211> 20

<212> DNA

<213> Homo sapiens

<400> 378

tgatcagggc ttagagggtc 20

<210> 379

<211> 20

<212> DNA

<213> Homo sapiens

<400> 379

actccctatt gttctcccct 20

<210> 380

<211> 20

<212> DNA

<213> Homo sapiens

<400> 380

ctccttgaca gatgtgaccc 20

<210> 381

<211> 20

<212> DNA

<213> Homo sapiens

<400> 381

ttttggagtc tgagccacaa 20

<210> 382

<211> 19

<212> DNA

<213> Homo sapiens

<400> 382

ttgaagtccc gttgctgat 19

<210> 383

<211> 20

<212> DNA

<213> Homo sapiens

<400> 383

ttggggtcag ttctaacagt 20

<210> 384

<211> 20

<212> DNA

<213> Homo sapiens

<400> 384

ttttcaccac ctcttcctc 20

<210> 385

<211> 20

<212> DNA

<213> Homo sapiens

<400> 385

acctgaccac aagctttaca 20

<210> 386

<211> 20

<212> DNA

<213> Homo sapiens

<400> 386

cacatattgg cgcacagtac 20

<210> 387

<211> 20

<212> DNA

<213> Homo sapiens

<400> 387

gccatgcacc gatgaaaaat 20

<210> 388

<211> 20

<212> DNA

<213> Homo sapiens

<400> 388

ttgtgaggag atttctgggc 20

<210> 389

<211> 20

<212> DNA

<213> Homo sapiens

<400> 389

cacactaaga gcactgggaa 20

<210> 390

<211> 20

<212> DNA

<213> Homo sapiens

<400> 390

atgacctagc acatcttccc 20

<210> 391

<211> 20

<212> DNA

<213> Homo sapiens

<400> 391

acattttccc cattccatgc 20

<210> 392

<211> 20

<212> DNA

<213> Homo sapiens

<400> 392

gtctgtcaac cacactttgc 20

<210> 393

<211> 20

<212> DNA

<213> Homo sapiens

<400> 393

ctgtctctcc ttgtgcaaa 20

<210> 394

<211> 20

<212> DNA

<213> Homo sapiens

<400> 394

agtaacctgc gactctcagt 20

<210> 395

<211> 20

<212> DNA

<213> Homo sapiens

<400> 395

tagcatttaa ggagtgggct 20

<210> 396

<211> 20

<212> DNA

<213> Homo sapiens

<400> 396

ggcctcctca gtgatttgaa 20

<210> 397

<211> 20

<212> DNA

<213> Homo sapiens

<400> 397

ctttctttgc ctcccctgta 20

<210> 398

<211> 20

<212> DNA

<213> Homo sapiens

<400> 398

acttccattt gtgtcaacgg 20

<210> 399

<211> 20

<212> DNA

<213> Homo sapiens

<400> 399

tcttgctttg ggtagaggg 20

<210> 400

<211> 20

<212> DNA

<213> Homo sapiens

<400> 400

aaccacacct ccacaagaaa 20

<210> 401

<211> 20

<212> DNA

<213> Homo sapiens

<400> 401

caagatatga gggaggggaa 20

<210> 402

<211> 20

<212> DNA

<213> Homo sapiens

<400> 402

tctaacctgg gcccttctt 20

<210> 403

<211> 20

<212> DNA

<213> Homo sapiens

<400> 403

tgccctcca gaactgtaaa 20

<210> 404

<211> 20

<212> DNA

<213> Homo sapiens

<400> 404

gccaggtcac ttaacaaagc 20

<210> 405

<211> 19
<212> DNA
<213> Homo sapiens

<400> 405
caataaggcg ccaagttcg 19

<210> 406
<211> 20
<212> DNA
<213> Homo sapiens

<400> 406
gtcatcaggg gagcaaatgt 20

<210> 407
<211> 21
<212> DNA
<213> Homo sapiens

<400> 407
aacatgcaat ccctggaatt c 21

<210> 408
<211> 21
<212> DNA
<213> Homo sapiens

<400> 408
agttgtttca ggacaggatc t 21

<210> 409
<211> 21
<212> DNA
<213> Homo sapiens

<400> 409
tcctctgcc ttaataagc t 21

<210> 410
<211> 21
<212> DNA
<213> Homo sapiens

<400> 410
ttacaaggca tctgacagga a 21

<210> 411
<211> 21
<212> DNA
<213> Homo sapiens

<400> 411
ttactggtag gtttgagcac a 21

<210> 412
<211> 22

<212> DNA

<213> Homo sapiens

<400> 412

gagctacggt ctttctcatc ac 22

<210> 413

<211> 21

<212> DNA

<213> Homo sapiens

<400> 413

caccaattaa agtgtgctgc a 21

<210> 414

<211> 21

<212> DNA

<213> Homo sapiens

<400> 414

tccctccaa agtgccttat a 21

<210> 415

<211> 21

<212> DNA

<213> Homo sapiens

<400> 415

tggttggtt gggatacttg a 21

<210> 416

<211> 21

<212> DNA

<213> Homo sapiens

<400> 416

gaacccaaat cgatcatgca t 21

<210> 417

<211> 21

<212> DNA

<213> Homo sapiens

<400> 417

agagttaaac gtgcaatgtg g 21

<210> 418

<211> 22

<212> DNA

<213> Homo sapiens

<400> 418

gttcgttgg catagttgtt gt 22

<210> 419

<211> 21

<212> DNA

<213> Homo sapiens

<400> 419

agtttagcca aaggattcag c 21

<210> 420

<211> 22

<212> DNA

<213> Homo sapiens

<400> 420

tcaaccattt agaaccacct tg 22

<210> 421

<211> 21

<212> DNA

<213> Homo sapiens

<400> 421

aatgtccact ttagcggaga g 21

<210> 422

<211> 22

<212> DNA

<213> Homo sapiens

<400> 422

ggagtattct gttcatgttg gg 22

<210> 423

<211> 22

<212> DNA

<213> Homo sapiens

<400> 423

tttctagaat tgaggaaggg ca 22

<210> 424

<211> 21

<212> DNA

<213> Homo sapiens

<400> 424

aggataagac gaggcacaa t 21

<210> 425

<211> 22

<212> DNA

<213> Homo sapiens

<400> 425

ttctgtgtg acatgtacct ct 22

<210> 426

<211> 21

<212> DNA

<213> Homo sapiens

<400> 426

tccaacattt ctctctgtcc c 21

<210> 427

<211> 20

<212> DNA

<213> Homo sapiens

<400> 427

ataacgtgta ctctcagcc 20

<210> 428

<211> 21

<212> DNA

<213> Homo sapiens

<400> 428

gcacttgag gatgtaaaga c 21

<210> 429

<211> 21

<212> DNA

<213> Homo sapiens

<400> 429

tgatgcttt aggaccaggt t 21

<210> 430

<211> 22

<212> DNA

<213> Homo sapiens

<400> 430

aactccacag gaatcttct ga 22

<210> 431

<211> 20

<212> DNA

<213> Homo sapiens

<400> 431

catttctct gggaccgaat 20

<210> 432

<211> 21

<212> DNA

<213> Homo sapiens

<400> 432

ttctgaagct gacgaaattc c 21

<210> 433

<211> 21

<212> DNA

<213> Homo sapiens

<400> 433

gttgcttagt ccttgcttca c 21

<210> 434

<211> 21

<212> DNA

<213> Homo sapiens

<400> 434

aggtcattgg tctgcagtta t 21

<210> 435

<211> 21

<212> DNA

<213> Homo sapiens

<400> 435

agcatttaga gaacagcagt c 21

<210> 436

<211> 21

<212> DNA

<213> Homo sapiens

<400> 436

gtgtaagaag tgggtgggtt t 21

<210> 437

<211> 22

<212> DNA

<213> Homo sapiens

<400> 437

aaaggcagag cagtgtattt ag 22

<210> 438

<211> 22

<212> DNA

<213> Homo sapiens

<400> 438

agacaagaga acaatcaggt ga 22

<210> 439

<211> 21

<212> DNA

<213> Homo sapiens

<400> 439

caaagaagct ctaggacagg a 21

<210> 440

<211> 21

<212> DNA

<213> Homo sapiens

<400> 440

tgggtggagga aatcaatgtt g 21

<210> 441

<211> 20

<212> DNA

<213> Homo sapiens

<400> 441

cacaaggag gaaacgttct 20

<210> 442

<211> 21

<212> DNA

<213> Homo sapiens

<400> 442

tgagatttag tgccagctag a 21

<210> 443

<211> 21

<212> DNA

<213> Homo sapiens

<400> 443

aggattagtt tggctcctca g 21

<210> 444

<211> 21

<212> DNA

<213> Homo sapiens

<400> 444

cctgcactat ttctcaaag c 21

<210> 445

<211> 21

<212> DNA

<213> Homo sapiens

<400> 445

caatttcctt ctactgagc c 21

<210> 446

<211> 21

<212> DNA

<213> Homo sapiens

<400> 446

acgcttccca aatctatctg g 21

<210> 447

<211> 22

<212> DNA

<213> Homo sapiens

<400> 447

cttatttggtg tgccaatac ca 22

<210> 448

<211> 21
<212> DNA
<213> Homo sapiens

<400> 448
ttgcagcagg aacaccataa a 21

<210> 449
<211> 21
<212> DNA
<213> Homo sapiens

<400> 449
ctgttcatgt tgctaccaca g 21

<210> 450
<211> 21
<212> DNA
<213> Homo sapiens

<400> 450
ctgccttaga ttcactttcg g 21

<210> 451
<211> 21
<212> DNA
<213> Homo sapiens

<400> 451
ccatctgtga ggtcttcttt g 21

<210> 452
<211> 21
<212> DNA
<213> Homo sapiens

<400> 452
tccttggttg tgtatttagc c 21

<210> 453
<211> 20
<212> DNA
<213> Homo sapiens

<400> 453
agactcaact cacattggcc 20

<210> 454
<211> 20
<212> DNA
<213> Homo sapiens

<400> 454
ggtctgactc tgggtttgg 20

<210> 455
<211> 21

<212> DNA

<213> Homo sapiens

<400> 455

tttcatttca tctgcccac g 21

<210> 456

<211> 21

<212> DNA

<213> Homo sapiens

<400> 456

ttctgttatt cgccatcagt c 21

<210> 457

<211> 20

<212> DNA

<213> Homo sapiens

<400> 457

gaattgggaa ctgggaagc 20

<210> 458

<211> 21

<212> DNA

<213> Homo sapiens

<400> 458

gaactttgga gaggacagt t 21

<210> 459

<211> 21

<212> DNA

<213> Homo sapiens

<400> 459

aactgtcatg tgtgtctgct a 21

<210> 460

<211> 21

<212> DNA

<213> Homo sapiens

<400> 460

tgattccttc cacctaccaa a 21

<210> 461

<211> 21

<212> DNA

<213> Homo sapiens

<400> 461

gccaaaggtcc attatctcaa g 21

<210> 462

<211> 21

<212> DNA

<213> Homo sapiens

<400> 462

gaacctgcat tgtcattctc t 21

<210> 463

<211> 22

<212> DNA

<213> Homo sapiens

<400> 463

aagaacatca acaaactcca gg 22

<210> 464

<211> 21

<212> DNA

<213> Homo sapiens

<400> 464

tcaattctct ttcacacgtg c 21

<210> 465

<211> 21

<212> DNA

<213> Homo sapiens

<400> 465

aggtgctgga tctgaattc a 21

<210> 466

<211> 21

<212> DNA

<213> Homo sapiens

<400> 466

tccctctacc cgaatctctt a 21

<210> 467

<211> 21

<212> DNA

<213> Homo sapiens

<400> 467

tgggtttaa ggacactagc a 21

<210> 468

<211> 21

<212> DNA

<213> Homo sapiens

<400> 468

cgaaggtcac acagttagt c 21

<210> 469

<211> 21

<212> DNA

<213> Homo sapiens

<400> 469

atgtgccttg ttgattgatg g 21

<210> 470

<211> 21

<212> DNA

<213> Homo sapiens

<400> 470

agatggtatg tcacaaagca c 21

<210> 471

<211> 21

<212> DNA

<213> Homo sapiens

<400> 471

acactttgga gagcttcaga t 21

<210> 472

<211> 22

<212> DNA

<213> Homo sapiens

<400> 472

gtgcccagaa ttatttgtgt ct 22

<210> 473

<211> 21

<212> DNA

<213> Homo sapiens

<400> 473

gctctctgt ggaaacgatt a 21

<210> 474

<211> 21

<212> DNA

<213> Homo sapiens

<400> 474

agttgtttc tctggcctac t 21

<210> 475

<211> 21

<212> DNA

<213> Homo sapiens

<400> 475

accacctcaa agatttcatg g 21

<210> 476

<211> 22

<212> DNA

<213> Homo sapiens

<400> 476

gtcttcatct atttcgtgag cc 22

<210> 477

<211> 21

<212> DNA

<213> Homo sapiens

<400> 477

tcatcccaga ttcagaatgc c 21

<210> 478

<211> 21

<212> DNA

<213> Homo sapiens

<400> 478

cgttcaatga agtcccttgt c 21

<210> 479

<211> 21

<212> DNA

<213> Homo sapiens

<400> 479

ttcacaagaa ctctgctgga t 21

<210> 480

<211> 21

<212> DNA

<213> Homo sapiens

<400> 480

gaagccttct agtgggacta a 21

<210> 481

<211> 21

<212> DNA

<213> Homo sapiens

<400> 481

gttaggggtca tgggtcactt t 21

<210> 482

<211> 21

<212> DNA

<213> Homo sapiens

<400> 482

gcctttgtag agtggacttc t 21

<210> 483

<211> 21

<212> DNA

<213> Homo sapiens

<400> 483

ggcttctga tactgcttc c 21

<210> 484
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 484
 aggtgtgcaa tactcaagga a 21

 <210> 485
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 485
 aaggtcttag gagtgaggac a 21

 <210> 486
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 486
 tcgtgctatt tcagtcagat ct 22

 <210> 487
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 487
 tgtccagccg taacattca t 21

 <210> 488
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 488
 aatggacatc ttccaggtct g 21

 <210> 489
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 489
 tcaaattggg atcgattag g 21

 <210> 490
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 490
 atgcctgggt ttattcatct tg 22

