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(54) Title: CANCER-RELATED BIOLOGICAL MATERIALS IN MICROVESICLES

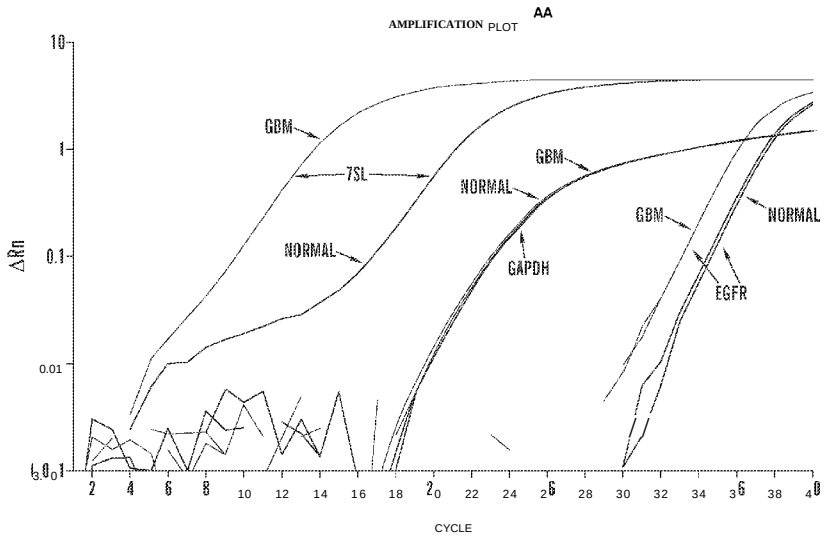

FIG. 33

AA Graphique d'amplification

(57) Abstract: Disclosed herein are methods for assaying a biological sample from a subject by analyzing components of microvesicle fractions in aid of risk, diagnosis, prognosis or monitoring of, or directing treatment of the subject for, a disease or other medical condition in the subject. Also disclosed are methods of treatment and identifying biomarkers using a microvesicle fraction of a subject. Kits, pharmaceutical compositions, and profiles related to the methods are also disclosed.

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CANCER-RELATED BIOLOGICAL MATERIALS IN MICROVESICLES

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of 35 U.S.C. § 119(e) to U.S. Provisional Application serial numbers 61/378,860 filed August 31, 2010; 61/421,421 filed December 9, 2010; 61/437,547 filed January 28, 2011; 61/438,199 filed January 31, 2011; and 61/493,261 filed June 03, 2011, the contents of each of which are incorporated herein by reference in their entirety.

GOVERNMENT SUPPORT

[0002] This invention was made with Government support under grants CA86355, CA69246, CA141226, and CA141150 awarded by National Cancer Institute. The Government has certain rights in the invention.

FIELD OF INVENTION

[0003] The present invention relates to the fields of biomarker analysis, diagnosis, prognosis, patient monitoring, therapy selection, risk assessment, and novel therapeutic agents for human or other animal subjects, particularly the profiling of biological materials from a microvesicle fraction of a biological sample, and novel therapies related to microvesicles.

BACKGROUND OF THE INVENTION

[0004] Increasing knowledge of the genetic and epigenetic changes occurring in cancer cells provides an opportunity to detect, characterize, and monitor tumors by analysing tumor-related nucleic acid sequences and profiles. Cancer-related changes include specific mutations in gene sequences (Cortez and Calin, 2009; Diehl et al., 2008; Network, 2008; Parsons et al., 2008), up- and down-regulation of mRNA and miRNA expression (Cortez and Calin, 2009; Itadani et al., 2008; Novakova et al., 2009), mRNA splicing variations, changes

in DNA methylation patterns (Cadieux et al., 2006; Kristensen and Hansen, 2009), amplification and deletion of genomic regions (Cowell and Lo, 2009), and aberrant expression of repeated DNA sequences (Ting et al., 2011). Various molecular diagnostic tests such as mutational analysis, methylation status of genomic DNA, and gene expression analysis may detect these changes.

[0005] Research uncovering the molecular mechanisms underlying cancer improves our understanding of how to select and design optimal treatment regimes for a patient' s disease based on the molecular makeup of his or her particular cancer. Over the past few years, this has led to a significant increase in the development of therapies specifically targeting gene mutations involved in disease progression. In parallel, the use of molecular diagnostic testing for cancer diagnosis, prognosis and treatment selection has expanded, driven by the need for more cost efficient applications of expensive therapies. Current molecular diagnostics has so far almost exclusively relied on assaying cancer cells from tissue biopsy by needle aspiration or surgical resection.

[0006] However, the ability to perform these tests using a blood sample is sometimes more desirable than using a tissue sample from a cancer patient because, frequently, fresh tissue samples are difficult or impossible to obtain, and archival tissue samples are often less relevant to the current status of the patient's disease. A less invasive approach using a more easily accessible biological sample, e.g., a blood sample, has wide ranging implications in terms of patient welfare, the ability to conduct longitudinal disease monitoring, and the ability to obtain expression profiles even when tissue cells are not easily accessible, e.g., in ovarian or brain cancer patients.

[0007] Currently, gene expression profiling of blood samples involves the analysis of RNA extracted from peripheral blood mononuclear cells (PBMC) (Hakonarson et al., 2005)

or circulating tumor cells (CTC) (Cristofanilli and Mendelsohn, 2006).

[0008] Many types of cancer cells release an abundance of small membrane-bound vesicles, which have been observed on their surface in culture (Skog et al., 2008). These microvesicles are generated and released through several processes and vary in size (from about 30 nm to about 1 μm in diameter) and content (Simons and Raposo, 2009). Microvesicles can bud/bleb off the plasma membrane of cells, much like retrovirus particles (Booth et al., 2006), be released by fusion of endosomal-derived multivesicular bodies with the plasma membrane (Lakkaraju and Rodriguez-Boulan, 2008), or be formed as apoptotic bodies during programmed cell death (Halicka et al., 2000). In addition, defective (i.e., non-infectious without helper-virus) retrovirus particles derived from human endogenous retroviral (HERV) elements may be found within microvesicle populations (Voisset et al., 2008).

[0009] Microvesicles from various cell sources have been studied with respect to protein and lipid content (Iero et al., 2008; Thery et al., 2002; Wieckowski and Whiteside, 2006). They have also been observed to contain cellular RNAs and mitochondria DNA (Baj-Krzyworzeka et al., 2006; Guescini et al.; Skog et al., 2008; Valadi et al., 2007) and may facilitate the transfer of genetic information between cells and/or act as a "release hatch" for DNA, RNA, and/or proteins that the cell is trying to eliminate. Both mRNA and miRNA in microvesicles are observed to be functional following uptake by recipient cells (Burghoff et al., 2008; Deregibus et al., 2007; Ratajczak et al., 2006; Skog et al., 2008; Valadi et al., 2007; Yuan et al., 2009) and it has also been shown that apoptotic bodies can mediate horizontal gene transfer between cells (Bergsmedh et al., 2001).

[0010] Knowing the expression profile, mutational profile, or both expression and mutational profiles of individual cancer is helpful for personalized medicine as many drugs

target specific pathways affected by the genetic status of the tumors. Detection of genetic biomarkers in blood samples from tumor patients is challenging due to the need for high sensitivity against a background of normal cellular nucleic acids found circulating in blood. Microvesicles released by tumor cells into the circulation can provide a window into the genetic status of individual tumors (Skog et al., 2008).

[0011] The present invention is directed to microvesicular nucleic acid profiles of microvesicle fractions obtained from a biological sample from a subject, methods for aiding in diagnosis, prognosis, patient monitoring, treatment selection, and risk assessment based on detecting the presence or absence of a genetic aberration in a nucleic acid profile, or changes in a polypeptide profile of a microvesicle fraction obtained from a biological sample from a patient, and therapeutic agents and methods of cancer treatment or prevention.

SUMMARY OF THE INVENTION

[0012] The present invention is based on the discovery of various types of cancer-related biological materials within microvesicles. The biological materials within microvesicles from a biological sample may be characterized and measured, and the results this analysis may be used to aid in biomarker discovery, as well as in diagnosis, prognosis, monitoring, treatment selection, or risk assessment for a disease or other medical condition.

[0013] In one aspect, the biological materials are nucleic acids and the invention is a method for assaying a biological sample comprising the steps of: a) obtaining or using a microvesicle fraction from a biological sample from a subject; b) extracting nucleic acid from the fraction; and c) detecting the presence or absence of a biomarker in the extracted nucleic acid. In a method for aiding in the diagnosis, prognosis or monitoring of a subject, the biomarker is a genetic aberration that is associated with the diagnosis, prognosis, or determination of the status or stage of a disease or other medical condition in the subject. In

a method for aiding in treatment selection for a subject in need of or potentially in need of therapeutic treatment, the biomarker is a genetic aberration that is associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other medical condition in the subject. In a method for aiding in a determination of a subject's risk of developing a disease or other medical condition, the biomarker is a genetic aberration that is associated with the subject's risk of developing a disease or other medical condition.

[0014] In some embodiments of the above methods, the genetic aberration is in or corresponds to a c-myc gene, a transposable element, a retrotransposon element, a satellite correlated gene, a repeated DNA element, a non-coding RNA other than miRNA, or a fragment of any of the foregoing.

[0015] In other embodiments of the above methods, the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof. For one example, the genetic aberration is in or corresponds to retrotransposon elements including LINE, SINE or HERV, or a fragment thereof. For another example, the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

[0016] In further embodiments of the above methods, the genetic aberration is in or corresponds to a satellite-correlated gene listed in Table 6, or a fragment thereof; a repeated DNA element listed in Table 8, or a fragment thereof; or a non-coding RNA listed in Table 9 (other than miRNA) or a fragment thereof. The non-coding RNA, for example, can be 7SL RNA.

[0017] In yet further embodiments of the above methods, the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof.

[0018] In another aspect, the biological material is protein or polypeptide and the invention is a method for assaying a biological sample from a subject comprising the steps of: a) obtaining or using a microvesicle fraction from a biological sample from a subject b) measuring a protein or polypeptide activity in the fraction; and c) determining whether the protein or polypeptide activity is higher or lower than a normal or average activity for the same protein or polypeptide. In a method for aiding in the diagnosis, prognosis or monitoring of a subject, an elevated or lowered activity is associated with a diagnosis, prognosis, status or stage of a disease or other medical condition in the subject. In a method for aiding in directing treatment of a subject, an elevated or lowered activity is associated with a disease or other medical condition or with the subject's responsiveness to a specific therapy for the disease or other medical condition. In a method in aid of a determination of a subject's risk of developing a disease or other medical condition, an elevated or lowered activity is associated with the subject's risk of developing a disease or other medical condition. In some embodiments of the foregoing methods, the polypeptide is an enzyme. For example, the polypeptide can be a reverse transcriptase and the method is to determine whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

[0019] In the present invention, the methods may further comprise a step of enriching the microvesicle fraction for microvesicles originating from a specific cell type. The enrichment may be achieved, for example, by affinity purification with antibody-coated magnetic beads.

[0020] In the present invention, the biological sample from a subject can be a bodily fluid, e.g., blood, serum, plasma, or urine. The subject can be a human subject. When the

subject is a human, the disease or other medical condition may be brain cancer such as medulloblastoma and glioblastoma, or melanoma.

[0021] In the present invention, the presence or absence of a biomarker in the extracted nucleic acid can be determined by various techniques, e.g., microarray analysis, PCR, quantitative PCR, Digital Gene Expression, or direct sequencing.

[0022] In yet another aspect, the present invention is a kit for genetic analysis of a microvesicle fraction obtained from a body fluid sample from a subject, comprising, in a suitable container, one or more reagents capable of hybridizing to or amplifying a nucleic acid corresponding to one or more of the genetic aberrations referenced above.

[0023] In yet another aspect, the present invention is an oligonucleotide microarray for genetic analysis of a microvesicle preparation from a body fluid sample from a subject, wherein the oligonucleotides on the array are designed to hybridize to one or more nucleic acids corresponding to one or more of the genetic aberrations referenced above.

[0024] In yet another aspect, the present invention is a profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject. The profile may be a genetic aberration in or corresponding to: a) cancer gene listed in Table 2 or 3, or a fragment thereof; b) a transposable element from the subject's genome, preferably an element listed in Table 4 or 5, or a fragment of any of the foregoing; c) a retrotransposon element from the subject's genome, preferably LINE, SINE or HERV, more preferably LINE1 (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment of any of the foregoing; d) a satellite correlated gene from the subject's genome, preferably a satellite correlated gene listed in Table 6, or a fragment of any of the foregoing; e) an element of repeated DNA from the subject's genome, preferably an element listed in Table 8, or a fragment of any of the foregoing; or f) a non-coding RNA other than miRNA, preferably a species listed in Table 9,

or a fragment of any of the foregoing. In one embodiment, the profile is a genetic aberration in the cancer gene c-myc. In another embodiment, the profile is a genetic aberration in the non-coding 7SL RNA.

[0025] In all of the foregoing nucleic acid-related embodiments of the invention, the genetic aberration can be a species of nucleic acid, the level of expression of a nucleic acid, a nucleic acid variant; or a combination of any of the foregoing. For example, the genetic aberration may be an RNA expression profile. For another example, the genetic aberration may be a fragment of a nucleic acid, and in some instances, the fragment contains more than 10 nucleotides.

[0026] In yet another aspect, the present invention is a method of identifying a potential new nucleic acid biomarker associated with a disease or other medical condition, status or stage of disease or other medical condition, a subject's risk of developing a disease or other medical condition, or a subject's responsiveness to a specific therapy for a disease or other medical condition. The method comprises the steps of: a) obtaining or using a microvesicle fraction from a biological sample from a subject; b) extracting nucleic acid from the fraction; c) preparing a profile according to any of the above-described profiles; and d) comparing the profile of step c) to a control or reference profile and selecting one or more potential new biomarkers based on one or more differences between the profile of step c) and the control or reference profile.

[0027] In yet anther aspect, the present invention is a method of treating a subject having a form of cancer in which cancer cells secrete microvesicles. The method comprises administering to the subject a therapeutically effective amount of a composition including an inhibitor of microvesicle secretion; an inhibitor of a reverse transcriptase; a microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles; or any

combination of the forgoing. In some embodiments, the inhibitor of microvesicle secretion is an inhibitor of RAB GTPase which may be Rab 27a, Rab 27b or Rab 35. In other embodiments, the inhibitor of a reverse transcriptase is a nucleoside analog selected from the group comprising 3'-azido2',3'-dideoxythymidine (AZT); 2',3'-dideoxyinosine (ddl), 2', 3'-didehyro-3'-deoxythymidine (d4T); nevirapine and efavirenz. In further embodiments, the inhibitor of a reverse transcriptase is RNAi targeting the reverse transcriptase gene. In still further embodiments, the microvesicle neutralizer is a biological agent that binds microvesicles and destroys the integrity of the microvesicles.

[0028] In yet another aspect, the present invention is a pharmaceutical composition comprising, in a suitable pharmaceutical carrier: a) an inhibitor of microvesicle secretion, particularly an inhibitor of RAB GTPase, and more particularly Rab 27a, Rab 27b or Rab 35); b) an inhibitor of reverse transcriptase, particularly a nucleoside analog, more particularly 3'-azido2',3'-dideoxythymidine (AZT); 2',3'-dideoxyinosine (ddl), 2',3'-didehyro-3'-deoxythymidine (d4T); nevirapine, or efavirenz, or an RNAi targeting the reverse transcriptase gene; c) a microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles, particularly a biological agent that binds microvesicles and destroys the integrity of the microvesicles; or d) a combination of any of the foregoing.

BRIEF DESCRIPTION OF THE DRAWINGS

[0029] Figure 1 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the meduUoblastoma cell line D384. Each bar represents the number of particles of a certain size that are present in the media and are released by one cell over 48 hours (hrs). The sum refers to the total number of particles released by one cell

over 48 hrs. ExoRNA refers to the total RNA yield in microvesicles from 1 x 10^6 cells over 48 hrs. The result is presented as the mean ± SEM (n=3).

[0030] Figure 2 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the meduUoblastoma cell line D425 in the same manner as in Figure 1.

[0031] Figure 3 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the meduUoblastoma cell line D458 in the same manner as in Figure 1.

[0032] Figure 4 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the melanoma cell line Yumel 0106 in the same manner as in Figure 1.

[0033] Figure 5 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the glioblastoma cell line 20/3 in the same manner as in Figure 1.

[0034] Figure 6 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the glioblastoma cell line 11/5 in the same manner as in Figure 1.

[0035] Figure 7 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the normal fibroblast cell line HF19 in the same manner as in Figure 1.

[0036] Figure 8 shows a graph depicting the quantification, size distribution and RNA yield of microvesicles purified from the normal fibroblast cell line HF27 in the same manner as in Figure 1.

[0037] Figure 9 shows a graph depicting the c-Myc gene yields in terms of genomic DNA extracted from cells of the following cell lines: one normal human fibroblast line (HF19), one GBM line (11/5), one atypical teratoid rhabdoid tumor (AT/RT) line (NS224) and three meduUoblastoma (MB) lines (D425, D458 and D384). Quantitative PCR was used to obtain c-Myc Ct values, which were normalized to GAPDH Ct values in the same preparation. The X-axis lists the names of the cell lines tested. The Y-axis is the fold change, represented as the ratio of the Ct value for each cell line to the Ct value for the normal fibroblast cell line HF19. In all cases, the Ct values are expressed as mean ± SEM (n=3) and analyzed by a two-tailed t-test.

[0038] Figure 10 shows a graph depicting the c-Myc gene yields in terms of RNA extracted from microvesicles secreted by cells of the same cell lines and in the same manner as in Figure 9. Quantitative Reverse Transcription PCR was used to obtain c-Myc RNA Ct values.

[0039] Figure 11 shows a graph depicting the c-Myc gene yields in terms of DNA extracted from microvesicles secreted by cells of the same cell lines and in the same manner as in Figure 9. Quantitative PCR was used to obtain c-Myc DNA Ct values.

[0040] Figure 12 shows a graph depicting the c-Myc gene yields in terms of RNA extracted from xenograft subcutaneous tumor cells. The subcutaneous tumors were generated by xenografting meduUoblastoma cells (MBT; D425 cell line) or epidermoid carcinoma (ECT; A431 cell line) cells in nude mice. The X-axis refers to the different tumor-bearing mice characterized by the type of tumor cell and the tumor mass weight at sacrifice. MBT

tumor mass weights are as follows: MBT 1: 3.4 g; MBT 2: 1.7 g; MBT 3: 2.4 g; MBT 4: 2.9 g; and MBT 5: 1.7 g. ECT tumor mass weights are as follows: ECT 1: 1.7 g; ECT 2: 2.3 g; ECT 3: 3.1 g; ECT 4: 1.9 g; and ECT 5: 2.2 g. Ct values were normalized to GAPDH. The Y-axis refers to the Ct values generated by quantitative reverse transcription PCR of the extracted RNA in each sample. For each RNA extract, two replicate qPCR were performed.

[0041] Figure 13 shows a gel picture depicting the c-Myc gene yields in terms of RNA extracted from serum microvesicles from mice that bear subcutaneous tumors. The subcutaneous tumors were generated by xenografting medulloblastoma cells (MBT; D425 cell line) in nude mice. C-Myc product was amplified by reverse transcription PCR method using human c-Myc specific primers and the RNA extracted from serum microvesicles as templates. The amplified c-Myc product should be 89 bp in length. The amplified c-Myc products were resolved by electrophoresis in a 2% agarose gel and visualized with ethidium bromide staining. The arrow points to the position where an 89bp product appears on the agarose gel. The lanes are referenced as follows: MW: DNA size marker; 1: MBT tumor mass weight of 3.4 g; 2: MBT tumor mass weight of 1.7 g; 3: MBT tumor mass weight of 2.4 g; 4: MBT tumor mass weight of 2.9 g; 5: MBT tumor mass weight of 1.7 g; NC: negative control where no RNA/cDNA was used.

[0042] Figure 14 shows a gel picture depicting the c-Myc gene yields in terms of RNA extracted from serum microvesicles from mice that bear subcutaneous tumors in the same manner as in Figure 13 except that the subcutaneous tumors were generated by xenografting epidermoid carcinoma (ECT; A431 cell line) in nude mice. The lanes are referenced as follows: MW: DNA size marker; 1: ECT tumor mass weight of 1.7 g; 2: ECT tumor mass weight of 2.3 g; 3: ECT tumor mass weight of 3.1 g; 4: ECT tumor mass weight

of 1.9 g; 5: ECT tumor mass weight of 2.2 g; NC: negative control where no RNA/cDNA was used.

[0043] Figure 15 shows a MA plot depicting relative levels of all represented RNA sequences (using 44,000 RNA probes on the Agilent microarray chip) in cells and microvesicles derived from the cells. The levels of transposon and retrotransposon sequences were compared to the rest of the RNA transcriptome in cells and microvesicles. ExoRNA and cellular RNA were isolated from GBM 20/3 cells and analyzed on an Agilent two-color 44k array. Y-axis (M) = $\log_2$Exo - $\log_2$Cell, X-axis (A) = 0.5 x ($\log_2$Exo + $\log_2$Cell).

[0044] Figure 16 shows a MA plot similar to the plot in Figure 15 except that the present plot only depicts relative levels of the following four HERV family sequences: HERV-H, HERV-K6, HERV-W and HERV-C, all of which are enriched in microvesicles more than 16-fold as compared to the host cells, i.e., $M \geq 4$.

[0045] Figure 17 shows a MA plot similar to the plot in Figure 15 except that the present plot only depicts relative levels of DNA transposons.

[0046] Figure 18 shows a MA plot similar to the plot in Figure 15 except that the present plot only depicts relative levels of LI sequences.

[0047] Figure 19 shows a MA plot similar to the plot in Figure 15 except that the present plot only depicts relative levels of HERV sequences with HERV-H, HERV-C, HERV-K6 and HERV-W being more than 16 fold enriched.

[0048] Figure 20 shows a MA plot similar to the plot in Figure 15 except that the present plot only depicts relative levels of Alu sequences.

[0049] Figures 21A, 21B and 21C show MA plots depicting relative expression levels of LI (Figure 21A), ALU (Figure 21B) and HERV-K (Figure 21C) RNA in cells and microvesicles derived from the cells. qRT-PCR was carried out for retrotransposon elements in cell RNA and exoRNA from three meduUoblastoma (D425, D384 and D458), one GBM (11/5), one melanoma (0106) and one human fibroblast (HF19) line. The RNA expression levels were measured and normalized to GAPDH. HERV-K RNA was not detectable in exoRNA from normal human fibroblasts (HF19), so it was given a Ct value of 36 (below detection limit).

[0050] Figure 22 shows a chart depicting the expression levels of HERV-K at different time points in HUVEC cells. The HUVEC cells were exposed to meduUoblastoma D384 microvesicles and their expression level of HERV-K RNA was analyzed by qRT-PCR over 72 hrs following exposure. MOCK is non-exposed cells. HERV-K was normalized to GAPDH. P values were calculated using the two-tailed t-test, comparing levels to MOCK infected cells.

[0051] Figures 23A, 23B and 23C show MA plots depicting relative levels of LI (Figure 23A), ALU (Figure 23B) and HERV-K (Figure 23C) DNA in cells and microvesicles derived from the cells. q-PCR was carried out for retrotransposon elements with cell genomic DNA and microvesicle DNA from three meduUoblastoma (D425, D384 and D458), one GBM (11/5), one melanoma (0106) and one human fibroblast (HF19) line. The DNA levels were measured and normalized to GAPDH. Results are expressed as average +SEM (n=3).

[0052] Figure 24 shows a chart depicting the Reverse Transcriptase (RT) activity in microvesicles secreted by three meduUoblastoma (D425, D384 and D458), one GBM (11/5), one melanoma (0106) and one human fibroblast (HF19) line. The RT activity was measured

in the microvesicles using the EnzChek RT Assay Kit (Invitrogen) and normalized to protein content. The RT activity is measured as RT units calculated based on the standard curve generated using Superscript III (Invitrogen). Results are expressed as average +SEM (n=3).

[0053] Figures 25A, 25B, 25C and 25D show charts depicting Bioanalyzer profiles of exoRNA and exoDNA from tumor or normal cell. Figure 25A depicts the profile of exoRNA from GBM 11/5 cells. Both 18S and 28S rRNA peaks are detectable (arrowheads). Figure 25B depicts the profile of exoDNA GBM 11/5 cells. Sizes ranged from 25 to 1000 nucleotides with a peak at 200 nt. Figure 25C depicts the profile of ExoRNA from human fibroblasts HF19, which was extracted and analyzed as in Figure 25A. The RNA yield was too low to yield distinct 18S and 28S rRNA peaks. After concentration, these peaks were visible (data not shown). Figure 25D depicts the profile of ExoDNA from human fibroblasts HF19, which was not readily detectable on the Bioanalyzer even after it was concentrated 30 times. Bioanalyzer profiles were generated using the RNA Pico Chip (Agilent).

[0054] Figures 26A and 26B show charts depicting the Bioanalyzer profiles of exoDNA from microvesicles isolated from medulloblastoma D384 cells. Figure 26A depicts the profile of exoDNA purified from externally DNase-treated microvesicles using the Agilent DNA 7500 bioanalyzer chip (Agilent Technologies Inc., Santa Clara, CA. Cat. Number 5067-1506) that detects dsDNA. Figure 26B depicts the profile of exoDNA after a second-strand synthesis treatment. Here the same sample as in (A) was subjected to second strand synthesis with Superscript Double-Stranded cDNA synthesis kit (Invitrogen) according to manufacturer's recommendation.

[0055] Figure 27 is an agarose gel picture depicting electrophoresis of GAPDH (112bp) PCR products using templates from different samples. The different samples were exoDNA samples extracted from microvesicles isolated from three medulloblastoma cell

lines (D425, D384 and D556) and genomic DNA extracted from L2132 normal fibroblasts as a control double stranded DNA, all four of which were mock treated or treated with SI nuclease enzyme which degrades single-stranded nucleic acids.

[0056] Figure 28 depicts representative bioanalyzer profiles of exoDNA extracted from medulloblastoma cell line D384 before and after SI nuclease treatment.

[0057] Figures 29A and 29B show charts depicting quantitative PCR results of c-Myc and POU5F1B, respectively, using as templates genomic DNA from cells or exoDNA extracted from microvesicles isolated from cells. Figure 29A depicts the results for c-Myc gene. Figure 29B depicts the results for POU5F1B, which gene sequence *(AF268618)* is found 319 kb upstream of the c-Myc gene in the genome, but still within the commonly amplified region in tumor cells. The cell lines are medulloblastoma cell lines D458 and D384, glioblastomas (11/5), and fibroblasts HF19.

[0058] Figure 30 illustrates the c-Myc copy number analysis results in tumor cell lines using an Affymetrix 250K SNP array. The c-Myc genomic region was analyzed in medulloblastoma lines, D425, D458 and D384, as well as rhabdoid tumor line, NS224.

[0059] Figures 31A and 3IB show charts depicting the qPCR results of the n-Myc gene in cells lines medulloblastoma D425, D458 and D384, rhabdoid tumor, GBM, and normal fibroblasts using genomic DNA Figure 31A or exoDNA Figure 3IB extracted from microvesicles isolated from the cells as templates.

[0060] Figure 32 shows a chart depicting the amount of exoDNA extracted from microvesicles isolated from medulloblastoma D384 cell culture media. D384 cells were seeded in 6-well plates and treated with increasing dosages of L-mimosine (200, 400 and 600 μM) or mock treated. Microvesicles were isolated from the medium after 48 hrs and ssDNA

was extracted using the Qiagen PCR purification kit. Single-stranded DNA yields were quantified using the Bioanalyzer and the yields were compared to mock treated cells (normalized to 1.0).

[0061] Figure 33 depicts the results of quantitative RT-PCR analysis of the expression levels of 7SL RNA, EGFR and GAPDH in microvesicles isolated from serum samples obtained from a GBM patient or a normal individual. The X-axis is the number of PCR cycles. The Y-axis is the fluorescent intensity (delta Rn) measured by the AB17500 machine.

[0062] Figure 34 depicts a series of signaling pathways related to cell proliferation, growth and/or survival.

DETAILED DESCRIPTION OF THE INVENTION

[0063] As described above, cell-derived vesicles are heterogeneous in size with diameters ranging from about 10 nm to about 1 μm. For example, "exosomes" have diameters of approximately 30 to 100 nm, with shedding microvesicles and apoptotic bodies often described as larger (Orozco and Lewis, 2010). Exosomes, shedding microvesicles, microparticles, nanovesicles, apoptotic bodies, nanoparticles and membrane vesicles co-isolate using various techniques and will, therefore, collectively be referred to throughout this specification as "microvesicles" unless otherwise expressly denoted.

[0064] The present invention is based on the discovery that cancer-related biological materials such as transposable elements, oncogenes, and reverse transcriptase (RT) can be detected in microvesicles.

[0065] The biological materials in microvesicles can be genetic materials, protein materials, lipid materials, or any combination of genetic, protein and lipid materials.

[0066] Genetic materials include nucleic acids, which can be DNA and its variations, e.g., double-stranded DNA ("dsDNA"), single-stranded DNA ("ssDNA"), genomic DNA, cDNA; RNA and its variations, e.g., mRNA, rRNA, tRNA, microRNA, siRNA, piwi-RNA, coding RNA, non-coding RNA, transposons, satellite repeats, minisatellite repeats, microsatellite repeats, Interspersed repeats such as short interspersed nuclear elements (SINES), e.g. but not limited to Alus, and long interspersed nuclear elements (LINES), e.g. but not limited to LINE-1, human endogenous retroviruses (HERVs), e.g. but not limited to HERV-K; or any combination of any of the above DNA and RNA species.

[0067] Protein materials can be any polypeptides and polypeptide variants recognized in the art. For convenience, "polypeptide" as disclosed in this application refers to both a polypeptide without modifications and a polypeptide variant with modifications. Polypeptides are composed of a chain of amino acids encoded by genetic materials as is well known in the art. For example, a reverse transcriptase is a polypeptide that can function as an enzyme to transcribe RNA into DNA. Polypeptide variants can include, e.g. polypeptides modified by acylation, ubiquitination, SUMOYlation, alkylation, amidation, glycosylation, hydroxylation, carboxylation, phosphorylations, oxidation, sulfation, selenoylation, nitrosylation, or glutathionylation.

[0068] Lipid materials include fats, waxes, sterols, fat-soluble vitamins (such as vitamins A, D, E and K), monoglycerides, diglycerides, phospholipids, fatty acids, glycerolipids, glycerophospholipids, sphingolipids, sterol lipids, prenol lipids, saccharolipids, and polyketides.

[0069] Microvesicles may be isolated from tissue, cells or other biological samples from a subject. For example, the biological sample may be a bodily fluid from the subject, preferably collected from a peripheral location. Bodily fluids include but are not limited to blood, plasma, serum, urine, sputum, spinal fluid, pleural fluid, nipple aspirates, lymph fluid,

fluid of the respiratory, intestinal, and genitourinary tracts, tear fluid, saliva, breast milk, fluid from the lymphatic system, semen, cerebrospinal fluid, intra-organ system fluid, ascitic fluid, tumor cyst fluid, amniotic fluid and combinations thereof. In some embodiments, the preferred bodily fluid for use as the biological sample is urine. In other embodiments, the preferred bodily fluid is serum.

[0070] The term "subject" is intended to include all animals shown to or expected to harbor nucleic acid-containing microvesicles. In particular embodiments, the subject is a mammal, e.g., a human or nonhuman primate, a dog, cat, horse, cow, other farm animal, or rodent (e.g. a mouse, rat, guinea pig, etc.). In one embodiment, the subject is an avian, amphibian or fish. The terms "subject," "individual" and "patient" are used interchangeably herein.

[0071] Methods for isolating microvesicles from a biological sample and extracting biological materials from the isolated microvesicles are described in this application as well as in scientific publications and patent applications, e.g. (Chen et al., 2010; Miranda et al., 2010; Skog et al., 2008). See also WO 2009/100029, WO 2011/009104, WO 2011/031892 and WO 201 1/031877. These publications are incorporated herein by reference for their disclosure pertaining to isolation and extraction methods and techniques.

[0072] A profile, as used herein, refers to a set of data or a collection of characteristics or features, which can be determined through the quantitative or qualitative analysis of one or more biological materials, particularly biological materials contained in microvesicles isolated from a subject. The biological materials, extraction of the biological materials, and various types of analysis of the biological materials are described herein. A control or reference profile is a profile obtained from the literature, from an independent subject or subjects, or from the same subject at a different time point.

[0073] In one aspect, the present invention includes a profile of one or more nucleic acids extracted from microvesicles. The nucleic acids include both RNA and DNA. A nucleic acid profile may be an RNA profile, a DNA profile, or may include profiles of both RNA and DNA. In other aspects, the present invention includes a profile of one or more protein or polypeptide species extracted from microvesicles, particularly, a level of protein activity.

[0074] In all of the various aspects of the invention described herein in relation to RNA, the RNA can be coding RNA, e.g., messenger RNA. The RNA can also be non-coding RNA (ncRNA), e.g., ribosomal RNA (rRNA), transfer RNA (tRNA), microRNA, and other non-coding transcripts that may originate from genomic DNA. See Table 9 for more examples of non-coding RNA. Non-coding RNA transcripts may include transcripts from satellite repeats or from transposons, which may be Class I retrotransposons or Class II DNA transposons.

[0075] In all of the various aspects of the invention described herein in relation to DNA, the DNA can be single-stranded DNA, e.g., cDNA, which is reverse transcribed from RNA. Reverse transcription is usually mediated by reverse transcriptase encoded by a reverse transcriptase gene in a cell. The DNA can also be single stranded DNA generated during DNA replication. Genomic DNA replicates in the nucleus while the cell is dividing. Some of the replicated DNA may come off its template, be exported out of the nucleus, and packaged into microvesicles. The DNA can further be fragments of double-stranded DNA.

[0076] In addition, the DNA can be non-coding DNA (ncDNA). The human genome contains only about 20,000 protein-coding genes, representing less than 2% of the genome. The ratio of non-coding to protein-coding DNA sequences increases as a function of developmental complexity (Mattick, 2004). Prokaryotes have less than 25% ncDNA, simple eukaryotes have between 25-50%, more complex multicellular organisms like plants and

animals have more than 50% ncDNA, with humans having about 98.5% ncDNA (Mattick, 2004)

[0077] Some of the ncDNA from the genome is transcribed into ncRNA. NcRNAs have been implicated in many important processes in the cell, e.g., enzymes (ribozymes), binding specifically to proteins (aptamers), and regulating gene activity at both the transcriptional and post-transcriptional levels. Examples of ncRNA classes and examples of their functions are shown in Table 9.

[0078] Many of the ncRNA species have multiple functions. For example, Ribonuclease P (RNase P) is a ribozyme which is involved in maturation of tRNA by cleaving the precursor tRNA, and nuclear RNaseP can also act as a transcription factor (Jarrous and Reiner, 2007). In addition, bifunctional RNAs have also been described that function both as mRNA and as regulatory ncRNAs (Dinger et al., 2008) or have two different ncRNA functions (Ender et al., 2008).

[0079] One example of the many long ncRNAs is the X-inactive specific transcript (Xist) expressed by the inactive X-chromosome, which is used to silence the extra X-chromosome in females (Ng et al., 2007). This RNA transcript binds to and inactivates the same X chromosome from which it is produced.

[0080] Another example is the HOX antisense intergenic RNA (HOTAIR) (Rinn et al., 2007). This RNA is expressed from chromosome 12, but controls gene expression on chromosome 2, affecting the skin phenotype on different parts of the body surface (Rinn et al., 2007) and also being involved in cancer metastasis (Gupta et al., 2010).

[0081] Yet another example of ncRNA is PCA3, a biomarker for prostate cancer (Day et al., 201 1). PCA3 can be readily measured in the RNA from urine microvesicles which can be extracted using a rapid filtration concentrator method (Miranda et al., 2010; Nilsson et al.,

2009). Another biomarker for prostate cancer is PCGEM1, which is an ncRNA transcript over-expressed in prostate cancer (Srikantan et al., 2000).

[0082] Yet another example of ncRNA is NEAT2/MALAT1, which has been found to be upregulated during metastasis of non-small cell lung cancer, and was correlated with poor patient survival (Ji et al., 2003).

[0083] Microvesicles contain a substantial array of the cellular gene expression profile from the cells from which they originate (their parent cells) at any given time. That is, substantially all the RNAs expressed in the parent cell are present within the microvesicle, although the quantitative levels of these RNAs may differ in the microvesicle compared to the parent cell. Substantially all the genes from the parent cell can, therefore, be tracked in the microvesicle fraction. In addition, microvesicles contain DNA from the parent cell, which corresponds to diagnostically relevant aspects of the subject's genome. Therefore, a nucleic acid profile from microvesicles may be associated with a disease or other medical condition.

[0084] In one embodiment, the disease is a neurological disease or other medical condition, e.g., Alzheimer's disease. The nucleic acid profile for Alzheimer's disease may be a profile of early-onset familial Alzheimer's disease, associated genes including, but not limited to, amyloid beta (A4) precursor protein gene, presenilin 1 and presenilin 2.

[0085] In another embodiment, the disease is a cancer. The microvesicular nucleic acid profile for cancer may, e.g., include nucleic acids of one or more cancer-related genes (e.g., known or suspected oncogenes or tumor suppressor genes; or genes whose expression levels correlate with the expression levels of nearby satellites). The determination of a cancer nucleic acid profile, including such cancer related genes, can aid in understanding the status of the cancer cells. In one embodiment, the oncogenes or tumor suppressor genes are one or more of those listed in Tables 2 and 3. In another embodiment, the cancer-related genes are

one or more of those genes whose expression levels correlate with the expression levels of nearby satellites, such as but not limited to the satellite correlated genes listed in Table 6.

[0086] In some instances, the cancer-related gene is c-myc. The copy number of c-myc oncogene is usually increased in tumor cells, e.g., meduUablastoma cells. The detection of increased c-myc gene copy number in microvesicles indicates an increased c-myc copy number in tumor cells that secret the microvesicles.

[0087] In other instances, the cancer-related gene is one or more members in the signaling pathways depicted in **Fig. 34.** These signaling pathways control the growth, proliferation and/or survival of cells (Alessi et al., 2009; Dowling et al.; Hanahan and Weinberg, 2000; Sarbassov et al., 2006). These pathways are sometimes cross-linked to each other, and thus enable extracellular signals to elicit multiple biological effects. For example, the growth promoting Ras protein interacts with the survival promoting PI3K and thus growth signals can concurrently evoke survival signals in the cell (Hanahan and Weinberg, 2000).

[0088] For one example, the member is from the RAS/RAF/MEK/MAPK pathway related to melanoma, brain and lung cancers. The MAP kinase is a convergence point for diverse receptor-initiated signaling events at the plasma membrane. The RAS/RAF/MEK/MAPK pathway regulates cell proliferation, differentiation, migration and invasion (Hanahan and Weinberg, 2000). In addition, extracellular signal-regulated kinases (ERKs) become activated upon integrin ligation and, thereby, regulate cell migration (Klemke et al., 1997).

[0089] For another sample, the member is from the PI3K/PTEN/AKT pathway related to prostate, bladder and kidney cancers. The PI3K/PTEN/AKT pathway is responsible for regulating cell survival (Cheng et al., 2008). Genetic variations in AKT1,

AKY2, PIK3CA, PTEN, and FRAP1 are associated with clinical outcomes in patients who receive chemoradiotherapy (Hildebrandt et al., 2009). Therefore, the determination of genetic variations in members of the pathway may help evaluating cancer treatment efficacy.

[0090] The microvesicular nucleic acid profile of the present invention may also reflect the nucleic acid profile of DNA repeats and/or transposable elements in cells from which the microvesicles originate.

[0091] DNA repeats include one or more repeated DNA elements that are composed of arrays of tandemly repeated DNA with the repeat unit being a simple or moderately complex sequence. The array of tandemly repeated DNA can be of varying size, thereby giving rise to categories of megasatellite, satellite, minisatellite and microsatellite repeats. See Table 7. Repeated DNA of this type is not transcribed and accounts for the bulk of the heterochromatic regions of the genome, being notably found in the vicinity of the centromeres (i.e., pericentromeric heterochromatin). The base composition, and therefore density, of such DNA regions is dictated by the base composition of constituent short repeat units and may diverge from the overall base composition of other cellular DNA. The nucleic acid profiles of the present invention comprising satellite repeats may include profiles of satellite repeat DNA and/or profiles of transcripts that are transcribed from satellite repeats.