 <210> 491

<211> 21
<212> DNA
<213> Homo sapiens

<400> 491
ggagaagttt gggttgatc c 21

<210> 492
<211> 21
<212> DNA
<213> Homo sapiens

<400> 492
tgataggagc catcagttct t 21

<210> 493
<211> 21
<212> DNA
<213> Homo sapiens

<400> 493
agcagatgtt gttagcttct c 21

<210> 494
<211> 21
<212> DNA
<213> Homo sapiens

<400> 494
ttctctgtca cttccatgag g 21

<210> 495
<211> 22
<212> DNA
<213> Homo sapiens

<400> 495
ccagtaactt attctgccag ag 22

<210> 496
<211> 21
<212> DNA
<213> Homo sapiens

<400> 496
tgagagacaa gctgcattac a 21

<210> 497
<211> 22
<212> DNA
<213> Homo sapiens

<400> 497
gcacagaaat tacagttcat gg 22

<210> 498
<211> 21

<212> DNA

<213> Homo sapiens

<400> 498

gctctcgat ctgacagtga a 21

<210> 499

<211> 21

<212> DNA

<213> Homo sapiens

<400> 499

caggcatctt ggttttagt g 21

<210> 500

<211> 21

<212> DNA

<213> Homo sapiens

<400> 500

cgatgatgaac agtgaatgact t 21

<210> 501

<211> 21

<212> DNA

<213> Homo sapiens

<400> 501

cgccatttgt tctctattc a 21

<210> 502

<211> 21

<212> DNA

<213> Homo sapiens

<400> 502

ttcgtagct actgggtact c 21

<210> 503

<211> 21

<212> DNA

<213> Homo sapiens

<400> 503

ccacccttta cacctatcca a 21

<210> 504

<211> 21

<212> DNA

<213> Homo sapiens

<400> 504

agatgcaca aaggagaaga c 21

<210> 505

<211> 22

<212> DNA

<213> Homo sapiens

<400> 505

tctactgtgt caaagcagat tg 22

<210> 506

<211> 21

<212> DNA

<213> Homo sapiens

<400> 506

ttcttcttag ccttccttc c 21

<210> 507

<211> 21

<212> DNA

<213> Homo sapiens

<400> 507

tctctggctg tgcagtaa t 21

<210> 508

<211> 21

<212> DNA

<213> Homo sapiens

<400> 508

aaactcccag cttaatccc t 21

<210> 509

<211> 21

<212> DNA

<213> Homo sapiens

<400> 509

aagaatgggt gagtgggtt c 21

<210> 510

<211> 21

<212> DNA

<213> Homo sapiens

<400> 510

ggaaactgaa ttgccaagtc t 21

<210> 511

<211> 20

<212> DNA

<213> Homo sapiens

<400> 511

ctcccaactt ttatgcagcc 20

<210> 512

<211> 21

<212> DNA

<213> Homo sapiens

<400> 512
gctcagggaa tatcttggga a 21

<210> 513
<211> 21
<212> DNA
<213> Homo sapiens

<400> 513
acattcagca agtaggaagg a 21

<210> 514
<211> 20
<212> DNA
<213> Homo sapiens

<400> 514
cccagaagag cagtaacaac 20

<210> 515
<211> 20
<212> DNA
<213> Homo sapiens

<400> 515
gaaaaagggg gataggcatt 20

<210> 516
<211> 21
<212> DNA
<213> Homo sapiens

<400> 516
ccaacaact gcaataaaag g 21

<210> 517
<211> 20
<212> DNA
<213> Homo sapiens

<400> 517
accgaaattg ctgtctcta 20

<210> 518
<211> 20
<212> DNA
<213> Homo sapiens

<400> 518
ccttagtgtg acaggacagg 20

<210> 519
<211> 20
<212> DNA
<213> Homo sapiens

<400> 519

ccaagacaac taggccaatg 20

<210> 520

<211> 21

<212> DNA

<213> Homo sapiens

<400> 520

gaagagatga tgcaaaagag c 21

<210> 521

<211> 20

<212> DNA

<213> Homo sapiens

<400> 521

tccaagcaag ggatctcttc 20

<210> 522

<211> 20

<212> DNA

<213> Homo sapiens

<400> 522

gaatggtcag ggaaggggtt 20

<210> 523

<211> 20

<212> DNA

<213> Homo sapiens

<400> 523

agtcttcagc catcttcctg 20

<210> 524

<211> 21

<212> DNA

<213> Homo sapiens

<400> 524

gcatttcag gctttacaag t 21

<210> 525

<211> 20

<212> DNA

<213> Homo sapiens

<400> 525

ctctctctcc ctggtcagat 20

<210> 526

<211> 20

<212> DNA

<213> Homo sapiens

<400> 526

cagcaattct caggctcaga 20

<210> 527

<211> 21

<212> DNA

<213> Homo sapiens

<400> 527

tctgaaacaa agcctcctta g 21

<210> 528

<211> 21

<212> DNA

<213> Homo sapiens

<400> 528

aggataaggt ttcccatgct c 21

<210> 529

<211> 21

<212> DNA

<213> Homo sapiens

<400> 529

atgtatctga aggagctctg c 21

<210> 530

<211> 20

<212> DNA

<213> Homo sapiens

<400> 530

ggccttcac acaacaaca 20

<210> 531

<211> 20

<212> DNA

<213> Homo sapiens

<400> 531

tgtgtcccat ctacaaagcc 20

<210> 532

<211> 20

<212> DNA

<213> Homo sapiens

<400> 532

tcctgaact cttccaagc 20

<210> 533

<211> 20

<212> DNA

<213> Homo sapiens

<400> 533

tgtttctctg tccaagtcca 20

<210> 534

<211> 19
<212> DNA
<213> Homo sapiens

<400> 534
cagcatccat cgctcgaaa 19

<210> 535
<211> 20
<212> DNA
<213> Homo sapiens

<400> 535
ggtattggtg ggggaaatga 20

<210> 536
<211> 24
<212> DNA
<213> Homo sapiens

<400> 536
gcactgctgt aaaagatcta tgag 24

<210> 537
<211> 19
<212> DNA
<213> Homo sapiens

<400> 537
actcaaaggc acatttcgc 19

<210> 538
<211> 22
<212> DNA
<213> Homo sapiens

<400> 538
attctattcc gatcacagcc tt 22

<210> 539
<211> 20
<212> DNA
<213> Homo sapiens

<400> 539
ctacctgaca aatggagctt 20

<210> 540
<211> 21
<212> DNA
<213> Homo sapiens

<400> 540
gaaatggcca tgtgtactga g 21

<210> 541
<211> 20

<212> DNA

<213> Homo sapiens

<400> 541

gaagcctctc aagctacaag 20

<210> 542

<211> 22

<212> DNA

<213> Homo sapiens

<400> 542

gaatgagatt agggagcaaa gt 22

<210> 543

<211> 20

<212> DNA

<213> Homo sapiens

<400> 543

ggaagtaaga agagtgtctgc 20

<210> 544

<211> 20

<212> DNA

<213> Homo sapiens

<400> 544

gtctctgatt gaagaagtgt 20

<210> 545

<211> 19

<212> DNA

<213> Homo sapiens

<400> 545

ctgctccttt gtctctgt 19

<210> 546

<211> 21

<212> DNA

<213> Homo sapiens

<400> 546

taaggtgaga gtgtgaggaa g 21

<210> 547

<211> 21

<212> DNA

<213> Homo sapiens

<400> 547

ccaggggaac atttactcag a 21

<210> 548

<211> 20

<212> DNA

<213> Homo sapiens

<400> 548

agggtacatg taaggcagct 20

<210> 549

<211> 20

<212> DNA

<213> Homo sapiens

<400> 549

ttctgtggca ttgtgtcttg 20

<210> 550

<211> 20

<212> DNA

<213> Homo sapiens

<400> 550

ccccaaattt accccactct 20

<210> 551

<211> 20

<212> DNA

<213> Homo sapiens

<400> 551

atccctagca ctttcaggac 20

<210> 552

<211> 20

<212> DNA

<213> Homo sapiens

<400> 552

ttaccaatcc atccagcctg 20

<210> 553

<211> 20

<212> DNA

<213> Homo sapiens

<400> 553

agaagctaaa caggttgccc 20

<210> 554

<211> 20

<212> DNA

<213> Homo sapiens

<400> 554

cataagagca cagccaagat 20

<210> 555

<211> 20

<212> DNA

<213> Homo sapiens

<400> 555

tgtcctgccca cttttacatc 20

<210> 556

<211> 21

<212> DNA

<213> Homo sapiens

<400> 556

gagctaagca gaacctaagg a 21

<210> 557

<211> 21

<212> DNA

<213> Homo sapiens

<400> 557

ttaagcaaca ggaacctacc c 21

<210> 558

<211> 21

<212> DNA

<213> Homo sapiens

<400> 558

gccaagggta atcatagcaa c 21

<210> 559

<211> 21

<212> DNA

<213> Homo sapiens

<400> 559

tcataatgaa acccttgctg c 21

<210> 560

<211> 21

<212> DNA

<213> Homo sapiens

<400> 560

aatcctagtg catgagactc c 21

<210> 561

<211> 21

<212> DNA

<213> Homo sapiens

<400> 561

tactgcctgc atcattacca c 21

<210> 562

<211> 21

<212> DNA

<213> Homo sapiens

<400> 562

attaacaatg aggagccagg t 21

<210> 563

<211> 21

<212> DNA

<213> Homo sapiens

<400> 563

gagagatggt tgagaaatgc c 21

<210> 564

<211> 21

<212> DNA

<213> Homo sapiens

<400> 564

actacaacca ccaattacag c 21

<210> 565

<211> 21

<212> DNA

<213> Homo sapiens

<400> 565

agtgacattt ccaagggctt t 21

<210> 566

<211> 21

<212> DNA

<213> Homo sapiens

<400> 566

ggagatggga agacgattag a 21

<210> 567

<211> 22

<212> DNA

<213> Homo sapiens

<400> 567

agtccttcag tcttacatgg gt 22

<210> 568

<211> 21

<212> DNA

<213> Homo sapiens

<400> 568

tagtttctgt gatcctggca g 21

<210> 569

<211> 20

<212> DNA

<213> Homo sapiens

<400> 569

tttctccag ctgttcctag 20

<210> 570

<211> 21

<212> DNA

<213> Homo sapiens

<400> 570

tacggaactt cgaatcaact c 21

<210> 571

<211> 21

<212> DNA

<213> Homo sapiens

<400> 571

tcaagtcacc ctcattgtag g 21

<210> 572

<211> 21

<212> DNA

<213> Homo sapiens

<400> 572

tgtaacgtgg atgtgagatt g 21

<210> 573

<211> 21

<212> DNA

<213> Homo sapiens

<400> 573

ttgagctaag tctgcatcac t 21

<210> 574

<211> 21

<212> DNA

<213> Homo sapiens

<400> 574

ctagagaaag caacgcctaa g 21

<210> 575

<211> 21

<212> DNA

<213> Homo sapiens

<400> 575

agcaccttcc atagcttctt t 21

<210> 576

<211> 21

<212> DNA

<213> Homo sapiens

<400> 576

gtgtcttctg atggccaaat g 21

<210> 577

<211> 21
<212> DNA
<213> Homo sapiens

<400> 577
aatcaggtga aaggtacctc c 21

<210> 578
<211> 21
<212> DNA
<213> Homo sapiens

<400> 578
ccttcacaat tcagggaaca a 21

<210> 579
<211> 21
<212> DNA
<213> Homo sapiens

<400> 579
tggaccagct tctatgcaat t 21

<210> 580
<211> 21
<212> DNA
<213> Homo sapiens

<400> 580
aatgaccctt acaactccga a 21

<210> 581
<211> 21
<212> DNA
<213> Homo sapiens

<400> 581
tttgggaagt gattgtgaag g 21

<210> 582
<211> 21
<212> DNA
<213> Homo sapiens

<400> 582
tcagctgcat agaccttgtt t 21

<210> 583
<211> 21
<212> DNA
<213> Homo sapiens

<400> 583
tcatttggtc tcattacggg c 21

<210> 584
<211> 20

<212> DNA

<213> Homo sapiens

<400> 584

ttctacctgg gttctctgg 20

<210> 585

<211> 21

<212> DNA

<213> Homo sapiens

<400> 585

taacttctg agcacacatc a 21

<210> 586

<211> 21

<212> DNA

<213> Homo sapiens

<400> 586

gggtaaattc aggaatgcac a 21

<210> 587

<211> 21

<212> DNA

<213> Homo sapiens

<400> 587

atttctctg gtgagttgc g 21

<210> 588

<211> 21

<212> DNA

<213> Homo sapiens

<400> 588

cctcttctg acatgttgtt g 21

<210> 589

<211> 21

<212> DNA

<213> Homo sapiens

<400> 589

gttggtgcca gattgtaact t 21

<210> 590

<211> 21

<212> DNA

<213> Homo sapiens

<400> 590

gcctggctca ataatagtc t 21

<210> 591

<211> 21

<212> DNA

<213> Homo sapiens

<400> 591

atgttcctt ctctacgtt g 21

<210> 592

<211> 20

<212> DNA

<213> Homo sapiens

<400> 592

gagtgagcg ctaccttat 20

<210> 593

<211> 20

<212> DNA

<213> Homo sapiens

<400> 593

agaatggga atggaagga 20

<210> 594

<211> 20

<212> DNA

<213> Homo sapiens

<400> 594

cacaatacat gggctgttt 20

<210> 595

<211> 21

<212> DNA

<213> Homo sapiens

<400> 595

ccactccaac tctgtttta c 21

<210> 596

<211> 21

<212> DNA

<213> Homo sapiens

<400> 596

gatgtggatt gtcttgttg c 21

<210> 597

<211> 22

<212> DNA

<213> Homo sapiens

<400> 597

agccttcat tgcacattc ag 22

<210> 598

<211> 20

<212> DNA

<213> Homo sapiens

<400> 598

tcccaccaca agaccaattt 20

<210> 599

<211> 21

<212> DNA

<213> Homo sapiens

<400> 599

gaagataggt ggtggagttc a 21

<210> 600

<211> 21

<212> DNA

<213> Homo sapiens

<400> 600

ctgtttgaat gaagttggct g 21

<210> 601

<211> 21

<212> DNA

<213> Homo sapiens

<400> 601

tatacatggg tgggatttgc c 21

<210> 602

<211> 21

<212> DNA

<213> Homo sapiens

<400> 602

tttgtgatgg accatctaac c 21

<210> 603

<211> 20

<212> DNA

<213> Homo sapiens

<400> 603

gaagatctgg tgtcccacta 20

<210> 604

<211> 20

<212> DNA

<213> Homo sapiens

<400> 604

atctgaagat ctccgtggta 20

<210> 605

<211> 21

<212> DNA

<213> Homo sapiens

<400> 605

atgtatgaac catttctgc t 21

<210> 606

<211> 22

<212> DNA

<213> Homo sapiens

<400> 606

agcacagaat tgaatgaagg aa 22

<210> 607

<211> 20

<212> DNA

<213> Homo sapiens

<400> 607

gcatgagtaa ggctgaagtg 20

<210> 608

<211> 24

<212> DNA

<213> Homo sapiens

<400> 608

aaaggcttat attgctttg aatc 24

<210> 609

<211> 20

<212> DNA

<213> Homo sapiens

<400> 609

ttgctgttgt tgggatcaag 20

<210> 610

<211> 20

<212> DNA

<213> Homo sapiens

<400> 610

gcttctgcat ccacctatct 20

<210> 611

<211> 20

<212> DNA

<213> Homo sapiens

<400> 611

aaaagctgcc taaatgcca 20

<210> 612

<211> 20

<212> DNA

<213> Homo sapiens

<400> 612

agtcagcaag ttagcagaaa 20

<210> 613

<211> 20

<212> DNA

<213> Homo sapiens

<400> 613

cccacattta tccctgtcc 20

<210> 614

<211> 20

<212> DNA

<213> Homo sapiens

<400> 614

tgtctgattc catcttccc 20

<210> 615

<211> 19

<212> DNA

<213> Homo sapiens

<400> 615

cagccaccaa aacacaatg 19

<210> 616

<211> 20

<212> DNA

<213> Homo sapiens

<400> 616

aaggcctgtt ttgtgtgtag 20

<210> 617

<211> 21

<212> DNA

<213> Homo sapiens

<400> 617

acagtcaca gatctttaag c 21

<210> 618

<211> 23

<212> DNA

<213> Homo sapiens

<400> 618

ggcattataa agagatagct cca 23

<210> 619

<211> 20

<212> DNA

<213> Homo sapiens

<400> 619

tgttttcct tgccctgtaa 20

<210> 620

<211> 20
<212> DNA
<213> Homo sapiens

<400> 620
taaccagatg aatgagggca 20

<210> 621
<211> 20
<212> DNA
<213> Homo sapiens

<400> 621
caacaagcca aaaccacatc 20

<210> 622
<211> 20
<212> DNA
<213> Homo sapiens

<400> 622
gttggttctt gaagacctga 20

<210> 623
<211> 22
<212> DNA
<213> Homo sapiens

<400> 623
tgtggttaagt agtctctaaa ga 22

<210> 624
<211> 20
<212> DNA
<213> Homo sapiens

<400> 624
accaaatttc cagatcacgg 20

<210> 625
<211> 20
<212> DNA
<213> Homo sapiens

<400> 625
aatgaatggt catggctcac 20

<210> 626
<211> 20
<212> DNA
<213> Homo sapiens

<400> 626
gccctgaagc acattaaagt 20

<210> 627
<211> 20

<212> DNA

<213> Homo sapiens

<400> 627

gcctccaggt ttatgacaac 20

<210> 628

<211> 20

<212> DNA

<213> Homo sapiens

<400> 628

cagctctatt ccccttctga 20

<210> 629

<211> 20

<212> DNA

<213> Homo sapiens

<400> 629

ccttgaagg gaaagttgat 20

<210> 630

<211> 18

<212> DNA

<213> Homo sapiens

<400> 630

gtcccaccct gctcttag 18

<210> 631

<211> 20

<212> DNA

<213> Homo sapiens

<400> 631

cagagtaaga cagtgggaca 20

<210> 632

<211> 20

<212> DNA

<213> Homo sapiens

<400> 632

aagtgtggtg cataaaggat 20

<210> 633

<211> 20

<212> DNA

<213> Homo sapiens

<400> 633

ctgtaagaag gagggttgg 20

<210> 634

<211> 20

<212> DNA

<213> Homo sapiens

<400> 634

gaggttgatg agaggtaggg 20

<210> 635

<211> 20

<212> DNA

<213> Homo sapiens

<400> 635

agccagggat attgtgaag 20

<210> 636

<211> 20

<212> DNA

<213> Homo sapiens

<400> 636

caggtaatg tgtgtccag 20

<210> 637

<211> 20

<212> DNA

<213> Homo sapiens

<400> 637

ttgattcca tgcagaagg 20

<210> 638

<211> 20

<212> DNA

<213> Homo sapiens

<400> 638

taattggcc ttaggggtg 20

<210> 639

<211> 21

<212> DNA

<213> Homo sapiens

<400> 639

tccataaaag gtgcttaaag c 21

<210> 640

<211> 20

<212> DNA

<213> Homo sapiens

<400> 640

ttgtatcaca ccatcgtgga 20

<210> 641

<211> 20

<212> DNA

<213> Homo sapiens

<400> 641

actgctgaga acaatcatgc 20

<210> 642

<211> 20

<212> DNA

<213> Homo sapiens

<400> 642

ggtgtggaga attgtttgc 20

<210> 643

<211> 20

<212> DNA

<213> Homo sapiens

<400> 643

tgatattagg cgggtggcta 20

<210> 644

<211> 20

<212> DNA

<213> Homo sapiens

<400> 644

tctcacctaa aatctggggc 20

<210> 645

<211> 22

<212> DNA

<213> Homo sapiens

<400> 645

aggactgtga cactttatct tt 22

<210> 646

<211> 21

<212> DNA

<213> Homo sapiens

<400> 646

atgcgaggta gaaaatgaga g 21

<210> 647

<211> 21

<212> DNA

<213> Homo sapiens

<400> 647

tgtggcttta aggttctgaa g 21

<210> 648

<211> 20

<212> DNA

<213> Homo sapiens

<400> 648

tcgttgctat tctgcttga 20

<210> 649

<211> 20

<212> DNA

<213> Homo sapiens

<400> 649

tccctttgt gggttcttg 20

<210> 650

<211> 20

<212> DNA

<213> Homo sapiens

<400> 650

tgccgcact cttcattaat 20

<210> 651

<211> 20

<212> DNA

<213> Homo sapiens

<400> 651

actggcttct cctcattagt 20

<210> 652

<211> 20

<212> DNA

<213> Homo sapiens

<400> 652

actgattgc catgtagagc 20

<210> 653

<211> 20

<212> DNA

<213> Homo sapiens

<400> 653

gaatgcata ttgcctgcca 20

<210> 654

<211> 20

<212> DNA

<213> Homo sapiens

<400> 654

tcactcgctt agaattgtgc 20

<210> 655

<211> 21

<212> DNA

<213> Homo sapiens

<400> 655

accattaact tcctgcaaac t 21

<210> 656

<211> 20

<212> DNA

<213> Homo sapiens

<400> 656

taaagcccca taccaggatt 20

<210> 657

<211> 20

<212> DNA

<213> Homo sapiens

<400> 657

ccaaaaatca cccatatgcg 20

<210> 658

<211> 20

<212> DNA

<213> Homo sapiens

<400> 658

ataaccaggg tgctcaaag 20

<210> 659

<211> 19

<212> DNA

<213> Homo sapiens

<400> 659

tccacagcag aagtaacga 19

<210> 660

<211> 21

<212> DNA

<213> Homo sapiens

<400> 660

aggaaagcta tgaagaaagg g 21

<210> 661

<211> 20

<212> DNA

<213> Homo sapiens

<400> 661

agctccagag tgtcagtatt 20

<210> 662

<211> 22

<212> DNA

<213> Homo sapiens

<400> 662

ttgattcca gcactgaact tt 22

<210> 663

<211> 20
<212> DNA
<213> Homo sapiens

<400> 663
tgtttgattt ttcaggctga 20

<210> 664
<211> 20
<212> DNA
<213> Homo sapiens

<400> 664
ctggtcattc ctgagtgct 20

<210> 665
<211> 24
<212> DNA
<213> Homo sapiens

<400> 665
tcctgtttta cacttttcta actt 24

<210> 666
<211> 20
<212> DNA
<213> Homo sapiens

<400> 666
acctcaacct gtttagcac 20

<210> 667
<211> 20
<212> DNA
<213> Homo sapiens

<400> 667
cagtgtgtgt catgccaaat 20

<210> 668
<211> 21
<212> DNA
<213> Homo sapiens

<400> 668
ggtctatgtt aatcttgggc c 21

<210> 669
<211> 21
<212> DNA
<213> Homo sapiens

<400> 669
agccagtctg tatctaaagg t 21

<210> 670
<211> 20

<212> DNA

<213> Homo sapiens

<400> 670

actcttgggg ttcttcagt 20

<210> 671

<211> 21

<212> DNA

<213> Homo sapiens

<400> 671

cgaaccaaaa gcaaaatcct t 21

<210> 672

<211> 20

<212> DNA

<213> Homo sapiens

<400> 672

aatctatgga ggtcactggg 20

<210> 673

<211> 20

<212> DNA

<213> Homo sapiens

<400> 673

aggctcttgt agtttgcttg 20

<210> 674

<211> 20

<212> DNA

<213> Homo sapiens

<400> 674

gtgagagcca atagagtgtg 20

<210> 675

<211> 20

<212> DNA

<213> Homo sapiens

<400> 675

gcatggtgtg tgaaagtgat 20

<210> 676

<211> 20

<212> DNA

<213> Homo sapiens

<400> 676

atgctgcttt tgactgatgt 20

<210> 677

<211> 20

<212> DNA

<213> Homo sapiens

<400> 677

cgaagctgta ttctgtctc 20

<210> 678

<211> 19

<212> DNA

<213> Homo sapiens

<400> 678

atggactaac tggagagcg 19

<210> 679

<211> 20

<212> DNA

<213> Homo sapiens

<400> 679

atgtctgcc agtaaacaca 20

<210> 680

<211> 20

<212> DNA

<213> Homo sapiens

<400> 680

tgccactaaa cacctaagga 20

<210> 681

<211> 20

<212> DNA

<213> Homo sapiens

<400> 681

ttggaaattt tggggtcagg 20

<210> 682

<211> 20

<212> DNA

<213> Homo sapiens

<400> 682

ttctgacctc ccttactgag 20

<210> 683

<211> 19

<212> DNA

<213> Homo sapiens

<400> 683

tatgtgcttg cgatgtgtt 19

<210> 684

<211> 20

<212> DNA

<213> Homo sapiens

<400> 684

gaaccttagg gccagtctat 20

<210> 685

<211> 21

<212> DNA

<213> Homo sapiens

<400> 685

agaacctgat gtgttttcct c 21

<210> 686

<211> 20

<212> DNA

<213> Homo sapiens

<400> 686

atgtgagaga agcaaaaccc 20

<210> 687

<211> 20

<212> DNA

<213> Homo sapiens

<400> 687

gtagttgtct tgagggcttt 20

<210> 688

<211> 20

<212> DNA

<213> Homo sapiens

<400> 688

cctggtaac aacatatggg 20

<210> 689

<211> 21

<212> DNA

<213> Homo sapiens

<400> 689

agaatattgc attggccag a 21

<210> 690

<211> 21

<212> DNA

<213> Homo sapiens

<400> 690

aaagctatgc aaatagtggc a 21

<210> 691

<211> 20

<212> DNA

<213> Homo sapiens

<400> 691

agttccaac agaggcta 20

<210> 692

<211> 20

<212> DNA

<213> Homo sapiens

<400> 692

agttataggt gaggaagggc 20

<210> 693

<211> 20

<212> DNA

<213> Homo sapiens

<400> 693

cactgcaaaa gaaggaggtt 20

<210> 694

<211> 21

<212> DNA

<213> Homo sapiens

<400> 694

tctcaacatc gctgatctag t 21

<210> 695

<211> 20

<212> DNA

<213> Homo sapiens

<400> 695

aggtagctgg aaaaggagaa 20

<210> 696

<211> 21

<212> DNA

<213> Homo sapiens

<400> 696

tgaaattgcc cagaattgag t 21

<210> 697

<211> 20

<212> DNA

<213> Homo sapiens

<400> 697

atttctctgg acttctgaca 20

<210> 698

<211> 21

<212> DNA

<213> Homo sapiens

<400> 698

tgttattcct cttctgtcc a 21

<210> 699

<211> 20

<212> DNA

<213> Homo sapiens

<400> 699

taaccacaca actacagctt 20

<210> 700

<211> 20

<212> DNA

<213> Homo sapiens

<400> 700

attcaaaatg gggacgagag 20

<210> 701

<211> 19

<212> DNA

<213> Homo sapiens

<400> 701

tcccagtttg ctactctgg 19

<210> 702

<211> 24

<212> DNA

<213> Homo sapiens

<400> 702

tctcattatg tgaagattgc ttic 24

<210> 703

<211> 23

<212> DNA

<213> Homo sapiens

<400> 703

ttaagattaa gcagtcttct tgg 23

<210> 704

<211> 20

<212> DNA

<213> Homo sapiens

<400> 704

caacagatct gattctgccc 20

<210> 705

<211> 20

<212> DNA

<213> Homo sapiens

<400> 705

catgtgttcc aaagttggct 20

<210> 706

<211> 21
<212> DNA
<213> Homo sapiens

<400> 706
actatagcat tagggtgagg g 21

<210> 707
<211> 20
<212> DNA
<213> Homo sapiens

<400> 707
gagatttgga catgcttca 20

<210> 708
<211> 19
<212> DNA
<213> Homo sapiens

<400> 708
cccaccacca gttgtcatc 19

<210> 709
<211> 21
<212> DNA
<213> Homo sapiens

<400> 709
gccactcact tcctagataa t 21

<210> 710
<211> 20
<212> DNA
<213> Homo sapiens

<400> 710
acagtatctc agggccttat 20

<210> 711
<211> 21
<212> DNA
<213> Homo sapiens

<400> 711
tcagtagttc ctcatgct a 21

<210> 712
<211> 20
<212> DNA
<213> Homo sapiens

<400> 712
aatgcatgaa agtccaggaa 20

<210> 713
<211> 21

<212> DNA

<213> Homo sapiens

<400> 713

acatgcactc ttgtctatg c 21

<210> 714

<211> 22

<212> DNA

<213> Homo sapiens

<400> 714

cacatatact ggctttctgg tc 22

<210> 715

<211> 19

<212> DNA

<213> Homo sapiens

<400> 715

gcacatgtca ttagcaggg 19

<210> 716

<211> 20

<212> DNA

<213> Homo sapiens

<400> 716

acatgtctca ttatggagcc 20

<210> 717

<211> 20

<212> DNA

<213> Homo sapiens

<400> 717

acaaagacag gaatagggct 20

<210> 718

<211> 24

<212> DNA

<213> Homo sapiens

<400> 718

caatctgctg acttgcttct tttc 24

<210> 719

<211> 21

<212> DNA

<213> Homo sapiens

<400> 719

ctttggctca gaatctcca a 21

<210> 720

<211> 21

<212> DNA

<213> Homo sapiens

<400> 720

tgtatgagga ccagcagtaa a 21

<210> 721

<211> 20

<212> DNA

<213> Homo sapiens

<400> 721

tcttttcccc ttgtgcatag 20

<210> 722

<211> 20

<212> DNA

<213> Homo sapiens

<400> 722

gcttagtgtg tgtgatccgt 20

<210> 723

<211> 20

<212> DNA

<213> Homo sapiens

<400> 723

actcaccttt cccaagaaga 20

<210> 724

<211> 20

<212> DNA

<213> Homo sapiens

<400> 724

tggtagtggg aagaggttga 20

<210> 725

<211> 20

<212> DNA

<213> Homo sapiens

<400> 725

gcatggagaa caaaagctga 20

<210> 726

<211> 20

<212> DNA

<213> Homo sapiens

<400> 726

tgtgagcaag aaactgaagg 20

<210> 727

<211> 20

<212> DNA

<213> Homo sapiens

<400> 727

agtatcactt gtccagctca 20

<210> 728

<211> 20

<212> DNA

<213> Homo sapiens

<400> 728

cacaggacta ggtaggcttt 20

<210> 729

<211> 21

<212> DNA

<213> Homo sapiens

<400> 729

gtgttaacag cttcccttc a 21

<210> 730

<211> 23

<212> DNA

<213> Homo sapiens

<400> 730

tcatgtacag aaagaattag cct 23

<210> 731

<211> 20

<212> DNA

<213> Homo sapiens

<400> 731

agaggccaag tgaccaaata 20

<210> 732

<211> 21

<212> DNA

<213> Homo sapiens

<400> 732

aagccagtaa ttcatttcc c 21

<210> 733

<211> 21

<212> DNA

<213> Homo sapiens

<400> 733

ccatgacata acacatcacc a 21

<210> 734

<211> 20

<212> DNA

<213> Homo sapiens

<400> 734

atagatttcc tctgggctg 20

<210> 735

<211> 20

<212> DNA

<213> Homo sapiens

<400> 735

ccacctctgt acccactatc 20

<210> 736

<211> 20

<212> DNA

<213> Homo sapiens

<400> 736

ttccctggaa gatagccaat 20

<210> 737

<211> 20

<212> DNA

<213> Homo sapiens

<400> 737

tggacacgta aaagaagggtg 20

<210> 738

<211> 20

<212> DNA

<213> Homo sapiens

<400> 738

ctgagaacct tgtccaactg 20

<210> 739

<211> 20

<212> DNA

<213> Homo sapiens

<400> 739

tttcgctagt ctttgcaactt 20

<210> 740

<211> 20

<212> DNA

<213> Homo sapiens

<400> 740

gcggcaataa ttgtcacaaa 20

<210> 741

<211> 20

<212> DNA

<213> Homo sapiens

<400> 741

cagaaatgtg tcaggctaca 20

<210> 742
<211> 20
<212> DNA
<213> Homo sapiens

<400> 742
aactcttcat ttgacgggg 20

<210> 743
<211> 20
<212> DNA
<213> Homo sapiens

<400> 743
tgggttgtgc tgtgtttag 20

<210> 744
<211> 19
<212> DNA
<213> Homo sapiens

<400> 744
gctcagctcc ttcatctg 19

<210> 745
<211> 20
<212> DNA
<213> Homo sapiens

<400> 745
aggacattca gcctatttc 20

<210> 746
<211> 20
<212> DNA
<213> Homo sapiens

<400> 746
acacagtatc aaggtaaca 20

<210> 747
<211> 20
<212> DNA
<213> Homo sapiens

<400> 747
gcagaaccac agtctatgag 20

<210> 748
<211> 21
<212> DNA
<213> Homo sapiens

<400> 748
aatgctcaa gttattccag a 21

<210> 749

<211> 20
<212> DNA
<213> Homo sapiens

<400> 749
aagagagaag cgacaaaacc 20

<210> 750
<211> 20
<212> DNA
<213> Homo sapiens

<400> 750
aatgagaagg aattgggtgc 20

<210> 751
<211> 20
<212> DNA
<213> Homo sapiens

<400> 751
aatgaagtgt tagggccatc 20

<210> 752
<211> 21
<212> DNA
<213> Homo sapiens

<400> 752
gctcatcaca gttaaggag t 21

<210> 753
<211> 20
<212> DNA
<213> Homo sapiens

<400> 753
atgtggaagc aagagaaagg 20

<210> 754
<211> 20
<212> DNA
<213> Homo sapiens

<400> 754
tgaaaggtga agtggctttt 20

<210> 755
<211> 20
<212> DNA
<213> Homo sapiens

<400> 755
gtaagtaagg ggtcctagct 20

<210> 756
<211> 20

<212> DNA

<213> Homo sapiens

<400> 756

tgtgacttcc atgaaactgg 20

<210> 757

<211> 20

<212> DNA

<213> Homo sapiens

<400> 757

gctgacaaac taacctcca 20

<210> 758

<211> 20

<212> DNA

<213> Homo sapiens

<400> 758

aaaacctccc aaaacagact 20

<210> 759

<211> 20

<212> DNA

<213> Homo sapiens

<400> 759

agtttagtgg ccacgtgaaa 20

<210> 760

<211> 20

<212> DNA

<213> Homo sapiens

<400> 760

ggcagaagtt tcaattccct 20

<210> 761

<211> 20

<212> DNA

<213> Homo sapiens

<400> 761

aaagcctctg ttgcacttt 20

<210> 762

<211> 20

<212> DNA

<213> Homo sapiens

<400> 762

tcagtcagct tcttgagtca 20

<210> 763

<211> 20

<212> DNA

<213> Homo sapiens

<400> 763

tgtttcattt gggcatgga 20

<210> 764

<211> 21

<212> DNA

<213> Homo sapiens

<400> 764

tacagcacta ggatcactct g 21

<210> 765

<211> 20

<212> DNA

<213> Homo sapiens

<400> 765

atgcatgttt ctgcaaagg 20

<210> 766

<211> 20

<212> DNA

<213> Homo sapiens

<400> 766

gtaggattca gggcatttca 20

<210> 767

<211> 19

<212> DNA

<213> Homo sapiens

<400> 767

aactggaact gagcgtgag 19

<210> 768

<211> 20

<212> DNA

<213> Homo sapiens

<400> 768

tgtatgcagt tacctccaga 20

<210> 769

<211> 20

<212> DNA

<213> Homo sapiens

<400> 769

ggatgtatac cagacccctt 20

<210> 770

<211> 20

<212> DNA

<213> Homo sapiens

<400> 770
cgaaagatgt tagcacctca 20

<210> 771
<211> 20
<212> DNA
<213> Homo sapiens

<400> 771
aattggcttt gcagtgttc 20

<210> 772
<211> 20
<212> DNA
<213> Homo sapiens

<400> 772
gcttgctggt aggaggtata 20

<210> 773
<211> 20
<212> DNA
<213> Homo sapiens

<400> 773
ctggaaacgg aaggaagtg 20

<210> 774
<211> 20
<212> DNA
<213> Homo sapiens

<400> 774
ctgtgttcag taagggtg 20

<210> 775
<211> 20
<212> DNA
<213> Homo sapiens

<400> 775
gacagtgaag tgtgatcggt 20

<210> 776
<211> 20
<212> DNA
<213> Homo sapiens

<400> 776
tggatgatgct gtttggaaa 20

<210> 777
<211> 22
<212> DNA
<213> Homo sapiens

<400> 777

ttcttcagg cagaagaaat ga 22

<210> 778

<211> 24

<212> DNA

<213> Homo sapiens

<400> 778

aagttccatt actgtattga aaat 24

<210> 779

<211> 20

<212> DNA

<213> Homo sapiens

<400> 779

ggacgtacgt gcttattca 20

<210> 780

<211> 21

<212> DNA

<213> Homo sapiens

<400> 780

cagcctgata ttccattga g 21

<210> 781

<211> 20

<212> DNA

<213> Homo sapiens

<400> 781

tcatgaggct gagtgagtat 20

<210> 782

<211> 20

<212> DNA

<213> Homo sapiens

<400> 782

aaagctctcc tatctccagt 20

<210> 783

<211> 21

<212> DNA

<213> Homo sapiens

<400> 783

acaaagagtc tggactatcc t 21

<210> 784

<211> 21

<212> DNA

<213> Homo sapiens

<400> 784

tgctaaaaa tacccaaagc t 21

<210> 785

<211> 20

<212> DNA

<213> Homo sapiens

<400> 785

ccaagacact cactccaaag 20

<210> 786

<211> 20

<212> DNA

<213> Homo sapiens

<400> 786

ccaggaaaag gagcagtttt 20

<210> 787

<211> 20

<212> DNA

<213> Homo sapiens

<400> 787

gttcaactct ttctgcgaac 20

<210> 788

<211> 20

<212> DNA

<213> Homo sapiens

<400> 788

ccacttcttc tgttccaac 20

<210> 789

<211> 19

<212> DNA

<213> Homo sapiens

<400> 789

gggaagggca tgctaata 19

<210> 790

<211> 20

<212> DNA

<213> Homo sapiens

<400> 790

tgttcaatca cctctccatc 20

<210> 791

<211> 20

<212> DNA

<213> Homo sapiens

<400> 791

agaggagagg ctaagcttg 20

<210> 792

<211> 20
<212> DNA
<213> Homo sapiens

<400> 792
acaagagagg aagctgtcag 20

<210> 793
<211> 20
<212> DNA
<213> Homo sapiens

<400> 793
agccccttct tcctattct 20

<210> 794
<211> 20
<212> DNA
<213> Homo sapiens

<400> 794
agggaagcag gattttaacg 20

<210> 795
<211> 20
<212> DNA
<213> Homo sapiens

<400> 795
aagttcaca ataccaggt 20

<210> 796
<211> 20
<212> DNA
<213> Homo sapiens

<400> 796
tcgcagaatg gacaagtact 20

<210> 797
<211> 20
<212> DNA
<213> Homo sapiens

<400> 797
ggctcccaga tttgatcat 20

<210> 798
<211> 20
<212> DNA
<213> Homo sapiens

<400> 798
cctagaactg caaaacacct 20

<210> 799
<211> 21

<212> DNA

<213> Homo sapiens

<400> 799

ttccattatt ttctaccgg c 21

<210> 800

<211> 20

<212> DNA

<213> Homo sapiens

<400> 800

cagtccaaca aagaggtcac 20

<210> 801

<211> 20

<212> DNA

<213> Homo sapiens

<400> 801

ttgtgtgtgt tgaagcctag 20

<210> 802

<211> 20

<212> DNA

<213> Homo sapiens

<400> 802

agtgggggta ggaagaaaaa 20

<210> 803

<211> 20

<212> DNA

<213> Homo sapiens

<400> 803

gttccaacaa tgtaaggcac 20

<210> 804

<211> 20

<212> DNA

<213> Homo sapiens

<400> 804

ggaaccctct atggtaaag 20

<210> 805

<211> 20

<212> DNA

<213> Homo sapiens

<400> 805

attgctgtgt agttcctga 20

<210> 806

<211> 20

<212> DNA

<213> Homo sapiens

<400> 806

tttcttgcca ccattctgac 20

<210> 807

<211> 20

<212> DNA

<213> Homo sapiens

<400> 807

cacacgttct aaccaagtgc 20

<210> 808

<211> 21

<212> DNA

<213> Homo sapiens

<400> 808

tagccacatc ttaacagacc t 21

<210> 809

<211> 20

<212> DNA

<213> Homo sapiens

<400> 809

attcctgagg gtgacatgaa 20

<210> 810

<211> 20

<212> DNA

<213> Homo sapiens

<400> 810

cctgccccat caacttaaaa 20

<210> 811

<211> 18

<212> DNA

<213> Homo sapiens

<400> 811

ctgggtgcag aggatctc 18

<210> 812

<211> 22

<212> DNA

<213> Homo sapiens

<400> 812

ttgagttgaa ctttgcttta ga 22

<210> 813

<211> 20

<212> DNA

<213> Homo sapiens

<400> 813
gaactaggag acactgggtt 20

<210> 814
<211> 21
<212> DNA
<213> Homo sapiens

<400> 814
caagaatagc taactggtgc t 21

<210> 815
<211> 21
<212> DNA
<213> Homo sapiens

<400> 815
agttacacac tgaatcatgg g 21

<210> 816
<211> 20
<212> DNA
<213> Homo sapiens

<400> 816
cccatgtggc ttactaata 20

<210> 817
<211> 20
<212> DNA
<213> Homo sapiens

<400> 817
gattgtggtc acgtggagag 20

<210> 818
<211> 20
<212> DNA
<213> Homo sapiens

<400> 818
cagatccagg tattcgaga 20

<210> 819
<211> 20
<212> DNA
<213> Homo sapiens

<400> 819
acaacaaca ccattacca 20

<210> 820
<211> 20
<212> DNA
<213> Homo sapiens

<400> 820

tggccatagt actgcttgta 20

<210> 821

<211> 20

<212> DNA

<213> Homo sapiens

<400> 821

tgtctcactg ttgggaactt 20

<210> 822

<211> 20

<212> DNA

<213> Homo sapiens

<400> 822

ttgtctgta tcctatgccc 20

<210> 823

<211> 20

<212> DNA

<213> Homo sapiens

<400> 823

gctgacaaaa ttggatccca 20

<210> 824

<211> 20

<212> DNA

<213> Homo sapiens

<400> 824

aaaatcctcc tgagtcctct 20

<210> 825

<211> 20

<212> DNA

<213> Homo sapiens

<400> 825

ttcactgggc tcttcagcta 20

<210> 826

<211> 20

<212> DNA

<213> Homo sapiens

<400> 826

aaagggcagg agttaggtaa 20

<210> 827

<211> 20

<212> DNA

<213> Homo sapiens

<400> 827

aggcataaga aaccaggttg 20

<210> 828
<211> 20
<212> DNA
<213> Homo sapiens

<400> 828
gtagttcggg ccaatgtcag 20

<210> 829
<211> 20
<212> DNA
<213> Homo sapiens

<400> 829
gatggtcaca attgcagggt 20

<210> 830
<211> 20
<212> DNA
<213> Homo sapiens

<400> 830
gccaaagatc tcaattgcc 20

<210> 831
<211> 20
<212> DNA
<213> Homo sapiens

<400> 831
gaccaagact gtctctcctt 20

<210> 832
<211> 22
<212> DNA
<213> Homo sapiens

<400> 832
taatgggtcaa atccctctca aa 22

<210> 833
<211> 20
<212> DNA
<213> Homo sapiens

<400> 833
catgtaggct gaagactcct 20

<210> 834
<211> 20
<212> DNA
<213> Homo sapiens

<400> 834
tttctctcca aactggttgc 20

<210> 835

<211> 21
<212> DNA
<213> Homo sapiens

<400> 835
tacaggcaag aaatagtgtc t 21

<210> 836
<211> 20
<212> DNA
<213> Homo sapiens

<400> 836
ttcagcaaga atggggattc 20

<210> 837
<211> 20
<212> DNA
<213> Homo sapiens

<400> 837
caaagagaga gccatcacag 20

<210> 838
<211> 21
<212> DNA
<213> Homo sapiens

<400> 838
tgagaacact gctatttctg c 21

<210> 839
<211> 18
<212> DNA
<213> Homo sapiens

<400> 839
gcatggtcag gacattgg 18

<210> 840
<211> 20
<212> DNA
<213> Homo sapiens

<400> 840
gattgaatca ggaggaagc 20

<210> 841
<211> 23
<212> DNA
<213> Homo sapiens

<400> 841
agcttaaatg atgaagtgtc ttc 23

<210> 842
<211> 20

<212> DNA

<213> Homo sapiens

<400> 842

ttctcctacg tatcttgga 20

<210> 843

<211> 20

<212> DNA

<213> Homo sapiens

<400> 843

acctgggaca taacctgat 20

<210> 844

<211> 20

<212> DNA

<213> Homo sapiens

<400> 844

ccattttcct actgcgtgtc 20

<210> 845

<211> 20

<212> DNA

<213> Homo sapiens

<400> 845

gaacatacca aacctactgg 20

<210> 846

<211> 20

<212> DNA

<213> Homo sapiens

<400> 846

acccaatgat gtacagttcc 20

<210> 847

<211> 22

<212> DNA

<213> Homo sapiens

<400> 847

acctattcga ctgaaactc ag 22

<210> 848

<211> 20

<212> DNA

<213> Homo sapiens

<400> 848

atttctgcac aactgtcca 20

<210> 849

<211> 20

<212> DNA

<213> Homo sapiens

<400> 849

gctgtaatgt gactaacct 20

<210> 850

<211> 20

<212> DNA

<213> Homo sapiens

<400> 850

tttcccgagg ttcacagata 20

<210> 851

<211> 20

<212> DNA

<213> Homo sapiens

<400> 851

gaacttggtg gacccaaaac 20

<210> 852

<211> 20

<212> DNA

<213> Homo sapiens

<400> 852

cattgcactg tgatgtcatg 20

<210> 853

<211> 20

<212> DNA

<213> Homo sapiens

<400> 853

gcactggaaa ttgacatcac 20

<210> 854

<211> 20

<212> DNA

<213> Homo sapiens

<400> 854

gggagaggct gaaagaagaa 20

<210> 855

<211> 20

<212> DNA

<213> Homo sapiens

<400> 855

tgtatcactt cctcatgcca 20

<210> 856

<211> 20

<212> DNA

<213> Homo sapiens

<400> 856

ccaagagttt cctgtttcca 20

<210> 857

<211> 22

<212> DNA

<213> Homo sapiens

<400> 857

atgacacata catccattta ca 22

<210> 858

<211> 20

<212> DNA

<213> Homo sapiens

<400> 858

ctcaaactgc ccagtgattt 20

<210> 859

<211> 20

<212> DNA

<213> Homo sapiens

<400> 859

tcctagcttg ccaaagaaat 20

<210> 860

<211> 20

<212> DNA

<213> Homo sapiens

<400> 860

cctcctctcc aggcatTTTA 20

<210> 861

<211> 20

<212> DNA

<213> Homo sapiens

<400> 861

aacagagtag cacagagagt 20

<210> 862

<211> 20

<212> DNA

<213> Homo sapiens

<400> 862

ttcagagaga cagacagcat 20

<210> 863

<211> 20

<212> DNA

<213> Homo sapiens

<400> 863

agaggaaaat cacaagcagt 20

<210> 864

<211> 20

<212> DNA

<213> Homo sapiens

<400> 864

tttgaacc caacagacct 20

<210> 865

<211> 20

<212> DNA

<213> Homo sapiens

<400> 865

aatccacaca ccaacagagg 20

<210> 866

<211> 21

<212> DNA

<213> Homo sapiens

<400> 866

tggtcacatc tggtggttg c 21

<210> 867

<211> 21

<212> DNA

<213> Homo sapiens

<400> 867

gttactcggg gggatatt t 21

<210> 868

<211> 21

<212> DNA

<213> Homo sapiens

<400> 868

aagaaacacc agcatcagtt c 21

<210> 869

<211> 21

<212> DNA

<213> Homo sapiens

<400> 869

aggttagag gtgagtgaac a 21

<210> 870

<211> 22

<212> DNA

<213> Homo sapiens

<400> 870

agaaacttca ctgtttcca ct 22

<210> 871

<211> 21

<212> DNA

<213> Homo sapiens

<400> 871

tgtgatggac attggtacct g 21

<210> 872

<211> 21

<212> DNA

<213> Homo sapiens

<400> 872

atatcatctg cctgtcccaa c 21

<210> 873

<211> 21

<212> DNA

<213> Homo sapiens

<400> 873

gagtgtctctg tgttgtttc a 21

<210> 874

<211> 22

<212> DNA

<213> Homo sapiens

<400> 874

tcagtgggta gctcttgaat at 22

<210> 875

<211> 21

<212> DNA

<213> Homo sapiens

<400> 875

actctctctt cacacatgca a 21

<210> 876

<211> 21

<212> DNA

<213> Homo sapiens

<400> 876

gtgttgaagt cagtaaagcc t 21

<210> 877

<211> 21

<212> DNA

<213> Homo sapiens

<400> 877

tgctttcaca tggcactaga t 21

<210> 878

<211> 21
<212> DNA
<213> Homo sapiens

<400> 878
ggagagagaa atcccaactg a 21

<210> 879
<211> 21
<212> DNA
<213> Homo sapiens

<400> 879
gggagatgtc aacactaggt c 21

<210> 880
<211> 20
<212> DNA
<213> Homo sapiens

<400> 880
atatgacatg gtggctctcc 20

<210> 881
<211> 21
<212> DNA
<213> Homo sapiens

<400> 881
aacatagagc catgggaggt a 21

<210> 882
<211> 21
<212> DNA
<213> Homo sapiens

<400> 882
gatagccttc aaatcatgcc t 21

<210> 883
<211> 21
<212> DNA
<213> Homo sapiens

<400> 883
gaaagcgggt gaacaacaat a 21

<210> 884
<211> 21
<212> DNA
<213> Homo sapiens

<400> 884
gatagagagc acaaagagca t 21

<210> 885
<211> 21

<212> DNA

<213> Homo sapiens

<400> 885

aacaagagga ataggagcca g 21

<210> 886

<211> 21

<212> DNA

<213> Homo sapiens

<400> 886

tggtgtctga tagtaacaaa g 21

<210> 887

<211> 21

<212> DNA

<213> Homo sapiens

<400> 887

actattgaac tgttggttc g 21

<210> 888

<211> 21

<212> DNA

<213> Homo sapiens

<400> 888

tccactaaag agcaacaaaa c 21

<210> 889

<211> 21

<212> DNA

<213> Homo sapiens

<400> 889

tgaagtggc agtaacaatg g 21

<210> 890

<211> 21

<212> DNA

<213> Homo sapiens

<400> 890

attcagagc tccttgtcc t 21

<210> 891

<211> 21

<212> DNA

<213> Homo sapiens

<400> 891

ggcaaagaaa tctggtgttc a 21

<210> 892

<211> 21

<212> DNA

<213> Homo sapiens

<400> 892

ttgctggtg ataggcattt g 21

<210> 893

<211> 21

<212> DNA

<213> Homo sapiens

<400> 893

attcccgcaa ttgtgagatt c 21

<210> 894

<211> 22

<212> DNA

<213> Homo sapiens

<400> 894

aaagaggtag agaactcaga cc 22

<210> 895

<211> 21

<212> DNA

<213> Homo sapiens

<400> 895

gtcttcatga acgttgccaa t 21

<210> 896

<211> 21

<212> DNA

<213> Homo sapiens

<400> 896

cttctcaggg ctcttgtgt a 21

<210> 897

<211> 21

<212> DNA

<213> Homo sapiens

<400> 897

gcaacagaaa ccaagattcc t 21

<210> 898

<211> 22

<212> DNA

<213> Homo sapiens

<400> 898

tcattgtcta cctcaaagag ca 22

<210> 899

<211> 21

<212> DNA

<213> Homo sapiens

<400> 899

ctctgaagga acaaaggatg g 21

<210> 900

<211> 21

<212> DNA

<213> Homo sapiens

<400> 900

cattagaatg cggtggtttc a 21

<210> 901

<211> 21

<212> DNA

<213> Homo sapiens

<400> 901

gatgtctggg ctgaggttta a 21

<210> 902

<211> 21

<212> DNA

<213> Homo sapiens

<400> 902

ttcctcttga agatgcactg g 21

<210> 903

<211> 21

<212> DNA

<213> Homo sapiens

<400> 903

ccagcatgtg aggaattgaa c 21

<210> 904

<211> 21

<212> DNA

<213> Homo sapiens

<400> 904

cccacttagt catccacaca t 21

<210> 905

<211> 21

<212> DNA

<213> Homo sapiens

<400> 905

gtttcacaca ccagaagaga g 21

<210> 906

<211> 21

<212> DNA

<213> Homo sapiens

<400> 906

ccatacacct gctctgacat t 21

<210> 907

<211> 21

<212> DNA

<213> Homo sapiens

<400> 907

atcagtaaca gtccattgc t 21

<210> 908

<211> 21

<212> DNA

<213> Homo sapiens

<400> 908

catgaggcat ttgatccatg g 21

<210> 909

<211> 21

<212> DNA

<213> Homo sapiens

<400> 909

accctgtttc actgaacaac t 21

<210> 910

<211> 21

<212> DNA

<213> Homo sapiens

<400> 910

ccctgtaatg agagcgttat t 21

<210> 911

<211> 22

<212> DNA

<213> Homo sapiens

<400> 911

gagagaatgg gttaaactcg cc 22

<210> 912

<211> 21

<212> DNA

<213> Homo sapiens

<400> 912

ctgcctgact tagccttaa t 21

<210> 913

<211> 21

<212> DNA

<213> Homo sapiens

<400> 913

aaccagaatg ttactagccc a 21

<210> 914
<211> 21
<212> DNA
<213> Homo sapiens

<400> 914
caatcctgtg tgtttagtgg a 21

<210> 915
<211> 20
<212> DNA
<213> Homo sapiens

<400> 915
tgtggaagc attgactctt 20

<210> 916
<211> 21
<212> DNA
<213> Homo sapiens

<400> 916
tcctgtgaga aatggagctt t 21

<210> 917
<211> 22
<212> DNA
<213> Homo sapiens

<400> 917
gttgccaagc ttaaatacct gt 22

<210> 918
<211> 21
<212> DNA
<213> Homo sapiens

<400> 918
ccacaacaac ataaacactg c 21

<210> 919
<211> 21
<212> DNA
<213> Homo sapiens

<400> 919
tctccaggc atattcattg c 21

<210> 920
<211> 21
<212> DNA
<213> Homo sapiens

<400> 920
atccattctc tctactggg a 21

<210> 921

<211> 22
<212> DNA
<213> Homo sapiens

<400> 921
ggctagaggg tgattataag ct 22

<210> 922
<211> 21
<212> DNA
<213> Homo sapiens

<400> 922
tactcatccc gatttctcc c 21

<210> 923
<211> 21
<212> DNA
<213> Homo sapiens

<400> 923
ttctcttct cttctgggca g 21

<210> 924
<211> 21
<212> DNA
<213> Homo sapiens

<400> 924
ttgtgagact caaggccatt t 21

<210> 925
<211> 21
<212> DNA
<213> Homo sapiens

<400> 925
ttggtagaga gaggccattt g 21

<210> 926
<211> 21
<212> DNA
<213> Homo sapiens

<400> 926
ggaggaagct ctgaagaca t 21

<210> 927
<211> 21
<212> DNA
<213> Homo sapiens

<400> 927
agcatcttcc gtttaactcc a 21

<210> 928
<211> 20

<212> DNA

<213> Homo sapiens

<400> 928

ctgcctgccca agtatgttct 20

<210> 929

<211> 21

<212> DNA

<213> Homo sapiens

<400> 929

ctactccttg tgtcattggc t 21

<210> 930

<211> 21

<212> DNA

<213> Homo sapiens

<400> 930

tgattctgag acacgtgctt a 21

<210> 931

<211> 21

<212> DNA

<213> Homo sapiens

<400> 931

cttgaggacc ttcatgctt g 21

<210> 932

<211> 21

<212> DNA

<213> Homo sapiens

<400> 932

ttgtgatttc aggtaggagg g 21

<210> 933

<211> 21

<212> DNA

<213> Homo sapiens

<400> 933

ttccctcaga gacagtatcc t 21

<210> 934

<211> 20

<212> DNA

<213> Homo sapiens

<400> 934

aaaggaggtc tggcttgaa 20

<210> 935

<211> 21

<212> DNA

<213> Homo sapiens

<400> 935

gcataaacct ggactgtgaa a 21

<210> 936

<211> 20

<212> DNA

<213> Homo sapiens

<400> 936

cactcagcga ttctctcac 20

<210> 937

<211> 21

<212> DNA

<213> Homo sapiens

<400> 937

aaagccagac acagactagt t 21

<210> 938

<211> 20

<212> DNA

<213> Homo sapiens

<400> 938

attcctggga ccacaagcat 20

<210> 939

<211> 20

<212> DNA

<213> Homo sapiens

<400> 939

tattgcctca tgtggttg 20

<210> 940

<211> 22

<212> DNA

<213> Homo sapiens

<400> 940

gtgttgactt gaaaggaatc ac 22

<210> 941

<211> 21

<212> DNA

<213> Homo sapiens

<400> 941

caggtagga atgacagtgg g 21

<210> 942

<211> 21

<212> DNA

<213> Homo sapiens

<400> 942

ttaggttacc cagggacgtt a 21

<210> 943

<211> 21

<212> DNA

<213> Homo sapiens

<400> 943

cggtttgctt tctgaacaac a 21

<210> 944

<211> 21

<212> DNA

<213> Homo sapiens

<400> 944

catttgggac ccttgaaac t 21

<210> 945

<211> 21

<212> DNA

<213> Homo sapiens

<400> 945

ggttatctct gggcaaagtt c 21

<210> 946

<211> 21

<212> DNA

<213> Homo sapiens

<400> 946

tagagagcag agaacaaacc c 21

<210> 947

<211> 21

<212> DNA

<213> Homo sapiens

<400> 947

ataagggcatt ttggaggga a 21

<210> 948

<211> 21

<212> DNA

<213> Homo sapiens

<400> 948

aatgcacact tagacaccac a 21

<210> 949

<211> 21

<212> DNA

<213> Homo sapiens

<400> 949

ggattgctac ccaggagata a 21

<210> 950

<211> 21

<212> DNA

<213> Homo sapiens

<400> 950

agaggttctg tgtatgagtg t 21

<210> 951

<211> 21

<212> DNA

<213> Homo sapiens

<400> 951

tagagaattg tacgctggac a 21

<210> 952

<211> 21

<212> DNA

<213> Homo sapiens

<400> 952

tctggagaaa tgcacaagag a 21

<210> 953

<211> 21

<212> DNA

<213> Homo sapiens

<400> 953

tgggttagaa catggtgctt a 21

<210> 954

<211> 21

<212> DNA

<213> Homo sapiens

<400> 954

atcgcatcac acccttacta t 21

<210> 955

<211> 21

<212> DNA

<213> Homo sapiens

<400> 955

ggaaatttag ctgacatgg c 21

<210> 956

<211> 22

<212> DNA

<213> Homo sapiens

<400> 956

tttgtaaac cacagtcct ac 22

<210> 957
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 957
 ggtactggag agcatagaag a 21

<210> 958
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 958
 aaacaagcta tcttcaggca g 21

<210> 959
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 959
 cgaacaatca gagactcgac t 21

<210> 960
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 960
 ctggttgaca atctgcaagt t 21

<210> 961
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 961
 accatccaag tcgtcttcat a 21

<210> 962
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 962
 atagctacgc ataccctgta g 21

<210> 963
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 963
 agcagaagaa acagtaaggc a 21

<210> 964

<211> 20
<212> DNA
<213> Homo sapiens

<400> 964
acccagggac ctattgttc 20

<210> 965
<211> 21
<212> DNA
<213> Homo sapiens

<400> 965
caagggctca ggtcttcatt a 21

<210> 966
<211> 21
<212> DNA
<213> Homo sapiens

<400> 966
tcactgtgac ttggagacta a 21

<210> 967
<211> 21
<212> DNA
<213> Homo sapiens

<400> 967
tgctctgctt cactgtgatt a 21

<210> 968
<211> 22
<212> DNA
<213> Homo sapiens

<400> 968
gatgaatgac taatagccca cg 22

<210> 969
<211> 21
<212> DNA
<213> Homo sapiens

<400> 969
ccatgtttag ttggtgctg t 21

<210> 970
<211> 20
<212> DNA
<213> Homo sapiens

<400> 970
agccaagtga ggtgctaaat 20

<210> 971
<211> 21

<212> DNA

<213> Homo sapiens

<400> 971

tcaggagagaa atgatgtcac c 21

<210> 972

<211> 21

<212> DNA

<213> Homo sapiens

<400> 972

cagtagctgg caagaatcat c 21

<210> 973

<211> 21

<212> DNA

<213> Homo sapiens

<400> 973

caacactgct agaattccca a 21

<210> 974

<211> 21

<212> DNA

<213> Homo sapiens

<400> 974

cctgagaagc acctgattgt a 21

<210> 975

<211> 20

<212> DNA

<213> Homo sapiens

<400> 975

tgtgtgcaga aatcccagga 20

<210> 976

<211> 21

<212> DNA

<213> Homo sapiens

<400> 976

aactggagcc atataacgat g 21

<210> 977

<211> 21

<212> DNA

<213> Homo sapiens

<400> 977

gaaatggtgc cctattgttg a 21

<210> 978

<211> 22

<212> DNA

<213> Homo sapiens

<400> 978

tcttaccatgc agtcatactc ct 22

<210> 979

<211> 22

<212> DNA

<213> Homo sapiens

<400> 979

gtccctcagt aacaccatct ta 22

<210> 980

<211> 21

<212> DNA

<213> Homo sapiens

<400> 980

gaagcaagag gatcaggcaa t 21

<210> 981

<211> 21

<212> DNA

<213> Homo sapiens

<400> 981

agtgtttcag aggcttgaaa g 21

<210> 982

<211> 21

<212> DNA

<213> Homo sapiens

<400> 982

atccggcatc ctttaaactc t 21

<210> 983

<211> 21

<212> DNA

<213> Homo sapiens

<400> 983

aggctaggaa gaaatgggaa a 21

<210> 984

<211> 21

<212> DNA

<213> Homo sapiens

<400> 984

acacatatgc tctgtctctc a 21

<210> 985

<211> 21

<212> DNA

<213> Homo sapiens

<400> 985

agttagttat cacctcgtcc c 21

<210> 986

<211> 22

<212> DNA

<213> Homo sapiens

<400> 986

tgtgtatttc cctctagttg ca 22

<210> 987

<211> 21

<212> DNA

<213> Homo sapiens

<400> 987

agcctctttc tacatcgttc g 21

<210> 988

<211> 21

<212> DNA

<213> Homo sapiens

<400> 988

ttacctgtgc agaagagtga c 21

<210> 989

<211> 21

<212> DNA

<213> Homo sapiens

<400> 989

tcttgtgttc tagcgtgttt g 21

<210> 990

<211> 21

<212> DNA

<213> Homo sapiens

<400> 990

tgtggtagt cagaaatgtg g 21

<210> 991

<211> 21

<212> DNA

<213> Homo sapiens

<400> 991

gggtcctgat gagtcttctg c 21

<210> 992

<211> 21

<212> DNA

<213> Homo sapiens

<400> 992

tggtgccttt gtttattcag c 21

<210> 993

<211> 21

<212> DNA

<213> Homo sapiens

<400> 993

tgttatgtgc cagggtttaa c 21

<210> 994

<211> 21

<212> DNA

<213> Homo sapiens

<400> 994

attggttcca gatacagtcg a 21

<210> 995

<211> 21

<212> DNA

<213> Homo sapiens

<400> 995

ggaaggaagt acagcatgga t 21

<210> 996

<211> 21

<212> DNA

<213> Homo sapiens

<400> 996

ccttattgaa gctgaccatg c 21

<210> 997

<211> 21

<212> DNA

<213> Homo sapiens

<400> 997

cagtgggaaa tgtgcttaca t 21

<210> 998

<211> 21

<212> DNA

<213> Homo sapiens

<400> 998

aaagggccta tattcaccag a 21

<210> 999

<211> 22

<212> DNA

<213> Homo sapiens

<400> 999

agagccattt aagactctct gt 22

<210> 1000

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1000

tacctgttc tctgcctcaa t 21

<210> 1001

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1001

tttagaagga tgtggacagg g 21

<210> 1002

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1002

agcaggacat ggactcaaa 20

<210> 1003

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1003

gcggctcttg ttctgaaat c 21

<210> 1004

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1004

acaggtagga gttcagagac a 21

<210> 1005

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1005

tttctattc tgctctctg ct 22

<210> 1006

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1006

aaatgctgct cagggttaga g 21

<210> 1007

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1007

caactttact ctgcacagct c 21

<210> 1008

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1008

cagtgccact acaaagaaat ca 22

<210> 1009

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1009

agaagcagag gttggatatg g 21

<210> 1010

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1010

ccacaatccc atagtcacca t 21

<210> 1011

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1011

gctggttctt gttgctgata a 21

<210> 1012

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1012

tccctcacga cttatgttg a 21

<210> 1013

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1013

ctaccttctc cagtgcacta t 21

<210> 1014

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1014

ggacctctct ttgaaatgga c 21

<210> 1015

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1015

tgggttgtgt ttctctgact t 21

<210> 1016

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1016

tacaagcctc cttaaccct t 21

<210> 1017

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1017

aaagggttg atacagttgg g 21

<210> 1018

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1018

aggatttgga gagcaagaaa ga 22

<210> 1019

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1019

gcaaactgga gctaaagtca t 21

<210> 1020

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1020

ttggttgcta gctctcaaat g 21

<210> 1021

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1021

ttcaatgccc ttactctcc t 21

<210> 1022

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1022

gcttgaggcg catatgattg 20

<210> 1023

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1023

catatggtgc ttgttctggg 20

<210> 1024

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1024

caaactcacc acccttcatt c 21

<210> 1025

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1025

ccttagccct gcaaataaca c 21

<210> 1026

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1026

tcacagatac ggacaagctc 20

<210> 1027

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1027

gccacaggta tcaatcatt c 21

<210> 1028

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1028

gcttctgtgg cactaatcaa g 21

<210> 1029

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1029

gccttattga ctactggac tg 22

<210> 1030

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1030

gtcagggatt agaggcagaa c 21

<210> 1031

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1031

caatcacttg gtcagatagt gt 22

<210> 1032

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1032

agtggagagg ttgagtatag tg 22

<210> 1033

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1033

tgagaaggga ggaagaatgt g 21

<210> 1034

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1034

aaggtaaac tctccattcc a 21

<210> 1035

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1035

ggagatgtct ttgccctgat t 21

<210> 1036

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1036

ggcctcgtt tgccttaag a 21

<210> 1037

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1037

agtattgctt tgagggtct a 21

<210> 1038

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1038

agctatcatg taagtcactc cc 22

<210> 1039

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1039

aggaaattca gtacctcagc t 21

<210> 1040

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1040

caacctctc attgtgaag ct 22

<210> 1041

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1041

ggtgacttg cttccaag 20

<210> 1042

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1042

gctgacaaac ggaggagag 20

<210> 1043

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1043

tggtctcat caggcacaat g 21

<210> 1044

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1044

accatttggtg tgatccagaa c 21

<210> 1045

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1045

cttgcttga gtgcggtaca 20

<210> 1046

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1046

gcctctcagt ttctcttat ag 22

<210> 1047

<211> 24

<212> DNA

<213> Homo sapiens

<400> 1047

cctagatcag tgcagagaat ttag 24

<210> 1048

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1048

ctttagtgtg gaggcctcat tc 22

<210> 1049

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1049

ctgacatcga tggaattctg g 21

<210> 1050

<211> 21
<212> DNA
<213> Homo sapiens

<400> 1050
acactgcacg aatggaagat c 21

<210> 1051
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1051
ataaacttgg tgctcagtgg t 21

<210> 1052
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1052
acaagcatta cagaattcgg c 21

<210> 1053
<211> 24
<212> DNA
<213> Homo sapiens

<400> 1053
actgacagat tctcacctat atca 24

<210> 1054
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1054
ggatcaaagc cactctagac t 21

<210> 1055
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1055
ttgagatggc atcaagttca ag 22

<210> 1056
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1056
actggattca tgcgttatca ag 22

<210> 1057
<211> 21

<212> DNA

<213> Homo sapiens

<400> 1057

tattcttggtg tggaccctgt g 21

<210> 1058

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1058

tgatattgca tgaaagtccc tg 22

<210> 1059

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1059

tcacacatga ggagtagaca 20

<210> 1060

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1060

cacagcagga gacatgagaa 20

<210> 1061

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1061

tttctcctg gcttgatcac 20

<210> 1062

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1062

caaaggagag aagtgaccca 20

<210> 1063

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1063

ctacgagtga aacagagtgc 20

<210> 1064

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1064

agactaaaag cctccaagcc 20

<210> 1065

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1065

tagaatatgt caccagccc 20

<210> 1066

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1066

acagaatcat cccatagcca 20

<210> 1067

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1067

cgccattctg tgcttaattt g 21

<210> 1068

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1068

gtgaagcaag agaaagcaag a 21

<210> 1069

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1069

tgattcggct gcaggttatt 20

<210> 1070

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1070

ctggcttcaa atgcatctga 20

<210> 1071

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1071
actgggaaat tggaattcgc 20

<210> 1072
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1072
ggtaaaactg cctggaaact 20

<210> 1073
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1073
agaccacggg ctctatctat 20

<210> 1074
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1074
catcttgctt attggcttac ga 22

<210> 1075
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1075
gaggtagagg cagtgtcttg 20

<210> 1076
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1076
tagtcctga actccctggt 20

<210> 1077
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1077
ccagcttagc gtctgtttt 20

<210> 1078
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1078

gaccacaact atcaagagca c 21

<210> 1079

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1079

ccaaagaaag gttgaagccc 20

<210> 1080

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1080

aataatgtgc actgtgatgg c 21

<210> 1081

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1081

tttaagggtc tgatggttgc 20

<210> 1082

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1082

gaaaatgccc atcgtctcaa 20

<210> 1083

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1083

attccttgc ttccccctc 20

<210> 1084

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1084

tcatttctct agcccaaaga tg 22

<210> 1085

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1085

ttggttggtt gacttcagcc 20

<210> 1086

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1086

gctcagtgac agttgggatt 20

<210> 1087

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1087

gtctgtctc tcttctcca ct 22

<210> 1088

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1088

ttagagcag gtggaaacga 20

<210> 1089

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1089

cttgggttt tatcggtgc t 21

<210> 1090

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1090

gttgctgga ttgctctaaa 20

<210> 1091

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1091

aaatcacgac gtaggaaacc 20

<210> 1092

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1092

tcacctgga gcaggtcata 20

<210> 1093

<211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1093
 cgaagaaggt ctgggagatg 20

 <210> 1094
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 1094
 caccattggt tcatcaggac t 21

 <210> 1095
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 1095
 ttgcatcatc agctcacata c 21

 <210> 1096
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1096
 agacctggaa aatgatgggt 20

 <210> 1097
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1097
 cctggaagtg tgtaacaagc 20

 <210> 1098
 <211> 21
 <212> DNA
 <213> Homo sapiens

 <400> 1098
 ctccctagca aaaacttctc a 21

 <210> 1099
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1099
 tgccttattc actgtgcaac 20

 <210> 1100
 <211> 20

<212> DNA

<213> Homo sapiens

<400> 1100

tgatggccta gtgagttcc 20

<210> 1101

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1101

tgcaatgtaa caaaagcgtg 20

<210> 1102

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1102

gccacatttg cttcacaca 20

<210> 1103

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1103

acgtcattgg gttcatggc 19

<210> 1104

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1104

attttacccc cttaggcacc 20

<210> 1105

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1105

tcttctacac agcccttcag 20

<210> 1106

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1106

attgggatcg tcagcatcaa 20

<210> 1107

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1107

tgattgtctt gtccactggt 20

<210> 1108

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1108

acatcacact tcatgccctt 20

<210> 1109

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1109

atgaaggcat taggagggag 20

<210> 1110

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1110

aaagtggaga agtggcagat 20

<210> 1111

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1111

ccttaggatt ctgagaggag ag 22

<210> 1112

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1112

agggcttctg attgatttgc 20

<210> 1113

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1113

cagggtagtc gggatttctc 20

<210> 1114

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1114

cccggtaatg atctacagca 20

<210> 1115

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1115

aacggcactt gggtcacta 19

<210> 1116

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1116

actctgaact cctcctcctg 20

<210> 1117

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1117

tttgctcaca cacaagacac 20

<210> 1118

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1118

acgactgcat cctttcatg 20

<210> 1119

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1119

ccatcatagc ctacaaatac cc 22

<210> 1120

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1120

agagagttga aaatatcccc ca 22

<210> 1121

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1121

actttcttga acacccagct 20

<210> 1122

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1122

tgctgtgtc ctactttcc 20

<210> 1123

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1123

tgactgccca agaattgaca 20

<210> 1124

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1124

ccgaacacgc tgtatgtatt 20

<210> 1125

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1125

ggaaggggaat tgaagcacag 20

<210> 1126

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1126

tcatcctatc caccaacctg 20

<210> 1127

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1127

aatgaactgg ccctgactta 20

<210> 1128

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1128

taagatacca taccgcagct 20

<210> 1129

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1129

tcagcgttca tggtagcaat a 21

<210> 1130

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1130

gtttccaac caacaacaa g 21

<210> 1131

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1131

tctatcggga tggagagtga 20

<210> 1132

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1132

gttcagacag gtggactagg 20

<210> 1133

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1133

aagcaacctg ggaaattgtg 20

<210> 1134

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1134

gggttaaggt tgctgggtta 20

<210> 1135

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1135

gtgaaatgtg gttgtagtgc a 21

<210> 1136

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1136
gtgactgcct tgcttcattt 20

<210> 1137
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1137
cagttctgga gccttctact 20

<210> 1138
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1138
ttagggcagg atgtacagaa 20

<210> 1139
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1139
gctggtgacc ttcatccaag 20

<210> 1140
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1140
taaaaccatg ttcggggca 19

<210> 1141
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1141
ctacctgtcc gtttcctta c 21

<210> 1142
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1142
gacaaagatg actggaggtg a 21

<210> 1143
<211> 21

<212> DNA

<213> Homo sapiens

<400> 1143

gggtggatgg tgagatatgt g 21

<210> 1144

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1144

cttcaaacct gatccatgtg c 21

<210> 1145

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1145

gcagaaacag catgaatctc c 21

<210> 1146

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1146

tgacttcaaa catcccatcc a 21

<210> 1147

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1147

gtgggatgag ttctagagga a 21

<210> 1148

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1148

agtcacacac atacacacag t 21

<210> 1149

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1149

acgactccc tgtgtaactt a 21

<210> 1150

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1150

ccttctcttg tctctagtc c 21

<210> 1151

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1151

ctggaaatac acacacacct g 21

<210> 1152

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1152

atttgtaaac caccacttc g 21

<210> 1153

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1153

tcactgtgct gacaaatcct a 21

<210> 1154

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1154

cccatcatca tcccttcaga c 21

<210> 1155

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1155

tcatcacttt atcctccag t 21

<210> 1156

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1156

atgggcacag gtaaagagtt t 21

<210> 1157

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1157

tttctaagct gagtctgagg t 21

<210> 1158

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1158

ttactgttg aatgccagct c 21

<210> 1159

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1159

tcccttctcc catcacaatt c 21

<210> 1160

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1160

gaagactgca tgtgtgtcct a 21

<210> 1161

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1161

ttctactct caactgaacc a 21

<210> 1162

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1162

tcaggagct tctaattaag ga 22

<210> 1163

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1163

aagatgatcc caggcttaag g 21

<210> 1164

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1164

gttgagggtt gctgatcttg g 21

<210> 1165

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1165

caaagataga ttgcacacc a 21

<210> 1166

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1166

gagctggaca aattaaatg c 21

<210> 1167

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1167

ccagtgcatt tggtttgaca 20

<210> 1168

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1168

tatgtgaatc ctctgtgtgg c 21

<210> 1169

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1169

agcttctctc tcattctgct t 21

<210> 1170

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1170

gactcccgat tcatttgct g 21

<210> 1171

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1171

tccaatcgt tgtgaaacat ac 22

<210> 1172

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1172

tctttacagg aagtgggac c 21

<210> 1173

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1173

taagttcaga tcagggagca g 21

<210> 1174

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1174

gttgaaagtc ttacagaacg ct 22

<210> 1175

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1175

caacataggc acattgtcct c 21

<210> 1176

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1176

gtcaggcctc ataactctct t 21

<210> 1177

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1177

gttgtgtggc ttctctatc a 21

<210> 1178

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1178

cctgcagctc tgtgtaaatt t 21

<210> 1179

<211> 21
<212> DNA
<213> Homo sapiens

<400> 1179
ctttggccag ttctttctct c 21

<210> 1180
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1180
gtggcccagc attattgtt 20

<210> 1181
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1181
tcttggtgtg acttgctaac a 21

<210> 1182
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1182
tttctggctg agataagacc c 21

<210> 1183
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1183
acaattccgt ggtatacagc t 21

<210> 1184
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1184
tgattgtgcc ctaaccaaac t 21

<210> 1185
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1185
tgtcgtatcc tgctgttag a 21

<210> 1186
<211> 21

<212> DNA

<213> Homo sapiens

<400> 1186

tcaggagtaa agtcaggacc t 21

<210> 1187

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1187

tgagctgatt tactgtgaca c 21

<210> 1188

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1188

tagcaccttg acttcaggat t 21

<210> 1189

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1189

tgaggttggg aagggccaat t 21

<210> 1190

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1190

cagcttctct tcctcttctc t 21

<210> 1191

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1191

acagtgagag gaaagaacag c 21

<210> 1192

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1192

ggaaataaat tgtgagctgg c 21

<210> 1193

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1193

agacagccct tcaatccata c 21

<210> 1194

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1194

cctacatccc ttctccttt c 21

<210> 1195

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1195

tcacccatct tccaattagc t 21

<210> 1196

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1196

tttctaagca caaactgaca cc 22

<210> 1197

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1197

gatgtttgca ctggagggat a 21

<210> 1198

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1198

gaagactaaa tgttgccga a 21

<210> 1199

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1199

gtagagagag ggaggatcac a 21

<210> 1200

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1200

cttgccatga agtttgacca g 21

<210> 1201

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1201

aggatgagca ttgtaacct g 21

<210> 1202

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1202

tgtcgcttcc aaattaccca c 21

<210> 1203

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1203

catacaagtg ctctgttagg c 21

<210> 1204

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1204

aggacttgga accagaaaga c 21

<210> 1205

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1205

aaagagggt gatatcgtct g 21

<210> 1206

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1206

ctcactgcaa actatggaac c 21

<210> 1207

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1207

tattctgcc atcttctcc t 21

<210> 1208

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1208

ggagacagcc caaacataga 20

<210> 1209

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1209

agcaatggg aagtctgga t 21

<210> 1210

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1210

ctggtcagt agagaaggga a 21

<210> 1211

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1211

tttctccact ggcatgaact 20

<210> 1212

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1212

catgatcaca attccaagcc a 21

<210> 1213

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1213

acccagtcaa gttacagtct t 21

<210> 1214

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1214

tgtaaagcat atcaaggga cg 22

<210> 1215

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1215

tgcaagagata tgttcccga t 21

<210> 1216

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1216

agaagacagt acaaggaagg c 21

<210> 1217

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1217

tggttgccat ttgttctct c 21

<210> 1218

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1218

ttgaaggcaa gagaagttg g 21

<210> 1219

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1219

gccaaggaaa tgtagggaaa g 21

<210> 1220

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1220

aaccttcaca cctagagaca g 21

<210> 1221

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1221

gcataacagg gaaagtcacc t 21

<210> 1222

<211> 21
<212> DNA
<213> Homo sapiens

<400> 1222
aggatgtag tggttgggt a 21

<210> 1223
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1223
tctgacactg acctcaact 20

<210> 1224
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1224
gaaacattgc ttccctcca 20

<210> 1225
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1225
ttccacacat ctcttccg 20

<210> 1226
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1226
gggagccttg aaaacctgaa 20

<210> 1227
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1227
attgtagcg ttgtcagca 19

<210> 1228
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1228
ttctgcac ttgtagaccc 20

<210> 1229
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1229

gggctaattgt ttgctcca 20

<210> 1230

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1230

tggtgattag agctccccc 20

<210> 1231

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1231

agaggtttct tccccgtg 19

<210> 1232

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1232

tagtgccctc tattgtgct 20

<210> 1233

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1233

actgctggac ttgaaatgc 20

<210> 1234

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1234

caaacagtga gatgtggctg 20

<210> 1235

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1235

ttgcttctg aaaactggtt c 21

<210> 1236

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1236

attccaatca cgtctctgca 20

<210> 1237

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1237

acaatctcac agcctggaaa 20

<210> 1238

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1238

tcagatgggt gaggttcttg 20

<210> 1239

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1239

ctgctccttc cctccaatta 20

<210> 1240

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1240

aaatgccagt cctgtaaagg 20

<210> 1241

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1241

tgtcccattg cttaggaagt 20

<210> 1242

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1242

tgtgtgatcc agagacccta 20

<210> 1243

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1243
accaatgtag acttagcggg 20

<210> 1244
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1244
actctcatat tgcccactt 20

<210> 1245
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1245
ccagggattg atgtactggt 20

<210> 1246
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1246
aattctggtc tatctggcgt 20

<210> 1247
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1247
gccagccctt ttacacatatt 20

<210> 1248
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1248
aactacacca tcccctgttt 20

<210> 1249
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1249
ccattcaaa catgtggtc 20

<210> 1250
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1250

agattataag aaggcaggga ac 22

<210> 1251

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1251

gtagagggt taaaacatgt cc 22

<210> 1252

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1252

acaagaacac agtcgttaag c 21

<210> 1253

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1253

tctctccttc actccctca 20

<210> 1254

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1254

tgtccacccc tcttgattg 20

<210> 1255

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1255

ttagcttct cctgccttg 20

<210> 1256

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1256

agaagcaatt caccaggtca 20

<210> 1257

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1257

tggagtcaga agtgtgtgtt 20

<210> 1258

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1258

tctggtgtca aagcttaggg 20

<210> 1259

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1259

tgccgatgat gtgtgttttg 20

<210> 1260

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1260

gtcccttcc taatcccaaa 20

<210> 1261

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1261

aggaatgtta agttgcagca 20

<210> 1262

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1262

tatgcagttt tacccttcc 20

<210> 1263

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1263

ttctgtgtgg tctcctcttg 20

<210> 1264

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1264

atggagggac aagtgagaca 20

<210> 1265

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1265
ggggaacatg gagctgtaaa 20

<210> 1266
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1266
ggacccccta ccacatttac 20

<210> 1267
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1267
agatggagaa atgtgcagag a 21

<210> 1268
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1268
atgactgcat ccaagagca 19

<210> 1269
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1269
cagaattcc aggcagttgt 20

<210> 1270
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1270
gaatccagaa gctcagtcct t 21

<210> 1271
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1271
agccctggaa tcttgacatt 20

<210> 1272
<211> 19

<212> DNA

<213> Homo sapiens

<400> 1272

gtgcattata cggatggcc 19

<210> 1273

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1273

ggtagagggt cctgtgattc 20

<210> 1274

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1274

gtaactgcta gccactgagt 20

<210> 1275

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1275

gccttttgg gaatcctagt 20

<210> 1276

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1276

aagggtggaa gcacattgac 20

<210> 1277

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1277

atagaggaac aagctgcaca 20

<210> 1278

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1278

ctcgtccctt gcacatctta 20

<210> 1279

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1279

agggtggggaa gaacaaaaca 20

<210> 1280

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1280

gagagtaggt gcagggaac 20

<210> 1281

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1281

atcccgcatc ctaaccaca 20

<210> 1282

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1282

gactaagcaa aagcatctcc c 21

<210> 1283

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1283

ttcttacagg ctcagggtat 20

<210> 1284

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1284

cccatagctt aaccctaca a 21

<210> 1285

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1285

tcttcattt actgtctagc ac 22

<210> 1286

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1286

tcatacccta tcctgtgat c 21

<210> 1287

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1287

tctgccctt gattgtttc c 21

<210> 1288

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1288

gcctttatc catatgccac c 21

<210> 1289

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1289

gccctcaact ttgctttca 20

<210> 1290

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1290

aaaaacctgc actgtgtcg 20

<210> 1291

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1291

ttttacagc aatcttcaact gc 22

<210> 1292

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1292

taagccggaa tgattgtaa gg 22

<210> 1293

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1293

taccctttgg cttaacagct 20

<210> 1294

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1294

agttgtcatg ttgggctcat 20

<210> 1295

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1295

tgtcctaagt tacctgtctg ac 22

<210> 1296

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1296

gccctggaaa gtactgtaac a 21

<210> 1297

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1297

tgttacagcc aggctttcat 20

<210> 1298

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1298

caacgaacac agggtttaca 20

<210> 1299

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1299

ccaggactct ctcttttct c 21

<210> 1300

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1300

gacacataag accactttag gc 22

<210> 1301

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1301

gatatgttct ggaggactgc t 21

<210> 1302

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1302

tgattctcac aggctccttg 20

<210> 1303

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1303

tgatggaagt ttctaggcca gt 22

<210> 1304

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1304

aacactcttg ctccctatgt 20

<210> 1305

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1305

tttctctccc agcttgatct t 21

<210> 1306

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1306

ctgtgcagag acgaactaag 20

<210> 1307

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1307

ctctcggagc aaagacctt 19

<210> 1308

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1308
acctcataag taogcccatc 20

<210> 1309
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1309
tgatcttctt ttgctcctgt 20

<210> 1310
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1310
atgacgacga tgttgagag 20

<210> 1311
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1311
tccttcagca agcctctttt 20

<210> 1312
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1312
tgagggtgat aacctgtgag 20

<210> 1313
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1313
ggcttgaagt ttgtctgtga 20

<210> 1314
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1314
ggatttcac attgctcagc 20

<210> 1315
<211> 21

<212> DNA

<213> Homo sapiens

<400> 1315

tagcatgaga gtgaactgag g 21

<210> 1316

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1316

cagccacata gcccatatct 20

<210> 1317

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1317

tgcccatgag tctactgtg 20

<210> 1318

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1318

aagtggaactg agggacaatt 20

<210> 1319

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1319

tcagactgag cattaaatca cc 22

<210> 1320

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1320

taggtctgga agaatgccag 20

<210> 1321

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1321

agtatcttgg gcttggaca 20

<210> 1322

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1322

gctccacttc cagtctttct 20

<210> 1323

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1323

ttggaatagt gagcctccct 20

<210> 1324

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1324

tctggggctc ttgtctttg 20

<210> 1325

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1325

attttctct ccctgtagct 20

<210> 1326

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1326

ctgggcacac tgtattacca 20

<210> 1327

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1327

caccacgttt ctaatgcaga 20

<210> 1328

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1328

gagtgaaaa aggtccacgc 20

<210> 1329

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1329
cagaggaaag acacagtgtc 20

<210> 1330
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1330
tcttggtttt gaggctgtca 20

<210> 1331
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1331
atcagcctaa ttctcccac 20

<210> 1332
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1332
atcccccatc atccatactc 20

<210> 1333
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1333
catagctagg cctgtgagtg 20

<210> 1334
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1334
tcagcttgct ccttctctg 19

<210> 1335
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1335
ctaggtcctc agcagtgttt 20

<210> 1336
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1336

tcccagagtt aacaataccc c 21

<210> 1337

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1337

ccatttgcac tgccgatttc 20

<210> 1338

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1338

actagtccca aaagcctaca c 21

<210> 1339

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1339

aacagcagcg tcagaataac 20

<210> 1340

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1340

aggtctttac gggaaggaaa 20

<210> 1341

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1341

tgaggagaa gtttgtagg 20

<210> 1342

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1342

ccctgtctaa agagccatgt 20

<210> 1343

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1343

gtttggagtt tcgatgcctt 20

<210> 1344

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1344

atgttttggt cctgggagaa 20

<210> 1345

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1345

ggaagtgggt agggcagatt 20

<210> 1346

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1346

agcccagtaa agataagagg c 21

<210> 1347

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1347

ccctccctt tcatcaaga 20

<210> 1348

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1348

ctgaaacctt ctcttagcc 20

<210> 1349

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1349

attatccaac ctgacctgca 20

<210> 1350

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1350

aggtgcaaag ctgtcatg 19

<210> 1351

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1351
aatgccaaga ttgtcctca 20

<210> 1352
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1352
tgcgaaacct cagtgatca 19

<210> 1353
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1353
cacttccttc agcacacttt 20

<210> 1354
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1354
ccggctctct atgaaagtga 20

<210> 1355
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1355
acttgtctgt ctgcctgttt 20

<210> 1356
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1356
ctgatgcgct gaaaaccaa 19

<210> 1357
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1357
ttccatgtgt tcttctccc 20

<210> 1358
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1358

agcagtaggg ttaacaggag 20

<210> 1359

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1359

gcagcaatgt ttcggtgta 19

<210> 1360

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1360

tactaatggc tgggggtaac 20

<210> 1361

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1361

ctgatgaggc taaaggacca 20

<210> 1362

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1362

cagagttctc catcccagac 20

<210> 1363

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1363

ctgagttcct cctttgcct 20

<210> 1364

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1364

gcaaaagggtg gtgtagctg 20

<210> 1365

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1365

atccacatcc catgcctaag 20

<210> 1366

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1366

tctattcctt tggcacctcc 20

<210> 1367

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1367

aggaaaggag agcttgtcc 20

<210> 1368

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1368

cctttcagct tccaagtcct 20

<210> 1369

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1369

gctctcttcc tccactaaa a 21

<210> 1370

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1370

actgcctgtg ttttcttct 20

<210> 1371

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1371

aaagcaattt cttccccagc 20

<210> 1372

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1372

tgctgttgc cattcctct 20

<210> 1373

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1373

tgactgtgac ttgtgcttc 20

<210> 1374

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1374

gaattacatt tccctgggcg 20

<210> 1375

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1375

tgaaaccgtc ttcttgtct 20

<210> 1376

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1376

tttaaagcag agcaggacct 20

<210> 1377

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1377

tttatgacac acagagcagc 20

<210> 1378

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1378

atgtgttga cccttcct 20

<210> 1379

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1379

atcctgaagt tgtccacat c 21

<210> 1380

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1380

gaccctgctt tgttactagg a 21

<210> 1381

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1381

tggacatgga cattcaacg 20

<210> 1382

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1382

aaaaatgctt ccactgcct 20

<210> 1383

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1383

gcacctccaa caacattcaa 20

<210> 1384

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1384

ttggaaatgg ggctggag 18

<210> 1385

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1385

actggtctat tgggggaaaa t 21

<210> 1386

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1386

agtgttagga aagcagagtg 20

<210> 1387
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1387
tggacagggt ttcacaagat 20