[0092] DNA repeats may serve as biomarkers of cancer cells. For example, some satellite repeats like HSATII are over-expressed in many types of cancers including pancreatic, lung, kidney, ovarian and prostate cancers (Ting et al., 2011). The RNA expression level of such satellite repeats correlates with cancer disease status. DNA repeats encompassed within the scope of the present invention can be one or more of those recited in Table 8. In some embodiments, the DNA repeats may be HSATII, ALR, $(CATTC)_n$, or a combination of the HSATII, ALR, and $(CATTC)_n$.

[0093] Transposable elements encompassed within the scope of the present invention may be one or more DNA transposons and/or retrotransposons. The retrotransposon can be one or more of those recited in Tables 3 and 4. In other embodiments, the retrotransposon can be one or more LINEs, Alus, HERVs or a combination of the LINEs, Alus and HERVs.

[0094] Transposable elements can serve as biomarkers of cancer cells. These repetitive elements constitute almost 50% of the human genome and include: half a million LINE-1 (LI) elements, of which about 100 are transcriptionally active and encode proteins involved in retrotransposition, including reverse transcriptase (RT) and integrase; a million Alu elements, which depend on LI functions for integration; and thousands of provirus HERV sequences, some of which contain near-to-full length coding sequences(Goodier and Kazazian, 2008; Voisset et al., 2008). Without being bound by theory, increased expression of retrotransposon elements in cancer appears to result in part from overall hypomethylation of the genome, which is also associated with genomic instability (Daskalos et al., 2009; Estecio et al., 2007) and tumor progression (Cho et al., 2007; Roman-Gomez et al., 2008).

[0095] Increased transcription of retrotransposon elements in the human genome has been noted in a number of cancer cell types. For example, increased expression of LI and HERV, as well as formation of retrovirus-like particles, has been reported in tumor tissue from breast cancer, melanoma, germ cell carcinoma and prostate cancer. See US 7,776,523 and Bratthauer et al., 1994; Golan et al., 2008; Ruprecht et al., 2008. Retrotransposon RNA and proteins, as well as antibodies against HERV proteins and virus-like particles, have also been found in blood of some cancer patients (Contreras-Galindo et al., 2008; Kleiman et al., 2004; Ruprecht et al., 2008; Wang-Johanning et al., 2008).

[0096] High level expression of retrotransposon genes and/or endogenous reverse transcriptase are sometimes associated with cancer. For example, human LINE-1 p40 protein

is often expressed at a higher level in breast cancer than in normal mammary gland (Asch et al., 1996). Thus, the microvesicular nucleic acid profiles of retrotransposable elements are suitable for use in aiding the diagnosis, prognosis, and/or monitoring of medical conditions such as cancer, as well as for use in aiding in treatment selection for therapies whose efficacy is affected by the subject's genetic make-up.

[0097] In one embodiment of the present invention, the microvesicular profile(s) of retrotransposable element(s) are determined by analyzing the content of microvesicles originating from brain cancer, e.g., medullablastoma, glioblastoma, lymphoma, and breast cancer cells. In one instance, the profile comprises one or more RNA expression levels of LI, Alu and HERV elements. In another instance, the profile comprises one or more DNA levels of LI and HERV elements.

[0098] In one embodiment, the profile comprises a profile of the HERV-K element. For example, the profile may comprise the expression of the HERV-K element in microvesicles isolated from plasma from a subject. The expression of the HERV-K element may be assessed by determining the expression of any gene that the HERV-K element may encode, e.g., the group-specific antigen gene (gag), the protease gene (prt), the polymerase gene (pol), and the envelope gene (env) (Lower et al., 1996).

[0099] In one instance, the present invention may comprise a profile of the expression of the gag gene in microvesicles. The gag gene is from the HERV-K element and the profile of gag expression reflects the profile of HERV-K expression. The expression of the gag gene can be measured by methods known in the art, e.g., quantitative reverse transcription PCR analysis.

[00100] In another instance, the present invention may comprise a profile of the expression of the env gene in microvesicles. The env gene is from the HERV-K element and the profile of env expression reflects the profile of HERV-K expression. The expression of

env gene can be measured by methods known in the art, e.g., quantitative reverse transcription PCR analysis.

[00101] In addition to the mRNA expression levels of one or more nucleic acids, the nucleic acid profiles of the present invention may also comprise the copy number of one or more nucleic acids, the fusion of several nucleic acids, the mutations of one or more nucleic acids, the alternative splicing of one or more nucleic acids, the methylation of one or more nucleic acids, and the single nucleotide polymorphism of one or more nucleic acids. The nucleic acids may correspond to genes, repeats, transposable elements, or other non-coding parts of the genomes of various organisms, including human beings.

[00102] The present invention encompasses all forms of cancer and pre-cancerous conditions. For example, without limitation, the present invention encompasses cancer and pre-cancer cells in brain, esophagus, lung, liver, stomach, ovary, testicle, kidney, skin, colon, blood, prostate, breast, uterus, and spleen.

[00103] The profile of nucleic acids can be obtained through analyzing nucleic acids obtained from isolated microvesicles according to standard protocols in the art.

[00104] In one embodiment, the nucleic acid is DNA. The analysis of the DNA may be performed by one or more various methods known in the art, including microarray analysis for determining the nucleic acid species in the extract, Quantitative PCR for measuring the expression levels of genes, DNA sequencing for detecting mutations in genes, and bisulfite methylation assays for detecting methylation patterns of genes.

[00105] In some embodiments of the present invention, data analysis may be performed by any of a variety of methods know in the art, e.g., Clustering Analysis, Principle Component Analysis, Linear Discriminant Analysis, Receiver Operating Characteristic Curve Analysis, Binary Analysis, Cox Proportional Hazards Analysis, Support Vector Machines

and Recursive Feature Elimination (SVM-RFE), Classification to Nearest Centroid, Evidence-based Analysis, or a combination thereof.

[00106] In another embodiment, the nucleic acid extracted and analyzed from the microvesicles is RNA. In some instance, the RNA may be subject to Digital Gene Expression (DGE) analysis (Lipson et al., 2009). In this method, the RNA may be digested and converted into single stranded cDNA which may then be subject to sequencing analysis on a DNA sequencing machine, e.g., the HeliScope™ Single Molecule Sequencer from Helicos Biosciences as described in a publication by Ting et al. (Ting et al., 2011).

[00107] In other instances, the RNA is preferably reverse-transcribed into complementary DNA (cDNA) before further amplification. Such reverse transcription may be performed alone or in combination with an amplification step. One example of a method combining reverse transcription and amplification steps is reverse transcription polymerase chain reaction (RT-PCR), which may be further modified to be quantitative, e.g., quantitative RT-PCR as described in US Patent No. 5,639,606, which is incorporated herein by reference for this teaching. Another example of the method comprises two separate steps: a first step of reverse transcription to convert RNA into cDNA and a second step of quantifying the amount of cDNA using quantitative PCR.

[00108] Nucleic acid amplification methods include, without limitation, polymerase chain reaction (PCR) (US Patent No. 5,219,727) and its variants such as in situ polymerase chain reaction (US Patent No. 5,538,871), quantitative polymerase chain reaction (US Patent No. 5,219,727), nested polymerase chain reaction (US Patent No. 5,556,773), self-sustained sequence replication and its variants (Guatelli et al., 1990), transcriptional amplification system and its variants (Kwoh et al., 1989), Qb Replicase and its variants (Miele et al., 1983), cold-PCR (Li et al., 2008), BEAMing (Li et al., 2006) or any other nucleic acid amplification methods, followed by the detection of the amplified molecules using techniques well known

to those of skill in the art. Especially useful are those detection schemes designed for the detection of nucleic acid molecules if such molecules are present in very low numbers. The foregoing references are incorporated herein for their teachings of these methods. In other embodiment, the step of nucleic acid amplification is not performed. Instead, the extracted nucleic acids are analyzed directly, e.g., through next-generation sequencing.

[00109] The analysis of nucleic acids present in the isolated microvesicles can be quantitative, qualitative, or both quantitative and qualitative. For quantitative analysis, the amounts (expression levels), either relative or absolute, of specific nucleic acids of interest within the isolated microvesicles are measured with methods known in the art (some of which are described below). For qualitative analysis, the species of specific nucleic acids of interest within the isolated particles, whether wild type or variants, are identified with methods known in the art.

[00110] The present invention further encompasses methods of creating and using the microvesicular nucleic acid profiles described herein. In one embodiment of a method for creating a microvesicular profile, the method comprises the steps of isolating microvesicles from a biological sample (e.g., from a body fluid) obtained from a subject or obtaining a microvesicle fraction isolated from a biological sample obtained from a subject, extracting nucleic acids from the isolated microvesicles or microvesicle fraction (or obtaining such as extraction), and determining the profile of the nucleic acids in the extract.

[00111] The microvesicular profiles of the present invention may be used in methods of aiding diagnosis, prognosis, monitoring, therapy selection, or risk assessment of a disease or other medical condition for a subject as described herein and in the claims.

[00112] In some embodiments of the present invention, the one or more nucleic acid(s) may be one or more genes listed in Table 2 (cancer genes), Table 3 (cancer-related somatic mutations) and Table 6 (satellite-correlated genes). In one embodiment, the one or more

nucleic acid(s) may be a fragment of a c-myc gene, for example, a fragment of c-myc gene containing more than 10 nucleotides. The fragment may contain incrementally longer sequences of 15, 20, 25, 30, 35, 40, 45, 50, 55, 60 nucleotides, up to the full length of the gene.

[00113] In other embodiments, the one or more nucleic acids may be one or more sequences listed in Table 4 (GBM transposable elements), Table 5 (human transposable elements) and Table 8 (repeated DNA). In one embodiment, the one or more nucleic acids may be LI, Alu, HERV, fragments thereof, or any combination of any of the foregoing. The fragment may contain incrementally longer sequences of 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60 nucleotides up to the full length of each gene sequence.

[00114] In one embodiment, the invention comprises microvesicular profiles and methods based on microvesicular polypeptide species, polypeptide activities, or both the species and activities of polypeptides. The polypeptide may be any polypeptide in microvesicles. In some embodiments, the polypeptide is a reverse transcriptase. The activity of the reverse transcriptase (RT) can be measured by standard protocols known in the art. For example, the RT activity can be measured by the EnzChek RT Assay Kit (Invitrogen).

[00115] The human endogenous retrovirus K (HERV-K) reverse transcriptase may serve as a breast cancer prognostic marker (Golan et al., 2008). As such, one particular embodiment of the present invention encompasses profiles and related methods based on detecting the activity of HERV-K reverse transcriptase in microvesicles.

[00116] The present invention also includes a kit for genetic analysis of a microvesicle preparation from a biological sample (e.g., a bodily fluid sample) from a subject. The kit in a suitable container may include one or more reagents capable of hybridizing to or amplifying one or more nucleic acids extracted from microvesicles. In some embodiments, the nucleic acids correspond to one or more of those genes listed in Tables 2, 3, 4, 5, 6 and/or 8. In some

further embodiments, the nucleic acids correspond to one or more RNA transcripts of one or more genes listed in Tables 2, 3, 4, 5, 6 and/or 8. In other further embodiments, the nucleic acid is DNA corresponding to one or more of the genes listed in Tables 2, 3, 4, 5, 6 and/or 8.

[00117] The present invention further includes an oligonucleotide microarray for genetic analysis of a microvesicle preparation from a body fluid sample from a subject, wherein the various oligonucleotides on the array are designed to hybridize exclusively to nucleic acids corresponding to one or more genes listed in Tables 2, 3, 4, 5, 6 and/or 8. The arrays can be made by standard methods known in the art. For example, SurePrint Technology (Agilent Technologies Corp.) may be used to make as many as 8 arrays on a single slide.

[00118] The present invention also includes a method of aiding the discovery of one or more biomarkers for a disease or other medical condition. The method may comprise, e.g., the steps of isolating microvesicles from subjects having a disease or other medical condition of interest and also from subjects who do not have the disease or other medical condition of interest; measuring the level of one or more target biological materials extracted from the isolated microvesicles from each of the subjects; comparing the measured levels of the one or more target biological materials from each of the subjects; and determining whether there is a statistically significant difference in the measured levels. The step of determination of a statistically significant difference in the measured levels identifies the one or more target biological materials as potential biomarkers for the disease or other medical condition. As an alternative to isolating microvesicles, the method may be carried out with pre-isolated microvesicle fractions.

[00119] The one or more biomarkers and nucleic acids in each of the various embodiments of the invention described herein can be one or a collection of genetic aberrations. The term "genetic aberration" is used herein to refer to the nucleic acid amounts

as well as nucleic acid variants within the nucleic acid-containing particles. Specifically, genetic aberrations include, without limitation, over-expression of a gene (e.g., an oncogene) or a panel of genes, under-expression of a gene (e.g., a tumor suppressor gene such as p53 or RB) or a panel of genes, alternative production of splice variants of a gene or a panel of genes, gene copy number variants (CNV) (e.g., DNA double minutes) (Hahn, 1993), nucleic acid modifications (e.g., methylation, acetylation and phosphorylations), single nucleotide polymorphisms (SNPs) (e.g., polymorphisms in Alu elements), chromosomal rearrangements (e.g., inversions, deletions and duplications), and mutations (insertions, deletions, duplications, missense, nonsense, synonymous or any other nucleotide changes) of a gene or a panel of genes, which mutations, in many cases, ultimately affect the activity and function of the gene products, lead to alternative transcriptional splice variants and/or changes of gene expression level, or combinations of any of the foregoing.

[00120] Genetic aberrations can be found in many types of nucleic acids. The determination of such genetic aberrations can be performed by a variety of techniques known to the skilled practitioner. For example, expression levels of nucleic acids, alternative splicing variants, chromosome rearrangement and gene copy numbers can be determined by microarray analysis (see, e.g., US Patent Nos. 6,913,879, 7,364,848, 7,378,245, 6,893,837 and 6,004,755) and quantitative PCR. Particularly, copy number changes may be detected with the Illumina Infinium II whole genome genotyping assay or Agilent Human Genome CGH Microarray (Steemers et al., 2006).

[00121] Nucleic acid modifications can be assayed by methods described in, e.g., US Patent No. 7,186,512 and patent publication WO/2003/023065. Particularly, methylation profiles may be determined by Illumina DNA Methylation OMA003 Cancer Panel.

[00122] SNPs and mutations can be detected by hybridization with allele-specific probes, enzymatic mutation detection, chemical cleavage of mismatched heteroduplex

(Cotton et al., 1988), ribonuclease cleavage of mismatched bases (Myers et al., 1985), mass spectrometry (US Patent Nos. 6,994,960, 7,074,563, and 7,198,893), single strand conformation polymorphism (SSCP) (Orita et al., 1989), denaturing gradient gel electrophoresis (DGGE)(Fischer and Lerman, 1979a; Fischer and Lerman, 1979b), temperature gradient gel electrophoresis (TGGE) (Fischer and Lerman, 1979a; Fischer and Lerman, 1979b), restriction fragment length polymorphisms (RFLP) (Kan and Dozy, 1978a; Kan and Dozy, 1978b), oligonucleotide ligation assay (OLA), allele-specific PCR (ASPCR) (US Patent No. 5,639,611), ligation chain reaction (LCR) and its variants (Abravaya et al., 1995; Landegren et al., 1988; Nakazawa et al., 1994), flow-cytometric heteroduplex analysis (WO/2006/113590), nucleic acid sequencing, and combinations/modifications thereof.

[00123] Nucleic acid sequencing is to determine the base pair sequences of nucleic acids. Two traditional techniques for sequencing DNA are the Sanger dideoxy termination method (Sanger et al., 1977) and the Maxam-Gilbert chemical degradation method (Maxam and Gilbert, 1977). Both methods deliver four samples with each sample containing a family of DNA strands in which all strands terminate in the same nucleotide. Gel electrophoresis, or more recently capillary array electrophoresis is used to resolve the different length strands and to determine the nucleotide sequence, either by differentially tagging the strands of each sample before electrophoresis to indicate the terminal nucleotide, or by running the samples in different lanes of the gel or in different capillaries. Related methods using dyes or fluorescent labels associated with the terminal nucleotide have been developed, where sequence determination is also made by gel electrophoresis and automated fluorescent detectors. For example, the Sanger-extension method has recently been modified for use in an automated micro-sequencing system which requires only sub-microliter volumes of reagents and dye-labelled dideoxyribonucleotide triphosphates. U.S. Patent No. 5,846,727.

[00124] More recently, high throughput DNA sequencing methods of various types have been developed and used to delineate nuclei acis sequences. These new methods are applied in sequencing machines including the 454 GenomeSequencer FLX instrument (Roche Applied Science), the Illumina (Solexa) Genome Analyzer, the Applied Biosystems ABI SOLiD system, the Helicos single-molecule sequencing device (HeliScope), and the Ion semiconductor sequencing by Ion Torrent Systems Inc. See also US patent application publications No. 20110111401 and No. 20110098193. It is understood that as the sequencing technology evolves, the analysis of nucleic acids obtained in the invention may be performed using any new sequencing method as one skilled in the art sees appropriate.

[00125] Gene expression levels may be determined by the serial analysis of gene expression (SAGE) technique (Velculescu et al., 1995), quantitative PCR, quantitative reverse transcription PCR, microarray analysis, and next generation DNA sequencing as known in the art.

[00126] In general, the methods for analyzing genetic aberrations are reported in numerous publications, not limited to those cited herein, and are available to skilled practitioners. The appropriate method of analysis will depend upon the specific goals of the analysis, the condition/history of the patient, and the specific cancer(s), diseases or other medical conditions to be detected, monitored or treated. The forgoing references are incorporated herein for their teaching of these methods.

[00127] Many biomarkers may be associated with the presence or absence of a disease or other medical condition in a subject. Therefore, detection of the presence or absence of such biomarkers in nucleic acids extracted from isolated microvesicles, according to the methods disclosed herein, may aid diagnosis of the disease or other medical condition in the subject.

[00128] For example, as described in WO 2009/100029, detection of the presence or

absence of the EGFRvIII mutation in nucleic acids extracted from microvesicles isolated from a patient serum sample aided in the diagnosis and/or monitoring of glioblastoma in the patient. This is so because the expression of the EGFRvIII mutation is specific to some tumors and defines a clinically distinct subtype of glioma (Pelloski et al., 2007).

[00129] For another example, as described in WO 2009/100029, detection of the presence or absence of the TMPRSS2-ERG fusion gene, PCA-3, or both TMPRSS2-ERG and PCA-3 in nucleic acids extracted from microvesicles isolated from a patient's urine sample may aid in the diagnosis of prostate cancer in the patient.

[00130] Further, many biomarkers may be associated with disease or medical status monitoring in a subject. Therefore, the detection of the presence or absence of such biomarkers in a nucleic acid extraction from isolated microvesicles, according to the methods disclosed herein, may aid in monitoring the progress or reoccurrence of a disease or other medical condition in a subject.

[00131] For example, as described in WO 2009/100029, the determination of matrix metalloproteinase (MMP) levels in nucleic acids extracted from microvesicles isolated from an organ transplantation patient may be used to monitor the post-transplantation condition, as a significant increase in the expression level of MMP-2 after kidney transplantation may indicate the onset and/or deterioration of post-transplantation complications. Similarly, a significantly elevated level of MMP-9 after lung transplantation, suggests the onset and/or deterioration of bronchiolitis obliterans syndrome.

[00132] Many biomarkers have also been found to influence the effectiveness of treatment in a particular patient. Therefore, the detection of the presence or absence of such biomarkers in a nucleic acid extraction from isolated microvesicles, according to the methods disclosed herein, may aid in evaluating the efficacy of a given treatment in a given patient. For example, as disclosed in Table 1 in the publication by Furnari et al. (Furnari et al., 2007),

biomarkers, e.g., mutations in a variety of genes, affect the effectiveness of specific medicines used in chemotherapy for treating brain tumors. The identification of these and other biomarkers in nucleic acids extracted from isolated particles from a biological sample from a patient can guide the skilled practitioner in the selection of treatment for the patient.

[00133] Without limitation, all of the methods mentioned above may further comprise the step of enriching the isolated microvesicles for microvesicles originating from a specific cell type. For example, the cell can be a cancer or pre-cancer cell.

[00134] Another aspect of the present invention is a method of treating a subject suffering from a form of cancer in which the cancer cells secret microvesicles. The method comprises administering to the subject a therapeutically effective amount of a composition comprising: an inhibitor of microvesicle secretion; an inhibitor of a reverse transcriptase; another microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles; or any combination of the inhibitors/neutralizers.

[00135] In one embodiment, the inhibitor of microvesicle secretion is an inhibitor of the Rab GTPase pathway (Ostrowski et al.).

[00136] In some instances, the Rab GTPases are Rab 27a and Rab 27b. The inhibition of the Rab 27a and Rab 27b can be effectuated by silencing the Slp4 gene (also known as SYTL4, synaptotagmin-like 4) and the Slac2b gene (also known as EXPH5, exophilin5), respectively. Gene silencing techniques are well known in the art. One example of such a gene silencing technique is an RNA interference technique that selectively silences genes by delivering shRNA with viral vectors (Sliva and Schnierle).

[00137] In other instances, the Rab GTPase is Rab35. The inactivation of Rab35 decreases microvesicle secretion. Therefore, silencing Rab35 may decrease the secretion of microvesicles by cells. Inactivation of Rab35 may be achieved by administering TBCIDIOB (TBC1 domain family, member 10B) polypeptide (Sliva and Schnierle).

[00138] In another embodiment, instead of, or in addition to, inhibiting microvesicle secretion, the reverse transcriptase activity is inhibited by administration of an RT inhibitor. RT inhibitors may be any one of 3'-azido2',3'-dideoxythymidine (AZT), 2',3'-dideoxyinosine (ddl), 2',3'-didehyro-3'-deoxythymidine (d4T), nevirapine and efavirenz.

[00139] Further, a microvesicle neutralizer may be used to block the effects of microvesicles. For example, such neutralizer may bind to microvesicles and destroy the integrity of microvesicles so that the biological materials in microvesicles are not transferred to other intact cells.

[00140] It should be understood that this invention is not limited to the particular methodologies, protocols and reagents, described herein, which may vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims.

[00141] The contents of earlier filed provisional applications USSN 61/378,860, filed August 31, 2010, USSN 61/421,421, filed December 9, 2010, USSN 61/437,547, filed January 28, 2011, USSN 61/438,199, filed January 31, 2011, and 61/493,261 filed June 03, 201 1 are herein incorporated by reference in their entirety.

[00142] All patents, patent applications, and publications cited herein are expressly incorporated herein by reference for the purpose of describing and disclosing, for example, the methodologies and techniques described in such publications that might be used in connection with the present invention. These publications are provided solely for their disclosure prior to the filing date of the present application. Nothing in this regard should be construed as an admission that the inventors are not entitled to antedate such disclosure by virtue of prior invention or for any other reason. All statements as to the date or representation as to the contents of these documents is based on the information available to

the applicants and does not constitute any admission as to the correctness of the dates or contents of these documents.

[00143] The present invention may be as defined in any one of the following numbered paragraphs.

1. A method for assaying a biological sample from a subject in aid of diagnosis, prognosis or monitoring of a disease or other medical condition in the subject, comprising the steps of:
   a. obtaining or using a microvesicle fraction from a biological sample from a subject;
   b. extracting nucleic acid from the fraction; and
   c. detecting the presence or absence of a biomarker in the extracted nucleic acid;
   wherein the biomarker is a genetic aberration associated with diagnosis, prognosis, status or stage of a disease or other medical condition, and wherein the genetic aberration is in or corresponds to:
      i. a c-myc gene;
      ii. a transposable element;
      iii. a retrotransposon element;
      iv. a satellite correlated gene;
      v. a repeated DNA element;
      vi. non-coding RNA other than miRNA; or
      vii. a fragment of any of the foregoing.

2. The method of paragraph 1, wherein the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof.

3. The method of paragraph 1, wherein the genetic aberration is in or corresponds to a retrotransposon element that is LINE, SINE or HERV, or a fragment thereof.

4. The method of paragraph 3, wherein the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

5. The method of paragraph 1, wherein the genetic aberration is in or corresponds to a satellite correlated gene listed in Table 6, or a fragment thereof.

6. The method of paragraph 1, wherein the genetic aberration is in or corresponds to a repeated DNA element listed in Table 8, or a fragment thereof.

7. The method of paragraph 1, wherein the genetic aberration is in or corresponds to a non-coding RNA listed in Table 9 (or a fragment thereof), other than miRNA.

8. The method of paragraph 7, wherein the non-coding RNA is 7SL.

9. A method for assaying a biological sample from a subject in aid of directing treatment of the subject for a disease or other medical condition, comprising the steps of :

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other medical condition, and wherein the genetic aberration is in or corresponds to:

i. a c-myc gene;

ii. a transposable element;

iii. a retrotransposon element;

iv. a satellite correlated gene;

v. a repeated DNA element;

vi. non-coding RNA other than miRNA; or

vii. a fragment of any of the foregoing.

10. The method of paragraph 9, wherein the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof.

11. The method of paragraph 9, wherein the genetic aberration is in or corresponds to a retrotransposon element that is LINE, SINE or HERV, or a fragment thereof.

12. The method of paragraph 11, wherein the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

13. The method of paragraph 9, wherein the genetic aberration is in or corresponds to a satellite correlated gene listed in Table 6, or a fragment thereof.

14. The method of paragraph 9, wherein the genetic aberration is in or corresponds to a repeated DNA element listed in Table 8, or a fragment thereof.

15. The method of paragraph 9, wherein the genetic aberration is in or corresponds to a non-coding RNA listed in Table 9 (or a fragment thereof), other than miRNA.

16. The method of paragraph 15, wherein the non-coding RNA is 7SL.

17. A method for assaying a biological sample from a subject in aid of a determination of the subject's risk of developing a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid, wherein the biomarker is a genetic aberration associated with a determination of the subject's risk of developing a disease or other medical condition, and wherein the genetic aberration is in or corresponds to:

i. a c-myc gene;

ii. a transposable element;

iii. a retrotransposon element;

iv. a satellite correlated gene;

v. a repeated DNA element;

vi. non-coding RNA other than miRNA; or

vii. a fragment of any of the foregoing.

18. The method of paragraph 17, wherein the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof.

19. The method of paragraph 17, wherein the genetic aberration is in or corresponds to a retrotransposon element that is LINE, SINE or HERV, or a fragment thereof.

20. The method of paragraph 19, wherein the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

21. The method of paragraph 17, wherein the genetic aberration is in or corresponds to a satellite correlated gene listed in Table 6, or a fragment thereof.

22. The method of paragraph 17, wherein the genetic aberration is in or corresponds to a repeated DNA element listed in Table 8, or a fragment thereof.

23. The method of paragraph 17, wherein the genetic aberration is in or corresponds to a non-coding RNA listed in Table 9 (or a fragment thereof), other than miRNA.

24. The method of paragraph 23, wherein the non-coding RNA is 7SL.

25. A method for assaying a biological sample from a subject in aid of diagnosis, prognosis or monitoring of a disease or other medical condition in the subject, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with diagnosis, prognosis, status or stage of a disease or other medical condition, and wherein the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof.

26. A method for assaying a biological sample from a subject in aid of directing treatment of the subject for a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other

medical condition, and wherein the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof

27. A method for assaying a biological sample from a subject in aid of a determination of the subject's risk of developing a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with a determination of the subject's risk of developing a disease or other medical condition, and wherein the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof.

28. A method for assaying a biological sample from a subject in aid of diagnosis, prognosis or monitoring of a disease or other medical condition in the subject, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. measuring a polypeptide activity in the fraction; and

c. determining whether the polypeptide activity is higher or lower than a normal or average activity for the polypeptide;

wherein an elevated or lowered activity is associated with diagnosis, prognosis, status or stage of a disease or other medical condition.

29. The method of paragraph 28, wherein the polypeptide is an enzyme.

30. The method of paragraph 29, wherein the enzyme is reverse transcriptase.

31. The method of paragraph 30, wherein step (c) involves determining whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

32. A method for assaying a biological sample from a subject in aid of directing treatment of the subject for a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. measuring a polypeptide activity in the fraction; and

c. determining whether the polypeptide activity is higher or lower than a normal or average activity for the same polypeptide;

wherein an elevated or lowered activity is associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other medical condition.

33. The method of paragraph 32, wherein the polypeptide is an enzyme.

34. The method of paragraph 33, wherein the enzyme is reverse transcriptase.

35. The method of paragraph 34, wherein step (c) involves determining whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

36. A method for assaying a biological sample from a subject in aid of a determination of the subject's risk of developing a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. measuring a polypeptide activity in the fraction; and

c. determining whether the polypeptide activity is higher or lower than a normal or average activity for the same polypeptide;

wherein an elevated or lowered activity is associated with a subject's risk of developing a disease or other medical condition.

37. The method of paragraph 36, wherein the polypeptide is an enzyme.

38. The method of paragraph 37, wherein the enzyme is reverse transcriptase.

39. The method of paragraph 38, wherein step (c) involves determining whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

40. The method of any of paragraphs 1-27, wherein the genetic aberration is:

a. a species of nucleic acid;

b. the level of expression of a nucleic acid;

c. a nucleic acid variant; or

d. a combination of any of the foregoing.

41. The method of any of paragraphs 1-27, wherein the nucleic acid is RNA and the genetic aberration is an expression profile.

42. The method of any of paragraphs 1-27, wherein the fragment contains more than 10 nucleotides.

43. The method of any of paragraphs 1-39, wherein the biological sample is a bodily fluid.

44. The method of paragraph 43, wherein the bodily fluid is blood, serum, plasma, or urine.

45. The method of any of paragraphs 1-39, wherein the subject is a human subject.

46. The method of paragraph 45, wherein the disease or other medical condition is brain cancer.

47. The method of paragraph 46, wherein the brain cancer is medulloblastoma or glioblastoma.

48. The method of paragraph 45, wherein the disease or other medical condition is melanoma.

49. The method of any of paragraphs 1-27, wherein the step of detecting the presence or absence of a biomarker in the extracted nucleic acid comprises microarray analysis, PCR, quantitative PCR, Digital Gene Expression, or direct sequencing.

50. The method of any of paragraphs 1-39, further comprising the step of enriching the microvesicle fraction for microvesicles originating from a specific cell type.

51. A kit for genetic analysis of a microvesicle fraction obtained from a body fluid sample from a subject, comprising, in a suitable container, one or more reagents capable of

hybridizing to or amplifying a nucleic acid corresponding to one or more of the genetic aberrations referenced in any of paragraphs 1-27.

52. An oligonucleotide microarray for genetic analysis of a microvesicle preparation from a body fluid sample from a subject, wherein the oligonucleotides on the array are designed to hybridize to one or more nucleic acids corresponding to one or more of the genetic aberrations referenced in any of paragraphs 1-27.

53. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to a cancer gene listed in Table 2 or 3, or a fragment thereof.

54. The profile of paragraph 53, wherein the cancer gene is a c-myc gene.

55. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to transposable element from the subject's genome, preferably an element listed in Table 4 or 5, or a fragment of any of the foregoing.

56. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to a retrotransposon element from the subject's genome, preferably LINE, SINE or HERV, more preferably LINE1 (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment of any of the foregoing.

57. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to a satellite correlated gene from the subject's genome, preferably a satellite correlated gene listed in Table 6, or a fragment of any of the foregoing.

58. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to an element of repeated DNA from the subject's genome, preferably an element listed in Table 8, or a fragment of any of the foregoing.

59. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to non-

coding RNA other than miRNA, preferably a species listed in Table 9, or a fragment of any of the foregoing.

60. The profile of paragraph 59, wherein the non-coding RNA is 7SL.

61. The profile of any of paragraphs 53-60, wherein the genetic aberration is:
    a. a species of nucleic acid;
    b. the level of expression of a nucleic acid;
    c. a nucleic acid variant; or
    d. a combination of any of the foregoing.

62. A method of identifying a potential new nucleic acid biomarker associated with a disease or other medical condition, status or stage of disease or other medical condition, a subject's risk of developing a disease or other medical condition, or a subject's responsiveness to a specific therapy for a disease or other medical condition, comprising the steps of:
    (a) obtaining or using a microvesicle fraction from a biological sample from a subject;
    (b) extracting nucleic acid from the fraction;
    (c) preparing a profile according to any of paragraphs 53-60; and
    (d) comparing the profile of step (c) to a control or reference profile and selecting one or more potential new biomarkers based on one or more differences between the profile of step (c) and the control or reference profile.

63. A method of treating a subject having a form of cancer in which cancer cells secrete microvesicles, the method comprising administering to the subject a therapeutically effective amount of a composition comprising:
    a. an inhibitor of microvesicle secretion;
    b. an inhibitor of a reverse transcriptase;
    c. a microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles; or
    d. any combination of the forgoing.

64. The method of paragraph 63, wherein the inhibitor of microvesicle secretion is an inhibitor of RAB GTPase.

65. The method of paragraph 64, where in the Rab GTPase is Rab 27a, Rab 27b or Rab 35.

66. The method of paragraph 63, wherein the inhibitor of a reverse transcriptase is a nucleoside analog selected from the group comprising 3'-azido2',3'-dideoxythymidine (AZT), 2',3'-dideoxyinosine (ddl), 2',3'-didehyro-3'-deoxythymidine (d4T), nevirapine and efavirenz.

67. The method of paragraph 63, wherein the inhibitor of a reverse transcriptase is RNAi targeting the reverse transcriptase gene.

68. The method of paragraph 63, wherein the microvesicle neutralizer is a biological agent that binds microvesicles and destroys the integrity of the microvesicles.

69. A pharmaceutical composition comprising, in a suitable pharmaceutical carrier: (a) an inhibitor of microvesicle secretion, particularly an inhibitor of RAB GTPase, and more particularly Rab 27a, Rab 27b or Rab 35); (b) an inhibitor of reverse transcriptase, particularly a nucleoside analog, more particularly 3'-azido2',3'-dideoxythymidine (AZT), 2',3'-dideoxyinosine (ddl), 2',3'-didehyro-3'-deoxythymidine (d4T), nevirapine, or efavirenz, or an RNAi targeting the reverse transcriptase gene; (c) a microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles, particularly a biological agent that binds microvesicles and destroys the integrity of the microvesicles; or (d) a combination of any of the foregoing.

1.

[00144] The invention is further illustrated by the following examples, which should not be construed as further limiting. Examples of the disclosed subject matter are set forth below. Other features, objects, and advantages of the disclosed subject matter will be apparent from the detailed description, figures, examples and claims. Methods and materials substantially similar or equivalent to those described herein can be used in the practice or testing of the presently disclosed subject matter. Exemplary methods and materials are now described as follows.

EXAMPLES

Example 1 Cultured cells release an abundance of microvesicles

[00145] We found that cultured tumor cells as well as normal cells release microvesicles. Here, we analyzed microvesicles produced by tumor cells from glioblastoma (GBM), a common and malignant brain tumor in adults; medulloblastoma, a common and malignant tumor in children with frequent amplification of c-Myc(Bigner et al., 1990); atypical teratoid rhabdoid tumor (AT/RT), a high-grade malignant tumor in children(Tez et al., 2008); and malignant melanoma, a peripheral tumor which can metastasize to the brain(Jemal et al., 2008). We analyzed microvesicles produced by epidermoid carcinoma cells as a control for the study. Increased expression of EGFR, but not c-Myc gene, was found in epidermoid carcinoma cells (Giard et al., 1973).

[00146] We cultured glioblastoma, medulloblastoma, melanoma and normal human fibroblast cells and monitored the release of microvesicles from each cell type. Specifically, primary GBM cell lines 20/3 and 11/5 were generated in our laboratory from tumor specimens kindly provided by Dr. Bob Carter (Massachusetts General Hospital), and diagnosed as GBM by a neuropathologist at Massachusetts General Hospital (Skog et al., 2008). Glioblastoma cells were cultured in Dulbecco modified essential medium (DMEM; Invitrogen, Carlsbad, CA) containing 10% fetal bovine serum (FBS; JRH Biosciences, Carlsbad, CA), and penicillin and streptomycin (10 IU/ml and 10 μg/ml, respectively; Cellgro, Herndon, VA).

[00147] Primary medulloblastoma cell lines D458, D384 and D425, as well as rhabdoid AT/RT tumor cell line, NS224, were provided by Drs. Y.-J. Cho and S.L. Pomeroy (Children's Hospital, Boston, MA). All medulloblastoma cell lines were cultured in suspension in DMEM containing 10% FBS, 1 x GlutaMAX (Invitrogen) and

penicillin/streptomycin. Rhabdoid tumor cell line NS224 was cultured in suspension in DMEM/F12 containing B27 supplement, 20 ng/ml EGF, 20 ng/ml FGF and penicillin/streptomycin.

[00148] Melanoma cell line, Yumel 0106, was kindly provided by Dr. R. Halaban (Yale New Haven Hospital, New Haven, CT) and cultured in OptiMEM (Invitrogen) containing 10% FBS and penicillin/streptomycin. Epidermoid carcinoma cell line, A431 (ATCC) was kindly provided by Huilin Shao (Massachusetts General Hospital) and cultured in DMEM containing 10% FBS and penicillin/streptomycin.

[00149] Normal human fibroblast lines, HF19 and HF27 were derived from human skin biopsies in the Breakefield laboratory; L2131 was derived in Dr. Christine Klein's laboratory (Univ. Ltibeck, Ltibeck, Germany) and cultured in DMEM supplemented with 10% FBS, 10 mM HEPES (Invitrogen) and penicillin/streptomycin. All cells were grown in media with 5% exosome-depleted fetal bovine serum (dFBS) (Skog et al., 2008). All cell lines were used over a few passages, as microvesicle yield tended to change over extended passages.

[00150] To characterize the size distribution and amount of microvesicles released from tumor cells and normal fibroblasts in culture using Nanosight LM10 nanoparticle tracking analysis (NTA), we isolated microvesicles from the culture media of three medulloblastoma cell lines (D384, D425 and D458), one melanoma (Yumel 0106), two GBMs (20/3 and 11/5) and two normal fibroblasts (HF19 and HF27). The media was first spun at 500 x g for 10 min. The supernatant was removed and spun again at 16,500 x g, filtered through a 0.22 μm filter and used for Nanosight analysis. The nanosight LM10 nanoparticle characterization system (NanoSight Ltd, UK) equipped with a blue laser (405

nm) illumination was used for real-time characterization of the vesicles. The result is presented as the average ± SEM of three independent experiments.

[00151] We found that medulloblastoma cells released more microvesicles/cell than the other cells types analyzed. The amount of microvesicles released by each cell type was: 13,400-25, 300/cell/48 hrs for medulloblastomas **(Figs. 1-3),** 12,600/cell/48 hrs for the melanoma **(Fig. 4),** 7,000-1 3,OOO/cell/48 hrs for the GBM cells **(Figs. 5-6),** and 3,800-6,200/cell/48 hrs for the normal human fibroblasts **(Fig. 7-8).** Normal human fibroblasts were of low passage and grew with similar rates as the tumor lines in culture, but were of larger size and hence greater surface area per cell.

[00152] To measure the amount of RNA in the microvesicles released in the culture media from these cells, we collected each conditioned medium after culturing for 48 hr and isolated microvesicles by differential centrifugation and filtration through a 0.22 μm filter followed by ultracentrifugation at 110,000 **x** g as detailed in WO 2009/100029.

[00153] For purposes of RNA extraction from microvesicles, microvesicle pellets generated from 39 ml conditioned medium produced from 0.5 x 10^6 - 3.5 x 10^6 cells over 48 hours were resuspended in 50 μï¸ PBS and incubated at 37°C for 30 min with DNAse I (DNA-free™ kit, Ambion) and Exonuclease III (Fermentas, Glen Burnie, MD), according to the manufacturer's instructions. After treatment, the enzymes were inactivated (using the kit's inactivation reagent and heat inactivation, respectively) and samples processed for RNA extraction.

[00154] Microvesicles were lysed in 300 μï MirVana lysis buffer (Ambion, Austin, TX) followed by extraction with an equal amount of acid-phenol:chloroform. After centrifugation at 10,000 **x** g for 5 min, the upper aqueous phase was removed and further processed to extract RNA using the mirVana RNA isolation kit (Ambion), according to the

manufacturer's instructions. RNA extracts were then treated with DNAse (DNA-free kit, Ambion) to exclude DNA carryover. RNA was quantified using a Nanodrop ND-1000 (Thermo Fisher Scientific, Waltham, MA) and the quantity and size ranges were evaluated using a 2100 Bioanalyzer (Agilent, Santa Clara, CA).