<210> 1388
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1388
ctcctctcca tcttccagg 20

<210> 1389
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1389
ataggctgac ttccacatct c 21

<210> 1390
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1390
tgtgggggtc aattctaacg 20

<210> 1391
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1391
ccaacgggta gtggtagatt 20

<210> 1392
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1392
cttaccacac ttcttctga 20

<210> 1393
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1393
cctgtcacia ctgccttg 19

<210> 1394

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1394
ttgccattt tgtgatgcca 20

<210> 1395
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1395
ggagtttcag gttggcagaa 20

<210> 1396
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1396
acagcttgct tcaaactaca 20

<210> 1397
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1397
ttgaaggggc aaaatacagc 20

<210> 1398
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1398
gccccaaatt gtaacaaagc 20

<210> 1399
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1399
tgacgaagac tccaacacaa 20

<210> 1400
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1400
aagtcaggga aatgaagctg 20

<210> 1401
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1401

gtaacacagt gtccttctc 20

<210> 1402

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1402

ggccccaatt agctgatttc 20

<210> 1403

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1403

ctgagcaggg aaaaatccag 20

<210> 1404

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1404

acaaaggatt caggtagcagt 20

<210> 1405

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1405

acaggtttg ctctcagga 20

<210> 1406

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1406

ggcaagttg tctggtcat t 21

<210> 1407

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1407

ccatctgcat ctgtctcctt 20

<210> 1408

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1408

gctcctctcc ttctccctt 19

<210> 1409

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1409

tgtataaggg caatcgtggt 20

<210> 1410

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1410

aaggaaccag gtcagacaag 20

<210> 1411

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1411

gttagaaggc aaacatcatg c 21

<210> 1412

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1412

tgcagtcata ggaaaaggct 20

<210> 1413

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1413

gcagtcagaa tggttggc 19

<210> 1414

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1414

agacattggt ttggtggtt c 21

<210> 1415

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1415

acacaaatga aagcccgta 20

<210> 1416

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1416

ggtctgctgt ttctcttgc 20

<210> 1417

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1417

agagccttac caagctgaag 20

<210> 1418

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1418

gggatgggta ctagtgggg 20

<210> 1419

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1419

ttacactcgc cttcaaaca 20

<210> 1420

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1420

gagagaggag gagttggaag 20

<210> 1421

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1421

atccacgaca tccaaaatca 20

<210> 1422

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1422

ttgtgcaaga agaaacctgc 20

<210> 1423

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1423

ggccttgcatt aaaccacatt 20

<210> 1424

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1424

tttgaattg gtcctgcct 20

<210> 1425

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1425

caagtatttc atggcgctcc 20

<210> 1426

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1426

gtcaacagta tcagcttcca a 21

<210> 1427

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1427

tgggcttctt ttcatccg 20

<210> 1428

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1428

tcaacaagct ctctgttcac 20

<210> 1429

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1429

gtgcaaacag tgacctcaat 20

<210> 1430

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1430

gctgggctgc tttatttct 20

<210> 1431

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1431

ggaattgtgg ggtcaaatgg 20

<210> 1432

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1432

ctagtgttc tacctccaga c 21

<210> 1433

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1433

aaccacacac taacagggaa 20

<210> 1434

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1434

tctagttgc cctcttccc 20

<210> 1435

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1435

cgaattgctt cctgctctg 20

<210> 1436

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1436

tctatcacag caggaaatca ct 22

<210> 1437

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1437
tcttcgtgtt tctctagccc 20

<210> 1438
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1438
ttgaagagct aaagggggag 20

<210> 1439
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1439
tgtcaccgta ctacctaagc 20

<210> 1440
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1440
agtacgctcc ttgcagag 19

<210> 1441
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1441
ttacggggac acaaaatggt 20

<210> 1442
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1442
ctgtgctttg cccttgaag 19

<210> 1443
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1443
aagtaacccc atatgccact 20

<210> 1444
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1444

acattcaggc tgtcacacat 20

<210> 1445

<211> 23

<212> DNA

<213> Homo sapiens

<400> 1445

tcatgtcact agttttataa ggc 23

<210> 1446

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1446

agtagtgagg ctccaaagtg 20

<210> 1447

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1447

tgggaggagt ttgctgttta 20

<210> 1448

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1448

ttctaagcct gtgactgaca 20

<210> 1449

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1449

tgaacctgac tttcctggg 20

<210> 1450

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1450

gccattctat catctcgga 20

<210> 1451

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1451

agtctctccc tgaaaccca 19

<210> 1452

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1452

aagagttggc ttggagttga 20

<210> 1453

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1453

cccacaatta tgaaaggagg t 21

<210> 1454

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1454

ttgaccagga caaatgagga 20

<210> 1455

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1455

cactttgttg gtctgggtca 20

<210> 1456

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1456

gggactctag gtgggggttaa 20

<210> 1457

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1457

gtttatgcct tgggattgcc 20

<210> 1458

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1458
gtgtggaag gatgctagga 20

<210> 1459
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1459
gaaagtgact cctccctgac 20

<210> 1460
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1460
ccaggttctg ttctctgca 20

<210> 1461
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1461
gtgagacatg gttgctgttc 20

<210> 1462
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1462
ctttctcctg ctccacctat 20

<210> 1463
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1463
ctatgtgtgt tccaacccga 20

<210> 1464
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1464
gggaccttct aacctgtgt 20

<210> 1465
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1465

cgggatttg aaaaggcaga 20

<210> 1466

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1466

gtgtgtctc tcagctctc 20

<210> 1467

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1467

gttctctggt taaggccctt 20

<210> 1468

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1468

cctctcacc tataagcccc 20

<210> 1469

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1469

taggggacag taagccagat 20

<210> 1470

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1470

acgatggacc tctgtgaac 20

<210> 1471

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1471

attcccatcc atccatcact c 21

<210> 1472

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1472

tcgttttgg atggtggtg 20

<210> 1473

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1473

gaagttcctc cagtagactc a 21

<210> 1474

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1474

ttgtttgagt ctgggaggaa 20

<210> 1475

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1475

aatactgtga gactgccacc 20

<210> 1476

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1476

cagtcacgga aagtaccctc 20

<210> 1477

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1477

accatgtttc cctctgtcac 20

<210> 1478

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1478

ttaccaaggg acaggatgga 20

<210> 1479

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1479

ccctagaggt caaggtatgg 20

<210> 1480

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1480
ataggccctg tgtgttagtt 20

<210> 1481
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1481
agaaagtccc ctccatttct 20

<210> 1482
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1482
gccaatgccca aagtcagtta 20

<210> 1483
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1483
gaggacgagt tgaacaaagc 20

<210> 1484
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1484
atactggtct caaggtagca c 21

<210> 1485
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1485
accaagtga gctgagttaa tg 22

<210> 1486
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1486
cccagataca ctctgcttc 20

<210> 1487
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1487

caaacatgag aggggggagaa 20

<210> 1488

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1488

aaacacagca atgaggaagg 20

<210> 1489

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1489

gatactcccc tgtgttgctt 20

<210> 1490

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1490

gctcttacta ggatggcagg 20

<210> 1491

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1491

gtttccagca gcaatccttt 20

<210> 1492

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1492

ctgtgcagaa gggtagct 19

<210> 1493

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1493

aaacccctgc taccctaaat 20

<210> 1494

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1494

aatgccccaga tgctgttttc 20

<210> 1495

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1495

gagtggttgt tctctccaga t 21

<210> 1496

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1496

cagtctagaa gctcacccag 20

<210> 1497

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1497

tctcctctac ccctacactg 20

<210> 1498

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1498

ggtgtaaagtg tggcctctcc 20

<210> 1499

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1499

aaaagctac aaactctggc 20

<210> 1500

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1500

tttactggg agactgatgc 20

<210> 1501

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1501
ctgttctgtt cctgaggcta 20

<210> 1502
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1502
tgtgtatcca ttgcctcatc t 21

<210> 1503
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1503
gaagaggggtg tgtgtaggac 20

<210> 1504
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1504
tggttgctct tcctagttcc 20

<210> 1505
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1505
caatgtggag gaagctcttg 20

<210> 1506
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1506
ttgcacaccc aatatgtctac 20

<210> 1507
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1507
tccaaggttt ctctagcgac 20

<210> 1508
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1508

tcgctattct ccttgccata 20

<210> 1509

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1509

aacagcctct ttccttagca 20

<210> 1510

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1510

tttttggtc agtgggatgt 20

<210> 1511

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1511

ctgttcattc ttctcaggg c 21

<210> 1512

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1512

ttcccagacc cataaactac 20

<210> 1513

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1513

tgctcagatt tcagcttct 20

<210> 1514

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1514

gtcagcgatg tggatgtcta 20

<210> 1515

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1515

aactgactcc atgacctgtg 20

<210> 1516

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1516

gaagctgcta ctggtgaac 20

<210> 1517

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1517

tttcctcct gttctgtgc 20

<210> 1518

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1518

ttctcaaatg caaccactcc 20

<210> 1519

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1519

ctggcccttc aattcatgc 20

<210> 1520

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1520

ccagcagtac cgatcaga g 21

<210> 1521

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1521

cagaaggcag gagatggatt 20

<210> 1522

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1522

aagcaaccat ttctgagc 20

<210> 1523

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1523
tcacccttca tctaccact 20

<210> 1524
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1524
aagctggtga cctctacag 20

<210> 1525
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1525
aaaattctgg ttggggagga 20

<210> 1526
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1526
ccatacctca tctgctctgt 20

<210> 1527
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1527
ggctgtccct gaactacttt 20

<210> 1528
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1528
cttggcttaa actctgctcc 20

<210> 1529
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1529
gacttgaaca caccctcaga 20

<210> 1530
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1530

aggagaagag accattgcag 20

<210> 1531

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1531

ttagctaagt ctgtgcggag 20

<210> 1532

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1532

gaagcaacac tgtacacgc 19

<210> 1533

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1533

tctgataaag gctggctcat 20

<210> 1534

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1534

taaaacagtg ccgctacttc 20

<210> 1535

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1535

agtgctatga gtcttggtcc 20

<210> 1536

<400> 1536

000

<210> 1537

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1537

gcagagaaat gggtaaggg 20

<210> 1538

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1538

ggtagagggtg ggttatctgt 20

<210> 1539

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1539

ctgtaaattct ccgggggtg 19

<210> 1540

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1540

ggcgagaatg gagagagaaa 20

<210> 1541

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1541

tccaagcca ggattctttt 20

<210> 1542

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1542

gaacaagtac aaccgtgcag 20

<210> 1543

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1543

acaaatgcc catatcaacc 20

<210> 1544

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1544

ggaaagaggc ctggagtaat 20

<210> 1545

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1545

tttcactgg atgtcgtcat 20

<210> 1546

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1546

aggacaaagt ttcagcctct 20

<210> 1547

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1547

actcaggaca cgactcata c 21

<210> 1548

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1548

acatctttgg ctactggtt 20

<210> 1549

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1549

tcacagtggg cttcattcag 20

<210> 1550

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1550

agctggaatc tatgtaggat gg 22

<210> 1551

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1551

ctgcggaagg atctagtctt 20

<210> 1552

<211> 22
<212> DNA
<213> Homo sapiens

<400> 1552
tgagaagtat tcagcatttc cc 22

<210> 1553
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1553
cactcacgga ctttaggc 19

<210> 1554
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1554
aaaaaaaaa aaaaaaaa 18

<210> 1555
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1555
tcacacgcca ggttattaca 20

<210> 1556
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1556
aagtgggtt gcagtttga 20

<210> 1557
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1557
atgtacgtgt gtgtccatgt 20

<210> 1558
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1558
aggcgggttg gtcaataata 20

<210> 1559
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1559

ccacaaatcc catcaacaca 20

<210> 1560

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1560

tttcacagta acatcggcac 20

<210> 1561

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1561

ctgacagcct gcatttgatt 20

<210> 1562

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1562

tttctggag taaagcgatc t 21

<210> 1563

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1563

cccacaatca cccatctcta 20

<210> 1564

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1564

tatctcactc cacagcttcc 20

<210> 1565

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1565

acaggtagtt tgggtgtgtc 20

<210> 1566

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1566

gctgttgaat gccagaactt 20

<210> 1567

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1567

atagggtcgg ttttggctg 20

<210> 1568

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1568

catcatccct gtcattccca 20

<210> 1569

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1569

gtgggctaag aaaacacctc 20

<210> 1570

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1570

attgtggttt gtggcatgtg 20

<210> 1571

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1571

ccagattcag cctgtattcc 20

<210> 1572

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1572

gcccattgaa gtaaacagtc 20

<210> 1573

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1573
aggttgaca taatagtgt gc 22

<210> 1574
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1574
aatcctttcc ccactcactg 20

<210> 1575
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1575
cacaaagcag ttccatgtcc 20

<210> 1576
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1576
ggacaatttc tcactgcc 20

<210> 1577
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1577
aaggggtgtt gttagatgt 20

<210> 1578
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1578
gcatcacaca cagcagatac 20

<210> 1579
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1579
aaaatgtccg tccagatga 20

<210> 1580
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1580

gggggaaaat gtgtgtgtt 20

<210> 1581

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1581

aactgttagc ttctccaccc 20

<210> 1582

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1582

cgagtgtagg ttccggtta 20

<210> 1583

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1583

agaatgccca ttccaggagt 20

<210> 1584

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1584

atatgtggtt tgaggtcagc t 21

<210> 1585

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1585

ggctttggtc acatggaga 19

<210> 1586

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1586

tgaggcaaga ttcagtgact 20

<210> 1587

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1587

actcatcft gacagcagct 20

<210> 1588

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1588

cacttcctca tgatgtttg ga 22

<210> 1589

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1589

ggccagccca ctatttttg 20

<210> 1590

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1590

ctcagggtgg agtttcaaac 20

<210> 1591

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1591

gatctttctt cccctcctcc 20

<210> 1592

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1592

tgtacatcca ccactgttt g 21

<210> 1593

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1593

agcggtagta agaaggcaaa 20

<210> 1594

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1594

agacaggtga ccattttccc 20

<210> 1595

<211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1595
 tgtggaactt ttgagccaga 20

<210> 1596
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 1596
 cataacgaaa tagggccttc c 21

<210> 1597
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 1597
 atttctgcct ctctcttc c 21

<210> 1598
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1598
 tcatcaagtc acctctccac 20

<210> 1599
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1599
 tggaaaacta gacagcagcc 20

<210> 1600
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1600
 ggaaagggga aaaggtgaca 20

<210> 1601
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 1601
 ctgtcctctg tccacataa 20

<210> 1602
 <211> 20

<212> DNA

<213> Homo sapiens

<400> 1602

tttctgagtc cattcccat 20

<210> 1603

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1603

ggccatcctg atatctcca 20

<210> 1604

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1604

cagagagatg cagaggttca 20

<210> 1605

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1605

tgtgtgtgag ctgctgaat 20

<210> 1606

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1606

ggtttcccat cctaccacat 20

<210> 1607

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1607

ggtgctttg ttgccttact 20

<210> 1608

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1608

actagaaagc aggtacagt 20

<210> 1609

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1609

gcttttcca actctgctg 20

<210> 1610

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1610

caacagacaa gtcacctct 20

<210> 1611

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1611

ggtctctct ggactcaaa 20

<210> 1612

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1612

gaaagcagta gttcaggtg t 21

<210> 1613

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1613

tgaaagactc tgtgccatg 20

<210> 1614

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1614

cactacacgc tcagaacaaa 20

<210> 1615

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1615

aaggcaagca ataatgaggc 20

<210> 1616

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1616

ggacagtctg tgaaaattgc t 21

<210> 1617

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1617

acaaacaacc cttaatgccc 20

<210> 1618

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1618

tgaaacagtg aatccgcaat 20

<210> 1619

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1619

aagggaaatg tggatgcagt a 21

<210> 1620

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1620

ttgaagggaa gcggaaagt 19

<210> 1621

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1621

atttcagct aatgatgctc c 21

<210> 1622

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1622

gctcacttac gcattaacca 20

<210> 1623

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1623

acaggcaaaa ttcagttgga 20

<210> 1624

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1624

aggctgaatc acgtcaaaac 20

<210> 1625

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1625

cctcgtcac atttgacgc 19

<210> 1626

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1626

tgtctgggtt caactgttg 20

<210> 1627

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1627

atthtgcacg cctgttgaga 20

<210> 1628

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1628

gctctcctca aaaccaagt 20

<210> 1629

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1629

cttaatgagg gggcaciaag 20

<210> 1630

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1630

tttctgtcca gtctccacc 20

<210> 1631

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1631

tacaggaccg tcagtgagag 20

<210> 1632

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1632

ttagctactg acgcttcacc 20

<210> 1633

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1633

gcacagacaa catgctagtt 20

<210> 1634

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1634

ttagtctgtt cactggcaca 20

<210> 1635

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1635

cttatcagca gggcacagt 19

<210> 1636

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1636

ttgcatcaaa caaagccaca 20

<210> 1637

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1637

gagagacaag tcaccccttc 20

<210> 1638

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1638
agtcaactac aaatggggga 20

<210> 1639
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1639
gtgccaaaat caacgaaagc 20

<210> 1640
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1640
aaggagggag tacaaagtga g 21

<210> 1641
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1641
atcacatfff cagcacgagg 20

<210> 1642
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1642
caggaggagg tgatttgaa 20

<210> 1643
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1643
agaactgaga ggggagcata 20

<210> 1644
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1644
cagtcaccaa caaaggcttt 20

<210> 1645
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1645

tccccatctc cctaactcat 20

<210> 1646

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1646

ttttctgct gcatccaagg 20

<210> 1647

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1647

actgtacgcc atgaaaaaca 20

<210> 1648

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1648

ggcaaatcaa gtgagctgac 20

<210> 1649

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1649

cgtgggtgga gaattcaca 20

<210> 1650

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1650

acttaggtca gttgcttgg 20

<210> 1651

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1651

gacttcacgc gcacgtactt 20

<210> 1652

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1652

tcgaggcaaa attagcatgg 20

<210> 1653

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1653

gacttatctg ctttcacccc 20

<210> 1654

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1654

ccccatgaac ctaagaccat 20

<210> 1655

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1655

tctggacatg tctttgcgta 20

<210> 1656

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1656

ctccaggaca tctcagcaat 20

<210> 1657

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1657

cctctcgtgt gggaaatgta 20

<210> 1658

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1658

tatctctggc tacctcctgt 20

<210> 1659

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1659
cccatccct gtaccaaag 19

<210> 1660
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1660
ctgcagagat attccatggc 20

<210> 1661
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1661
aaagctgggt tcttaggctt 20

<210> 1662
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1662
gctgttttag gggcacattt 20

<210> 1663
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1663
aagaggcaat gtggaggtta 20

<210> 1664
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1664
gccccaaaca tctgcctttt a 21

<210> 1665
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1665
tggttcaaa taactgggct 20

<210> 1666
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1666

agagcacaca gaacagaact 20

<210> 1667

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1667

ctggtggatt tctcgtcaga 20

<210> 1668

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1668

taggtgttg tgtgaggctt 20

<210> 1669

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1669

gcctcactgc tcctatcttt 20

<210> 1670

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1670

ctctagcagc tgttcctcc 19

<210> 1671

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1671

cgtcgtatct ctggctttgt 20

<210> 1672

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1672

gtccccaacc tcattttca 20

<210> 1673

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1673

tctcaaaga tggctgcaaa 20

<210> 1674

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1674

agtataacca gatagccgtg c 21

<210> 1675

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1675

tgtcctcagg gcaataaagt 20

<210> 1676

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1676

tttgctgctt gaagtggaac 20

<210> 1677

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1677

gctgcaatga cctgatttct 20

<210> 1678

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1678

tccctctctc ctccaaatga 20

<210> 1679

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1679

tgccacagta ggtataggtt g 21

<210> 1680

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1680

ccctcgccct aaagaaacta 20

<210> 1681

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1681
cccctgaatc cctacatcat 20

<210> 1682
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1682
tgttgtacaa gtgagccatt c 21

<210> 1683
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1683
accaagcaat caactcactc t 21

<210> 1684
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1684
gccaatttg tctagccaat a 21

<210> 1685
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1685
ctactgatcc caaagaaggc a 21

<210> 1686
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1686
gtgaaagggt ctatctgcca a 21

<210> 1687
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1687
ggcataccga gcatacatag a 21

<210> 1688
<211> 21

<212> DNA

<213> Homo sapiens

<400> 1688

cacctgttc accaaatcac t 21

<210> 1689

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1689

tctcatgctc tgacagacaa g 21

<210> 1690

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1690

ttgtcctgtt tctctgtga c 21

<210> 1691

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1691

cacaggactg catgcctatt a 21

<210> 1692

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1692

gactctctca gcatcgagtt t 21

<210> 1693

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1693

ctgatggaag ggcattatcc a 21

<210> 1694

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1694

ttctggttcc ataaatccat gc 22

<210> 1695

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1695

gggattattg ttggctactg ag 22

<210> 1696

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1696

aattggtgac ctagggatca g 21

<210> 1697

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1697

gggtttggta agggagaatg a 21

<210> 1698

<211> 23

<212> DNA

<213> Homo sapiens

<400> 1698

aagacatccc agttatgcat tgt 23

<210> 1699

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1699

agatgggagg gagattagac a 21

<210> 1700

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1700

gagtagcaac aacacatgga g 21

<210> 1701

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1701

ttctcctca ttagccacac a 21

<210> 1702

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1702

agtcgcact gtactcttct g 21

<210> 1703

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1703

acaaatgggt catgatgggtg g 21

<210> 1704

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1704

ggtactcacg ttccagtttc c 21

<210> 1705

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1705

gttcatttct acagtcagg c 21

<210> 1706

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1706

ctctcactgt gctgcttaaa g 21

<210> 1707

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1707

caaagaattc cacagagatg gg 22

<210> 1708

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1708

tgagctacag acaagattgc a 21

<210> 1709

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1709

tcacatggga tcgacatatg c 21

<210> 1710

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1710

ccacacaatt tctggctat g 21

<210> 1711

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1711

tcttgcttct ggagagttct t 21

<210> 1712

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1712

agggtatgca gacttcagga a 21

<210> 1713

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1713

aagccaattc tgctctcta g 21

<210> 1714

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1714

tccctcctt attctggcaa c 21

<210> 1715

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1715

gcttcaaaca ctctaaagg c 21

<210> 1716

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1716

tgccattaat gagaagtgt g 21

<210> 1717

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1717

tgccaatcct gttaaacaac tc 22

<210> 1718

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1718

cccgaaacatt gataacagaa ga 22

<210> 1719

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1719

gcaactcagg aaagactaca tc 22

<210> 1720

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1720

ttaagaaagt acccatcctc cc 22

<210> 1721

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1721

gtcatgcctt acaacttagc a 21

<210> 1722

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1722

aatctttgcc aaggtagag c 21

<210> 1723

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1723

gccacttata cctccagaca t 21

<210> 1724

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1724
ccacaatcct gaatgcatg 20

<210> 1725
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1725
ctgcaaggta caacacaagt c 21

<210> 1726
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1726
atctctgtgc cagcaagtat t 21

<210> 1727
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1727
attgggaaac tgtcactgat g 21

<210> 1728
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1728
gccctaataag agaagcaaag c 21

<210> 1729
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1729
gggagccaat cagatagaag t 21

<210> 1730
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1730
gggaagttgg gctatttaat gc 22

<210> 1731
<211> 21

<212> DNA

<213> Homo sapiens

<400> 1731

aactgtgtag agcgaccaa t 21

<210> 1732

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1732

cagtaaggcc atggtctaga t 21

<210> 1733

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1733

ctcagaacat ttgcaccttc t 21

<210> 1734

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1734

acctgataca atggagcatg t 21

<210> 1735

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1735

gggacctaaa ctctttgga a 21

<210> 1736

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1736

tctgcagtgg tgttatctag t 21

<210> 1737

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1737

cacttaagtt tccacgccag 20

<210> 1738

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1738

gtaatggcga gaggttaaag c 21

<210> 1739

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1739

tttaggtatc gaagttgggt ca 22

<210> 1740

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1740

gataagtttg gaagctgcat ca 22

<210> 1741

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1741

aagctctgcc attgacttta c 21

<210> 1742

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1742

ccctacagaa ccgaggaatc 20

<210> 1743

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1743

tcaatctttg catacacagc c 21

<210> 1744

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1744

gtaggtttac atggacagat gc 22

<210> 1745

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1745

tcttctgttt agtgctgtgg t 21

<210> 1746

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1746

caagttcatt tcttcctgc a 21

<210> 1747

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1747

tgcaggaata catggtagac a 21

<210> 1748

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1748

cataggcctt catgtctctc a 21

<210> 1749

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1749

tatgagggtg cactaacaga t 21

<210> 1750

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1750

ggtgctacta ctggtgtatg t 21

<210> 1751

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1751

gccatgcaat atcaaatccc a 21

<210> 1752

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1752

gaaaccaaag actagtgcag c 21

<210> 1753

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1753

atgactaaca ctctgccaag t 21

<210> 1754

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1754

aacaaatgca tcccagacag a 21

<210> 1755

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1755

gcagagagga gtatgtgga t 21

<210> 1756

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1756

atgggtcatt ctacgaagca a 21

<210> 1757

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1757

tggtgtgtgt ggtgataatt ag 22

<210> 1758

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1758

agtgaccctc tgaataacct g 21

<210> 1759

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1759

tcagcaagta aacctgagac c 21

<210> 1760

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1760

gtaccttcac cctccagatc 20

<210> 1761

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1761

tcatcaaatt gccactcct a 21

<210> 1762

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1762

catcagactg tcttgcctt c 21

<210> 1763

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1763

catctctgct gacatttccc a 21

<210> 1764

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1764

gaagatcagg gtattgctga aa 22

<210> 1765

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1765

ttttaggtc attcagcctc c 21

<210> 1766

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1766

tggctaggat tcacttagga aa 22

<210> 1767

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1767

gcaaacaggg tgaattatgc t 21

<210> 1768

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1768

agaagtctgg gaaacgaaga g 21

<210> 1769

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1769

cagatgctcc attactaggt g 21

<210> 1770

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1770

cacatggaga aaggtgaatc a 21

<210> 1771

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1771

tccatccaa tactgccttc 20

<210> 1772

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1772

tctggctcaa aggatcacat g 21

<210> 1773

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1773

aagatcccat tgaccctgaa t 21

<210> 1774

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1774

ccacaggctc tctagaacta a 21

<210> 1775

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1775

ttgagagggg ttacaagggt c 21

<210> 1776

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1776

cttctcctac tctgcattct ca 22

<210> 1777

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1777

gacattagtg gattcaggcc a 21

<210> 1778

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1778

gctgaagtgg aggcaattaa c 21

<210> 1779

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1779

tataactgtt gagtctgccc a 21

<210> 1780

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1780

actgagctta cattcatgca c 21

<210> 1781

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1781

gccactttct ctgcaaagaa t 21

<210> 1782

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1782

acttctacg gactcaaac t 21

<210> 1783

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1783

ggctctcatt acaattggct g 21

<210> 1784

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1784

attgctttca gtgggtggatt g 21

<210> 1785

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1785

ggaatgaaac agaggagtcc c 21

<210> 1786

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1786

aagatgctag aaaccacaa g 21

<210> 1787

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1787

aatgggtggg ttacagagag 20

<210> 1788

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1788
gcatttggac atgaacaagc 20

<210> 1789
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1789
cattggtggg tggatagctg 20

<210> 1790
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1790
accaggagga gaaaagcaaa 20

<210> 1791
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1791
cggaaaacaa accctgaagt 20

<210> 1792
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1792
acctgcatat tgagccatac 20

<210> 1793
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1793
tgttctttca ctttagccc c 21

<210> 1794
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1794
tttctagaac cctcagcaac t 21

<210> 1795
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1795

cccccaacag ttttagtgg t 21

<210> 1796

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1796

aaggcaaaac actcccttt 20

<210> 1797

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1797

cagtgattgc ctctagaaaa gg 22

<210> 1798

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1798

ctaagcagat tgaagcagct 20

<210> 1799

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1799

tgtccccagg ctaagaatc 20

<210> 1800

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1800

agccagaata agcaactgtc 20

<210> 1801

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1801

tttctctat cccagcttgc 20

<210> 1802

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1802

agtacagagg ataacaagg t 21

<210> 1803

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1803

ctcccatcag taccctctct 20

<210> 1804

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1804

ggaatgccta aaccatactg t 21

<210> 1805

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1805

agtggatatt caatgctcta cc 22

<210> 1806

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1806

gcagtacatc gtcctggaa 19

<210> 1807

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1807

cctgagcgag aagaaattg t 21

<210> 1808

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1808

ggaactgaac aagaagtga g 21

<210> 1809

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1809

acctactctt attccgcact 20

<210> 1810

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1810
tgacagcctc tctctcaat 20

<210> 1811
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1811
aaaaaaaaaa aaaaaaaaa 18

<210> 1812
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1812
gctgttttc tgtgtgctc 20

<210> 1813
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1813
atgtattcc ttagcgccc 20

<210> 1814
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1814
aatttgcaa gacttccggt 20

<210> 1815
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1815
tccagttgt gaacattgc 20

<210> 1816
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1816
atgggtttt gcacagatga c 21

<210> 1817
<211> 19

<212> DNA

<213> Homo sapiens

<400> 1817

gggagtcaga aggaggtca 19

<210> 1818

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1818

cctcttttg catgaacctg a 21

<210> 1819

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1819

ccttaccctt tccactcaga 20

<210> 1820

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1820

gactggtata atctgccgt g 21

<210> 1821

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1821

tgtctgcatc ttgatctctg g 21

<210> 1822

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1822

ggtccacag catttgagc 19

<210> 1823

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1823

aggagccctt aactatggtg 20

<210> 1824

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1824

tggcttgggt attgcagata 20

<210> 1825

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1825

ggggacagta gaagatgagt 20

<210> 1826

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1826

agttgttctt ggacggactt 20

<210> 1827

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1827

agaatttccc tgtcatacc a 21

<210> 1828

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1828

agtgagtgaa cttgccatca 20

<210> 1829

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1829

ggcttttctc tgcactgatt 20

<210> 1830

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1830

gcaaaggaaa caggctaact a 21

<210> 1831

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1831

atggcagctg aatcgatct t 21

<210> 1832

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1832

taggtgatgg gcaaattctc a 21

<210> 1833

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1833

gaaatgcctt cccacttaca at 22

<210> 1834

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1834

attggcaaat gtacctgaag c 21

<210> 1835

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1835

caatgattgc tctgtgcc a 21

<210> 1836

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1836

agctgtcctc ctctccatat a 21

<210> 1837

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1837

ggcgttcaag ttactcgatt g 21

<210> 1838

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1838

tagtgactag ctttggagag t 21

<210> 1839

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1839

agccaatgat cccttatgac tt 22

<210> 1840

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1840

aactaaactg gtaggcaatc g 21

<210> 1841

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1841

caatcagacc acaggaagga a 21

<210> 1842

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1842

gatgtgttta ttgcctgtgg t 21

<210> 1843

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1843

gctccttca tagtttcagg g 21

<210> 1844

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1844

acacactgca gttctcacta ta 22

<210> 1845

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1845

tgaatcaagt gacatgacag c 21

<210> 1846

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1846

ttcttacagt cctcagcact t 21

<210> 1847

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1847

ccactaggct gcactaatgt a 21

<210> 1848

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1848

cactagcttc tgtaactgtg tg 22

<210> 1849

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1849

gtctcacact gctcatttcc a 21

<210> 1850

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1850

cactaggggt catcagctgt t 21

<210> 1851

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1851

caaccaacat tagagtgacc c 21

<210> 1852

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1852

gctggttgag agagagagag a 21

<210> 1853

<211> 21
<212> DNA
<213> Homo sapiens

<400> 1853
acaccagccg aatacagatt t 21

<210> 1854
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1854
tgcttcatac ctttctgctt c 21

<210> 1855
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1855
atttcccatg cctttcaact c 21

<210> 1856
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1856
tctctcagta ggcgtcttta a 21

<210> 1857
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1857
tgactgctac gctagacttg 20

<210> 1858
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1858
ggatagagga aaccaggtg 20

<210> 1859
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1859
ggctctttca aagtatccag g 21

<210> 1860
<211> 22

<212> DNA

<213> Homo sapiens

<400> 1860

agactttctt tgttgccttc ag 22

<210> 1861

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1861

gcctcaacaa ttcagtccac 20

<210> 1862

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1862

cataagttgc tggaagagaa ca 22

<210> 1863

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1863

tcgactgctt taagtgaagg a 21

<210> 1864

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1864

accagtgatt agtgtttctc ct 22

<210> 1865

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1865

caagacacac acaaacacac a 21

<210> 1866

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1866

ggtaagagtt gccctaattg c 21

<210> 1867

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1867

gcttggcttc tcacaaatgt 20

<210> 1868

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1868

gtttgccagt agaaatggga 20

<210> 1869

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1869

gtaaagtgtt cagaggacgg 20

<210> 1870

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1870

actagggaga agaattggca g 21

<210> 1871

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1871

ccagttcatt ccagcttcca 20

<210> 1872

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1872

gatcgccaac ctgtttata ag 22

<210> 1873

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1873

gctgtcaaag tggagataac c 21

<210> 1874

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1874

aacgcttcca tccaccta t 21

<210> 1875

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1875

acctgcctgt ctaccatta a 21

<210> 1876

<211> 23

<212> DNA

<213> Homo sapiens

<400> 1876

gatactttcc ttctccaga tct 23

<210> 1877

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1877

ggccgcagtt ttgatttag 20

<210> 1878

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1878

tggaaggac gggttgta 19

<210> 1879

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1879

tgaatcatgc tgggagaac 20

<210> 1880

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1880

atagaagagg taccagcaa 20

<210> 1881

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1881

ccctgactat gctaagttgc 20

<210> 1882

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1882

tgcaagcaaa atgaaaccag 20

<210> 1883

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1883

aaaaaaaaaa aaaaaaaaa 18

<210> 1884

<211> 19

<212> DNA

<213> Homo sapiens

<400> 1884

cagctgctcc ttcttagc 19

<210> 1885

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1885

tatactgcc aaggtgacct 20

<210> 1886

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1886

gaagcataat gagaacctcc a 21

<210> 1887

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1887

aacccaactt gcagacaatc 20

<210> 1888

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1888

atctgtttgc tgtgtcagaa 20

<210> 1889

<211> 23

<212> DNA

<213> Homo sapiens

<400> 1889

tccagatata ttcaaaaggg aga 23

<210> 1890

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1890

agggttttat caaagcccca 20

<210> 1891

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1891

gggacttgat gttctaagca a 21

<210> 1892

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1892

cctacatgat acgcacagtc 20

<210> 1893

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1893

aaaaaaaaa aaaaaaaaa 18

<210> 1894

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1894

gtttttctct acccagcaca 20

<210> 1895

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1895

ctctaatttg ccaccctctt t 21

<210> 1896

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1896
gaacgctaaa gctttccca 20

<210> 1897
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1897
tcttctctct gccaaagtaga 20

<210> 1898
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1898
ataacactgt ccttctgggc 20

<210> 1899
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1899
gagccctactc tctgatacga 20

<210> 1900
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1900
ccagttgttc acttctctga t 21

<210> 1901
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1901
gccttaaaac caaactgtgt 20

<210> 1902
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1902
ctggacttca atcacccaag 20

<210> 1903
<211> 20

<212> DNA

<213> Homo sapiens

<400> 1903

tgaacaaatt gctgtgctga 20

<210> 1904

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1904

cccctaaat gaaagtggc 20

<210> 1905

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1905

aaaaaaaaa aaaaaaaa 18

<210> 1906

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1906

tgagtgttg gaattttgca 20

<210> 1907

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1907

ggttggctac ttcattgtac 20

<210> 1908

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1908

tcactgcatt cctagaacct 20

<210> 1909

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1909

ataactcagg caaatgggg 20

<210> 1910

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1910

ccttctgctc tcactttacg 20

<210> 1911

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1911

ggatactagc agaggtggag 20

<210> 1912

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1912

tgtacacaat atgccaggaa c 21

<210> 1913

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1913

gcacttgagt tatgggactt 20

<210> 1914

<211> 23

<212> DNA

<213> Homo sapiens

<400> 1914

tgtgatatgt agtgtgtatc agt 23

<210> 1915

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1915

gaatgtgttc aaaggagggt 20

<210> 1916

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1916

gatgaagggg attacgggaa 20

<210> 1917

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1917

tttaggaagc agcacaagaa 20

<210> 1918

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1918

gagggtgctg gggttatc 18

<210> 1919

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1919

cccgaagca ctaccttt 20

<210> 1920

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1920

ttcatgagct gcaatgtgt 20

<210> 1921

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1921

tgctatgaaa agagggacca 20

<210> 1922

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1922

gtcctggatc tacacgtgaa 20

<210> 1923

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1923

gtaaatctgt gtgccagcaa 20

<210> 1924

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1924

taaaagaggc gtgtggaaaa 20

<210> 1925

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1925

ccagtagctt gtgatgtgta 20

<210> 1926

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1926

tacaggcctc tgaaagatga 20

<210> 1927

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1927

agagcatgct agacgtcttt 20

<210> 1928

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1928

ctgggctgta attaaggctc 20

<210> 1929

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1929

aacacctgca cacttgaaa 20

<210> 1930

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1930

aatgaacttt gtgggctgaa 20

<210> 1931

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1931

ccacactctc actggttcta 20

<210> 1932

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1932

cacagtggat acctcaggaa 20

<210> 1933

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1933

ccaacacagg aggaactttt 20

<210> 1934

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1934

gagaaaagcc aacaaaaatg tg 22

<210> 1935

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1935

tgtcattact agaagcacct tt 22

<210> 1936

<211> 23

<212> DNA

<213> Homo sapiens

<400> 1936

tggtgtgagt tcaggagggt tta 23

<210> 1937

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1937

accatttctg acagaacaga 20

<210> 1938

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1938

tgatgcttaa acacatgcct 20

<210> 1939

<211> 20
<212> DNA
<213> Homo sapiens

<400> 1939
aagggatatg cagcttggtc 20

<210> 1940
<211> 18
<212> DNA
<213> Homo sapiens

<400> 1940
aaaaaaaaaa aaaaaaaaa 18

<210> 1941
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1941
gttgatcacc aaatgcacc ac 22

<210> 1942
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1942
ctcagattcc agagccctc 19

<210> 1943
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1943
acattgctag cagctttgt 20

<210> 1944
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1944
acttgccaag aacagtatct g 21

<210> 1945
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1945
ttccttcttc caggtgaaca 20

<210> 1946
<211> 20

<212> DNA
<213> Homo sapiens

<400> 1946
tgttctcct tcactcgggc 20

<210> 1947
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1947
tgtcaccttg cagatacagg 20

<210> 1948
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1948
attgttcaca gggtaagtc 20

<210> 1949
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1949
atgagccagg agaatacatca 20

<210> 1950
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1950
catcatttca aaggggctca 20

<210> 1951
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1951
tcttctctaa caccactcc 20

<210> 1952
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1952
acccttacca aagtagcatc 20

<210> 1953
<211> 20
<212> DNA

<213> Homo sapiens

<400> 1953

atcacgacgc ctgtttatt 20

<210> 1954

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1954

actttcctgc caacaatctc 20

<210> 1955

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1955

ttgatagttg catctgggga 20

<210> 1956

<211> 22

<212> DNA

<213> Homo sapiens

<400> 1956

tttgtaact aacgtgattc ca 22

<210> 1957

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1957

cccactctcc atgtgttctt 20

<210> 1958

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1958

tcctgcttca actcaatagc 20

<210> 1959

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1959

acccttcatt ttcgtatgtc 20

<210> 1960

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1960
acagttatgg aggaattgcg 20

<210> 1961
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1961
tcaaacctct tttatctgtc cc 22

<210> 1962
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1962
atttcacgta acactctggt 20

<210> 1963
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1963
ctctggcaaa actttctgga t 21

<210> 1964
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1964
gcttctcatg ctacactg 19

<210> 1965
<211> 21
<212> DNA
<213> Homo sapiens

<400> 1965
aatatgactt gcccttttga a 21

<210> 1966
<211> 19
<212> DNA
<213> Homo sapiens

<400> 1966
tcacagccag ttacacaga 19

<210> 1967
<211> 20
<212> DNA
<213> Homo sapiens

<400> 1967

ctacagtga gaagagtccc 20

<210> 1968

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1968

ttggttcat gtggcttga 20

<210> 1969

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1969

tcctctccc caacttctt 20

<210> 1970

<211> 21

<212> DNA

<213> Homo sapiens

<400> 1970

ctttagattc cagggctctt g 21

<210> 1971

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1971

tgaaagcgtg aaaatcagct 20

<210> 1972

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1972

actcgatccc taggtaatgt 20

<210> 1973

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1973

acaagtgggt agggatgttc 20

<210> 1974

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1974

gcacaagttt tcagggaatg 20

<210> 1975

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1975

gtggaaagtc tcgtcagaat 20

<210> 1976

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1976

tccacctctg agcataacat 20

<210> 1977

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1977

aaaaaaaaaa aaaaaaaaa 18

<210> 1978

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1978

aaaaaaaaaa aaaaaaaaa 18

<210> 1979

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1979

ccatcccact tctccagata 20

<210> 1980

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1980

ccaccttctt gcttaaagaa 20

<210> 1981

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1981

ctccttactt gcactgagtt 20

<210> 1982

<211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1982
 gggaaaactt acgggaactt 20

 <210> 1983
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <400> 1983
 tagaaatgtt taggggtcat ga 22

 <210> 1984
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1984
 taccctctt ttccatctgc 20

 <210> 1985
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1985
 gcattttgac aggaaagtgg 20

 <210> 1986
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1986
 tagggccaca gtttctcaat 20

 <210> 1987
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1987
 gaatgagaaa tctggcagga 20

 <210> 1988
 <211> 20
 <212> DNA
 <213> Homo sapiens

 <400> 1988
 tcagatgcct gatgaccata 20

 <210> 1989
 <211> 20

<212> DNA

<213> Homo sapiens

<400> 1989

aatatgcagt gggtaggagc 20

<210> 1990

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1990

gacaacagct gacttcatt 20

<210> 1991

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1991

cactctctgg aacaaacaca 20

<210> 1992

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1992

gttttgaggc ggtttcatga 20

<210> 1993

<211> 18

<212> DNA

<213> Homo sapiens

<400> 1993

aaaaaaaaa aaaaaaaaa 18

<210> 1994

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1994

gaacacctca aagttgctca 20

<210> 1995

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1995

aagaagcaag gacaaggatg 20

<210> 1996

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1996

gaaacaacca ccacaacaaa 20

<210> 1997

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1997

ccaccatgtt tacaccgttt 20

<210> 1998

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1998

tttaccatg aattgctgca 20

<210> 1999

<211> 20

<212> DNA

<213> Homo sapiens

<400> 1999

agtttcatt tgttcaggga 20

<210> 2000

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2000

ttcggatggc ttgattgtc 20

<210> 2001

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2001

cattgtaaat taaacggcct c 21

<210> 2002

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2002

ctaatgcaag ctgcttctct 20

<210> 2003

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2003
tgtctagtgg taatctggg 20

<210> 2004
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2004
tctggacagt ggagttgaa 20

<210> 2005
<211> 18
<212> DNA
<213> Homo sapiens

<400> 2005
aaaaaaaaa aaaaaaaaa 18

<210> 2006
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2006
aggagagaca taactggtct 20

<210> 2007
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2007
attgcaatgt ctgtggatgt 20

<210> 2008
<211> 19
<212> DNA
<213> Homo sapiens

<400> 2008
aagaagttga ggtagcacg 19

<210> 2009
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2009
agtgctcttt cctccagttc 20

<210> 2010
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2010

ttgaacctga aaggaactgt g 21

<210> 2011

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2011

gctcaatcac ctgtccctt 20

<210> 2012

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2012

cattgaagct cactctaagg g 21

<210> 2013

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2013

ctaaagtgtg ggtaggggt 20

<210> 2014

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2014

tgcccttacat ttctgtggg 20

<210> 2015

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2015

gccataagat ttcccactc 20

<210> 2016

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2016

acaaagcaag aggatgaaac a 21

<210> 2017

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2017

caaagcacca tcaacactta 20

<210> 2018

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2018

cactgcaact cctagaatga 20

<210> 2019

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2019

tgtggggaaa ttgctgttta 20

<210> 2020

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2020

gtatgggcag ctgtaacttg 20

<210> 2021

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2021

tcacaagcca ctgaaaatgt 20

<210> 2022

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2022

tgtatgttaa gctagccaac a 21

<210> 2023

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2023

tgtgttattg aactttgcca 20

<210> 2024

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2024

ttcatcccta cctcatcacc 20

<210> 2025

<211> 21
<212> DNA
<213> Homo sapiens

<400> 2025
agatcacttt tggctgtaac c 21

<210> 2026
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2026
caagtgacaa tctcagccaa 20

<210> 2027
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2027
gcattttcag atggttccct 20

<210> 2028
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2028
atggagagtt tgagtggagt 20

<210> 2029
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2029
ctgccactgg gtttatagaa aa 22

<210> 2030
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2030
acacctttac tcctgtggat 20

<210> 2031
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2031
gatgtagggc cttatccaca 20

<210> 2032
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2032

agcttggtga tcttcaaaca 20

<210> 2033

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2033

tgaaatggtg ggtaatgctc 20

<210> 2034

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2034

catgcaagtt cacgaggtta 20

<210> 2035

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2035

agtcgagga agaagcaact 20

<210> 2036

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2036

gagtccaatc tttccaca 20

<210> 2037

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2037

tccactgctg tcttaccctt 20

<210> 2038

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2038

ggacagaaca gctacaaagg 20

<210> 2039

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2039

ctggctgtg aattagagg 20

<210> 2040

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2040

gtaagatggt ggcaggat 19

<210> 2041

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2041

agaagggtc aaaacacatc 20

<210> 2042

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2042

tcatgtaggc ttctgatt t 21

<210> 2043

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2043

tgtagctctt gacctagcaa 20

<210> 2044

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2044

taagttcacg gtgaagtcaa c 21

<210> 2045

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2045

gtggcttcaa ctaactggac 20

<210> 2046

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2046
accgtaagt gttgagtga 20

<210> 2047
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2047
tgtagaagta gggttgcgt 20

<210> 2048
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2048
caggggacat ttgaagatgg 20

<210> 2049
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2049
gaaattgtgc agtgaaagca 20

<210> 2050
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2050
atgtaagaag tgcgttgctt a 21

<210> 2051
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2051
agatctggaa tctgagactc c 21

<210> 2052
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2052
tataggataa ggtcaagcag gt 22

<210> 2053
<211> 18
<212> DNA
<213> Homo sapiens

<400> 2053

aaaaaaaaa aaaaaaaaa 18

<210> 2054

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2054

tcagtgaatg aggaatcatg c 21

<210> 2055

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2055

ttctcaggag taccacaagc 20

<210> 2056

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2056

ggatgaaaca cagaacctg 20

<210> 2057

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2057

cagatccctt tcatttgca 20

<210> 2058

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2058

ggaaaagtc tcaattaggc 20

<210> 2059

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2059

ctggcagtta tagtcaccaa 20

<210> 2060

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2060

aggaagtcct tatgatgcca 20

<210> 2061

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2061

gctggtgaag ttggagtttt 20

<210> 2062

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2062

gctgggttta agccacatat 20

<210> 2063

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2063

tgtagcctaa atagcagcct 20

<210> 2064

<211> 23

<212> DNA

<213> Homo sapiens

<400> 2064

aggaattgct ttatttttaa cca 23

<210> 2065

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2065

gctgcttca ggttttgtg 20

<210> 2066

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2066

atggtgcaga aaagagcaat 20

<210> 2067

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2067

gtgtggtgcc attttcttc 20

<210> 2068

<211> 20
<212> DNA
<213> Homo sapiens

<400> 2068
gaacaataact ttctccccgg 20

<210> 2069
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2069
gaaatggcca tgctaggaat 20

<210> 2070
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2070
actccagta acatggatgc 20

<210> 2071
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2071
gaaacaccca gacttgtagc 20

<210> 2072
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2072
ttaaacttt gtgtgcgtgt 20

<210> 2073
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2073
cctccaggaa cttgttcag 20

<210> 2074
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2074
aaaaaccttc acaaacccca 20

<210> 2075
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2075

gagtgatatt tgtctcgctg 20

<210> 2076

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2076

actagccacac taatgttgct 20

<210> 2077

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2077

cgattatcag aacagatgag gt 22

<210> 2078

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2078

attgcacagc tgaaaatcct 20

<210> 2079

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2079

ggcacactga ccgtatttat 20

<210> 2080

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2080

tggtagtggg tcaggaattt 20

<210> 2081

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2081

tctcttgaaa agaaaggcgg 20

<210> 2082

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2082

tgaattacac agcaaagccc 20

<210> 2083

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2083

ctgccaatgg gatcgaattt 20

<210> 2084

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2084

gagtgacgct gttcattctt 20

<210> 2085

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2085

gatagtaacc ggggtagca 20

<210> 2086

<211> 18

<212> DNA

<213> Homo sapiens

<400> 2086

aaaaaaaaaa aaaaaaaaa 18

<210> 2087

<211> 23

<212> DNA

<213> Homo sapiens

<400> 2087

tctaataagg gattgatgga gtt 23

<210> 2088

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2088

gggagatttc ctgctttag 20

<210> 2089

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2089
aatccatgca gcttctctct 20

<210> 2090
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2090
tgcattgtct ctggtttgaa 20

<210> 2091
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2091
tcctgaatgc atccttaacc 20

<210> 2092
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2092
tgggaaaggt gagaaggatt 20

<210> 2093
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2093
ttcgggaccc atacctaaaa 20

<210> 2094
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2094
tcttttctgg acccacatga 20

<210> 2095
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2095
gacctctaca tctgtatctt cc 22

<210> 2096
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2096

cccttcattt tctgtcccat 20

<210> 2097

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2097

tcagccttga gtattagcct a 21

<210> 2098

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2098

aagtttgcca tgaaggtcat 20

<210> 2099

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2099

gacttctggg tgtttcctca 20

<210> 2100

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2100

atgtgtctat tgcctacct 20

<210> 2101

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2101

tgcggaagt tcacatgaa 19

<210> 2102

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2102

gtgaactca ggctgctta 19

<210> 2103

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2103

tggttcgtc ccgtaaataag 20

<210> 2104

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2104

aattcctttc aatgctggct 20

<210> 2105

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2105

agaaagacac atatgcatg g 21

<210> 2106

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2106

ttgttggtgt cagttctgaa 20

<210> 2107

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2107

tgtaggaaca gattagggca 20

<210> 2108

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2108

ctccaagctg atatgccatc 20

<210> 2109

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2109

ccacccctca ttcttcctt 20

<210> 2110

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2110

gggtccttcg ttctgttt 20

<210> 2111

<211> 21
<212> DNA
<213> Homo sapiens

<400> 2111
taggaaacag gctaaaaggg a 21

<210> 2112
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2112
tactgtgtag aaggcagtgt 20

<210> 2113
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2113
gctaaggaca aagaaccact 20

<210> 2114
<211> 18
<212> DNA
<213> Homo sapiens

<400> 2114
aaaaaaaaa aaaaaaaaa 18

<210> 2115
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2115
tggctaagac caggattgtt 20

<210> 2116
<211> 18
<212> DNA
<213> Homo sapiens

<400> 2116
aaaaaaaaa aaaaaaaaa 18

<210> 2117
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2117
tgataggcag atcattcccc 20