[00155] ExoRNA in microvesicles was measured using a 2100 Bioanalyzer (Agilent) with RNA 6000 Pico Chip for RNA. The Bioanalyzer RNA 6000 Pico Chip kit detects mainly single strand nucleic acids, but can also detect double strand DNA when present in large amounts. As shown in **Figs. 1-8,** the amount of RNA in microvesicles (exoRNA) from meduUoblastoma cells was 120- to 310-fold higher than the amount of exoRNA from normal fibroblasts; the amount of exoRNA from glioblastoma cells was 2.8- to 6.5-fold higher than from normal fibroblasts; and the amount from exoRNA from melanoma cells was similar to that from normal fibroblasts even though melanoma cells shed more than twice as many microvesicles. Thus, meduUoblastoma tumor cells, in particular, release abundant microvesicles with a high content of exoRNA.

Example 2 Characterization of RNA and DNA in microvesicles

[00156] To characterize the RNA and DNA in microvesicles, we isolated microvesicles from culture media of meduUoblastoma cell line D384, glioblastoma cell line 11/5 and fibroblast cell line H19 as detailed in Example 1. Isolated microvesicles were treated extensively with DNase prior to nucleic acid extraction to reduce the chance of external DNA contamination. Isolated microvesicles may also be treated with RNase prior to nucleic acid extraction although such treatment did not affect the RNA yield from microvesicles probably due to the absence of any significant amounts of external RNA.

[00157] ExoRNA was extracted from isolated microvesicles as detailed in Example 1.

[00158] For exoDNA extraction, microvesicle pellets generated from 39 ml conditioned medium produced from 0.5 x 10^6 - 3.5 x 10^6 cells over 48 hr were resuspended in 50 µL PBS and incubated at 37°C for 30 min with DNAse **I** (DNA-free™ kit, Ambion) and Exonuclease **III** (Fermentas, Glen Burnie, MD), according to manufacturer's instructions. After treatment, the enzymes were inactivated (using the kit's inactivation reagent and heat inactivation, respectively) and samples processed for DNA extraction.

[00159] Microvesicles were lysed in 300 µï MirVana lysis buffer (Ambion, Austin, TX) followed by extraction with an equal amount of acid-phenol:chloroform. After centrifugation at 10,000 **x** g for 5 min, the upper aqueous phase was removed and further processed to extract DNA using the Qiagen PCR purification kit according to manufacturer's instructions. DNA extracts were then treated with RNase (e.g., RNase A, Fermentas, Glen Burnie, MD) to exclude RNA carryover. DNA were quantified using a Nanodrop ND-1000 (Thermo Fisher Scientific, Waltham, MA) and the quantity and size ranges were evaluated using a 2100 Bioanalyzer (Agilent, Santa Clara, CA). ExoDNA in microvesicles was measured using a 2100 Bioanalyzer (Agilent) with RNA 6000 Pico Chip and/or DNA 7500 LabChip kits. The Bioanalyzer RNA 6000 Pico Chip kit detects mainly single stranded ("ss") nucleic acids, but can also detect double-stranded DNA (dsDNA) when present in large amounts, while the DNA 7500 LabChip kit only detects dsDNA. SI nuclease (200 U/ml; Fermentas) was also used to digest single stranded nucleic acid at 37°C for 30 min. Genomic cell DNA was isolated from cells with the Flexigene DNA kit (Qiagen, Valencia, CA), according to manufacturers' recommendation.

[00160] As shown in **Figs. 25A** and **25C,** the RNA profile varied among cell types and culture conditions, but in general, RNA with intact 18S and 28S ribosomal peaks were isolated from microvesicles.

[00161] The DNA profile also varied among cell types. ExoDNA was much more abundant in microvesicles secreted by glioblastoma tumor cells **(Fig. 25B)** as compared to normal fibroblast cells **(Fig. 25D).**

[00162] We also found that exoDNA was primarily single stranded. When exoDNA from meduUoblastoma tumor cells (D384) was analyzed using a dsDNA detection chip, no DNA was detected **(Fig. 26A).** However, when this same exoDNA was subjected to second strand synthesis, this same chip detected abundant dsDNA **(Fig. 26B).** Similar results were obtained with exoDNA extracted from microvesicles secreted by GBM cells (GBM 20/3).

[00163] That exoDNA was primarily single stranded DNA was also supported by our SI exonuclease assays and PicoGreen assays. In the SI exonuclease assays, we isolated exoDNA from three meduUoblastoma cell lines (D435, D384, D556) and gDNA from one normal human fibroblast cell line (L2132). Samples were incubated with SI nuclease (200U/ml) at 37° C for 30 minutes or MOCK treated. PCR for the house-keeping gene GAPDH was then performed on treated and MOCK treated samples. SI exonuclease specifically digests single stranded nucleic acids. As shown in **Fig. 27,** without SI treatment, the bands for exoDNAs extracted from microvesicles secreted by meduUoblastoma cell lines (D425m, D384 and D556) were observed on the gel. In contrast, after SI treatment, the bands for exoDNAs extracted from microvesicles secreted by meduUoblastoma cell lines (D425m, D384 and D556) did not show up. As a control, the band for the genomic DNA extracted from fibroblast cell line L2132 still showed up after SI exonuclease digestion. Therefore, exoDNA was sensitive to SI exonuclease digestion, suggesting that exoDNA is likely to be single stranded DNA.

[00164] Further, quantitative analysis of exoDNA using PicoGreen® (Thermo Scientific, Waltham, MA), which is a sensitive dsDNA binding fluorescent dye, showed an

18-fold lower amount of nucleic acids in comparison with the amount detected using the Bioanalyzer RNA chip. Since the Bioanalyzer RNA chip detection method can detect only single stranded nucleic acids, the exoDNA extract contained mainly single stranded nucleic acids.

Example 3 c-Myc oncogene amplification in cultured medulloblastoma tumor cells can be detected in both exoRNA and exoDNA

[00165] We detected c-Myc oncogene amplification using either exoRNA or exoDNA from medulloblastoma tumor cells. To measure the amount of c-Myc amplification, we extracted exoRNA and exoDNA, from culture media of three medulloblastoma cell lines (D458, D425 and D384), one atypical teratoid/rhabdoid (AT/RT) tumor cell line NS224, one glioblastoma cell line (11/5), and one normal fibroblast cell line H19 using the same method as detailed in Example 1, respectively. The genomic DNA from each of the same cell lines was extracted according to standard protocols in the art, which can be found in books such as *Molecular Cloning: A Laboratory Manual* (3-Volume Set) Ed. Joseph Sambrook, David W. Russel, and Joe Sambrook, Cold Spring Harbor Laboratory, 3rd edition (January 15, 2001), ISBN: 0879695773. The extracted nucleic acids were then used in PCR analysis to measure the level of amplifications.

[00166] For PCR analysis of exoRNA, total exoRNA (50 ng) was converted into cDNA with the Sensiscript RT Kit (Qiagen) using random primers, according to the manufacturer's instructions, and a 1:20 fraction (corresponding to 2.5 ng reverse transcribed RNA) was used for quantitative PCR (qPCR). For PCR analysis of the gDNA and exoDNA, qPCR was carried out using 10 ng DNA as a template. All reactions were performed in a 25µ1reaction using Power SYBR® Green PCR Master Mix (Applied Biosystems, Foster City, CA) and 160 nM of each primer. Amplification conditions consisted of: (1) 1 cycle of

50°C, 2 min; (2) 1 cycle of 95°C, 10 min; (3) 40 cycles of 95°C, 15 sec; and 60°C, 1 min, and (4) a dissociation stage consisting of 1 cycle of 95°C, 15 sec; 60°C, 20 sec; and 95°C, 15 sec on the 7000 ABI Prism PCR system (Applied Biosystems). Cycle threshold ("Ct") values were analyzed in auto mode and manually inspected for accuracy. The Ct values of both RNA and DNA levels were normalized to the housekeeping gene GAPDH in each sample. Primer dimers were excluded by evaluation of dissociation curve and agarose gel electrophoresis.

[00167] Sequences of the primers used were as follows **n-Myc** primers: 1) Forward TCTACCCGGACGAAGATGAC (SEQ ID NO: 1), Reverse AGCTCGTTCTCAAGCAGCAT (SEQ ID NO: 2) (primers within exon 2); **c-Myc** primer: Forward TCAAGAGGCGAACACACAAC (SEQ ID NO: 3), Reverse TAACTACCTTGGGGGCCTTT (SEQ ID NO: 4) (both primers in exon 3); **c-Myc** primer: Forward CCTACCCTCTCAACGACAGC (SEQ ID NO: 5), Reverse CTCTGACCTTTTGCCAGGAG (SEQ ID NO: 6) (spanning intron 2). **c-Myc** human specific primers: Forward CAACCCTTGCCGCATCCAC (SEQ ID NO: 7), Reverse AGTCGCGTCCTTGCTCGG (SEQ ID NO: 8) (both primers in exon 1). **POU5F1B** primers: Forward ATCCTGGGGGTTCTATTTGG (SEQ ID NO: 9), Reverse CTCCAGGTTGCCTCTCACTC (SEQ ID NO: 10); and **GAPDH** primers: Forward CTCTGCTCCTCCTGTTCGAC (SEQ ID NO: 11) (exon 8), Reverse ACGACCAAATCCGTTGACTC (SEQ ID NO: 12) (exon 9).

[00168] Levels of c-Myc amplification were measured at the genomic level (gDNA) by qPCR **(Fig. 9).** All three medulloblastoma cell lines had significant amplifications of c-Myc sequences (16-34-fold) compared to fibroblasts and other tumor cell types. RNA and DNA were extracted from microvesicles shed by these cell lines and quantitated by RT-PCR

and PCR respectively, using primers in exon 3 with values for c-Myc sequences normalized to glyceraldehyde 3-phosphate dehydrogenase (GAPDH), a housekeeping gene constitutively expressed in cells and found in exoRNA [14] and here in exoDNA. Microvesicles from all meduUoblastoma cell lines showed elevated levels of c-Myc sequences, both for exoRNA (8-45-fold) and exoDNA (10-25 fold), compared to microvesicles from fibroblasts and tumor cells with diploid c-Myc copy numbers **(Figs. 10-11).** Also, using primers that span a full intron, we successfully detected a 1.6 kb fragment corresponding to the unspliced c-Myc genomic DNA (verified by sequencing) in exoDNA from all three meduUoblastoma cell lines, but not in any of the other cell lines.

[00169] Furthermore, to establish that this genomic fragment of c-Myc in microvesicles was derived from a genomic amplicon, we verified the presence of elevated levels of a flanking gene, POU5F1B gene(Storlazzi et al., 2006) at levels matching those of c-Myc **(Fig. 29B).** POU5F1B PCR product was also verified by sequencing.

[00170] Levels of n-Myc sequences in cellular genomic DNA (gDNA) or exoRNA were also measured by qPCR and qRT-PCR and none of the other tumor types showed genomic amplification of n-Myc sequences or elevated levels of n-Myc exoRNA **(Figs. 31A** and **B).**

[00171] The levels of c-Myc DNA quantitated for gDNA and exoDNA/RNA in these meduUoblastoma lines were also compared to levels estimated by 250K single nucleotide polymorphism (SNP) analysis. For gene copy number estimation by the SNP array analysis, genomic DNA was extracted from meduUoblastoma cell pellets using the Puregene DNA Extraction Kit (Gentra Systems, Minneapolis, MN), according to the manufacturer's instructions. To obtain signal intensities and genotype calls, genomic DNA samples were digested, labeled and hybridized to Affymetrix 250K Styl SNP arrays, according to the

manufacturer's protocol (Affymetrix, Santa Clara, CA). Signal intensities were normalized using rank invariant set normalization, and copy numbers for altered genomic regions were inferred using the GLAD (Gain and Loss of DNA) algorithm available in the Genepattern software package (www.genepattern.org). C-Myc and n-Myc copy numbers were inferred by analyzing the smoothed copy number data at genomic regions ch8q24.12 and ch2p24, respectively.

[00172] The results are shown in Table **1** and in Fig. **30** in a representative heat map. Increased levels of c-Myc exoDNA corresponded well to the genomic copy number estimated by 250k SNP and qPCR in medulloblastoma lines, as compared to normal diploid levels in other cell lines, with correspondingly elevated c-Myc exoRNA in medulloblastoma microvesicles.

Table **1.** Assessment of c-Myc gene amplification levels in different cell types.

	Method	**c-Myc genomic copy number**	**c-Myc amount exoRNA[a]**	**c-Myc amount exoDNA[b]**
D425	FISH 250k SNP[c] qPCR	>25 15 8±3.6	8±2.0	13±0.2
D384	250k SNP qPCR	25 12±4.7	42±22	25±3.7
D458	250k SNP qPCR	17 17±3.0	45±11	10±0.6
NS224	250k SNP qPCR	2 2	0.8±0.3	4.2±0.1
GBM11/5	qPCR	2	2.8±1.4	0.4±0.1
HF19	qPCR	2	1	1

[a]2.5 ng reverse transcribed exoRNA and 10 ng of exoDNA were used as template for qPCR. All values were normalized to GAPDH mRNA.
[b]*FISH* = Fluorescence *in situ* hybridization of metaphase chromosome spread.[63]
[c]See representative heat map shown in Fig. 30.

Example 4 c-Myc oncogene amplification in xenografted medulloblastoma tumor cells *in vivo* can be detected with both exoRNA and exoDNA

[00173] To assess the potential diagnostic utility of using exoRNA to detect c-Myc amplification in tumors, human medulloblastoma cells (c-Myc amplified) and epidermoid carcinoma tumor cells (non-amplified) were grown as xenograft tumors in nude mice. In the xenograft experiments, two groups of five adult immunodeficient mice (nu/nu NCI) were each injected subcutaneously in both flanks with 5×10^6 medulloblastoma cells (line D425) or epidermoid carcinoma cells (line A431). Tumors were allowed to grow for three weeks; the mice were then sacrificed and blood was drawn by cardiac puncture. Approximately 1 ml of blood was obtained from each mouse and allowed to clot at room temperature for 15 min and then centrifuged at 1300 x g for 10 min. The serum was then filtered through a 0.22 μm filter and stored at -80°C. Samples were thawed and centrifuged for 1 hr at 100,000 x g to obtain microvesicles for RNA extraction, as described above.

[00174] As shown in **Fig. 12,** microvesicles were isolated from serum samples in tumor-bearing mice and exoRNA was extracted from the isolated microvesicles. Human c-Myc was detected in exoRNAs from 2/5 (40%) of the medulloblastoma-bearing mice **(Fig. 13)** and from 0/5 (0%) of the epidermoid carcinoma-bearing mice **(Fig. 14).**

Example 5 Retrotransposon elements are enriched in tumor microvesicles

[00175] We analyzed the RNA species in cellular RNA and exoRNA preparations from a low passage GBM line by microarray analysis using a whole genome array (Agilent Technologies). Briefly, RNA was extracted from microvesicles, as described above. RNA (0.5 μg) was used for linear T7-based amplification and Cy-3/Cy-5 labeling (Agilent Low RNA Input Linear Amp Kit, Agilent Technologies) following the manufacturer's protocol. The microarray experiments were performed by Miltenyi Biotec (Auburn, CA) using the

Agilent whole human genome microarray, 4 x 44K (44,000 probes), two-color array. The array was performed on two different RNA preparations from primary GBM cells and their microvesicles.

[00176] The microarray results have been deposited with a Geo accession number GSE13470. The results indicate the presence of higher transcription levels of a number of retrotransposon sequences in exoRNA extracts as compared to cellular RNA extracts.

[00177] From the two-color Agilent array data, we generated MA plots as previously described(Storey and Tibshirani, 2003). The intensities of the expression levels for each transcript were obtained from the array data for both exoRNA extracts from microvesicles and cellular RNA extracts from cells. The intensity of exoRNA is here designated "Microvesicle." The intensity of cellular RNA is here designated "Cell". The log ratio of the intensities of microvesicle/cell is plotted on the Y-axis ($M = \log_2 Microvesicle - logiCell$) and the mean log expression of the two on the X-axis ($A = 0.5 \times (\log_2 Microvesicle + logiCell)$).

[00178] As shown in **Fig. 15,** the microarray data was represented on a MA plot as the cumulative abundance (in microvesicles and cells) of specific RNAs (X-axis) and the relative ratio of these RNAs in microvesicles versus cells (Y-axis). The Y-axis scale was log2, so RNAs above 4 or below -4 on the Y-axis have at least a 16-fold different level in the microvesicles vs. cells. There were many RNA species that were at least 16 fold more abundant in microvesicles than in cells (M value above 4). Similarly, there were also many RNA species that were at least 16 fold less abundant in microvesicles than in cells (M value below -4).

[00179] As shown in **FIG. 17,** RNA from DNA transposons was similar in content in cells and microvesicles with the M values spreading between -4 and 4. In contrast, as shown in **Figs. 18-20,** RNA from retrotransposons, e.g. HERV, Alu and LI, was frequently higher in

microvesicles than in cells. This was particularly notable for the HERV sequences. As shown in **Fig. 16,** HERV-H was the most abundant and microvesicle-enriched in these GBM cells, followed by HERV-C, HERV-K6 and HERV-W. Therefore, some retrotransposon RNAs, e.g., HERV RNA, may be selectively packaged or enriched, in tumor microvesicles.

[00180] Since only a selected subset of transposon/retrotransposon probes are represented on the Agilent arrays, other retrotransposons that are not represented on the Agilent arrays may be enriched in microvesicles from tumor cells as well.

[00181] Since LI and HERV-K retrotransposons, as well as Alu elements (Goodier and Kazazian, 2008), have been implicated in tumor progression, we further assayed their levels in cellular RNA and exoRNA from tumor and normal cells by qRT-PCR (again with the caveat that the primers used only detect a subset of these sequences). See **Figs. 21A-C.** The expression levels were normalized to that of the GAPDH mRNA. LI and Alu sequences were abundant in both cells and microvesicles (high values on the X-axis) and enriched in most of the microvesicles compared to the cells (M>0). The levels of retrotransposon sequences tended to be higher in exoRNA vs. cellular RNA, with HERV-K being relatively high in some tumors. Interestingly, HERV-K RNA was not detectable in exoRNA from normal human fibroblasts (HF19), with a Ct value of 36 (below detection limit). This difference between levels of HERV-K RNA in microvesicles from fibroblasts and tumor cells is shown in the MA plot **(Fig. 21C).**

Example 6 The non-coding 7SL RNA in microvesicles as biomarkers for cancer cells

[00182] We found that the expression profiles of the non-coding 7SL RNA in microvesicles from plasma may serve as biomarkers for glioblastoma. We obtained de-identified blood samples from a GBM patient and healthy control from the biobank at Massachusetts General Hospital. We took the serum for each blood sample and isolated

microvesicles from the serum using the method as described in Example 1. RNA was extracted from the isolated microvesicles for further analysis. The expression levels of the 7SL RNA, EGFR and GAPDH were determined using qRT-PCR following a procedure as detailed in Example 3. The primers used for the qRT-PCR are as follows: 7SL-RNA: Forward primer 5' CAAAACTCCCGTGCTGATCA 3' (SEQ ID NO: 13), Reverse primer 5' GGCTGGAGTGCAGTGGCTAT 3' (SEQ ID NO: 14), Probe (FAM labeled MGB probe), 5' TGGGATCGCGCCTGT 3' (SEQ ID NO: 15); EGFR: Forward primer 5' TATGTCCTCATTGCCCTCAACA 3' (SEQ ID NO: 16), Reverse primer 5' CTGATGATCTGCAGGTTTTCCA 3' (SEQ ID NO: 17), Probe (FAM labeled MGB probe), 5' AAGGAATTCGCTCCACTG 3' (SEQ ID NO: 18); GAPDH, huGAPDH ID 4326317E from the vendor Applied Biosystems Inc..

[00183] The results show that the expression profile of the 7SL RNA in microvesicles correlates with the disease status of the subject from which the microvesicles were isolated **(Fig. 34).** The expression levels of the 7SL RNA in microvesicles from GBM serum samples were about 200 times higher than the levels from normal serum samples. In contrast, the expression levels of EGFR in microvesicles from GBM serum samples were about 2 times higher than the levels from normal serum samples. Further, the expression levels of GAPDH in microvesicles from GBM serum samples were roughly the same as the levels in normal serum samples.

[00184] As such, one aspect of the present invention is directed to the profile of 7SL RNA in microvesicles isolated from a subject, e.g., a human being. The profile of 7SL RNA may be the expression profile of the 7SL RNA. The profile of 7SL RNA may be correlated with the medical condition of the subject wherefrom the microvesicles are isolated.

[00185] Another aspect of the present invention is directed to a method of aiding the diagnosis, prognosis or selection of treatment therapy of a medical condition by determining the profile of the 7SL RNA. The determination of the profile of 7SL RNA may be the determination of the expression profile of the 7SL RNA. Since the profile of 7SL RNA may be correlated with the medical condition of the subject wherefrom the microvesicles are isolated, the determination of the profile in microvesicles may therefore aid the diagnosis, prognosis or selection of treatment therapy for the subject.

Example 7 Retrotransposon elements in tumor microvesicles are transferrable

[00186] To determine whether microvesicles could transfer HERV-K RNA to normal cells, human umbilical vein endothelial cells (HUVEC) were exposed to microvesicles from medulloblastoma cells and levels of HERV-K RNA were measured in HUVEC cells over time. Human umbilical vein endothelial cells (HUVEC) cells, kindly provided by Dr. Jonathan Song (Massachusetts General Hospital), were cultured in gelatin - coated flasks in endothelial basal medium (Lonza, Walkersville, MD) supplemented with hEGF, hydrocortisone, GA-1000 and FBS (Singlequots from Lonza). All cell lines were used over a few passages, as microvesicle yield tended to change over extended passages.

[00187] Specifically, HUVEC cells were seeded in 12-well plates at a density of 1.5 x 10^5 cells/well. Microvesicles were isolated from 1.2 x 10^7 D384 cells over a 48 hour period and added to each well in a total volume of 400 µï DMEM. Mock treated cells were incubated in 400 µï exosome-free DMEM. The cells were incubated for 2 hrs at 37°C and were then replenished with 1.5 ml DMEM (with 5% dFBS). Cells were collected at different time points after the microvesicle exposure and cell RNA was extracted for qRT-PCR analysis. The result is presented as the average ± SEM of three independent experiments.

[00188] As shown in **Fig. 22,** HERV-K RNA expression was increased in HUVEC cells at 2, 6, 12, 24, 48 and 72 hours after microvesicle exposure. The increased HERV-K RNA expression in HUVEC cells indicated that the microvesicles contained active HERV-K genes and such genes were transferred to the HUVEC cells.

Example 8 Retrotransposon elements in the form of exoDNA were enriched in tumor microvesicles with elevated RT activities

[00189] ExoDNA was also analyzed at the retrotransposon level with qPCR. ExoDNAs were extracted from microvesicles as detailed in Example 2. gDNA were extracted from cells as detailed in Example 3. The primers used for qPCR are as follows: GAPDH primers: Forward CTCTGCTCCTCCTGTTCGAC (SEQ ID NO: 19) (exon 8), Reverse ACGACCAAATCCGTTGACTC (SEQ ID NO: 20) (exon 9); LI primers: Forward TAAGGGCAGCCAGAGAGAAA (SEQ ID NO: 21), Reverse GCCTGGTGGTGACAAAATCT (SEQ ID NO: 22); HERV-K6 primers: Forward GGAGAGAAGCTGTCCTGTGG (SEQ ID NO: 23), Reverse TGACTGGACTTGCACGTAGG (SEQ ID NO: 24); Alu primers: Forward CATGTGGGTTAGCCTGGTCT (SEQ ID NO: 25), Reverse TTCCCACATTGCGTCATTTA (SEQ ID NO: 26).

[00190] The exoDNA levels were compared to nuclear gDNA isolated from the cells in MA plots. The levels of exoDNA in microvesicles and gDNA in corresponding cells were normalized to levels of GAPDH. The exoDNA (presumably originating from the cytoplasmic compartment) and gDNA (isolated from the nuclear compartment of the cells) showed clearly different patterns ($M \neq 0$). LI was slightly enriched in all medulloblastomas **(Fig. 23A).** HERV-K DNA was enriched in two of the medulloblastomas (D425 and D384)

(Fig. 23C). In contrast, Alu was not enriched in any of the meduUoblastoma tested **(Fig. 23B).**

[00191] We further found that the enrichment of the transposable elements at the exoDNA level in the meduUoblastoma cell lines corresponded to high levels of endogenous Reverse Transcription (RT) activity in exosomes. To measure RT activities, microvesicles were lysed in RIPA buffer [50 mM Tris-HCl (pH 8); 150 mM NaCl, 2.5% sodium dodecyl sulfate, 2.5% deoxycholic acid, 2.5% Nonidet P-40] for 20 min at 4°C. Exosomal debris was removed by centrifugation at 14,000 x g for 15 min. Proteins were quantified by Bradford assay and diluted 1:6 for each RT reaction. The RT assay was performed using the EnzCheck RT assay kit (Invitrogen) on a 25 µï¸ reaction, as described by the manufacturer. Fluorescence signal of the samples was measured before and after the RT incubation. The difference between the two values indicates newly synthesized DNA. Serial dilutions of Superscript™ III First Strand (Invitrogen) were used as standards. The result is presented as the average ± SEM of three independent experiments.

[00192] As shown in **Fig. 24,** RT activities in the 0106, GBM1 1/5, GBM 20/3 and HF19 cells are significantly less than those in D384, D425 and D458 cells. This decreased RT activities correlate well with the reduced levels of LI and HERV-K exoDNA in 0106, GBM11/5, GBM 20/3 and HF19 cells (as shown by the negative values on the MA plots in **Fig. 23 A and C).** Such correlation suggests that a fraction of exoDNA may be cDNA.

[00193] In addition, we found that exoDNA might also include fragments of genomic DNA. We used L-mimosine to inhibit DNA replication and examined whether the inhibition affected the yield of exoDNA. If the exoDNA yield is decreased after inhibition, it is very likely that exoDNA may contain fragments of genomic DNA.

[00194] Specifically, D384 cells were plated on 6-well plates (2 x 106 cells/well) and treated with increasing amounts (200, 400 and 600 μM) of L-mimosine (Sigma-Aldrich, St. Louis, MO) which is an inhibitor of DNA replication. The drug was added at one time point and 48 hrs after, the media was collected and processed for the isolation of microvesicles. Cell viability was assessed by cell count using the Countess Automated Cell Counter (Invitogen). SsDNA yields are normalized to one.

[00195] As shown in **Fig. 32,** the exoDNA yield in microvesicles was decreased by about 50% following inhibition of DNA replication with L-mimosine. Therefore, some of the exoDNA may also be fragments of genomic DNA generated during DNA replication and mitosis.

[00196] While the present invention has been disclosed with reference to certain embodiments, numerous modifications, alterations, and changes to the described embodiments are possible without departing from the sphere and scope of the present invention, as defined in the appended claims. Accordingly, it is intended that the present invention not be limited to the described embodiments, but that it has the full scope defined by the language of the following claims, and equivalents thereof.

Table 2 Cancer genes.

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
ABL1	25	P00519	9q34.1	CML, ALL	–	–	L	Dom	T	*BCR, ETV6*
ABL2	27	P42684	1q24-q25	AML	–	–	L	Dom	T	*ETV6*
AF15Q14	57082	NP_065113	15q14	AML	–	–	L	Dom	T	*MLL*
AF1Q	10962	Q13015	1q21	ALL	–	–	L	Dom	T	*MLL*
AF3p21	51517	Q9NZQ3	3p21	ALL	–	–	L	Dom	T	*MLL*
AF5q31	27125	NP_055238	5q31	ALL	–	–	L	Dom	T	*MLL*
AKT2	208	P31751	19q13.1-q13.2	Ovarian, pancreatic	–	–	E	Dom	A	
ALK	238	Q9UM73	2p23	ALCL	–	–	L	Dom	T	*NPM1, TPM3, TFG, TPM4, ATIC, CLTC, MSN, ALO17*
ALO17	57714	XP_290769	17q25.3	ALCL	–	–	L	Dom	T	*ALK*
APC	324	P25054	5q21	Colorectal, pancreatic, desmoid, hepatoblastoma, glioma, other CNS	Colorectal, pancreatic, desmoid, hepatoblastoma, glioma, other CNS	Adenomatous polyposis coli; Turcot syndrome	E, M, O	Rec	D‡, Mis, N, F, S	–
ARHGEF12	23365	NP_056128	11q23.3	AML	–	–	L	Dom	T	*MLL*
ARHH	399	Q15669	4p13	NHL	–	–	L	Dom	T	*BCL6*
ARNT	405	P27540	1q21	AML	–	–	L	Dom	T	*ETV6*
ASPSCR1	79058	NP_076988	17q25	Alveolar soft part sarcoma	–	–	M	Dom	T	*TFE3*
ATF1	466	P18846	12q13	Malignant melanoma of soft parts, angiomatoid fibrous histiocytoma	–	–	E, M	Dom	T	*EWSR1*
ATIC	471	P31939	2q35	ALCL	–	–	L	Dom	T	*ALK*
ATM	472	Q13315	11q22.3	T-PLL	Leukaemia, lymphoma, medulloblastoma, glioma	Ataxia telangiectasia	L, O	Rec	D, Mis, N, F, S	–
BCL10	8915	O95999	1p22	MALT	–	–	L	Dom	T	*IGHa*
BCL11A	53335	NP_060484	2p13	B-CLL	–	–	L	Dom	T	*IGHa*
BCL11B	64919	NP_612808	14q32.1	T-ALL	–	–	L	Dom	T	*TLX3*
BCL2	596	P10415	18q21.3	NHL, CLL	–	–	L	Dom	T	*IGHa*
BCL3	602	P20749	19q13	CLL	–	–	L	Dom	T	*IGHa*
BCL5	603	I52586	17q22	CLL	–	–	L	Dom	T	*MYC*
BCL6	604	P41182	3q27	NHL, CLL	–	–	L	Dom	T, Mis	*IG* loci, *ZNFN1A1, LCP1, PIM1, TFRC, MHC2TA, NACA, HSPCB, HSPCA*

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
										, *HIST1H4I, IL21R, POU2AF1, ARHH, EIF4A2*
BCL7A	605	NP_066273	12q24.1	B-NHL	–	–	L	Dom	T	*MYC*
BCL9	607	O00512	1q21	B-ALL	–	–	L	Dom	T	*IGHa, IGLa*
BCR	613	P11274	22q11.21	CML, ALL	–	–	L	Dom	T	*ABL1, FGFR1*
BHD	201163	NP_659434	17p11.2		Renal, fibrofolliculomas, trichodiscomas	Birt–Hogg–Dube syndrome	E, M	Rec?	Mis, N, F	–
BIRC3	330	Q13489	11q22-q23	MALT	–	–	L	Dom	T	*MALT1*
BLM	641	P54132	15q26.1	–	Leukaemia, lymphoma, skin squamous cell, other cancers	Bloom Syndrome	L, E	Rec	Mis, N, F	–
BMPR1A	657	P36894	10q22.3	–	Gastrointestinal polyps	Juvenile polyposis	E	Rec	Mis, N, F	–
BRAF	673	P15056	7q34	Melanoma, colorectal, papillary thyroid, borderline ovarian, NSCLC, cholangiocarcinoma	–	–	E	Dom	M	–
BRCA1	*672*	P38398	17q21	Ovarian	Breast, ovarian	Hereditary breast/ovarian	E	Rec	D, Mis, N, F, S	–
BRCA2	675	P51587	13q12	Breast, ovarian, pancreatic	Breast, ovarian, pancreatic, leukaemia (FANCB, FANCD1)	Hereditary breast/	L, E ovarian	Rec	D, Mis, N,	– *F, S*
BRD4	23476	O60885	19p13.1	Lethal midline carcinoma of young people	–	–	E	Dom	T	*NUT*
BTG1	694	P31607	12q22	BCLL	–	–	L	Dom	T	*MYC*
CBFA2T1	862	Q06455	8q22	AML	–	–	L	Dom	T	*MLL, RUNX1*
CBFA2T3	863	NP_005178	16q24	AML	–	–	L	Dom	T	*RUNX1*
CBFB	865	Q13951	16q22	AML	–	–	L	Dom	T	*MYH11*
CBL	867	P22681	11q23.3	AML	–	–	L	Dom	T	*MLL*
CCND1	595	P24385	11q13	CLL, B-ALL, breast	–	–	L, E	Dom	T	*IGHa, FSTL3*
CDH1	999	P12830	16q22.1	Lobular breast, gastric	Gastric	Familial gastric carcinoma	E	Rec	Mis, N, F, S	–
CDK4	1019	P11802	12q14	–	Melanoma	Familial malignant melanoma	E	Dom	Mis	–

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
CDKN2A-p14^{ARF}	1029	NP_478102	9p21	Melanoma, multiple other	Melanoma, pancreatic	Familial malignant melanoma	L, E, M, O	Rec	D, S	–
CDKN2A-p16^{INK4A}	1029	P42771	9p21	Melanoma, multiple other	Melanoma, pancreatic	Familial malignant melanoma	L, E, M, O	Rec	D, Mis, N, F, S	–
CDX2	1045	Q99626	13q12.3	AML	–	–	L	Dom	T	*ETV6*
CEBPA	1050	NP_004355	11p15.5	AML, MDS	–	–	L	Dom	Mis, N, F	–
CEP1	11064	NP_008949	9q33	MPD/NHL	–	–	L	Dom	T	*FGFR1*
CHIC2	26511	NP_036242	4q11-q12	AML	–	–	L	Dom	T	*ETV6*
CHN1	1123	P15882	2q31-q32.1	Extraskeletal myxoid chondrosarcoma	–	–	M	Dom	T	*TAF15*
CLTC	1213	Q00610	17q11-qter	ALCL	–	–	L	Dom	T	*ALK*
COL1A1	1277	P02452	17q21.31-q22	Dermatofibrosarcoma protuberans	–	–	M	Dom	T	*PDGFB*
COPEB	1316	Q99612	10p15	Prostatic, glioma	–	–	E, O	Rec	Mis, N	–
COX6C	1345	P09669	8q22-q23	Uterine leiomyoma	–	–	M	Dom	T	*HMGA2*
CREBBP	1387	Q92793	16p13.3	AL, AML	–	–	L	Dom	T	*MLL, MORF, RUNXBP2*
CTNNB1	1499	P35222	3p22-p21.3	Colorectal, ovarian, hepatoblastoma, others	–	–	E, M, O	Dom	H, Mis	–
CYLD	1540	NP_056062	16q12-q13	Cylindroma	Cylindroma	Familial cylindromatosis	E	Rec	Mis, N, F, S	–
D10S170	8030	NP_005427	10q21	Papillary thyroid, CML	–	–	E	Dom	T	*RET, PDGFRB*
DDB2	1643	Q92466	11p12	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum E	E	Rec	M, N	–
DDIT3	1649	P35638	12q13.1-q13.2	Liposarcoma	–	–	M	Dom	T	*FUS*
DDX10	1662	Q13206	11q22-q23	AML§	–	–	L	Dom	T	*NUP98*
DEK	7913	P35659	6p23	AML	–	–	L	Dom	T	*NUP214*
EGFR	1956	P00533	7p12.3-p12.1	Glioma	–	–	O	Dom	A, O‖	–
EIF4A2	1974	Q14240	3q27.3	NHL	–	–	L	Dom	T	*BCL6*
ELKS	23085	NP_055879	12p13.3	Papillary thyroid	–	–	E	Dom	T	*RET*
ELL	8178	P55199	19p13.1	AL	–	–	L	Dom	T	*MLL*
EP300	2033	Q09472	22q13	Colorectal, breast, pancreatic, AML	–	–	L, E	Rec	T	*MLL, RUNXBP2*
EPS15	2060	P42566	1p32	ALL	–	–	L	Dom	T	*MLL*
ERBB2	2064	P04626	17q21.1	Breast, ovarian, other	–	–	E	Dom	A	–

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				tumour types						
ERCC2	2068	P18074	19q13.2-q13.3	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum D	E	Rec	M, N, F, S	–
ERCC3	2071	P19447	2q21	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum B	E	Rec	M, S	–
ERCC4	2072	Q92889	16p13.3-	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum F	E	Rec	M, N, F	–
ERCC5	2073	P28715	13q33	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum G	E	Rec	M, N, F	–
ERG	2078	P11308	21q22.3	Ewing's sarcoma	–	–	M	Dom	T	*EWSR1*
ETV1	2115	P50549	7p22	Ewing's sarcoma	–	–	M	Dom	T	*EWSR1*
ETV4	2118	P43268	17q21	Ewing's sarcoma	–	–	M	Dom	T	*EWSR1*
ETV6	2120	P41212	12p13	Congenital fibrosarcoma, multiple leukaemia and lymphoma, secretory breast	–	–	L, E, M	Dom	T	*NTRK3, RUNX1, PDGFRB, ABL1, MNI, ABL2, FACL6, CHIC2, ARNT, JAK2, EVI1, CDX2, STL*
EVI1	2122	Q03112	3q26	AML, CML	–	–	L	Dom	T	*RUNX1, ETV6*
EWSR1	2130	NP_005234	22q12	Ewing's sarcoma, desmoplastic small round cell, ALL	–	–	L, M	Dom	T	*FLI1, ERG, ZNF278, NR4A3, TEC, FEV, ATF1, ETV1, ETV4, WT1, ZNF384*
EXT1	2131	NP_000118	8q24.11-q24.13	–	Exostoses, osteosarcoma	Multiple exostoses type 1	M	Rec	Mis, N, F, S	–
EXT2	2132	Q93063	11p12-p11	–	Exostoses, osteosarcoma	Multiple exostoses type 2	M	Rec	Mis, N, F, S	–
FACL6	23305	NP_056071	5q31	AML, AEL	–	–	L	Dom	T	*ETV6*
FANCA	2175	NP_000126	16q24.3	–	AML, leukaemia	Fanconi anaemia A	L	Rec	D, Mis, N, F, S	–
FANCC	2176	Q00597	9q22.3	–	AML, leukaemia	Fanconi anaemia C	L	Rec	D, Mis, N, F, S	–
FANCD2	2177	NP_149075	3o26	–	AML,	Fanconi	L	Rec	D, Mis, N,	–

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					leukaemia	anaemia D2			F	
FANCE	2178	NP_068741	6p21-p22	–	AML, leukaemia	Fanconi anaemia E	L	Rec	N, F, S	–
FANCF	2188	Q9NPJ8	11plS	–	AML, leukaemia	Fanconi anaemia F	L	Rec	N, F	–
FANCG	2189	O15287	9pl3	–	AML, leukaemia	Fanconi anaemia G	L	Rec	Mis, N, F, S	–
FEV	54738	NP_059991	2q36	Ewing's sarcoma	–	–	M	Dorn	T	*EWSR1*
FGFR1	2260	P11362	8pll.2-pll.l	MPD/NHL	–	–	L	Dom	T	*BCR, FOP, ZNF198, CEPl*
FGFRIOP	11116	NP_008976	6q27	MPD/NHL	–	–	L	Dom	T	*FGFR1*
FGFR2	2263	P21802	10q26	Gastric	–	–	E	Dom	Mis	-
FGFR3	2261	P22607	4pl6.3	Bladder, MM	–	–	L, E	Dom	Mis, T	*IGHa*
FH	2271	P07954	lq42.1	–	Leiomyomatosis, renal	Hereditary leiomyomatosis and renal-cell cancer	E, M	Rec	Mis, N, F	–
FIP1L1	81608	NP_1 12179	4ql2	Idiopathic hypereosinophilic syndrome	–	–	L	Dom	T	*PDGFRA*
FLI1	2313	Q01543	l lq24	Ewing's sarcoma	–	–	M	Dom	T	*EWSR1*
FLT3	2322	P36888	..13.ql2	AML, ALL	–	–	L	Dom	Mis, O	-
FLT4	2324	P35916	5q35.3	Angiosarcoma	–	–	M	Dom	Mis	-
FNBP1	23048	XP_052666	9q23	AML	–	–	L	Dom	T	*MLL*
FOXOIA	2308	Q12778	13ql4.1	Alveolar rhabdomyosarcomas	–	–	M	Dom	T	*PAX3*
FOX03A	2309	043524	6q21	AL	–	–	L	Dom	T	*MLL*
FSTL3	10272	095633	19pl3	B-CLL	–	–	L	Dom	T	*CCND1*
FUS	2521	P35637	16pl l.2	Liposarcoma	–	–	M	Dom	T	*DDIT3*
GAS7	8522	060861	17p	AML§	–	–	L	Dom	T	*MLL*
GATA1	2623	P15976	Xp 11.23	Megakaryoblastic leukaemia of Down syndrome	–	–	L	Dom	Mis, F	–
GMPS	8833	P49915	3q24	AML	–	–	L	Dom	T	*MLL*
GNAS	2778	P04895	20ql3.2	Pituitary adenoma	–	–	E	Dom	Mis	-
GOLGA5	9950	NP_005104	14q	Papillary thyroid	–	–	E	Dom	T	*RET*
GPC3	2719	P51654	Xq26.1	–	Wilms' tumour	Simpson-Golabi-Behmel O syndrome	O	Rec	T, D, Mis, N, F, S	–
GPHN	10243	Q9NQX3	14q24	AL	–	–	L	Dom	T	*MLL*
GRAF	23092	NP_055886	5q31	AML, MDS	–	–	L	Dom	T, F, S	*MLL*
HEI10	57820	NP_067001	14ql l.l	Uterine leiomyoma	–	–	M	Dom	T	*HMGA2*
HIP1	3092	000291	7qll.23	CMML	–	–	L	Dom	T	*PDGFRB*
HIST1H4I	8294	NP_003486	6p21.3	NHL	–	–	L	Dom	T	*BCL6*
HLF	3131	Q16534	17q22	ALL	–	–	L	Dom	T	*TCF3*
HMGA2	8091	P52926	12ql5	Lipoma	–	–	M	Dom	T	*LHFP, RAD51LI, LPP, HEI10,*

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										COX6C
HOXA11	3207	P31270	7p15-p14.2	CML	–	–	L	Dom	T	*NUP98*
HOXA13	3209	P31271	7p15-p14.2	AML	–	–	L	Dom	T	*NUP98*
HOXA9	3205	P31269	7p15-p14.2	AML[§]	–	–	L	Dom	T	*NUP98*
HOXC13	3229	P31276	12q13.3	AML	–	–	L	Dom	T	*NUP98*
HOXD11	3237	P31277	2q31-q32	AML	–	–	L	Dom	T	*NUP98*
HOXD13	3239	P35453	2q31-q32	AML[§]	–	–	L	Dom	T	*NUP98*
HRAS	3265	P01112	11p15.5	Infrequent sarcomas, rare other types	–	–	L, M	Dom	Mis	–
HRPT2	3279	NP_013522	1q21-q31	Parathyroid adenoma	Parathyroid adenoma, multiple ossifying jaw fibroma	Hyperpara-thyroidism jaw tumour syndrome	E, M	Rec	Mis, N, F	–
HSPCA	3320	P07900	1q21.2-q22	NHL	–	–	L	Dom	T	*BCL6*
HSPCB	3326	P08238	6p12	NHL	–	–	L	Dom	T	*BCL6*
IGHα	3492	–	14q32.33	MM, Burkitt's lymphoma, NHL, CLL, B-ALL, MALT	–	–	L	Dom	T	*MYC, FGFR3, PAX5, IRTA1, IRF4, CCND1, BCL9, BCL6, BCL8, BCL2, BCL3, BCL10, BCL11A. LHX4*
IGKα	50802	–	2p12	Burkitt's lymphoma	–	–	L	Dom	T	*MYC*
IGLα	3535	–	22q11.1-q11.2	Burkitt's lymphoma	–	–	L	Dom	T	*BCL9, MYC*
IL21R	50615	Q9HBE5	16p11	NHL	–	–	L	Dom	T	*BCL6*
IRF4	3662	Q15306	6p25-p23	MM	–	–	L	Dom	T	*IGHα*
IRTA1	83417	NP_112572	1q21	B-NHL	–	–	L	Dom	T	*IGHα*
JAK2	3717	O60674	9p24	ALL, AML	–	–	L	Dom	T	*ETV6*
KIT	3815	P10721	4q12	GIST, AML, TGCT	GIST, epithelioma	Familial gastrointestinal stromal	L, M, O	Dom	Mis, O	–
KRAS2	3845	NP_004976	12p12.1	Pancreatic, colorectal, lung, thyroid, AML, others	–	–	L, E, M, O	Dom	Mis	–
LAF4	3899	P51826	2q11.2-q12	ALL	–	–	L	Dom	T	*MLL*
LASP1	3927	Q14847	17q11-q21.3	AML	–	–	L	Dom	T	*MLL*
LCK	3932	NP_005347	1p35-p34.3	T-ALL	–	–	L	Dom	T	*TRBα*
LCP1	3936	P13796	13q14.1-q14.3	NHL	–		L	Dom	T	*BCL6*
LCX	80312	XP_167612	10q21	AML	–	–	L	Dom	T	*MLL*
LHFP	10186	NP_005771	13q12	Lipoma	–	–	M	Dom	T	*HMGA2*

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LMO1	4004	P25800	11p15	T-ALL	–	–	L	Dom	T	*TRDα*
LMO2	4005	P25791	11p13	T-ALL	–	–	L	Dom	T	*TRDα*
LPP	4026	NP_005569	3q28	Lipoma, leukaemia	–	–	L, M	Dom	T	*HMGA2, MLL*
LYL1	4066	P12980	19p13.2-p13.1	T-ALL	–	–	L	Dom	T	*TRBα*
MADH4	4089	Q13485	18q21.1	Colorectal, pancreatic, small intestine	Gastrointestinal polyps	Juvenile polyposis	E	Rec	D, Mis, N, F	–
MALT1	10892	Q9UDY8	18q21	MALT	–	–	L	Dom	T	*BIRC3*
MAML2	84441	XP_045716	11q22-q23	Salivary-gland mucoepidermoid	–	–	E	Dom	T	*MECT1*
MAP2K4	6416	P45985	17p11.2	Pancreatic, breast, colorectal	–	–	E	Rec	D, Mis, N	–
MDS1	4197	Q13465	3q26	MDS, AML	–	–	L	Dom	T	*RUNX1*
MECT1	94159	AAK93832.1	19p13	Salivary-gland mucoepidermoid	–	–	E	Dom	T	*MAML2*
MEN1	4221	O00255	11q13	Parathyroid	Parathyroid adenoma, pituitary adenoma, pancreatic islet cell, carcinoid	Multiple endocrine neoplasia type 1	E	Rec	D, Mis, N, F, S	–
MET	4233	P08581	7q31	Papillary renal, head-neck squamous cell	Papillary renal	Familial papillary renal	E	Dom	Mis	–
MHC2TA	4261	P33076	16p13	NHL	–	–	L	Dom	T	*BCL6*
MLF1	4291	P58340	3q25.1	AML	–	–	L	Dom	T	*NPM1*
MLH1	4292	P40692	3p21.3	Colorectal, endometrial, ovarian, CNS	Colorectal, endometrial, ovarian, CNS	Hereditary non-polyposis colorectal, Turcot syndrome	E, O	Rec	D, Mis, N, F, S	–

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
MLL	4297	Q03164	1lq23	AML, ALL	–	–	L	Dom	T, O	*MLL, MLLT1, MLLT2, MLLT3, MLLT4, MLLT7, MLLT10, MLLT6, ELL, EPS15, AF1Q, CREBBP, SH3GL1, FNBP1, PNUTL1, MSF, GPHN, GMPS, SSH3BP1, ARHGEF12, GAS7, FOXO3A, LAF4, LCX, SEPT6, LPP, CBFA2T1, GRAF, EP300, PICALM*
MLLT1	4298	Q03111	19p13.3	AL	–	–	L	Dom	T	*MLL*
MLLT10	8028	P55197	10p12	AL	–	–	L	Dom	T	*MLL, PICALM*
MLLT2	4299	P51825	4q21	AL	–	–	L	Dom	T	*MLL*
MLLT3	4300	P42568	9p22	ALL	–	–	L	Dom	T	*MLL*
MLLT4	4301	P55196	6q27	AL	–	–	L	Dom	T	*MLL*
MLLT6	4302	P55198	17q21	AL	–	–	L	Dom	T	*MLL*
MLLT7	4303	NP_005929	Xq13.1	AL	–	–	L	Dom	T	*MLL*
MN1	4330	Q10571	22q13	AML, meningioma	–	–	L, O	Dom	T	*ETV6*
MSF	10801	NP_006631	17q25	AML[§]	–	–	L	Dom	T	*MLL*
MSH2	4436	P43246	2p22-p21	Colorectal, endometrial, ovarian	Colorectal, endometrial, ovarian	Hereditary non-polyposis colorectal	E	Rec	D, Mis, N, F, S	–
MSH6	2956	P52701	2p16	Colorectal	Colorectal, endometrial, ovarian	Hereditary non-polyposis colorectal	E	Rec	Mis, N, F, S	–
MSN	4478	P26038	Xq11.2-q12	ALCL	–	–	L	Dom	T	*ALK*
MUTYH	4595	NP_036354	1p34.3-1p32.1		Colorectal	Adenomatous polyposis coli	E	Rec	Mis, N, F, S	–
MYC	4609	P01106	8q24.12-q24.13	Burkitt's lymphoma, amplified in other cancers,	–	–	L, E	Dom	A, T	*IGKα, BCL5, BCL7A, BTG1,*

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				B-CLL						*TRAα, IGHα*
MYCL1	4610	P12524	1p34.3	Small cell lung	–	–	E	Dom	A	–
MYCN	4613	P04198	2p24.1	Neuroblastoma	–	–	O	Dom	A	–
MYH11	4629	P35749	16p13.13-p13.12	AML	–	–	L	Dom	T	*CBFB*
MYH9	4627	P35579	22q13.1	ALCL	–	–	L	Dom	T	*ALK*
MYST4	23522	NP_036462	10q22	AML	–	–	L	Dom	T	*CREBBP*
NACA	4666	NP_005585	12q23-q24.1	NHL	–	–	L	Dom	T	*BCL6*
NBS1	4683	NP_002476	8q21	–	NHL, glioma, medulloblastoma, rhabdomyosarcoma	Nijmegen breakage syndrome	L, E, M, O	Rec	Mis, N, F	–
NCOA2	10499	Q15596	8q13.1	AML	–	–	L	Dom	T	*RUNXBP2*
NCOA4	8031	Q13772	10q11.2	Papillary thyroid	–	–	E	Dom	T	*RET*
NF1	4763	P21359	17q12	Neurofibroma, glioma	Neurofibroma, glioma	Neurofibromatosis type 1	O	Rec	D, Mis, N, F, S, O	–
NF2	4771	P35240	22q12.2	Meningioma, acoustic neuroma	Meningioma, acoustic neuroma	Neurofibromatosis type 2	O	Rec	D, Mis, N, F, S, O	–
NOTCH1	4851	P46531	9q34.3	T-ALL	–	–	L	Dom	T	*TRBα*
NPM1	4869	P06748	5q35	NHL, APL, AML	–	–	L	Dom	T	*ALK, RARA, MLF1*
NR4A3	8013	Q92570	9q22	Extraskeletal myxoid chondrosarcoma	–	–	M	Dom	T	*EWSR1*
NRAS	4893	P01111	1p13.2	Melanoma, MM, AML, thyroid	–	–	L, E	Dom	Mis	–
NSD1	64324	NP_071900	5q35	AML	–	–	L	Dom	T	*NUP98*
NTRK1	4914	P04629	1q21-q22	Papillary thyroid	–	–	E	Dom	T	*TPM3, TPR, TFG*
NTRK3	4916	Q16288	15q25	Congenital fibrosarcoma, secretory breast	–	–	E, M	Dom	T	*ETV6*
NUMA1	4926	NP_006176	11q13	APL	–	–	L	Dom	T	*RARA*
NUP214	8021	P35658	9q34.1	AML	–	–	L	Dom	T	*DEK, SET*
NUP98	4928	P52948	11p15	AML	–	–	L	Dom	T	*HOXA9, NSD1, WHSC1L1, DDX10, TOP1, HOXD13, PMX1, HOXA13, HOXD11, HOXA11, RAP1GDS1*

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NUT	256646	XP_171724	15q13	Lethal midline carcinoma of young people	–	–	E	Dom	T	*BRD4*
OLIG2	10215	Q13516	21q22.11	T-ALL	–	–	L	Dom	T	*TRAα*
PAX3	5077	P23760	2q35	Alveolar rhabdomyosarcoma	–	–	M	Dom	T	*FOXO1A*
PAX5	5079	Q02548	9p13	NHL	–	–	L	Dom	T	*IGHα*
PAX7	5081	P23759	1p36.2-p36.12	Alveolar rhabdomyosarcoma	–	–	M	Dom	T	*FOXO1A*
PAX8	7849	Q06710	2q12-q14	Follicular thyroid	–	–	E	Dom	T	*PPARG*
PBX1	5087	NP_002576	1q23	Pre-B-ALL	–	–	L	Dom	T	*TCF3*
PCM1	5108	NP_006188	8p22-p21.3	Papillary thyroid	–	–	E	Dom	T	*RET*
PDGFB	5155	P01127	22q12.3-q13.1	DFSP	–	–	M	Dom	T	*COL1A1*
PDGFRA	5156	P16234	4q11-q13	GIST	–	–	M, O	Dom	Mis, O	–
PDGFRB	5159	NP_002600	5q31-q32	MPD, AML, CMML, CML	–	–	L	Dom	T	*ETV6, TRIP11, HIP1, RAB5EP, H4*
PICALM	8301	Q13492	11q14	T-ALL, AML	–	–	L	Dom	T	*MLLT10, MLL*
PIM1	5292	P11309	6p21.2	NHL	–	–	L	Dom	T	*BCL6*
PML	5371	P29590	15q22	APL	–	–	L	Dom	T	*RARA*
PMS1	5378	P54277	2q31-q33	–	Colorectal, endometrial, ovarian	Hereditary non-polyposis colorectal cancer	E	Rec	Mis, N	–
PMS2	5395	P54278	7p22	–	Colorectal, endometrial, ovarian, medulloblastoma, glioma	Hereditary non-polyposis colorectal cancer, Turcot syndrome	E	Rec	Mis, N, F	–
PMX1	5396	P54821	1q24	AML	–	–	L	Dom	T	*NUP98*
PNUTL1	5413	NP_002679	22q11.2	AML	–	–	L	Dom	T	*MLL*
POU2AF1	5450	Q16633	11q23.1	NHL	–	–	L	Dom	T	*BCL6*
PPARG	5468	P37231	3p25	Follicular thyroid	–	–	E	Dom	T	*PAX8*
PRCC	5546	Q92733	1q21.1	Papillary renal	–	–	E	Dom	T	*TFE3*
PRKAR1A	5573	P10644	17q23-q24	Papillary thyroid	Myxoma, endocrine, papillary thyroid	Carney complex	E, M	Dom, Rec	T, Mis, N, F, S	*RET*
PRO1073	29005	Q9UHZ2	11q31.1	Renal-cell carcinoma (childhood epithelioid)	–	–	E	Dom	T	*TFEB*
PSIP2	11168	NP_150091	9p22.2	AML	–	–	L	Dom	T	*NUP98*
PTCH	5727	Q13635	9q22.3	Skin basal cell, medulloblastoma	Skin basal cell, medulloblastoma	Nevoid basal-cell carcinoma syndrome	E, M	Rec	Mis, N, F, S	–

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
PTEN	5728	O00633	10q23.3	Glioma, prostatic, endometrial	Harmartoma, glioma, prostatic, endometrial	Cowden syndrome, Bannayan–Riley–Ruvalcaba syndrome	L, E, M, O	Rec	D, Mis, N, F, S	–
PTPN11	5781	Q06124	12q24.1	JMML, AML, MDS	–	–	L	Dom	Mis	–
RAB5EP	9135	NP_004694	17p13	CMML	–	–	L	Dom	T	*PDGFRB*
RAD51L1	5890	NP_002868	14q23-q24.2	Lipoma, uterine leiomyoma	–	–	M	Dom	T	*HMGA2*
RAP1GDS1	5910	P52306	4q21-q25	T-ALL	–	–	L	Dom	T	*NUP98*
RARA	5914	P10276	17q12	APL	–	–	L	Dom	T	*PML, ZNF145, TIF1, NUMA1, NPM1*
RB1	5925	P06400	13q14	Retinoblastoma, sarcoma, breast, small-cell lung	Retinoblastoma, sarcoma, breast, small-cell lung	Familial retinoblastoma	L, E, M, O	Rec	D, Mis, N, F, S	–
RECQL4	9401	O94761	8q24.3	–	Osteosarcoma, skin basal and squamous cell	Rothmund–Thompson syndrome	M	Rec	N, F, S	–
REL	5966	Q04864	2p13-p12	Hodgkin Lymphoma	–	–	L	Dom	A	–
RET	5979	P07949	10q11.2	Medullary thyroid, papillary thyroid, pheochromocytoma	Medullary thyroid, papillary thyroid, pheochromocytomaneoplasia	Multiple endocrine 2A/2B	E, O	Dom	T, Mis, N, F	*H4, PRKAR1A, NCOA4, PCM1, GOLGA5, TRIM33*
RPL22	6146	P35268	3q26	AML, CML	–	–	L	Dom	T	*RUNX1*
RUNX1	861	Q01196	21q22.3	AML, pre-B-ALL	–	–	L	Dom	T	*RPL22, MDS1, EVI1, CBFA2T3, CBFA2T1, ETV6*
RUNXBP2	799	NP_006757	8p11	AML	–	–	L	Dom	T	*CREBBP, NCOA2, EP300*
SBDS	51119	Q9Y3A5	7q11	–	AML, MDS	Schwachman–Diamond syndrome	L	Rec	Gene conversion	–
SDHB	6390	P21912	1p36.1-p35	–	Paraganglioma, pheochromocytoma	Familial paraganglioma	O	Rec	Mis, N, F	–
SDHC	6391	O75609	1q21	–	Paraganglioma, pheochromocytoma	Familial paraganglioma	O	Rec	Mis, N, F	–
SDHD	6392	O14521	11q23	–	Paraganglioma, pheochromoc	Familial paraganglioma	O	Rec	Mis, N, F, S	–

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
					ytoma					
SEPT6	23157	NP_055944	Xq24	AML	–	–	L	Dom	T	*MLL*
SET	6418	Q01105	9q34	AML	–	–	L	Dom	T	*NUP214*
SFPQ	6421	P23246	1p34.3	Papillary renal cell	–	–	E	Dom	T	*TFE3*
SH3GL1	6455	Q99961	19p13.3	AL	–	–	L	Dom	T	*MLL*
SMARCB1	6598	Q12824	22q11	Malignant rhabdoid	Malignant rhabdoid	Rhabdoid predisposition syndrome	M	Rec	D, N, F, S	–
SMO	6608	Q99835	7q31-q32	Skin basal cell	–	–	E	Dom	Mis	–
SS18	6760	Q15532	18q11.2	Synovial sarcoma	–	–	M	Dom	T	*SSX1, SSX2*
SS18L1	26039	O75177	20q13.3	Synovial sarcoma	–	–	M	Dom	T	*SSX1*
SSH3BP1	10006	NP_005461	10p11.2	AML	–	–	L	Dom	T	*MLL*
SSX1	6756	Q16384	Xp11.23-p11.22	Synovial sarcoma	–	–	M	Dom	T	*SS18*
SSX2	6757	Q16385	Xp11.23-p11.22	Synovial sarcoma	–	–	M	Dom	T	*SS18*
SSX4	6759	O60224	Xp11.23	Synovial sarcoma	–	–	M	Dom	T	*SS18*
STK11	6794	Q15831	19p13.3	NSCLC	Jejunal harmartoma, ovarian, testicular, pancreatic	Peutz–Jeghers syndrome	E, M, O	Rec	D, Mis, N,	–
STL	7955	NOPROTEIN	6q23	B-ALL	–	–	L	Dom	T	*ETV6*
SUFU	51684	NP_057253	10q24.32	Medulloblastoma	Medulloblastoma	Medulloblastoma predisposition	O	Rec	D, F, S	–
TAF15	8148	Q92804	17q11.1-q11.2	Extraskeletal myxoid chondrosarcomas, ALL	–	–	L, M	Dom	T	*TEC, CHN1, ZNF384*
TAL1	6886	P17542	1p32	Lymphoblastic leukaemia/ biphasic	–	–	L	Dom	T	*TRDα*
TAL2	6887	Q16559	9q31	T-ALL	–	–	L	Dom	T	*TRBα*
TCF1	6927	P20823	12q24.2	Hepatic adenoma, hepatocellular carcinoma	Hepatic adenoma, hepatocellular carcinoma	Familial hepatic adenoma	E	Rec	Mis, F	–
TCF12	6938	Q99081	15q21	Extraskeletal myxoid chondrosarcoma	–	–	M	Dom	T	*TEC*
TCF3	6929	P15923	19p13.3	pre-B-ALL	–	–	L	Dom	T	*PBX1, HLF, TFPT*
TCL1A	8115	NP_068801	14q32.1	T-CLL	–	–	L	Dom	T	*TRAα*
TEC	7006	P42680	4p12	Extraskeletal myxoid chondrosarcoma	–	–	M	Dom	T	*EWSR1, TAF15, TCF12*
TFE3	7030	P19532	Xp11.22	Papillary renal, alveolar soft part sarcoma	–	–	E	Dom	T	*SFPQ, ASPSCR1, PRCC*
TFEB	7942	P19484	6p21	Renal (childhood epithelioid)	–	–	E, M	Dom	T	*ALPHA*
TFG	10342	NP_006061	3q11-q12	Papillary thyroid,	–	–	E, L	Dom	T	*NTRK1, ALK*

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
				ALCL						
TFPT	29844	NP_037474	19q13	Pre-B-ALL	–	–	L	Dom	T	*TCF3*
TFRC	7037	P02786	3q29	NHL	–	–	L	Dom	T	*BCL6*
TIF1	8805	O15164	7q32-q34	APL	–	–	L	Dom	T	*RARA*
TLX1	3195	P31314	10q24	T-ALL	–	–	L	Dom	T	*TRBα, TRDα*
TLX3	30012	O43711	5q35.1	T-ALL	–	–	L	Dom	T	*BCL11B*
TNFRSF6	355	P25445	10q24.1	TGCT, nasal NK/T lymphoma, skin squamous-cell carcinoma (burn-scar related)	–	–	L, E, O	Rec	Mis	–
TOP1	7150	P11387	20q12-q13.1	AML[§]	–	–	L	Dom	T	*NUP98*
TP53	7157	P04637	17p13	Breast, colorectal, lung, sarcoma, adrenocortical, glioma, multiple other types	Breast, sarcoma, adrenocortical carcinoma, glioma, multiple other types	Li–Fraumeni syndrome	L, E, M, O	Rec	Mis, N, F	–
TPM3	7170	P06753	1q22-q23	Papillary thyroid, ALCL	–	–	E, L	Dom	T	*NTRK1, ALK*
TPM4	7171	P07226	19p13.1	ALCL	–	–	L	Dom	T	*ALK*
TPR	7175	P12270	1q25	Papillary thyroid	–	–	E	Dom	T	*NTRK1*
TRAα	6955	–	14q11.2	T-ALL	–	–	L	Dom	T	*ATL, OLIG2, MYC, TCL1A*
TRBα	6957	–	7q35	T-ALL	–	–	L	Dom	T	*HOX11, LCK, NOTCH1, TAL2, LYL1*
TRDα	6964	–	14q11	T-cell leukaemia	–	–	L	Dom	T	*TAL1, HOX11, TLX1, LMO1, LMO2*
TRIM33	51592	Q9UPN9	1p13	Papillary thyroid	–	–	E	Dom	T	*RET*
TRIP11	9321	NP_004230	14q31-q32	AML	–	–	L	Dom	T	*PDGFRB*
TSC1	7248	Q92574	9q34	–	Hamartoma, renal cell	Tuberous sclerosis 1	E, O	Rec	D, Mis, N, F, S	–
TSC2	7249	P49815	16p13.3	–	Hamartoma, renal cell	Tuberous sclerosis 2	E, O	Rec	D, Mis, N, F, S	–
TSHR	7253	P16473	14q31	Toxic thyroid adenoma	Thyroid adenoma	–	E	Dom	Mis	–
VHL	7428	P40337	3p25	Renal, hemangioma, pheochromocytoma	Renal, hemangioma, pheochromocytoma	von Hippel–Lindau syndrome	E, M, O	Rec	D, Mis, N, F, S	–
WAS	7454	P42768	Xp11.23-p11.22	–	Lymphoma	Wiskott–Aldrich syndrome	L	Rec	Mis, N, F, S	–
WHSC1L1	54904	NP_060248	8p12	AML	–	–	L	Dom	T	*NUP98*

Symbol	Locuslink ID	Protein ID*	Chromosome band	Tumour types (somatic)	Tumour types (germline)	Cancer syndrome	Tissue type	Cancer molecular genetics	Mutation type	Translocation partner
WRN	7486	Q14191	8p12-p11.2	–	Osteosarcoma, meningioma, others	Werner syndrome	L, E, M, O	Rec	Mis, N, F, S	–
WT1	7490	NP_000369	11p13	Wilms', desmoplastic small round cell	Wilms'	Denys–Drash syndrome, Frasier syndrome, Familial Wilms' tumour	O	Rec	D, Mis, N, F, S	*EWSR1*
XPA	7507	P23025	9q22.3	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum A	E	Rec	Mis, N, F, S	–
XPC	7508	Q01831	3p25	–	Skin basal cell, skin squamous cell, melanoma	Xeroderma pigmentosum C	E	Rec	Mis, N, F, S	–
ZNF145	7704	Q05516	11q23.1	APL	–	–	L	Dom	T	*RARA*
ZNF198	7750	Q9UBW7	13q11-q12	MPD/NHL	–	–	L	Dom	T	*FGFR1*
ZNF278	23598	NP_055138	22q12-q14	Ewing's sarcoma	–	–	M	Dom	T	*EWSR1*
ZNF384	171017	NP_597733	12p13	ALL	–	–	L	Dom	T	*EWSR1, TAF15*
ZNFN1A1	10320	NP_006051	7p12	ALL, DLBCL	–	–	L	Dom	T	*BCL6*

*From Swiss-Prot/Refseq. ‡D (large deletion) covers the abnormalities that result in allele loss/loss of heterozygosity at many recessive cancer genes. §Refers to cases of acute myeloid leukaemia that are associated with treatment. ‖O (other) in the 'mutation type' column refers primarily to small in-frame deletions/insertions as found in KIT/PDGFRA, and larger duplications/insertions as found in FLT3 and EGFR. Note that where an inversion/large deletion has been shown to result in a fusions protein, these have been listed under translocations. The Wellcome Trust Sanger Institute web version of the cancer-gene set can be found at http://www.sanger.ac.uk/genetics/CPG/Census/. A, amplification; AEL, acute eosinophilic leukaemia; AL, acute leukaemia; ALCL, anaplastic large-cell lymphoma; ALL, acute lymphocytic leukaemia; AML, acute myelogenous leukaemia; APL, acute promyelocytic leukaemia; B-ALL, B-cell acute lymphocytic leukaemia; B-CLL, B-cell lymphocytic leukaemia; B-NHL, B-cell non-Hodgkin's lymphoma; CLL, chronic lymphatic leukaemia; CML, chronic myeloid leukaemia; CMML, chronic myelomonocytic leukaemia; CNS, central nervous system; D, large deletion; DFSP, dermatofibrosarcoma protuberans; DLBCL, diffuse large B-cell lymphoma; Dom, dominant; E, epithelial; F, frameshift; GIST, gastrointestinal stromal tumour; JMML, juvenile myelomonocytic leukaemia; L, leukaemia/lymphoma; M, mesenchymal; MALT, mucosa-associated lymphoid tissue; MDS, myelodysplastic syndrome; MM, multiple myeloma; Mis, missense; N, nonsense; NHL, non-Hodgkin's lymphoma; NK/T, natural killer T cell; NSCLC, non-small-cell lung cancer; O, other; pre-B-ALL, pre-B-cell acute lymphoblastic leukaemia; Rec, recessive; S, splice site; T, translocation; T-ALL, T-cell acute lymphoblastic leukaemia; T-CLL, T-cell chronic lymphocytic leukaemia; TGCT, testicular germ-cell tumour; T-PLL, T-cell prolymphocytic leukaemia.

Table 3 List of genes which contain cancer-related somatic mutations. The list was adapted from Sanger Center's COSMIC database(Bamford et al., 2004; Forbes et al., 2008; Forbes et al.; Forbes et al.; Friedberg; Pleasance et al.). The gene names are uniquely assigned by HUGO Gene Nomenclature Committee (http://www.genenames.org/index.html, accessed January 31. 2011).

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
39340	A1BG	A1CF	A2BP1	A2LD1
A2M	A2ML1	A2RRG4_HUMAN	A3GALT2	A4D198_HUMAN
A4D226_HUMAN	A4GALT	A4GNT	AAAS	AACS
AADAC	AADACL2	AADACL3	AADACL4	AADAT
AAGAB	AAK1	AAMP	AANAT	AARS
AARS2	AARSD1	AASDH	AASDHPPT	AASS
AATF	AATK	AB019437_1	ABAT	ABBA-1
ABCA1	ABCA10	ABCA12	ABCA13	ABCA2
ABCA3	ABCA4	ABCA5	ABCA6	ABCA7
ABCA8	ABCA9	ABCB1	ABCB10	ABCB11
ABCB4	ABCB5	ABCB6	ABCB7	ABCB8
ABCB9	ABCC1	ABCC10	ABCC11	ABCC12
ABCC2	ABCC3	ABCC4	ABCC5	ABCC6
ABCC8	ABCC9	ABCD1	ABCD2	ABCD3
ABCD4	ABCE1	ABCF1	ABCF2	ABCF3
ABCG1	ABCG2	ABCG4	ABCG5	ABCG8
ABHD1	ABHD10	ABHD11	ABHD12	ABHD12B
ABHD13	ABHD14A	ABHD14B	ABHD15	ABHD2
ABHD3	ABHD4	ABHD5	ABHD6	ABHD8
ABI1	ABI2	ABI3	ABI3BP	ABL1
ABL2	ABLIM1	ABLIM3	ABO	ABP1
ABR	ABRA	ABT1	ABTB1	ABTB2
AC002472.13	AC007731_16	AC008537_5-2	AC008969.1	AC010872_2
AC012100.1	AC013469_8-2	AC021593.2	AC022098.2	AC023469_1
AC027369_8	AC068473.1	AC079612.1	AC092070_2	AC093393.1
AC097374_3	AC099524.1	AC103710_2	AC112491_4	AC114273.2
AC120042.2	AC127391_4	AC142381_2	AC142381_2_ENST00000356559	ACAA1
ACAA2	ACACA	ACACB	ACAD10	ACAD11
ACAD8	ACAD9	ACADL	ACADM	ACADS
ACADSB	ACADVL	ACAN	ACAP1	ACAP2
ACAP3	ACAT1	ACAT2	ACBD3	ACBD4
ACBD5	ACBD6	ACBD7	ACCN1	ACCN2
ACCN3	ACCN4	ACCN5	ACCS	ACCSL
ACD	ACE	ACE2	ACER1	ACER2
ACER3	ACHE	ACIN1	ACLY	ACMSD
ACN9	ACO1	ACO2	ACOT1	ACOT11
ACOT12	ACOT13	ACOT2	ACOT4	ACOT6
ACOT7	ACOT8	ACOT9	ACOX1	ACOX2
ACOX3	ACOXL	ACP1	ACP2	ACP5
ACP6	ACPL2	ACPP	ACPT	ACR

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ACRBP	ACRC	ACRV1	ACSBG 1	ACSBG2
ACSF2	ACSF3	ACSL1	ACSL3	ACSL4
ACSL5	ACSL6	ACSM1	ACSM2A	ACSM2B
ACSM3	ACSM5	ACSS1	ACSS2	ACSS3
ACTA1	ACTA2	ACTB	ACTBL2	ACTC1
ACTG 1	ACTG2	ACTL6A	ACTL6B	ACTL7A
ACTL7B	ACTL8	ACTL9	ACTN1	ACTN2
ACTN3	ACTN4	ACTR1 0	ACTR1 A	ACTR1 B
ACTR2	ACTR3	ACTR3B	ACTR5	ACTR6
ACTR8	ACTRT1	ACTRT2	ACVR1	ACVR1 B
ACVR1 C	ACVR2A	ACVR2B	ACVRL1	ACY1
ACY3	ACYP1	ACYP2	ADA	ADAD1
ADAD2	ADAL	ADAM1 0	ADAM1 1	ADAM1 2
ADAM1 5	ADAM1 7	ADAM1 8	ADAM1 9	ADAM2
ADAM20	ADAM21	ADAM22	ADAM22 _ENS T0000031 5984	ADAM23
ADAM28	ADAM29	ADAM30	ADAM32	ADAM33
ADAM7	ADAM8	ADAM9	ADAMDEC1	ADAMTS1
ADAMTS1 0	ADAMTS1 2	ADAMTS1 3	ADAMTS1 4	ADAMTS1 5
ADAMTS1 6	ADAMTS1 6_ENS T000002741 8 1	ADAMTS1 7	ADAMTS1 8	ADAMTS1 9
ADAMTS2	ADAMTS20	ADAMTS3	ADAMTS4	ADAMTS5
ADAMTS6	ADAMTS6 _ENS T00000381 055	ADAMTS7	ADAMTS8	ADAMTS9
ADAMTSL1	ADAMTSL1 _ENS T00000380548	ADAMTSL2	ADAMTSL3	ADAMTSL4
ADAMTSL5	ADAP1	ADAP2	ADAR	ADARB1
ADARB2	ADAT1	ADAT2	ADAT3	ADC
ADCK1	ADCK2	ADCK4	ADCK5	ADCY1
ADCY1 0	ADCY2	ADCY3	ADCY4	ADCY5
ADCY6	ADCY7	ADCY8	ADCY9	ADCYAP1
ADCYAP1 R 1	ADD1	ADD2	ADD3	ADH1 A
ADH1 B	ADH4	ADH5	ADH6	ADH7
ADHFE1	ADM	ADI POQ	ADI POR1	ADI POR2
ADK	ADM	ADM2	ADNP	ADN P2
ADO	ADORA1	ADORA2A	ADORA2B	ADORA3
ADPGK	ADPRH	ADPRHL1	ADPRHL2	ADRA1 A
ADRA1 B	ADRA1 D	ADRA2A	ADRA2B	ADRA2C
ADRB1	ADRB2	ADRB3	ADRBK1	ADRBK2
ADRM1	ADSL	ADSS	ADSSL1	AEBP1
AEN	AES	AFAP1	AFAP1 L 1	AFAP1 L2
AFF1	AFF2	AFF3	AFF4	AFG3L2
AFM	AFMI D	AFP	AFTPH	AGA
AGAP1	AGAP2	AGAP3	AGAP4	AGAP5
AGAP7	AGAP8	AGBL2	AGBL4	AGBL5
AGC1	AGER	AGFG 1	AGFG2	AGGF1
AGK	AGL	AGMAT	AGPAT1	AGPAT2
AGPAT3	AGPAT4	AGPAT5	AGPAT6	AGPAT9
AGPHD1	AGPS	AGR2	AGR3	AGRN
AGRP	AGT	AGTPBP1	AGTR1	AGTR2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
AGTRAP	AGXT	AGXT2	AGXT2L1	AGXT2L2
AHCTF1	AHCTF1 P	AHCY	AHCYL1	AHCYL2
AHDC1	AHI 1	AHNAK	AHNAK2	AHR
AHRR	AHSA1	AHSA2	AHSG	AHSP
AICDA	AIDA	AIF1	AIF1 L	AIF1_ENSTO 0000376051
AIFM1	AIFM2	AIFM3	AIG 1	AIM1
AIM1 L	AIM2	AIMP1	AIMP2	AIP
AIPL1	AIRE	AJAP1	AK1	AK2
AK3	AK3L1	AK5	AK7	AKAP1
AKAP1 0	AKAP1 1	AKAP1 2	AKAP1 3	AKAP1 4
AKAP2	AKAP3	AKAP4	AKAP5	AKAP6
AKAP7	AKAP8	AKAP9	AKAP9_NM_00 5751	AKD1
AKI RIN1	AKI RIN2	AKNA	AKNAD1	AKR1 A 1
AKR1 B 1	AKR1 B 10	AKR1 B 1P8	AKR1 C 1	AKR1 C2
AKR1 C3	AKR1 C4	AKR1 CL1	AKR1 D 1	AKR1 E2
AKR7A2	AKR7A3	AKR7L	AKT1	AKT1 S 1
AKT2	AKT3	AKTIP	AL1 2 1675_36-2	AL1 22001_3 2
AL1 6 1645_14	AL5 12274_9	ALAD	ALAS1	ALAS2
ALB	ALCAM	ALDH 16A1	ALDH1 8A1	ALDH 1A 1
ALDH 1A2	ALDH 1A3	ALDH 1B 1	ALDH1 L 1	ALDH 1L2
ALDH2	ALDH3A1	ALDH3A2	ALDH3B2	ALDH4A1
ALDH5A1	ALDH6A1	ALDH7A1	ALDH8A1	ALDH9A1
ALDOA	ALDOB	ALDOC	ALG1	ALG 10
ALG 10B	ALG 11	ALG 12	ALG1 3	ALG 14
ALG 1L	ALG2	ALG5	ALG6	ALG8
ALG9	ALK	ALKBH1	ALKBH2	ALKBH3
ALKBH4	ALKBH5	ALKBH6	ALKBH7	ALKBH8
ALLC	ALMS1	ALOX1 2	ALOX1 2B	ALOX1 2P2
ALOX1 5	ALOX1 5B	ALOX5	ALOX5AP	ALOXE3
ALPI	ALPK1	ALPK2	ALPK2_ENSTO 0000361 673	ALPK3
ALPL	ALPP	ALPPL2	ALS2	ALS2CL
ALS2CR1 1	ALS2CR1 2	ALS2CR8	ALX1	ALX3
ALX4	AMAC1	AMAC1 L2	AMACR	AMBN
AMBP	AMBRA1	AMD1	AMDH D 1	AMDHD2
AMELX	AMELY	AMFR	AMH	AMHR2
AMICA1	AMIG01	AMIG02	AMIG03	AMMECR1
AMMECR1 L	AMN	AMOT	AMOTL1	AMOTL2
AMPD1	AMPD2	AMPD2_ENST 00000393689	AMPD3	AMPH
AMT	AMTN	AMY1 A	AMY1 B	AMY1 C
AMY2A	AMY2B	AMZ1	AMZ2	ANAPC1
ANAPC1 0	ANAPC1 1	ANAPC1 3	ANAPC2	ANAPC4
ANAPC5	ANAPC7	ANG	ANGEL1	ANG EL2
ANG PT1	ANG PT2	ANG PT4	ANGPTL1	ANG PTL2
ANG PTL3	ANG PTL4	ANG PTL5	ANGPTL6	ANG PTL7
ANK1	ANK2	ANK3	ANKAR	ANKDD1 A

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ANKFN 1	ANKFY1	ANKH	ANKHD1	ANKHD1 - EIF4EBP3
ANKK1	ANKLE2	ANKMY1	ANKMY2	ANKRA2
ANKRD1	ANKRD1 0	ANKRD1 1	ANKRD1 2	ANKRD1 3A
ANKRD1 3B	ANKRD1 3C	ANKRD1 3D	ANKRD1 6	ANKRD1 7
ANKRD1 8A	ANKRD2	ANKRD20A1	ANKRD20A2	ANKRD20A3
ANKRD20A4	ANKRD20A5	ANKRD22	ANKRD23	ANKRD24
ANKRD26	ANKRD27	ANKRD28	ANKRD29	ANKRD30A
ANKRD31	ANKRD32	ANKRD33	ANKRD34A	ANKRD34B
ANKRD35	ANKRD37	ANKRD39	ANKRD40	ANKRD42
ANKRD43	ANKRD44	ANKRD45	ANKRD46	ANKRD49
ANKRD5	ANKRD50	ANKRD52	ANKRD53	ANKRD54
ANKRD55	ANKRD56	ANKRD57	ANKRD58	ANKRD6
ANKRD60	ANKRD7	ANKRD9	ANKS1 A	ANKS3
ANKS4B	ANKS6	ANKZF1	ANLN	ANO1 0
AN02	AN03	AN04	AN05	AN06
AN07	AN08	AN09	ANP32B	ANP32C
ANP32D	ANP32E	ANPEP	ANTXR1	ANTXRL
ANUBL1	ANXA1	ANXA1 0	ANXA1 1	ANXA1 3
ANXA2	ANXA3	ANXA4	ANXA5	ANXA6
ANXA7	ANXA8	ANXA8L1	ANXA8L2	ANXA9
AOAH	AOC2	AOC3	AOF2	AOX1
AP001 01 1.2_ENST00000261 598	AP001 01 1.3_ENST00000320876	AP005901 _2	AP1 AR	AP1 B1
AP1 G1	AP1 G2	AP1 M1	AP1 M2	AP1 S1
AP1 S2	AP1 S3	AP2A1	AP2A2	AP2B1
AP2M1	AP2S1	AP3B1	AP3B2	AP3D1
AP3M1	AP3M2	AP3S1	AP3S2	AP4B1
AP4E1	AP4M1	AP4S1	APAF1	APBA1
APBA2	APBA3	APBB1	APBB1 IP	APBB2
APBB3	APC	APC2	APCDD1	APCDD1 L
APCS	APEH	APEX1	APEX2	APH1 A
APH1 B	API5	API P	APITD1	APLF
APLN	APLNR	APLP1	APLP2	APOA1
APOA1 BP	APOA2	APOA4	APOA5	APOB
APOB48R	APOBEC1	APOBEC2	APOBEC3A	APOBEC3B
APOBEC3C	APOBEC3D	APOBEC3F	APOBEC3G	APOBEC3H
APOBEC4	APOC1	APOC2	APOC3	APOC4
APOD	APOE	APOH	APOL1	APOL2
APOL3	APOL4	APOL5	APOL6	APOLD1
APOM	APOO	APOOL	APP	APPBP2
APPL1	APPL2	APRT	APTX	AQP1
AQP1 0	AQP1 1	AQP1 2A	AQP2	AQP3
AQP4	AQP5	AQP6	AQP7	AQP8
AQP9	AQR	AR	ARAF	ARAP1
ARAP2	ARAP3	ARC	ARCN1	ARD1 B
AREG	ARF1	ARF3	ARF4	ARF5
ARF6	ARFGAP1	ARFGAP2	ARFGAP3	ARFGEF1
ARFGEF2	ARFIP1	ARFIP2	ARFRP1	ARG 1
ARG2	ARG FX	ARGLU1	ARHGAP1	ARHGAP1 0