<210> 2118
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2118

gcaaatggca aagggaac 20

<210> 2119

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2119

cacggctagt gtcatttt 19

<210> 2120

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2120

ccgtaatacc caagtcatt g 21

<210> 2121

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2121

agcaaaactaa aacagcaact tc 22

<210> 2122

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2122

agcctgctat cttcactgg 19

<210> 2123

<211> 23

<212> DNA

<213> Homo sapiens

<400> 2123

accacatata tagagacttt gaa 23

<210> 2124

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2124

ctccagactc tgcaaggat 19

<210> 2125

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2125

ttcctgttg ctctgatca 20

<210> 2126

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2126

ccacaaagat gaaggccaag 20

<210> 2127

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2127

ccatacctta gttctcaggg t 21

<210> 2128

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2128

gtaagagaga gctgggacaa 20

<210> 2129

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2129

tgtgaccatc ctatccacaa 20

<210> 2130

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2130

agaaccagtt gtacgagttc 20

<210> 2131

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2131

agtccttctcc ctctctgtc 20

<210> 2132

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2132

gccctttct ctcttgacc 20

<210> 2133

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2133

tctgttcca agtattcctg g 21

<210> 2134

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2134

accacttag cccatctctt 20

<210> 2135

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2135

gtggtggatt attgagctgg 20

<210> 2136

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2136

tgcttaatgg gatcattgac c 21

<210> 2137

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2137

cccacatagt gcaaaagaca 20

<210> 2138

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2138

gtatgtgtga agtagccgag 20

<210> 2139

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2139

tggtcctaac tcagacctt 20

<210> 2140

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2140

aacatgaagg gaaggttg 20

<210> 2141

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2141

tatacttcaa ctgcaggca g 21

<210> 2142

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2142

gccaaagaca atgagagagt c 21

<210> 2143

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2143

atttagcagc catgaccagt a 21

<210> 2144

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2144

tgggccaatt cctaaccat t 21

<210> 2145

<211> 23

<212> DNA

<213> Homo sapiens

<400> 2145

cgatctcatg aataagtctg acc 23

<210> 2146

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2146

tggaaagcag actaacagtg a 21

<210> 2147

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2147

gggaccctat gtagagattg t 21

<210> 2148

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2148

ggagcccaag gatgtattag a 21

<210> 2149

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2149

ctaatagctg gttctgcaca c 21

<210> 2150

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2150

gatgaaatga atgctgactc tc 22

<210> 2151

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2151

aaactgaagc ttcgagaacc c 21

<210> 2152

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2152

tgccgacaac tactttaggt a 21

<210> 2153

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2153

tgtatccaat cacctgtcag a 21

<210> 2154

<211> 21
<212> DNA
<213> Homo sapiens

<400> 2154
cagcacctta agcagaaatc a 21

<210> 2155
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2155
aagcccttca tccattctc t 21

<210> 2156
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2156
atcttggtgc catcttaagg t 21

<210> 2157
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2157
agcaaaccacaa tcgcaaaacta g 21

<210> 2158
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2158
aatcatcatc ttcacagct cg 22

<210> 2159
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2159
ccttcgcct tgcttatatg g 21

<210> 2160
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2160
actactcaac agcctaccaa a 21

<210> 2161
<211> 21

<212> DNA

<213> Homo sapiens

<400> 2161

tggagctggg aactttaatg t 21

<210> 2162

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2162

gaagagagag agaatgcgtg t 21

<210> 2163

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2163

gacatggata ttctggtgcc a 21

<210> 2164

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2164

ctgttgcaag atgacccaaa t 21

<210> 2165

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2165

agatacacac acgttcacaa ac 22

<210> 2166

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2166

gatggcaatg ctgataacg a 21

<210> 2167

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2167

ttccatgaag ttctcaaga ct 22

<210> 2168

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2168

ccaccacat accctgaaat t 21

<210> 2169

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2169

gtaacacacg gatgctgaag 20

<210> 2170

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2170

tggacacgag gctatttga g 21

<210> 2171

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2171

ggcttaagaa ggagagtgg t 21

<210> 2172

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2172

tagttcctt tggccttct c 21

<210> 2173

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2173

ctaggggtcc cagttcaca a 21

<210> 2174

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2174

gaaacaacat tgagggcatt g 21

<210> 2175

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2175
gagctcttg aagtagaagc a 21

<210> 2176
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2176
ccattccaac aaagcttccg 20

<210> 2177
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2177
ctactgccc tattgtgctg a 21

<210> 2178
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2178
ccaggggtgt tgaaggtaga a 21

<210> 2179
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2179
ctggaggtaa gaaggaatgc a 21

<210> 2180
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2180
atgtgggact cttgctctc 20

<210> 2181
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2181
atgaatacag cttgcatgg c 21

<210> 2182
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2182

gttaaagcat tcacagccct c 21

<210> 2183

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2183

ctgggacttg tctatctcc t 21

<210> 2184

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2184

atgtctgtcc aagtgaacag t 21

<210> 2185

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2185

aaagtatcca gaccagaac c 21

<210> 2186

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2186

ataggccagc actccaaata a 21

<210> 2187

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2187

caaatcaagt cccatggtag g 21

<210> 2188

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2188

ctttccgtct ttataggcag c 21

<210> 2189

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2189

agaaatcgtg ttacagcct a 21

<210> 2190

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2190

ccgtaaatga agtggcttga a 21

<210> 2191

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2191

cctttcttgc aaccttgaga t 21

<210> 2192

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2192

ctctagatgc tcaacctcag g 21

<210> 2193

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2193

aataacagtc caccagaacc a 21

<210> 2194

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2194

tccaaggacc tgcaaatgtt a 21

<210> 2195

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2195

aggttacatc attcaccac a 21

<210> 2196

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2196

atgaagacaa tgacatctgc g 21

<210> 2197

<211> 21
<212> DNA
<213> Homo sapiens

<400> 2197
cacttgcat ggtaggga c 21

<210> 2198
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2198
acctccacct tattgtca a 21

<210> 2199
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2199
gaattgcaaa ggatgggtag g 21

<210> 2200
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2200
ctgcattgtg agtccatga a 21

<210> 2201
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2201
tcctatcttc atccctctc c 21

<210> 2202
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2202
ttccatttag cctccatct g 21

<210> 2203
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2203
tagcttatg ggcctgttc t 21

<210> 2204
<211> 21

<212> DNA

<213> Homo sapiens

<400> 2204

ccacctctca aaccagatt t 21

<210> 2205

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2205

gtcagcgtat ttgggattga at 22

<210> 2206

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2206

aaatctgccca cccatttctt c 21

<210> 2207

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2207

tattctgagt tctaccagg t 21

<210> 2208

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2208

tacatgagac ccagaaacag a 21

<210> 2209

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2209

cttcttgga gactatcagg a 21

<210> 2210

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2210

aagctgctaa atctgtaggg a 21

<210> 2211

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2211

ctgaccagac ctgttgacta a 21

<210> 2212

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2212

tgatatgttc agtttgcta cc 22

<210> 2213

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2213

agcttgagtt tcttgctggg 20

<210> 2214

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2214

ttcccgcaaa gtagaagcta t 21

<210> 2215

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2215

aaacgcatac aaacaggaga c 21

<210> 2216

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2216

cttctaacc catcacctgc t 21

<210> 2217

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2217

cacccaaact cacaggtaca a 21

<210> 2218

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2218

tgaattctga gatcgagagc c 21

<210> 2219

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2219

agattaactg ttgcctcact g 21

<210> 2220

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2220

caagacagtg cattccatgg 20

<210> 2221

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2221

ccaaggaaag agttgagaag g 21

<210> 2222

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2222

tgagtgcagt cgataaggaa g 21

<210> 2223

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2223

aacaccgaga aagagagaga g 21

<210> 2224

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2224

tgtactgctt tcgtcttatg c 21

<210> 2225

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2225

catattcgca ctgtatagcc g 21

<210> 2226

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2226

ctgatggatt ctctggtgtg a 21

<210> 2227

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2227

tcaaggagaa gagagagggg a 21

<210> 2228

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2228

tctcccaaag cagacaaaga c 21

<210> 2229

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2229

agtcagttgt tacgtgcaaa g 21

<210> 2230

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2230

aaaggtttgt tcatcctccc t 21

<210> 2231

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2231

acagagcacg caatatagga a 21

<210> 2232

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2232

ctgcattcac ccatgtactt t 21

<210> 2233

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2233

tccagccata ccatgtctat c 21

<210> 2234

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2234

ctcactaggg aagaacagca g 21

<210> 2235

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2235

tgctgggtct gagtgttata aa 22

<210> 2236

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2236

gttgtgtgaa tgggtctgtt a 21

<210> 2237

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2237

ggcccagaag actcttgtaa t 21

<210> 2238

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2238

cgacctacat cagctaattg t 21

<210> 2239

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2239

aagggaagaa taacaatggt gc 22

<210> 2240

<211> 21
<212> DNA
<213> Homo sapiens

<400> 2240
atgggagtat gggagtagga a 21

<210> 2241
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2241
ttggtggctt gcagagattt 20

<210> 2242
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2242
tcacacgatc atcatactca ca 22

<210> 2243
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2243
ggtagcagat gactagacga t 21

<210> 2244
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2244
acgcctctgt catttcctaa c 21

<210> 2245
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2245
cagttgactc aatgggtcaa t 21

<210> 2246
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2246
ataggttaca gattgccacg t 21

<210> 2247
<211> 21

<212> DNA

<213> Homo sapiens

<400> 2247

gatgctgcta tcaaaggaac a 21

<210> 2248

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2248

aagacaaaga gatggaaggc a 21

<210> 2249

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2249

aataccctct tccctcctc a 21

<210> 2250

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2250

ccaccgtcaa tatttatcag ct 22

<210> 2251

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2251

gcctcagtcc aaatcttaga t 21

<210> 2252

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2252

ccttaggatt ctcaaagagt gt 22

<210> 2253

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2253

gcagtacaga ttcttgaaca gt 22

<210> 2254

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2254

agaggattag atgtcttgct gt 22

<210> 2255

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2255

tactgcaggc aattcaggta a 21

<210> 2256

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2256

gaagagggtcc agtaagtgag g 21

<210> 2257

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2257

ttgtgagtcc ttgtctcctt g 21

<210> 2258

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2258

gacgactaag acattgcac a 21

<210> 2259

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2259

agaagtctct ctccgttggt t 21

<210> 2260

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2260

cttaatgtgca tcaactgtgc t 21

<210> 2261

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2261
agtgctctc agaatcagga c 21

<210> 2262
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2262
tttattccc tacgcaaagc c 21

<210> 2263
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2263
agccttgat gactgagtg a 21

<210> 2264
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2264
ttggttcta ttctgactg c 21

<210> 2265
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2265
ttagagcttg ctagatcgg g 21

<210> 2266
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2266
gaaatcccaa actgcctgaa a 21

<210> 2267
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2267
atccttcttg tgaaccttc t 21

<210> 2268
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2268

accagatgca tgtgattaaa gg 22

<210> 2269

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2269

gtgtactcta ggctactgtc a 21

<210> 2270

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2270

gtcagcagca agtaaaggtt c 21

<210> 2271

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2271

catctagtca aggggtccac a 21

<210> 2272

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2272

caagtcatgc tccaaactgt t 21

<210> 2273

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2273

aggacttagg acaacagaga a 21

<210> 2274

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2274

tgcccaacac catctcta a 21

<210> 2275

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2275

gccttcac ctcagaactt c 21

<210> 2276

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2276

agggtatcta ttctccggac a 21

<210> 2277

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2277

atttgcccaa gtaagttcca c 21

<210> 2278

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2278

tggaagtaca tgggatgcat t 21

<210> 2279

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2279

cttgaagagt tccaatgcca a 21

<210> 2280

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2280

cgctgctgtt taaatcgatc a 21

<210> 2281

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2281

gctctgcttt gctcaaattc t 21

<210> 2282

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2282

tgagctccag aattagatgt gt 22

<210> 2283

<211> 22
<212> DNA
<213> Homo sapiens

<400> 2283
aacacctcct ttctcactac ag 22

<210> 2284
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2284
acaaacttca ttcaccgcag 20

<210> 2285
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2285
aactacgccca cccaactaaa 20

<210> 2286
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2286
gcttcagtgt aaccatgact c 21

<210> 2287
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2287
tgcacaatta agctacttct cc 22

<210> 2288
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2288
caacaccaaa cttgcctgaa t 21

<210> 2289
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2289
tccacaattt ctacagcaac c 21

<210> 2290
<211> 21

<212> DNA

<213> Homo sapiens

<400> 2290

gtgtcatttg attggtgctc t 21

<210> 2291

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2291

gggtgtttca gtaggttagg at 22

<210> 2292

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2292

tgggattcta atgtctggtg c 21

<210> 2293

<211> 18

<212> DNA

<213> Homo sapiens

<400> 2293

agagggtggtt ggttggtt 18

<210> 2294

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2294

gggcatcctg tctgaaatat g 21

<210> 2295

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2295

aagaagcgca gatacagtac a 21

<210> 2296

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2296

cacagcaagt ttgaacctag t 21

<210> 2297

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2297

agtgcaaatg atgacctgtt g 21

<210> 2298

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2298

gaactgttgc atgagaggta c 21

<210> 2299

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2299

ctttgtcctt ctctgttg t 21

<210> 2300

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2300

tttcttctag agtccagagg tg 22

<210> 2301

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2301

attctcttct ctctccagc c 21

<210> 2302

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2302

tatggctttg ctacctgtc a 21

<210> 2303

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2303

ctatttctct ggctcttgac c 21

<210> 2304

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2304

ttcttaaacc tctgtgtggc t 21

<210> 2305

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2305

tggacaaaca agaactgggt a 21

<210> 2306

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2306

ccatgatcac tgaaaccaac a 21

<210> 2307

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2307

ccatatgccc tgctctttaa g 21

<210> 2308

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2308

gggtggacaa agcaattcaa a 21

<210> 2309

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2309

cagcattcaa ttcattcttg tg 22

<210> 2310

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2310

aagtagaagc aagccctgaa t 21

<210> 2311

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2311

gtgtgtagg gatgagaatt at 22

<210> 2312

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2312

tcaggtgaagc ttccctccac 20

<210> 2313

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2313

actggttgta gaaaggacct c 21

<210> 2314

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2314

agtaagaggc cagaagtcag a 21

<210> 2315

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2315

gcagtgcagg cctatatata g 21

<210> 2316

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2316

aaatctctga gtcggccata a 21

<210> 2317

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2317

aggcatggca aacttacttg 20

<210> 2318

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2318

catttcactt tcgaggatgg t 21

<210> 2319

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2319

gtcagactaa agtgaggacc a 21

<210> 2320

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2320

ccagccctac ctaaagtga t 21

<210> 2321

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2321

cccttcaca agactctt c 21

<210> 2322

<211> 18

<212> DNA

<213> Homo sapiens

<400> 2322

aaaaaaaaa aaaaaaaa 18

<210> 2323

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2323

ccaaatgtag aacaggatca gc 22

<210> 2324

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2324

tagcagtagg tgtggcttc 20

<210> 2325

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2325

ttggattctc ttggtgtga g 21

<210> 2326

<211> 22
<212> DNA
<213> Homo sapiens

<400> 2326
caacgccttg gtatagttg tg 22

<210> 2327
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2327
ccaggtgccca tcgttaaaga a 21

<210> 2328
<211> 18
<212> DNA
<213> Homo sapiens

<400> 2328
aaaaaaaaa aaaaaaaaa 18

<210> 2329
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2329
ggataagtca actaccatgg tt 22

<210> 2330
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2330
aatggaatta ctcagctgtg g 21

<210> 2331
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2331
ggcagaaact gatagagact g 21

<210> 2332
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2332
accatgttct gactacctct t 21

<210> 2333
<211> 23

<212> DNA

<213> Homo sapiens

<400> 2333

agtcctgaat caatgtctaa cac 23

<210> 2334

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2334

tggtccctgt gcttgatat 20

<210> 2335

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2335

tggttttct ttctcggta 20

<210> 2336

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2336

ccaaggctgc tttaattcca 20

<210> 2337

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2337

caaaactatcg ctgaggacct 20

<210> 2338

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2338

gtctgctgcc attgagttat 20

<210> 2339

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2339

gctcacccctc tcttctctct 20

<210> 2340

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2340

acctgtttct cccagttaca 20

<210> 2341

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2341

gcccataaaa gagaaaccag 20

<210> 2342

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2342

ctccatcagt gcagaagtcc 20

<210> 2343

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2343

acagtcagca gccctaaaat 20

<210> 2344

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2344

gcctccttca cataatgcag 20

<210> 2345

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2345

ttgtcaacag agagtcagct 20

<210> 2346

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2346

ctgaaatggt ctgggagtct 20

<210> 2347

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2347
tcaaagacag agtgagtgga 20

<210> 2348
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2348
tttgggggtt acacttcata g 21

<210> 2349
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2349
agccagcaga ataataccag g 21

<210> 2350
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2350
acctcatctt ttgtcagcct 20

<210> 2351
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2351
acagttccat aggcagggtt 20

<210> 2352
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2352
gcagttccag atccaatatg c 21

<210> 2353
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2353
tttgggaaag atgggagagc 20

<210> 2354
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2354

ttgcaggtaa ggtacagaag a 21

<210> 2355

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2355

cttcagctgc atcttgagc 19

<210> 2356

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2356

ggcacttcaa aaacaaaccc 20

<210> 2357

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2357

agggttttat ggtctcctgg 20

<210> 2358

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2358

tcaacacgga gaactgaaaa c 21

<210> 2359

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2359

tccgtgtaaa tgaacaaagc ac 22

<210> 2360

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2360

ttcagggaat ggttgcatt 20

<210> 2361

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2361

gagatgccat tccaaaagg 20

<210> 2362

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2362

ccctaccata gtgccagatg 20

<210> 2363

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2363

cagctttcag tgacagagga 20

<210> 2364

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2364

ccaaaggcag atgagtgtt 20

<210> 2365

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2365

gcctgggata gaaatgggaa 20

<210> 2366

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2366

ggaaaggaaa ggaagctgtg 20

<210> 2367

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2367

tcagagaggt ctgctgaag 20

<210> 2368

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2368

tctctctgtt gcttgttcc t 21

<210> 2369

<211> 20
<212> DNA
<213> Homo sapiens

<400> 2369
cgcatgtggt agatcatcag 20

<210> 2370
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2370
tataacaccc tcacctcca 20

<210> 2371
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2371
cacccaaatc acctgctat g 21

<210> 2372
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2372
caactaccgt ggattccgtt 20

<210> 2373
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2373
tctatcatga gtcgctcca 20

<210> 2374
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2374
tttctgtcac ttctgggct 20

<210> 2375
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2375
cgtgtgttc tagtcattg t 21

<210> 2376
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2376

gggctcagag ggaatatcag 20

<210> 2377

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2377

ccgacgaatg gatgaaagac 20

<210> 2378

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2378

acccaaattc catgcctact 20

<210> 2379

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2379

tgtacagcag tctccagaaa 20

<210> 2380

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2380

gccctcttac cctttctcat 20

<210> 2381

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2381

cattcaaaga tcagaccag g 21

<210> 2382

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2382

atctgtgatt gctgccctc 19

<210> 2383

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2383

ctagaaactc ccaggacaga 20

<210> 2384

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2384

catgtgtgga aaggattggt 20

<210> 2385

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2385

tatgaatgaa ccgtggctca 20

<210> 2386

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2386

aagttgagtc gttgtccca 20

<210> 2387

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2387

tagtgttca ggagcgtgtt 20

<210> 2388

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2388

ccaggacaag cagacatttt 20

<210> 2389

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2389

gctgctggtg attttgaag a 21

<210> 2390

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2390

ctctgggcaa acaagaaacc 20

<210> 2391

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2391

gtgtgtgttt gtggaagtgt 20

<210> 2392

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2392

aaagcccaat ctctctggtt a 21

<210> 2393

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2393

taggcgggct tattgtgttt 20

<210> 2394

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2394

tcaatgtaaa ctgccgggag 20

<210> 2395

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2395

atgggagtcg aatggtgtaa a 21

<210> 2396

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2396

taacattga gggcatggga 20

<210> 2397

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2397

cagaataccc tcactgtgct 20

<210> 2398

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2398

ggagataaca gcagaggtcc 20

<210> 2399

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2399

tgtgggtgat atctgtgtct 20

<210> 2400

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2400

gccatcctgt aactgaatgc 20

<210> 2401

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2401

gtattttccc ttgccgcag 20

<210> 2402

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2402

attacagcaa agaacgtggc 20

<210> 2403

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2403

tctgtgtgtt ttgcattggc 20

<210> 2404

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2404

gtgacagttt tccaaggcat 20

<210> 2405

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2405

gcattacttt ttcgcacact 20

<210> 2406

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2406

ggggattgtt ttaagcaggc 20

<210> 2407

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2407

ccattgttct caccaactct 20

<210> 2408

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2408

cctgaaacac aagcagcag 19

<210> 2409

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2409

agctgcctat ttgattgggtg 20

<210> 2410

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2410

cagtacagtc agccttcctt 20

<210> 2411

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2411

tgattcaaa ctacccaag 20

<210> 2412

<211> 20
<212> DNA
<213> Homo sapiens

<400> 2412
ccgaaaagag gcaagcaatt 20

<210> 2413
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2413
gtcacctcaa cctaactcca 20

<210> 2414
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2414
gcaacagtct acccgtctag 20

<210> 2415
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2415
atcaatgctc tgacctctg 20

<210> 2416
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2416
atacatcagg cctccagaat t 21

<210> 2417
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2417
cacatcttta gagctcaggt ga 22

<210> 2418
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2418
ccatcacttc acaatccaca c 21

<210> 2419
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2419

aatcctgcag tcattctccc 20

<210> 2420

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2420

caagtctggt ttgtgagaag c 21

<210> 2421

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2421

gggagcttct gtagtctttg a 21

<210> 2422

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2422

taaggagagc aggacttaca g 21

<210> 2423

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2423

ccaacggttc attgtcgtg t 21

<210> 2424

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2424

ccttgctctg ttaatgggtt t 21

<210> 2425

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2425

aacaatgctt aacgggaatc c 21

<210> 2426

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2426

gcagagttca tagaagggtc a 21

<210> 2427

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2427

aaaccgagac gaccacctaa t 21

<210> 2428

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2428

gagtgatgat gagccatgat g 21

<210> 2429

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2429

ggatattgga gatagcaggc a 21

<210> 2430

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2430

gtttggcact gcaactagat a 21

<210> 2431

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2431

tgaaataagg gaagccacac a 21

<210> 2432

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2432

tccttagtgt gccaatagc c 21

<210> 2433

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2433

ttaatgtgga gagacaggcc 20

<210> 2434

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2434

caatgcatct tactcacct t 21

<210> 2435

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2435

agtatggaag tgggaattgg a 21

<210> 2436

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2436

ttgcttcac agaaactct c 21

<210> 2437

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2437

aaccgaccta ttcaaagtc t 21

<210> 2438

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2438

tgtgaagcga atacagctca a 21

<210> 2439

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2439

gttctaacta caccaggctc t 21

<210> 2440

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2440

gtatgagtgt aggtgtggag g 21

<210> 2441

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2441

aatctggatc tagcgaagga c 21

<210> 2442

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2442

taatgagaag gcaggatgag g 21

<210> 2443

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2443

aagacaactc tctaggcctc a 21

<210> 2444

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2444

gtttatgggt gtccctggag a 21

<210> 2445

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2445

tccaccttct gatcacacaa t 21

<210> 2446

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2446

aagatcaggt accaaggcat t 21

<210> 2447

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2447

atgatgtgaa gtccatgggt a 21

<210> 2448

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2448

tccaaattga cttccatgag c 21

<210> 2449

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2449

gtggtttcag gaattggag g 21

<210> 2450

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2450

tatttgctgc ttcattcttc cc 22

<210> 2451

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2451

aagtcattac gtccacact g 21

<210> 2452

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2452

aaagtcatca gaagggtagc a 21

<210> 2453

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2453

aatgatgccg aacagtgagt a 21

<210> 2454

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2454

aatgtaagac agggacagag a 21

<210> 2455

<211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2455
 tgaattccac agtccagtca a 21

<210> 2456
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2456
 aatgccttca aagacagtga c 21

<210> 2457
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2457
 cacacctgca attgagatga a 21

<210> 2458
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2458
 gtcacgatga tgcaacagct a 21

<210> 2459
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2459
 ttccacggta agaggagcaa a 21

<210> 2460
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2460
 ttctctctag gcaggtgaac t 21

<210> 2461
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 2461
 accctttgaa agaaccagga a 21

<210> 2462
 <211> 21

<212> DNA

<213> Homo sapiens

<400> 2462

aatgagccac tgttctctag g 21

<210> 2463

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2463

atttcacat tagggcctca a 21

<210> 2464

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2464

gaacttcct gcttcctct 20

<210> 2465

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2465

aaatactgg ctgtgacat g 21

<210> 2466

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2466

aagacccttg agaactcca a 21

<210> 2467

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2467

atgtgtaaag acgtcctgga a 21

<210> 2468

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2468

tctatgtgga gggatttgac a 21

<210> 2469

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2469

ttcctgaagt ttatggtgca ac 22

<210> 2470

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2470

aaggttgaat gaggatcaag c 21

<210> 2471

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2471

gaggaagaa cacaacacat g 21

<210> 2472

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2472

cagactagcc tacaatcctc c 21

<210> 2473

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2473

cattcaggtt cttaagggt g 21

<210> 2474

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2474

gaaaggcaga cgatgaaaga g 21

<210> 2475

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2475

atctccatca gcacaggaat t 21

<210> 2476

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2476

gcagtgtgac atctgtgaat g 21

<210> 2477

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2477

agactttcct gttcctcttc a 21

<210> 2478

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2478

tttacaatga actagccagg c 21

<210> 2479

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2479

taacatctgc ctgaaagctt c 21

<210> 2480

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2480

ctcgtgtgtg caatttgga t 21

<210> 2481

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2481

ggagagatgg agaagacctt t 21

<210> 2482

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2482

aatgtattac tgtgctccg t 21

<210> 2483

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2483

accacctgcc actgtataaa t 21

<210> 2484

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2484

aattcttctt ctggtgcaag g 21

<210> 2485

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2485

ttgccctttg aactgtgat c 21

<210> 2486

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2486

aagcacacta aggcctgata a 21

<210> 2487

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2487

tcagtatcca ttcagcatcc a 21

<210> 2488

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2488

taaccgaagc ccatactctg 20

<210> 2489

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2489

tccttactcc agataccga t 21

<210> 2490

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2490

tctggcttct ttcttgaga g 21

<210> 2491

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2491

gcaacattca ttcatcctg c 21

<210> 2492

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2492

catcacgaca tccattcca c 21

<210> 2493

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2493

gtggttatta tcggtgggtg a 21

<210> 2494

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2494

ctgccattcc ttgttccaa 20

<210> 2495

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2495

atttgactt gaagcagcct 20

<210> 2496

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2496

ctgtattctt tgtccaccac c 21

<210> 2497

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2497

gacaggacac cttggattga t 21

<210> 2498

<211> 20
<212> DNA
<213> Homo sapiens

<400> 2498
gagtaattcc cccgatgcag 20

<210> 2499
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2499
tgagaatcat tgagccaaac c 21

<210> 2500
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2500
aattgtgagc gttagagtc 20

<210> 2501
<211> 21
<212> DNA
<213> Homo sapiens

<400> 2501
ccagtgggtc ttaacattga g 21

<210> 2502
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2502
aaaaggctag tagagggtgc 20

<210> 2503
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2503
tcgctgaaga actgagacac 20

<210> 2504
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2504
gggaagtgat tggagagagg 20

<210> 2505
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2505

ccgcttgga tagagtgcg 20

<210> 2506

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2506

ttgaggtgt caggaaagct 20

<210> 2507

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2507

tctgggaaa gggtcattct 20

<210> 2508

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2508

tctctccat gcactccac 19

<210> 2509

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2509

gatctgaccc tctgctcac 19

<210> 2510

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2510

cctgaaagat gcatggttg 20

<210> 2511

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2511

gccacagaac aaccagattc 20

<210> 2512

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2512

tggggttaag agctcaagag 20

<210> 2513

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2513

agtggtgatg actctgcaa 20

<210> 2514

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2514

gccccattat cctccttgt 20

<210> 2515

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2515

caaatcagac ccactaagca c 21

<210> 2516

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2516

tgtttggac tgctcactc 20

<210> 2517

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2517

attatcatgc tcactcctcc a 21

<210> 2518

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2518

gacatagcac gggagagta 19

<210> 2519

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2519

gctagtggcg ttttaggaaa 20

<210> 2520

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2520

tcgcttggaa gtcatagcc 19

<210> 2521

<211> 23

<212> DNA

<213> Homo sapiens

<400> 2521

cagagctgct ttgaagataa tcc 23

<210> 2522

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2522

gaagcctgat agatgtgcct 20

<210> 2523

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2523

tacctctgcc tccaattgtc 20

<210> 2524

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2524

cccatgtaga caaagtgtt 20

<210> 2525

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2525

ggcaggtttg tcttacagtt 20

<210> 2526

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2526

tgtgagattg cattccccctt 20

<210> 2527

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2527

cggtcagag aaagatcagg 20

<210> 2528

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2528

aaacatttgt aaccactccc tg 22

<210> 2529

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2529

cctgtaatat gggactcctg g 21

<210> 2530

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2530

ccaaaccaca cacacaaact 20

<210> 2531

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2531

aggagaagga catttcacag g 21

<210> 2532

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2532

aggccgataa gacaagggtc 20

<210> 2533

<211> 19

<212> DNA

<213> Homo sapiens

<400> 2533

gtttcccata gagccctgg 19

<210> 2534

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2534

ctccactctc tccaaccaac 20

<210> 2535

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2535

aaactgtgaa aggacgagga 20

<210> 2536

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2536

tcccttgctt ttgtaccagg 20

<210> 2537

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2537

catgtgtgta ctgtgcctca 20

<210> 2538

<211> 21

<212> DNA

<213> Homo sapiens

<400> 2538

tcttcactg tcactatggg g 21

<210> 2539

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2539

aaatgcagct tccaacatc 20

<210> 2540

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2540

gagacttct ggaggacgaa 20

<210> 2541

<211> 22
<212> DNA
<213> Homo sapiens

<400> 2541
gaaacgtaat ttagtgactg gc 22

<210> 2542
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2542
atgtgtctat tgctacctgt ga 22

<210> 2543
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2543
ctccttcatt ttgctggtgg 20

<210> 2544
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2544
ggtgatcatt tgtctgcaca 20

<210> 2545
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2545
tgaagggatg aaggcagaag 20

<210> 2546
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2546
attgtgttgt ccttccgttt 20

<210> 2547
<211> 20
<212> DNA
<213> Homo sapiens

<400> 2547
ctgaagcatc actggcattg 20

<210> 2548
<211> 20

<212> DNA

<213> Homo sapiens

<400> 2548

aagctttag tctggtagc 20

<210> 2549

<211> 22

<212> DNA

<213> Homo sapiens

<400> 2549

tccctctgta ctatgtagca tg 22

<210> 2550

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2550

ttcatttccc ttgttgccc 20

REFERENCES CITED IN THE DESCRIPTION

Cited references

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- [US7868017B \[0004\]](#)
- [US8008018B \[0004\]](#)
- [US8195415B \[0004\]](#)
- [US8296076B \[0004\]](#)
- [US8682594B \[0004\]](#)
- [US20110201507A \[0004\]](#)
- [US20120270739A \[0004\]](#)
- [WO2016189368A \[0004\] \[0024\]](#)
- [US20160340733A \[0004\] \[0024\]](#)

Non-patent literature cited in the description

- CHIU, R. W. et al.Proc. Natl. Acad. Sci. USA, 2008, vol. 105, 20458-20463 [0003]
- FAN, H.C. et al.Proc. Natl. Acad. Sci. USA, 2008, vol. 105, 16266-162710 [0003]
- PALOMAKI, G.E. et al.Genet. Med., 2011, vol. 13, 913-920 [0003]
- EHRICH, M. et al.Am. J. Obstet. Gynecol., 2011, vol. 204, 205e1-11 [0003]
- CHEN, E.Z. et al.PLoS One, 2011, vol. 6, e21791- [0003]
- SEHNERT, A.J. et al.Clin. Chem., 2011, vol. 57, 1042-1049 [0003]
- PALOMAKI, G.E. et al.Genet. Med., 2012, vol. 14, 296-305 [0003]
- BIANCHI, D.W. et al.Obstet. Gynecol., 2012, vol. 119, 890-901 [0003]
- ZIMMERMAN, B et al.Prenat. Diag, 2012, vol. 32, 1233-1241 [0003]
- NICOLAIDES, K.H. et al.Prenat. Diagn, 2013, vol. 33, 575-579 [0003]
- SPARKS, A.B. et al.Prenat. Diagn., 2012, vol. 32, 3-9 [0003]
- KOUMBARIS, G. et al.Clinical chemistry, 2016, vol. 62, 6848-855 [0004] [0024] [0091] [0092] [0093] [0097] [0098] [0098]
- MEYER, MKIRCHNER, MCold Spring Harb. Protoc., 2010, vol. 2010, 6 [0024]
- LIAO, G.J. et al.PLoS One, 2012, vol. 7, e38154- [0024]
- MARICIC, T. et al.PLoS One, 2010, vol. 5, e14004- [0024]
- TEWHEY, R. et al.Genome Biol., 2009, vol. 10, R116- [0024]
- TSANGARAS, K. et al.PLoS One, 2014, vol. 9, e109101- [0024]
- EICHLER, E.E.Trends Genet., 2001, vol. 17, 661-669 [0034]
- TODD, J et al.Nature Reviews Genet., 2012, vol. 13, 36-46 [0035]
- JIANG et al.Proceedings of the National Academy of Sciences, 2015, vol. 112, 11E1317-E1325 [0068] [0085] [0151] [0156]
- CHAN, K.C.Clin. Chem., 2004, vol. 50, 88-92 [0068]
- FORBES, S.A. et al.Curr. Protocol Hum. Genetic, 2016, vol. 91, 10.11.1-10.11.37 [0072]
- FORBES, S.A. et al.Nucl. Acids Res, 2017, vol. 45, D777-D783 [0072]
- PRIOR et al.Cancer Res., 2012, vol. 72, 2457-2467 [0072]
- SHAR, N.A. et al.Mol. Canc., 2016, vol. 15, 76- [0072]
- MARTIN, M. et al.EMB.netJournal, 2011, vol. 17.1, [0101]
- LI, H.DURBIN, R.Bioinformatics, 2009, vol. 25, 1754-1760 [0101]
- TARASOV, ARTEM et al.Sambamba: fast processing of NGS alignment formats.Bioinformatics, 2015, vol. 31.12, 2032-2034 [0101]
- LI, H. et al.Bioinformatics, 2009, vol. 25, 2078-2079 [0102]

Patentkrav

1. Fremgangsmåde til påvisning af en eller flere tumorbiomarkører i en DNA-prøve fra et individ, der har eller er mistænkt for at have en tumor, hvilken fremgangsmåde omfatter:

- 5 (a) at forberede et sekventeringsbibliotek fra DNA-prøven;
- (b) at hybridisere sekventeringsbiblioteket til en pulje af dobbeltstrengede target-indfangningssekvenser (TACS), der binder til en eller flere tumorbiomarkørsekvenser af interesse, hvor :
 - 10 (i) hver medlemssekvens i puljen af TACS er mellem 150-260 basepar i længden, hvor hver medlemssekvens har en 5'-ende og en 3'-ende;
 - (ii) hvor fortrinsvis og valgfrit hver medlemssekvens binder til tumorbiomarkørsekvensen af interesse mindst 50 basepar væk, på både 5'-enden og 3'-enden, fra regioner der rummer kopinummervariationer (CNV'er), segmentale duplikationer eller repetitive DNA-elementer; og
 - 15 (iii) GC-indholdet i puljen af TACS er mellem 19 % og 80 %, som bestemt ved at beregne GC-indholdet for hvert medlem i puljen af TACS;
 - (iv) puljen af TACS omfatter et antal TACS-familier, der hver er rettet mod en forskellig tumorbiomarkørsekvens af interesse, hvor hver TACS-familie omfatter et antal medlemssekvenser, hvor hver medlemssekvens
 - 20 binder til den samme tumorbiomarkørsekvens af interesse, men har forskellig start- og/eller stoppositioner i forhold til et referencekoordinatsystem for tumorbiomarkørsekvensen af interesse, eventuelt hvor start- og/eller stoppositionerne for medlemssekvenserne inden for en TACS-familie i forhold til et referencekoordinatsystem for tumorbiomarkøren er forskudt med 5 til 10 basepar;
 - 25 (c) at isolere medlemmer af sekventeringsbiblioteket der binder til puljen af TACS for at opnå et beriget bibliotek;
 - (d) at amplificere og sekventere det berigede bibliotek;
 - (e) at aligne det berigede bibliotek ind efter et referencegenom for derved
 - 30 at opnå læsedybdeinformation og alleliske tællinger; og
 - (f) at udføre statistisk analyse på de berigede bibliotekssekvenser, eventuelt kun ved brug af fragmenter af et specifikt størrelsesområde, for der-

ved at påvise tumorbiomarkøren eller tumorbiomarkørerne i DNA-prøven,

hvor sekventeringen af det berigede bibliotek tilvejebringer en læsedybde for de genomiske sekvenser af interesse og læsedybder for referenceloci, og den statistiske analyse omfatter anvendelse af en algoritme, der sekventielt tester læsedybden af loci fra de genomiske sekvenser af interesse mod læsedybden af referenceloci, hvilken algoritme omfatter trin til:

5

(a) at fjerne utilstrækkeligt sekventerede loci,

10

(b) at afhjælpe bias af GC-indhold, og

(c) at bestemme genetisk status;

og/eller

hvor sekventeringen af det berigede bibliotek tilvejebringer antallet og størrelsen af sekventerede fragmenter for TACS-specifikke koordinater,

15

og den statistiske analyse omfatter anvendelse af en algoritme, der sekventielt tester fragmentstørrelsesforholdet for den genomiske sekvens af interesse mod fragmentstørrelsesforholdet af referenceloci, hvilken algoritme omfatter trin af :

(a) at fjerne outliers i fragmentstørrelse,

20

(b) at beregne fragmentstørrelsesforholdet, og

(c) at bestemme genetisk status.

2. Fremgangsmåden ifølge krav 1, hvor bias af GC-indhold afhjælpes ved at gruppere loci med matchende GC-indhold.

25

3. Fremgangsmåde ifølge krav 1 til 2, hvor puljen af TACS omfatter mindst 5 forskellige TACS-familier, eventuelt hvor hver TACS-familie omfatter mindst 3 medlemssekvenser.

30

4. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 3, hvor medlemmer af sekventeringsbiblioteket der binder til puljen af TACS, er delvist komplementære til TACS'ene.

5. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 4, hvor puljen af TACS er fikseret til en fast bærer, eventuelt hvor TACS'ene er biotinyleret og er bundet til streptavidin-belagte magnetiske perler.

5 6. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 5, hvor DNA-prøven omfatter cellefrit tumor-DNA (cftDNA).

7. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 6, hvor DNA-prøven er udvalgt fra en gruppe, der består af: en plasmaprøve, en urinprøve,
10 en sputumprøve, en cerebrospinalvæskeprøve, en ascitesprøve og en pleural effusionsprøve fra et individ med eller mistænkt for at have en tumor.

8. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 7, hvor DNA-prøven er fra en vævsprøve fra et individ, der har eller er mistænkt for at have
15 en tumor .

9. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 8, hvor den statistiske analyse omfatter en segmenteringsalgoritme .

20 10. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 9, hvor den statistiske analyse omfatter et scorebaseret klassifikationssystem .

11. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 10, hvor puljen af TACS binder til et antal tumorbiomarkørsekvenser af interesse, der er udvalgt
25 fra en gruppe som omfatter: AKT1, ALK, APC, AR, ARAF, ATM, BAP1, BARD1, BMPR1A, BRAF, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A (p14ARF), CDKN2A (p16INK4a), CHEK2, CTNNB1, DDB2, DDR2, DICER1, EGFR, EPCAM, ERBB2, ERBB3, ERBB4, ERCC1, ERCC2, ERCC3, ERCC4, ERCC5, ESR1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI,
30 FANCL, FANCM, FBXW7, FGFR1, FGFR2, FLT3, FOXA1, FOXL2, GATA3, GNA11, GNAQ, GNAS, GREM1, HOXB13, IDH1, IDH2, JAK2, KEAP1, KIT, KRAS, MAP2K1, MAP3K1, MEN1, MET, MLH1, MPL, MRE11A, MSH2, MSH6, MTOR, MUTYH, MYC, MYCN, NBN, NPM1, NRAS, NTRK1, PALB2, PDGFRA,

PIK3CA, PIK3CB, PMS2, POLD1, POLE, POLH, PTEN, RAD50, RAD51C, RAD51D, RAF1, RB1, RET, ROS1, RUNX1, SDHA, SDHAF2, SDHB, SDHC, SDHD, SLX4, SMAD4, SMARCA4, SPOP, STAT, STK11, TMPRSS2, TP53, VHL, XPA, XPC, EGFR_6240, KRAS_521, EGFR_6225, NRAS_578, NRAS_580, PIK3CA_763, EGFR_13553, EGFR_18430, BRAF_476, KIT_1314, NRAS_584, EGFR_12378 og kombinationer deraf.

12. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 11 der yderligere omfatter at stille en diagnose for individet baseret på påvisning af mindst én tumorbiomarkørsekvens.

13. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 12 der yderligere omfatter at udvælge et terapeutisk behandlingsregime for individet baseret på påvisning af mindst én tumorbiomarkørsekvens.

14. Fremgangsmåde ifølge et hvilket som helst af kravene 1 til 13 der yderligere omfatter overvågning af behandlingseffektiviteten af et terapeutisk behandlingsregime for individet baseret på påvisning af mindst én tumorbiomarkørsekvens.

DRAWINGS

Fig. 1

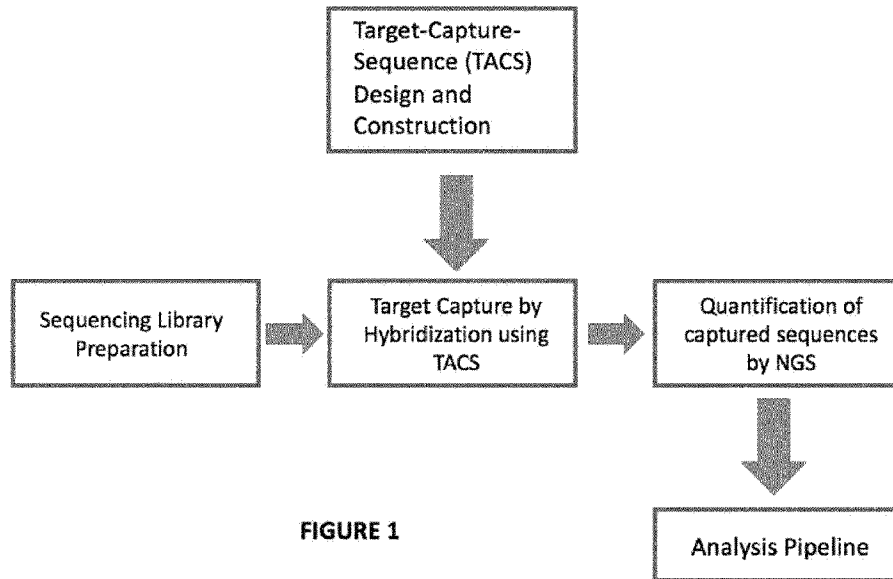


FIG 2

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	91049752	91050001	TCT TCT CGT TCA AGA TGC CG	AAG GGT GGA AGC ACA TTG AC	1, 2
chr13	92177139	92177388	AAA TTA CAT GCA AGG CTA CCA C	ATA GAG GAA CAA GCT GCA CA	3, 4
chr13	93071049	93071298	ACA GGA AGA AAG GGG AGT TAC	CTC GTC CCT TGC ACA TCT TA	5, 6
chr13	94326973	94327222	TTG AGG TTG TGT GAT GTG TC	AGG TGG GGA AGA ACA AAA CA	7, 8
chr13	94415507	94415756	TAA GCA GAG GTT TTG TTG CC	GAG AGT AGG TGC AGG GAA AC	9, 10
chr13	95600034	95600283	GTG AAG TAT TTG CTG CCA CC	ATC CCG CAT TCT TAA CCA CA	11, 12
chr13	112910529	112910778	ATG GTC ATC TCA ACA GCA CA	GAC TAA GCA AAA GCA TCT CCC	13, 14
chr13	53328405	53328654	TCC ACT GAC GTT GAG ATT CG	TTC TTA CAG GCT CAG GGT AT	15, 16
chr13	20533985	20534234	CGA ACC TCC TTG ACC TCT TA	CCC ATA GCT TAA CCC CTA CAA	17, 18
chr13	20535728	20535977	GTT ATG TTG ATA GGG GAA GGT T	TCT TCA TCT TAC TGT CTA GCA C	19, 20
chr13	20544227	20544476	AAG CCC TCT ACT CCA TCT GT	TCA TAC CCT ATC CCT GTG ATC	21, 22
chr13	20567359	20567607	TCA GAA CTC GTC AGT GGA AG	TCT TGC CCT TCA TTT GTT TCC	23, 24
chr13	20577159	20577407	GAA GGG CCA GAC AGC TTA T	GCC TTT TAT CCA TAT GCC ACC	25, 26
chr13	20598772	20599021	ATT TGC TTT GTT TTT GTG CCT	GCC CTC AAC TTT GCT TTT CA	27, 28
chr13	20600556	20600804	GAT CAT TGC TTT GTT TGG ACC	AAA AAC CTG CAC TGT GTT CG	29, 30
chr13	20610779	20611027	AGG AGA GGA AAA ATC TTG ACC	TTT TTA CAG CAA TCT TCA CTG C	31, 32

FIGURE 2 (Page 1 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	20621336	20621585	CTG CCT GCA GCC ATT ATT GT	TAA GCC GGA ATG ATT TGT AAG G	33, 34
chr13	20624392	20624641	CCT TGG GGT ATG TTT GTT ATG T	TAC CCT TTG GCT TAA CAG CT	35, 36
chr13	20625461	20625710	ACT TTT TCT GTA TCA GTC ACG G	AGT TGT CAT GTT GGG CTC AT	37, 38
chr13	20632609	20632857	CTG CTT TTG TGT GTT CCC TT	TGT CCT AAG TTA CCT GTC TGA C	39, 40
chr13	20635196	20635444	CCA GTT CCT GTT TTT CTG CC	GGC CTG GAA AGT ACT GTA ACA	41, 42
chr13	21127405	21127653	GCC TTC ACT GAT CCT ACT TTC	TGT TAC AGC CAG GCT TTC AT	43, 44
chr13	21163998	21164247	GGA TAT GGG GTA GGT TTT TGT	CAA CGA ACA CAG GGT TTA CA	45, 46
chr13	21170950	21171199	ACT CAT AGA ACT GGG GCT TT	CCA GGA CTC TCT CTT TTC TTC	47, 48
chr13	21172515	21172764	CTT TGT AGG TCC TCC AGA GA	GAC ACA TAA GAC CAC TTT AGG C	49, 50
chr13	21173774	21174022	CCT GTT TTC AGT GGG TTG AA	GAT ATG TTC TGG AGG ACT GCT	51, 52
chr13	21182580	21182828	CCA CGT TGT ACC TTT CCA TG	TGA TTC TCA CAG GCT CCT TG	53, 54
chr13	21203385	21203634	GAG ATT CAA AAC AGT GGT GGC	TGA TGG AAG TTT CTA GGT CAG T	55, 56
chr13	21217173	21217422	ACA ACA CTG TCC TTG GGT T	AAC ACT CTT GCT CCC TAT GT	57, 58
chr13	21228403	21228652	TAA ATG TCC TGT GTG CTC GG	TTT CTC TCC CAG CTT GAT CTT	59, 60
chr13	21237418	21237666	GAC AGG ACA CAT GGA GAG AG	CTG TGC AGA GAC GAA CTA AG	61, 62
chr13	21239719	21239968	AAC TGA TGG TGA TTT GCA TGT	CTC TCG GAG CAA AGA CCT T	63, 64

FIGURE 2 (Page 2 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	21245232	21245481	GGC TTC TGG AAA CAT CTT GC	ACC TCA TAA GTA CGC CCA TC	65, 66
chr13	21251423	21251672	CAA TAG AAG TAG GGG GTG AGG	TGA TCT TCC TTT GCT CCT GT	67, 68
chr13	21276601	21276850	AGC TGG GAT GGG TTG TTT AT	ATG ACG ACG ATG TTG GAG AG	69, 70
chr13	21296989	21297237	GCC AGT TGT CAG AAG AAT CC	TCC TTC AGC AAG CCT CTT TT	71, 72
chr13	21321012	21321261	CAA CTG CAT TCC AAA ACA GC	TGA GGG TGA TAA CCT GTG AG	73, 74
chr13	21330138	21330386	GAA GGG AAA CAG TCA GAA AGA	GGC TTG AAG TTT GTC TGT GA	75, 76
chr13	21348854	21349102	TCA AGC GCC GTA AGT ATG TA	GGA TTT TCA CAT TGC TCA GC	77, 78
chr13	21351692	21351941	TAA CCA TAA CAT CCA GGG CA	TAG CAT GAG AGT GAA CTG AGG	79, 80
chr13	21356527	21356775	TTG TAA GCT GGC ACA CTG AA	CAG CCA CAT AGC CCA TAT CT	81, 82
chr13	21361621	21361869	TTA AGA AAG TGC CGT GTT GC	TGC CCA TGA GTC TAC TTG TG	83, 84
chr13	21396343	21396591	ATG GGT CCA TGA AGA GAA GC	AAG TGG ACT GAG GGA CAA TT	85, 86
chr13	21399744	21399992	AGT TGT TTC CAG TAC TGC CA	TCA GAC TGA GCA TTA AAT CAC C	87, 88
chr13	21417352	21417601	GTA TGC TTT CAA GTG ACG CC	TAG GTC TGG AAG AAT GCC AG	89, 90
chr13	21422981	21423229	GAA GAC AAT GCA ATG AGG TGT	AGT ATC TTG GGC TTG TGA CA	91, 92
chr13	21607075	21607324	ACA CCC AAT GAG AAC AGG AA	GCT CCA CTT CCA CTC TTT CT	93, 94
chr13	21631007	21631256	TGA TGG AGG AAG TGT GAA GC	TTG GAA TAG TGA GCC TCC CT	95, 96

FIGURE 2 (Page 3 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	22114658	22114907	TGG CTT TTC TGT AGT TTG GG	TCT GGG GCT CTT TGT CTT TG	97, 98
chr13	22130956	22131205	AGC AGC AAG AGT TGA GAA GA	ATT TTT CCT CCC CTG TAG CT	99, 100
chr13	22189915	22190164	GGC TTT GAA AAA TCA CCA TGG	CTG GGC ACA CTG TAT TAC CA	101, 102
chr13	22270443	22270692	AGA GGT TTC CAT CGT TGC TA	CAC CAC GTT TCT AAT GCA GA	103, 104
chr13	22396225	22396474	AAC AGC CCC AAA CTT CCT AC	GAG TTG AAA AAG GTC CAC GC	105, 106
chr13	22609278	22609527	ATC ACT GCC AAC AAG CCA TT	CAG AGG AAA GAC ACA GTG CT	107, 108
chr13	22691882	22692131	TGA GTT GTG GGG GAT AAA GG	TCT TGG TTT TGA GGC TGT CA	109, 110
chr13	22765144	22765393	TCT GGG CAC TTT CCT TAT GA	ATC AGC CTA ATT CTC CCC AC	111, 112
chr13	27175379	27175628	GCA GTT TTG AGG GGA GAA GA	ATC CCC CAT CAT CCA TAC TC	113, 114
chr13	27405837	27406086	TTC ATG ATG CCA CCT CCT C	CAT AGC TAG GCC TGT GAG TG	115, 116
chr13	27646720	27646969	GCC CAA ATA CCC CTT CAG TA	TCA GCT TGC TCC TTC TCT G	117, 118
chr13	27674747	27674996	GCA CCT CAA TCC CGT ACA AT	CTA GGT CCT CAG CAG TGT TT	119, 120
chr13	27969360	27969609	GGC TTT TAA GCA GCT GTG TA	TCC CAG AGT TAA CAA TAC CCC	121, 122
chr13	27978231	27978480	TCT CCA GAT CGA AAC AGC AT	GCA TTT GCA CTG CCG ATT TC	123, 124
chr13	28003481	28003730	TCA TTC AAA GCC AAG ATG CC	ACT AGT CCC AAA AGC CTA CAC	125, 126
chr13	28073180	28073429	ACA CGC TAC ATA GAC ACT GG	AAC AGC AGC GTC AGA ATA AC	127, 128