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ARHGAP1 1A	ARHGAP1 1B	ARHGAP1 2	ARHGAP1 5	ARHGAP1 7
ARHGAP1 8	ARHGAP1 9	ARHGAP1 9_ENST00000358531	ARHGAP20	ARHGAP21
ARHGAP22	ARHGAP23	ARHGAP24	ARHGAP25	ARHGAP26
ARHGAP27	ARHGAP28	ARHGAP29	ARHGAP30	ARHGAP31
ARHGAP32	ARHGAP32_ENST00000310343	ARHGAP33	ARHGAP36	ARHGAP4
ARHGAP5	ARHGAP6	ARHGAP8	ARHGAP9	ARHG DIA
ARHG DIB	ARHG DIG	ARHG EF1	ARHGEF1 0	ARHG EF1 0L
ARHG EF1 0_ENST00000398564	ARHG EF1 1	ARHG EF1 2	ARHGEF1 5	ARHG EF1 6
ARHG EF1 7	ARHG EF1 8	ARHG EF1 9	ARHGEF2	ARHG EF3
ARHG EF4	ARHG EF5	ARHG EF5L	ARHGEF6	ARHG EF7
ARHG EF9	ARI D 1A	ARI D 1B	ARID2	ARI D3A
ARI D3B	ARI D3C	ARI D4A	ARID4B	ARI D4B_ENST00000264183
ARI D5A	ARI D5B	ARIH1	ARIH2	ARL1
ARL1 0	ARL1 1	ARL1 3A	ARL1 3B	ARL1 4
ARL1 5	ARL1 7B	ARL2	ARL2BP	ARL3
ARL4A	ARL4C	ARL4D	ARL4P	ARL5A
ARL5B	ARL5C	ARL6	ARL6I P 1	ARL6IP4
ARL6IP5	ARL6IP6	ARL8A	ARL8B	ARL9
ARMC1	ARMC1 0	ARMC2	ARMC3	ARMC4
ARMC6	ARMC7	ARMC8	ARMC9	ARMCX1
ARMCX2	ARMCX3	ARMCX4	ARMCX5	ARMCX6
ARNT	ARNT2	ARNTL	ARNTL2	ARPC1 A
ARPC1 B	ARPC2	ARPC3	ARPC4	ARPC5
ARPC5L	ARPM1	ARPP-21	ARPP1 9	ARR3
ARRB1	ARRB2	ARRDC1	ARRDC2	ARRDC3
ARRDC4	ARSA	ARSB	ARSD	ARSE
ARSF	ARSG	ARSH	ARSI	ARSJ
ARSK	ART1	ART3	ART4	ART5
ARTN	ARV1	ARVCF	ARX	AS3MT
ASAH1	ASAH2	ASAH2B	ASAM	ASAP1
ASAP2	ASAP3	ASB1	ASB1 0	ASB1 1
ASB1 2	ASB1 3	ASB1 4	ASB1 5	ASB1 6
ASB1 7	ASB1 8	ASB2	ASB3	ASB4
ASB5	ASB6	ASB7	ASB8	ASB9
ASCC1	ASCC2	ASCC3	ASCL1	ASCL2
ASCL3	ASCL4	ASF1 B	ASG R 1	ASGR1_ENST00000380920
ASGR2	ASH1 L	ASH2L	ASI P	ASL
ASMT	ASMTL	ASNA1	ASNS	ASNSD1
ASNS_ENSTOOO00394309	ASPA	ASPDH	ASPH	ASPHD1
ASPHD2	ASPM	ASPN	ASPRV1	ASPSCR1
ASRGL1	ASS1	ASTE1	ASTL	ASTN1
ASTN2	ASXL1	ASXL2	ASXL3	ASZ1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ATAD1	ATAD2	ATAD2B	ATAD2B_ENST00000238789	ATAD3A
ATAD3B	ATAD3B_ENSTO0000378741	ATAD5	ATCAY	ATE1
ATF1	ATF2	ATF3	ATF4	ATF5
ATF6	ATF6B	ATF7IP	ATF7IP2	ATG10
ATG12	ATG16L1	ATG16L2	ATG2A	ATG2B
ATG3	ATG4A	ATG4A_ENST00000372232	ATG4C	ATG4D
ATG5	ATG7	ATG9A	ATG9B	ATHL1
ATIC	ATL1	ATL2	ATL3	ATM
ATMIN	ATN1	ATOH1	ATOH7	ATOH8
ATP10A	ATP10B	ATP10D	ATP11A	ATP11B
ATP11C	ATP12A	ATP13A1	ATP13A2	ATP13A3
ATP13A4	ATP13A5	ATP1A1	ATP1A2	ATP1A3
ATP1A4	ATP1B1	ATP1B2	ATP1B3	ATP1B4
ATP2A1	ATP2A2	ATP2A3	ATP2B1	ATP2B2
ATP2B3	ATP2B3_ENSTO00003701 86	ATP2B4	ATP2C1	ATP2C2
ATP4A	ATP4B	ATP5A1	ATP5B	ATP5C1
ATP5D	ATP5E	ATP5F1	ATP5G1	ATP5G2
ATP5G3	ATP5H	ATP5I	ATP5J	ATP5J2
ATP5L	ATP50	ATP5S	ATP5SL	ATP6AP1
ATP6AP1L	ATP6AP2	ATP6V0A1	ATP6V0A2	ATP6V0A4
ATP6V0B	ATP6V0C	ATP6V0D1	ATP6V0D2	ATP6V0E1
ATP6V0E2L	ATP6V1A	ATP6V1B1	ATP6V1B2	ATP6V1C1
ATP6V1C2	ATP6V1D	ATP6V1E1	ATP6V1E2	ATP6V1F
ATP6V1G1	ATP6V1G2	ATP6V1G3	ATP6V1H	ATP7A
ATP7B	ATP8A1	ATP8A2	ATP8B1	ATP8B2
ATP8B4	ATP9A	ATP9B	ATPAF1	ATPAF2
ATPBD3	ATPBD4	ATPGD1	ATPIF1	ATR
ATRIP	ATRN	ATRNL1	ATRX	ATXN1
ATXN10	ATXN2	ATXN2L	ATXN3	ATXN3L
ATXN7	ATXN7L1	ATXN7L2	ATXN7L3	AUH
AUP1	AURKA	AURKAIP1	AURKB	AURKC
AUTS2	AVEN	AVIL	AVL9	AVP
AVPI1	AVPR1A	AVPR1B	AVPR2	AWAT1
AWAT2	AXIN1	AXIN2	AXL	AZGP1
AZI1	AZI2	AZIN1	AZU1	B2M
B3GALNT1	B3GALNT2	B3GALT1	B3GALT2	B3GALT4
B3GALT5	B3GALT6	B3GALTL	B3GAT1	B3GAT2
B3GAT3	B3GNT1	B3GNT2	B3GNT3	B3GNT4
B3GNT5	B3GNT6	B3GNT7	B3GNT8	B3GNTL1
B3Gn-T6	B4GALNT1	B4GALNT2	B4GALNT3	B4GALNT4
B4GALT1	B4GALT2	B4GALT3	B4GALT4	B4GALT5
B4GALT6	B4GALT7	B7	B9D1	B9D2
BAALC	BAAT	BACE1	BACE2	BACH1
BACH2	BAD	BAG1	BAG2	BAG3
BAG4	BAG5	BAHD1	BAM	BAI2
BAI3	BAIAP2	BAIAP2L1	BAIAP2L2	BAIAP3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
BAK1	BAMBI	BANF1	BANF2	BANK1
BANP	BAP1	BARD1	BARHL1	BARHL2
BARX1	BARX2	BASP1	BAT1	BAT2
BAT2D1	BAT2D1 _ENSTO 0000392078	BAT3	BAT4	BAT5
BATF	BATF2	BATF3	BAX	BAZ1 A
BAZ1 B	BAZ2A	BAZ2B	BBC3	BBOX1
BBS1	BBS1 0	BBS1 2	BBS2	BBS4
BBS5	BBS7	BBS9	BBX	BCAM
BCAN	BCAP29	BCAP31	BCAR1	BCAR3
BCAS1	BCAS2	BCAS3	BCAS4	BCAS4 _ENS T000003587 91
BCAT1	BCAT2	BCCI P	BCDIN3D	BCH E
BCKDHA	BCKDHB	BCKDK	BCL1 0	BCL1 1A
BCL1 1B	BCL2	BCL2A1	BCL2L1	BCL2L1 0
BCL2L1 1	BCL2L1 2	BCL2L1 3	BCL2L1 4	BCL2L1 5
BCL2L2	BCL3	BCL6	BCL6B	BCL7A
BCL7B	BCL7C	BCL9	BCL9L	BCLAF1
BCM01	BC02	BCOR	BCORL1	BCORL2
BCR	BCS1 L	BDH1	BDH2	BDKRB1
BDKRB2	BDNF	BDP1	BECN1	BEGAIN
BEND2	BEND3	BEND4	BEN D5	BEND6
BEND7	BEST1	BEST2	BEST3	BEST4
BET1	BET1 L	BEX1	BEX2	BEX4
BEX5	BFAR	BFSP1	BFSP2	BGLAP
BGN	BHLHA1 5	BHLHB9	BHLHE22	BHLH E23
BHLH E40	BHLH E41	BHMT	BHMT2	BICC1
BICD1	BICD2	BID	BIK	BIN1
BIN2	BIRC2	BIRC3	BIRC5	BIRC6
BIRC7	BIRC8	BIVM	BLCAP	BLI D
BLK	BLM	BLMH	BLNK	BLOC1 S1
BL0C1 S2	BLOC1 S3	BLVRA	BLVRB	BLYM _HUM AN
BLZF1	BMF	BMI 1	BMP1	BMP1 0
BMP1 5	BMP2	BMP2K	BMP2KL	BMP2K _ENS T000003350 16
BMP3	BMP4	BMP5	BMP6	BMP7
BMP8A	BMP8B	BMPER	BMPR1 A	BMPR1 B
BMPR2	BMS1	BMX	BNC1	BNC2
BNI P1	BNI P2	BNI P3	BNI P3L	BNI PL
BOC	BOD1	BOD1 L	BOK	BOLA1
BOLA2	BOLA2B	BOLA3	BOLL	BOP1
BPGM	BPHL	BPI	BPIL1	BPIL2
BPIL3	BPNT1	BPTF	BPY2B	BPY2C
BRAF	BRAP	BRCA1	BRCA2	BRCC3
BRD1	BRD2	BRD2 _ENSTOO 000395289	BRD3	BRD3 _ENST 00000303407
BRD4	BRD4 _ENSTOOO 00263377	BRD7	BRD8	BRD9

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
BRDT	BRE	BRF1	BRF2	BRI3
BRI3BP	BRIP1	BRIX1	BRMS1	BRMS1L
BRP44	BRP44L	BRPF1	BRPF3	BRS3
BRSK1	BRSK2	BRWD1	BRWD3	BSCL2
BSDC1	BSG	BSN	BSND	BSPRY
BST1	BST2	BSX	BTAF1	BTBD1
BTBD10	BTBD11	BTBD12	BTBD16	BTBD17
BTBD2	BTBD3	BTBD6	BTBD7	BTBD8
BTBD9	BTBD9_ENSTOO000403056	BTC	BTD	BTF3
BTF3L1	BTF3L3	BTF3L4	BTG1	BTG2
BTG3	BTG4	BTK	BTLA	BTN1A1
BTN2A1	BTN2A2	BTN2A3	BTN3A1	BTN3A2
BTN3A3	BTNL2	BTNL8	BTNL9	BTRC
BUB1	BUB1B	BUB3	BUD13	BUD31
BVES	BYSL	BZRAP1	BZW1	BZW2
C10orf10	C1Oorf104	C1Oorf107	C1Oorf11	C10orf111
C10orf113	C1Oorf113_ENST000003771_18	C10orf114	C10orf116	C10orf118
C1Oorf119	C1Oorf12	C1Oorf120	C1Oorf125	C1Oorf128
C10orf129	C1Oorf131	C1Oorf137	C1Oorf18	C10orf2
C10orf25	C10orf26	C10orf27	C10orf28	C10orf31
C10orf32	C10orf35	C10orf4	C10orf46	C10orf47
C10orf53	C10orf54	C10orf57	C10orf58	C10orf6
C10orf61	C10orf62	C10orf64	C10orf68	C10orf71
C10orf71_ENSTO00003741_44	C10orf72	C10orf76	C10orf78	C10orf79
C10orf81	C10orf82	C10orf84	C10orf88	C10orf90
C10orf91	C10orf92	C10orf93	C10orf95	C10orf96
C10orf99	C11orf1	C11orf10	C11orf16	C11orf17
C11orf2	C11orf24	C11orf30	C11orf34	C11orf35
C11orf40	C11orf41	C11orf42	C11orf44	C11orf45
C11orf46	C11orf47	C11orf48	C11orf49	C11orf51
C11orf52	C11orf53	C11orf54	C11orf57	C11orf58
C11orf59	C11orf60	C11orf61	C11orf63	C11orf65
C11orf66	C11orf67	C11orf68	C11orf70	C11orf73
C11orf74	C11orf75	C11orf76	C11orf77	C11orf82
C11orf83	C11orf84	C11orf85	C11orf86	C11orf87
C11orf88	C11orf9	C11orf92	C12orf10	C12orf11
C12orf12	C12orf23	C12orf24	C12orf26	C12orf28
C12orf29	C12orf32	C12orf34	C12orf35	C12orf36
C12orf37	C12orf39	C12orf4	C12orf40	C12orf42
C12orf43	C12orf44	C12orf45	C12orf48	C12orf49
C12orf5	C12orf50	C12orf52	C12orf54	C12orf55
C12orf56	C12orf57	C12orf59	C12orf60	C12orf61
C12orf62	C12orf63	C12orf64	C12orf65	C12orf66
C12orf67	C12orf68	C12orf69	C12orf72	C12orf74
C12orf76	C13orf1	C13orf15	C13orf16	C13orf23
C13orf26	C13orf27	C13orf28	C13orf30	C13orf31
C13orf33	C13orf34	C13orf35	C13orf36	C13orf37

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
C13orf39	C13orf40	C14orf1	C14orf100	C14orf101
C14orf102	C14orf104	C14orf105	C14orf106	C14orf109
C14orf115	C14orf118	C14orf119	C14orf126	C14orf128
C14orf129	C14orf135	C14orf138	C14orf142	C14orf143
C14orf145	C14orf147	C14orf148	C14orf149	C14orf153
C14orf156	C14orf159	C14orf166	C14orf167	C14orf173
C14orf174	C14orf177	C14orf178	C14orf179	C14orf180
C14orf181	C14orf182	C14orf183	C14orf2	C14orf20
C14orf21	C14orf23	C14orf28	C14orf37	C14orf38
C14orf39	C14orf4	C14orf43	C14orf45	C14orf48
C14orf49	C14orf50	C14orf68	C14orf73	C14orf79
C14orf80	C14orf93	C15orf17	C15orf2	C15orf23
C15orf24	C15orf26	C15orf27	C15orf29	C15orf32
C15orf33	C15orf38	C15orf39	C15orf40	C15orf42
C15orf43	C15orf44	C15orf48	C15orf52	C15orf53
C15orf54	C15orf55	C15orf56	C15orf57	C15orf58
C15orf59	C15orf63	C16orf11	C16orf13	C16orf3
C16orf35	C16orf38	C16orf42	C16orf45	C16orf46
C16orf48	C16orf5	C16orf53	C16orf54	C16orf55
C16orf57	C16orf58	C16orf59	C16orf61	C16orf62
C16orf63	C16orf65	C16orf68	C16orf7	C16orf70
C16orf71	C16orf72	C16orf73	C16orf75	C16orf78
C16orf79	C16orf80	C16orf85	C16orf87	C16orf88
C16orf89	C16orf91	C16orf92	C16orf93	C17orf101
C17orf102	C17orf103	C17orf28	C17orf37	C17orf38
C17orf39	C17orf42	C17orf46	C17orf47	C17orf48
C17orf49	C17orf50	C17orf53	C17orf55	C17orf56
C17orf57	C17orf58	C17orf59	C17orf60	C17orf61
C17orf62	C17orf64	C17orf65	C17orf66	C17orf67
C17orf68	C17orf70	C17orf71	C17orf74	C17orf76
C17orf77	C17orf79	C17orf80	C17orf81	C17orf82
C17orf85	C17orf87	C17orf90	C17orf91	C17orf92
C17orf97	C17orf98	C18orf1	C18orf10	C18orf19
C18orf21	C18orf22	C18orf25	C18orf26	C18orf32
C18orf34	C18orf45	C18orf54	C18orf55	C18orf56
C18orf62	C18orf8	C19orf10	C19orf12	C19orf16
C19orf18	C19orf2	C19orf20	C19orf21	C19orf22
C19orf24	C19orf26	C19orf28	C19orf29	C19orf29_ENST00000429344
C19orf33	C19orf35	C19orf36	C19orf39	C19orf40
C19orf41	C19orf42	C19orf43	C19orf44	C19orf45
C19orf46	C19orf47	C19orf48	C19orf50	C19orf51
C19orf52	C19orf53	C19orf56	C19orf57	C19orf59
C19orf6	C19orf60	C19orf61	C19orf63	C19orf67
C19orf75	C1D	C1GALT1	C1GALT1C1	C1QA
C1QB	C1QBP	C1QC	C1QL1	C1QL2
C1QL3	C1QL4	C1QTNF1	C1QTNF2	C1QTNF3
C1QTNF4	C1QTNF5	C1QTNF6	C1QTNF7	C1QTNF8
C1QTNF9	C1RL	C1S	C1orf100	C1orf101
C1orf103	C1orf105	C1orf106	C1orf107	C1orf109

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
C 1orf1 11	C 1orf1 12	C 1orf1 13	C 1orf1 14	C 1orf1 15
C 1orf1 16	C 1orf1 22	C 1orf1 23	C 1orf1 24	C 1orf1 25
C 1orf1 27	C 1orf1 28	C 1orf1 29	C 1orf1 30	C 1orf1 3 1
C 1orf1 35	C 1orf1 4	C 1orf1 4 1	C 1orf1 44	C 1orf1 46
C 1orf1 47	C 1orf1 50	C 1orf1 5 1	C 1orf1 56	C 1orf1 58
C 1orf1 6 1	C 1orf1 62	C 1orf1 63	C 1orf1 64	C 1orf1 67
C 1orf1 68	C 1orf1 70	C 1orf1 72	C 1orf1 73	C 1orf1 74
C 1orf1 75	C 1orf1 77	C 1orf1 82	C 1orf1 83	C 1orf1 86
C 1orf1 87	C 1orf1 89	C 1orf1 90	C 1orf1 92	C 1orf1 94
C 1orf1 98	C 1orf201	C 1orf21	C 1orf21 0	C 1orf21 2
C 1orf21 3	C 1orf21 6	C 1orf21 8	C 1orf220	C 1orf222
C 1orf227	C 1orf229	C 1orf25	C 1orf26	C 1orf31
C 1orf34	C 1orf35	C 1orf38	C 1orf43	C 1orf49
C 1orf50	C 1orf51	C 1orf52	C 1orf54	C 1orf55
C 1orf56	C 1orf57	C 1orf58	C 1orf59	C 1orf61
C 1orf63	C 1orf64	C 1orf65	C 1orf66	C 1orf67
C 1orf68	C 1orf69	C 1orf74	C 1orf77	C 1orf83
C 1orf84	C 1orf85	C 1orf86	C 1orf87	C 1orf88
C 1orf89	C 1orf9	C 1orf91	C 1orf92	C 1orf93
C 1orf94	C 1orf95	C 1orf96	C2	C20orf 103
C20orf1 06	C20orf1 07	C20orf1 08	C20orf 11	C20orf 111
C20orf1 12	C20orf1 14	C20orf 118	C20orf1 33	C20orf1 34
C20orf1 34_ENST 00000330271	C20orf1 35	C20orf1 4 1	C20orf1 44	C20orf1 5 1
C20orf 152	C20orf1 60	C20orf1 65	C20orf1 66	C20orf 177
C20orf1 85	C20orf1 86	C20orf1 87	C20orf1 9 1	C20orf 194
C20orf1 95	C20orf1 96	C20orf1 97	C20orf20	C20orf200
C20orf201	C20orf24	C20orf26	C20orf27	C20orf29
C20orf3	C20orf30	C20orf4	C20orf43	C20orf46
C20orf54	C20orf62	C20orf7	C20orf70	C20orf71
C20orf72	C20orf74	C20orf78	C20orf79	C20orf80
C20orf85	C20orf94	C20orf95	C20orf96	C21 orf1 05
C21 orf1 24	C21 orf1 3	C21 orf1 5	C21 orf2	C21 orf29
C21 orf33	C21 orf34	C21 orf45	C21 orf56	C21 orf57
C21 orf58	C21 orf59	C21 orf62	C21 orf63	C21 orf66
C21 orf7	C21 orf70	C21 orf74	C21 orf88	C21 orf89
C21 orf9	C21 orf91	C22orf1 3	C22orf 15	C22orf23
C22orf24	C22orf25	C22orf26	C22orf28	C22orf29
C22orf30	C22orf31	C22orf32	C22orf33	C22orf36
C22orf39	C22orf40	C22orf42	C22orf43	C22orf9
C2CD2	C2CD2L	C2CD3	C2CD4A	C2CD4B
C2orf 15	C2orf 16	C2orf 18	C2orf24	C2orf27A
C2orf27B	C2orf28	C2orf29	C2orf3	C2orf34
C2orf39	C2orf40	C2orf42	C2orf43	C2orf44
C2orf47	C2orf48	C2orf49	C2orf50	C2orf51
C2orf52	C2orf53	C2orf54	C2orf55	C2orf56
C2orf57	C2orf60	C2orf61	C2orf62	C2orf63
C2orf63 _ENSTOO 0004071 22	C2orf64	C2orf65	C2orf66	C2orf67
C2orf68	C2orf69	C2orf7	C2orf70	C2orf71

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
C2orf76	C2orf77	C2orf79	C2orf80	C2orf82
C2orf83	C2orf84	C2orf85	C2orf86	C2orf88
C3	C3AR1	C3P1	C3orf1	C3orf1 4
C3orf 15	C3orf 17	C3orf 18	C3orf 19	C3orf20
C3orf21	C3orf22	C3orf23	C3orf24	C3orf25
C3orf26	C3orf27	C3orf28	C3orf30	C3orf31
C3orf32	C3orf33	C3orf34	C3orf35	C3orf36
C3orf37	C3orf38	C3orf39	C3orf43	C3orf45
C3orf46	C3orf49	C3orf53	C3orf54	C3orf57
C3orf58	C3orf59	C3orf62	C3orf63	C3orf64
C3orf67	C3orf70	C3orf72	C3orf75	C3orf77
C4A	C4B	C4BPA	C4BPB	C4orf1 4
C4orf 17	C4orf 19	C4orf21	C4orf22	C4orf23
C4orf26	C4orf27	C4orf31	C4orf32	C4orf33
C4orf34	C4orf35	C4orf36	C4orf37	C4orf39
C4orf40	C4orf41	C4orf42	C4orf43	C4orf44
C4orf46	C4orf49	C4orf50	C4orf6	C4orf7
C5	C5AR1	C5orf1 3	C5orf1 5	C5orf22
C5orf23	C5orf24	C5orf28	C5orf30	C5orf32
C5orf33	C5orf34	C5orf35	C5orf36	C5orf37
C5orf38	C5orf39	C5orf4	C5orf40	C5orf41
C5orf42	C5orf43	C5orf45	C5orf46	C5orf48
C5orf49	C5orf5	C5orf50	C5orf51	C5orf53
C5orf54	C5orf56	C6	C6orf1	C6orf1 0
C6orf 103	C6orf1 05	C6orf1 06	C6orf1 08	C6orf1 14
C6orf1 15	C6orf1 18	C6orf1 2	C6orf1 20	C6orf1 24
C6orf1 25	C6orf1 29	C6orf1 30	C6orf1 34	C6orf1 36
C6orf1 38	C6orf1 42	C6orf1 45	C6orf1 46	C6orf1 5
C6orf1 50	C6orf 153	C6orf 154	C6orf 162	C6orf1 63_ENST00000369574
C6orf1 65	C6orf1 67	C6orf1 68	C6orf 170	C6orf 173
C6orf 174	C6orf 182	C6orf1 86	C6orf1 9 1	C6orf 192
C6orf1 95	C6orf201	C6orf203	C6orf204	C6orf21 1
C6orf21 3	C6orf21 8	C6orf221	C6orf222	C6orf223
C6orf224	C6orf225	C6orf227	C6orf25	C6orf26
C6orf27	C6orf35	C6orf47	C6orf48	C6orf49
C6orf57	C6orf58	C6orf62	C6orf64	C6orf70
C6orf72	C6orf81	C6orf87	C6orf89	C6orf94
C6orf97	C6orf98	C7	C7orf 11	C7orf 16
C7orf20	C7orf23	C7orf25	C7orf26	C7orf27
C7orf28A	C7orf28B	C7orf29	C7orf30	C7orf31
C7orf33	C7orf34	C7orf36	C7orf41	C7orf42
C7orf43	C7orf44	C7orf45	C7orf46	C7orf47
C7orf49	C7orf50	C7orf51	C7orf52	C7orf53
C7orf54	C7orf55	C7orf58	C7orf59	C7orf60
C7orf62	C7orf63	C7orf64	C7orf66	C7orf68
C7orf69	C7orf70	C7orf72_ENST00000297001	C8A	C8B
C8G	C8orf1 2	C8orf1 3	C8orf1 4	C8orf30A
C8orf31	C8orf33	C8orf34	C8orf37	C8orf38

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
C8orf4	C8orf40	C8orf41	C8orf44	C8orf45
C8orf46	C8orf47	C8orf55	C8orf58	C8orf59
C8orf76	C8orf79	C8orf8	C8orf80	C8orf82
C8orf84	C8orf85	C8orf86	C9	C9orf1 00
C9orf 102	C9orf 103	C9orf1 06	C9orf 11	C9orf1 14
C9orf1 16	C9orf1 17	C9orf1 19	C9orf1 23	C9orf1 25
C9orf1 28	C9orf1 29	C9orf1 3 1	C9orf1 35	C9orf1 39
C9orf1 40	C9orf1 42	C9orf1 44	C9orf1 50	C9orf 152
C9orf 153	C9orf1 56	C9orf1 6	C9orf 163	C9orf 164
C9orf1 67	C9orf 170	C9orf1 7 1	C9orf21	C9orf23
C9orf24	C9orf25	C9orf3	C9orf30	C9orf37
C9orf4	C9orf40	C9orf41	C9orf43	C9orf46
C9orf47	C9orf48	C9orf5	C9orf50	C9orf51
C9orf56	C9orf6	C9orf62	C9orf64	C9orf66
C9orf68	C9orf7	C9orf71	C9orf72	C9orf75
C9orf78	C9orf79	C9orf80	C9orf82	C9orf84
C9orf85	C9orf86	C9orf89	C9orf9	C9orf91
C9orf93	C9orf95	C9orf96	C9orf98	C9orf98 _EN ST00000298 545
CA1	CA1 0	CA1 1	CA1 2	CA1 3
CAM	CA2	CA3	CA4	CA5A
CA5B	CA5BP	CA6	CA7	CA8
CA9	CAB39	CAB39L	CABC1	CABIN1
CABLES1	CABLES2	CABP1	CABP2	CABP4
CABP5	CABP7	CABYR	CACHD1	CACNA1 A
CACNA1 A_ ENST 0000035701 8	CACNA1 B	CACNA1 C	CACNA1 D	CACNA1 E
CACNA1 F	CACNA1 G	CACNA1 H	CACNA1 H_EN ST0000035859 0	CACNA1 1
CACNA1 S	CACNA2D1	CACNA2D2	CACNA2D3	CACNB1
CACNB2	CACNB3	CACNG 1	CACNG2	CACNG3
CACNG4	CACNG5	CACNG6	CACNG7	CACNG8
CACYBP	CAD	CADM1	CADM2	CADM3
CADM4	CAD PS	CADPS2	CAGE1	CALB1
CALB2	CALCA	CALCB	CALCOC01	CALCOC02
CALCR	CALCR L	CALD1	CALHM1	CALHM2
CALM1	CALM2	CALM3	CALML3	CALML4
CALML5	CALML6	CALN 1	CALR	CALR3
CALU	CALY	CAMK1	CAMK1 D	CAMK1 G
CAMK2A	CAMK2B	CAMK2D	CAMK2G	CAMK2N1
CAMK2N2	CAMK4	CAMKK1	CAMKK2	CAMKV
CAMKV _ENSTOO 000477224	CAMLG	CAMP	CAMSAP1	CAMSAP1 L 1
CAMTA1	CAMTA2	CAND1	CAND2	CANT1
CANX	CAP1	CAP2	CAPG	CAPN1
CAPN1 0	CAPN1 1	CAPN1 2	CAPN1 3	CAPN2
CAPN3	CAPN5	CAPN6	CAPN7	CAPN9
CAPNS1	CAPRIN1	CAPRIN2	CAPS	CAPS2
CAPSL	CAPZA1	CAPZA2	CAPZA3	CAPZB

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CARD1 0	CARD1 1	CARD1 4	CARD1 6	CARD1 7
CARD1 8	CARD6	CARD8	CARD9	CARHSP1
CARKD	CARM1	CARS	CARS2	CARTPT
CASC1	CASC3	CASC4	CASC5	CASD1
CASK	CASKIN 1	CASKIN2	CASP1	CASP1 0
CASP1 4	CASP2	CASP3	CASP4	CASP5
CASP6	CASP7	CASP8	CASP9	CASQ1
CASQ2	CASR	CASS4	CAST	CASZ1
CAT	CATSPER1	CATSPER2	CATSPER3	CATSPER4
CATSPERB	CATSPERG	CAV1	CAV2	CAV3
CBARA1	CBFA2T2	CBFA2T3	CBFB	CBL
CBLB	CBLC	CBLL1	CBLN1	CBLN2
CBLN3	CBLN4	CBR1	CBR3	CBR4
CBS	CBW D 1	CBW D2	CBWD3	CBW D5
CBW D6	CBX1	CBX2	CBX3	CBX4
CBX5	CBX6	CBX7	CBX8	CBY1
CC2D1 A	CC2D1 B	CC2D2A	CC2D2B	CCAR1
CCBE1	CCBL1	CCBL2	CCBL2_ENSTO 0000370491	CCBP2
CCDC1 0 1	CCDC1 02A	CCDC1 02B	CCDC1 03	CCDC1 04
CCDC1 05	CCDC1 06	CCDC1 07	CCDC1 08	CCDC1 09A
CCDC1 09B	CCDC1 1	CCDC1 10	CCDC1 11	CCDC1 12
CCDC1 13	CCDC1 14	CCDC1 15	CCDC1 16	CCDC1 17
CCDC1 2	CCDC1 20	CCDC1 2 1	CCDC1 22	CCDC1 23
CCDC1 24	CCDC1 25	CCDC1 26	CCDC1 27	CCDC1 28
CCDC1 3	CCDC1 30	CCDC1 32	CCDC1 32_EN ST0000030586 6	CCDC1 34
CCDC1 35	CCDC1 37	CCDC1 38	CCDC1 4	CCDC1 40
CCDC1 4 1	CCDC1 42	CCDC1 44B	CCDC1 44NL	CCDC1 46
CCDC1 47	CCDC1 48	CCDC1 49	CCDC1 5	CCDC1 5 1
CCDC1 53	CCDC1 55	CCDC1 57	CCDC1 58	CCDC1 60
CCDC1 8	CCDC1 9	CCDC21	CCDC22	CCDC23
CCDC24	CCDC25	CCDC27	CCDC28A	CCDC28B
CCDC29	CCDC3	CCDC30	CCDC33	CCDC34
CCDC35	CCDC36	CCDC37	CCDC38	CCDC39
CCDC40	CCDC41	CCDC42	CCDC46	CCDC47
CCDC48	CCDC50	CCDC51	CCDC52	CCDC54
CCDC55	CCDC56	CCDC58	CCDC59	CCDC6
CCDC60	CCDC62	CCDC63	CCDC64	CCDC65
CCDC66	CCDC67	CCDC68	CCDC69	CCDC7
CCDC70	CCDC71	CCDC72	CCDC73	CCDC74A
CCDC74B	CCDC76	CCDC77	CCDC78	CCDC8
CCDC80	CCDC81	CCDC82	CCDC83	CCDC84
CCDC85A	CCDC85B	CCDC86	CCDC87	CCDC88A
CCDC88B	CCDC89	CCDC9	CCDC90A	CCDC90B
CCDC91	CCDC92	CCDC93	CCDC94	CCDC96
CCDC97	CCDC99	CCHCR1	CCIN	CCK
CCKAR	CCKBR	CCL1	CCL1 1	CCL1 3
CCL1 4	CCL1 5	CCL1 6	CCL1 7	CCL1 8
CCL1 9	CCL2	CCL20	CCL21	CCL22

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CCL23	CCL24	CCL25	CCL26	CCL27
CCL28	CCL3	CCL3L1	CCL3L3	CCL4
CCL4L1	CCL4L2	CCL5	CCL7	CCL8
CCM2	CCNA1	CCNA2	CCNB1	CCNB1 IP1
CCNB2	CCNB3	CCNB3 _ENST 00000376042	CCNC	CCND1
CCND2	CCND3	CCNDBP1	CCNE1	CCNE2
CCNF	CCNG1	CCNG2	CCNH	CCNI
CCNI2	CCNJ	CCNJL	CCNL1	CCNL2
CCNO	CCNT1	CCNT2	CCNY	CCNYL1
CCNYL2	CCPG 1	CCR1	CCR1 0	CCR2
CCR3	CCR4	CCR5	CCR6	CCR7
CCR8	CCR9	CCRL1	CCRL2	CCRN4L
CCS	CCT2	CCT3	CCT4	CCT5
CCT6A	CCT6B	CCT7	CCT8	CCT8L1
CCT8L2	CD1 0 1	CD1 09	CD1 4	CD1 5 1
CD1 60	CD1 63	CD1 63L1	CD1 64	CD1 64L2
CD1 80	CD1 9	CD1 A	CD1 B	CD1 C
CD1 D	CD1 E	CD2	CD200	CD200R1
CD200R1 L	CD207	CD209	CD22	CD226
CD244	CD247	CD248	CD27	CD274
CD276	CD28	CD2AP	CD2BP2	CD300A
CD300C	CD300E	CD300LB	CD300LD	CD300LF
CD300LG	CD302	CD320	CD33	CD34
CD36	CD36 _ENSTOOO 00433696	CD37	CD38	CD3D
CD3E	CD3EAP	CD3G	CD4	CD40
CD40LG	CD44	CD46	CD47	CD48
CD5	CD52	CD53	CD55	CD58
CD59	CD5L	CD6	CD63	CD68
CD69	CD7	CD70	CD72	CD74
CD79A	CD79B	CD80	CD81	CD82
CD83	CD84	CD86	CD8A	CD8B
CD9	CD93	CD96	CD97	CD99
CD99L2	CDA	CDADC1	CDAN1	CDC1 23
CDC1 4A	CDC1 4B	CDC1 6	CDC20	CDC20B
CDC23	CDC25A	CDC25B	CDC25C	CDC26
CDC27	CDC2L2	CDC34	CDC37	CDC37L1
CDC37P1	CDC40	CDC42	CDC42BPA	CDC42BPB
CDC42BPG	CDC42EP1	CDC42EP2	CDC42EP3	CDC42EP4
CDC42EP5	CDC42SE1	CDC42SE2	CDC45L	CDC5L
CDC6	CDC7	CDC73	CDCA2	CDC A3
CDCA4	CDCA5	CDCA7	CDCA7L	CDCA8
CDCP1	CDCP2	CDH1	CDH1 0	CDH1 1
CDH1 2	CDH1 3	CDH1 5	CDH1 6	CDH1 7
CDH1 8	CDH1 9	CDH2	CDH20	CDH22
CDH23	CDH24	CDH26	CDH3	CDH4
CDH5	CDH6	CDH7	CDH8	CDH9
CDHR1	CDHR5	CDIPT	CDK1	CDK1 0
CDK1 1B	CDK1 2	CDK1 3	CDK1 4	CDK1 5