FIGURE 2 (Page 4 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	28077809	28078058	CAA TCG AGG TCA CAT TCA CC	AGG TCT TTA CGG GAA GGA AA	129, 130
chr13	28212786	28213035	TGA CAC GCT GAA GAA AAT AGC	TGA GGG AGA AGT TTG GTA GG	131, 132
chr13	28302961	28303210	GGA GGG AAT GGC AGA AGT AA	CCC TGT CTA AAG AGC CAT GT	133, 134
chr13	28325874	28326123	GGA TTT TCA GAG CAG AGG TTG	GTT TGG AGT TTC GAT GCC TT	135, 136
chr13	28395893	28396142	AAG AGT TGC CTG TAC CCT TC	ATG TTT TGG TCC TGG GAG AA	137, 138
chr13	28549591	28549840	GTC TCT TTA CTG GGA GCG T	GGA AGT GGT TAG GGC AGA TT	139, 140
chr13	28592602	28592851	ACA TTG CCC CTG ACA ACA TA	AGC CCA GTA AAG ATA AGA GGC	141, 142
chr13	28608293	28608542	TCA TTA TCT GAG GAG CCG G	CCC TTC CCT TTC ATC CAA GA	143, 144
chr13	28617043	28617292	GGC TCC ATA ATC TTC TGC AAT	CTG AAA CCT TCT CCT TAG CC	145, 146
chr13	28622471	28622720	CGT ACA TCT GAT TTG TGG GT	ATT ATC CAA CCT GAC CTG CA	147, 148
chr13	28623594	28623843	TGC CAC TGA TGA TAC AAA AGC	AGG TGC AAA GCT GTT CAT G	149, 150
chr13	28941450	28941699	GAA ACG TGT GGT GTC CTC TA	AAT GCC AAG ATT GTC CTT CA	151, 152
chr13	28958898	28959147	AGT GTT TGG GGC TCT ATC AG	TGC GAA ACC TCA GTG ATC A	153, 154
chr13	28960375	28960624	CTT TCC CTT TTG AGT CCT GC	CAC TTC CTT CAG CAC ACT TT	155, 156
chr13	29003985	29004234	TCT CGC TTA CCT TGC TAC AT	CCG GCT CTC TAT GAA AGT GA	157, 158
chr13	29052686	29052935	AAA GCG GGA ATT GGA ACT TT	ACT TGT CTG TCT GCC TGT TT	159, 160

FIGURE 2 (Page 5 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	52293092	52293341	GGG GAA CAT TGG GAA GAG AT	CTG ATG CGC TGA AAA CCA A	161, 162
chr13	52302656	52302905	TCT ACC AGC TAC AAA CCC AT	TTC CAT GTG TTC TTC CTC CC	163, 164
chr13	53286404	53286653	TCA GCC AAT ACC CAT AGC AG	AGC AGT AGG GTT AAC AGG AG	165, 166
chr13	53306303	53306552	AAT CAG AGG AAG ATG GGT CG	GCA GCA ATG TTT CGG TGT A	167, 168
chr13	53497224	53497473	GAG AAC TCC ACC CTG TGT TT	TAC TAA TGG CTG GGG GTA AC	169, 170
chr13	53548644	53548893	GGG AGT GTG TGA ATG TGT CT	CTG ATG AGG CTA AAG GAC CA	171, 172
chr13	53652715	53652964	AAG CTT TAC ATC ATG GCA CTG	CAG AGT TCT CCA TCC CAG AC	173, 174
chr13	53861872	53862121	AAA GGT CCA TAG GCT CAC AT	CTG AGT TCC TCC TTT TGC CT	175, 176
chr13	53897429	53897678	TTG ACC AAT GCC ATT AAG CC	GCA AAA GGT GGT GTT AGC TG	177, 178
chr13	53938205	53938454	ACC AGG GAA ATG TTA GCT TCT	ATC CAC ATC CCA TGC CTA AG	179, 180
chr13	54626806	54627055	TGC TCT GTT ATG GTT GGA GTT	TCT ATT CCT TTG GCA CCT CC	181, 182
chr13	54740174	54740423	GAA GCG GCA GTA ATT CAG GA	AGG AAA GGA GAG CTT TGT CC	183, 184
chr13	54753834	54754083	AAC TGT GTC CTA AGC AGT GA	CCT TTC AGC TTC CAA GTC CT	185, 186
chr13	54768238	54768487	GTC ACC TCC AGA GCT TTC AT	GCT CTC TTC CTC CCA CTA AAA	187, 188
chr13	54773333	54773582	GAA CAA TCC AAC CTG AGA ACT	ACT GCC TGT GTT TTC TTC CT	189, 190
chr13	54910969	54911218	TGA TTG TCC TCT ACC ATG CAT	AAA GCA ATT TCT TCC CCA GC	191, 192

FIGURE 2 (Page 6 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	54917347	54917596	AGG CTT GAA ACA CCA CCT TTA	TGT CTG TTG CCA TTC CTT CT	193, 194
chr13	54926251	54926500	TTG ATT TGT TGG GTG GTT GG	TGA CTG TGA CTT GTG CTT TC	195, 196
chr13	55009732	55009981	TGC CAA TCT GAG GTT TTT CC	GAA TTA CAT TTC CCT GGG CG	197, 198
chr13	59785342	59785591	ACT CTG CTT TAG GGC TTC TG	TGA AAC CGT CTT CCT TGT CT	199, 200
chr13	60086302	60086551	GCA GAA AAG CTC CCA AAC AA	TTT AAA GCA GAG CAG GAC CT	201, 202
chr13	60668020	60668269	GAA AAG AGG TGG AGA GGG AG	TTT ATG ACA CAC AGA GCA GC	203, 204
chr13	60707747	60707996	AGG ACC CTT TTG CTG ATT TC	ATG TGT TTG ACC CTT TCC CT	205, 206
chr13	60975949	60976198	CTG GCC CAA GTG CAT ACA TA	ATC CTG AAG TTG TTC CAC ATC	207, 208
chr13	61177164	61177413	AAC CAG AGA GAC ACC TTG AC	GAC CCT GCT TTG TTA CTA GGA	209, 210
chr13	61495655	61495904	TCC TCC CTA TCT CCT GTG AC	TGG ACA TGG ACA TTT CAA CG	211, 212
chr13	67720914	67721163	ACT CTG CCA GAA AAG CCT AC	AAA AAT GCT TCC ACT TGC CT	213, 214
chr13	67799557	67799806	CCT TTG TCT TGA AGC CTC CT	GCA CCT CCA ACA ACA TTC AA	215, 216
chr13	70101783	70102032	TTG ACT GAG CAG AGT AGA GC	TTG GAA ATG GGG CTG GAG	217, 218
chr13	71512697	71512946	TTT TAC CTA CAA GCA AAG AGA G	ACT GGT CTA TTG GGG GAA AAT	219, 220
chr13	71821654	71821903	TCA CCA ACA GAG GAT CAA ACT	AGT GTT AGG AAA GCA GAG TG	221, 222
chr13	72405844	72406093	CCG AGG GAT AAC ATA CAG CT	TGG ACA GGG TTT CAC AAG AT	223, 224

FIGURE 2 (Page 7 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	74087455	74087704	CAC TAG TCA CAG AAG CAG GT	CTC CTC TCC ATC TTT CCA GG	225, 226
chr13	74192477	74192726	GTA GAA ACC CCG AGA CAA CT	ATA GGC TGA CTT CCA CAT CTC	227, 228
chr13	74260893	74261142	CAA TTT GCT GTT CAG AGG CT	TGT GGG GGT CAA TTC TAA CG	229, 230
chr13	78218064	78218313	TCA TGA TGT GGC TTA GTG GG	CCA ACG GGT AGT GGT AGA TT	231, 232
chr13	88033439	88033688	TAC ACC CAC ATG CAT ACA CA	CTT ACC CCA CTT CTT CCT GA	233, 234
chr13	90954378	90954627	GAA GTG TGC ATG GGA GAG T	CCT GTC ACA ACT GCC TTT G	235, 236
chr13	91290109	91290358	TTT GGG TGG CTC TAT GTT AGG	TTT GCC ATT TTG TGA TGC CA	237, 238
chr13	91874767	91875016	CTC CTT GAC TCA TTT CCC GT	GGA GTT TCA GGT TGG CAG AA	239, 240
chr13	92125914	92126163	ACA GTA CCA CTG CCA AGA AA	ACA GCT TGC TTC AAA CTA CA	241, 242
chr13	92308079	92308328	CTG CTA GTC TGT CAG GAG AG	TTG AAG GGG CAA AAT ACA GC	243, 244
chr13	92971372	92971621	GGG CAG CAC TAT AAA CAT CC	GCC CCA AAT TCT AAC AAA GC	245, 246
chr13	94063232	94063481	GAC ATT CCC TTC CAT TGA GC	TGA CGA AGA CTC CAA CAC AA	247, 248
chr13	94453836	94454085	TTC CTG GTA AAT GTG CTG GT	AAG TCA GGG AAA TGA AGC TG	249, 250
chr13	94713643	94713892	GGC CAG ATT TGC AGT GAT TT	GTA ACA CAG TGC TGC TTC TC	251, 252
chr13	95766126	95766375	AGA ATC AAC AAC AAT GGC AGG	GGC CCC AAT TAG CTG ATT TC	253, 254
chr13	95814599	95814848	CTC TGA GGA AAG CTT GTA GGA	CTG AGC AGG GAA AAA TCC AG	255, 256

FIGURE 2 (Page 8 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	111956688	111956937	AGG TTT TCG TTC TGC TTC AG	ACA AAG GAT TCA GGT GCA GT	257, 258
chr13	112517966	112518215	CGG GTC AGT GAT TCT AGC T	ACA GGT TTT GCT CTT CAG GA	259, 260
chr13	112531519	112531768	GTC ACT ATG GAA TGG GGG TT	GGC AAG TTT GTC TGG TTC ATT	261, 262
chr13	112986709	112986958	GCT TCT TCC CCG CAA TAT GA	CCA TCT GCA TCT GTC TCC TT	263, 264
chr13	113000054	113000303	CGG TTC ACA GTC AAT GGC TA	GCT CCT CTC CTT CTC CCT T	265, 266
chr13	21391429	21391678	TAC CCA ACA AGC CAG AGA AAT	TGT ATA AGG GCA ATC GTG GT	267, 268
chr13	21394616	21394865	AGA GGG AAA GTG CAA GGA AT	AAG GAA CCA GGT CAG ACA AG	269, 270
chr13	21404268	21404516	GTT TTT CAG CAC ACT GTC CC	GTT AGA AGG CAA ACA TCA TGC	271, 272
chr13	21618233	21618482	ACC ACA TTA CTC ACA ACC CT	TGC AGT CAT AGG AAA AGG CT	273, 274
chr13	21619521	21619769	AAG CCC TTT TCA TCT CCA CA	GCA GTC AGAATG GTT TGG C	275, 276
chr13	21629602	21629851	CCA GAG CTG AGA CAA CTA CT	AGA CAT TGG TTT GGT TGG TTC	277, 278
chr13	21654127	21654376	GAA GCA ATT CCT CAC ACC AC	ACA CAA ATG AAA GCC CGT AC	279, 280
chr13	22215795	22216044	TTC AGT CAG AAT GAG GAG CC	GGT CTG CTG TTT CTC TTT GC	281, 282
chr13	22227261	22227510	CTC CTC TCC CCT CTG ATT TT	AGA GCC TTA CCA AGC TGA AG	283, 284
chr13	22243011	22243260	TTT TAA AGC GAC AGT CAC ACG	GGG ATG GTT ACT TAG TGG GG	285, 286
chr13	22255153	22255402	TCC TCT GCC TTC TAC CCT TT	TTA CAC TCG CCT TCC AAA CA	287, 288

FIGURE 2 (Page 9 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	22639387	22639636	TGT TGT GCC TTT TGT TGT GG	GAG AGA GGA GGA GTT GGA AG	289, 290
chr13	27183101	27183350	TTA GGA GGT AAG GCT GCA AAA A	ATC CAC GAC ATC CAA AAT CA	291, 292
chr13	27387690	27387939	CTG TCA GCA ATT TCA GGT CAG	TTG TGC AAG AAG AAA CCT GC	293, 294
chr13	30466189	30466438	AGA CAA AGG CTT CAC GGA AC	GGC CTT GCA TAA ACC ACA TT	295, 296
chr13	30977198	30977447	TTG CTC TGT TGT TTG AAG GT	TTT GTA ATT GGT CCT CGC CT	297, 298
chr13	31061235	31061484	ATC AAT GCA GGT GAG TGT GA	CAA GTA TTT CAT GGC GCT CC	299, 300
chr13	31205037	31205286	CAC TCC ACA TAA GCC TCA GA	GTC AAC AGT ATC AGC TTC CAA	301, 302
chr13	32625308	32625557	AGG ATG TAG TTG GGT GAG GA	TGG GCT TCT TTT TCA TTC CG	303, 304
chr13	34428102	34428351	CAG TCA TCA CGG GGA GAT AC	TCA ACA AGC TCT CTG TTC AC	305, 306
chr13	36054899	36055148	GAC AGA TAT TTG TGC AGG GT	GTG CAA ACA GTG ACC TCA AT	307, 308
chr13	36105686	36105935	TCC TAG CCC TTA CCT TTC CT	GCT GGG CTG CTT TAA TTT CT	309, 310
chr13	40676702	40676951	AGC CTG AAT GTC ACT GAT CA	GGA ATT GTG GGG TCA AAT GG	311, 312
chr13	40745383	40745632	ACT CAT CAC TTC TGG CTG C	CTA GTG CTT CTA CCT CCA GAC	313, 314
chr13	49281723	49281972	TCT TGT GTT TCC TGC CCT AT	AAC CAC ACA CTA ACA GGG AA	315, 316
chr13	53624527	53624776	TTG CTG TGG ATG AGA ATG GA	TCT AGT TTG CCC TCT TTC CG	317, 318
chr13	60069277	60069526	TGA GGG CAG AAA GAA ACA GA	CGA ATT GCT TCC TTG CTC TG	319, 320

FIGURE 2 (Page 10 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	60654975	60655224	GGG GTC ACA CAT CAC TTT TC	TCT ATC ACA GCA GGA AAT CAC T	321, 322
chr13	61151386	61151635	ATA GGG TCA CAA TCC ACT GC	TCT TCG TGT TTC TCT AGC GC	323, 324
chr13	62064603	62064852	ATA TTG AGC CCC GCA TGT TA	TTG AAG AGC TAA AGG GGG AG	325, 326
chr13	71479359	71479608	GGT TGC AGG AGA AAG AAC AT	TGT CAC CGT ACT ACC TAA GC	327, 328
chr13	39233534	39233783	TGC CAT GTA ATT GCC AAG AT	AGT ACG CTC CTT TGC AGA G	329, 330
chr13	39281667	39281916	CCT GTT CTC CAT CCC TCT G	TTA CGG GGA CAC AAA ATG GT	331, 332
chr13	39343524	39343773	TCA CAA ACT ACC CAA CAC CTA	CTG TGC TTT GCC CTT GAA G	333, 334
chr13	39444897	39445146	CAG AAT TAG TTG GGG AGC TGT	AAG TCA ACC CAT ATG CCA CT	335, 336
chr13	39469458	39469707	GCC ATC TCC TGA AAT AGT GC	ACA TTC AGG CTG TCA CAC AT	337, 338
chr13	39486237	39486486	GCA AGT GTT CCC ATC TAG AA	ATC ATG TCA CTA GTT TTA TAA GGC	339, 340
chr13	39541262	39541511	ATT GAT ACC CCT CTC CCC AG	AGT ACT GAG GCT CCA AAG TG	341, 342
chr13	39597307	39597556	AAG TAA GCT GTC TCC TGG C	TGG GAG GAG TTT GCT GTT TA	343, 344
chr13	39662550	39662799	AGG TTG GTT GGC ATG AAG AA	TTT TAA GCC TGT GAC TGA CA	345, 346
chr13	39681445	39681694	ACC AGA GTT TCA AGA CAA GC	TGA ACC TGA CTT TCC TTG GG	347, 348
chr13	39707053	39707302	TTT TAC ACA GCA GGC CTC TT	GGC ATT CTA TCA TCT CGG GA	349, 350
chr13	39791099	39791348	GCA ACT CCA AAT TAT CAG GGC	AGT CTC TCC CTG AAA CCC A	351, 352

FIGURE 2 (Page 11 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	39882804	39883053	CAG CAC CTT CCC TTA GCA AA	AAG AGT TGG CTT GGA GTT GA	353, 354
chr13	39887397	39887646	CTT GTT GTC TTG TAG CCC TG	CCC ACA ATT ATG AAA GCA GGT	355, 356
chr13	40023278	40023527	CAC AGA TAC AGA CGT CCA CA	TTG ACC AGG ACA AAT GAG GA	357, 358
chr13	40038277	40038526	AGC TCA GCA ATT AAA CAG TCC	CAC TTT GTT GGT CTG GGT CA	359, 360
chr13	40071926	40072175	TGT TGA GAG TGC CAG AGA TG	GGG ACT CTA GGT GGG GTT AA	361, 362
chr13	40138914	40139163	CTT CCA CCT TCT GCC AAT GA	GTT TAT GCC TTG GGA TTG CC	363, 364
chr13	40171414	40171663	TTC TGA CAT TTG CAA GCA CC	GTG TGG TAA GGA TGC TAG GA	365, 366
chr13	40405751	40406000	CTG TTG CTA GTT TCT TGG GC	GAA AGT GAC TCC TCC CTG AC	367, 368
chr13	40483291	40483540	TTT TCC AGT CCC AGC ACA T	CCA GGT TCT GTT CTC TGT CA	369, 370
chr13	40562330	40562579	TCT CTC TCT TCC TGA AAC AGC	GTG AGA CAT GGT TGC TGT TC	371, 372
chr13	40590631	40590880	AAC CTC TGC TTT CTG TAG TGA	CTT TCT CCT GCT CCA CCT AT	373, 374
chr13	40633944	40634193	GAG AGA ATG CAA GGT TCA GC	CTA TGT GTG TTC CAA CCC GA	375, 376
chr13	40644042	40644291	TAC AGC ATC AAA GAG GAA GC	GGG ACC TTC TAA CCA TGT GT	377, 378
chr13	40661582	40661831	GAG GGG ATG AGG GGA AAA AG	CGG GAT TTT GAA AAG GCA GA	379, 380
chr13	40667939	40668188	CAT GAC CTC TGA CGG ATC TG	GTG TTG TCT CTC AGC TCC TC	381, 382
chr13	40684306	40684555	AGG CAA TGA GGT CAA GGA C	GTT CTC TGG TTA AGG CCC TT	383, 384

FIGURE 2 (Page 12 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	40747946	40748195	ATG ATG GCC CCA ACT TGT TC	CCT CTT CAC CTA TAA GCC CC	385, 386
chr13	40767281	40767530	TTC TAG ACA CTG AGG GAG CA	TAG GGG ACA GTA AGC CAG AT	387, 388
chr13	41165017	41165266	AAC GCT ACA CTT TAC GAG CT	ACG ATG GAC CTC TGT TGA AC	389, 390
chr13	41176869	41177118	TCA ACA CTA CCT GCC AAT CA	ATT CCC ATC CAT CCA TCA CTC	391, 392
chr13	41573543	41573792	TGC CGA CAC AAA AGA ATG C	TGG TTT TTG GAT GGT GGT TG	393, 394
chr13	41581284	41581533	AAA GTG TTC CTC CCT GCT G	GAA GTT CCT CCA GTA GAC TCA	395, 396
chr13	41588844	41589093	AGG AGC AAA ATA GTC TGG CT	TTG TTT GAG TCT GGG AGG AA	397, 398
chr13	41628316	41628565	ACC ACT CTT GAA TCA TTG CAG	AAT ACT GTG AGA CTG CCA CC	399, 400
chr13	41633944	41634193	CCA GCC AAT TTT CTC TTT CCC	CAG TCA CGG AAA GTA CCC TC	401, 402
chr13	41827812	41828061	ACT GTC CCT ACT GCC AAT TT	ACC ATG TTT CCC TCT GTC AC	403, 404
chr13	42280338	42280587	ATC TGG TTT GAA CTT GCC AAC	TTA CCA AGG GAC AGG ATG GA	405, 406
chr13	42349979	42350228	CAC TCT GAA TAG CTC TCC CC	CCC TAG AGG TCA AGG TAT GG	407, 408
chr13	42589616	42589865	TTA TCC GGG ACA GTT TCA GG	ATA GGC CCT GTG TGT TAG TT	409, 410
chr13	42773088	42773337	GAA TCT TTT GGC CCA CAC TG	AGA AAG TCC CCT CCA TTT CT	411, 412
chr13	42811933	42812182	GTC AGA CAC ACT TAG CTG GT	GCC AAT GCC AAA GTC AGT TA	413, 414
chr13	44211957	44212206	ACA CAT TTC ACC TTC ACC CT	GAG GAC GAG TTG AAC AAA GC	415, 416

FIGURE 2 (Page 13 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	44239246	44239495	GCA CTA ATC CAG GGG CTT AA	ATA CTG GTC TCA AGG TAG CAC	417, 418
chr13	44247433	44247682	CCC CTT ACC ACC ACT TCT AC	AGC AAG TGA AGC TCA GTT AAT G	419, 420
chr13	44359516	44359765	TTC AGA TCC CTT AAG CAC GC	CCC AGA TAC ACT CCT GCT TC	421, 422
chr13	44388992	44389241	ACC TAA GGC CTC AAA TTC CA	CAA ACA TGA GAG GGG GAG AA	423, 424
chr13	44493443	44493692	CAG ACC ACG GGC ATA AGA AA	AAA CAC AGC AAT GAG GAA GG	425, 426
chr13	44557886	44558135	TGG ATG TGT GGA TTT GCA GA	GAT ACT CCC CTG TGT TGC TT	427, 428
chr13	44959162	44959411	CTG GCT GTC TTC TGG GAA A	GCT CTT ACT AGG ATG GCA GG	429, 430
chr13	45043950	45044199	CAA GCA GAA CTG AGA AGA GTC	GTT TCC AGC AGC AAT CCT TT	431, 432
chr13	45115235	45115484	AGT GGA ACG AGG ATT GTG TT	CTG TGC AGA AGG GTT AGC T	433, 434
chr13	45147386	45147635	CTC CCA TCT GAA ACT GCT GA	AAA CCC CTG CTA CCC AAA AT	435, 436
chr13	47067063	47067312	ACA TCA CAA CCA CCC TGA C	AAT GCC CAG ATG CTG TTT TC	437, 438
chr13	47120595	47120844	GTG TTG ACC TGA TTT GCC AA	GAG TGG TTG TTC TCT CCA GAT	439, 440
chr13	47154937	47155186	GAA CAA AGA GGA ACA GAG CC	CAG TCT AGA AGC TCA CCC AG	441, 442
chr13	47258834	47259083	TTC ATG ATT CCA GGG TCC TC	TCT CCT CTA GCC CTA CAC TG	443, 444
chr13	47261849	47262098	GGA CGG ATT TAG TGT ACA TTG G	GGT GTA AAT GTG GCC TCT CC	445, 446
chr13	47286641	47286890	TTT CCT TCC AAC ACC ACA GA	ACA AAG CTA CAA ACT CTG GC	447, 448

FIGURE 2 (Page 14 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	47314093	47314342	TCC TTA GGG TTC TGC GAA AT	TTT CAC TGG GAG ACT GAT GC	449, 450
chr13	47623498	47623747	GGA AAC TCC CTG CCT TCT AC	CTG TTC TGT TCC TGA GGC TA	451, 452
chr13	48562058	48562307	TCT TCC AAA CAC CAG CTC TA	TGT GTA TCC ATT GCC TCA TCT	453, 454
chr13	48698166	48698415	ACT CAA TGG AAG GAA GGG C	GAA GAG GGT GTG TGT AGG AC	455, 456
chr13	48762184	48762433	AAG GAC TTG TGC TGT ATT GC	TGG TTG CTC TTC CTA GTT CC	457, 458
chr13	48806515	48806764	GAC GGG AGC CAG TAT TCT AC	CAA TGT GGA GGA AGC TCT TG	459, 460
chr13	48811339	48811588	GGG ATT GAG AGC TTG GTT CT	TTG CAC ACC CAA TAT GCT AC	461, 462
chr13	49119202	49119451	CTC CCC ACC AAG ATG TTC AA	TCC AAG GTT TCT CTA GCG AC	463, 464
chr13	49479756	49480005	GTT TTG GGT CAT GCA GTG TT	TCG CTA TTC TCC TTG CCA TA	465, 466
chr13	49505070	49505319	GAC AAA AAC ACT TGC CAG AC	AAC AGC CTC TTT CCT TAG CA	467, 468
chr13	49530727	49530976	AAC CAT GGC TTT GCA ACT AC	TTT TTG GCT CAG TGG GAT GT	469, 470
chr13	50387096	50387317	GGA ACC CTC TGC TAT TTT GC	CTG TTC ATT CTT CTT CAG GGC	471, 472
chr13	50960526	50960775	TAC TCC TTG TGT GAA CCC CT	TTT CCG AGC CCA TAA ACT AC	473, 474
chr13	51783208	51783457	ACC TTT ACC CCA TAC CAT CC	TGC TCA GAT TTC AGC TTC CT	475, 476
chr13	51816719	51816968	CAT TCC TTT GGT TGG TGT CC	GTG AGC GAT GTG GAT GTC TA	477, 478
chr13	51825241	51825490	CTA ATG GGC CTG TTG TTC CT	AAC TGA CTC CAT GAC CTG TG	479, 480

FIGURE 2 (Page 15 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	52025153	52025402	CAA CCT ACC TGC CCA TAG TT	GAA GCT GCT ACT TGG TGA AC	481, 482
chr13	52249504	52249753	CGT AGC AAA TTA TGG CGA GG	TTT TCC TCC TGT TCT GTT GC	483, 484
chr13	29111011	29111260	GGT CAG AAG GGA AAG GGT TC	TTC TCA AAT GCA ACC ACT CC	485, 486
chr13	29192994	29193243	CCA GAT TAA AAC GTG GTG CC	CTG GCC CTT CAA TTT CAT GC	487, 488
chr13	29233772	29234021	CCC ACA ACT ATA GGT CGC AT	CCA GCA GTA CCG ATA TCA GAG	489, 490
chr13	29310139	29310388	AGT TGT TCC ATT TCT ACC AGC	CAG AAG GCA GGA GAT GGA TT	491, 492
chr13	29563140	29563389	TTG GCT GCA CTT TGA GTC A	AAG CAA CCA TTT TCC TGA GC	493, 494
chr13	29580073	29580322	CAG ATG GCC CAT TGT AAC AA	TCA CCC TTC ATC TAC CCA CT	495, 496
chr13	29929175	29929424	TAT TGA GGT TCC CGT GCT G	AAG CTG GTG ACC TTC TAC AG	497, 498
chr13	29934475	29934724	AGA ATG TGA AGT GGC TCC AT	AAA ATT CTG GTT GGG GAG GA	499, 500
chr13	29939640	29939889	TTT GGG TTT GTG TGT GTG TG	CCA TAG CTC ATC TGC TCT GT	501, 502
chr13	29957853	29958102	AGG AAT CTC TCT CTG CCA AG	GGC TGT CCC TGA ACT ACT TT	503, 504
chr13	29995732	29995981	TCT TCA AGG CAG GTC ATA GG	CTT GGC TTA AAC TCT GCT CC	505, 506
chr13	30003375	30003624	GAA ACC TAA GAC GTT CCA CTG	GAC TTG AAC ACA CCC TCA GA	507, 508
chr13	30014954	30015203	GAG TGA AGG GAT TGG AGC AA	AGG AGA AGA GAC CAT TGC AG	509, 510
chr13	30114022	30114271	ATG TCT CAG GCT AGG TGT TC	TTA GCT AAG TCT GTG CGG AG	511, 512

FIGURE 2 (Page 16 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	30145894	30146143	ACA CTC ACA AAG CCC AGT TA	GAA GCA ACA CTG TAC ACG C	513, 514
chr13	30187253	30187502	GTG CAG ACT CAT GTT ATG GC	TCT GAT AAA GGC TGG CTC AT	515, 516
chr13	30421518	30421767	AGG ATC TCA AAG CAC CAC AG	TAA AAC AGT GCC GCT ACT TC	517, 518
chr13	30531947	30532196	AAC GGG AAG AGG GAA ACT TT	AGT GCT ATG AGT CTT GGT CC	519, 520
chr13	30778718	30778967	ATG TTC AAC AGA GTC AGG CT	GGA AAA CAT GCG GTG GTC TA	521, 522
chr13	30905760	30906009	CAG TAA CAG TCC AGG GTC TT	GCA GAG AAA TGG GTT AAG GG	523, 524
chr13	31011560	31011809	AGT CTG GGA GCC TAG AAT CA	GGT AGA GGT GGG TTA TCT GT	525, 526
chr13	31089936	31090185	CAT TGT AGT TTC AGG ACA CCA A	CTG TAA ATC TCC GGG GGT G	527, 528
chr13	31227324	31227573	ACC ACA GAA TGA CTT GCA GC	GGC GAG AAT GGA GAG AGA AA	529, 530
chr13	31430437	31430686	TTT CAC GTG TAA CAG GAG CA	TCC CAA GCC AGG ATT CTT TT	531, 532
chr13	31575060	31575309	TGC TAC AGC GAA AAT GGT CT	GAA CAA CTA CAA CCG TGC AG	533, 534
chr13	31641685	31641934	TCC ACT GCT TAG TTT GCC TT	ACA AAT GCC CCA TAT CAA CC	535, 536
chr13	31718167	31718416	ACA GGT GGG GAG AAA AGG TA	GGA AAG AGG CCT GGA GTA AT	537, 538
chr13	31723797	31724044	CTG CCA CTA CTA CAC AGC TA	TTT CCA CTG GAT GTC GTC AT	539, 540
chr13	32249897	32250146	ATG GGT CTC TGG AAT GCA TG	AGG ACA AAG TTT CAG CCT CT	541, 542
chr13	32296888	32297137	AGT TCT CCA CAG CAC ATC AT	ACT CAG GAC ACG ACT TCA TAC	543, 544

FIGURE 2 (Page 17 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	32311823	32312072	TCT TTC ATC TCA GCT CTG CA	ACA TCT TTG GCT CAC TGG TT	545, 546
chr13	32316395	32316644	CGG AAC AGT ATT TTG AGG GG	TCA CAG TGG GCT TCA TTC AG	547, 548
chr13	32321163	32321412	TTT GGC TGT TTC CTG TTT CC	AGC TGG AAT CTA TGT AGG ATG G	549, 550
chr13	32348262	32348511	ACC TAA CTT GCC TTG TCC TT	CTG CGG AAG GAT CTA GTC TT	551, 552
chr13	32565108	32565357	ACA GGA GAA CAA GCA GCA TA	TGA GAA GTA TTC AGC ATT TCC C	553, 554
chr13	32578964	32579213	CAG CCT AGT ATA TGG GAA CGT	CAC TCA CGG ACT TTT AGG C	555, 556
chr13	32584041	32584290	ACC CAT ATG TAG TAT CGC TCT TG		557, 558
chr13	32596887	32597136	TAT GGG TTT TTC TGC TCC ACT	TCA CAC GCC AGG TTA TTA CA	559, 560
chr13	32651705	32651954	AAA TGT GAG GGA GAG TCG TC	AAG TGG GTT TGC AGT TTG GA	561, 562
chr13	32760468	32760717	GCA GGA CCC TTC AGC ATT A	ATG TAC GTG TGT GTC CAT GT	563, 564
chr13	32829312	32829561	GAC TGG ATG ATG CAA AGG TG	AGG CGG GTT GGT CAA TAA TA	565, 566
chr13	32852622	32852871	AAC ATT TGC AGG GGG ATC AA	CCA CAA ATC CCA TCA ACA CA	567, 568
chr13	32872003	32872252	AAA GAT GCC TCC TTG TGT CT	TTT CAC AGT AAC ATC GGC AC	569, 570
chr13	33535420	33535669	AAG TTA TCT GCC CAG GGA AA	CTG ACA GCC TGC ATT TGA TT	571, 572
chr13	33634729	33634978	TCC TGG CTA GTT TTG CTG AA	TTT CCT GGA GTA AAG CGA TCT	573, 574
chr13	33660366	33660615	CTC CTT GCT TGC CTT TAC AC	CCC ACA ATC ACC CAT CTC TA	575, 576

FIGURE 2 (Page 18 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	33742309	33742558	AGC CTT AAT TCC CCA TGC AT	TAT CTC ACT CCA CAG CTT CC	577, 578
chr13	33760763	33761012	TTT TTC TGT GGA GTG TGG CT	ACA GGT AGT TTG GTG GTG TC	579, 580
chr13	33787480	33787729	AAA GAG TCA ACC ATG CAC TG	GCT GTT GAA TGC CAG AAC TT	581, 582
chr13	33803219	33803468	GGT GAA GCA GCC TGA ATA AA	ATA GGG TCG GTT TTG GTC TG	583, 584
chr13	33925858	33926107	TCT TTG TAC CAA GCT GCC A	CAT CAT CCC TGT CAT TCC CA	585, 586
chr13	34286418	34286667	GCT TCT ACT TTC CCC TCC AG	GTG GGC TAA GAA AAC ACC TC	587, 588
chr13	34301780	34302029	AGA AAA GCC AAC CTC CTC TT	ATT GTG GTT TGT GGC ATG TG	589, 590
chr13	34380783	34381032	CCA GGG TAC TAA AAG GGG AC	CCA GAT TCA GCC TGT ATT CC	591, 592
chr13	35504924	35505173	TTG TGG GTC AAT GTC AAC AC	GCC CAT GGA AGT AAA CAG TC	593, 594
chr13	35532835	35533084	AGA AAA GGT GGA GGA AGG GA	AGG TTT GAC ATA ATA GTG CTG C	595, 596
chr13	35538772	35539021	GGA GTT GTT TAC AGG TGG ACT	AAT CCT TTC CCC ACT CAC TG	597, 598
chr13	36233165	36233414	TAG CTT CCA ATT CAC AGG TCA	CAC AAA GCA GTT CCA TGT CC	599, 600
chr13	36343466	36343715	TTA AAT GCG CCA AGT CCC TA	GGA CAA TTT CTC ACT TGC CA	601, 602
chr13	36348003	36348252	ATT TCC TGG CTC AAG CTC TT	AAG GGG TGT TGT TAG ATG CT	603, 604
chr13	36380590	36380839	CTT GGA CCA GGA ATG CTC TA	GCA TCA CAC ACA GCA GAT AC	605, 606
chr13	36386774	36387023	AGG CAG TCA GAT CCA CCT AT	AAA ATG TCC GTC CCA GAT GA	607, 608

FIGURE 2 (Page 19 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr13	36410707	36410956	AAA ATT GCC TGC TGT TTG GA	GGG GGA AAA TGT GTT GTG TT	609, 610
chr13	36427833	36428082	GCA CCA TCA TGA AAC CTC CT	AAC TGT TAG CTT CTC CAC CC	611, 612
chr13	36445018	36445267	ATA GGC CAG TCT CAG GTA GA	CGA GTG TAG GTT CCG GTT TA	613, 614
chr13	36451093	36451342	AGA TTG CAG CCT ACC CAA AG	AGA ATG CCC ATT TCA GGA GT	615, 616
chr13	36568336	36568585	TTG ACT GAA GTG TTC CAG GT	ATA TGT GGT TTG AGG TCA GCT	617, 618
chr13	36576882	36577131	GCT TCT TTC AAC CAT CCA CC	GGC TTT GGT CAC ATG GAG A	619, 620
chr13	36663599	36663848	GCA GCA CTC AAC TAT TCC AC	TGA GGC AAG ATT CAG TGA CT	621, 622
chr13	37595672	37595921	CAG CAG TTA TGG CAC CAG TG	ACT TCA TCT TGA CAG CAG CT	623, 624
chr13	38283224	38283473	GAG AGT GTG GAG GCA GAA AA	CAC TTC CTC ATG ATG TTT TGG A	625, 626
chr13	38320894	38321143	GCC CAA CTT ATT TTC CAG CT	GGC CAG CCC ACT TAT TTT TG	627, 628
chr13	38361974	38362223	TCA AGC CCC TTA GAT TGA ACA	CTC AGG GTG GAG TTT CAA AC	629, 630
chr13	38380696	38380945	GCT GGG CAT GTA GAA CTC AA	GAT CTT TCT TCC CCT CCT CC	631, 632
chr13	38789453	38789702	GGG AAA TTG TCA AGG GCT TT	TGT ACA TCC ACC ACT TGT TTG	633, 634
chr13	39009512	39009761	CTT AGT TGC TGT TGT GCT TCT	AGC GGT AGT AAG AAG GCA AA	635, 636
chr13	39096011	39096260	AGT TGT AGC TGT ATC TCG GT	AGA CAG GTG ACC ATT TTC CC	637, 638
chr13	39202882	39203131	AGC TGA GTC ATG TTT AAG GC	TGT GGA ACT TTT GAG CCA GA	639, 640

FIGURE 2 (Page 20 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	44004660	44004909	CAA TTC AGA CTT TGC CCA AAC	CAT AAC GAA ATA GGG CCT TCC	641, 642
chrX	44005572	44005821	CAA TCA TTC CCA CAG TTC CAA	ATT TCT GCC TCT TCT CTT CCC	643, 644
chrX	80622102	80622351	CTG TGA TGG TCC ATT CAA GG	TCA TCA AGT CAC CTC TCC AC	645, 646
chrX	81576088	81576337	TAG CTG GAA ATT GCA AGG AG	TGG AAA ACT AGA CAG CAG CC	647, 648
chrX	83458870	83459119	TCT GTT CAC CTG AGC CTT T	GGA AAG GGG AAA AGG TGA CA	649, 650
chrX	83461989	83462238	TAA CTT GGA CTG TGA ACC CA	CTG TCC TCT GTG CCA CAT AA	651, 652
chrX	83972195	83972444	CGC AAC AGG ATG AAG GAA AT	TTT CTG AGT CCA TTC CCC AT	653, 654
chrX	83973091	83973340	GAC TCA CAC TCT TAA AGC CT	GGC CAT CCT GAT ATC TTC CA	655, 656
chrX	84308155	84308404	AAT TTA GGT AGC ACT GAC CCC	CAG AGA GAT GCA GAG GTT CA	657, 658
chrX	84412933	84413182	CTG GGG AAT TAG GAA GCA GA	TGT GTG TGA GCT AGC TGA AT	659, 660
chrX	84530826	84531075	ATG ACA AGG CTG GCT CAT C	GGT TTC CCA TCC TAC CAC AT	661, 662
chrX	84531356	84531605	TTA GTT TTG CCA TGT GGT GG	GGT GCT TTT GTT GCC TTA CT	663, 664
chrX	84561384	84561633	TGG TGA GGG AGT GTT CTT TT	ACT AGA AAG CAG GGT ACA GT	665, 666
chrX	85583338	85583587	TCA TTG GGG GAG TCA TTC AC	GCT TTT TCC AAC TTC TGC TG	667, 668
chrX	85584098	85584347	GAA GTG GTG TGA TGA GGG TG	CAA CAG ACA AGT CAC CTC CT	669, 670
chrX	85643367	85643616	AAG TTA GGC CCT GTT AAG CA	GGT TCT TCC TGG ACT TCA AA	671, 672

FIGURE 2 (Page 21 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	85643847	85644096	TCT TGG TCG GAG TCA GAA AT	GAA AGC AGT AGT TTC AGG TGT	673, 674
chrX	85644765	85645014	GTA AAA GAG GTT GGG ATG CC	TGA AAG ACT CTG TTG CCA TG	675, 676
chrX	85682212	85682461	CGT TGG ACA TGG ATC ATA CC	CAC TAC ACG CTC AGA ACA AA	677, 678
chrX	85715710	85715959	TCA CAA CAA GGG AAA TAG CCT A	AAG GCA AGC AAT AAT GAG GC	679, 680
chrX	85764768	85765017	TAG TCA GGT AAA CAA CGC CT	GGA CAG TCT GTG AAA ATT GCT	681, 682
chrX	85988749	85988998	TCT GTT TCT TGT TTG GCT GAG	ACA AAC AAC CCT TAA TGC CC	683, 684
chrX	85989214	85989463	ACA TAG GTC ACA CAA AGG GT	TGA AAC AGT GAA TCC GCA AT	685, 686
chrX	85997574	85997823	GTG TGA CAC TTT TCT GCC TT	AAG GGA AAT GTG GAT GCA GTA	687, 688
chrX	87225841	87226090	CTG GAA ATA GAA GGC CTT TGC	TTG AAG GGA AGC GGA AAG T	689, 690
chrX	91517109	91517358	TCT TGG TCT GGG AAT AAG CC	ATT TCC AGC TAA TGA TGC TCC	691, 692
chrX	91517578	91517827	TGC CCC TAT GAA CAA CAG AA	GCT CAC TTA CGC ATT AAC CA	693, 694
chrX	94601042	94601291	TGA ACG TCT TGC TTA CCC AC	ACA GGC AAA ATT CAG TTG GA	695, 696
chrX	95282210	95282459	GAA GGA AGG CAG AGG TCA A	AGG CTG AAT CAC GTC AAA AC	697, 698
chrX	95700693	95700942	CTT CCA CAA AGT CCT GCA AC	CCT CGT TCA CAT TTG ACG C	699, 700
chrX	96016317	96016566	ATG TGA ACC ATT GAG AGG CA	TGT CTG GGT TCA ACT GTT TG	701, 702
chrX	96474722	96474971	AAG AGA AAC TAC CCT GGC AA	ATT TTG CAT GCC TGT TGA GA	703, 704

FIGURE 2 (Page 22 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	96475190	96475439	GCA TGT AGT TCA GTT CAG GC	GCT CTC CTC AAA ACC CAA GT	705, 706
chrX	96522258	96522507	ATG AAA TGT AAT GGG GTG CG	CTT AAT GAG GGG GCA CAA AG	707, 708
chrX	96685785	96686034	TTT TGG CAG TGA TGA CCT TG	TTT TCG TCC AGT CTT CCA CC	709, 710
chrX	982226881	98227130	TTC TTG GCT TTT CTG ACC CT	TAC AGG ACC GTC AGT GAG AG	711, 712
chrX	98227467	98227716	TTG AGA AAG AGC CCA ACA GAA	TTA GCT ACT GAC GCT TCA CC	713, 714
chrX	98314697	98314946	GAA AAT AAC ACA GTA GGG ATG C	GCA CAG ACA ACA TGC TAG TT	715, 716
chrX	98331718	98331967	GAA TGG AGA GGC AGT TTT CA	TTA GTC TGT TCA CTG GCA CA	717, 718
chrX	102986351	102986600	CAC CCT TTT CCT GTT TTG CA	CTT ATC AGC AGG GCA CAG T	719, 720
chrX	112117885	112118134	AGA AGA AAC TTG CAG TGT TGG	TTG CAT CAA ACA AAG CCA CA	721, 722
chrX	116461543	116461792	TGC AGC ATT ATT CTT TCT GGG	GAG AGA CAA GTC ACC CCT TC	723, 724
chrX	116746667	116746916	ACA CAC ATA TTA GGG AAC AGC	AGT CAA CTA CAA ATG GGG GA	725, 726
chrX	117121287	117121536	GAG TGT AGG TGC TTG GGT AT	GTG CCA AAA TCA ACG AAA GC	727, 728
chrX	117494627	117494876	CCT TAG AAT CCT AGC GCC TT	AAG GAG GGA GTA CAA AGT GAG	729, 730
chrX	118400460	118400709	TCA TGA GGT TGC CAG TGT TT	ATC ACA TTT TCA GCA CGA GG	731, 732
chrX	119760145	119760394	CCC CAT ACA TCA TCA CAT GC	CAG GGA GGG ATG ATT TGG AA	733, 734
chrX	120436725	120436974	GGG TAA TGC TTT CTT GGG GA	AGA ACT GAG AGG GGA GCA TA	735, 736

FIGURE 2 (Page 23 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	120437307	120437556	ACT TGA GAA GGG AAG GCA AG	CAG TCA CCA ACA AAG GCT TT	737, 738
chrX	121854317	121854566	CTC CTG GTG GCT TAT TTT TGA	TCC CCA TCT CCC TAA CTC AT	739, 740
chrX	121855104	121855353	TCT GGA TTT TGG CTA CTC ATG A	TTT TTC TGC TGC ATC CAA GG	741, 742
chrX	122863038	122863287	GTA GTC CTC CTT TGC CCT TC	ACT GTA CGC CAT GAA AAA CA	743, 744
chrX	123203756	123204005	GAC ATG CAC AGA TCG AAA CC	GGC AAA TCA AGT GAG CTG AC	745, 746
chrX	123989030	123989279	CGC ATT TGA CAA CAG GGA TC	CGT GGG TGG AGA ATT TCA CA	747, 748
chrX	124394967	124395216	AAG CCA CCT GTT CTC TCT CA	ACT TAG GTC AGT TGC TTG GT	749, 750
chrX	125455385	125455634	ATT CCA ACC ATT CCG ACA CC	GAC TTC ATC AGC ACG TAC TT	751, 752
chrX	125500101	125500350	AAA GAA AAT GGT GAA CGT GC	TGC AGG CAA AAT TAG CAT GG	753, 754
chrX	125500582	125500831	TGA TCA GGG CTT TAG AGG TC	GAC TTA TCT GCT TTC ACC CC	755, 756
chrX	127973758	127974007	ACT CCC TAT TGT TCT CCC CT	CCC CAT GAA CCT AAG ACC AT	757, 758
chrX	128274367	128274616	CTC CTT GAC AGA TGT GAC CC	TCT GGA CAT GTC TTT GCG TA	759, 760
chrX	128274689	128274938	TTT TGG AGT CTG AGC CAC AA	CTC CAG GAC ATC TCA GCA AT	761, 762
chrX	128275238	128275487	TTG AAG TCC CGT TGC TGA T	CCT CTC GTG TGG GAA ATG TA	763, 764
chrX	128694864	128695113	TTG GGG TCA GTT CTA ACA GT	TAT CTC TGG CTA CCT CCT GT	765, 766
chrX	131201343	131201592	TTT TCA CCA CCT CTT CCC TC	CCC CAT CCC TGT ACC AAA G	767, 768

FIGURE 2 (Page 24 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	132160888	132161137	ACC TGA CCA CAA GCT TTA CA	CTG CAG AGA TAT TCC ATG GC	769, 770
chrX	133560531	133560780	CAC ATA TTG GCG CAC ACT AC	AAA GCT GGG TTC TTA GGC TT	771, 772
chrX	133847304	133847553	GCC ATG CAC CGA TGA AAA AT	GCT GTT TTA GGG GCA CAT TT	773, 774
chrX	133886077	133886326	TTG TGA GGA GAT TTC TGG GC	AAG AGG CAA TGT GGA GGT TA	775, 776
chrX	133886778	133887027	CAC ACT AAG AGC ACT GGG AA	GCC CAA ACA ATC TGC CTT TTA	777, 778
chrX	135279738	135279987	ATG ACC TAG CAC ATC TTC CC	TGG CTT CAA ATA ACT GGG CT	779, 780
chrX	135581031	135581280	ACA TTT TCC CCA TTC CAT GC	AGA GCA CAC AGA ACA GAA CT	781, 782
chrX	136941543	136941792	GTC TGT CAA CCA CAC TTT GC	CTG GTG GAT TTC TCG TCA GA	783, 784
chrX	138913313	138913562	CTG TCT CTC CTT TTG CCA AA	TAG GTG TTT GTG TGA GGC TT	785, 786
chrX	138913920	138914169	AGT AAC CTG CGA CTC TCA GT	GCC TCA CTG CTC CTA TCT TT	787, 788
chrX	139857034	139857283	TAG CAT TTA AGG AGT GGG CT	CTC TAG CAG CTG TTC CTC C	789, 790
chrX	139857318	139857567	GGC CTC CTC AGT GAT TTG AA	CGT CGT ATC TCT GGC TTT GT	791, 792
chrX	141400062	141400311	CTT TCT TTG CCT CCC CTG TA	GTC CCC AAC CTC ATC TTT CA	793, 794
chrX	141408144	141408393	ACT TCC ATT TGT GTC AAC GG	TCT TCA AAG ATG GCT GCA AA	795, 796
chrX	141408548	141408797	TCT TGC TTT GGG TTA GAG GG	AGT ATA ACC AGA TAG CGG TGC	797, 798
chrX	142517923	142518172	AAC CAC ACC TCC ACA AGA AA	TGT CCT CAG GGC AAT AAA GT	799, 800

FIGURE 2 (Page 25 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	143466384	143466633	CAA GAT ATG AGG GAG GGG AA	TTT GCT GCT TGA AGT GGA AC	801, 802
chrX	147766073	147766322	TCT AAC CTG GGC CCT TTC TT	GCT GCA ATG ACC TGA TTT CT	803, 804
chrX	147869477	147869726	TGC CCT TCC AGA ACT GTA AA	TCC CTC TCT CCT CCA AAT GA	805, 806
chrX	147880766	147881015	GGC AGG TCA CTT AAC AAA GC	TGG CAC AGT AGG TAT AGG TTG	807, 808
chrX	147881811	147882060	CAA TAA GGC GCC AAG TTC G	CCC TCG CCC TAA AGA AAC TA	809, 810
chrX	151796091	151796340	GTC ATC AGG GGA GCA AAT GT	CCC CTG AAT CCC TAC CTC AT	811, 812
chrX	104102171	104102420	AAC ATG CAA TCC CTG GAA TTC	TGT TGT ACA AGT GAG CCA TTC	813, 814
chrX	104124449	104124698	AGT TGT TTC AGG ACA GGA TCT	ACC AAG CAA TCA ACT CAC TCT	815, 816
chrX	104234605	104234854	TCC TCC TGC CTT TAA TAA GCT	GCC CAA TTT GTC TAG CCA ATA	817, 818
chrX	104235195	104235444	TTA CAA GGC ATC TGA CAG GAA	CTA CTG ATC CCA AAG AAG GCA	819, 820
chrX	104291380	104291629	TTA CTG GTA GGT TTG AGC ACA	GTG AAA GGT TCT ATC TGC CAA	821, 822
chrX	104291786	104292035	GAG CTA CGT TCT TTC TCA TCA C	GGC ATA CCG AGC ATA CAT AGA	823, 824
chrX	104647680	104647929	CAC CAA TTA AAG TGT GCT GCA	CAC CTG TTT CAC CAA ATC ACT	825, 826
chrX	104648691	104648940	TCC CTT CCA AAG TGC CTT ATA	TCT CAT GCT CTG ACA GAC AAG	827, 828
chrX	106886942	106887191	TGG TTG GTT TGG GAT ACT TGA	TTG TCC TGT TTC TCT TGT GAC	829, 830
chrX	3343487	3343736	GAA CCC AAA TCG ATC ATG CAT	CAC AGG ACT GCA TGC CTA TTA	831, 832

FIGURE 2 (Page 26 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	4013011	4013260	AGA GTT AAA CGT GCA ATG TGG	GAC TCT CTC AGC ATC GAG TTT	833, 834
chrX	5008870	5009119	GTT CGT TGG TCA TAG TTG TTG T	CTG ATG GAA GGG CAT TAT CCA	835, 836
chrX	5687782	5688031	AGT TTA GCC AAA GGA TTC AGC	TTC TGG TTC CAT AAA TCC ATG C	837, 838
chrX	5717003	5717252	TCA ACC ATT TAG AAC CAC CTT G	GGG ATT ATT GTT GGC TAC TGA G	839, 840
chrX	5808998	5809247	AAT GTC CAC TTT AGC GGA GAG	AAT TGG TGA CCT AGG GAT CAG	841, 842
chrX	5814187	5814436	GGA GTA TTC TGT TCA TGT TGG G	GGG TTT GGT AAG GGA GAA TGA	843, 844
chrX	5836574	5836823	TTT CTA GAA TTG AGG AAG GGC A	AA GAC ATC CCA GTT ATG CAT TGT	845, 846
chrX	5849776	5850025	AGG ATA AGA CGA GGC ATC AAT	AGA TGG GAG GGA GAT TAG ACA	847, 848
chrX	6895474	6895723	TTC TGT GTT GAC ATG TAC CTC T	GAG TAG CAA CAA CAC ATG GAG	849, 850
chrX	6965226	6965475	TCC AAC ATT TCT CTC TGT CCC	TTC TCC TTC ATT AGC CAC ACA	851, 852
chrX	6965573	6965822	ATA ACG TGT ACT CCT CAG CC	AGT CTG CAC TCT ACT CTT CTG	853, 854
chrX	7152743	7152992	GCA CTT GGA GGA TGT AAA GAC	ACA AAT GGT TCA TGA TGG TGG	855, 856
chrX	9529739	9529988	TGT ATG CTT TAG GAC CCA GTT	GGT ACT CAC GTT TCA GTT TCC	857, 858
chrX	9605323	9605572	AAC TCC ACA GGA ATC TTT CTG A	GTT CAT TTC TAC AGT CCA GGC	859, 860
chrX	9615158	9615407	CAT TTC TCC TGG GAC CGA AT	CTC TCA CTG TGC TGC TTA AAG	861, 862
chrX	9766329	9766578	TTC TGA AGC TGA CGA AAT TCC	CAA AGA ATT CCA CAG AGA TGG G	863, 864