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CDK1 6	CDK1 7	CDK1 8	CDK1 9	CDK1 _ENST 00000395284
CDK2	CDK20	CDK2AP1	CDK2AP2	CDK3
CDK4	CDK5	CDK5R1	CDK5R2	CDK5RAP1
CDK5RAP2	CDK5RAP3	CDK6	CDK7	CDK8
CDK9	CDKAL1	CDKL1	CDKL2	CDKL3
CDKL4	CDKL5	CDKN1 A	CDKN1 B	CDKN1 C
CDKN2A	CDKN2AI P	CDKN2AI PNL	CDKN2B	CDKN2C
CDKN2D	CDKN2a(p1 4)	CDKN3	CDNF	CD01
CDON	CDR1	CDR2	CDRT1	CDRT1 5
CDRT4	CDS1	CDS2	CDSN	CDT1
CDV3	CDX1	CDX2	CDX4	CDY1
CDY1 B	CDY2A	CDY2B	CDYL	CDYL2
CEACAM1	CEACAM1 8	CEACAM1 8_E NST00000451 6 26	CEACAM1 9	CEACAM20
CEACAM3	CEACAM4	CEACAM5	CEACAM6	CEACAM7
CEACAM8	CEBPA	CEBPB	CEBPE	CEBPG
CEBPZ	CECR1	CECR2	CECR5	CECR6
CEL	CELA1	CELA2A	CELA2B	CELA3A
CELA3B	CELF1	CELF2	CELF3	CELF4
CELF5	CELF6	CELP	CELSR1	CELSR2
CELSR3	CEMP1	CEND1	CENPA	CEN PB
CEN PC1	CEN PE	CEN PF	CENPH	CEN PI
CEN PJ	CEN PK	CEN PL	CENPM	CEN PN
CEN PO	CEN PP	CEN PQ	CENPT	CEN PV
CEP1 10	CEP1 20	CEP1 35	CEP1 52	CEP1 64
CEP1 70	CEP1 70L	CEP1 92	CEP250	CEP290
CEP55	CEP57	CEP63	CEP68	CEP70
CEP72	CEP76	CEP78	CEP97	CEPT1
CER1	CERCAM	CERK	CERKL	CES1
CES1 _ENST000 00360526	CES2	CES3	CES7	CES8
CETN1	CETN2	CETN3	CETP	CFB
CFC1	CFC1 B	CFD	CFDP1	CFH
CFHR1	CFHR2	CFHR3	CFHR4	CFHR5
CFI	CFL1	CFL2	CFLAR	CFP
CFTR	CGA	CGB	CGB1	CGB2
CGB5	CGB7	CGB8	CGGBP1	CGI-77
CGN	CGNL1	CGREF1	CG RRF1	CH25H
CHAC1	CHAC2	CHAD	CHADL	CHAF1 A
CHAF1 B	CHAT	CHCHD1	CHCHD1 0	CHCHD2
CHCHD3	CHCHD4	CHCHD5	CHCHD6	CHCHD7
CHCHD8	CHCHD9	CHD1	CHD1 L	CHD2
CHD3	CHD4	CHD5	CHD6	CHD7
CHD8	CHD9	CHDH	CHEK1	CHEK2
CHERP	CHFR	CHGA	CHGB	CHI3L1
CHI3L2	CHIA	CHIC1	CHIC2	CHID1
CHIT1	CHKA	CHKB	CHL1	CHM
CHML	CHMP2A	CHMP2B	CHMP4A	CHMP4B
CHMP4C	CHMP5	CHMP6	CHMP7	CHN1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CHN2	CHODL	CHORDC1	CHP	CHP2
CHPF	CHPF2	CHPT1	CHRAC1	CHRD
CHRDL1	CHRDL2	CHRFAM7A	CHRM1	CHRM2
CHRM3	CHRM5	CHRNA1	CHRNA1 0	CHRNA2
CHRNA3	CHRNA4	CHRNA5	CHRNA6	CHRNA7
CHRNA9	CHRNB1	CHRNB2	CHRNB3	CHRNB4
CHRND	CHRNE	CHRNG	CHST1	CHST1 0
CHST1 1	CHST1 2	CHST1 3	CHST1 4	CHST1 5
CHST2	CHST3	CHST4	CHST5	CHST6
CHST7	CHST8	CHST9	CHSY1	CHSY3
CHTF1 8	CHTF8	CHUK	CHURC1	CIA01
CIAPIN1	CIB1	CIB2	CIB3	CIB4
CIC	CIDEA	CIDEB	CIDEC	CIITA
CILP	CILP2	CINP	CIR1	CIRBP
CIRH1 A	CISD1	CISD1 B	CISD2	CISH
CIT	CITED1	CITED2	CITED4	CIZ1
CKAP2	CKAP2L	CKAP4	CKAP5	CKB
CKLF	CKM	CKMT1 A	CKMT1 B	CKMT2
CKS1 B	CKS2	CLASP1	CLASP2	CLC
CLCA1	CLCA2	CLCA3P	CLCA4	CLCC1
CLCF1	CLCN1	CLCN2	CLCN3	CLCN4
CLCN5	CLCN6	CLCN7	CLCNKA	CLCNKB
CLDN1	CLDN1 0	CLDN1 1	CLDN1 2	CLDN1 4
CLDN1 5	CLDN1 6	CLDN1 7	CLDN1 8	CLDN1 9
CLDN2	CLDN20	CLDN22	CLDN3	CLDN4
CLDN5	CLDN6	CLDN7	CLDN8	CLDN9
CLDND1	CLDND2	CLEC1 0A	CLEC1 1A	CLEC1 2A
CLEC1 2B	CLEC1 4A	CLEC1 6A	CLEC1 8A	CLEC1 8B
CLEC1 8C	CLEC1 A	CLEC1 B	CLEC2B	CLEC2D
CLEC3A	CLEC3B	CLEC4A	CLEC4C	CLEC4D
CLEC4E	CLEC4F	CLEC4G	CLEC4M	CLEC5A
CLEC6A	CLEC7A	CLEC9A	CLECL1	CLGN
CLIC1	CLIC2	CLIC3	CLIC4	CLIC5
CLIC6	CLIP1	CLIP2	CLIP3	CLIP4
CLK1	CLK2	CLK3	CLK4	CLLU1
CLLU1 0 S	CLMN	CLN3	CLN5	CLN6
CLN8	CLNS1 A	CLOCK	CLP1	CLPB
CLPP	CLPS	CLPTM1	CLPTM1 L	CLPX
CLRN1	CLRN2	CLRN3	CLSPN	CLSTN1
CLSTN2	CLSTN3	CLTA	CLTB	CLTC
CLTCL1	CLU	CLUAP1	CLUL1	CLVS2
CLYBL	CMA1	CMAS	CMBL	CMC1
CMKLR1	CMPK1	CMPK2	CMTM1	CMTM2
CMTM3	CMTM4	CMTM5	CMTM6	CMTM7
CMTM8	CMYA5	CNBP	CNDP1	CNDP2
CNFN	CNGA1	CNGA2	CNGA3	CNGA4
CNGB1	CNGB3	CNIH	CNIH2	CNIH3
CNIH4	CNKSR1	CNKSR2	CNKSR3	CNN1
CNN2	CNN3	CNNM1	CNNM2	CNNM3
CNNM4	CNO	CNOT1	CNOT1 0	CNOT2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CNOT3	CNOT4	CNOT6	CNOT6L	CNOT7
CNOT8	CNP	CNPY1	CNPY2	CNPY3
CNPY4	CNR1	CNR2	CNRIP1	CNST
CNTD1	CNTD2	CNTF	CNTFR	CNTLN
CNTN1	CNTN2	CNTN3	CNTN4	CNTN5
CNTN6	CNTNAP1	CNTNAP2	CNTNAP3	CNTNAP4
CNTNAP5	CNTROB	COASY	COBL	COBLL1
COBRA1	COCH	COE4_HUMAN	COG1	COG2
COG3	COG4	COG5	COG6	COG7
COG8	COIL	COL10A1	COL11A1	COL12A1
COL13A1	COL14A1	COL15A1	COL16A1	COL17A1
COL18A1	COL19A1	COL1A1	COL1A2	COL20A1
COL22A1	COL23A1	COL24A1	COL25A1	COL27A1
COL28A1	COL2A1	COL3A1	COL4A1	COL4A2
COL4A3	COL4A3BP	COL4A4	COL4A5	COL4A6
COL5A1	COL5A2	COL5A3	COL6A1	COL6A2
COL6A3	COL6A6	COL7A1	COL8A1	COL8A2
COL9A1	COL9A2	COL9A3	COLEC10	COLEC11
COLEC12	COLO	COMMD1	COMMD10	COMMD2
COMMD3	COMMD4	COMMD5	COMMD6	COMMD7
COMMD8	COMMD9	COMP	COMT	COMTD1
COPA	COPB1	COPB2	COPE	COPG
COPS2	COPS3	COPS4	COPS5	COPS6
COPS7A	COPS7B	COPS8	COPZ1	COQ10A
COQ10B	COQ2	COQ3	COQ4	COQ5
COQ6	COQ7	COQ9	CORIN	COR01A
COR01B	COR01C	COR02A	COR02B	COR06
COR07	CORT	COTL1	COX10	COX11
COX15	COX16	COX17	COX18	COX19
COX4I1	COX4I2	COX4NB	COX5A	COX5B
COX6A1	COX6A2	COX6B1	COX6B1_ENST00000392201	COX6B2
COX6BP3	COX6C	COX7A1	COX7A2	COX7A2L
COX7AP2	COX7B	COX7B2	COX7C	COX8A
COX8C	CP	CP110	CPA1	CPA2
CPA3	CPA4	CPA5	CPA6	CPAMD8
CPB1	CPB2	CPD	CPE	CPEB1
CPEB2	CPEB3	CPEB4	CPLX2	CPLX3
CPLX4	CPM	CPN1	CPN2	CPNE1
CPNE2	CPNE3	CPNE4	CPNE5	CPNE6
CPNE7	CPNE8	CPNE9	CPO	CPOX
CPPED1	CPS1	CPSF1	CPSF2	CPSF3
CPSF3L	CPSF4	CPSF4L	CPSF6	CPSF7
CPT1A	CPT1B	CPT1C	CPT2	CPVL
CPXCR1	CPXM1	CPXM2	CPZ	CR1
CR1L	CR2	CRABP1	CRABP2	CRADD
CRAT	CRB1	CRB2	CRB3	CRBN
CRCP	CRCT1	CREB1	CREB3	CREB3L1
CREB3L2	CREB3L3	CREB3L4	CREB5	CREBBP
CREBL2	CREBZF	CREG1	CREG2	

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CRELD1	CRELD2	CREM	CREM_ENSTO0000395887	CRH
CRHBP	CRHR1	CRHR2	CRIM1	CRIP1
CRIP2	CRIP3	CRIPAK	CRIPT	CRISP1
CRISP2	CRISP3	CRISPLD1	CRISPLD2	CRK
CRKL	CRLF1	CRLF2	CRLF3	CRLS1
CRMP1	CRNKL1	CRNN	CROCC	CROT
CRP	CRSP3	CRTAC1	CRTAM	CRTAP
CRTC1	CRTC2	CRTC3	CRX	CRY1
CRY2	CRYAA	CRYAB	CRYBA1	CRYBA2
CRYBA4	CRYBB1	CRYBB2	CRYBB3	CRYBG3
CRYGA	CRYGB	CRYGC	CRYGD	CRYGN
CRYGS	CRYL1	CRYM	CRYZ	CRYZL1
CS	CSAD	CSAG1	CSAG2	CSAG3
CSAG4	CSDA	CSDC2	CSDE1	CSE1L
CSF1	CSF1R	CSF2	CSF2RA	CSF2RB
CSF3	CSF3R	CSGALNACT1	CSGALNACT2	CSH1
CSH2	CSHL1	CSK	CSMD1	CSMD1_ENST0000031 8252
CSMD2	CSMD3	CSN2	CSN3	CSNK1A1
CSNK1A1L	CSNK1D	CSNK1E	CSNK1E_ENST00000403904	CSNK1G1
CSNK1G2	CSNK1G3	CSNK2A1	CSNK2A2	CSNK2B
CSPG4	CSPG5	CSPP1	CSRNP1	CSRNP2
CSRNP3	CSRP1	CSRP2	CSRP2BP	CSRP3
CST1	CST11	CST2	CST3	CST4
CST5	CST6	CST7	CST8	CST9
CST9L	CSTA	CSTB	CSTF1	CSTF2
CSTF2T	CSTF3	CSTL1	CT45-1	CT45A2
CT45A3	CT45A4	CT45A5	CT45A6	CT47A1
CT47A10	CT47A11	CT47A2	CT47A3	CT47A4
CT47A5	CT47A6	CT47A7	CT47A8	CT47A9
CTAG1A	CTAG1B	CTAG2	CTAG2_ENST00000247306	CTAGE5
CTBP1	CTBP2	CTBS	CTCF	CTCFL
CTD-2267G17_3	CTDP1	CTDSP1	CTDSP2	CTDSPL
CTDSPL2	CTF1	CTGF	CTH	CTHRC1
CTLA4	CTNNA1	CTNNA2	CTNNA2_ENST00000466387	CTNNA3
CTNNAL1	CTNNB1	CTNNBIP1	CTNNBL1	CTNND1
CTNND2	CTNS	CTPS	CTPS2	CTR9
CTRB1	CTRB2	CTRC	CTRL	CTSA
CTSB	CTSC	CTSD	CTSE	CTSF
CTSG	CTSH	CTSK	CTSL1	CTSL2
CTSL3	CTSO	CTSS	CTSW	CTSZ
CTTN	CTTNBP2	CTTNBP2NL	CTU2	CTXN1
CTXN3	CU041_HUMAN	CU085_HUMAN	CUBN	CUEDC1
CUEDC2	CUL1	CUL2	CUL3	CUL4A

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
CUL4B	CUL4B _ENSTOO 000371 322	CUL5	CUL7	CUL9
CUTA	CUTC	CUX1	CUX1 _ENSTOO 000292538	CUX2
CUZD1	CWC22	CWC27	CWF1 9L1	CWF1 9L2
CWH43	CX3CL1	CX3CR1	CXADR	CXCL1
CXCL1 0	CXCL1 1	CXCL1 2	CXCL1 3	CXCL1 4
CXCL1 6	CXCL1 7	CXCL2	CXCL3	CXCL5
CXCL6	CXCL9	CXCR1	CXCR2	CXCR3
CXCR4	CXCR5	CXCR6	CXCR7	CXXC1
CXXC4	CXXC5	CXorfl	CXorfl 5	CXorfl 9
CXorf21	CXorf22	CXorf23	CXorf24	CXorf25
CXorf26	CXorf27	CXorf28	CXorf29	CXorf30
CXorf31	CXorf35	CXorf36	CXorf38	CXorf40A
CXorf40B	CXorf41	CXorf42	CXorf48	CXorf56
CXorf57	CXorf58	CXorf59	CXorf61	CXorf62
CXorf65	CXorf66	CXorf67	CYB561	CYB561 D 1
CYB561 D2	CYB5A	CYB5B	CYB5D1	CYB5D2
CYB5R1	CYB5R2	CYB5R3	CYB5R4	CYBA
CYBASC3	CYBB	CYBRD1	CYC1	CYCS
CYCSP52	CYFIP1	CYFIP2	CYGB	CYHR1
CYLC1	CYLC2	CYLD	CYP1 1A 1	CYP1 1B 1
CYP1 1B2	CYP1 7A1	CYP1 9A1	CYP1 A 1	CYP1 A2
CYP1 B 1	CYP20A1	CYP21 A2	CYP24A1	CYP26A1
CYP26B1	CYP26C1	CYP27A1	CYP27B1	CYP27C1
CYP2A1 3	CYP2A6	CYP2A7	CYP2B6	CYP2B7P1
CYP2C1 8	CYP2C1 9	CYP2C8	CYP2C9	CYP2D6
CYP2E1	CYP2F1	CYP2J2	CYP2R1	CYP2S1
CYP2U1	CYP2W 1	CYP39A1	CYP3A4	CYP3A43
CYP3A5	CYP3A7	CYP46A1	CYP4A1 1	CYP4A22
CYP4B1	CYP4F1 1	CYP4F1 2	CYP4F2	CYP4F22
CYP4F3	CYP4F8	CYP4V2	CYP4X1	CYP4Z1
CYP51 A 1	CYP7A1	CYP7B1	CYP8B1	CYR61
CYS1	CYSLTR1	CYSLTR2	CYTH1	CYTH2
CYTH3	CYTH4	CYTI P	CYTL1	CYTSA
CYTSB	CYYR1	CYorf 15B	CaMKI b	D2HGDH
D4S234E	DAAM1	DAAM2	DAB1	DAB2
DAB2I P	DACH1	DACH2	DACH2 _ENST 000003731 3 1	DACT1
DACT2	DAD1	DAG 1	DAG LA	DAG LB
DAK	DALRD3	DAMS_HUMA N	DAND5	DAO
DAOA	DAP	DAP3	DAPK1	DAPK2
DAPK3	DAPL1	DAPP1	DARC	DARS
DARS2	DAXX	DAZ2	DAZ3	DAZAP1
DAZAP2	DAZL	DBC1	DBF4	DBF4B
DBF4B _ENSTOO 00031 5005	DBH	DBI	DBN1	DBNDD1
DBNDD2	DBNL	DBP	DBR1	DBT
DBX1	DBX2	DCAF1 0	DCAF1 2	DCAF1 2L1
DCAF1 2L2	DCAF1 3	DCAF1 5	DCAF1 6	DCAF1 7

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
DCAF4	DCAF4L1	DCAF4L2	DCAF5	DCAF6
DCAF7	DCAF8	DCAF8L1	DCAF8L2	DCAKD
DCBLD1	DCBLD2	DCC	DCD	DCDC1
DCDC2	DCDC5	DCHS1	DCHS2	DCI
DCK	DCLK1	DCLK2	DCLK3	DCLRE1 A
DCLRE1 B	DCLRE1 C	DCLRE1 C_ENST00000378278	DCN	DCP1 A
DCP1 B	DCP2	DCPS	DCST1	DCST2
DCT	DCTD	DCTN1	DCTN3	DCTN4
DCTN5	DCTN6	DCTPP1	DCUN1 D1	DCUN1 D2
DCUN1 D3	DCUN1 D4	DCUN1 D5	DCX	DCXR
DDA1	DDAH1	DDAH2	DDB1	DDB2
DDC	DDHD1	DDHD2	DDI1	DDI2
DDIT3	DDIT4	DDIT4L	DDN	DDO
DDOST	DDR1	DDR2	DDRGK1	DDT
DDTL	DDX1	DDX10	DDX11	DDX12
DDX12_ENSTOO000432996	DDX17	DDX18	DDX19A	DDX19B
DDX20	DDX21	DDX23	DDX24	DDX25
DDX26B	DDX27	DDX28	DDX31	DDX39
DDX3X	DDX3Y	DDX4	DDX41	DDX42
DDX43	DDX46	DDX47	DDX49	DDX5
DDX50	DDX51	DDX52	DDX53	DDX54
DDX55	DDX56	DDX58	DDX59	DDX6
DDX60	DDX60L	DDX60_ENSTO0000393743	DEAF1	01-Dec
DECR1	DECR2	DEDD	DEDD2	DEF6
DEF8	DEFA1	DEFA1B	DEFA3	DEFA4
DEFA5	DEFA6	DEFB1	DEFB103A	DEFB103B
DEFB104A	DEFB104B	DEFB105A	DEFB105B	DEFB106A
DEFB106B	DEFB107A	DEFB107B	DEFB108B	DEFB110
DEFB111	DEFB112	DEFB113	DEFB114	DEFB115
DEFB116	DEFB118	DEFB119	DEFB121	DEFB123
DEFB124	DEFB125	DEFB126	DEFB127	DEFB128
DEFB129	DEFB130	DEFB131	DEFB132	DEFB134
DEFB135	DEFB136	DEFB4A	DEGS1	DEGS2
DEK	DEM1	DENND1A	DENND1B	DENND1C
DENND2A	DENND2C	DENND2D	DENND3	DENND4A
DENND4B	DENND4C	DENND5A	DENND5B	DEPDC1
DEPDC1B	DEPDC4	DEPDC5	DEPDC6	DEPDC7
DERL1	DERL2	DERL3	DES	DET1
DEXI	DFFA	DFFB	DFNA5	DFNB31
DFNB59	DGAT1	DGAT2	DGAT2L6	DGCR14
DGCR2	DGCR6	DGCR6L	DGCR8	DGKA
DGKB	DGKD	DGKE	DGKG	DGKH
DGKI	DGKK	DGKQ	DGKZ	DGUOK
DHCR24	DHCR7	DHDDS	DHDH	DHDPSL
DHFR	DHFRL1	DHH	DHODH	DHPS
DHRS1	DHRS11	DHRS12	DHRS13	DHRS2
DHRS3	DHRS4	DHRS4L2	DHRS7	DHRS7B

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
DHRS9	DHRSX	DHTKD1	DHX1 5	DHX1 6
DHX29	DHX30	DHX32	DHX33	DHX34
DHX35	DHX36	DHX37	DHX38	DHX40
DHX57	DHX58	DHX8	DHX9	DIABLO
DIAPH1	DIAPH2	DIAPH3	DICER1	DID01
DIMT1 L	DI01	DI03	DIP2B	DIP2C
DIRAS1	DIRAS2	DIRAS3	DIRC1	DIRC2
DIS3	DIS3L	DIS3L2	DISC1	DISP1
DISP2	DIXDC1	DKC1	DKFZP434P1 7 50	DKFZP5640 0823
DKFZP566M1 14	DKK1	DKK2	DKK3	DKK4
DKKL1	DLAT	DLC1	DLC1 _ENSTOO 00031 6609	DLD
DLEC1	DLEU2L	DLG1	DLG2	DLG3
DLG4 _ENSTOOO 0029381 3	DLG5	DLGAP1	DLGAP2	DLGAP2 _EN ST00000356 067
DLGAP3	DLGAP4	DLGAP5	DLK1	DLK2
DLL1	DLL3	DLL4	DLST	DLX1
DLX2	DLX3	DLX4	DLX5	DLX6
DMAP1	DMBT1	DMBX1	DMC1	DMD
DMD _ENSTOOOO 0378687	DMG DH	DMKN	DMP1	DMPK
DMRT1	DMRT2	DMRT2 _ENST 00000302441	DMRT3	DMRTA1
DMRTB1	DMRTC1	DMRTC1 B	DMRTC2	DMTF1
DMWD	DMXL1	DMXL2	DNA2L	DNAH1
DNAH1 0	DNAH1 0_same_ name	DNAH1 1	DNAH1 2L	DNAH1 4
DNAH1 7	DNAH1 _ENSTOO 000420323	DNAH2	DNAH3	DNAH5
DNAH6	DNAH7	DNAH8	DNAH9	DNAI 1
DNAI2	DNAJA1	DNAJA2	DNAJA3	DNAJA4
DNAJB1	DNAJB1 1	DNAJB1 2	DNAJB1 3	DNAJB1 4
DNAJB2	DNAJB4	DNAJB5	DNAJB6	DNAJB7
DNAJB8	DNAJB9	DNAJC1	DNAJC1 0	DNAJC1 1
DNAJC1 2	DNAJC1 3	DNAJC1 4	DNAJC1 5	DNAJC1 6
DNAJC1 7	DNAJC1 8	DNAJC1 9	DNAJC2	DNAJC21
DNAJC22	DNAJC24	DNAJC25	DNAJC25-GNG1 0	DNAJC27
DNAJC28	DNAJC3	DNAJC30	DNAJC4	DNAJC5
DNAJC5B	DNAJC5G	DNAJC6	DNAJC7	DNAJC8
DNAJC9	DNAL4	DNALI 1	DNAPTP6	DNASE1
DNASE1 L1	DNASE1 L2	DNASE1 L3	DNASE2	DNASE2B
DND1	DNER	DNHD1 _ENST 00000254579	DNHL1	DNLZ
DNM1	DNM1 L	DNM2	DNM3	DNMBP
DNMT1	DNMT3A	DNMT3B	DNMT3L	DNPEP
DNTT	DNTTI P1	DOC2A	DOCK1	DOCK1 0
DOCK1 0_ENSTO 0000373702	DOCK1 1	DOCK2	DOCK3	DOCK3 _ENS T000002660

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
				37
DOCK4	D0CK5	DOCK6	DOCK7	DOCK8
DOCK9	DOHH	DOK1	DOK2	DOK3
DOK4	DOK5	DOK6	DOK7	DOLK
DOLPP1	DOM3Z	DONSON	DOPEY1	DOPEY2
DOT1 L	DPAGT1	DPCR1	DPEP1	DPEP2
DPEP3	DPF1	DPF2	DPH1	DPH1 - OVCA2
DPH2	DPH3	DPH3B	DPH5	DPMI
DPM2	DPM3	DPP1 0	DPP3	DPP4
DPP6	DPP7	DPP8	DPP9	DPPA2
DPP A3	DPPA4	DPPA5	DPRX	DPT
DPY1 9L1	DPY1 9L2	DPY1 9L3	DPY1 9L4	DPY30
DPYD	DPYS	DPYSL2	DPYSL3	DPYSL4
DPYSL5	DQX1	DR1	DRAM1	DRAM2
DRAP1	DRD1	DRD2	DRD3	DRD4
DRD5	DRD5P1	DRG1	DRG2	DRP2
DSC1	DSC2	DSC3	DSCAM	DSCAML1
DSCC1	DSCR3	DSCR4	DSCR6	DSE
DSEL	DSG 1	DSG2	DSG3	DSG4
DSN1	DSP	DSPP	DST	DSTN
DSTYK	DST_ENSTOOOO 0370754	DST_ENSTOOO 00370769	DTD1	DTHD1
DTL	DTNA	DTNB	DTNBP1	DTWD1
DTWD2	DTX1	DTX2	DTX3	DTX3L
DTX4	DTYMK	DULLARD	DUOX1	DUOX2
DU0XA1	DUOXA2	DUPD1	DUS1 L	DUS2L
DUS3L	DUS4L	DUSP1	DUSP1 0	DUSP1 1
DUSP1 2	DUSP1 3	DUSP1 3_ENS T00000356369	DUSP1 4	DUSP1 5
DUSP1 6	DUSP1 8	DUSP1 9	DUSP2	DUSP21
DUSP22	DUSP23	DUSP26	DUSP27	DUSP28
DUSP3	DUSP4	DUSP5	DUSP5P	DUSP6
DUSP7	DUSP8	DUSP9	DUT	DUXA
DVL1	DVL2	DVL3	DYDC1	DYDC2
DYM	DYNC1 H 1	DYNC1 I1	DYNC1 I2	DYNC1 LI1
DYNC1 LI2	DYNC2H1	DYNC2H1 _EN ST0000039809 3	DYNC2LI 1	DYNLL1
DYNLL2	DYNLRB1	DYNLRB2	DYNLT1	DYNLT3
DYRK1 A	DYRK1 B	DYRK2	DYRK3	DYRK4
DYSF	DYSFI P 1	DYX1 C 1	DZIP1	DZI P 1 L
DZI P3	E2F1	E2F2	E2F3	E2F4
E2F5	E2F6	E2F7	E2F8	E4F1
EAF1	EAF2	EAPP	EARS2	EBAG9
EBF1	EBF3	EBI3	EBNA1 BP2	EBP
EBPL	ECD	ECE1	ECE2	ECEL1
ECH1	ECHDC1	ECHDC2	ECHDC3	ECHS1
ECM1	ECM2	ECOP	ECSIT	ECT2
ECT2L	EDA	EDA2R	EDAR	EDARADD

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
EDC3	EDC4	EDDM3A	EDDM3B	EDEM1
EDEM2	EDEM3	EDF1	EDG6	EDIL3
EDN1	EDN2	EDN3	EDNRA	EDNRB
EEA1	EED	EEF1A1	EEF1A1P11	EEF1A2
EEF1B2	EEF1D	EEF1E1	EEF2	EEF2K
EEFSEC	EEPD1	EFCAB1	EFCAB2	EFCAB3
EFCAB4A	EFCAB4B	EFCAB5	EFCAB6	EFCAB7
EFEMP1	EFEMP2	EFHA1	EFHA2	EFHB
EFHC1	EFHC2	EFHD1	EFHD2	EFNA1
EFNA2	EFNA3	EFNA4	EFNA5	EFNB1
EFNB2	EFNB3	EFR3A	EFS	EFTUD1
EFTUD2	EGF	EGFL4	EGFL6	EGFL7
EGFL8	EGFLAM	EGFR	EGFR_ENSTO0000344576	EGLN1
EGLN2	EGLN3	EGR1	EGR2	EGR3
EGR4	EHBP1	EHBP1L1	EHD1	EHD2
EHD3	EHD4	EHF	EHHADH	EHMT1
EHMT2	EI24	EID1	EID2	EID2B
EIF1	EIF1AD	EIF1AX	EIF1AY	EIF1B
EIF2A	EIF2AK1	EIF2AK2	EIF2AK3	EIF2AK4
EIF2A_ENSTOOO00487799	EIF2B1	EIF2B2	EIF2B3	EIF2B4
EIF2B5	EIF2C1	EIF2C2	EIF2C3	EIF2C4
EIF2S1	EIF2S2	EIF2S3	EIF3A	EIF3B
EIF3C	EIF3CL	EIF3D	EIF3E	EIF3EIP
EIF3F	EIF3G	EIF3H	EIF3I	EIF3J
EIF3K	EIF3M	EIF3S8	EIF4A1	EIF4A2
EIF4A3	EIF4B	EIF4E	EIF4E2	EIF4E3
EIF4EBP1	EIF4EBP2	EIF4EBP3	EIF4ENIF1	EIF4G1
EIF4G2	EIF4G3	EIF4H	EIF5	EIF5A
EIF5A2	EIF5B	EIF6	ELAC1	ELAC2
ELANE	ELAVL1	ELAVL2	ELAVL3	ELAVL4
ELF1	ELF2	ELF3	ELF4	ELF5
ELFN2	ELK1	ELK3	ELK4	ELL
ELL2	ELL3	ELM01	ELM02	ELM03
ELMOD2	ELMOD3	ELN	ELOF1	ELOVL1
ELOVL2	ELOVL3	ELOVL4	ELOVL5	ELOVL6
ELOVL7	ELP2	ELP3	ELP4	ELSPBP1
ELTD1	EMB	EMCN	EMD	EME1
EME2	EMID1	EMID2	EMILIN1	EMILIN2
EMILIN3	EML1	EML2	EML3	EML4
EML5	EMP1	EMP2	EMP3	EMR1
EMR2	EMR3	EMR4	EMX1	EMX2
EN1	EN2	ENAH	ENAM	ENC1
ENDOD1	ENDOG	ENDOU	ENG	ENGASE
ENHO	ENKUR	EN01	EN02	EN03
EN04	ENOPH 1	ENOSF1	ENOX1	EN0X2
ENPEP	ENPP1	ENPP2	ENPP3	ENPP4
ENPP5	ENPP6	ENPP7	ENSA	ENSG00000038102

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ENSG000001 062 32	ENSG000001 078 16	ENSG000001 1 5339	ENSG000001 1 7540	ENSG00000 11851 9
ENSG000001 189 28	ENSG000001 232 57	ENSG000001 2 4224	ENSG000001 2 4677	ENSG00000 124854
ENSG000001 249 15	ENSG000001 256 3 1	ENSG000001 2 5822	ENSG000001 2 5881	ENSG00000 125964
ENSG000001 260 02	ENSG000001 262 17	ENSG000001 2 8422	ENSG000001 2 8563	ENSG00000 129973
ENSG000001 302 25	ENSG000001 302 4 1	ENSG000001 3 1484	ENSG000001 3 521 3	ENSG00000 135702
ENSG000001 357 49	ENSG000001 370 2 1	ENSG000001 3 7746	ENSG000001 3 9239	ENSG00000 140209
ENSG000001 428 32	ENSG000001 429 5 1	ENSG000001 4 391 0	ENSG000001 4 4396	ENSG00000 145642
ENSG000001 467 36	ENSG000001 471 13	ENSG000001 4 8667	ENSG000001 4 871 3	ENSG00000 148805
ENSG000001 496 18	ENSG000001 496 58	ENSG000001 5 0980	ENSG000001 5 3081	ENSG00000 154732
ENSG000001 563 67	ENSG000001 565 09	ENSG000001 5 781 9	ENSG000001 5 7999	ENSG00000 1581 85
ENSG000001 583 0 1	ENSG000001 584 03	ENSG000001 5 9239	ENSG000001 6 1643	ENSG00000 162568
ENSG000001 626 2 1	ENSG000001 626 44	ENSG000001 6 2734	ENSG000001 6 2767	ENSG00000 162872
ENSG000001 631 44	ENSG000001 631 82	ENSG000001 6 361 2	ENSG000001 6 4 159	ENSG00000 164236
ENSG000001 642 4 1	ENSG000001 645 00	ENSG000001 6 4845	ENSG000001 6 4860	ENSG00000 164946
ENSG000001 651 14	ENSG000001 651 24	ENSG000001 6 5429	ENSG000001 6 5851	ENSG00000 165935
ENSG000001 660 13	ENSG000001 663 29	ENSG000001 6 6492	ENSG000001 6 6593	ENSG00000 166707
ENSG000001 672 8 1	ENSG000001 673 90	ENSG000001 6 7433	ENSG000001 6 7442	ENSG00000 167475
ENSG000001 680 38	ENSG000001 681 13	ENSG000001 6 8561	ENSG000001 6 9664	ENSG00000 169697
ENSG000001 702 38	ENSG000001 708 17	ENSG000001 7 0987	ENSG000001 7 1084	ENSG00000 17 1459
ENSG000001 7 18 4 1	ENSG000001 7 18 78	ENSG000001 7 1995	ENSG000001 7 2070	ENSG00000 17221 2
ENSG000001 722 6 1	ENSG000001 727 64	ENSG000001 7 2786	ENSG000001 7 2823	ENSG00000 172895
ENSG000001 728 99	ENSG000001 729 00	ENSG000001 7 2963	ENSG000001 7 3 115	ENSG00000 17321 3
ENSG000001 736 09	ENSG000001 736 7 1	ENSG000001 7 3679	ENSG000001 7 3774	ENSG00000 173780
ENSG000001 738 20	ENSG000001 738 63	ENSG000001 7 3961	ENSG000001 7 3968	ENSG00000 174028

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ENSG000001 74057	ENSG000001 74104	ENSG000001 74121	ENSG000001 74126	ENSG00000 174144
ENSG000001 74398	ENSG000001 74440	ENSG000001 74459	ENSG000001 74483	ENSG00000 174658
ENSG000001 74681	ENSG000001 74880	ENSG000001 75117	ENSG000001 75143	ENSG00000 175267
ENSG000001 75822	ENSG000001 75856	ENSG000001 76050	ENSG000001 76207	ENSG00000 176220
ENSG000001 76757	ENSG000001 76819	ENSG000001 76900	ENSG000001 76937	ENSG00000 176951
ENSG000001 76960	ENSG000001 77111	ENSG000001 77634	ENSG000001 77835	ENSG00000 177858
ENSG000001 77863	ENSG000001 78006	ENSG000001 78225	ENSG000001 78322	ENSG00000 178510
ENSG000001 78546	ENSG000001 78585	ENSG000001 79294	ENSG000001 79312	ENSG00000 179326
ENSG000001 79360	ENSG000001 79574	ENSG000001 79702	ENSG000001 79755	ENSG00000 179824
ENSG000001 79851	ENSG000001 80150	ENSG000001 80494	ENSG000001 80518	ENSG00000 180519
ENSG000001 80649	ENSG000001 80715	ENSG000001 80882	ENSG000001 81437	ENSG00000 181669
ENSG000001 81882	ENSG000001 81922	ENSG000001 82053	ENSG000001 82065	ENSG00000 182150
ENSG000001 82553	ENSG000001 82625	ENSG000001 82729	ENSG000001 82933	ENSG00000 182957
ENSG000001 83000	ENSG000001 83059	ENSG000001 83096	ENSG000001 83122	ENSG00000 183144
ENSG000001 83190	ENSG000001 83239	ENSG000001 83317	ENSG000001 83355	ENSG00000 183397
ENSG000001 83405	ENSG000001 83445	ENSG000001 83455	ENSG000001 83514	ENSG00000 183627
ENSG000001 83817	ENSG000001 83851	ENSG000001 83920	ENSG000001 83981	ENSG00000 183983
ENSG000001 84008	ENSG000001 84064	ENSG000001 84100	ENSG000001 84263	ENSG00000 184352
ENSG000001 84353	ENSG000001 84391	ENSG000001 84490	ENSG000001 84493	ENSG00000 184521
ENSG000001 84543	ENSG000001 84653	ENSG000001 84673	ENSG000001 84844	ENSG00000 184888
ENSG000001 84902	ENSG000001 85034	ENSG000001 85055	ENSG000001 85082	ENSG00000 185095
ENSG000001 85319	ENSG000001 85448	ENSG000001 85467	ENSG000001 85636	ENSG00000 185641
ENSG000001 85685	ENSG000001 85758	ENSG000001 85834	ENSG000001 85863	ENSG00000 185929
ENSG000001 85945	ENSG000001 85956	ENSG000001 86218	ENSG000001 86259	ENSG00000 186381
ENSG000001 86400	ENSG000001 86414	ENSG000001 86483	ENSG000001 86659	ENSG00000 186663

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ENSG000001 86709	ENSG000001 86728	ENSG000001 86743	ENSG000001 86756	ENSG00000 186773
ENSG000001 86787	ENSG000001 87042	ENSG000001 87072	ENSG000001 87080	ENSG00000 187522
ENSG000001 87534	ENSG000001 87544	ENSG000001 87600	ENSG000001 87615	ENSG00000 187653
ENSG000001 87661	ENSG000001 87686	ENSG000001 87791	ENSG000001 87809	ENSG00000 187828
ENSG000001 87851	ENSG000001 87900	ENSG000001 87938	ENSG000001 87963	ENSG00000 187988
ENSG000001 87999	ENSG000001 88013	ENSG000001 88023	ENSG000001 88031	ENSG00000 188075
ENSG000001 88082	ENSG000001 88144	ENSG000001 88292	ENSG000001 88405	ENSG00000 188423
ENSG000001 88438	ENSG000001 88447	ENSG000001 88463	ENSG000001 88469	ENSG00000 188604
ENSG000001 88668	ENSG000001 88683	ENSG000001 88796	ENSG000001 88831	ENSG00000 188841
ENSG000001 88873	ENSG000001 88890	ENSG000001 88912	ENSG000001 88926	ENSG00000 188974
ENSG000001 88985	ENSG000001 88989	ENSG000001 89118	ENSG000001 89119	ENSG00000 189128
ENSG000001 89244	ENSG000001 89258	ENSG000001 89279	ENSG000001 89290	ENSG00000 189311
ENSG000001 89378	ENSG000001 89384	ENSG000001 96076	ENSG000001 96094	ENSG00000 196115
ENSG000001 96121	ENSG000001 96183	ENSG000001 96230	ENSG000001 96285	ENSG00000 196292
ENSG000001 96306	ENSG000001 96454	ENSG000001 96527	ENSG000001 96681	ENSG00000 196690
ENSG000001 96926	ENSG000001 96930	ENSG000001 96940	ENSG000001 96960	ENSG00000 197023
ENSG000001 97049	ENSG000001 97149	ENSG000001 97185	ENSG000001 97218	ENSG00000 197246
ENSG000001 97320	ENSG000001 97335	ENSG000001 97369	ENSG000001 97407	ENSG00000 197438
ENSG000001 97450	ENSG000001 97475	ENSG000001 97481	ENSG000001 97490	ENSG00000 197526
ENSG000001 97575	ENSG000001 97585	ENSG000001 97608	ENSG000001 97630	ENSG00000 197680
ENSG000001 97799	ENSG000001 97825	ENSG000001 97865	ENSG000001 97883	ENSG00000 198059
ENSG000001 98079	ENSG000001 98107	ENSG000001 98154	ENSG000001 98179	ENSG00000 198229
ENSG000001 98273	ENSG000001 98322	ENSG000001 98326	ENSG000001 98475	ENSG00000 198544
ENSG000001 98615	ENSG000001 98616	ENSG000001 98649	ENSG000001 98684	ENSG00000 198694
ENSG000001 98706	ENSG000001 98725	ENSG000001 98726	ENSG000001 98731	ENSG00000 198760

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ENSG000001 98778	ENSG000001 98789	ENSG000001 98801	ENSG000001 98810	ENSG00000 198902
ENSG000001 98921	ENSG000001 98957	ENSG000001 98965	ENTHD1	ENTPD1
ENTPD2	ENTPD3	ENTPD4	ENTPD5	ENTPD6
ENTPD7	ENTPD8	ENY2	EOMES	EP300
EP400	EPAS1	EPB41	EPB41 L1	EPB41 L2
EPB41 L3	EPB41 L4A	EPB41 L4B	EPB41 L5	EPB42
EPB49	EPC1	EPC2	EPCAM	EPDR1
EPGN	EPHA1	EPHA10	EPHA2	EPHA3
EPHA4	EPHA5	EPHA6	EPHA7	EPHA8
EPHB1	EPHB1_ENSTOO00039801 5	EPHB2	EPHB3	EPHB4
EPHB6	EPHX1	EPHX2	EPHX3	EPHX4
EPM2A	EPN2	EPN3	EPO	EPOR
EPRS	EPS15	EPS15L1	EPS8	EPS8L1
EPS8L2	EPS8L3	EPSTI1	EPX	EPYC
ERAL1	ERAP1	ERAP2	ERAS	ERBB2
ERBB2IP	ERBB3	ERBB3_ENST000002671 01	ERBB4	ERC1
ERCC1	ERCC2	ERCC3	ERCC4	ERCC5
ERCC6	ERCC6L	ERCC8	EREG	ERF
ERG	ERGIC1	ERGIC2	ERGIC3	ERH
ERI1	ERI2	ERI3	ERICH1	ERLEC1
ERLIN2	ERMAP	ERMN	ERMP1	ERN1
ERN2	ER01L	ER01LB	ERP27	ERP29
ERP44	ERRFI1	ERVFC1	ERVWE1	ESAM
ESC01	ESC02	ESD	ESF1	ESM1
ESPL1	ESPN	ESPNL	ESR1	ESR2
ESRP1	ESRP2	ESRRA	ESRRB	ESRRG
ESSPL	ESX1	ESYT1	ESYT2	ESYT3
ETAA1	ETF1	ETFA	ETFB	ETFDH
ETHE1	ETNK1	ETNK2	ETS1	ETS2
ETV1	ETV2	ETV3	ETV3L	ETV4
ETV5	ETV6	ETV7	EVC	EVC2
EVI2A	EVI2B	EVI5	EVI5L	EVL
EVPL	EVX1	EVX2	EWSR1	EXD1
EXD3	EXDL2	EX01	EXOC1	EXOC2
EX0C3	EXOC3L	EXOC3L2	EXOC4	EXOC5
EX0C6	EXOC6B	EXOC7	EXOC8	EXOG
EX0SC1	EXOSC10	EXOSC2	EXOSC3	EXOSC4
EX0SC5	EXOSC6	EXOSC7	EXOSC8	EXOSC9
EXPH5	EXT1	EXT2	EXTL1	EXTL2
EXTL3	EYA1	EYA2	EYA3	EYA4
EYS	EZH1	EZH2	EZH2_ENSTOO000350995	EZR
F10	F11	F11R	F12	F13A1
F13B	F2	F2R	F2RL1	F2RL2
F2RL3	F3	F5	F7	F8