FIGURE 2 (Page 27 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	9793372	9793621	GTT GCT TAG TCC TTG CTT CAC	TGA GCT ACA GAC AAG ATT GCA	865, 866
chrX	9849298	9849547	AGG TCA TTG GTC TGC AGT TAT	TCA CAT GGG ATC GAC ATA TGC	867, 868
chrX	9850182	9850431	AGC ATT TAG AGA ACA GCA GTC	CCA CAC AAT TTC CTG GCT ATG	869, 870
chrX	10002581	10002830	GTG TAA GAA GTG GTT GGG TTT	TCT TGC TTC TGG AGA GTT CTT	871, 872
chrX	10301512	10301761	AAA GGC AGA GCA GTG TAT TTA G	AGG TTA TGC AGA CTT CAG GAA	873, 874
chrX	10354762	10355011	AGA CAA GAG AAC AAT CAG GTG A	AAG CCA ATT CTG CCT CTC TAG	875, 876
chrX	10375361	10375610	CAA AGA AGC TCT AGG ACA GGA	TCC CTT CCT TAT TCT GGC AAC	877, 878
chrX	10384260	10384509	TGG TGG AGG AAA TCA ATG TTG	GCT TCA AAC ACT CTA AAG GGC	879, 880
chrX	10398645	10398894	CAC AAG GGA GGA AAC GTT CT	TGC CAT TAA TGA GAA GTG CTG	881, 882
chrX	10572719	10572968	TGA GAT TTA GTG CCA GCT AGA	TGG CAA TCC TGT TAA ACA ACT C	883, 884
chrX	10579800	10580049	AGG ATT AGT TTG GCT CCT CAG	CCC GAA CAT TGA TAA CAG AAG A	885, 886
chrX	10580482	10580731	CCT GCA CTA TTT CCT CAA AGC	GCA ACT CAG GAA AGA CTA CAT C	887, 888
chrX	10627502	10627751	CAA TTT CCT TCT CAC TGA GCC	TTA AGA AAG TAC CCA TCC TCC C	889, 890
chrX	10645064	10645313	ACG CTT CCC AAA TCT ATC TGG	GTC ATG CCT TAC AAC TTA GCA	891, 892
chrX	10669664	10669913	CTT ATT TGT GTG CCC AAT ACC A	AAT CTT TGC CAA GGT ATG AGC	893, 894
chrX	10709674	10709923	TTG CAG CAG GAA CAC CAT AAA	GCC ACT TAT ACC TCC AGA CAT	895, 896

FIGURE 2 (Page 28 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	10710087	10710336	CTG TTC ATG TTG CTA CCA CAG	CCA CAA TCC TGA ATG CCA TG	897, 898
chrX	11139863	11140112	CTG CCT TAG ATT CAC TTT CGG	CTG CAA GGT ACA ACA CAA GTC	899, 900
chrX	11658912	11659161	CCA TCT GTG AGG TCT TCT TTG	ATC TCT GTG CCA GCA AGT ATT	901, 902
chrX	11681358	11681607	TCC TTG GTT GTG TAT TTA GCC	ATT GGG AAA CTG TCA CTG ATG	903, 904
chrX	11686196	11686445	AGA CTC AAC TCA CAT TGG CC	GGC CTA ATA GAG AAG CAA AGC	905, 906
chrX	11686913	11687162	GGT CTG ACT CTG TGG TTT GG	GGG AGC CAA TCA GAT AGA AGT	907, 908
chrX	11687182	11687431	TTT CAT TTC ATC CTG CCC ATG	GGG AAG TTG GGC TAT TTA ATG C	909, 910
chrX	11917847	11918096	TTC TGT TAT TCG CCA TCA GTC	AAC TGT GTA GAG CGA CCA AAT	911, 912
chrX	12016474	12016723	GAA TTG GGA ACT TGG GAA GC	CAG TAA GGC CAT GGT CTA GAT	913, 914
chrX	12158815	12159064	GAA CTT TGG AGA GGA CAG TGT	CTC AGA ACA TTT GCA CCT TCT	915, 916
chrX	12485152	12485401	AAC TGT CAT GTG TCT CTG CTA	ACC TGA TAC AAT GGA GCA TGT	917, 918
chrX	12608017	12608266	TGA TTC CTT CCA CCT ACC AAA	GGG ACC TAA ACT CCT TTG GAA	919, 920
chrX	12724960	12725209	GCC AAG GTC CAT TAT CTC AAG	TCT GCA GTG GTG TTA TCT AGT	921, 922
chrX	12841791	12842040	GAA CCT GCA TTG TCA TTC TCT	CAC TTA AGT TTC CAC GCC AG	923, 924
chrX	12904558	12904807	AAG AAC ATC AAC AAA CTC CAG G	GTA ATG GCG AGA GGT TAA AGC	925, 926
chrX	12937788	12938037	TCA ATT CTC TTT CAC ACG TGC	TTT AGG TAT CGA AGT TGG GTC A	927, 928

FIGURE 2 (Page 29 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	12938100	12938349	AGG TGC TGG ATC TTG AAT TCA	GAT AAG TTT GGA AGC TGC ATC A	929, 930
chrX	12992266	12992515	TCC CTC TAC CCG AAT CTC TTA	AAG CTC TGC CAT TGA CTT TAG	931, 932
chrX	12995926	12996175	TGG GTT TAA AGG ACA CTA GCA	CCC TAC AGA ACC GAG GAA TC	933, 934
chrX	12997273	12997522	CGA AGG TCA CAC AGT TTA GTC	TCA ATC TTT GCA TAC ACA GCC	935, 936
chrX	13293562	13293811	ATG TGC CTT GTT GAT TGA TGG	GTA GGT TTA CAT GGA CAG ATG C	937, 938
chrX	13338207	13338456	AGA TGG TAT GTC ACA AAG CAC	TCT TCT GTT TAG TGC TGT GGT	939, 940
chrX	13340422	13340671	ACA CTT TGG AGA GCT TCA GAT	CAA GTT CAT TTC TTC CCT GCA	941, 942
chrX	13351532	13351781	GTG CCC AGA ATT ATT TGT GTC T	TGC AGG AAT ACA TGG TAG ACA	943, 944
chrX	13624857	13625106	GCT CTC TTG TGG AAA CGA TTA	CAT AGG CCT TCA TGT CTC TCA	945, 946
chrX	15525635	15525884	AGT TTG TTT CTC TGG CCT ACT	TAT GAG GGT GCA CTA ACA GAT	947, 948
chrX	15543469	15543718	ACC ACC TCA AAG ATT TCA TGG	GGT GCT ACT ACT GGT GTA TGT	949, 950
chrX	15543853	15544102	GTC TTC ATC TAT TTC GTG AGC C	GCC ATG CAA TAT CAA ATC CCA	951, 952
chrX	15844810	15845059	TCA TCC CAG ATT CAG AAT GCC	GAA ACC AAA GAC TAG TGC AGC	953, 954
chrX	16860721	16860970	CGT TCA ATG AAG TCC CTT GTC	ATG ACT AAC ACT CTG CCA AGT	955, 956
chrX	16861729	16861978	TTC ACA AGA ACT CTG CTG GAT	AAC AAA TGC ATC CCA GAC AGA	957, 958
chrX	18307677	18307926	GAA GCC TTC TAG TGG GAC TAA	GCA GAG AGG AGT ATG TGG TAT	959, 960

FIGURE 2 (Page 30 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	18600682	18600931	GTT AGG GTC ATG GGT CAC TTT	ATG GGT CAT TCT ACG AAG CAA	961, 962
chrX	19376384	19376633	GCC TTT GTA GAG TGG ACT TCT	TGG TGT GTG TGG TGA TAA TTA G	963, 964
chrX	20026004	20026253	GGC TTC TTG ATA CTG CTT TCC	AGT GAC CCT CTG AAT AAC CTG	965, 966
chrX	20627108	20627357	AGG TGT GCA ATA CTC AAG GAA	TCA GCA AGT AAA CCT GAG ACC	967, 968
chrX	21537202	21537451	AAG GTC TTA GGA GTG AGG ACA	GTA CCT TCA CCC TCC AGA TC	969, 970
chrX	21629967	21630216	TCC TGC TAT TTC AGT CAG ATC T	TCA TCA AAT TGC CCA CTC CTA	971, 972
chrX	21887062	21887311	TGT CCA GCC GTA ACA TTT CAT	CAT CAG ACT GTC TTG CCT TTC	973, 974
chrX	22202443	22202692	AAT GGA CAT CTT TCA GGT CTG	CAT TCT TGC TGA CAT TTC CCA	975, 976
chrX	23018625	23018874	TCA AAT TGG GAT CGC ATT AGG	GAA GAT CAG GGT ATT GCT GAA A	977, 978
chrX	23019006	23019255	ATG CCT GGG TTT ATT CAT CTT G	TTT GTA GGT CAT TCA GCC TCC	979, 980
chrX	24521325	24521774	GGA GAA CTT TGG GTT TGA TCC	TGG CTA GGA TTC ACT TAG GAA A	981, 982
chrX	24522047	24522296	TGA TAG GAG CCA TCA GTT CTT	GCA AAC AGG GTG AAT TAT GCT	983, 984
chrX	25401534	25401783	AGC AGA TGT TGT TAG CTT TCC	AGA AGT CTG GGA AAC GAA GAG	985, 986
chrX	25403300	25403549	TTC TCT GTC ACT TCC ATG AGG	CAG ATG CTC CAT TAC TAG GTG	987, 988
chrX	28689766	28690015	CCA GTA ACT TAT TCT GCC AGA G	CAC ATG GAG AAA GGT GAA TCA	989, 990
chrX	28693600	28693849	TGA GAG ACA AGC TGC ATT ACA	TCC CAT CCA ATA CTG CCT TC	991, 992

FIGURE 2 (Page 31 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	28717026	28717275	GCA CAG AAA TTA CAG TTC ATG G	TCT GGC TCA AAG GAT CAC ATG	993, 994
chrX	28720131	28720380	GCT CTC CTA TCT GAC AGT GAA	AAG ATC CCA TTG ACC CTG AAT	995, 996
chrX	28808128	28808377	CAG GCA TCT TGG TTT GTA GTG	CCA CAG GCT CTC TAG AAC TAA	997, 998
chrX	28824813	28825062	CGT GAT GAA CAG TGA TGA CTT	TTG AGA GGG TTT ACA AGG TCC	999, 1000
chrX	28825844	28826093	CGC CAT TTG TTC TCC TAT TCA	CTT CTC CTA CTC TGC ATT CTC A	1001, 1002
chrX	29487025	29487274	TTC GTT AGC TAC TGG GTA CTC	GAC ATT AGT GGA TTC AGG CCA	1003, 1004
chrX	30847194	30847443	CCA CCC TTT ACA CCT ATC CAA	GCT GAA GTG GAG GCA ATT AAC	1005, 1006
chrX	32660941	32661190	AGA GTG CAC AAA GGA GAA GAC	TAT AAC TGT TCA GTC TGC CCA	1007, 1008
chrX	32949975	32950224	TCT ACT GTG TCA AAG CAG ATT G	ACT GAG CTT ACA TTC ATG CAC	1009, 1010
chrX	35971182	35971431	TTC TTC CTA GCC TTC CTT TCC	GCC ACT TTC TCT GCA AAG AAT	1011, 1012
chrX	35971544	35971793	TCT CTG GCT GTG CAG TAA ATT	ACT TCC TAC GCA CTC AAA TCT	1013, 1014
chrX	43599991	43600240	AAA CTC CCA GCT TTA ATC CCT	GGC TCT CAT TAC AAT TGG CTG	1015, 1016
chrX	43600262	43600511	AAG AAT GGG TGA GTT GGG TTC	ATT GCT TTC AGT GGT GGA TTG	1017, 1018
chrX	43807492	43807741	GCA AAC TGA ATT GCC AAG TCT	GGA ATG AAA CAG AGG AGT CCC	1019, 1020
chrX	63137429	63137678	CTC CCA ACT TTT ATG CAG CC	AAG ATG CTA GAA ACC CAC AAG	1021, 1022
chrX	63137928	63138177	GCT CAG GGA ATA TCT TGG GAA	AAT GGG TGG GTT ACA GAG AG	1023, 1024

FIGURE 2 (Page 32 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	74269728	74269977	ACA TTC AGC AAG TAG GAA GGA	GCA TTT GGA CAT GAA CAA GC	1025, 1026
chrX	74270926	74271175	CCC AGA AGA GCA GTA ACA AC	CAT TGG TGG GTG GAT AGC TG	1027, 1028
chrX	74282022	74282271	GAA AAA GGG GGA TAG GCA TT	ACC AGG AGG AGA AAA GCA AA	1029, 1030
chrX	74329664	74329913	CCC AAC AAC TGC AAT AAA AGG	CGG AAA ACA AAC CCT GAA GT	1031, 1032
chrX	74344769	74345018	ACC GAA ATT GCT TGC TGT TA	ACC TGC ATA TTG AGC CAT AC	1033, 1034
chrX	74741441	74741690	CCT TAG TGT GAC AGG ACA GG	TGT TCT TTC ACT TTT AGC CCC	1035, 1036
chrX	76192017	76192266	CCA AGA CAA CTA GGC CAA TG	TTT CTA GAA CCC TCA GCA ACT	1037, 1038
chrX	76194203	76194452	GAA GAG ATG ATG CAA AAG AGC	CCC CCA ACA GTT TTT AGT GGT	1039, 1040
chrX	76221949	76222198	TCC AAG CAA GGG ATC TCT TC	AAG GCA AAA CAC TCC CTT TT	1041, 1042
chrX	76226569	76226818	GAA TGG TCA GGG AAG GGT TT	CAG TGA TTG CCT CTA GAA AAG G	1043, 1044
chrX	76234682	76234931	AGT CTT CAG CCA TCT TCC TG	CTA AGC AGA TTG AAG CAG CT	1045, 1046
chrX	76308591	76308840	GCA TTT CCA GGC TTT ACA AGT	TGT CCC CAG GCT TAA GAA TC	1047, 1048
chrX	76647025	76647274	CTC TCT CTC CCT GGT CAG AT	AGC CAG AAT AAG CAA CTG TC	1049, 1050
chrX	76711476	76711725	CAG CAA TTC TCA GGC TCA GA	TTT CTC CTA TCC CAG CTT GC	1051, 1052
chrX	76759387	76759636	TCT GAA ACA AAG CCT CCT TAG	ACT ACA GAG GAT AAC AAG GGT	1053, 1054
chrX	76778190	76778439	AGG ATA AGG TTT CCC ATG CTC	CTC CCA TCA GTA CCC TCT CT	1055, 1056

FIGURE 2 (Page 33 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	76778847	76779096	ATG TAT CTG AAG GAG CTC TGC	GGA ATG CCT AAA CCA TAC TGT	1057, 1058
chrX	76875971	76876220	GGC CTT CAT CAC AAA CAA CA	AGT GGT ATT TCA ATG CTC TAC C	1059, 1060
chrX	76923678	76923927	TGT CTC CCA TCT ACA AAG CC	GCA GTA CAT CGT CCT GGA A	1061, 1062
chrX	76937441	76937690	TCC TTG AAC TCT TTC CAA GC	CCT GAG CGA GAA GAA ATT TGT	1063, 1064
chrX	76938848	76939097	TGT TTT CCT GTC CAA GTC CA	GGA ACT GAA CAA GAA GTG GAG	1065, 1066
chrX	76939481	76939730	CAG CAT CCA TCG CTC GAA A	ACC TAC TCT TAT TCC GCA CT	1067, 1068
chrX	76949897	76950146	GGT ATT GGT GGG GGA AAT GA	TGA CAG CCT CTC TCT TCA AT	1069, 1070
chrX	76951314	76951563	GCA CTG CTG TAA AAG ATC TAT GAG		1071, 1072
chrX	77040328	77040577	ACT CAA AGG CAC ATT TCG C	GCT GTT TTT CTG TGT GCT TC	1073, 1074
chrX	77168344	77168593	ATT CTA TTC CGA TCA CAG CCT T	ATG TAT TTC CTT TAG CGC CC	1075, 1076
chrX	77634270	77634519	CTA CCT GAC AAA TGG AGC TT	AAT TTT GCA AGA CTT CCG GT	1077, 1078
chrX	78176076	78176325	GAA ATG GCC ATG TCT ACT GAG	TCC CAG TTG TGA ACA TTT GC	1079, 1080
chrX	78176555	78176804	GAA GCC TCT CAA GCT ACA AG	ATG GGT TTT TGC ACA GAT GAC	1081, 1082
chrX	78178901	78179150	GAA TGA GAT TAG GGA GCA AAG T	GGG AGT CAG AAG GAG GTC A	1083, 1084
chrX	78208245	78208494	GCA AGT AAG AAG AGT GCT GC	CCT CTT TTT GCA TGA ACC TGA	1085, 1086
chrX	78290291	78290540	GCT CCT GAT TGA AGA AGT GT	CCT TAC CCT TTC CAC TCA GA	1087, 1088

FIGURE 2 (Page 34 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	78401753	78402002	CTG CTC CTT TGT CTC CTG T	GAC TGG TAT AAT CTT GCC GTG	1089, 1090
chrX	78403248	78403497	TAA GGT GAG AGT GTG AGG AAG	TGT CTG CAT CTT GAT CTC TGG	1091, 1092
chrX	78405536	78405785	CCA GGG GAA CAT TTA CTC AGA	GGT TCC ACA GCA TTT GAG C	1093, 1094
chrX	78411791	78412040	AGG GTA CAT GTA AGG CAG CT	AGG AGC CCT TAA CTA TGG TG	1095, 1096
chrX	78427326	78427575	TTC TGT GGC ATT GTG TCT TG	TGG CTT GGG TAT TGC AGA TA	1097, 1098
chrX	78430991	78431240	CCC CAA ATT TAC CCC ACT CT	GGG GAC AGT AGA AGA TGA GT	1099, 1100
chrX	78431372	78431621	ATC CCT AGC ACT TTC AGG AC	AGT TGT TTC TGG ACG GAC TT	1101, 1102
chrX	78437851	78438100	TTA CCA ATC CAT CCA GCC TG	AGA ATT TCC CTG TCC ATA CCA	1103, 1104
chrX	78526539	78526788	AGA AGC TAA ACA GGT TGC CC	AGT GAG TGA ACT TGC CAT CA	1105, 1106
chrX	78531686	78531935	CAT AAG AGC ACA GCC AAG AT	GGC TTT TCT CTG CAC TGA TT	1107, 1108
chrX	78996675	78996924	TGT CCT GCC ACT TTT ACA TC	GCA AAG GAA ACA GGC TAA CTA	1109, 1110
chrX	107682036	107682285	GAG CTA AGC AGA ACC TAA GGA	ATG GCA GCT GAA TCG ATA TCT	1111, 1112
chrX	107683930	107684179	TTA AGC AAC AGG AAC CTA CCC	TAG CTG ATG GGC AAA TTC TCA	1113, 1114
chrX	110366745	110366994	GCC AAG GGT AAT CAT AGC AAC	GAA ATG CCT TCC CAC TTA CAA T	1115, 1116
chrX	110367927	110368176	TCA TAA TGA AAC CCT TGC TGC	ATT GGC AAA TGT ACC TGA AGC	1117, 1118
chrX	110368330	110368579	AAT CCT AGT GCA TGA GAC TCC	CAA TGA TTG CTC TTG TGC CAA	1119, 1120

FIGURE 2 (Page 35 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	110443307	110443556	TAC TGC CTG CAT CAT TAC CAC	AGC TGT CCT CCT CTC CAT ATA	1121, 1122
chrX	110466084	110466333	ATT AAC AAT GAG GAG CCA GGT	GGC GTT CAA GTT ACT CGA TTG	1123, 1124
chrX	110537791	110538040	GAG AGA TGG TTG AGA AAT GCC	TAG TGA CTA GCT TTG GAG AGT	1125, 1126
chrX	110538060	110538309	ACT ACA ACC ACC AAT TAC AGC	AGC CAA TGA TCC CTT ATG ACT T	1127, 1128
chrX	110538444	110538693	AGT GAC ATT TCC AAG GGC TTT	AAC TAA ACT GGT AGG CAA TCG	1129, 1130
chrX	110575740	110575989	GGA GAT GGG AAG ACG ATT AGA	CAA TCA GAC CAC AGG AAG GAA	1131, 1132
chrX	110576099	110576348	AGT CTT TCA GTC TTA CAT GGG T	GAT GTG TTT ATT GCC TGT GGT	1133, 1134
chrX	110950649	110950898	TAG TTT CTG TGA TCC TGG CAG	GCT CCT TTC ATA GTT TCA GGG	1135, 1136
chrX	110971144	110971393	TTT CTC CCA GCT GTT CCT AG	ACA CAC TGC AGT TGT CAC TAT A	1137, 1138
chrX	121597454	121597703	TAC GGA ACT TCG AAT CAA CTC	TGA ATC AAG TGA CAT GAC AGC	1139, 1140
chrX	135558463	135558712	TCA AGT CAC CCT CAT TGT AGG	TTT TTA CAG TCC TCA GCA CTT	1141, 1142
chrX	135570815	135571064	TGT AAC GTG GAT GTG AGA TTG	CCA CTA GGC TGC ACT AAT GTA	1143, 1144
chrX	135760826	135761075	TTG AGC TAA GTC TGC ATC ACT	CAC TAG CTT CTG TAA CTG TGT G	1145, 1146
chrX	135831981	135832230	CTA GAG AAA GCA ACG CCT AAG	GTC TCA CAC TGC TCA TTT CCA	1147, 1148
chrX	136044394	136044643	AGC ACC TTC CAT AGC TTC TTT	CAC TAG GGT TCA TCA GCT GTT	1149, 1150
chrX	136318161	136318410	GTG TCT TCT GAT GGC CAA ATG	CAA CCA ACA TTA GAG TGA CCC	1151, 1152

FIGURE 2 (Page 36 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	136320360	136320609	AAT CAG GTG AAA GGT ACC TCC	GCT GGT TGA GAG AGA GAG AGA	1153, 1154
chrX	139380500	139380749	GCT TCA CAA TTC AGG GAA CAA	ACA CCA GCC GAA TAC AGA TTT	1155, 1156
chrX	139381074	139381323	TGG ACC CAG TTC TAT GCA ATT	TGC TTC ATA CCT TTC TGC TTC	1157, 1158
chrX	144897923	144898172	AAT GAC CCT TAC AAC TCC GAA	ATT TCC CAT GCC TTT CAA CTC	1159, 1160
chrX	144908837	144909086	TTT GGG AAG TGA TTG TGA AGG	TCT CTC AGT AGG CGT CTT TAA	1161, 1162
chrX	144958353	144958602	TCA GCT GCA TAG ACC TTG TTT	TGA CTG CTA GGC TAG ACT TG	1163, 1164
chrX	144959377	144959626	TCA TTT GTT CTC ATT ACG GGC	GGA TAG AGG AAA CCC AGG TG	1165, 1166
chrX	145799354	145799603	TTT TAC CTG GGT TCT CTT GG	GGC TCT TTC AAA GTA TCC AGG	1167, 1168
chrX	145922717	145922966	TAA CTT CCT GAG CAC ACA TCA	AGA CTT TCT TTG TTG CCT TCA G	1169, 1170
chrX	146994477	146994726	GGG TAA ATT CAG GAA TGC ACA	GCC TCA ACA ATT CAG TCC AC	1171, 1172
chrX	146995311	146995560	ATT TCT TCT GGT GAG TTT GCG	CAT AAG TTG CTG GAA GAG AAC A	1173, 1174
chrX	147540977	147541226	CCT CTT CCT GAC ATG TTG TTG	TGG ACT GCT TTA AGT GAA GGA	1175, 1176
chrX	149764787	149765036	GTT GGT GCC AGA TTG TAA CTT	ACC AGT GAT TAG TGT TTC TCC T	1177, 1178
chrX	150808513	150808762	GCC TGG CTC AAT AAT AGT CCT	CAA GAC ACA CAC AAA CAC ACA	1179, 1180
chrX	150809248	150809497	ATG TTG CCT TCT CTA CGT TTG	GGT AAG AGT TGC CCT AAT GTC	1181, 1182
chrX	150942801	150943050	GAG TGG AGC GCT ACC TTT AT	GCT TGG CTT CTC ACA AAT GT	1183, 1184

FIGURE 2 (Page 37 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chrX	79712826	79713075	AGA ATG GGA AAT GGG AAG GA	GTT TGC CAG TAG AAA TGG GA	1185, 1186
chrX	80374192	80374441	CAC AAT ACA TGG GCT GCT TT	GTA AAG TGT TCA GAG GAC GG	1187, 1188
chrX	80491243	80491492	CCA CTC CAA CTC TGC TTT TAC	ACT AGG GAG AAG AAT TGG CAG	1189, 1190
chrX	80514786	80515035	GAT GTG GAT TGT CTT TGT TGC	CCA GTT CAT TCC AGC TTC CA	1191, 1192
chrX	80553311	80553560	AGC CTT TCA TTG CAC ATT TCA G	GAT CGC CAA CCT GTT TTA TAA G	1193, 1194
chrX	104028154	104028403	TCC CAC CAC AAG ACC AAT TT	GCT GTC AAA GTG GAG ATA ACC	1195, 1196
chrX	104039199	104039448	GAA GAT AGG TGG TGG AGT TCA	AAC GCT TCC ATC CAC CTA ATT	1197, 1198
chrX	104101675	104101924	CTG TTT GAA TGA AGT TGG CTG	ACC TGC CTG TCT TAC CAT TAA	1199, 1200
chr21	17021878	17022127	TAT ACA TGG GTG GGA TTT GTC	GAT ACT TTC CTT TCT CCA GAT CT	1201, 1202
chr21	17046718	17046967	TTT GTG ATG GAC CAT CTA ACC	GGC CGC AGT TTT TGA TTT AG	1203, 1204
chr21	17088576	17088825	GAA CAT CTG CTG TCC CAC TA	TGG GAA GGA CGG TTT CTT A	1205, 1206
chr21	17134784	17135033	ATC TGA AGA TCT CCG TCG TA	TGA ATC ATG CTG TGG AGA AC	1207, 1208
chr21	17161709	17161958	ATG TAT GAA CCA TTT CCT GCT	ATA GAA GAG GTA CCC AGC AA	1209, 1210
chr21	17183683	17183932	AGC ACA GAA TTG AAT GAA GGA A	CCC TGA CTA TGC TAA GTT GC	1211, 1212
chr21	17301983	17302232	GCA TGA GTA AGG CTG AAG TG	TGC AAG CAA AAT GAA ACC AG	1213, 1214
chr21	17302814	17303063	AAA GGC TTA TAT TGC TTT TGA ATC A		1215, 1216

FIGURE 2 (Page 38 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	17336649	17336898	TTG CTG TTG TTG GGA TGA AG	CAG CTG CTC CTT CTT TAG C	1217, 1218
chr21	17346228	17346477	GCT TCT GCA TCC ACC TAT CT	TAT ACT GCC AAA GGT GAC CT	1219, 1220
chr21	17348050	17348299	AAA AGC TGC CTA AAA TGC CA	GAA GCA TAA TGA GAA CCT CCA	1221, 1222
chr21	17351309	17351558	AGT CAG CAA GTT AGC AGA AA	AAC CCA ACT TGC AGA CAA TC	1223, 1224
chr21	17362239	17362488	CCC ACA TTT ATC CCT TGT CC	ATC TGT TTG CTG TGT CAG AA	1225, 1226
chr21	17367713	17367962	TGT CTG ATT CCA TCT TTC CC	TCC AGA TAT ATT CAA AAG GGA GA	1227, 1228
chr21	17506670	17506919	CAG CCA CCA AAA CAC AAT G	AGG TTT TTA TCA AAG CCC CA	1229, 1230
chr21	17548792	17549041	AAG GCC TGT TTT GTG TGT AG	GGC ACT TGA TGT TCT AAG CAA	1231, 1232
chr21	17591325	17591574	ACA GCT CAC AGA TCT TTA AGC	CCT ACA TGA TAC GCA CAG TC	1233, 1234
chr21	17695933	17696182	GGC ATT ATA AAG AGA TAG CTC CA		1235, 1236
chr21	19087043	19087292	TGT TTT TCC TTG CCC TGT AA	GTT TTT CTC TAC CCA GCA CA	1237, 1238
chr21	19178365	19178614	TAA CCA GAT GAA TGA GGG CA	CTC TAA TTT GCC ACC CTC TTT	1239, 1240
chr21	22579319	22579568	CAA CAA GCC AAA ACC ACA TC	GAA CGG TAA AGC TTT TCC CA	1241, 1242
chr21	22605212	22605461	GTT GGT TCT TGA AGA CCT GA	TCT TTC TCC TGC CAA GTA GA	1243, 1244
chr21	22964667	22964916	TCT GGT AAG TAG TCT CTA AAG A	ATA ACA CTG TCC TTC TGG GC	1245, 1246
chr21	22984832	22985081	ACC AAA TTT CCA GAT CAC GG	GAG CCT ACT CTC TGA TAC GA	1247, 1248

FIGURE 2 (Page 39 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	22985386	22985635	AAT GAA TGG TCA TGG CTC AC	CCA GTT GTT CAC TTC TCT GAT	1249, 1250
chr21	36076596	36076845	GCC CTG AAG CAC ATT AAA GT	GCC TTA AAA CCA AAC TGT GT	1251, 1252
chr21	36169368	36169617	GCC TCC AGG TTT ATG ACA AC	CTG GAC TTC AAT CAC CCA AG	1253, 1254
chr21	36789088	36789337	CAG CTC TAT TCC CCT TCT GA	TGA ACA AAT TGC TGT GCT GA	1255, 1256
chr21	37939587	37939836	CCT TGG AAG GGA AAG TTG AT	CCC CCT AAA TGA AAG TGG TC	1257, 1258
chr21	37959766	37960015	GTG CCA CCC TGC TCT TAG		1259, 1260
chr21	37983316	37983565	CAG AGT AAG ACA GTG GGA CA	TGA GTG CTT GGA ATT TTG CA	1261, 1262
chr21	38559539	38559788	AAG TGT GGT GCA TAA AGG AT	GGT TGG CTA CTT CAT GGT AC	1263, 1264
chr21	38751525	38751774	CTG TAA GAA GGA GGG TTT GG	TCA CTG CAT TCC TAG AAC CT	1265, 1266
chr21	39173262	39173511	GAG GTT GAT GAG AGG TAG GG	ATA ACT CAG GCA AAA TGG GG	1267, 1268
chr21	39285267	39285516	AGC CAG GGA TAT TGT TCA AG	CCT TCT GCT CTC ACT TTA CG	1269, 1270
chr21	39330340	39330589	CAG GTA AGT GTG TGT TCC AG	GGA TAC TAG CAG AGG TGG AG	1271, 1272
chr21	39442392	39442641	TTG ATT TCC ATG CAG AAG GG	TGT ACA CAA TAT GCC AGG AAC	1273, 1274
chr21	39499219	39499468	TAA TTT GGC CTT AGG GGT TG	GCA CTT GAG TTA TGG GAC TT	1275, 1276
chr21	39541298	39541547	TCC ATA AAA GGT GCT TAA AGC	TGT GAT ATG TAG TGT GTA TCA GT	1277, 1278
chr21	39563720	39563969	TTG TAT CAC ACC ATC GTG GA	GAA TGT GTT CAA AGG AGG GT	1279, 1280

FIGURE 2 (Page 40 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	39584873	39585122	ACT GCT GAG AAC AAT CAT GC	GAT GAA GGG GAT TAC GGG AA	1281, 1282
chr21	46530377	46530731	GCT GTG GAG AAT TTG TTT GC	TTT AGG AAG CAG CAC AAG AA	1283, 1284
chr21	46534043	46534292	TGA TAT TAG GCG GTG GCT TA	GAG GGT GCT GGG GTT ATC	1285, 1286
chr21	46535763	46536012	TCT CAC CTA AAA TCT GGG GC	CCC GAA AGC ACT TAC CTT TT	1287, 1288
chr21	46537454	46537703	AGG ACT GTG ACA CTT TAT CTT T	TTC ATG AGC TGC AAT GTG TT	1289, 1290
chr21	46542089	46542338	ATG CGA GGT AGA AAA TGA GAG	TGC TAT GAA AAG AGG GAC CA	1291, 1292
chr21	46556856	46557105	TGT GGC TTT AAG GTT CTG AAG	GTG CTG GAT CTA CAC GTG AA	1293, 1294
chr21	46564465	46564714	TGG TTG CTA TTC TGC TTT GA	GTA AAT CTG TGT GCC AGC AA	1295, 1296
chr21	46567255	46567504	TCC CTT TTG TGG TTT CTT GG	TAA AAG AGG CGT GTG GAA AA	1297, 1298
chr21	46572969	46573218	TTG CCG CAC TCT TCA TTA AT	CCA GTA GCT TGT GAT GTG TA	1299, 1300
chr21	46605329	46605578	ACT GGC TTC TCC TCA TTA GT	TAC AGG CCT CTG AAA GAT GA	1301, 1302
chr21	32134809	32135058	ACT GAT TTG CCA TGT AGA GC	AGA GCA TGC TAG AGG TCT TT	1303, 1304
chr21	32148136	32148385	GAA TGT CAT ATT GCC TGC CA	CTG GGC TGT AAT TAA GGC TC	1305, 1306
chr21	32165994	32166243	TCA CTC GCT TAG AAT GTT GC	AAC ACC TGC ACA CTT TGA AA	1307, 1308
chr21	32174173	32174422	ACC ATT AAC TTC CTG CAA ACT	AAT GAA CTT TGT GGG CTG AA	1309, 1310
chr21	32179882	32180131	TAA AGC CCC ATA CCA GGA TT	CCA CAC TCT CAC TGG TTC TA	1311, 1312

FIGURE 2 (Page 41 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	32181384	32181633	CCA AAA ATC ACC CAT ATG CG	CAC AGT GGA TAC CTC AGG AA	1313, 1314
chr21	32184463	32184712	ATA ACC CAG GTG CTT CAA AG	CCA ACA CAG GAG GAA CTT TT	1315, 1316
chr21	32201994	32202243	TCC ACA GCA GAA GTA ACG A	GAG AAA AGC CAA CAA AAA TGT G	1317, 1318
chr21	32208609	32208858	AGG AAA GCT ATG AAG AAA GGG	TGT CAT TAC TAG AAG CAC CTT T	1319, 1320
chr21	32319600	32319849	AGC TCC AGA GTG TCA GTA TT	TGG TGT GAG TTC AGG AGG GTT TA	1321, 1322
chr21	35034581	35034830	TTG ATT TCC AGC ACT GAA CTT T	ACC ATT TCT GAC AGA ACA GA	1323, 1324
chr21	35060177	35060426	TGT TTG ATT TTT CAG GCT GA	TGA TGC TTA AAC ACA TGC CT	1325, 1326
chr21	35070605	35070854	CTG GTC ATT CCT GAG TGT CT	AAG GGA TAT GCA GCT TGT TC	1327, 1328
chr21	35093305	35093554	TCC TGT TTT ACA CTT TTC TAA CTT T		1329, 1330
chr21	35094930	35095179	ACC TCA ACC TGT TTT AGC AC	GTT GTC ATT CAA ATG TCA CCA C	1331, 1332
chr21	35099418	35099667	CAG TGT GTG TCA TGC CAA AT	CTC AGA TTC CAG AGC CCT C	1333, 1334
chr21	35138457	35138706	GGT CTA TGT TAA TCT TGG GCC	ACA TTG CTA GCA GCT TTT GT	1335, 1336
chr21	35152877	35153126	AGC CAG TCT GTA TCT AAA GGT	ACT TGC CAA GAA CAG TAT CTG	1337, 1338
chr21	35157173	35157422	ACT CTT GGG GTT TCT TCA GT	TTC CTT CTT CCA GGT GAA CA	1339, 1340
chr21	35161795	35162044	CGA ACC AAA AGC AAA ATC CTT	TGT TTC TCC TTC ATC TGG TC	1341, 1342
chr21	35296082	35296331	AAT CTA TGG AGG TCA CTG GG	TGT CAC CTT GCA GAT ACA GG	1343, 1344

FIGURE 2 (Page 42 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	35450331	35450580	AGG TCC TTG TAG TTT GCT TG	ATT GTT CAC AGG GTC AAG TC	1345, 1346
chr21	35473022	35473271	GTG AGA GCC AAT AGA GTG TG	ATG AGC CAG GAG AAT CAT CA	1347, 1348
chr21	35473971	35474220	GCA TGG TGT GTG AAA GTG AT	CAT CAT TTC AAA GGG GCT CA	1349, 1350
chr21	35498164	35498413	ATG CTG CTT TTG ACT GAT GT	TCT TCT CTA ACA CCC ACT CC	1351, 1352
chr21	35540943	35541192	CGA AGC TGT ATT CCT GTC TC	ACC CTT ACC AAA GTA GCA TC	1353, 1354
chr21	35702965	35703214	ATG GAC TAA CTG CAG AGC G	ATC AGG ACG CCT TGT TTA TT	1355, 1356
chr21	28574819	28575068	ATG TCC TGC CAG TAA ACA CA	ACT TTC CTG CCA ACA ATC TC	1357, 1358
chr21	28586377	28586626	TGC CAC TAA ACA CCT AAG GA	TTG ATA GTT GCA TCT GGG GA	1359, 1360
chr21	28597009	28597258	TTG GAA ATT TTG GGG TCA GG	TTT GTT AAC TAA CGT GAT TCC A	1361, 1362
chr21	28616121	28616370	TTG TGA CCT CCC TTA CTG AG	CCC ACT CTC CAT GTG TTC TT	1363, 1364
chr21	28631408	28631657	TAT GTG CTT GCG ATG TGT T	TCC TGC TTC AAC TCA ATA CG	1365, 1366
chr21	28891355	28891604	GAA CCT TAG GGC CAG TCT AT	ACC CCT CAT TTT CGT ATG TC	1367, 1368
chr21	28892223	28892472	AGA ACC TGA TGT GTT TTC CTC	ACA GTT ATG GAG GAA TTG CG	1369, 1370
chr21	28919446	28919695	ATG TGA GAG AAG CAA AAC CC	TCA AAC CTC TTT TAT CTG TCC C	1371, 1372
chr21	29012106	29012355	GTA GTT GTC TTG AGG GCT TT	ATT TCA CGT AAC ACT CTG GT	1373, 1374
chr21	29021007	29021256	CCT GGT CAA CAA CAT ATG GG	CTC TGG CAA AAC TTT CTG GAT	1375, 1376

FIGURE 2 (Page 43 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	29753618	29753867	AGA ATA TTG CAT TTG GCC AGA	GCT TCT CAT GCT CAC ACT G	1377, 1378
chr21	29796479	29796728	AAA GCT ATG CAA ATA GTG GCA	AAT ATG ACT TGC CCT TTT GAA	1379, 1380
chr21	29812165	29812414	AGT TCC CAA CAG AGG CTA AT	TCA CAG CCA GTT ACA CAG A	1381, 1382
chr21	29813966	29814215	AGT TAT AGG TGA GGA AGG GC	CTA CAG TGC AGA AGA GTC CC	1383, 1384
chr21	29814951	29815200	CAC TGC AAA AGA AGG AGG TT	TTG GTT TCA TGT GGC TTT GA	1385, 1386
chr21	29820028	29820277	TCT CAA CAT CGC TGA TCT AGT	TCC TTC TCC CCA ACT TTC TT	1387, 1388
chr21	29825992	29826241	AGG TAG CTG GAA AAG GAG AA	CTT TAG ATT CCA GGG CTC TTG	1389, 1390
chr21	29827616	29827865	TGA AAT TGC CCA GAA TTG AGT	TGA AAG CGT GAA AAT CAG CT	1391, 1392
chr21	29841662	29841911	ATT TTC CTG GAC TTC TGA CA	ACT CGA TCC CTA GGT AAT GT	1393, 1394
chr21	29884231	29884480	TGT TAT TCC TCT TCC TGT CCA	ACA AGT GGG TAG GGA TGT TC	1395, 1396
chr21	29898255	29898504	TAA CCA CAC AAC TAC AGC TT	GCA CAA GTT TTC AGG GAA TG	1397, 1398
chr21	30368230	30368479	ATT CAA AAT GGG GAC GAG AG	GTG GAA AGT CTC GTC AGA AT	1399, 1400
chr21	30413906	30414155	TCC CAG TTT GCT ACT CTG G	TCC ACC TCT GAG CAT AAC AT	1401, 1402
chr21	30415555	30415804	TCT CAT TAT GTG AAG ATT GCT TTC		1403, 1404
chr21	30428953	30429202	TTA AGA TTA AGC AGT CTT CTT GG		1405, 1406
chr21	30477650	30477899	CAA CAG ATC TGA TTC TGC CC	CCA TCC CAC TTC TCC AGA TA	1407, 1408

FIGURE 2 (Page 44 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	30528161	30528410	CAT GTG TTT CAA AGT TGG CT	CCA CCT TCC TGC TTA AAG AA	1409, 1410
chr21	30550132	30550381	ACT ATA GCA TTA GGG TGA GGG	CTC CTT ACT TGC ACT GAG TT	1411, 1412
chr21	30580738	30580987	GAG ATT TGG ACA TGC TTT CA	GGG AAA ACT TAC GGG AAC TT	1413, 1414
chr21	30600446	30600695	CCC ACC ACC AGT TGT CAT C	TAG AAA TGT TTA GGG TGC ATG A	1415, 1416
chr21	30628668	30628917	GCC ACT CAC TTC CTA GAT AAT	TAC CCC TCT TTT CCA TCT GC	1417, 1418
chr21	30660609	30660858	ACA CTA TCT CAG GGC CTT AT	GCA TTT TGA CAG GAA AGT GG	1419, 1420
chr21	30680391	30680640	TCA GTA GTT CCT CAG ATG CTA	TAG GGC CAC AGT TTC TCA AT	1421, 1422
chr21	30720214	30720463	AAT GCA TGA AAG TCC AGG AA	GAA TGA GAA ATC TGG CAG GA	1423, 1424
chr21	30782462	30782711	ACA TGC ACT CTT GTC TTA TGC	TCA GAT GCC TGA TGA CCA TA	1425, 1426
chr21	30810199	30810448	CAC ATA TAC TGG CTT TCT GGT C	AAT ATG CAG TGG GTA GGA GC	1427, 1428
chr21	30849402	30849651	GCA CAT GTC ATT AGC AGG G	GAC AAC AGC TGA CTT CCA TT	1429, 1430
chr21	30868525	30868774	ACA TGC TCA ATT ATG GAG CC	CAC TCT CTG GAA CAA ACA CA	1431, 1432
chr21	30988776	30989025	ACA AAG ACA GGA ATA GGG CT	GTT TTG AGG CGG TTT CAT GA	1433, 1434
chr21	31012406	31012655	CAA TCT GCT GAC TTG CTT CTT TTC A		1435, 1436
chr21	31032720	31032969	CTT TGG CTC AGA ATC TTC CAA	GAA CAC CTC AAA GTT GCT CA	1437, 1438
chr21	31085356	31085605	TGT ATG AGG ACC AGC AGT AAA	AAG AAG CAA GGA CAA GGA TG	1439, 1440

FIGURE 2 (Page 45 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	31494755	31495004	TCT TTT CCC CTT GTG CAT AG	GAA ACA ACC ACC ACA ACA AA	1441, 1442
chr21	31560667	31560916	GCT TAG TGT GTG TGA TCC GT	CCA CCA TGT TTA CAC GGT TT	1443, 1444
chr21	31605973	31606222	ACT CAC CTT TCC CAA GAA GA	TTT ACC CAT GAA TTG CTG CA	1445, 1446
chr21	31621826	31622075	TGG TAG TGG GAA GAG GTT GA	AGT TTG CAT TTG TTC AGG GA	1447, 1448
chr21	31653822	31654071	GCA TGG AGA ACA AAA GCT GA	TTC GGA TGG CTT TGA TTG TC	1449, 1450
chr21	31670830	31671079	TCT GAG CAA GAA ACT GAA GG	CAT TGT AAA TTA AAC GGC CTC	1451, 1452
chr21	31691347	31691596	AGT ATC ACT TGT CCA GCT CA	CTA ATG CAA GCT GCT TCT CT	1453, 1454
chr21	31708936	31709185	CAC AGG ACT AGG TAG GCT TT	TGT CTA GTG GTA ATC TGG GG	1455, 1456
chr21	31733443	31733692	GTG TTA ACA GCT TTC CCT TCA	TCT GGA CAG TGG AGT TGA AA	1457, 1458
chr21	31768996	31769245	TCA TGT ACA GAA AGA ATT AGC CT		1459, 1460
chr21	31886189	31886438	ACA GGC CAA CTG ACC AAA TA	AGG AGA CAC ATA ACT GGT CT	1461, 1462
chr21	31886808	31887057	AAG CCA GTA ATT CAT CTT CCC	ATT GCA ATG TCT CTG GAT GT	1463, 1464
chr21	32119833	32120082	CCA TGA CAT AAC ACA TCA CCA	AAG AAG TTG AGG TAG CAC G	1465, 1466
chr21	32125263	32125512	ATA GAT TTC CTC CTG GGC TG	AGT GTC CTT TCC TCC AGT TC	1467, 1468
chr21	25795207	25795456	CCA CCT CTG TAC CCA CTA TC	TTG AAC CTG AAA GGA ACT GTG	1469, 1470
chr21	25802273	25802522	TTC CCT GGA AGA TAG CCA AT	GCT CAA TCA CCT GTT CCC TT	1471, 1472

FIGURE 2 (Page 46 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	26355452	26355702	TGG ACA CGT AAA AGA AGG TG	CAT TGA AGC TCA CTC TAA GGG	1473, 1474
chr21	26365770	26366019	CTG AGA ACC TTG TCC AAC TG	CTA AAG TTT GGG TTA GGG GT	1475, 1476
chr21	26373440	26373689	TTT CGC TAG TCT TTG CAC TT	TGC CTT ACA TTT TCT GTG GG	1477, 1478
chr21	26374774	26375023	GGG GCA ATA ATT GTC ACA AA	GCC ATA AGA TTT CCC CAC TC	1479, 1480
chr21	26390279	26390528	CAG AAA TGT GTC AGG CTA CA	ACA AAG CAA GAG GAT GAA ACA	1481, 1482
chr21	26390951	26391200	AAC TCT TCA TTT TGA CGG GG	CAA AGC ACC ATC AAC ACT TA	1483, 1484
chr21	26402802	26403051	TGG GTT GTG CTG TTG TTT AG	CAC TGC AAC TCC TAG AAT GA	1485, 1486
chr21	26496769	26497018	GCT CAG CTC CTT TCA TCT G	TGT GGG GAA ATT GCT GTT TA	1487, 1488
chr21	26515400	26515649	AGG ACA TTC AGC CTA TTT GC	GTA TGG GCA GCT GTA ACT TG	1489, 1490
chr21	26571662	26571911	ACA CAG TAT CAA GGT CAA CA	TCA CAA GCC ACT GAA AAT GT	1491, 1492
chr21	26589786	26590035	GCA GAA CCA CAG TCT ATG AG	TCT ATG TTA AGC TAG CCA ACA	1493, 1494
chr21	26604824	26605073	AAT GCT CCA AGT TAT TCC AGA	TGT GTT ATT GAA CTT TGC CA	1495, 1496
chr21	26933670	26933919	AAG AGA GAA GCG ACA AAA CC	TTC ATC CCT ACC TCA TCA CC	1497, 1498
chr21	26950703	26950952	AAT GAG AAG GAA TTG GGT GC	AGA TCA CTT TTG GCT GTA ACC	1499, 1500
chr21	27045134	27045383	AAT GAA GTG TTA GGG CCA TC	CAA GTG ACA ATC TCA GCC AA	1501, 1502
chr21	27398390	27398639	GCT CAT CAC AGT TTA AGG AGT	GCA TTT TCA GAT GGT TCC CT	1503, 1504

FIGURE 2 (Page 47 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	27441346	27441595	ATG TGG AAG CAA GAG AAA GG	ATG GAG AGT TTG AGT GGA GT	1505, 1506
chr21	27465490	27465739	TGA AAG GTG AAG TGG CTT TT	CTG CCA CTG GGT TTA TAG AAA A	1507, 1508
chr21	27485182	27485431	GTA AGT AAG GGG TCC TAG CT	ACA CCT TTA CTC CTG TGG AT	1509, 1510
chr21	27486006	27486255	TGT GAC TTC CAT GAA ACT GG	GAT GTA GGG CCT TAT CCA CA	1511, 1512
chr21	27502429	27502678	GCT GAC AAA CTA AGC TTC CA	AGC TTG GTG ATC TTC AAA CA	1513, 1514
chr21	27520192	27520441	AAA ACC TCC CAA AAC AGA CT	TGA AAT GGT GGG TAA TGC TC	1515, 1516
chr21	27539803	27540052	AGT TTA GTG GCC ACG TGA AA	CAT GCA AGT TCA CGA GGT TA	1517, 1518
chr21	27623130	27623379	GGC AGA AGT TTC AAT TCC CT	AGT CTG AGG AAG AAG CAA CT	1519, 1520
chr21	27623692	27623941	AAA GCC TCT GTT TGC ACT TT	GAG TCC AAT CTT TTC CCA CA	1521, 1522
chr21	27763679	27763928	TCA GTC AGC TTC TTG AGT CA	TCC ACT GCG TTC TTA TCC TT	1523, 1524
chr21	27894000	27894249	TGT TTC ATT TGG GTC ATG GA	GGA CAG AAC AGC TAC AAA GG	1525, 1526
chr21	27926498	27926747	TAC AGC ACT AGG ATC ACT CTG	CTG GCT TGT GAA TTA GAG GG	1527, 1528
chr21	28077177	28077426	ATG CAT GTT TCT TGC AAA GG	GTA AGA TGG TGG GCA GGA T	1529, 1530
chr21	28122462	28122711	GTA GGA TTC AGG GCA TTT CA	AGA AGG GCT CAA AAC ACA TC	1531, 1532
chr21	28161337	28161586	AAC TGG AAC TGA GCG TGA G	TCA TGT AGG CTT TCT GAT TTT	1533, 1534
chr21	28180925	28181174	TGT ATG CAG TTA CCT CCA GA	TGT AGC TCT TGA CCT AGC AA	1535, 1536

FIGURE 2 (Page 48 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	28275754	28276003	GGA TGT ATA CCA GAC CCC TT	TAA GTT CAC GGT GAA GTC AAC	1537, 1538
chr21	28291449	28291698	CGA AAG ATG TTA GCA CCT CA	GTG GCT TCA ACT AAC TGG AC	1539, 1540
chr21	28294820	28295069	AAT TGG CTT TGC AGT GTT TC	ACC CGT AAG TGT TTG AGT GA	1541, 1542
chr21	28295351	28295600	GCT TGC TGG TAG GAG GTA TA	TGT AGA AGT AGG GTT TGC GT	1543, 1544
chr21	28295857	28296106	CTG GAA ACC GAA GGA AGT TG	CAG GGG ACA TTT GAA GAT GG	1545, 1546
chr21	28311866	28312115	CTG TGT TCA GTA AGT GGC TG	GAA ATT GTG CAG TGA AAG CA	1547, 1548
chr21	28334784	28335033	GAC AGT GAA GTG TGA TGG TT	ATG TAA GAA GTG CGT TGC TTA	1549, 1550
chr21	28354814	28355063	TGG TGA TGC TGT TTT GGA AA	AGA TCT GGA ATC TGA GAC TCC	1551, 1552
chr21	28415341	28415590	TTT TTT CAG GCA GAA ATG A	TAT AGG ATA AGG TCA AGC AGG T	1553, 1554
chr21	28433186	28433435	AAG TTC CAT TAC TGT ATT GAA AAT T		1555, 1556
chr21	28450226	28450475	GCA CGT ACC TGC TTA TTT CA	TCA GTG AAT CAG GAA TCA TGC	1557, 1558
chr21	28474083	28474332	CAG CCT GAT ATT CCC ATT GAG	TTC TCA GGA GTA CCA CAA GC	1559, 1560
chr21	28491062	28491311	TCA TGA GGC TGA GTG AGT AT	GGA TGA AAC ACA GAA CCA TG	1561, 1562
chr21	28509439	28509688	AAA CCT CTC CTA TCT CCA GT	CAG ATC CCT TTC ATT TTG CA	1563, 1564
chr21	28534176	28534425	ACA AAG ACT CTG GAC TAT CCT	GGA AAA CTG CTC AAT TAG GC	1565, 1566
chr21	40042441	40042690	TGC CTA AAA ATA CCC AAA GCT	CTG GCA GTT ATA GTC ACC AA	1567, 1568