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
F8A1	F8A2	F8A3	F8_ENST00000360256	F9
FA2H	FA87B_HUMAN	FAAH	FAAH2	FABP1
FABP12	FABP2	FABP3	FABP4	FABP5
FABP6	FABP7	FABP9	FABPE_HUMAN	FADD
FADS1	FADS2	FADS3	FADS6	FAF1
FAF2	FAH	FAHD1	FAHD2A	FAHD2B
FAIM	FAIM2	FAIM3	FAM100A	FAM100B
FAM101A	FAM102A	FAM102B	FAM103A1	FAM104B
FAM105A	FAM105B	FAM107A	FAM107B	FAM108A1
FAM108A3	FAM108B1	FAM109A	FAM109B	FAM110A
FAM110B	FAM110C	FAM111A	FAM111B	FAM113A
FAM113B	FAM114A1	FAM114A2	FAM115A	FAM115C
FAM116A	FAM117A	FAM117B	FAM118A	FAM118B
FAM119A	FAM119B	FAM120A	FAM120AOS	FAM120B
FAM120C	FAM122A	FAM122B	FAM122C	FAM123A
FAM123B	FAM123C	FAM124A	FAM124B	FAM125A
FAM125B	FAM126A	FAM126B	FAM127A	FAM127B
FAM127C	FAM128A	FAM128B	FAM129A	FAM129B
FAM129C	FAM131A	FAM131B	FAM131C	FAM132A
FAM133A	FAM134A	FAM134B	FAM134C	FAM135A
FAM135B	FAM136A	FAM13A1	FAM13C	FAM149A
FAM150A	FAM151A	FAM151B	FAM153A	FAM153B
FAM153C	FAM154A	FAM154B	FAM155A	FAM155B
FAM156A	FAM156B	FAM158A	FAM159A	FAM160A2
FAM160B1	FAM161A	FAM161B	FAM162A	FAM162B
FAM163A	FAM163B	FAM164A	FAM164C	FAM165B
FAM166A	FAM167B	FAM168A	FAM168B	FAM169A
FAM170A	FAM171A1	FAM171B	FAM172A	FAM173A
FAM173B	FAM174A	FAM174B	FAM175A	FAM175B
FAM176A	FAM176B	FAM177A1	FAM177B	FAM178B
FAM179A	FAM179B	FAM180A	FAM181A	FAM181B
FAM184A	FAM184B	FAM186A	FAM186B	FAM187B
FAM188A	FAM188B	FAM189A1	FAM189A2	FAM189B
FAM18B	FAM18B2	FAM190A	FAM190B	FAM192A
FAM193A	FAM194A	FAM194B	FAM195A	FAM196A
FAM198A	FAM198B	FAM199X	FAM19A2	FAM19A3
FAM19A4	FAM19A5	FAM200A	FAM20A	FAM20B
FAM21A	FAM21C	FAM22A	FAM22D	FAM22F
FAM22G	FAM23A	FAM23B	FAM24A	FAM24B
FAM26A	FAM26D	FAM26E	FAM26F	FAM32A
FAM33A	FAM35A	FAM36A	FAM38B	FAM39B
FAM3A	FAM3B	FAM3C	FAM3D	FAM40A
FAM40B	FAM43A	FAM43B	FAM45A	FAM45B
FAM46A	FAM46B	FAM46C	FAM46D	FAM47A
FAM47B	FAM47C	FAM48A	FAM48B1	FAM48B2
FAM49A	FAM49B	FAM50A	FAM50B	FAM53A
FAM53B	FAM53C	FAM54A	FAM54B	FAM55A
FAM55C	FAM55D	FAM57A	FAM57B	FAM58A

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
FAM58B	FAM59A	FAM5B	FAM5C	FAM60A
FAM63A	FAM63B	FAM64A	FAM65A	FAM65B
FAM65C	FAM69B	FAM69C	FAM70A	FAM70B
FAM71A	FAM71B	FAM71C	FAM71E1	FAM71F1
FAM72A	FAM72B	FAM73A	FAM73B	FAM74A3
FAM75A1	FAM75A2	FAM75A6	FAM75A7	FAM76A
FAM76B	FAM78A	FAM78B	FAM81A	FAM81B
FAM82A1	FAM82A2	FAM82B	FAM83A	FAM83B
FAM83C	FAM83D	FAM83E	FAM83F	FAM83G
FAM83H	FAM84A	FAM84B	FAM86A	FAM86C
FAM87B	FAM89A	FAM89B	FAM8A1	FAM90A1
FAM90A20	FAM91A1	FAM92B	FAM96A	FAM98A
FAM98B	FAM98C	FAM9A	FAM9B	FAM9C
FANCA	FANCB	FANCC	FANCD2	FANCE
FANCF	FANCG	FANCI	FANCL	FANCM
FANK1	FAP	FAR1	FAR2	FARP1
FARP2	FARS2	FARSA	FARSB	FAS
FASLG	FASN	FASTK	FASTKD1	FASTKD2
FASTKD3	FASTKD5	FAT	FAT1	FAT2
FAT3	FAT4	FAT4_ENSTOO000394329	FATE1	FAU
FBF1	FBL	FBLIM1	FBLN1	FBLN2
FBLN2_ENSTOO000492059	FBLN5	FBLN7	FBN1	FBN2
FBN3	FBP1	FBP2	FBRSL1	FBXL12
FBXL13	FBXL14	FBXL15	FBXL16	FBXL17
FBXL18	FBXL19	FBXL2	FBXL20	FBXL21
FBXL21_ENSTOO0002971 58	FBXL22	FBXL3	FBXL4	FBXL5
FBXL6	FBXL7	FBXL8	FBXO10	FBX01 1
FBX01 5	FBX01 6	FBX01 7	FBX01 8	FBX02
FBX021	FBX022	FBX024	FBX025	FBX027
FBX028	FBX03	FBXO30	FBX031	FBX032
FBX033	FBX034	FBX036	FBX038	FBX039
FBX04	FBXO40	FBX041	FBX042	FBX043
FBX044	FBX045	FBX046	FBX047	FBX048
FBX05	FBX06	FBX07	FBX08	FBX09
FBXW10	FBXW11	FBXW12	FBXW2	FBXW4
FBXW5	FBXW7	FBXW7_NM_01831 5_2	FBXW8	FBXW9
FCAMR	FCAR	FCER1A	FCER1G	FCER2
FCF1	FCGBP	FCGR1A	FCGR1B	FCGR2A
FCGR2B	FCGR3A	FCGR3B	FCGRT	FCH01
FCHSD1	FCHSD2	FCN1	FCN2	FCN3
FCRL1	FCRL2	FCRL3	FCRL4	FCRL5
FCRL6	FCRLA	FCRLB	FDFT1	FDPS
FDX1	FDX1L	FDXR	FECH	FEM1A
FEM1B	FEM1C	FEN1	FER	FER1L6
FERD3L	FERMT1	FERMT2	FERMT3	FES
FETUB	FEV	FEZ1	FEZF1	FEZF2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
FFAR1	FFAR2	FFAR3	FGA	FGB
FGD1	FGD2	FGD3	FGD4	FGD5
FGD6	FGF1	FGF10	FGF11	FGF12
FGF13	FGF14	FGF16	FGF17	FGF18
FGF19	FGF2	FGF20	FGF21	FGF22
FGF23	FGF3	FGF4	FGF5	FGF6
FGF7	FGF7P2	FGF8	FGF9	FGFBP1
FGFBP2	FGFBP3	FGFR1	FGFR10P	FGFR10P2
FGFR1_ENSTOO000425967	FGFR2	FGFR3	FGFR4	FGFR4_ENST000002924 08
FGFRL1	FGG	FGGY	FGL1	FGL2
FGR	FH	FHAD1	FHDC1	FHIT
FHL1	FHL2	FHL3	FHL5	FHOD1
FHOD3	FIBCD1	FIBIN	FIBP	FICD
FIG4	FIGF	FIGN	FIGNL1	FILIP1
FILIP1L	FIP1L1	FIS1	FITM1	FITM2
FIZ1	FKBP10	FKBP11	FKBP14	FKBP1A
FKBP1B	FKBP1C	FKBP2	FKBP3	FKBP4
FKBP5	FKBP6	FKBP7	FKBP8	FKBP9
FKBP9L	FKBPL	FKRP	FKTN	FLAD1
FLCN	FLG	FLG2	FLU	FLII
FLJ10357	FLJ10404	FLJ10490	FLJ13236	FLJ13855
FLJ14075	FLJ14627	FLJ14775	FLJ16165	FLJ16171
FLJ16331	FLJ16360	FLJ16369	FLJ16542	FLJ20184
FLJ20273	FLJ20366	FLJ20584	FLJ23356	FLJ23584
FLJ25006	FLJ25917	FLJ31132	FLJ34521	FLJ35880
FLJ38348	FLJ38451	FLJ38576	FLJ39257	FLJ39369
FLJ41131	FLJ41603	FLJ42177	FLJ42418	FLJ42957
FLJ43374	FLJ43806	FLJ43980	FLJ44048	FLJ44060
FLJ44216	FLJ44635	FLJ44817	FLJ44874	FLJ45224
FLJ45422	FLJ45455	FLJ45831	FLJ45910	FLJ45983
FLJ46321	FLJ90650	FLNA	FLNB	FLNC
FLOT1	FLOT2	FLRT1	FLRT2	FLRT3
FLT1	FLT3	FLT3LG	FLT4	FLT4_ENSTO0000261937
FLVCR1	FLVCR2	FLYWCH1	FLYWCH2	FMN2
FMNL1	FMNL2	FMNL3	FM01	FM02
FM03	FM04	FM05	FM06P	FMOD
FMR1	FMR1NB	FN1	FN3K	FN3KRP
FNBP1L	FNBP1_ENSTOO00037241 6	FNBP4	FNDC1	FNDC3A
FNDC3B	FNDC4	FNDC5	FNDC7	FNDC8
FNIP1	FNIP2	FNTA	FNTB	FOLH1
FOLH1B	FOLR1	FOLR2	FOS	FOSB
FOSL1	FOSL2	FOXA1	FOXA2	FOXA3
FOXB1	FOXB2	FOXC1	FOXC2	FOXD2
FOXD3	FOXD4	FOXD4L1	FOXD4L2	FOXD4L3
FOXD4L4	FOXD4L6	FOXE1	FOXE3	FOXF1
FOXF2	FOXG1	FOXH1	FOXI1	FOXI2
FOXI3	FOXJ1	FOXJ2	FOXJ3	FOXK1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
FOXK2	F0XL1	F0XL2	F0XM1	FOXN1
FOXN2	F0XN3	F0XN4	F0X01	FOX03
FOX04	F0XP1	F0XP2	F0XP3	FOXP4
FOXQ1	F0XR1	F0XR2	F0XRED1	FOXRED2
FOXS1	FPGS	FPGT	FPR1	FPR2
FPR3	FRAG1	FRAS1	FRAS1_ENSTO0000325942	FRAT1
FRAT2	FREM1	FREM2	FREM3	FRG 1
FRG2	FRG2C	FRK	FRMD1	FRMD3
FRMD4A	FRMD4B	FRMD5	FRMD6	FRMD7
FRMD8	FRMPD1	FRMPD2	FRMPD2L1	FRMPD2L2
FRMPD3	FRMPD4	FRRS1	FRS2	FRS3
FRY	FRYL	FRZB	FSCB	FSCN1
FSCN3	FSD1	FSD2	FSHB	FSHR
FSIP1	FST	FSTL1	FSTL3	FSTL4
FSTL5	FTCD	FTH1	FTHL1 7	FTHL1 9
FTL	FTLP2	FTMT	FTO	FTSJ1
FTSJ2	FTSJ3	FTSJD1	FTSJD2	FUBP1
FUBP3	FUCA1	FUCA2	FUK	FUNDC1
FUNDC2	FUNDC2P1	FURIN	FUS	FUSIP1
FUT1	FUT1 0	FUT1 1	FUT2	FUT3
FUT4	FUT5	FUT6	FUT7	FUT8
FUT9	FUZ	FXC1	FXN	FXR1
FXYD1	FXYD2	FXYD3	FXYD4	FXYD5
FXYD6	FXYD7	FXYD8	FYC01	FYN
FYTTD1	FZD1	FZD1 0	FZD2	FZD3
FZD4	FZD5	FZD6	FZD7	FZD8
FZD9	FZR1	G0S2	G2E3	G3BP1
G3BP2	G6PC	G6PC2	G6PC3	G6PD
GAA	GAB1	GAB2	GAB3	GAB4
GABARAP	GABARAPL1	GABARAPL2	GABARAPL3	GABBR1
GABBR2	GABPA	GABPB1	GABPB2	GABRA1
GABRA2	GABRA3	GABRA4	GABRA5	GABRA6
GABRB1	GABRB2	GABRB3	GABRD	GABRE
GABRG 1	GABRG2	GABRP	GABRQ	GABRR1
GABRR2	GABRR3	GAD1	GAD2	GADD45A
GADD45B	GADD45G	GADD45GI P 1	GADL1	GAGE1
GAGE1 0	GAGE1 2C	GAGE1 2E	GAG E1 2F	GAGE1 2G
GAGE1 2H	GAGE1 2J	GAGE2C	GAG E2D	GAGE2E
GAK	GAL	GAL3ST1	GAL3ST2	GAL3ST3
GAL3ST4	GALC	GALE	GALK1	GALK2
GALM	GALNS	GALNT1	GALNT1 0	GALNT1 1
GALNT1 2	GALNT1 3	GALNT1 4	GALNT2	GALNT3
GALNT5	GALNT6	GALNT7	GALNT8	GALNT9
GALNTL1	GALNTL2	GALNTL4	GALNTL5	GALNTL6
GALP	GALR1	GALR2	GALR3	GALT
GAMT	GAN	GANAB	GANC	GAP43
GAPDH	GAPDHS	GAPT	GAPVD1	GAR1
GARNL3	GARS	GART	GAS1	GAS2
GAS2L1	GAS2L2	GAS2L3	GAS6	GAS7

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
GAS8	GAST	GATA1	GATA2	GATA3
GATA4	GATA5	GATA6	GATAD1	GATAD2A
GATAD2B	GATC	GATM	GATS	GATSL3
GBA	GBA2	GBAP	GBAS	GBF1
GBG5L_HUMAN	GBGT1	GBP1	GBP2	GBP3
GBP4	GBP5	GBP6	GBP7	GBX1
GBX2	GC	GCA	GCAT	GCC1
GCC2	GCDH	GCET2	GCH1	GCHFR
GCK	GCKR	GCLC	GCLM	GCM1
GCM2	GCN1 L1	GCNT1	GCNT2	GCNT3
GCNT4	GC0M1	GCSH	GDA	GDAP1
GDAP1 L1	GDAP2	GDE1	GDF1	GDF10
GDF11	GDF15	GDF2	GDF3	GDF5
GDF6	GDF7	GDF9	GDI1	GDI2
GDNF	GDPD1	GDPD2	GDPD3	GDPD4
GDPD5	GEFT	GEM	GEMIN4	GEMIN5
GEMIN6	GEMIN7	GEMIN8	GEN1	GFAP
GFER	GFI1	GFI1B	GFM1	GFM2
GF0D1	GF0D2	GFPT1	GFPT2	GFRA1
GFRA3	GFRA4	GFRAL	GGA1	GGA2
GGA3	GGCT	GGCX	GGH	GGN
GGNBP2	GGPS1	GGT1	GGT5	GGT6
GGT7	GGTLA4	GGTLC1	GGTLC2	GH1
GH2	GHDC	GHITM	GHR	GHRH
GHRHR	GHRL	GHSR	GIF	GIGYF1
GIGYF2	GIMAP1	GIMAP2	GIMAP4	GIMAP5
GIMAP6	GIMAP7	GIMAP8	GIN1	GINS1
GINS2	GINS3	GINS4	GIOT-1	GIP
GIPC1	GIPC2	GIPC3	GIPR	GIT1
GIT2	GIYD1	GIYD2	GJA1	GJA10
GJA3	GJA4	GJA5	GJA8	GJA9
GJB1	GJB2	GJB3	GJB4	GJB5
GJB6	GJB7	GJC1	GJC2	GJC3
GJD2	GJD4	GK	GK2	GK3P
GK5	GKAP1	GKN1	GKN2	GLA
GLB1	GLB1L	GLB1L2	GLB1L3	GLCCI1
GLCE	GLDC	GLDN	GLE1	GLE1L
GLG1	GLI1	GLI2	GLI3	GLI4
GLIPR1	GLIPR1L1	GLIPR1L2	GLIPR2	GLIS1
GLIS2	GLIS3	GLMN	GL01	GL0D4
GL0D5	GLP1R	GLP2R	GLRA1	GLRA2
GLRA3	GLRA4	GLRB	GLRX	GLRX2
GLRX3	GLRX5	GLRXP3	GLS	GLS2
GLT1D1	GLT25D1	GLT25D2	GLT28D1	GLT6D1
GLT8D1	GLT8D2	GLTP	GLTPD1	GLTPD2
GLTSCR2	GLUD1	GLUD2	GLUL	GLYAT
GLYATL1	GLYATL2	GLYCTK	GLYR1	GM2A
GMCL1	GMDS	GMEB1	GMEB2	GMFB
GMFG	GMIP	GML	GMNN	GMPPA
GMPPB	GMPR	GMPR2	GMPS	GNA11

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
GNA12	GNA13	GNA14	GNA15	GNAI1
GNAI2	GNAI3	GNAL	GNA01	GNAQ
GNAS	GNAS_ENSTOOO00371100	GNAS_NM_016592_1	GNAT1	GNAT2
GNAZ	GNB1	GNB1L	GNB2	GNB2L1
GNB3	GNB4	GNB5	GNE	GNG10
GNG11	GNG12	GNG13	GNG2	GNG3
GNG4	GNG5	GNG7	GNG8	GNGT1
GNGT2	GNL1	GNL2	GNL3	GNL3L
GNLY	GNMT	GNPAT	GNPDA1	GNPDA2
GNPNAT1	GNPTAB	GNPTG	GNRH1	GNRH2
GNRHR	GNRHR2	GNS	GOLGA1	GOLGA2
GOLGA2B	GOLGA3	GOLGA4	GOLGA5	GOLGA6A
GOLGA7	GOLGA7B	GOLGA8A	GOLGA8E	GOLGA8G
GOLGB1	GOLIM4	GOLM1	GOLPH3	GOLPH3L
GOLT1A	GOLT1B	GON4L	GOPC	GORAB
GORASP1	GORASP2	GOSR1	GOSR2	GOT1
GOT2	GP1BB	GP2	GP5	GP6
GP9	GPA33	GPAA1	GPAM	GPAT2
GPATCH1	GPATCH2	GPATCH3	GPATCH4	GPATCH8
GPBP1	GPBP1L1	GPC1	GPC2	GPC3
GPC4	GPC5	GPC6	GPCPD1	GPD1
GPD1L	GPD2	GPER	GPHA2	GPHB5
GPHN	GPI	GPIHBP1	GPKOW	GPLD1
GPM6A	GPM6B	GPN1	GPN2	GPN3
GPNMB	GPR1	GPR101	GPR107	GPR108
GPR109A	GPR110	GPR111	GPR112	GPR113
GPR114	GPR115	GPR116	GPR119	GPR12
GPR120	GPR123	GPR124	GPR125	GPR126
GPR128	GPR132	GPR133	GPR135	GPR137
GPR137B	GPR137C	GPR139	GPR141	GPR142
GPR143	GPR146	GPR148	GPR149	GPR15
GPR150	GPR151	GPR152	GPR153	GPR155
GPR156	GPR157	GPR158	GPR160	GPR161
GPR162	GPR165P	GPR17	GPR171	GPR172A
GPR172B	GPR173	GPR174	GPR176	GPR179
GPR18	GPR180	GPR182	GPR183	GPR19
GPR20	GPR21	GPR22	GPR25	GPR26
GPR27	GPR3	GPR31	GPR32	GPR34
GPR35	GPR37	GPR37L1	GPR39	GPR4
GPR42	GPR44	GPR45	GPR50	GPR52
GPR55	GPR56	GPR6	GPR61	GPR62
GPR63	GPR64	GPR65	GPR68	GPR75
GPR77	GPR78	GPR81	GPR82	GPR82_ENST00000302548
GPR83	GPR84	GPR85	GPR87	GPR88
GPR89A	GPR89B	GPR97	GPR98	GPRASP1
GPRASP2	GPRC5A	GPRC5B	GPRC5C	GPRC5D
GPRC6A	GPRIN1	GPRIN2	GPRIN3	GPS1
GPS2	GPSM1	GPSM2	GPSM3	GPT

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
GPT2	GPX1	GPX2	GPX3	GPX4
GPX5	GPX6	GPX7	GPX8	GRAMD1 A
GRAMD1 B	GRAMD1 C	GRAMD2	GRAMD3	GRAMD4
GRAP	GRAP2	GRASP	GRB10	GRB14
GRB2	GRB7	GREB1	GREB1_ENST00000381486	GREM1
GREM2	GRHL1	GRHL2	GRHL3	GRHPR
GRIA1	GRIA2	GRIA3	GRIA3_ENSTO0000264357	GRIA4
GRID1	GRID2	GRIK1	GRIK2	GRIK2_ENST00000421544
GRIK3	GRIK4	GRIK5	GRIN1	GRIN2A
GRIN2B	GRIN2C	GRIN2D	GRIN3A	GRIN3B
GRINA	GRINL1A	GRINL1B	GRIP1	GRIP2
GRIPAP1	GRK1	GRK4	GRK5	GRK6
GRK7	GRLF1	GRM1	GRM2	GRM3
GRM4	GRM4_ENSTOO003741 77	GRM5	GRM6	GRM7
GRM8	GRN	GRP	GRPEL1	GRPEL2
GRPR	GRRP1	GRTP1	GRWD1	GRXCR1
GRXCR2	GSC	GSC2	GSDMA	GSDMB
GSDMC	GSDMD	GSG1	GSG1L	GSG2
GSK3A	GSK3B	GSN	GSPT1	GSPT2
GSR	GSS	GSTA1	GSTA2	GSTA3
GSTA4	GSTA5	GSTCD	GSTK1	GSTM1
GSTM2	GSTM3	GSTM4	GSTM5	GST01
GST02	GSTP1	GSTT1	GSTT2	GSTT2B
GSTZ1	GSX1	GSX2	GTDC1	GTF2A1
GTF2A2	GTF2B	GTF2E1	GTF2E2	GTF2F1
GTF2F2	GTF2H1	GTF2H2	GTF2H2C	GTF2H3
GTF2H4	GTF2H5	GTF2I	GTF2IRD1	GTF2IRD2
GTF2IRD2B	GTF3C1	GTF3C2	GTF3C3	GTF3C4
GTF3C5	GTF3C6	GTPBP1	GTPBP10	GTPBP2
GTPBP3	GTPBP4	GTPBP5	GTPBP6	GTPBP8
GTSE1	GTSF1	GTSF1L	GUCA1A	GUCA1B
GUCA1C	GUCA2A	GUCA2B	GUCY1A2	GUCY1A3
GUCY2C	GUCY2D	GUCY2F	GUF1	GUK1
GUK1_ENSTOOO0036671 9	GULP1	GUSB	GUSL1_HUMAN	GXYLT1
GYG1	GYG2	GYLTL1B	GYPA	GYPB
GYPC	GYS1	GYS2	GZF1	GZMA
GZMB	GZMH	GZMK	GZMM	H19
H1F0	H1FNT	H1FOO	H1FX	H2AFB1
H2AFB2	H2AFB3	H2AFJ	H2AFV	H2AFX
H2AFY	H2AFY2	H2AFZ	H2AFZP2	H2BFM
H2BFWT	H3F3A	H3F3B	H3F3C	H6PD
HAAO	HABP2	HABP4	HACE1	HACL1
HADH	HADHA	HADHB	HAGH	HAGHL
HAL	HAMP	HAND1	HAND2	HA01
HA02	HAP1	HAPLN1	HAPLN2	HAPLN3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
HAPLN4	HARBI 1	HARS	HARS2	HAS1
HAS2	HAS3	HAT1	HAUS1	HAUS2
HAUS3	HAUS4	HAUS5	HAUS6	HAUS7
HAUS8	HAVCR1	HAVCR2	HAX1	HBA1
HBA2	HBB	HBD	HBE1	HBEGF
HBG 1	HBG2	HBM	HBP1	HBQ1
HBS1 L	HBXI P	HBZ	HCCS	HCFC1
HCFC1 R 1	HCFC2	HCG9	HCK	HCLS1
HCN1	HCN2	HCN3	HCN4	HCP1
HCP5	HCRT	HCRTR1	HCRTR2	HCST
HDAC1	HDAC1 0	HDAC1 1	HDAC2	HDAC3
HDAC4	HDAC5	HDAC6	HDAC7	HDAC8
HDAC9	HDC	HDDC2	HDDC3	HDGF
HDGF2	HDGFL1	HDGFRP3	HDHD1 A	HDHD2
HDHD3	HDLBP	HDX	HEATR1	HEATR2
HEATR3	HEATR4	HEATR5B	HEATR6	HEATR7B1
HEATR7B2	HEBP1	HEBP2	HECA	HECTD1
HECTD2	HECTD3	HECTD3 _ENS T000003721 72	HECW1	HECW2
HEG 1	HEJ1	HELB	HELLS	HELQ
HELT	HELZ	HEMGN	HEMK1	HEPACAM
HEPACAM2	HEPH	HEPHL1	HERC1	HERC2
HERC2P3	HERC3	HERC4	HERC5	HERC6
HERPUD1	HERPUD2	HERV-FRD	HES1	HES2
HES3	HES4	HES5	HES6	HES7
HESX1	HEXA	HEXB	HEXDC	HEXIM1
HEXIM2	HEY1	HEY2	HEYL	HFE
HFE2	HFM1	HGD	HG F	HGF AC
HGS	HGSNAT	HGSNAT _ENS T00000458501	HHAT	HHATL
HHEX	HHIP	HHIPL1	HHI PL2	HHLA3
HIAT1	HIATL1	HIATL2	HIBADH	HIBCH
HIC1	HIC2	HIF1 A	H IF 1A N	HIF3A
HIG D 1A	HIG D 1B	HIG D2A	HIGD2BP	HIN1 L_HUM AN
HINFP	HINT1	HINT2	HINT3	HIP1
HIP1 R	HIPK1	HIPK2	H IPK3	HIPK4
HIRA	HIRI P3	HIST1 H 1A	HIST1 H 1B	HIST1 H 1C
HIST1 H 1D	HIST1 H 1E	HIST1 H 1T	HIST1 H2AA	HIST1 H2AB
HIST1 H2AC	HIST1 H2AD	HIST1 H2AE	HIST1 H2AG	HIST1 H2AH
HIST1 H2AI	HIST1 H2AJ	HIST1 H2AK	HIST1 H2AL	HIST1 H2AM
HIST1 H2BA	HIST1 H2BB	HIST1 H2BC	HIST1 H2BD	HIST1 H2BE
HIST1 H2BF	HIST1 H2BG	HIST1 H2BH	HIST1 H2BI	HIST1 H2BJ
HIST1 H2BK	HIST1 H2BL	HIST1 H2BM	HIST1 H2BN	HIST1 H2B0
HIST1 H3A	HIST1 H3B	HIST1 H3C	HIST1 H3D	HIST1 H3E
HIST1 H3F	HIST1 H3G	HIST1 H3H	HIST1 H3I	HIST1 H3J
HIST1 H4A	HIST1 H4B	HIST1 H4C	HIST1 H4D	HIST1 H4E
HIST1 H4F	HIST1 H4G	HIST1 H4H	HIST1 H4I	HIST1 H4J
HIST1 H4K	HIST1 H4L	HIST2H2AA3	HIST2H2AA4	HIST2H2AB
HIST2H2AC	HIST2H2BE	HIST2H2BF	HIST2H3A	HIST2H3C

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
HIST2H3D	HIST2H4A	HIST2H4B	HIST3H2A	HIST3H2BB
HIST3H3	HIST4H4	HIVEP1	HIVEP2	HIVEP3
HJURP	HK1	HK2	HK3	HKDC1
HKR1	HLA-A	HLA-B	HLA-C	HLA-DMA
HLA-DMB	HLA-DOA	HLA-DOB	HLA-DPA1	HLA-DPB1
HLA-DQA1	HLA-DQA2	HLA-DQB1	HLA-DRA	HLA-DRB5
HLA-E	HLA-F	HLA-G	HLCS	HLF
HLTF	HLX	HM1 3	HMBOX1	HMBS
HMCN1	HMG 1L 1 0	HMG20A	HMG20B	HMGA1
HMGA2	HMGB1	HMGB1 L 1	HMGB2	HMGB3
HMGB4	HMGCL	HMGCLL1	HMGCR	HMGCS1
HMGCS2	HMGN1	HMGN2	HMGN3	HMGN4
HMGN5	HMGXB3	HMGXB4	HMHA1	HMHB1
HMMR	HMOX1	HMOX2	HMP1 9	HMX2
HMX3	HN1	HN1 L	HNF1 A	HNF1 B
HNF4A	HNF4G	HNMT	HNRNPA0	HNRNPA1
HNRNPA1 L2	HNRNPA2B1	HNRNPA3	HNRNPAB	HNRNPC
HNRNPCL1	HNRNPD	HNRNPF	HNRNPH1	HNRNPH2
HNRNPH3	HNRNPK	HNRNPL	HNRNPM	HNRNPR
HNRNPU	HNRNPUL1	HNRNPUL2	HNRPD	HNRPDL
HNRPF	HNRPH 1	HNRPL	HNRPLL	HNRPR
HNRPU	HOMER1	HOMER2	HOMER3	HOOK1
H00K2	HOOK3	HOPX	HORMAD1	HOXA1
H0XA1 0	HOXA1 1	HOXA1 3	HOXA2	HOXA3
H0XA4	HOXA5	HOXA6	HOXA7	HOXA9
H0XB1	HOXB1 3	HOXB2	HOXB3	HOXB4
H0XB5	HOXB6	HOXB7	HOXB8	HOXB9
HOXC1 0	HOXC1 1	HOXC1 2	HOXC1 3	HOXC4
H0XC5	HOXC6	HOXC8	HOXC9	HOXD1
HOXD1 0	HOXD1 1	HOXD1 3	HOXD3	HOXD4
H0XD8	HOXD9	HP	HP1 BP3	HPCA
HPCAL1	HPCAL4	HPD	HPDL	HPG D
HPG DS	HPN	HPR	HPRT1	HPS1
HPS3	HPS4	HPS5	HPS6	HPSE
HPSE2	HPX	HR	HRAS	HRASLS
HRASLS2	HRASLS5	HRAS_ENSTO 0000397594	HRC	HRCT1
HRG	HRH1	HRH2	HRH3	HRH4
HRK	HRNR	HRSP1 2	HS1 BP3	HS2ST1
HS3ST1	HS3ST2	HS3ST3A1	HS3ST3B1	HS3ST4
HS3ST5	HS6ST1	HS6ST1 P	HS6ST2	HS6ST3
HSCB	HSD1 1B 1	HSD1 1B 1L	HSD1 1B2	HSD1 7B1
HSD1 7B1 0	HSD1 7B1 1	HSD1 7B1 2	HSD1 7B1 3	HSD1 7B1 4
HSD1 7B2	HSD1 7B3	HSD1 7B4	HSD1 7B6	HSD1 7B7
HSD1 7B8	HSD3B1	HSD3B2	HSD3B7	HSDL1
HSDL2	HSF1	HSF2	HSF2BP	HSF4
HSF5	HSFX1	HSFY1	HSFY2	HSP90AA1
HSP90AA2	HSP90AB1	HSP90AB2P	HSP90AB6P	HSP90B1
HSPA1 2A	HSPA1 2B	HSPA1 3	HSPA1 4	HSPA1 A
HSPA1 B	HSPA1 L	HSPA2	HSPA4	HSPA4L

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
HSPA5	HSPA6	HSPA8	HSPA9	HSPB1
HSPB1 1	HSPB2	HSPB3	HSPB6	HSPB7
HSPB8	HSPB9	HSPBAP1	HSPBP1	HSPC1 59
HSPD1	HSPE1	HSPG2	HSPH1	HTATI P2
HTATSF1	HTN1	HTN3	HTR1 A	HTR1 B
HTR1 D	HTR1 E	HTR1 F	HTR2A	HTR2B
HTR2C	HTR3A	HTR3B	HTR3C	HTR3D
HTR3E	HTR4	HTR5A	HTR6	HTR7
HTRA1	HTRA2	HTRA3	HTRA4	HTT
HUMPPA	HUNK	HUS1	HUS1 B	HUWE1
HVCN1	HYAL1	HYAL2	HYAL3	HYAL4
HYDIN	HYI	HYLS1	HYOU1	IAH1
IAPP	IARS	IARS2	IBSP	IBTK
ICA1	ICA1 L	ICAM1	ICAM2	ICAM3
ICAM4	ICAM5	ICK	ICMT	ICOS
ICOSLG	ICT1	ID1	ID2	ID2B
ID3	ID4	IDE	IDH1	IDH2
IDH3A	IDH3B	IDH3G	IDI1	IDI2
ID01	IDS	IDUA	IER2	IER3
IER3I P 1	IER5	IER5L	IFF01	IFI1 6
IFI27	IFI27L1	IFI27L2	IFI30	IFI35
IFI44	IFI44L	IFI6	IFIH1	IFIT1
IFIT1 L	IFIT2	IFIT3	IFIT5	IFITM2
IFITM3	IFITM5	IFLTD1	IFNA1	IFNA1 0
IFNA1 3	IFNA1 4	IFNA1 6	IFNA1 7	IFNA2
IFNA21	IFNA4	IFNA5	IFNA6	IFNA7
IFNA8	IFNAR1	IFNAR2	IFNB1	IFNE
IFNG	IFNGR1	IFNGR2	IFNK	IFNW1
IFRD1	IFRD2	IFT1 22	IFT1 40	IFT1 72
IFT20	IFT52	IFT57	IFT74	IFT80
IFT81	IFT88	IGBP1	IGDCC3	IG DCC4
IG F 1	IG F 1 R	IG F2	IGF2AS	IG F2BP1
IG F2BP2	IG F2BP3	IG F2R	IGFALS	IG FBP1
IG FBP2	IG FBP3	IG FBP4	IGFBP5	IG FBP6
IG FBP7	IG FBPL1	IG FL3	IGFL4	IG FN1
IGHMBP2	IGHV1 0R1 5-1	IGHV1 0R1 5-5	IGJ	IGLL1
IGLL3	IGSF1	IGSF1 0	IGSF1 1	IGSF21
IGSF22	IGSF3	IGSF5	IGSF6	IGSF8
IGSF9	IGSF9B	IHH	IK	IKBI P
IKBKAP	IKBKB	IKBKE	IKBKG	IKZF1
IKZF2	IKZF3	IKZF4	IKZF4 _ ENSTO 0000262032	IKZF5
IL1 0	IL1 0RA	IL1 0RB	IL1 1	IL1 1RA
IL1 2A	IL1 2 B	IL1 2RB1	IL1 2RB2	IL1 3
IL1 3RA1	IL1 3RA2	IL1 5	IL1 5RA	IL1 6
IL1 7A	IL1 7 B	IL1 7C	IL1 7 D	IL1 7F
IL1 7RA	IL1 7RB	IL1 7RC	IL1 7RD	IL1 7RE
IL1 7REL	IL1 8	IL1 8BP	IL1 8R1	IL1 8RAP
IL1 9	IL1 A	IL1 B	IL1 F10	IL1 F5
IL1 F6	IL1 F7	IL1 F8	IL1 F9	IL1 R 1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
IL1 R2	IL1 RAP	IL1 RAPL1	IL1 RAPL2	IL1 RL1
IL1 RL2	IL1 RN	IL2	IL20	IL20RA
IL20RB	IL21	IL21 R	IL22	IL22RA1
IL22RA2	IL23A	IL23R	IL24	IL25
IL26	IL27	IL27RA	IL28A	IL28B
IL28RA	IL29	IL2RA	IL2RB	IL2RG
IL2RG _ENSTOOO 00374202	IL3	IL31	IL31 RA	IL32
IL33	IL34	IL3RA	IL4	IL4I 1
IL4R	IL5	IL5RA	IL6	IL6R
IL6ST	IL7	IL7R	IL8	IL9
IL9R	ILDR1	ILDR2	ILF2	ILF3
ILK	ILKAP	ILK_ENSTOOOO 0299421	ILVBL	IMMP1 L
IMMP2L	IMMT	IMP3	IMP4	IMP5
IMPA1	IMPA2	IMPACT	IMPAD1	IMPDH1
IMPDH2	IMPG 1	IMPG2	INA	INADL
INCA1	INCENP	INE1	INF2	INF2 _NEW
ING 1	ING2	ING3	ING4	ING5
INGX	INHA	INHBA	INHBB	INHBC
INHBE	INMT	INO80	INO80B	INO80C
INO80D	INO80E	INOC1	INPP1	INPP4A
INPP4B	INPP5A	INPP5B	INPP5B _ENST 00000373026	INPP5D
INPP5E	INPP5F	INPP5J	INPP5K	INPPL1
INS	INS-IG F2	INSC	INSIG1	INSIG2
INSL3	INSL4	INSL5	INSL6	INSM1
INSM2	INSR	INSRR	INTS1 0	INTS1 2
INTS2	INTS3	INTS4	INTS5	INTS6
INTS7	INTS8	INTS9	INTU	INVS
IP6K1	IP6K2	IP6K3	IPCEF1	IPMK
IP01 1	IP01 3	IP04	IP05	IP07
IP08	IP09	IPP	IPPK	IQCB1
IQCC	IQCD	IQCE	IQCF1	IQCF2
IQCG	IQCH	IQCK	IQGAP1	IQGAP2
IQGAP3	IQSEC1	IQSEC2	IQSEC3	IQUB
IRAKI	IRAKI BP1	IRAK2	IRAK3	IRAK4
IREB2	IRF1	IRF2	IRF2BP1	IRF2BP2
IRF3	IRF4	IRF5	IRF6	IRF7
IRF8	IRF9	IRGC	IRGQ	IRS1
IRS2	IRS4	IRX1	IRX2	IRX3
IRX4	IRX5	IRX6	ISCA1	ISCA2
ISCU	ISG1 5	ISG20	ISG20L2	ISL1
ISL2	ISLR	ISLR2	ISM1	ISM2
ISOC1	ISOC2	ISX	ISY1	ISYNA1
ITCH	ITFG1	ITFG2	ITFG3	ITGA1
ITGA1 0	ITGA1 1	ITGA2	ITGA2B	ITGA3
ITGA4	ITGA5	ITGA6	ITGA7	ITGA8
ITGA9	ITGAD	ITGAE	ITGAL	ITGAM
ITGAV	ITGAX	ITGB1	ITGB1 BP1	ITGB1 BP2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ITGB1 BP3	ITGB2	ITGB3	ITGB3BP	ITGB4
ITGB5	ITGB6	ITGB7	ITGB8	ITGBL1
ITIH1	ITIH2	ITIH3	ITIH4	ITIH5
ITIH5L	ITK	ITLN1	ITLN2	ITM2A
ITM2B	ITM2C	ITPA	ITPK1	ITPKA
ITPKB	ITPKC	ITPR1	ITPR2	ITPR3
ITPRIP	ITPRIPL1	ITPRIPL2	ITSN1	ITSN2
IVD	IVL	IVNS1 ABP	IWS1	IYD
IZUM01	JAG 1	JAG2	JAGN1	JAK1
JAK2	JAK3	JAKMI P 1	JAKMI P2	JAKMI P3
JAM2	JAM3	JARI D2	JAZF1	JDP2
JHDM1 D	JMJD1 C	JMJD4	JMJD5	JMJD6
JMJD7-PLA2G4B	JMY	J0SD1	J0SD2	JPH1
JPH2	JPH3	JPH4	JRKL	JSRP1
JTB	JUB	JUN	JUNB	JUND
JUP	K0087_HUMAN	K0401_HUMAN	KAAG 1	KAL1
KALRN	KANK1	KANK2	KANK3	KANK4
KARCA1	KARS	KAT2A	KAT2B	KAT5
KATNA1	KATNAL1	KATNAL2	KATNB1	KAZALD1
KBTBD1 0	KBTBD1 1	KBTBD2	KBTBD3	KBTBD4
KBTBD5	KBTBD6	KBTBD7	KBTBD8	KCNA1
KCNA1 0	KCNA2	KCNA3	KCNA4	KCNA5
KCNA6	KCNA7	KCNAB1	KCNAB2	KCNAB3
KCNB1	KCNB2	KCNC1	KCNC2	KCNC3
KCNC4	KCND1	KCND2	KCND3	KCN E 1
KCN E 1 L	KCN E2	KCN E3	KCNE4	KCNF1
KCNG 1	KCNG2	KCNG3	KCNG4	KCNH1
KCNH2	KCNH3	KCNH4	KCNH5	KCNH6
KCNH7	KCNH8	KCNI P 1	KCNI P2	KCNI P3
KCNI P4	KCNJ1	KCNJ1 0	KCNJ1 1	KCNJ1 2
KCNJ1 3	KCNJ1 4	KCNJ1 5	KCNJ1 6	KCNJ2
KCNJ3	KCNJ4	KCNJ5	KCNJ6	KCNJ8
KCNJ9	KCNK1	KCNK1 0	KCNK1 2	KCNK1 3
KCNK1 5	KCNK1 6	KCNK1 7	KCNK1 8	KCNK2
KCNK3	KCNK4	KCNK5	KCNK6	KCNK7
KCNK9	KCNMA1	KCNMB1	KCNMB2	KCNMB3
KCNMB4	KCNN1	KCNN1_ENST00000222249	KCNN2	KCNN3
KCNN4	KCNQ1	KCNQ2	KCNQ3	KCNQ4
KCNQ5	KCNRG	KCNS1	KCNS2	KCNS3
KCNT1	KCNT2	KCNV1	KCNV2	KCP
KCTD1	KCTD1 0	KCTD1 1	KCTD1 2	KCTD1 3
KCTD1 4	KCTD1 5	KCTD1 6	KCTD1 7	KCTD1 8
KCTD1 9	KCTD2	KCTD20	KCTD21	KCTD3
KCTD4	KCTD5	KCTD6	KCTD7	KCTD8
KCTD9	KCTD9L	KDELC1	KDELC2	KDELR1
KDELR2	KDELR3	KDM1 A	KDM1 B	KDM2A
KDM2B	KDM3A	KDM3B	KDM4A	KDM4B
KDM4C	KDM4D	KDM5A	KDM5B	KDM5C