FIGURE 2 (Page 49 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	40427338	40427587	CCA AGA CAC TCA CTC CAA AG	AGG AAG TCC TTA TGA TGC CA	1569, 1570
chr21	40509976	40510225	CCA GGA AAA GGA GCA GTT TT	GCT GGT GAA GTT GGA GTT TT	1571, 1572
chr21	405311291	405311540	GTT CAA CTC TTT CTG CGA AC	GCT GGG TTT AAG CCA CAT AT	1573, 1574
chr21	40578323	40578572	CCA CTT CTT CTG TTT CCA AC	TGT AGC CTA AAT AGC AGC CT	1575, 1576
chr21	40601158	40601407	GGG AAG GGC ATG CTA ATC A	AGG AAT TGC TTT TAT TTT AAC CA	1577, 1578
chr21	40630577	40630826	TGT TCA ATC ACC TCT CCA TC	GCT GCT TTC AGG TTT TTG TG	1579, 1580
chr21	41280723	41280972	AGA GGA GAG GCT AAG CTT TG	ATG GTG CAG AAA AGA GCA AT	1581, 1582
chr21	41607273	41607522	ACA AGA GAG GAA GCT GTC AG	GTG TGG TGC CAT TTT CTT TC	1583, 1584
chr21	41629820	41630069	AGC CCC TTT CTC CTT ATT CT	GAA CAA TAC TTT CTC CCC GG	1585, 1586
chr21	41703462	41703711	AGG GAA GCA GGA TTT TAA CG	GAA ATG GCC ATG CTA GGA AT	1587, 1588
chr21	41729089	41729338	AAG TTT CAC AAT ACC CAG GT	ACT TCC AGT AAC ATG GAT GC	1589, 1590
chr21	41761636	41761885	TCG CAG AAT GGA CAA GTA CT	GAA ACA CCC AGA CTT GTA GC	1591, 1592
chr21	41839021	41839270	GGC TCC CAG ATT TTG ATC AT	TTA AAT CTT TGT GTG CGT GT	1593, 1594
chr21	41908902	41909151	CCT AGA ACT GCA AAA CAC CT	CCT CCA GGA ACT TTG TTC AG	1595, 1596
chr21	41933321	41933570	TTG CAT TAT TTT CTC AGC GGC	AAA AAC CTT CAC AAA CCC CA	1597, 1598
chr21	41981868	41982117	CAG TCC AAC AAA GAG GTC AC	GAG TGG ATA TTG TCT CGC TG	1599, 1600

FIGURE 2 (Page 50 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	42029142	42029391	TTG TGT GTG TTG AAG CCT AG	ACT AGC CCA CTA ATG TTG CT	1601, 1602
chr21	42030642	42030891	AGT GGG GGT AGG AAG AAA AA	CGA TTA TCA GAA CAG ATG AGG T	1603, 1604
chr21	42080190	42080439	GTT CCA ACA ATG TAA GGC AC	ATT GCA CAG CTG AAA ATC CT	1605, 1606
chr21	42251219	42251468	GGA ACC CTC TAT GGT CAA AG	GGC ACA CTG ACC GTA TTT AT	1607, 1608
chr21	42559559	42559808	ATT GCT GTG TAG TTC CTT GA	TGG TAG TGG GTC AGG AAT TT	1609, 1610
chr21	42601828	42602077	TTT CTT GCC ACC ATT CTG AC	TCT CTT GAA AAG AAA GGC GG	1611, 1612
chr21	42851340	42851589	CAC ACG TTC TAA CCA AGT GC	TGA ATT ACA CAG CAA AGC CC	1613, 1614
chr21	42872713	42872962	TAG CCA CAT CTT AAC AGA CCT	CTG CCA ATG GGA TCG AAT TT	1615, 1616
chr21	43032728	43032977	ATT CCT GAG GGT GAC ATG AA	GAG TGA CGC TGT TCA TTC TT	1617, 1618
chr21	43406661	43406910	CCT GCC CCA TCA ACT TAA AA	GAT AGT AAC CGG GTG TAG CA	1619, 1620
chr21	46521300	46521549	CTG GGT GCA GAG GAT CTC		1621, 1622
chr21	16323548	16323797	TTG AGT TGA ACT TTG CTT TAG A	TCT AAT AAG GGA TTG ATG GAG TT	1623, 1624
chr21	16330249	16330498	GAA CTA GGA CAC ACT GGG TT	GGG AGA TTT CCT GCT TGT AG	1625, 1626
chr21	16332622	16332871	CAA GAA TAG CTA ACT GGT GCT	AAT CCA TGC AGC TTC TCT CT	1627, 1628
chr21	16333315	16333564	AGT TAC ACA CTG AAT CAT GGG	TGC ATT GTC TCT GGT TTG AA	1629, 1630
chr21	16335355	16335604	CCC ATG TGG CTT CAC TAA TA	TCC TGA ATG CAT CCT TAA CC	1631, 1632

FIGURE 2 (Page 51 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	16344361	16344610	GAT TGT GGT CAC GTG GAG AG	TGG GAA AGG TGA GAA GGA TT	1633, 1634
chr21	16349606	16349855	CAG ATC CAG GTA TTC GGA GA	TTC GGG ACC CAT ACC TAA AA	1635, 1636
chr21	16358650	16358899	ACA ACA ACA ACC ATT ACC CA	TCT TTT CTG GAC CCA CAT GA	1637, 1638
chr21	15713251	15713500	TGG CCA TAG TAC TGC TTG TA	GAC CTC TAC ATC TGT ATC TTC C	1639, 1640
chr21	15714357	15714606	TGT CTC ACT GTT GGG AAC TT	CCC TTC ATT TTC TGT CCC AT	1641, 1642
chr21	15725977	15726226	TTT CTC TGT ATC CTA TGC CC	TCA GCC TTG AGT ATT AGG CTA	1643, 1644
chr21	15731366	15731615	GCT GAC AAA ATT GGA TCC CA	AAG TTT GCC ATG AAG GTC AT	1645, 1646
chr21	15816232	15816481	AAA ATC CTC CTG AGT CCT CT	GAC TTC TGG TTG TTT CCT CA	1647, 1648
chr21	15843963	15844212	TTC ACT GGG CTC TTC AGC TA	ATG TGT CTA TTG CCC TAC CT	1649, 1650
chr21	15858450	15858699	AAA GGG CAG GAG TTA GGT AA	TGC GGG AAG TTC ACA TGA A	1651, 1652
chr21	15859015	15859264	AGG CAT AAG AAA CCA GGT TG	GTG AAC TTC AGG CTG CTT A	1653, 1654
chr21	16002625	16002874	GTA GTT CGG TCC AAT GTC AG	TGG TTT CGT CCC GTA AAT AG	1655, 1656
chr21	16030414	16030663	GAT GGT CAC AAT TGC AGG TT	AAT TCC TTT CAA TGC TGG CT	1657, 1658
chr21	16063119	16063368	GCC AAA GAT CTC AAT TGC CA	AGA AAG ACA CAT ATG CCA TGG	1659, 1660
chr21	16068358	16068607	GAC CAA GAC TGT CTC TGC TT	TTG TTG GTG TCA GTT CTG AA	1661, 1662
chr21	16071495	16071744	TAA TGG TCA AAT CCC TCT CAA A	TGT AGG AAC AGA TTA GGG CA	1663, 1664

FIGURE 2 (Page 52 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	16081282	16081531	CAT GTA GGC TGA AGA CTC CT	CTC CAA GCT GAT ATG CCA TC	1665, 1666
chr21	16115078	16115327	TTT CTC TCC AAA CTG GTT GC	CCA CCC CTC ATT TCT TCC TT	1667, 1668
chr21	16122085	16122334	TAC AGG CAA GAA ATA GTG TCT	GGG TCC TTC GTT TTC TGT TT	1669, 1670
chr21	16130688	16130937	TTC AGC AAG AAT GGG GAT TC	TAG GAA ACA GGC TAA AAG GGA	1671, 1672
chr21	16133865	16134114	CAA AGA GAG AGC CAT CAC AG	TAC TGT GTA GAA GGC AGT GT	1673, 1674
chr21	16139969	16140218	TGA GAA CAC TGC TAT TTC TGC	GCT AAG GAC AAA GAA CCA CT	1675, 1676
chr21	16141592	16141841	GCA TGG TCA GGA CAT TGG		1677, 1678
chr21	16160517	16160766	GAT TGA ATC AGG AGG GAA GC	TGG CTA AGA CCA GGA TTG TT	1679, 1680
chr21	16165861	16166110	AGC TTA AAT GAT GAA GTG CTT TC		1681, 1682
chr21	16189746	16189995	TTC TCC TAC GTA TCT TGG CA	TGA TAG GCA GAT CAT TCC CC	1683, 1684
chr21	16190806	16191055	ACC TGG GAC ATA ACC TTG AT	GCA AAT GGC AAA GGG AAA AC	1685, 1686
chr21	16192618	16192867	CCA TTT TCC TAC TGC GTG TC	CAC GGC TAG TGC TCA TTT T	1687, 1688
chr21	16195809	16196058	GAA CAT ACC AAA CCC ACT GG	CCG TAA TAC CCA AGT CAT CTG	1689, 1690
chr21	16198337	16198586	ACC CAA TGA TGT ACA GTT CC	AGC AAA CTA AAA CAG CAA CTT C	1691, 1692
chr21	16203731	16203980	ACC TAT TCG ACT TGA AAC TCA G	AGC CTG CTA TCT TCA CTG G	1693, 1694
chr21	16207035	16207284	ATT TCT GCA CAA CTG TTC CA	ACC ACA TAT ATA GAG ACT TTG AA	1695, 1696

FIGURE 2 (Page 53 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	16209341	16209590	GCT GTA ATG TGA CTA ACC CT	CTC CAG ACT CTG CAA GGA T	1697, 1698
chr21	16211270	16211519	TTT CCC GAG GTT CAC AGA TA	TTT CCT GTT GCT CTT GAT CA	1699, 1700
chr21	16219907	16220156	GAA CTT GTG TGA CCC AAA AC	CCA CAA AGA TGA AGG CCA AG	1701, 1702
chr21	16230785	16231034	CAT TGC ACT GTG ATG TCA TG	CCA TAC CTT AGT TCT CAG GGT	1703, 1704
chr21	16236026	16236275	GCA CTG GAA ATT GAC ATC AC	GTA AGA GAG AGC TGG GAC AA	1705, 1706
chr21	16241139	16241388	GGG AGA GGC TGA AAG AAG AA	TGT GAC CAT CCT ATC CAC AA	1707, 1708
chr21	16242812	16243061	TGT ATC ACT TCC TCA TGC CA	AGA ACC AGT TGT AGG AGT TC	1709, 1710
chr21	16246944	16247193	CCA AGA GTT TCC TGT TTC CA	AGT CTT CTC CCT TCC TTG TC	1711, 1712
chr21	16265484	16265733	ATG ACA CAT ACA TCC ATT TAC A	GCC CTT TTC TCT CTT TGA CC	1713, 1714
chr21	16273734	16273983	CTC AAA CTG CCC AGT GAT TT	TCT TGT TCC AAG TAT TCC TGG	1715, 1716
chr21	16275865	16276114	TCC TAG CTT GCC AAA GAA AT	ACC ACT TTA GCC CAT CTC TT	1717, 1718
chr21	16290234	16290483	CCT CCT CTC CAG GCA TTT TA	GTG GTG GAT TAT TGA GCT GG	1719, 1720
chr21	16295877	16296126	AAC AGA GTA GCA CAG AGA GT	TGC TTA ATG GGA TCA TTG ACC	1721, 1722
chr21	16296687	16296936	TTC AGA GAG ACA GAC ACC AT	CCC ACA TAG TGC AAA AGA CA	1723, 1724
chr21	16298842	16299091	AGA GGA AAA TCA CAA GCA GT	GTA TGT GTG AAG TAG CCG AG	1725, 1726
chr21	16316213	16316462	TTT GAA AAC CCA ACA GAC CT	TGG TCC TAA CTC AGA CCT TT	1727, 1728

FIGURE 2 (Page 54 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr21	16319836	16320085	AAT CCA CAC ACC AAC AGA GG	AAC ATG AAG GGA AGG TTG TG	1729, 1730
chr18	64634331	64634580	TGT TCA CAT CTG TTG GTT TGC	TAT ACT TCA ACT TGC AGG CAG	1731, 1732
chr18	64645925	64646174	GTT ACT CGG TGG GTG ATA TTT	GCC AAA GAC AAT GAG AGA GTC	1733, 1734
chr18	64975938	64976187	AAG AAA CAC CAG CAT CAG TTC	ATT TAG CAG CCA TGA CCA GTA	1735, 1736
chr18	64996573	64996822	AGG TTT AGA GGT GAG TGA ACA	TGG GCC AAT TCC TAA TCC ATT	1737, 1738
chr18	65066425	65066674	AGA AAC TTC ACT GTC TTC CAC T	CGA TCT CAT GAA TAA GTC TGA CC	1739, 1740
chr18	65073729	65073978	TGT GAT GGA CAT TGG TAC CTG	TGG AAA GCA GAC TAA CAG TGA	1741, 1742
chr18	65074170	65074419	ATA TCA TCT GCC TGT CCC AAC	GGG ACC CTA TGT AGA GAT TGT	1743, 1744
chr18	66343957	66344206	GAG TGC TCT GTG TTT GTT TCA	GGA GCC CAA GGA TGT ATT AGA	1745, 1746
chr18	66344406	66344655	TCA GTG GTG AGC TCT TGA ATA T	CTA ATA GCT GGT TCT GCA CAC	1747, 1748
chr18	66585247	66585496	ACT CTC TCT TCA CAC ATG CAA	GAT GAA ATG AAT GCT GAC TCT C	1749, 1750
chr18	66596489	66596738	GTG TTG AAG TCA GTA AAG CCT	AAA CTG AAG CTT CGA GAA CCC	1751, 1752
chr18	66601231	66601480	TGC TTT CAC ATG GCA CTA GAT	TGC CGA CAA CTA CTT TAG GTA	1753, 1754
chr18	69966208	69966457	GGA GAG AGA AAT CCC AAC TGA	TGT ATC CAA TCA CCT GTC AGA	1755, 1756
chr18	70089188	70089188	GGG AGA TGT CAA CAC TAG GTC	CAG CAC CTT AAG CAG AAA TCA	1757, 1758
chr18	70093364	70093613	ATA TGA CAT GGT GGC TCT CC	AAG CCC TTC ATC CAT TTC TCT	1759, 1760

FIGURE 2 (Page 55 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	70107935	70108184	AAC ATA GAG CCA TGG GAG GTA	ATC TTG GTG CCA TCT TAA GGT	1761, 1762
chr18	70198868	70199117	GAT AGC CTT CAA ATC ATG CCT	AGC AAA CCA ATC GCA AAC TAG	1763, 1764
chr18	70200128	70200377	GAA AGC GGG TGA ACA ACA ATA	AAT CAT CAT CTT CAT CAG CTC G	1765, 1766
chr18	70200907	70201156	GAT AGA GAG CAC AAA GAG CAT	CCT TTC GCC TTG CTT ATA TGG	1767, 1768
chr18	70674976	70675225	AAC AAG AGG AAT AGG AGC CAG	ACT ACT CAA CAG CCT ACC AAA	1769, 1770
chr18	70682967	70683216	TGG GTG CTG ATA GTA ACA AAG	TGG AGC TGG GAA CTT TAA TGT	1771, 1772
chr18	73541191	73541440	ACT ATT GAA CTG TTG GCT TCG	GAA GAG AGA GAG AAT GCG TGT	1773, 1774
chr18	73548315	73548564	TCC ACT AAA GAG CAA CCA AAC	GAC ATG GAT ATT CTG GTG CCA	1775, 1776
chr18	73605288	73605537	TGA AGT GGT CAG TAA CAA TGG	CTG TTG CAA GAT GAC CCA AAT	1777, 1778
chr18	73704485	73704734	ATT TCA GAG CTC CTT TGT CCT	AGA TAC ACA CAC GTT CAC AAA C	1779, 1780
chr18	73752546	73752795	GGC AAA CAA ATC TGG TGT TCA	GAT GGC AAT GCT TGA TAA CGA	1781, 1782
chr18	73764755	73765004	TTG CTG GTT GAT AGG CAT TTG	TTC CAT GAA GTT CCT CAA GAC T	1783, 1784
chr18	73768420	73768669	ATT CCC GCA ATT GTG AGA TTC	CCA CCC ACA TAC CCT GAA ATT	1785, 1786
chr18	73775027	73775276	AAA GAG GTA CAG AAC TCA GAC C	GTA ACA CAC GGA TGC TGA AG	1787, 1788
chr18	73788751	73789000	CTC TTC ATG AAC GTT GCC AAT	TGG ACA CGA GGC TAT TTG TAG	1789, 1790
chr18	73851108	73851357	CTT CTC AGG GCT CTT TGT GTA	GGC TTA AGA AGG AGA GTG GTT	1791, 1792

FIGURE 2 (Page 56 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	73854713	73854962	GCA ACA GAA ACC AAG ATT CCT	TAG TTT CCT TTG GCC TTC TCC	1793, 1794
chr18	73871422	73871671	TCA TTG TCT ACC TCA AAG AGC A	CTA GGG TTC CCA GTT CAC AAA	1795, 1796
chr18	73876103	73876352	CTC TGA AGG AAC AAA GGA TGG	GAA ACA ACA TTG AGG GCA TTG	1797, 1798
chr18	73879805	73880054	CAT TAG AAT GCG GTG GTT TCA	GAG CTC TTT GAA GTA GAA GCA	1799, 1800
chr18	73884248	73884497	GAT GTC TGG GCT GAG GTT TAA	GCA TTC CAA CAA AGC TTC CG	1801, 1802
chr18	73931865	73932114	TTC CTC TTG AAG ATG CAC TGG	CTA CTT GCC CTA TTG TGT CGA	1803, 1804
chr18	73938014	73938263	CCA GCA TGT GAG GAA TTG AAC	CCA GGG TGT TTG AAG GTA GAA	1805, 1806
chr18	73943212	73943461	CCC ACT TAG TCA TCC ACA CAT	CTG GAG GTA AGA AGG AAT GCA	1807, 1808
chr18	73947628	73947877	GTT TCA CAC ACC AGA AGA GAG	ATG TGG GAC TCT TTG CTC TC	1809, 1810
chr18	73964168	73964417	CCA TAC ACC TGC TCT GAC ATT	ATG AAT ACA GCT TTG CAT GGC	1811, 1812
chr18	73966321	73966570	ATC AGT AAC AGT CCC ATT GCT	GTT AAA GCA TTC ACA GCC CTC	1813, 1814
chr18	73974071	73974320	CAT GAG GCA TTT GAT CCA TGG	CTG GCA CTT GTC TAT CCT CCT	1815, 1816
chr18	73985549	73985798	ACC CTG TTT CAC TGA ACA ACT	ATG TCT GTC CAA GTG AAC AGT	1817, 1818
chr18	73987174	73987423	CCC TGT AAT GAG AGC GTT ATT	AAA GTA TCC AGA CCC AGA ACC	1819, 1820
chr18	48466086	48466335	GAG AGA ATG GGT TAA ATC TGC C	ATA GGC CAG CAC TCC AAA TAA	1821, 1822
chr18	48928528	48928777	CTG CCT GAC TTA GCC TTA AAT	CAA ATC AAG TCC CAT GGT AGG	1823, 1824

FIGURE 2 (Page 57 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	48929078	48929327	AAC CAG AAT GTT ACT AGC CCA	CTT TCC GTC TTT ATA GGC AGC	1825, 1826
chr18	48951524	48951773	CAA TCC TGT GTG TTT AGT GGA	AGA AAT CGT GTT CAC AGC CTA	1827, 1828
chr18	48951856	48952105	TGT GGG AAG CAT TGA CTC TT	CCG TAA ATG AAG TGG CTT GAA	1829, 1830
chr18	48959882	48960131	TCC TGT GAG AAA TGG AGC TTT	CCT TTC TTG CAA CCT TGA GAT	1831, 1832
chr18	48960304	48960553	GTT GCC AAG CTT AAA TAC CTG T	CTC TAG ATG CTC AAC CTC AGG	1833, 1834
chr18	49004516	49004765	CCA CAA CAA CAT AAA CAC TGG	AAT AAC AGT CCA CCA GAA CCA	1835, 1836
chr18	49006425	49006674	TCT TCC AGG CAT ATT CAT TGC	TCC AAG GAC CTG CAA ATG TTA	1837, 1838
chr18	49017695	49017944	ATC CAT TCT CTC TAC TTG GGA	AGG TTA CAT CAT TCA CCC ACA	1839, 1840
chr18	49148010	49148259	GGC TAG AGG GTG ATT ATA AGC T	ATG AAG ACA ATG ACA TCT GCG	1841, 1842
chr18	49149627	49149876	TAC TCA TCC CGA TTT CTT CCC	CAC TTG TCA TGG TTT AGG GAC	1843, 1844
chr18	49149933	49150182	TTC TCT TTC TCT TCT GGG CAG	ACC TCC ACC TTA TTG CTT CAA	1845, 1846
chr18	49150459	49150708	TTG TGA GAC TCA AGG CCA TTT	GAA TTG CAA AGG ATG GGT AGG	1847, 1848
chr18	50239403	50239652	TTG GTA GAG AGA GGC CAT TTG	CTG CAT TGT GAG TCC ATG TAA	1849, 1850
chr18	50242789	50243038	GGA GGA AGC TCT TGA AGA CAT	TCC TAT CTT CAT CCC TCT TCC	1851, 1852
chr18	50243069	50243318	AGC ATC TTC CGT TTA ACT CCA	TTT CAT TTA GCC TCC CAT CTG	1853, 1854
chr18	50243367	50243616	CTG CCT GCC AAG TAT GTT CT	TAG CTT TAT GGG CCT TGT TCT	1855, 1856

FIGURE 2 (Page 58 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	50247229	50247478	CTA CTC CTT GTG TCA TTG GCT	CCA CCT CTC AAA CCC AGA TTT	1857, 1858
chr18	50308727	50308976	TGA TTC TGA GAC AGG TGC TTA	GTC AGC CTA TTT GGG ATT GAA T	1859, 1860
chr18	50309031	50309280	CTT GAG GAC CTT TCA TGC TTG	AAA TCT GCC ACC CAT TTC TTC	1861, 1862
chr18	50338747	50338996	TTG TGA TTT CAG GTA GGA GGG	TAT TCT GAG TTC TAC CCA GGT	1863, 1864
chr18	50423284	50423533	TTC CCT CAG AGA CAG TAT CCT	TAC ATG AGA CCC AGA AAC AGA	1865, 1866
chr18	50424422	50424671	AAA GGA GGT CTG GCT TTG AA	CTT CTT GGC AGA CTA TCA GGA	1867, 1868
chr18	50424789	50425038	GCA TAA ACC TGG ACT GTG AAA	AAG CTG CTA AAT CTG TAG GGA	1869, 1870
chr18	50448837	50449086	CAC TCA GCG ATT CTC CTC AC	CTG ACC AGA CCT GTT GAC TAA	1871, 1872
chr18	50449492	50449741	AAA GCC AGA CAC AGA CTA GTT	TGA TAT GTT CAG TTT GCC TAC C	1873, 1874
chr18	50514079	50514328	ATT CCT GGG ACC ACA AGC AT	AGC TTG AGT TTC TTG CTG GG	1875, 1876
chr18	50519889	50520138	TAT TGC CTC ATG TGG TTG TG	TTC CCG CAA AGT AGA AGC TAT	1877, 1878
chr18	56064244	56064493	GTG TTG ACT TGA AAG GAA TCA C	AAA CGC ATA CAA ACA GGA GAC	1879, 1880
chr18	56148666	56148915	CAG GTT AGG AAT GAC AGT GGG	CTT CTA AAC CCA TCA CCT GCT	1881, 1882
chr18	56149037	56149286	TTA GGT TAC CCA GGG ACG TTA	CAC CCA AAC TCA CAG GTA CAA	1883, 1884
chr18	56244171	56244420	CGG TTT GCT TTC TGA ACA ACA	TGA ATT CTG AGA TCG AGA GCC	1885, 1886
chr18	56245242	56245491	CAT TTG GGA CCC TTT GAA ACT	AGA TTA ACT GTT GCC TCA CTG	1887, 1888

FIGURE 2 (Page 59 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	56247063	56247312	GGT TAT CTC TGG GCA AAG TTC	CAA GAC AGT GCA TTC CAT GG	1889, 1890
chr18	56527049	56527298	TAG AGA GCA GAG AAG AAA CCC	CCA AGG AAA GAG TTG AGA AGG	1891, 1892
chr18	56528011	56528260	ATA AGG GCA TTT GGA GGG AAA	TGA GTG CAG TCG ATA AGG AAG	1893, 1894
chr18	56532190	56532439	AAT GCA CAC TTA GAC ACC ACA	AAC ACC GAG AAA GAG AGA GAG	1895, 1896
chr18	56532882	56533131	GGA TTG CTA CCC AGG AGA TAA	TGT ACT GCT TTC GTC TTA TGC	1897, 1898
chr18	56534208	56534457	AGA GGT TCT GTG TAT GAG TGT	CAT ATT CGC ACT GTA TAG CCG	1899, 1900
chr18	56601487	56601736	TAG AGA ATT GTA CGC TGG ACA	CTG ATG GAT TCT CTG GTG TGA	1901, 1902
chr18	56633131	56633380	TCT GGA GAA ATG CAC AAG AGA	TCA AGG AGA ACA GAG AGG GTA	1903, 1904
chr18	56635259	56635508	TGG GTT AGA ACA TGG TGC TTA	TCT CCC AAA GCA GAC AAA GAC	1905, 1906
chr18	56719296	56719545	ATC GCA TCA CAC CCT TAC TAT	AGT CAG TTG TTA CGT GCA AAG	1907, 1908
chr18	58037828	58038077	GGA AAT TTA GCT TGA CAT GGC	AAA GGT TTG TTC ATC CTC CCT	1909, 1910
chr18	58038328	58038577	TTT GTA AAT CCA CAG TGC CTA C	ACA GAG CAC GCA ATA TAG GAA	1911, 1912
chr18	58039111	58039360	GGT ACT GGA GAG CAT AGA AGA	CTG CAT TCA CCC ATG TAC TTT	1913, 1914
chr18	58040290	58040539	AAA CAA GCT ATC TTC AGG CAG	TCC AGC CAT ACC ATG TCT ATC	1915, 1916
chr18	59424085	59424334	CGA ACA ATC AGA GAC TCG ACT	CTC ACT AGG GAA GAA CAG CAG	1917, 1918
chr18	59424765	59425014	CTG GTT GAC AAT CTG CAA GTT	TGC TGG GTC TGA GTG TTA TAA A	1919, 1920

FIGURE 2 (Page 60 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	59441324	59441573	ACC ATC CAA GTC GTC TTC ATA	GTT GTG TGA ATG GTG CTG TTA	1921, 1922
chr18	59499718	59499967	ATA GCT ACG CAT ACC CTG TAG	GGC CCA GAA GAC TCT TGT AAT	1923, 1924
chr18	59500226	59500475	AGC AGA AGA AAC AGT AAG GCA	CGA CCT ACA TCA GCT AAT GGT	1925, 1926
chr18	59507920	59508169	ACC CAG GGA CCT ATT TGT TC	AAG GGA AGA ATA ACA ATG GTG C	1927, 1928
chr18	59543044	59543293	CAA GGG CTC AGG TCT TCA TTA	ATG GGA GTA TGG GAG TAG GAA	1929, 1930
chr18	59556453	59556702	TCA CTG TGA CTT GGA GAC TAA	TTG GTG GCT TGC AGA GAT TT	1931, 1932
chr18	59614976	59615225	TGC TCT GCT TCA CTG TGA TTA	TCA CAC GAT CAT CAT ACT CAC A	1933, 1934
chr18	59625553	59625802	GAT GAA TGA CTA ATA GCC CAC G	GGT ACC AGA TGA CTA GAC GAT	1935, 1936
chr18	59631090	59631339	CCA TGT TTA GTT TGG TGC TGT	ACG CCT CTG TCA TTT CCT AAC	1937, 1938
chr18	59631779	59632028	AGC CAA GTG AGG TGC TAA AT	CAG TTG ACT CAA TGG TGC AAT	1939, 1940
chr18	59632388	59632637	TCA GGG AGA AAT GAT GTC ACC	ATA GGT TAC AGA TTG CCA CGT	1941, 1942
chr18	59695718	59695967	CAG TAG CTG GCA AGA ATC ATC	GAT GCT GCT ATC AAA GGA ACA	1943, 1944
chr18	59696087	59696336	CAA CAC TGC TAG AAT TCC CAA	AAG ACA AAG AGA TGG AAG GCA	1945, 1946
chr18	59696563	59696812	CCT GAG AAG CAC CTG ATT GTA	AAT ACC CTC TTC CCT TCC TCA	1947, 1948
chr18	59712419	59712668	TGT TGT CAG AAA TCC CAG GAA	CCA CCG TCA ATA TTT ATC AGC T	1949, 1950
chr18	59756979	59757228	AAC TGG AGC CAT ATA ACG ATG	GCC TCA GTC CAA ATC TTA GAT	1951, 1952

FIGURE 2 (Page 61 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	59770789	59771038	GAA ATG GTG CCC TAT TGT TGA	CCT TAG GAT TCT CAA AGA GTG T	1953, 1954
chr18	59805993	59806242	TCT TAC ATG CAG TCA TAC TCC T	GCA GTA CAG ATT CTT GAA CAG T	1955, 1956
chr18	59813876	59814125	GTC CCT CAG TAA CAC CAT CTT A	AGA GGA TTA GAT GTC TTG CTG T	1957, 1958
chr18	59855411	59855660	GAA GCA AGA GGA TCA GGC AAT	TAC TGC AGG CAA TTC AGG TAA	1959, 1960
chr18	59909054	59909303	AGT GTT TCA GAG GCT TGA AAG	GAA GAG GTC CAG TAA GTG AGG	1961, 1962
chr18	59909336	59909585	ATC CGG CAT CCT TTA AAC TCT	TTG TGA GTC CTT GTC TCC TTG	1963, 1964
chr18	59910140	59910389	AGG CTA GGA AGA AAT GGG AAA	GAC GAC TAA GAC ATT GCA TCA	1965, 1966
chr18	59910602	59910851	ACA CAT ATG CTC TGT CTC TCA	AGA AGT CTC TCT CCG TTG TTT	1967, 1968
chr18	59973803	59974052	AGT TAG TTA TCA CCT CGT CCC	CTT ATG TGC ATC AAC TGT GCT	1969, 1970
chr18	59996728	59996977	TGT GTA TTT CCC TCT AGT TGC A	AGT GTC TCT CAG AAT CAG GAC	1971, 1972
chr18	60010541	60010790	AGC CTC TTT CTA CAT CGT TCG	TTT ATT TCC CTA CGC AAA GCC	1973, 1974
chr18	60011381	60011630	TTA CCT GTG CAG AAG AGT GAC	AGC CTT TGA TGA CTG ACT TGA	1975, 1976
chr18	60240694	60240943	TCT TGT GTT CTA GCG TGT TTG	TTG GTT TCT ATT CTG CAC TGC	1977, 1978
chr18	60378353	60378602	TGT GGT TAG TCA GAA ATG TGG	TTA GAG CTT GCT AGT ATC GGG	1979, 1980
chr18	60384593	60384842	GGG TCC TGA TGA GTC TTT GTC	GAA ATC CCA AAC TGC CTG AAA	1981, 1982
chr18	60384979	60385228	TGG TGC CTT TGT TTA TTC AGC	ATC CTT CTT GTG AAC CTT CCT	1983, 1984

FIGURE 2 (Page 62 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	60389544	60389793	TGT TAT GTG CCA GGG TTT AAC	ACC AGA TGC ATG TGA TTA AAG G	1985, 1986
chr18	60401084	60401333	ATT GGT TCC AGA TAC AGT CGA	GTG TAC TCT AGG CTA CTG TCA	1987, 1988
chr18	60412199	60412448	GGA AGG AAG TAC AGC ATG GAT	GTG AGC AGC AAG TAA AGG TTC	1989, 1990
chr18	60420053	60420302	CCT TAT TGA AGC TGA CCA TGC	CAT CTA GTC AAG GGT TCC ACA	1991, 1992
chr18	60434561	60434810	CAG TGG GAA ATG TGC TTA CAT	CAA GTC ATG CTC CAA ACT GTT	1993, 1994
chr18	60449047	60449296	AAA GGG CCT ATA TTC ACC AGA	AGG ACT TAG GAC AAC AGA GAA	1995, 1996
chr18	60452471	60452720	AGA GCC ATT TAA GAC TCT CTG T	TGC CCA ACA CCA TCT CTA ATA	1997, 1998
chr18	60456757	60457006	TAC CTT GTT CTC TGC CTC AAT	GCC TTC ATC ACT CAG AAC TTC	1999, 2000
chr18	60467147	60467396	TTT AGA AGG ATG TGG ACA GGG	AGG GTA TCT ATT CTC CGG ACA	2001, 2002
chr18	60469757	60470006	AGC AGG ACA TGG ACT TCA AA	ATT TGC CCA AGT AAG TTC CAC	2003, 2004
chr18	60514168	60514417	GCG GCT CTT GTT TCT GAA ATC	TGG AAG TAC ATG GGA TGC ATT	2005, 2006
chr18	60537888	60538137	ACA GGT AGG AGT TCA GAG ACA	CTT GAA GAG TTC CAA TGC CAA	2007, 2008
chr18	60544380	60544629	TTT CCT ATT CTG CTC TTC TGC T	CGC TGC TGT TTA AAT CGA TCA	2009, 2010
chr18	60544742	60544991	AAA TGC TGC TCA GGG TTA GAG	GCT CTG CTT TGC TCA AAT TCT	2011, 2012
chr18	60545407	60545656	CAA CTT TAC TCT GCA CAG CTC	TGA GCT CCA GAA TTA GAT GTG T	2013, 2014
chr18	60611934	60612183	CAG TGC CAC TAC AAA GAA ATC A	AAC ACC TCC TTT CTC ACT ACA G	2015, 2016

FIGURE 2 (Page 63 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	60617081	60617330	AGA AGC AGA GGT TGG ATA TGG	ACA AAC TTC ATT CAC CGC AG	2017, 2018
chr18	60617641	60617890	CCA CAA TCC CAT ACT CAC CAT	AAC TAC GCC ACC CAA CTA AA	2019, 2020
chr18	60630438	60630687	GCT GGT TCT TGT TGC TGA TAA	GCT TCA GTG TAA CCA TGA CTC	2021, 2022
chr18	60630849	60631098	TCC CTC ACG ACT TAT GTT TGA	TGC ACA ATT AAG CTA CTT CTC C	2023, 2024
chr18	60639840	60640089	CTA CCT TCT CCA GTG CAC TAT	CAA CAC CAA ACT TGC CTG AAT	2025, 2026
chr18	60640300	60640549	GGA CCT CTC TTT GAA ATG GAG	TCC ACA ATT TCT ACA GCA AGC	2027, 2028
chr18	60776944	60777193	TGG GTT GTG TTT CTC TGA CTT	GTG TCA TTT GAT TGG TGC TCT	2029, 2030
chr18	60813738	60813987	TAC AAG CCT CCT TTA ACC CTT	GGG TGT TTC AGT AGG TTA GGA T	2031, 2032
chr18	60814585	60814834	AAA GGG TTT GAT ACA GTT GGG	TGG GAT TCT AAT GTC TGG TGC	2033, 2034
chr18	60938666	60938915	AGG TAT TGG AGA GCA AGA AAG A	AGA GGT GGT TGG TTG GTT	2035, 2036
chr18	60939202	60939451	GCA AAC TGG AGC TAA AGT CAT	GGG CAT CCT GTC TGA AAT ATG	2037, 2038
chr18	60950541	60950790	TTG GTT GCT AGC TCT CAA ATG	AAG AAG CGC AGA TAC AGT ACA	2039, 2040
chr18	60953225	60953474	TTC AAT GCC CTT ACT TCT CCT	CAC AGC AAG TTT GAA CCT AGT	2041, 2042
chr18	60958474	60958723	GCT TGA GGC GCA TAT GAT TG	AGT GCA AAT GAT GAC CTG TTG	2043, 2044
chr18	60960879	60961128	CAT ATG GTG CTT GTT CTG GG	GAA CTG TTG CAT GAG AGG TAC	2045, 2046
chr18	60965583	60965832	CAA ACT CAC CAC CCT TCA TTC	CTT TGT CCT TCT CTG TTG TGT	2047, 2048

FIGURE 2 (Page 64 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	60970051	60970300	CCT TAG CCC TGC AAA TAA CAC	TTT CTT CTA GAG TCC AGA GGT G	2049, 2050
chr18	60974839	60975088	TCA CAG ATA CGG ACA AGC TC	ATT CTC TTC TCT CTT CCA GCC	2051, 2052
chr18	60984378	60984627	GCC ACA GGT ATC AAT CAC TTC	TAT GGC TTT GCT ACC TTG TCA	2053, 2054
chr18	61055997	61056246	GCT TCT GTG GCA CTA ATC AAG	CTA TTT CTC TGG CTC TTG ACC	2055, 2056
chr18	61088669	61088918	GCC TTA TTG ACT TAC TGG ACT G	TTT TTA AAC CTC TGT GTG GCT	2057, 2058
chr18	61090462	61090711	GTC AGG GAT TAG AGG CAG AAC	TGG ACA AAC AAG AAC TGG GTA	2059, 2060
chr18	61100325	61100574	CAA TCA CTT GGT CAG ATA GTG T	CCA TGA TCA CTG AAA CCA ACA	2061, 2062
chr18	61154459	61154708	AGT GGA GAG GTT CAG TAT AGT G	CCA TAT GCC CTG CTC TTT AAG	2063, 2064
chr18	61162901	61163150	TGA GAA GGG AGG AAG AAT GTG	GGG TGG ACA AAG CAA TTC AAA	2065, 2066
chr18	61170629	61170878	AAG GTC AAA CTC TCC ATT CCA	CAG CAT TCA ATT CAT CCT TGT G	2067, 2068
chr18	61197492	61197741	GGA GAT GTC TTT GCC CTG ATT	AAG TAG AAG CAA GCC CTG AAT	2069, 2070
chr18	61213452	61213701	GGT CCT CGT TTG TCC TTA AGA	GTG TGG TAG GGA TGA GAA TTA T	2071, 2072
chr18	61213900	61214149	AGT ATT GCT TTG AGG GCT CTA	TCA GGT AAG CTT GCC TCC AC	2073, 2074
chr18	61216749	61216998	AGC TAT CAT GTA AGT CAC TCC C	ACT GGT TGT AGA AAG GAC CTC	2075, 2076
chr18	61232928	61233177	AGG AAA TTC AGT ACC TCA GCT	ACT AAG AGG CCA GAA GTC AGA	2077, 2078
chr18	61236079	61236328	CAA CCT TCT CAT TGT TGA AGC T	GCA CTG CAG GCC TAT ATA TAG	2079, 2080

FIGURE 2 (Page 65 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	61253277	61253526	GGT GAC TTT GCT TTC CCA AG	AAA TCT CTG AGT CGG CCA TAA	2081, 2082
chr18	61259478	61259727	GCT GAC AAA CGG AGG GAG AG	AGG CAT GGC AAA CTT ACT TG	2083, 2084
chr18	61264533	61264782	TGT TCT TCA TCA GGC ACA ATG	CAT TTC ACT TTC GAG GAT GGT	2085, 2086
chr18	61289440	61289689	ACC ATT TGT GTG ATC CAG AAC	GTC AGA CTA AAG TGA GGA CCA	2087, 2088
chr18	61368889	61369138	CTT GTC TTG AGT GCG GTA CA	CCA GCC CTA CCT AAA GTG AAT	2089, 2090
chr18	61370663	61370912	GCC TCT CAG TTT CCT CTT ATA G	CCC TTT CAC AAG ACT CTT CTC	2091, 2092
chr18	63685629	63685878	CCT AGA TCA GTG CAG AGA ATT TAG T		2093, 2094
chr18	63711583	63711832	CTT TAG TTT GGA GGC CTC ATT C	CCA AAT GTA GAA CAG GAT CAG C	2095, 2096
chr18	63721183	63721432	CTG ACA TCG ATG GAA TTC TGG	TAG CAG TAG GTG TGG CTT TC	2097, 2098
chr18	64379625	64379874	ACA CTG CAC GAA TGG AAG ATC	TTG GAT TCT CTT GGT TGT GAG	2099, 2100
chr18	64398368	64398617	ATA AAC TTG GTG CTC AGT GGT	CAA CGC TTT GGT ATA GTT TGT G	2101, 2102
chr18	64410092	64410341	ACA AGC ATT ACA GAA TTC GGC	CCA GGT GCC ATC GTT AAA GAA	2103, 2104
chr18	64412606	64412855	ACT GAC AGA TTC TCA CCT ATA TCA G		2105, 2106
chr18	64417267	64417516	GGA TCA AAG CCA CTC TAG ACT	GGA TAA GTC AAC TAC CAT GGT T	2107, 2108
chr18	64421562	64421811	TTG AGA TGG CAT CAA GTT CAA G	AAT GGA ATT ACT CAG CTG TGG	2109, 2110
chr18	64426871	64427120	ACT GGA TTC ATG CGT TAT CAA G	GGC AGA AAC TGA TAG AGA CTG	2111, 2112

FIGURE 2 (Page 66 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	64436287	64436536	TAT TCT TGT GTG GAC CCT GTG	ACC ATG TTC TGA GTA CCT CTT	2113, 2114
chr18	64593727	64593976	TGA TAT TGC ATG AAA GTC CCT G	AG TGC TGA ATC AAT GTC TAA CAC	2115, 2116
chr18	24962594	24962843	TCA CAC ATG AGG AGT AGA CA	TGG TCC CTG TGC TTT GAT AT	2117, 2118
chr18	24964748	24964997	CAC AGC AGG AGA CAT GAG AA	TGG CTT TTC TTT CCT CGG TA	2119, 2120
chr18	25003553	25003802	TTT CCT CCT GGC TTG ATC AC	CCA AGG CTG CTT TAA TTC CA	2121, 2122
chr18	25033345	25033594	CAA AGG AGA GAA GTG ACC CA	CAA ACT ATC GCT GAG GAC CT	2123, 2124
chr18	25037434	25037683	CTA CGA GTG AAA CAG AGT GC	GTC TGC TGC CAT TGA GTT AT	2125, 2126
chr18	25052992	25053241	AGA CTA AAA GCC TCC AAG CC	GCT CAC CCT CTC TTC TCT CT	2127, 2128
chr18	25080042	25080291	TAG AAT ATG TCA CCC AGC CC	ACC TGT TTC TCC CAG TTA CA	2129, 2130
chr18	25124915	25125164	ACA GAA TCA TCC CAT AGC CA	GCC CAT GAA AGA GAA ACC AG	2131, 2132
chr18	25128057	25128306	CGC CAT TCT GTG CTT AAT TTG	CTC CAT CAG TGC AGA AGT CC	2133, 2134
chr18	25140257	25140506	GTG AAG CAA GAG AAA GCA AGA	ACA GTC AGC AGC CCT AAA AT	2135, 2136
chr18	25140722	25140971	TGA TTC GGC TGC AGG TTA TT	GCC TCC TTC ACA TAA TGC AG	2137, 2138
chr18	25147759	25148008	CTG GCT TCA AAT GCA TCT GA	TTG TCA ACA GAG AGT CAG CT	2139, 2140
chr18	25157828	25158077	ACT GGG AAA TTG GAA TTC GC	CTG AAA TGG TCT GGG AGT CT	2141, 2142
chr18	25160244	25160493	GGT AAA ACT GCC TGG AAA CT	TCA AAG ACA GAG TGA GTG GA	2143, 2144

FIGURE 2 (Page 67 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	25166354	25166603	AGA CCA CGG GCT CTA TGT AT	TTT GGG GGT TAC ACT TCA TAG	2145, 2146
chr18	25172986	25173235	CAT CTT GCT TAT TGG CTT ACG A	AGC CAG CAG AAT AAT ACC AGG	2147, 2148
chr18	25174972	25175221	GAG GTA GAG GCA GTG TCT TG	ACC TCA TCT TTT GTC AGC CT	2149, 2150
chr18	25175640	25175889	TAG TCC TTG AAC TCC CTG GT	ACA GTT CCA TAG GCA GGT TT	2151, 2152
chr18	25182855	25183104	CCA GCT TAG CGT CTG TTT TT	GCA GTT CCA GAT CCA ATA TGC	2153, 2154
chr18	25198531	25198780	GAC CAC AAC TAT CAA GAG CAC	TTT GGG AAA GAT GGG AGA GC	2155, 2156
chr18	25201886	25202135	CCA AAG AAA GGT TGA AGC CC	TTG CAG GTA AGG TAC AGA AGA	2157, 2158
chr18	25209395	25209644	AAT AAT GTG CAC TGT GAT GGC	CTT CAG CTG CAT CTT GAG C	2159, 2160
chr18	25213880	25214129	TTT AAG GGT CTG ATG GTT GC	GGC ACT TCA AAA ACA AAC CC	2161, 2162
chr18	25216888	25217137	GAA AAT GCC CAT CGT CTC AA	AGG GTT TTA TGG TCT CCT GG	2163, 2164
chr18	25228617	25228866	ATT CCT TGT CTT TCC CCC TC	TCA ACA CGG AGA ACT GAA AAC	2165, 2166
chr18	25231535	25231784	TCA TTT CTC TAG CCC AAA GAT G	TCC GTG TAA ATG AAC AAA GCA C	2167, 2168
chr18	25245662	25245911	TTG GTT TGT TGA CTT CAG CC	TTT AGG GAA TGG TTT GCA TT	2169, 2170
chr18	25246300	25246549	GCT CAG TGA CAG TTG GCA TT	GAG ATG CCA TTC CCA AAA GG	2171, 2172
chr18	25254843	25255092	GTC TTG TCT CTC TTC TTC CAC T	CCC TAC CAT AGT GCC AGA TG	2173, 2174
chr18	25265476	25265725	TTT AGA GCA GGT GGA AAC GA	CAG CTT TCA GTG ACA GAG GA	2175, 2176

FIGURE 2 (Page 68 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	25278532	25278781	C TT GGG TTT TTA TGG GTT GCT	CCA AAG GCA GAT GAG TGT TT	2177, 2178
chr18	25279010	25279259	G TT GCC TGG ATT GCT CTA AA	GCC TGG GAT AGA AAT GGG AA	2179, 2180
chr18	25283817	25284066	AAA TCA CGA CGT AGG AAA CC	GGA AAG GAA AGG AAG CTG TG	2181, 2182
chr18	25292042	25292291	TCA CCT TGG AGC AGG TCA TA	TCA GAG AGG TCT TGC TGA AG	2183, 2184
chr18	25295429	25295678	CGA AGA AGG TCT GGG AGA TG	TCT CTC TGT TGC TTG TTT CCT	2185, 2186
chr18	25330345	25330594	CAC CAT TGT TTC ATC AGG ACT	CGC ATG TGG TAG ATC ATC AG	2187, 2188
chr18	25332963	25333212	TTG CAT CAT CAG CTC ACA TAC	TAT AAC ACC CTC ACC TCC CA	2189, 2190
chr18	25333284	25333533	AGA CCT GGA AAA TGA TGG GT	CAC CCA AAT CAC CTT GCT ATG	2191, 2192
chr18	25345252	25345501	CCT GGA AGT GTG TAA CAA GC	CAA CTA CCG TGG ATT CCG TT	2193, 2194
chr18	25384702	25384951	CTC CCT AGC AAA AAC TTC TCA	TCT ATC ATG AGT CGC TTC CA	2195, 2196
chr18	25510767	25511016	TGC CTT ATT CAC TGT GCA AC	TTT CTG TCA CTT TCT GGG CT	2197, 2198
chr18	25519108	25519357	TGA TGG CCT AGT GAG TTT CC	CGT GTG TTT CTA GTG CAT TGT	2199, 2200
chr18	25531724	25531973	TGC AAT GTA ACA AAA GCG TG	GGG CTC AGA GGG AAT ATC AG	2201, 2202
chr18	25543168	25543417	GCC ACA TTT GCT TTC ACA CA	CCG ACG AAT GGA TGA AAG AC	2203, 2204
chr18	25547425	25547674	ACG TCA TTG GGT TCA TGG C	ACC CAA ATT CCA TGC CTA CT	2205, 2206
chr18	25557343	25557592	ATT TTA CCC CCT TAG GCA CC	TGT ACA GCA GTC TCC AGA AA	2207, 2208

FIGURE 2 (Page 69 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	25564483	25564732	TCT TCT ACA CAG CCC TTC AG	GCC CTC TTA CCC TTT CTC AT	2209, 2210
chr18	25583087	25583336	ATT GGG ATC GTC AGC ATC AA	CAT TCA AAG ATC CAG ACC AGG	2211, 2212
chr18	25585083	25585332	TGA TTG TCT TGT CCA CTG GT	ATC TGT GAT TGC TGC CCT C	2213, 2214
chr18	25589902	25590151	ACA TCA CAC TTC ATG CCC TT	CTA GAA ACT CCC AGG ACA GA	2215, 2216
chr18	25601966	25602215	ATG AAG GCA TTA GGA GGG AG	CAT GTG TGG AAA GGA TTG GT	2217, 2218
chr18	25611986	25612235	AAA GTG GAG AAG TGG CAG AT	TAT GAA TGA ACC GTG GCT CA	2219, 2220
chr18	25617498	25617747	CCT TAG GAT TCT GAG AGG TGA G	AAG TTG AGT CGT TTG TCC CA	2221, 2222
chr18	25629105	25629354	AGG GCT TCT GAT TGA TTT GC	TAG TGT TTC AGG AGC GTG TT	2223, 2224
chr18	25631180	25631429	CAG GGT AGT CGG GAT TTC TC	CCA GGA CAA GCA GAC ATT TT	2225, 2226
chr18	25643639	25643888	CCC GGT AAT GAT CTA CAG CA	GCT GCT GGT GAT TTT TGA AGA	2227, 2228
chr18	25645371	25645620	AAC GGC ACT TGG TTC ACT A	CTC TGG GCA AAC AAG AAA CC	2229, 2230
chr18	25665025	25665274	ACT CTG AAC TCC TCC TCC TG	GTG TGT GTT TGT GGA AGT GT	2231, 2232
chr18	25666614	25666863	TTT GCT CAC ACA CAA GAC AC	AAA GCC CAA TCT CTC TGG TTA	2233, 2234
chr18	25667057	25667306	ACG ACT GCA TCC TTT TCA TG	TAG GCG GGC TTA TTG TGT TT	2235, 2236
chr18	25670741	25670990	CCA TCA TAG CCT ACA AAT ACC C	TCA ATG TAA ACT GCC GGG AG	2237, 2238
chr18	25673208	25673457	AGA GAG TTG AAA ATA TCC CCC A	ATG GGA GTC GAA TGG TGT AAA	2239, 2240

FIGURE 2 (Page 70 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	25681018	25681267	ACT TTC TTG AAC ACC CCA GT	TAA CAT TTG AGG GCA TGG GA	2241, 2242
chr18	25682079	25682328	TGC CTG TGT CCT ACT TTT CC	CAG AAT ACC CTC ACT GTG CT	2243, 2244
chr18	25689906	25690155	TGA CTG CCC AAG AAT GTA CA	GGA GAT AAC AGC AGA GGT CC	2245, 2246
chr18	25700540	25700789	CCG AAC ACG CTG TAT GTA TT	TGT GGG TGA TAT CTG TGT CT	2247, 2248
chr18	25703648	25703897	GGA AGG GAA TTG AAG CAC AG	GCC ATC CTG TAA CTG AAT GC	2249, 2250
chr18	25707188	25707437	TCA TCC TAT CCA CCA ACC TG	GTA TTT TCC CTT TGC CGC AG	2251, 2252
chr18	25716100	25716349	AAT GAA CTG GCC CTG ACT TA	ATT ACA GCA AAG AAC GTG GC	2253, 2254
chr18	25722951	25723200	TAA GAT ACC ATA CCG CAG CT	TCT GTG TGT TTT GCA TTG GT	2255, 2256
chr18	25725055	25725304	TCA GCG TTC ATG GTA CCA ATA	GTG ACA GTT TTC CAA GGC AT	2257, 2258
chr18	25748105	25748354	GTT TCC CAA CCA ACA AAC AAG	GCA TTA CTT TTT CGC ACA CT	2259, 2260
chr18	26214441	26214690	TCT ATC GGG ATG GAG ACT GA	GGG GAT TGT TTT AAG CAG GC	2261, 2262
chr18	26236788	26237037	GTT CAG ACA GGT GGA CTA GG	CCA TTG TTC TCA CCA ACT CT	2263, 2264
chr18	26261336	26261585	AAG CAA CCT GGG AAA TTG TG	CCT GAA ACA CAA GCA GCA G	2265, 2266
chr18	26265937	26266186	GGG TTA AGG TTG CTG GGT TA	AGC TGC CTA TTT GAT TGG TG	2267, 2268
chr18	26285286	26285535	GTG AAA TGT GGT TGT AGT GCA	CAG TAC AGT CAG CCT TCC TT	2269, 2270
chr18	26289006	26289255	GTG ACT GCC TTG CTT CAT TT	TGC ATT CAA ACT ACC CCA AG	2271, 2272

FIGURE 2 (Page 71 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	26308405	26308654	CAG TTC TGG AGC CTT CTA CT	CCG AAA AGA GGC AAG CAA TT	2273, 2274
chr18	26308962	26309211	TTA GGG CAG GAT GTA CAG AA	GTC ACC TCA ACC TAA CTC CA	2275, 2276
chr18	26312054	26312303	GCT GGT GAC CTT CAT TCA AG	GCA ACA CTC TAC CCG TCT AG	2277, 2278
chr18	26316149	26316398	TAA AAC CAT GTT CGG GGC A	ATC AAT GCT CTG ACC TCC TG	2279, 2280
chr18	47100905	47101154	CTA CCT GTC CGT TTC CCT TAC	ATA CAT CAG GCC TCC AGA ATT	2281, 2282
chr18	47130278	47130527	GAC AAA GAT GAC TGG AGG TGA	CAC ATC TTT AGA GCT CAG GTG A	2283, 2284
chr18	47366936	47367185	GGG TGG ATG GTG AGA TAT GTG	CCA TCA CTT CAC AAT CCA CAC	2285, 2286
chr18	47371131	47371380	CTT CAA ACC TGA TCC ATG TGC	AAT CCT GCA GTC ATC TTC CC	2287, 2288
chr18	47689868	47690117	GCA GAA ACA GCA TGA ATC TCC	CAA GTC TGG TTT GTG AGA AGC	2289, 2290
chr18	47690267	47690516	TGA CTT CAA ACA TCC CAT CCA	GGG AGC TTC TGT AGT CTT TGA	2291, 2292
chr18	47703689	47703938	GTG GGA TGA GTT CTA GAG GAA	TAA GGA GAG CAG GAC TTA CAG	2293, 2294
chr18	47708139	47708388	AGT CAC ACA CAT ACA CAC AGT	CCA ACG GTT CAT TTG TCG TAT	2295, 2296
chr18	47717445	47717694	ACG ACT TCC CTG TGT AAC TTA	CCT TGC TCT GTT AAT GGG TTT	2297, 2298
chr18	47738531	47738780	CCT TCT CTT GTC TCT AGT GCC	AAC AAT GCT TAA CGG GAA TCC	2299, 2300
chr18	47777438	47777687	CTG GAA ATA CAG ACA CAC CTG	GCA GAG TTC ATA GAA GGG TCA	2301, 2302
chr18	47794212	47794461	ATT TGT AAA CCA CCC ACT TCG	AAA CCG AGA CGA CCA CCT AAT	2303, 2304

FIGURE 2 (Page 72 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	47799400	47799649	TCA CTG TGC TGA CAA ATC CTA	GAG TGA TGA GCC ATG ATG	2305, 2306
chr18	47802662	47802911	CCC ATC ATC ATC CCT TCA GAC	GGG TAT TGG AGA TAG CAG GCA	2307, 2308
chr18	39874986	39875235	TCA TCA CTT TAT CCT CCC AGT	GTT TGG CAC TGC AAC TAG ATA	2309, 2310
chr18	39891490	39891739	ATG GGC ACA GGT AAA GAG TTT	TGA AAT AAG GGA AGC CAC ACA	2311, 2312
chr18	42204240	42204489	TTT GTA AGC TGA GTG TGA GGT	TCC TTA GTG TGC CAA TTA GCC	2313, 2314
chr18	42313146	42313395	TTA CTG TTT GAA TGC CAG CTC	TTA ATG TGG AGA GAC AGG CC	2315, 2316
chr18	42313939	42314188	TCC CTT CTC CCA TCA CAA TTC	CAA TGC ATC TTA CTC ACC CTT	2317, 2318
chr18	42314302	42314551	GAA GAC TGC ATG TGT GTC CTA	AGT ATG GAA GTG GGA ATT GGA	2319, 2320
chr18	42349923	42350172	TTC TCA CTC TCA ACT GAA CCA	TTG CTT CCA CAG AAA CTC TTC	2321, 2322
chr18	42407165	42407414	TCA GGG AGC TTC TAA TTA AGG A	AAC CGA CCT ATT CCA AAG TCT	2323, 2324
chr18	42418033	42418282	AAG ATG ATC CCA GGC TTA AGG	TCT GAA GCG AAT ACA GCT CAA	2325, 2326
chr18	42449702	42449951	GTT GAG GTT TGC TCA TCT TGG	GTT CTA ACT ACA CCA GGC TCT	2327, 2328
chr18	42450400	42450649	CAA AGA TAG ATT CGC ACA CCA	GTA TGA GTG TAG GTG TGG AGG	2329, 2330
chr18	42461427	42461676	GAG CTG GAC AAA TTA AAT GGC	AAT CTG GAT CTA GCG AAG GAC	2331, 2332
chr18	42462834	42463083	CCA GTG CAT TTG GTT TGA CA	TAA TGA GAA GGC AGG ATG AGG	2333, 2334
chr18	42468595	42468844	TAT GTG AAT CCT CTG TGT GGC	AAG ACA ACT CTC TAG GCC TCA	2335, 2336

FIGURE 2 (Page 73 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	42468938	42469187	AGC TTC TCT CTC ATT CTG CTT	GTT TAT GGT TGT CCC TGG AGA	2337, 2338
chr18	42644003	42644252	GAC TCC CGA TTT CAT TTG CTG	TCC ACC TTC TGA TCA CAC AAT	2339, 2340
chr18	42644494	42644743	TCC CAA TCG TTG TGA AAC ATA C	AAG ATC AGG TAC CAA GGC ATT	2341, 2342
chr18	42645387	42645636	TCT TTA CAG GAA GTT GGG ACC	ATG ATG TGA AGT CCA TGG TGA	2343, 2344
chr18	42741059	42741308	TAA GTT CAG ATC AGG GAG CAG	TCC AAA TTG ACT TCC ATG AGC	2345, 2346
chr18	42745733	42745982	GTT GAA AGT CTT ACA GAA CGC T	GTG GTT TCA GGA ATT TGG AGG	2347, 2348
chr18	42746460	42746709	CAA CAT AGG CAC ATT GTC CTC	TAT TTG CTG CTT CAT TCT TCC C	2349, 2350
chr18	42746911	42747160	GTC AGG CCT CAT AAC TCT CTT	AAG TCA TTA CGT CCC ACA CTG	2351, 2352
chr18	42747473	42747722	GTT GTG TGG CTT TCC TTA TCA	AAA GTC ATC AGA AGG GTA GCA	2353, 2354
chr18	43796659	43796908	CCT GCA GCT CTG TGT AAA TTT	AAT GAT GCC GAA CAG TGA GTA	2355, 2356
chr18	43820471	43820720	CTT TGG CCA GTT CTT TCT CTC	AAT GTA AGA CAG GGA CAG AGA	2357, 2358
chr18	43841913	43842162	GTG GCC CAG CAT TAT TTG TT	TGA ATT CCA CAG TCC AGT CAA	2359, 2360
chr18	43842202	43842451	TCT TGG TGT GAC TTG CTA ACA	AAT GCC TTC AAA GAC AGT GAC	2361, 2362
chr18	43842647	43842896	TTT CTG GCT GAG ATA AGA CCC	CAC ACC TGC AAT TGA GAT GAA	2363, 2364
chr18	43845701	43845950	ACA ATT CCG TGG TAT ACA GCT	GTG ATG ATG ATG CAA CAG CTA	2365, 2366
chr18	43846353	43846602	TGA TTG TGC CCT AAC CAA ACT	TTT CAC GGT AAG AGG AGC AAA	2367, 2368

FIGURE 2 (Page 74 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	43917652	43917901	TGT CGT ATC CTG CTG TTT AGA	TTC TCT CTA GGC AGG TGA ACT	2369, 2370
chr18	43918519	43918768	TCA GGA GTA AAG TCA GGA CCT	ACC CTT TGA AAG AAC CAG GAA	2371, 2372
chr18	43918998	43919247	TGA GCT GAT TTA CTG TGA CAC	AAT GAG CCA CTG TTC TCT AGG	2373, 2374
chr18	43919544	43919793	TAG CAC CTT GAC TTC AGG ATT	ATT TGC ACA TTA GGG CCT CAA	2375, 2376
chr18	44086123	44086372	TGA GGT TGG AAA GGG TCA ATT	GAA CTT CCC TGC TTC CTT CT	2377, 2378
chr18	44094299	44094548	CAG CTT TCC TTC CTC TTC TCT	AAA TAC TTG GCT GTG ACC ATG	2379, 2380
chr18	44167214	44167463	ACA GTG AGA GGA AAG AAC AGC	AAG ACC CTT GAG AAC TTC CAA	2381, 2382
chr18	44167791	44168040	GGA AAT AAA TTG TGA CCT GGC	ATG TGT AAA GAC GTC CTG GAA	2383, 2384
chr18	44168296	44168545	AGA CAG CCC TTC AAT CCA TAC	TCT ATG TGG AGG GAT TTG ACA	2385, 2386
chr18	44173512	44173761	CCT ACA TCC CTT CCT CCT TTC	TTC CTG AAG TTT ATG GTG CAA C	2387, 2388
chr18	44174626	44174875	TCA CCC ATC TTC CAA TTA GCT	AAG GTT GAA TGA GGA TCA AGC	2389, 2390
chr18	44857765	44858014	TTT CTA AGC ACA AAC TGA CAC C	GAG GGA AGA ACA CAA CAC ATG	2391, 2392
chr18	45110525	45110774	GAT GTT TGC ACT GGA GGG ATA	CAG ACT AGC CTA CAA TCC TCC	2393, 2394
chr18	45197621	45197870	GAA GAC TAA ATG TTG GCC GAA	CAT TCA GGT TCT TAA GGG CTG	2395, 2396
chr18	45197871	45198120	GTA GAG AGA GGG AGG ATC ACA	GAA AGG CAG ACG ATG AAA GAG	2397, 2398
chr18	45198760	45199009	CTT GCC ATG AAG TTT GAC CAG	ATC TCC ATC AGC ACA GGA ATT	2399, 2400

FIGURE 2 (Page 75 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	45234886	45235135	AGG ATG AGC ATT TGT AAC CTG	GCA GTG TGA CAT CTG TGA ATG	2401, 2402
chr18	45235523	45235772	TGT GGC TTT CAA ATT ACC CAC	AGA CTT TCC TCT TCC TCT TCA	2403, 2404
chr18	45238370	45238619	CAT ACA AGT GCT CTG TTA GGC	TTT ACA ATG AAC TAG CCA GGC	2405, 2406
chr18	45335896	45336145	AGG ACT TGG AAC CAG AAA GAC	TAA CAT CTG CCT GAA AGC TTC	2407, 2408
chr18	45336353	45336602	AAA GAG GGC TGA TAT CGT CTG	CTC GTG TGT GCA ATT TGG AAT	2409, 2410
chr18	45357461	45357710	CTC ACT GCA AAC TAT GGA ACC	GGA GAG ATG GAG AAG ACC TTT	2411, 2412
chr18	45357745	45357994	TAT TCT GCC CAT CTT CTT CCT	AAT GTA TTA CTG TGC TCC CGT	2413, 2414
chr18	45358502	45358751	GGA GAC AGC CCA AAC ATA GA	ACC ACC TGC CAC TGT ATA AAT	2415, 2416
chr18	45362379	45362628	AGC AAT GGT GAA GTT CTG GAT	AAT TCT TCT TCT GGT GCA AGG	2417, 2418
chr18	45397588	45397837	CTG GTC AGT GAG AGA AGG GAA	TTG CCC TTT GAA CTG TTG ATC	2419, 2420
chr18	45864183	45864432	TTT CTC CAC TGG CAT GAA CT	AAG CAC ACT AAG GCC TCA TAA	2421, 2422
chr18	46464382	46464631	CAT GAT CAC AAT TCC AAG CCA	TCA GTA TCC ATT CAG CAT CCA	2423, 2424
chr18	46473428	46473677	ACC CAG TCA AGT TAC AGT CTT	TAA CCG AAG CCC ATA CTC TG	2425, 2426
chr18	46474545	46474794	TGT AAA GCA TAT CAA GGG AAC G	TCC TTA CTC CAG ATA CCC GAT	2427, 2428
chr18	46481797	46482046	TGC AGA GAT ATG TTC CCG TAT	TCT GGC TTC TTT CTT GGA GAG	2429, 2430
chr18	46483016	46483265	AGA AGA CAG TAC AAG GAA GGC	GCA ACA TTC ATT TCA TCC TGC	2431, 2432

FIGURE 2 (Page 76 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	46589014	46589263	TGT TTG CCA TTT GTT CTC CTC	CAT CAC GAC ATC CAT TTC CAC	2433, 2434
chr18	46599847	46600096	TTG AAG GCA AGA GAA GTT TGG	GTG CTT ATT ATC GGT GGG TGA	2435, 2436
chr18	46601866	46602115	GCC AAG GAA ATG TAG GGA AAG	CTG CCA TTC CTT GTT TCC AA	2437, 2438
chr18	46983278	46983527	AAC CTT CAC ACC TAG AGA CAG	ATT TGG ACT TGA AGC AGC CT	2439, 2440
chr18	47013103	47013352	GCA TAA CAG GGA AAG TCA CCT	CTG TAT TCT TTG TCC ACC ACC	2441, 2442
chr18	47016802	47017051	AGG ATG TTA GTG GTT TGG GTA	GAC AGG ACA CCT TGG ATT GAT	2443, 2444
chr18	286722	286971	TCT GAC ACT GAC CTT CAA CT	GAG TAA TTC CCC CGA TGC AG	2445, 2446
chr18	298393	298642	GAA ACA TTG CTT TCC CTC CA	TGA GAA TCA TTG AGC CAA ACC	2447, 2448
chr18	338127	338376	TTG CAC ACA TCT CTT CTC CG	AAT TGT GAG CGT TAG AGT GC	2449, 2450
chr18	340427	340676	GGG AGC CTT GAA AAC CTG AA	CCA GTG GGT CTT AAC ATT GAG	2451, 2452
chr18	387135	387384	ATT GGT AGC GTT CTC AGC A	AAA AGG CTA GTA GAG GGT GC	2453, 2454
chr18	391175	391424	TTG CTG CAT CTT GTA GAC CC	TCG CTG AAG AAC TGA GAC AC	2455, 2456
chr18	434440	434689	GGG CTA ATG TTT TGC TTC CA	GGG AAG TGA TTG GAG AGA GG	2457, 2458
chr18	457527	457776	TGT TGA TTA GAG CTT CCC CC	CCG CTT GGT ATA GAG TGC TG	2459, 2460
chr18	460384	460633	AGA GGT TTT CTT CCC CGT G	TTG AGG TTG TCA GGA AAG CT	2461, 2462
chr18	469281	469530	TAG TGC CCT CTA TTG TGC CT	TCT TGG GAA AGG GTC ATT CT	2463, 2464

FIGURE 2 (Page 77 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	572716	572965	ACT GCT GGA CTT TGA AAT GC	TCT CTT CCA TGC ACT CCA C	2465, 2466
chr18	598352	598601	CAA ACA GTG AGA TGT GGC TG	GAT CTG ACC CTC TGC TCA C	2467, 2468
chr18	615413	615662	TTG CTT CCT GAA AAC TGG TTC	CCT GAA AGA TGC ATG GTT GG	2469, 2470
chr18	618280	618529	ATT CCA ATC AGG TCT CTG CA	GCC ACA GAA CAA CCA GAT TC	2471, 2472
chr18	901111	901360	ACA ATC TCA CAG CCT GGA AA	TGG GGT TAA GAG CTC AAG AG	2473, 2474
chr18	939383	939632	TCA GAT GGG TGA GGT TCT TG	AGT GTG GAT GAC TTC TGC AA	2475, 2476
chr18	26321283	26321532	CTG CTC CTT CCC TCC AAT TA	GCC CCA TTA TCC TCC TTT GT	2477, 2478
chr18	26337865	26338114	AAA TGC CAG TCC TGT AAA GG	CAA ATC AGA CCC ACT AAG CAC	2479, 2480
chr18	26345717	26345966	TGT CCC ATT GCT TAG GAA GT	TGT TTT GGA CTG CTT CAC TC	2481, 2482
chr18	26365387	26365636	TGT GTG ATC CAG AGA CCC TA	ATT ATC ATG CTC ACT CCT CCA	2483, 2484
chr18	26367518	26367767	ACC AAT GTA GAC TTA GCG GG	GAC ATA GCA CGG GAG GAG TA	2485, 2486
chr18	26392500	26392749	ACT CTC ATA TTG CCC CAC TT	GCT AGT GGC GTT TTA GGA AA	2487, 2488
chr18	26406499	26406748	CCA GGG ATT GAT GTA CTG GT	TCG CTT GGA AGT CAT AGC C	2489, 2490
chr18	26711590	26711839	AAT TCT GGT CTA TCT GGC GT	CAG AGC TGC TTT GAA GAT AAT CC	2491, 2492
chr18	26729342	26729591	GCC AGC CCT TTT CAC ATA TT	GAA GCC TGA TAG ATG TGC CT	2493, 2494
chr18	26733981	26734230	AAC TAC ACC ATC CCC TGT TT	TAC CTC TGC CTC CAA TTG TC	2495, 2496

FIGURE 2 (Page 78 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	26739336	26739585	CCA TTT CAA ACA TGC TGG TC	CCC ATG TAG ACA AAG TGC TT	2497, 2498
chr18	26750685	26750934	AGA TTA TAA GAA GGC AGG GAA C	GGC AGC TTT GTC TTA CAG TT	2499, 2500
chr18	26752487	26752736	GTA GAG GGC TTA AAA CAT GTC C	TGT GAG ATT GCA TTC CCC TT	2501, 2502
chr18	26757573	26757822	ACA AGA ACA CAG TCG TTA AGC	CGG GTC AGA GAA AGA TCA GG	2503, 2504
chr18	27244230	27244479	TCT CTC CTT CAC TCC CTT CA	AAA CAT TTG TAA CCA CTC CCT G	2505, 2506
chr18	35076347	35076596	TGT CCA CCC CTC TTT GAT TG	CCT GTA ATA TGG GAC TCC TGG	2507, 2508
chr18	35147912	35148161	TTT AGC TTC TCC TGC CTT TG	CCA AAC CAC ACA CAC AAA CT	2509, 2510
chr18	35282655	35282904	AGA AGC AAT TCA CCA GGT CA	AGG ACA AGG ACA TTT CAC AGG	2511, 2512
chr18	35292141	35292390	TGG AGT CAG AAG TGT GTG TT	AGG CCG ATA AGA CAA GGT TC	2513, 2514
chr18	35304247	35304496	TCT GGT GTC AAA GCT TAG GG	GTT TCC CAT AGA GCC CTG G	2515, 2516
chr18	35311302	35311551	TGC CGA TGA TGT GTG TTT TG	CTC CAC TCT CTC CAA CCA AC	2517, 2518
chr18	36463709	36463958	TGT CCC TTC CTA ATC CCA AA	AAA CTG TGA AAG GAC GAG GA	2519, 2520
chr18	36473033	36473282	AGG ATG TTT AAG TTG CAG CA	TCC CTT GCT TTT GTA CCA GG	2521, 2522
chr18	36475403	36475652	TAT GCA GTT TTA CCC CCT CC	CAT GTG TGT ACT GTG CCT CA	2523, 2524
chr18	36479145	36479394	TTC TGT GTG GTC TCC TCT TG	TCT TTC ACT GTC ACT ATG GGG	2525, 2526
chr18	36482038	36482287	ATG GAG GGA CAA GTG AGA CA	AAA TGC AGC TTC CCA ACA TC	2527, 2528

FIGURE 2 (Page 79 of 80)

chromosome	start	stop	forward primer	reverse primer	SEQ ID NOs:
chr18	36483959	36484208	GGG GAA CAT GGA GCT GTA AA	GAG ACT TTC TGG AGG ACG AA	2529, 2530
chr18	36485761	36486010	GGA CCC CCT ACC ACA TTT AC	GAA ACG TAA TTT AGT GAC TGG C	2531, 2532
chr18	36487627	36487876	AGA TGG AGA AAT GTG CAG AGA	ATG TGT CTA TTG CTA CCT GTG A	2533, 2534
chr18	36489135	36489384	ATG ACT GCA TCC AAG AGC A	CTC CTT CAT TTT GCT GGT GG	2535, 2536
chr18	36531244	36531493	CAG AAT TTC CAG GCA GTT GT	GGT GAT CAT TTG TCT GCA CA	2537, 2538
chr18	36554006	36554255	GAA TCC AGA AGC TCA GTC CTT	TGA AGG GAT GAA GGC AGA AG	2539, 2540
chr18	36558050	36558299	AGC CCT GGA ATC TTG ACA TT	ATT GTG TTG TCC TTC CGT TT	2541, 2542
chr18	36566619	36566868	GTG CAT TAT ACG CAT GGC C	CTG AAG CAT CAC TGG CAT TG	2543, 2544
chr18	1017928	1018177	GGT AGA GGG TCC TGT GAT TC	AAG CTT GTA GTC TGG GTA GC	2545, 2546
chr18	241538	241787	GTA ACT GCT AGC CAC TGA GT	TCC CTC TGT ACT ATG TAG CAT G	2547, 2548
chr18	242831	243080	GCC TTT TTG GGA ATC CTA GT	TTC ATT TCC CTT TGT TGC CC	2549, 2550

FIGURE 2 (Page 80 of 80)

Fig. 3



Fig. 4 A

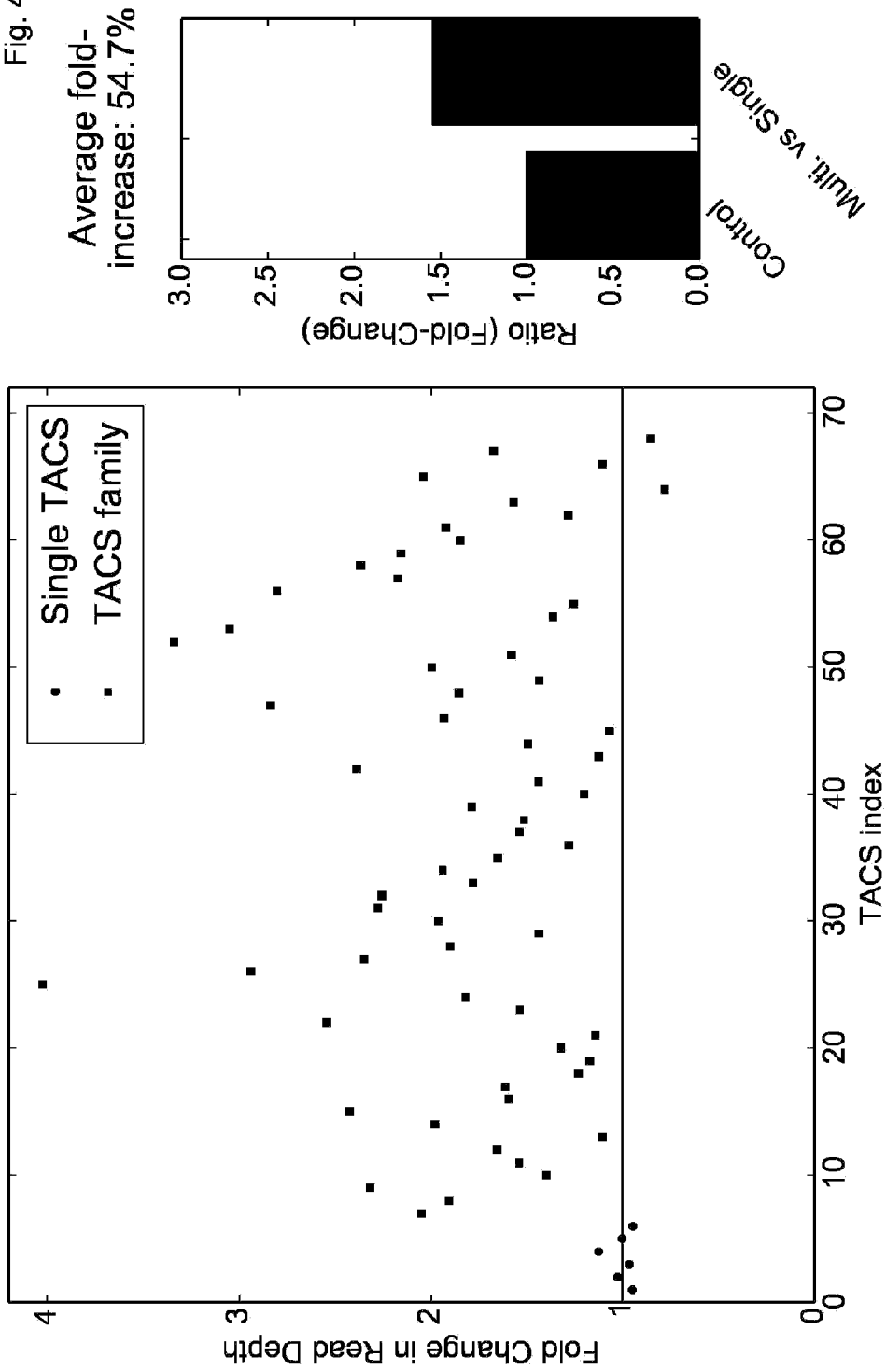


Fig 4B

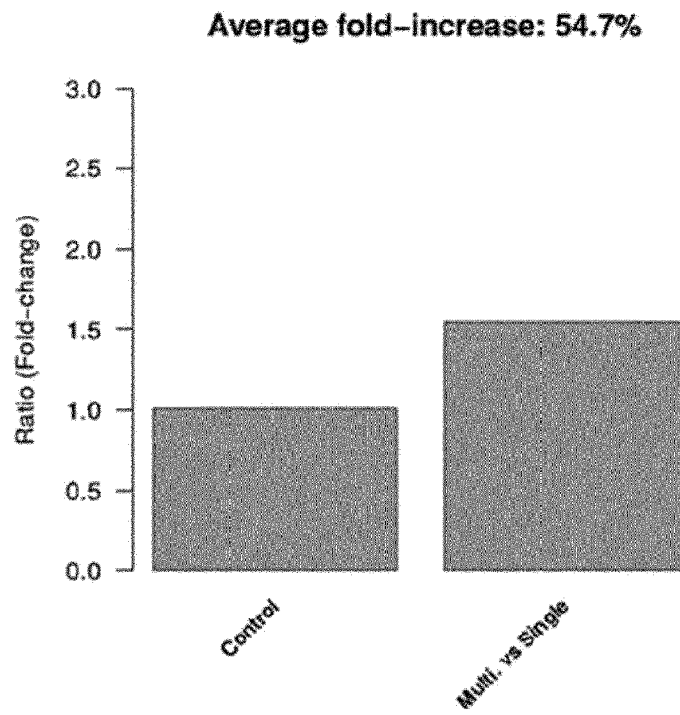


Fig 5

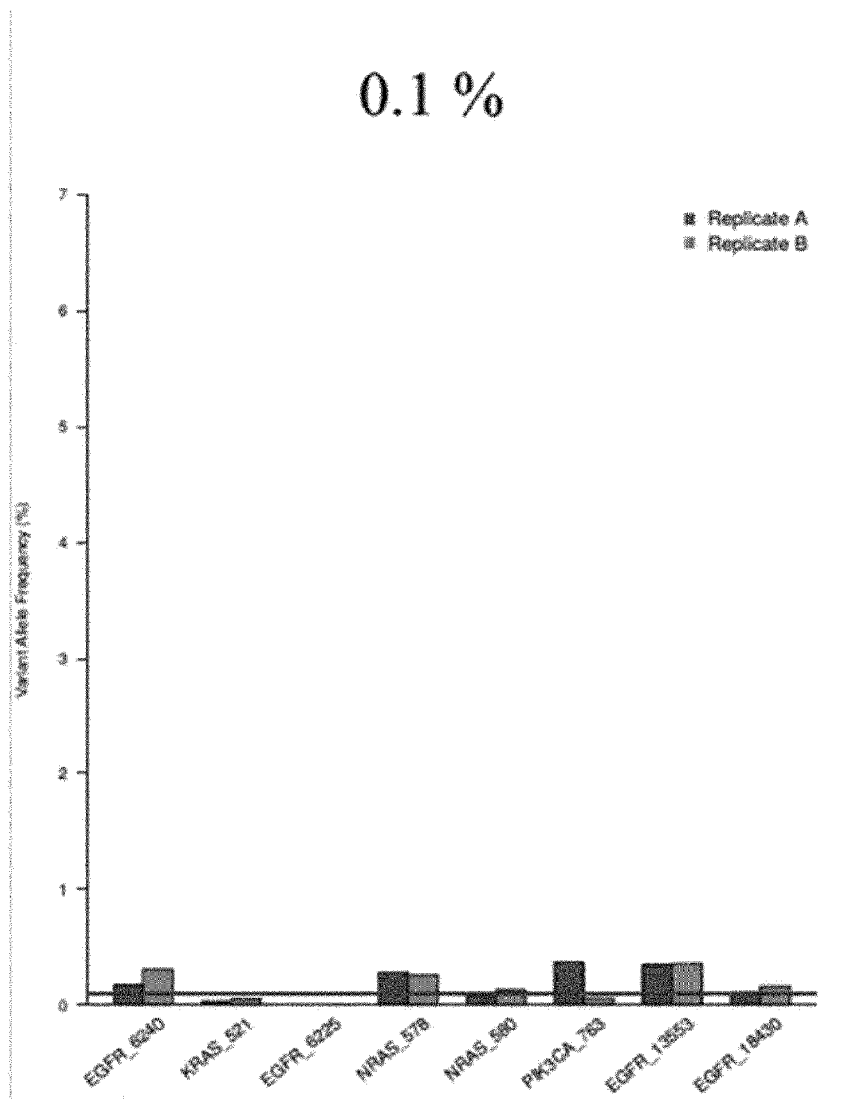


Fig. 5 Cont.

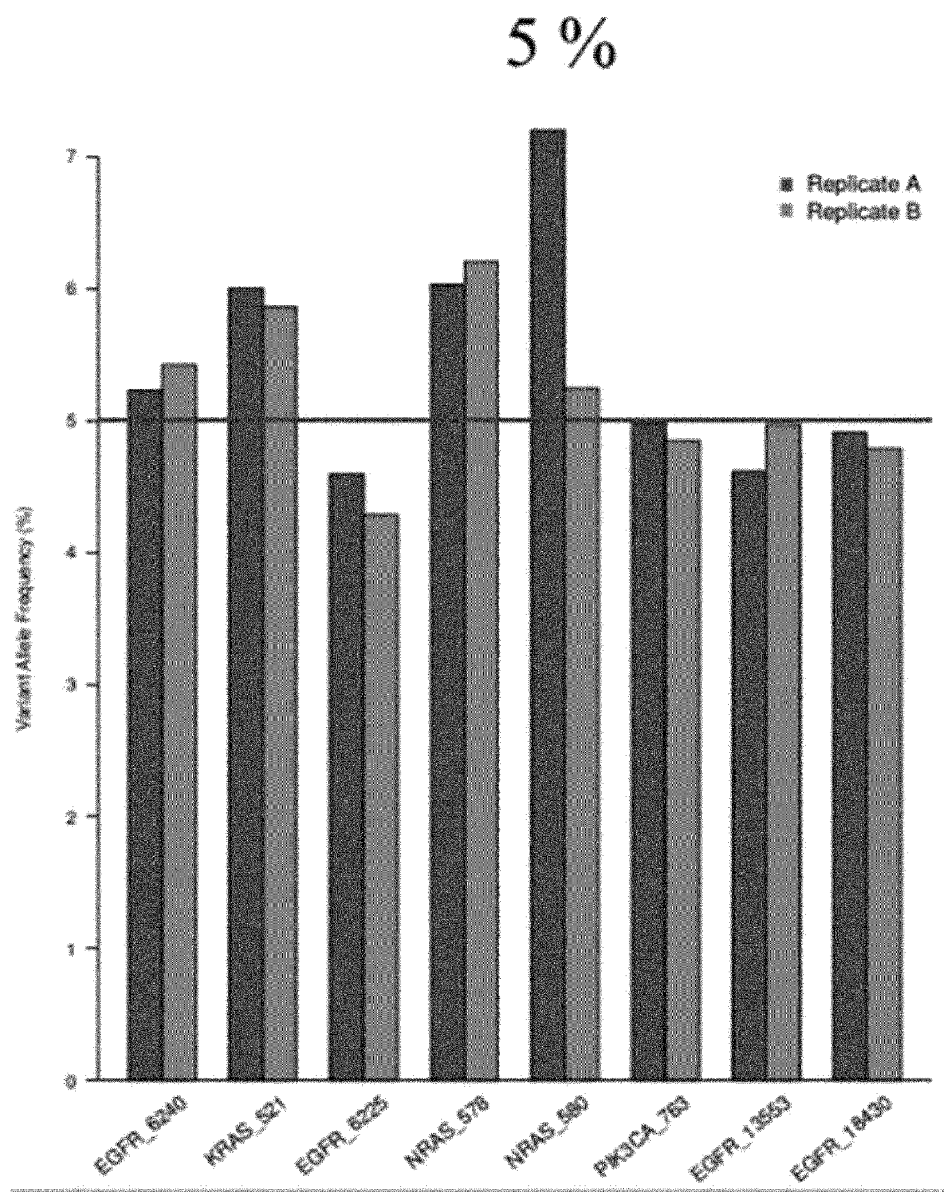


Fig. 6

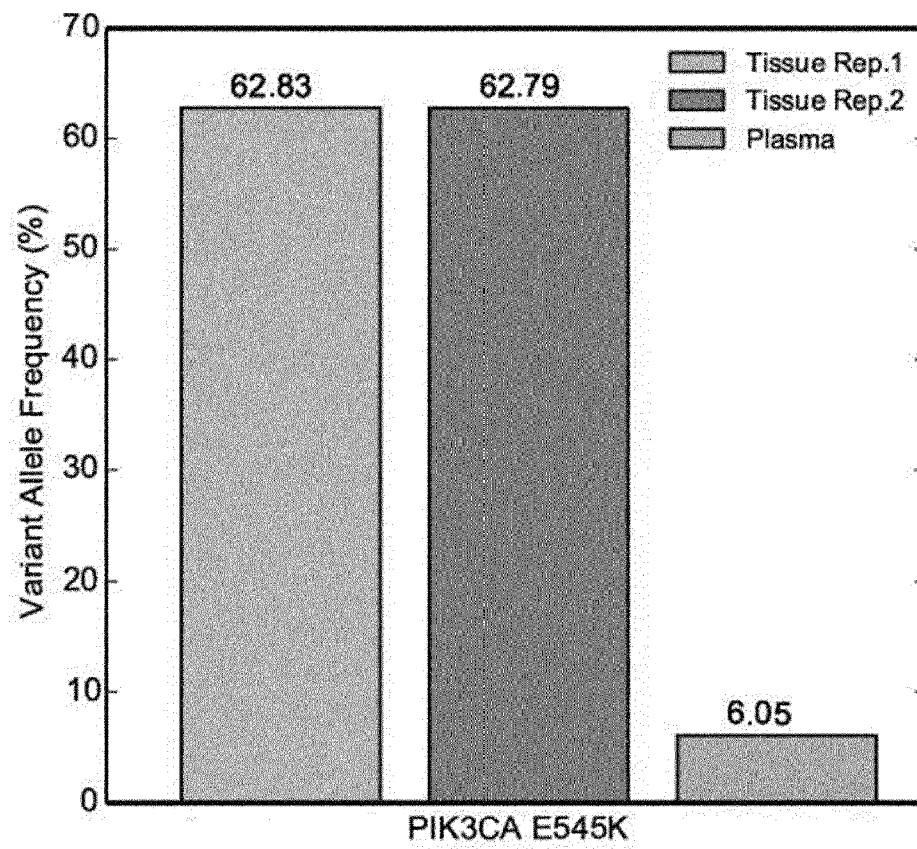


Fig. 6 cont

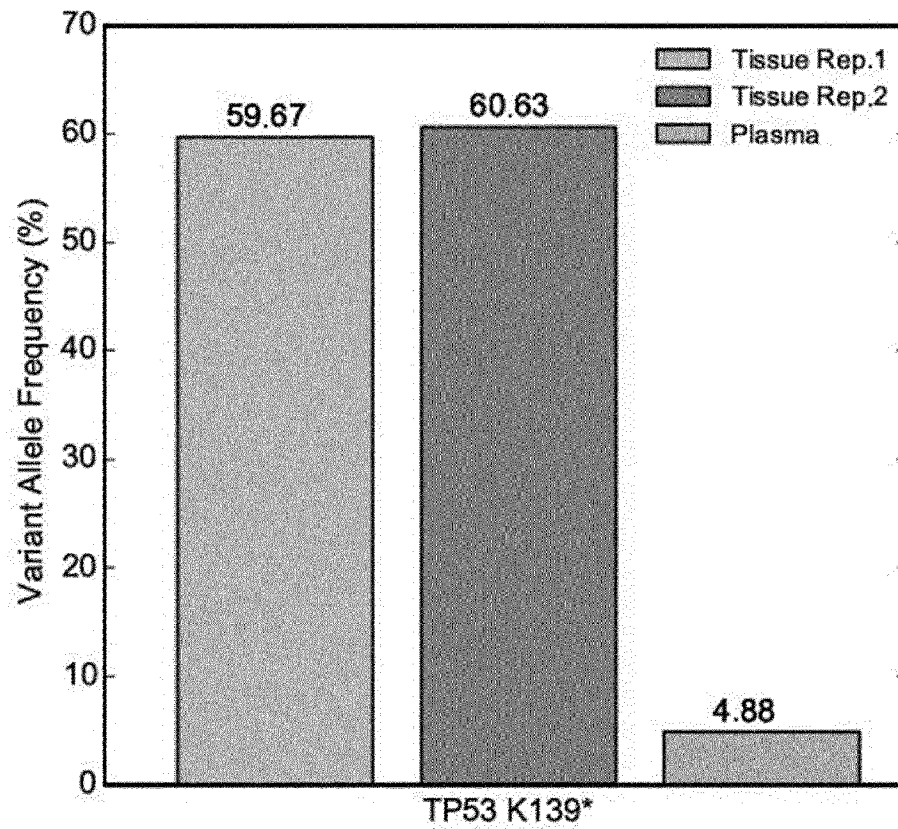


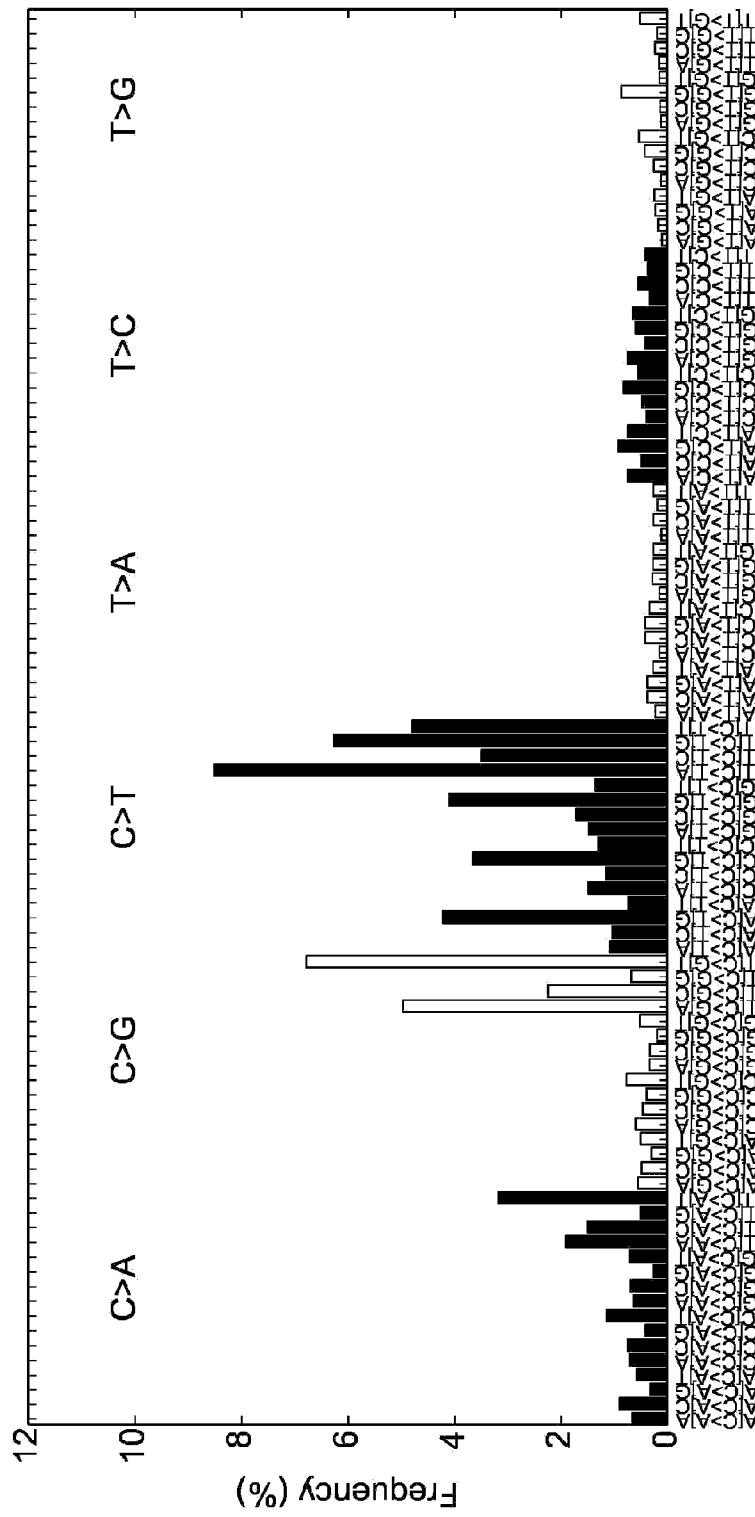
Fig. 7
Observed pattern of somatic SNVs

Fig. 8

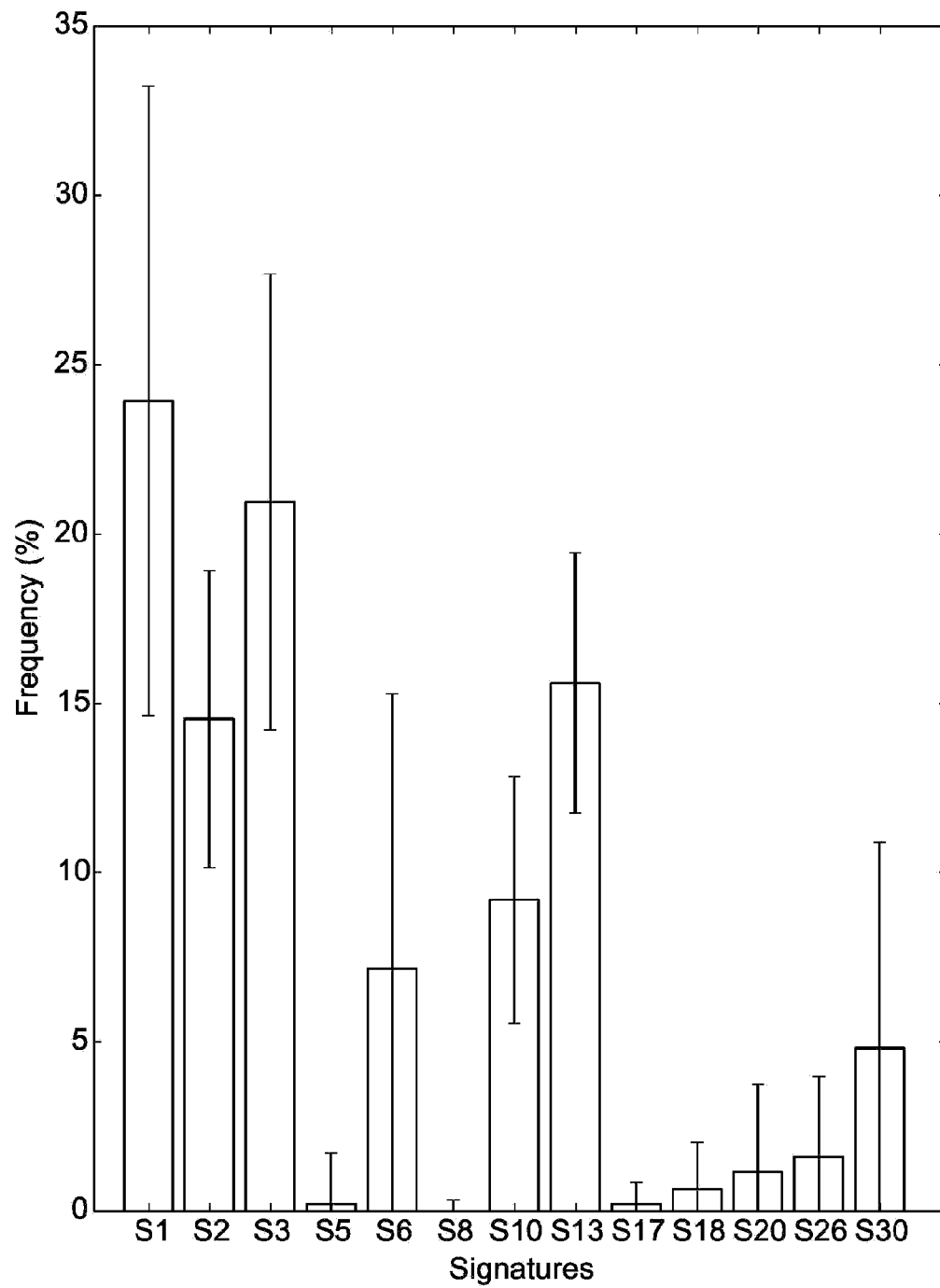


Fig 9

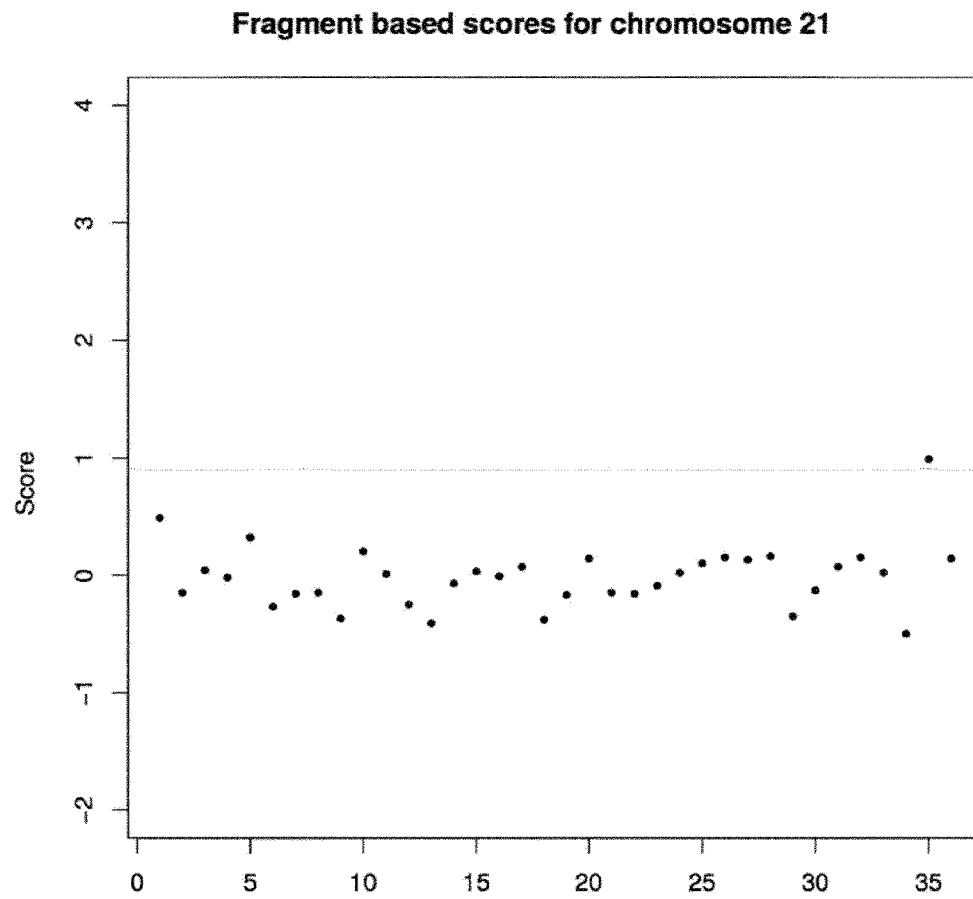


Fig 10

chromosome	start	stop	gene
chr1	115256347	115256588	NRAS
chr1	115256398	115256647	NRAS
chr1	115256410	115256649	NRAS
chr1	115256442	115256691	NRAS
chr1	115256467	115256726	NRAS
chr1	115256470	115256715	NRAS
chr1	115258538	115258778	NRAS
chr1	115258570	115258813	NRAS
chr1	115258607	115258846	NRAS
chr1	115258659	115258901	NRAS
chr3	178916725	178916970	PI3KCA
chr3	178916766	178917010	PI3KCA
chr3	178916782	178917028	PI3KCA
chr3	178916822	178917068	PI3KCA
chr3	178917417	178917566	PI3KCA
chr3	178917417	178917618	PI3KCA
chr3	178917420	178917590	PI3KCA
chr3	178917420	178917604	PI3KCA
chr3	178921331	178921578	PI3KCA
chr3	178921339	178921585	PI3KCA
chr3	178921347	178921596	PI3KCA
chr3	178921364	178921608	PI3KCA
chr3	178927888	178928114	PI3KCA
chr3	178927898	178928114	PI3KCA
chr3	178927974	178928182	PI3KCA
chr3	178935873	178936102	PI3KCA
chr3	178935930	178936133	PI3KCA
chr3	178935944	178936197	PIK3CA
chr3	178935995	178936197	PI3KCA
chr3	178936030	178936279	PI3KCA
chr3	178951914	178952159	PI3KCA
chr3	178951915	178952140	PI3KCA
chr3	178951921	178952140	PI3KCA
chr3	178951921	178952159	PI3KCA
chr3	178951948	178952109	PIK3CA
chr3	178952004	178952152	PIK3CA
chr3	178952010	178952109	PIK3CA
chr3	178952109	178952152	PIK3CA

Fig. 10 cont

chromosome	start	stop	gene
chr7	55241468	55241710	EGFR
chr7	55241542	55241789	EGFR
chr7	55241576	55241746	EGFR
chr7	55242269	55242500	EGFR
chr7	55242272	55242520	EGFR
chr7	55242280	55242532	EGFR
chr7	55242319	55242558	EGFR
chr7	55242332	55242584	EGFR
chr7	55242505	55242271	EGFR
chr7	55248852	55249080	EGFR
chr7	55248896	55249120	EGFR
chr7	55248933	55249182	EGFR
chr7	55248937	55249187	EGFR
chr7	55248961	55249208	EGFR
chr7	55259335	55259571	EGFR
chr7	55259337	55259586	EGFR
chr7	55259356	55259602	EGFR
chr7	55259368	55259570	EGFR
chr7	55259391	55259640	EGFR
chr12	25378488	25378688	KRAS
chr12	25378503	25378751	KRAS
chr12	25378546	25378778	KRAS
chr12	25378554	25378783	KRAS
chr12	25380153	25380359	KRAS
chr12	25380166	25380337	KRAS
chr12	25380167	25380326	KRAS
chr12	25380167	25380359	KRAS
chr12	25398080	25398329	KRAS
chr12	25398145	25398394	KRAS
chr12	25398153	25398397	KRAS
chr12	25398159	25398408	KRAS
chr12	25398186	25398433	KRAS