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
KDM5D	KDM6A	KDM6B	KDR	KDSR
KEAP1	KEL	KERA	KHDC1	KHDRBS1
KHDRBS2	KHDRBS3	KHK	KHNYN	KHSRP
KIAA0020	KIAA0090	KIAA0100	KIAA0101	KIAA0141
KIAA0146	KIAA0174	KIAA0182	KIAA0195	KIAA0196
KIAA0226	KIAA0226_ENST00000273582	KIAA0232	KIAA0240	KIAA0247
KIAA0284	KIAA0317	KIAA0319	KIAA0319L	KIAA0355
KIAA0368	KIAA0391	KIAA0406	KIAA0408	KIAA0415
KIAA0415_ENST00000450194	KIAA0427	KIAA0430	KIAA0467	KIAA0467_ENST00000372442
KIAA0494	KIAA0513	KIAA0528	KIAA0556	KIAA0562
KIAA0564	KIAA0649	KIAA0664	KIAA0664_ENST00000322335	KIAA0672
KIAA0701	KIAA0746	KIAA0748	KIAA0753	KIAA0776
KIAA0802	KIAA0831	KIAA0892	KIAA0895	KIAA0895L
KIAA0895_ENST00000338533	KIAA0907	KIAA0913	KIAA0922	KIAA0947
KIAA0953	KIAA1009	KIAA1012	KIAA1024	KIAA1033
KIAA1045	KIAA1109	KIAA1143	KIAA1147	KIAA1161
KIAA1191	KIAA1199	KIAA1210	KIAA1211	KIAA1217
KIAA1244	KIAA1267	KIAA1274	KIAA1279	KIAA1324
KIAA1324L	KIAA1328	KIAA1377	KIAA1404	KIAA1407
KIAA1409	KIAA1429	KIAA1430	KIAA1432	KIAA1443
KIAA1462	KIAA1467	KIAA1468	KIAA1486	KIAA1509
KIAA1522	KIAA1524	KIAA1529	KIAA1530	KIAA1539
KIAA1542	KIAA1543	KIAA1549	KIAA1586	KIAA1598
KIAA1609	KIAA1614	KIAA1618	KIAA1632	KIAA1644
KIAA1671	KIAA1683	KIAA1688	KIAA1704	KIAA1712
KIAA1715	KIAA1737	KIAA1751	KIAA1755	KIAA1772
KIAA1797	KIAA1804	KIAA1826	KIAA1841	KIAA1853
KIAA1875	KIAA1913	KIAA1919	KIAA1949	KIAA1958
KIAA1967	KIAA1984	KIAA2013	KIAA2018	KIAA2022
KIAA2026	KIDINS220	KIF11	KIF12	KIF13A
KIF13B	KIF14	KIF15	KIF16B	KIF17
KIF18A	KIF18B	KIF19	KIF1A	KIF1B
KIF1C	KIF20A	KIF20B	KIF21A	KIF21B
KIF22	KIF23	KIF25	KIF27	KIF2A
KIF2B	KIF2C	KIF3A	KIF3B	KIF3C
KIF4A	KIF5A	KIF5B	KIF5C	KIF6
KIF7	KIF9	KIFAP3	KIFC1	KIFC2
KIFC3	KIN	KIR2DL1	KIR2DL3	KIR2DL4
KIR2DS4	KIR3DL1	KIR3DL2	KIR3DL3	KIR3DX1
KIRREL	KIRREL2	KIRREL3	KISS1	KISS1R
KIT	KITLG	KL	KLB	KLC1
KLC2	KLC3	KLC4	KLF1	KLF10
KLF11	KLF12	KLF13	KLF14	KLF15
KLF16	KLF17	KLF2	KLF3	KLF4
KLF5	KLF6	KLF7	KLF8	KLF9

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
KLHDC1	KLHDC1 0	KLHDC2	KLHDC3	KLHDC4
KLHDC5	KLHDC6	KLHDC7A	KLHDC7B	KLHDC8A
KLHDC8B	KLHDC9	KLHL1	KLHL1 0	KLHL1 1
KLHL1 2	KLHL1 3	KLHL1 4	KLHL1 5	KLHL1 7
KLHL1 8	KLHL2	KLHL20	KLHL21	KLHL22
KLHL23	KLHL24	KLHL25	KLHL26	KLHL28
KLHL29	KLHL3	KLHL31	KLHL32	KLHL34
KLHL36	KLHL38	KLHL4	KLHL5	KLHL6
KLHL7	KLHL8	KLHL9	KLK1	KLK1 0
KLK1 1	KLK1 2	KLK1 3	KLK1 4	KLK1 5
KLK2	KLK3	KLK4	KLK5	KLK6
KLK7	KLK8	KLK9	KLKB1	KLRA1
KLRB1	KLRC1	KLRC2	KLRC3	KLRC4
KLRD1	KLRF1	KLRG 1	KLRG2	KLRK1
KMO	KNDC1	KNG 1	KNTC1	KPNA1
KPNA2	KPNA3	KPNA4	KPNA5	KPNA6
KPNA7	KPNB1	KPRP	KPTN	KRAS
KRBA1	KRBA2	KRCC1	KREMEN1	KREMEN2
KRI 1	KRIT1	KRR1	KRT1	KRT1 0
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KRT222	KRT23	KRT24	KRT25	KRT26
KRT27	KRT28	KRT3	KRT31	KRT32
KRT33A	KRT33B	KRT34	KRT35	KRT36
KRT37	KRT38	KRT39	KRT4	KRT40
KRT5	KRT6A	KRT6B	KRT6C	KRT7
KRT71	KRT72	KRT73	KRT74	KRT75
KRT76	KRT77	KRT78	KRT79	KRT8
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KRT85	KRT86	KRT9	KRTAP1 - 1	KRTAP1 -3
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KRTAP1 3-2	KRTAP1 3-3	KRTAP1 3-4	KRTAP1 5-1	KRTAP1 7-1
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KRTAP5-2	KRTAP5-3	KRTAP5-5	KRTAP5-6	KRTAP5-7
KRTAP5-8	KRTAP6-1	KRTAP6-2	KRTAP8-1	KRTAP9-2
KRTAP9-3	KRTAP9-4	KRTAP9-8	KRTAP9L2	KRTCAP2
KRTCAP3	KRTDAP	KSR1	KSR2	KTELC1
KTI 12	KTN1	KYNU	Klkbl4	L 1CAM
L 1TD1	L2HGDH	L3MBTL	L3MBTL2	L3MBTL3
L3MBTL4	LACE1	LACRT	LACTB	LACTB2
LAD1	LAG3	LAG E3	LAIR1	LAI R2
LALBA	LAMA1	LAMA2	LAMA3	LAMA4
LAMA5	LAMB1	LAMB2	LAMB3	LAMB4

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
LAMC1	LAMC2	LAMC3	LAMP1	LAMP2
LAMP3	LANCL1	LANCL2	LANCL3	LAP3
LAPTM4A	LAPTM4B	LAPTM5	LARG E	LARP1
LARP1 B	LARP4	LARP4B	LARP6	LARP7
LARS	LARS2	LAS1 L	LASP1	LASS1
LASS2	LASS3	LASS4	LASS5	LASS6
LAT	LAT2	LATS1	LATS2	LAX1
LAYN	LBH	LBP	LBR	LBX1
LBX2	LBXCOR1	LCA5	LCA5L	LCAP
LCAT	LCE1 A	LCE1 B	LCE1 C	LCE1 D
LCE1 E	LCE1 F	LCE2A	LCE2B	LCE2C
LCE2D	LCE3A	LCE3B	LCE3C	LCE3D
LCE3E	LCE4A	LCE5A	LCK	LCLAT1
LCMT1	LCMT2	LCN1	LCN1 0	LCN1 2
LCN1 5	LCN2	LCN6	LCN8	LCN9
LCOR	LCORL	LCP1	LCT	LCTL
LDB1	LDB2	LDB3	LDHA	LDHAL6A
LDHAL6B	LDHB	LDHC	LDHD	LDLR
LDLRAD1	LDLRAD2	LDLRAD3	LDLRAP1	LDOC1
LDOC1 L	LEAP2	LECT1	LECT2	LEF1
LEFTY1	LEFTY2	LEKR1	LELP1	LEMD1
LEMD2	LEMD3	LEN EP	LENG1	LENG8
LENG9	LE01	LEP	LEPR	LEPRE1
LEPREL1	LEPREL2	LEPROT	LEPROTL1	LETM1
LETM2	LETMD1	LFNG	LGALS1	LGALS1 2
LGALS1 3	LGALS1 4	LGALS2	LGALS3	LGALS3BP
LGALS4	LGALS7	LGALS8	LGALS9	LGALS9B
LGALS9C	LGI 1	LGI2	LG I3	LGI4
LGMN	LGR4	LGR5	LG R6	LGSN
LGTN	LHB	LHCGR	LHFP	LHFPL1
LHFPL2	LHFPL4	LHFPL5	LHPP	LHX1
LHX2	LHX3	LHX4	LHX5	LHX6
LHX8	LHX9	LIAS	LIF	LIFR
LIG 1	LIG3	LIG4	LILRA1	LILRA2
LILRA3	LILRA4	LILRA5	LILRA6	LILRB1
LILRB2	LILRB3	LILRB4	LILRB5	LIM2
LIMA1	LIMCH1	LIMD1	LIMD2	LIME1
LIMK1	LIMK2	LIMS1	LIMS2	LIMS3
LIN28	LIN28B	LIN52	LIN54	LIN7A
LIN7B	LIN7C	LIN9	LING01	LING02
LING04	LINS1	LIPA	LIPC	LIPE
LIPF	LIPG	LIPH	LIPI	LIPJ
LIPM	LIPT1	LIPT2	LITAF	LIX1
LIX1 L	LL0XNC01 - 209G1 _2	LL0XNC01 - 237H1 _1	LLGL1	LLGL2
LLPH	LMAN1	LMAN1 L	LMAN2	LMAN2L
LMBR1	LMBR1 L	LMBRD1	LMBRD2	LMCD1
LMF1	LMF2	LMLN	LMNA	LMNB1
LMNB2	LM01	LM02	LM03	LM04
LM07	LMOD1	LMOD2	LMTK2	LMTK3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
LMX1 A	LMX1 B	LNP1	LNPEP	LNX1
LNX2	LOC1 14984	LOC1 20364	LOC1 33308	LOC1 391 16
LOC1 39249	LOC1 39263	LOC1 39431	LOC1 3951 6	LOC1 39542
LOC1 4581 4	LOC1 4821 3	LOC1 52485	LOC1 53328	LOC1 57567
LOC1 58572	LOC1 58730	LOC1 58825	LOC1 58957	LOC1 651 86
LOC1 68850	LOC200420	LOC20351 0	LOC203604	LOC220686
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LOC283849	LOC284023	LOC2841 00	LOC284288	LOC286404
LOC286408	LOC28641 1	LOC286467	LOC286478	LOC28651 2
LOC286528	LOC3391 23	LOC340096	LOC340549	LOC340571
LOC340578	LOC340581	LOC341 457	LOC342541	LOC3441 65
LOC345630	LOC347376	LOC347381	LOC34741 1	LOC347421
LOC347424	LOC347549	LOC3491 36	LOC387867	LOC388972
LOC389669	LOC389841	LOC389842	LOC389846	LOC389848
LOC389858	LOC389873	LOC389888	LOC389895	LOC389899
LOC389900	LOC389901	LOC389904	LOC390335	LOC390956
LOC391 370	LOC392434	LOC392439	LOC392459	LOC392467
LOC392473	LOC392487	LOC39251 2	LOC392528	LOC392529
LOC392531	LOC392533	LOC392539	LOC392546	LOC392549
LOC392554	LOC392556	LOC392559	LOC401 052	LOC401 584
LOC401 588	LOC401 599	LOC401 605	LOC401 611	LOC401 613
LOC401 616	LOC401 621	LOC4021 20	LOC40241 4	LOC40241 8
LOC439951	LOC440055	LOC440345	LOC440354	LOC44091 7
LOC440925	LOC440944	LOC441 344	LOC441 480	LOC441 481
LOC441 483	LOC441 485	LOC441 486	LOC441 488	LOC441 493
LOC441 494	LOC441 496	LOC441 497	LOC441 498	LOC441 499
LOC441 504	LOC441 507	LOC441 510	LOC441 511	LOC441 513
LOC441 515	LOC441 526	LOC441 795	LOC442425	LOC442439
LOC442444	LOC442447	LOC442451	LOC442452	LOC442454
LOC442456	LOC442461	LOC442464	LOC442465	LOC442466
LOC442470	LOC493829	LOC51 058	LOC51 059	LOC51 123
LOC51 321	LOC541 473	LOC55954	LOC56901	LOC571 49
LOC642755	LOC643751	LOC645864	LOC646049	LOC646625
LOC646853	LOC646870	LOC646871	LOC649445	LOC649587
LOC64961 8	LOC649930	LOC650875	LOC651 21	LOC651 271
LOC651 503	LOC651 746	LOC6521 53	LOC652737	LOC6531 92
LOC653698	LOC653720	LOC7281 94	LOC728350	LOC728378
LOC729903	LOC730029	LOC730445	LOC730735	LOC731 028
LOC731 173	LOC731 740	LOC731 796	LOC731 890	LOC81 691
LOC88523	LOC91 461	LOC91 807	LOC92249	LOC93081
LOH1 2CR1	LONP1	LONP2	LONRF1	LONRF2
LONRF3	LOR	LOX	LOXL1	LOXL2
LOXL3	LOXL4	LPA	LPAL2	LPAR1
LPAR2	LPAR3	LPAR4	LPAR5	LPAR6
LPCAT1	LPCAT2	LPCAT3	LPCAT4	LPGAT1
LPHN 1	LPHN2	LPHN3	LPIN 1	LPIN2
LPIN3	LPL	LPO	LPP	LPPR2
LPPR4	LPXN	LRAT	LRBA	LRCH1
LRCH2	LRCH3	LRCH4	LRDD	LRFN1
LRFN2	LRFN3	LRFN4	LRFN5	LRG1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
LRGUK	LRIG 1	LRIG2	LRIG3	LRIT1
LRIT2	LRIT3	LRMP	LRP1	LRP1 0
LRP1 1	LRP1 2	LRP1 B	LRP2	LRP2BP
LRP3	LRP4	LRP5	LRP5L	LRP6
LRP8	LRPAP1	LRPPRC	LRRC1	LRRC1 0
LRRC1 4	LRRC1 4B	LRRC1 5	LRRC1 6A	LRRC1 6B
LRRC1 7	LRRC1 8	LRRC1 9	LRRC2	LRRC20
LRRC23	LRRC24	LRRC25	LRRC26	LRRC27
LRRC28	LRRC29	LRRC3	LRRC30	LRRC31
LRRC32	LRRC33	LRRC34	LRRC36	LRRC37A
LRRC37A2	LRRC37A3	LRRC37B	LRRC39	LRRC3B
LRRC4	LRRC40	LRRC41	LRRC42	LRRC43
LRRC45	LRRC46	LRRC47	LRRC49	LRRC4B
LRRC4C	LRRC50	LRRC52	LRRC55	LRRC56
LRRC57	LRRC59	LRRC6	LRRC61	LRRC66
LRRC67	LRRC68	LRRC7	LRRC8A	LRRC8B
LRRC8C	LRRC8D	LRRC8E	LRRCC1	LRRFI P 1
LRRFI P 1_ENSTO 0000392000	LRRFI P2	LRRIQ1	LRRIQ3	LRRK1
LRRK2	LRRK2_ENSTOO 00029891 0	LRRN1	LRRN2	LRRN3
LRRN4	LRRN4CL	LRRTM1	LRRTM3	LRRTM4
LRSAM1	LRTM1	LRTM2	LRTOMT	LRWD1
LSAMP	LSG 1	LSM1	LSM1 0	LSM1 1
LSM1 2	LSM1 4A	LSM1 4B	LSM2	LSM3
LSM4	LSM5	LSM6	LSMD1	LSP1
LSR	LSS	LST1	LTA	LTA4H
LTB	LTB4R	LTB4R2	LTBP1	LTBP2
LTBP3	LTBP4	LTBR	LTC4S	LTF
LTK	LTV1	LUC7L	LUC7L2	LUC7L3
LUM	LUZP1	LUZP2	LUZP4	LXN
LY6D	LY6E	LY6G5B	LY6G5C	LY6G6C
LY6G6D	LY6G6F	LY6H	LY6K	LY75
LY86	LY9	LY96	LYAR	LYG 1
LYG2	LYL1	LYN	LYNX1	LYNX1_ENS T0000031 75 43
LYPD1	LYPD2	LYPD3	LYPD4	LYPD5
LYPD6	LYPLA1	LYPLA2	LYPLAL1	LYRM1
LYRM2	LYRM4	LYRM5	LYRM7	LYSMD1
LYSMD2	LYSMD3	LYSMD4	LYST	LYVE1
LYZ	LYZL1	LYZL2	LYZL4	LYZL6
LZIC	LZTFL1	LZTR1	LZTS1	LZTS2
M6PR	MAB21 L 1	MAB21 L2	MACC1	MACF1
MACF1_ENSTOO 000361 689	MACR0D1	MACR0D2	MAD1 L 1	MAD2L1
MAD2L1 BP	MAD2L2	MADCAM1	MADD	MAEA
MAEL	MAF	MAF1	MAFA	MAFB
MAFF	MAFG	MAFK	MAG	MAGEA1
MAGEA1 0	MAGEA1 1	MAGEA1 2	MAG EA1 3P	MAGEA2
MAGEA2B	MAGE A3	MAGEA4	MAG EA5	MAGEA6

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
MAGEA8	MAGEA9	MAGEA9B	MAG EB1	MAGEB1 0
MAGEB1 6	MAGEB1 7	MAGEB1 8	MAG EB2	MAGEB3
MAGEB4	MAGEB5	MAGEB6	MAG EB6B	MAGEC1
MAGEC2	MAGEC3	MAGED1	MAG ED2	MAGED4B
MAGEE1	MAGEE2	MAGEF1	MAG EH1	MAG 11
MAG 11_ENSTOO 000402939	MAGI2	MAGI3	MAG IX	MAGOH
MAGOHB	MAGT1	MAK	MAK1 6	MAL
MALL	MALT1	MAMDC2	MAMDC4	MAML1
MAML2	MAMLD1	MAMSTR	MAN 1A 1	MAN1 A2
MAN1 B 1	MAN1 C 1	MAN2A1	MAN2A2	MAN2B1
MAN2B2	MAN2C1	MANBA	MANBAL	MANEA
MANEAL	MANSC1	MAOA	MAOB	MAPI A
MAPI B	MAPI D	MAPI LC3A	MAP1 LC3B	MAPI LC3B2
MAPI LC3C	MAP1 S	MAP2	MAP2K1	MAP2K2
MAP2K3	MAP2K4	MAP2K5	MAP2K6	MAP2K7
MAP3K1	MAP3K1 0	MAP3K1 1	MAP3K1 2	MAP3K1 3
MAP3K1 4	MAP3K1 5	MAP3K2	MAP3K3	MAP3K4
MAP3K5	MAP3K6	MAP3K6 _ENS T00000374040	MAP3K7	MAP3K8
MAP3K9	MAP4	MAP4K1	MAP4K2	MAP4K3
MAP4K4	MAP4K5	MAP6	MAP6D1	MAP7
MAP7D1	MAP7D2	MAP7D3	MAP9	MAPK1
MAPK1 0	MAPK1 1	MAPK1 2	MAPK1 3	MAPK1 4
MAPK1 5	MAPK1 IP1 L	MAPK3	MAPK4	MAPK6
MAPK7	MAPK8	MAPK8IP1	MAPK8I P2	MAPK8IP3
MAPK9	MAPKAP1	MAPKAPK2	MAPKAPK3	MAPKAPK5
MAPKBP1	MAPKSP1	MAPRE1	MAPRE2	MAPRE3
MAPT	01-Mar	10-Mar	02-Mar	03-Mar
04-Mar	05-Mar	06-Mar	07-Mar	08-Mar
09-Mar	MARCKS	MARCKSL1	MARCO	MARK1
MARK2	MARK3	MARK4	MARS	MARS2
MARVELD2	MARVELD3	MAS1	MAS1 L	MASP1
MASP2	MAST1	MAST2	MAST2 _ENST 00000361 297	MAST3
MAST4	MASTL	MAT1 A	MAT2A	MAT2B
MATK	MATN1	MATN4	MATR3	MAVS
MAX	MAZ	MB	MB3L2 _HUMA N	MBD1
MBD2	MBD3	MBD3L1	MBD3L2	MBD4
MBD5	MBD6	MBI P	MBL2	MBLAC1
MBLAC2	MBNL1	MBNL1 _ENST 00000282488	MBNL2	MBNL3
MBOAT1	MBOAT2	MBOAT4	MBOAT7	MBP
MBTD1	MBTPS1	MBTPS2	MC2R	MC3R
MC4R	MC5R	MCAM	MCART1	MCART2
MCART6	MCAT	MCC	MCCC1	MCCC2
MCCD1	MCC_ENSTOOOO 0408903	MCEE	MCF2	MCF2L
MCF2L2	MCFD2	MCHR1	MCHR2	MCL1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
MCM10	MCM2	MCM3	MCM3AP	MCM4
MCM5	MCM6	MCM7	MCM8	MCM9
MCOLN1	MCOLN2	MCOLN3	MCPH1	MCRS1
MCTP1	MCTP2	MCTS1	MDC1	MDFI
MDFIC	MDGA1	MDGA2	MDH1	MDH1B
MDH2	MDK	MDM1	MDM2	MDM4
MDN1	MDP1	MDS1	MDS2	ME1
ME2	ME3	MEA1	MEAF6	MECOM
MECP2	MECR	MED1	MEDI O	MED11
MED12	MED12L	MED13	MED13L	MED14
MED15	MED16	MED17	MED18	MED19
MED20	MED21	MED22	MED23	MED24
MED25	MED26	MED27	MED28	MED29
MED30	MED31	MED4	MED6	MED7
MED8	MED9	MEF2B	MEF2C	MEF2D
MEFV	MEGF10	MEGF11	MEGF6	MEM
MEIG1	MEIS1	MEIS2	MEIS3	MELK
MEM01	MEM01 P	MEN1	MEOX1	ME0X2
MEP1A	MEP1B	MEPCE	MEPE	MERTK
MESDC1	MESDC2	MESP1	MESP2	MEST
MET	METAP2	METRN	METRNL	METT10D
METT11D1	METT5D1	METTL1	METTL10	METTL11A
METTL12	METTL13	METTL14	METTL2A	METTL2B
METTL3	METTL4	METTL5	METTL6	METTL7A
METTL7B	METTL8	METTL9	MEX3A	MEX3B
MEX3C	MEX3D	MFAP1	MFAP2	MFAP3
MFAP3L	MFAP4	MFAP5	MFF	MFGE8
MFHAS1	MFI2	MFN1	MFN2	MFNG
MFRP	MFSD1	MFSD10	MFSD11	MFSD2A
MFSD3	MFSD4	MFSD5	MFSD6	MFSD6L
MFSD7	MFSD8	MFSD9	MGA	MGAM
MGAM_ENSTOO00047301 1	MGAT1	MGAT2	MGAT3	MGAT4A
MGAT4B	MGAT4C	MGAT5	MGAT5B	MGC15476
MGC17624	MGC33414	MGC33530	MGC42105	MGC57359
MGC99813	MGEA5	MGLL	MGMT	MGP
MGRN1	MGST1	MGST2	MGST3	MIA
MIA2	MIA3	MIB1	MIB2	MICA3_HUMAN
MICAL1	MICAL2	MICAL3	MICALCL	MICALL1
MICALL2	MICB	MIDI	MID1IP1	MID2
MIDN	MIER1	MIER2	MIER3	MIF
MIF4GD	MIIP	MINA	MINK1	MINPP1
MIOS	MIOX	MIP	MIPEP	MIPOL1
MIS12	MITD1	MITF	MIXL1	MKI67
MKI67IP	MKKS	MKL1	MKL2	MKLN1
MKNK1	MKNK2	MKNK2_ENST00000250896	MKRN1	MKRN2
MKRN3	MKRN4P	MKS1	MKX	MLANA
MLC1	MLEC	MLF1	MLF1IP	MLF2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
MLH1	MLH3	MLKL	MLL	MLL2
MLL3	MLL4	MLL5	MLLT1	MLLT1 0
MLLT1 1	MLLT3	MLLT4	MLLT6	MLN
MLNR	MLPH	MLST8	MLST8_ENSTO 0000301 724	MLX
MLXI P	MLXI PL	MLYCD	MMAA	MMAB
MMACHC	MMADHC	MMD	MMD2	MME
MMEL1	MMGT1	MMP1	MMP1 0	MMP1 1
MMP1 2	MMP1 3	MMP1 4	MMP1 5	MMP1 6
MMP1 7	MMP1 9	MMP2	MMP20	MMP21
MMP23B	MMP25	MMP26	MMP27	MMP28
MMP3	MMP7	MMP8	MMP9	MMPL1
MMRN1	MMRN2	MN1	MNAT1	MND1
MNDA	MNS1	MNT	MNX1	MOAP1
MOBKL1 A	MOBKL1 B	MOBKL2A	MOBKL2B	MOBKL2C
MOBKL3	MOBP	MOCOS	MOCS1	MOCS2
MOCS3	MOG	MOGAT1	MOGAT2	MOGAT3
MOGS	MON1 A	MON1 B	MON2	MORC1
MORC2	MORC3	MORC4	MORF4L1	MORF4L2
MORN1	MORN3	MORN4	MORN5	MOS
MOSC1	MOSC2	MOSPD1	MOSPD2	MOSPD3
MOV1 0	MOV1 0L1	MOXD1	MOXD1_ENST 00000336749	MPDU1
MPDZ	MPEG1	MPG	MPHOSPH 10	MPHOSPH6
MPHOSPH8	MPHOSPH9	MPI	MPL	MPND
MPO	MPP1	MPP2	MPP3	MPP4
MPP5	MPP6	MPP7	MPPE1	MPPED2
MPRI P	MPST	MPV1 7	MPV1 7L	MPV1 7L2
MPZ	MPZL1	MPZL2	MPZL3	MR1
MRAP	MRAP2	MRAS	MRC1	MRC1 L 1
MRC2	MRE1 1A	MREG	MRFAP1	MRFAP1 L 1
MRG PRD	MRG PRE	MRG PRF	MRGPRG	MRG PRX1
MRG PRX2	MRG PRX3	MRG PRX4	MRU	MRM1
MRO	MRP63	MRPL1	MRPL1 0	MRPL1 1
MRPL1 2	MRPL1 3	MRPL1 4	MRPL1 5	MRPL1 6
MRPL1 7	MRPL1 8	MRPL1 9	MRPL2	MRPL20
MRPL21	MRPL22	MRPL23	MRPL24	MRPL27
MRPL28	MRPL3	MRPL30	MRPL32	MRPL33
MRPL34	MRPL35	MRPL36	MRPL37	MRPL39
MRPL4	MRPL40	MRPL41	MRPL42	MRPL43
MRPL44	MRPL45	MRPL46	MRPL47	MRPL49
MRPL50	MRPL51	MRPL52	MRPL53	MRPL54
MRPL55	MRPL9	MRPS1 0	MRPS1 1	MRPS1 2
MRPS1 4	MRPS1 5	MRPS1 6	MRPS1 7	MRPS1 8A
MRPS1 8B	MRPS1 8C	MRPS2	MRPS21	MRPS22
MRPS23	MRPS24	MRPS25	MRPS26	MRPS27
MRPS28	MRPS30	MRPS31	MRPS33	MRPS34
MRPS35	MRPS36	MRPS5	MRPS6	MRPS7
MRPS9	MRRF	MRRFP1	MRS2	MRT04
MRVI 1	MS4A1	MS4A1 0	MS4A1 2	MS4A1 3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
MS4A1 4	MS4A1 5	MS4A2	MS4A3	MS4A4A
MS4A5	MS4A6A	MS4A6E	MS4A7	MS4A8B
MSC	MSGN1	MSH2	MSH3	MSH4
MSH5	MSH6	MSI 1	MSI2	MSL1
MSL2	MSL3	MSLN	MSLNL	MSMB
MSMP	MSN	MSR1	MSRA	MSRB2
MSRB3	MST1	MST1 R	MST4	MSTN
MST01	MSX1	MSX2	MT1 A	MT1 B
MT1 E	MT1 F	MT1 G	MT1 H	MT1 M
MT1 P2	MT1 X	MT2A	MT3	MT4
MTA1	MTA2	MTAC2D1	MTAP	MTBP
MTCH1	MTCH2	MTCP1	MTDH	MTERF
MTERFD1	MTERFD2	MTERFD3	MTF1	MTF2
MTFR1	MTG 1	MTHFD1	MTHFD1 L	MTHFD2
MTHFD2L	MTHFR	MTHFS	MTHFSD	MTI F2
MTI F3	MTL5	MTM1	MTMR1	MTMR1 0
MTMR1 1	MTMR1 2	MTMR1 4	MTMR1 5	MTMR2
MTMR3	MTMR3 _ENSTOO 000401 950	MTMR4	MTMR6	MTMR7
MTMR8	MTMR9	MTNR1 A	MTNR1 B	MT01
MTOR	MTP1 8	MTPAP	MTPN	MTR
MTRF1	MTRF1 L	MTRR	MTSS1	MTTP
MTUS1	MTUS2	MTUS2 _ENST 00000431 530	MTX1	MTX2
MUC1	MUC1 3	MUC1 5	MUC1 6	MUC1 6_ENS T00000331 9 86
MUC1 7	MUC2	MUC21	MUC4	MUC4 _ENST 000004051 67
MUC5AC	MUC7	MUCL1	MUDENG	MUL1
MUM1	MUM1 L 1	MURC	MUS81	MUSK
MUT	MUTED	MUTYH	MVD	MVK
MVP	MX1	MX2	MXD1	MXD3
MXD4	MXI 1	MXRA5	MXRA7	MXRA8
MYADM	MYADML2	MYB	MYBBP1 A	MYBL1
MYBL2	MYBPC1	MYBPC2	MYBPC3	MYBPH
MYBPHL	MYB _ENSTOOOO 0341 9 1 1	MYC	MYCBP	MYCBP2
MYCBPAP	MYCL1	MYCL1 _ENST 00000397332	MYCL2	MYCN
MYCT1	MYD88	MYEF2	MYEOV	MYEOV2
MYF5	MYF6	MYH1	MYH 10	MYH1 1
MYH1 4	MYH1 5	MYH1 6	MYH2	MYH3
MYH4	MYH6	MYH7	MYH7B	MYH8
MYH9	MYL1	MYL1 0	MYL1 2A	MYL1 2B
MYL2	MYL3	MYL4	MYL5	MYL6
MYL6B	MYL7	MYL9	MYLIP	MYLK
MYLK2	MYLK3	MYLK4	MYLPF	MYNN
MYO1 0	MY01 5A	MY01 6	MY01 8A	MY01 8B
MY01 A	MY01 B	MY01 C	MY01 D	MY01 E
MY01 F	MY01 G	MY03A	MY03B	MY05A

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
MY05B	MY05C	MY06	MY07A	MY09A
MY09B	MY09B _ENSTOO 00031 9396	MYOC	MYOCD	MYOD1
MYOF	MYOG	MYOHD1	MYOM1	MYOM2
MYOM3	MYOT	MYOZ1	MYOZ2	MYOZ3
MYPN	MYPOP	MYRI P	MYSM1	MYST1
MYST2	MYST3	MYST4	MYT1	MYT1 L
MZF1	Magmas _	N4BP1	N4BP2	N4BP2L1
N4BP2L2	N4BP3	N6AMT1	N6AMT2	NAA1 0
NAA1 5	NAA1 6	NAA20	NAA25	NAA30
NAA35	NAA38	NAA40	NAA50	NAAA
NAALAD2	NAALADL1	NAB1	NAB2	NACA
NACA2	NACA3P	NACC1	NACC2	NADK
NADSYN1	NAE1	NAF1	NAG6	NAGA
NAGK	NAGLU	NAG PA	NAGS	NAI F 1
NAI P	NALCN	NALP6	NAMPT	NANOG
NANOGP1	NANOS1	NANOS2	NANOS3	NAN P
NANS	NAP1 L 1	NAP1 L2	NAP1 L3	NAP1 L4
NAP1 L5	NAP1 L6	NAPA	NAPB	NAPEPLD
NAPRT1	NAPSA	NAPSB	NARF	NARFL
NARG2	NARS	NARS2	NASP	NAT1
NAT1 0	NAT1 4	NAT2	NAT6	NAT8
NAT8L	NAT9	NAV1	NAV2	NAV3
NBAS	NBEA	NBEAL1	NBEAL1 _ENS T00000449802	NBEAL2
NBL1	NBN	NBPF1 1	NBPF1 4	NBPF1 5
NBPF1 6	NBPF3	NBPF5	NBPF7	NBR1
NCALD	NCAM2	NCAN	NCAPD2	NCAPD3
NCAPG	NCAPG2	NCAPH	NCAPH2	NCBP1
NCBP2	NCBP2L	NCCRP1	NCDN	NCEH1
NCF1	NCF2	NCF4	NCK1	NCK2
NCKAP1	NCKAP1 L	NCKAP5L	NCKAP5 _ENS T00000405974	NCKI PSD
NCL	NCLN	NCOA1	NCOA2	NCOA3
NCOA4	NCOA5	NCOA6	NCOA7	NCOR1
NCOR2	NCR1	NCR2	NCR3	NCRNA0008 6
NCRNA001 03	NCRNA001 05	NCRNA001 69	NCRNA001 74	NCRNA001 7 5
NCRNA001 76	NCRNA001 88	NCS1	NCSTN	ND4
NDC80	NDE1	NDEL1	NDFIP1	NDFI P2
NDN	NDNL2	NDOR1	NDP	NDRG1
NDRG2	NDRG3	NDRG4	NDST1	NDST2
NDST3	NDST4	NDUFA1	NDUFA1 0	NDUFA1 1
NDUFA1 2	NDUFA1 3	NDUFA2	NDUFA3	NDUFA4
NDUFA4L2	NDUFA5	NDUFA6	NDUFA7	NDUFA8
NDUFA9	NDUFAB1	NDUFAF1	NDUFAF2	NDUFAF3
NDUFAF4	NDUFB1	NDUFB1 0	NDUFB1 1	NDUFB2
NDUFB3	NDUFB4	NDUFB5	NDUFB6	NDUFB7
NDUFB8	NDUFB9	NDUFC1	NDUFC2	NDUFS1
NDUFS2	NDUFS3	NDUFS4	NDUFS5	NDUFS6

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
NDUFS7	NDUFS8	NDUFV1	NDUFV2	NDUFV3
NEB	NEBL	NECAB1	NECAB2	NECAB3
NECAP1	NECAP2	NEDD1	NEDD4	NEDD4L
NEDD8	NEDD9	NEFH	NEFL	NEFM
NEG RI	NEIL1	NEIL2	NEIL3	NEK1
NEK1 0	NEK1 1	NEK2	NEK3	NEK4
NEK5	NEK6	NEK7	NEK8	NEK9
NELF	NELL1	NELL2	NENF	NE01
NES	NET1	NET01	NET02	NEU1
NEU2	NEU4	NEURL	NEURL2	NEURL3
NEURL4	NEURL4 _ENSTO 000031 561 4	NEUROD1	NEUROD2	NEUROD4
NEUR0D6	NEUR0G1	NEUROG2	NEUROG3	NEXN
NF1	NF2	NFAM1	NFASC	NFAT5
NFATC1	NFATC2	NFATC2IP	NFATC3	NFATC4
NFE2	NFE2L1	NFE2L2	NFE2L3	NFIA
NFIB	NFIB_ENSTOOOO 0397581	NFIC	NFIL3	NFIX
NFKB1	NFKB2	NFKBIA	NFKBIB	NFKBI D
NFKBI E	NFKBIL1	NFKBIL2	NFKBIZ	NFRKB
NFS1	NFU1	NFX1	NFXL1	NFYA
NFYB	NFYC	NGB	NG DN	NGEF
NGF	NGFR	NGFRAP1	NGLY1	NGRN
NHEDC1	NHEDC2	NHEJ1	NHLH1	NHLH2
NHLRC1	NHLRC2	NHLRC3	NHP2	NHP2L1
NHS	NHSL1	NHSL2	NICN1	NID1
NID2	NIF3L1	NIN	NINJ1	NINJ2
NINL	NIP7	NIPA1	N IPA2	NIPAL1
NIPAL2	NIPAL3	NIPAL4	N IPBL	NIPSNAP1
NIPSNAP3A	NIPSNAP3B	NISCH	NIT1	NIT2
NKAIN1	NKAIN2	NKAIN4	NKAP	NKAPL
NKD1	NKD2	NKG7	NKIRAS1	NKI RAS2
NKPD1	NKRF	NKTR	NKX2-1	NKX2-2
NKX2-3	NKX2-4	NKX2-5	NKX2-6	NKX2-8
NKX3-1	NKX3-2	NKX6-1	NKX6-2	NKX6-3
NLE1	NLGN1	NLGN2	NLGN3	NLGN4X
NLGN4Y	NLK	NLN	NLRC3	NLRC4
NLRC5	NLRP1	NLRP1 0	NLRP1 1	NLRP1 2
NLRP1 3	NLRP1 4	NLRP2	NLRP3	NLRP4
NLRP5	NLRP6	NLRP7	NLRP8	NLRP9
NLRX1	NMB	NMBR	NMD3	NME1
NME1 -NME2	NME2	NME2P1	NME3	NME4
NME5	NME6	NME7	NMI	NMNAT1
NMNAT2	NMNAT3	NMRAL1	NMS	NMT1
NMT2	NMU	NMUR1	NMUR2	NM_001 0129 84_2
NM_001 013679	NM_001 031 _4	NM_001 03969 0_2	NM_001 08047 0_1	NM_024534
NM_024588 _3	NM_032947 _3	NM_198455 _2	NNAT	NNMT
NNT	NOB1	NOBOX	NOC2L	NOC3L

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
NOC4L	NOD1	NOD2	NODAL	NOG
NOL11	NOL12	NOL3	NOL4	NOL6
NOL7	NOL9	NOLC1	NOM1	NOM01
NOM02	NOM03	NONO	NOP10	NOP14
NOP16	NOP2	NOP56	NOP58	NOS1
NOS1AP	NOS1AP_ENSTO0000361897	NOS2	NOS3	NOSIP
NOSTRIN	NOTCH1	NOTCH2	NOTCH2NL	NOTCH3
NOTCH4	NOTUM	NOV	NOVA1	NOVA2
NOX1	NOX3	NOX4	NOX5	NOXA1
NOX01	NP12_HUMAN	NPAS1	NPAS2	NPAS3
NPAS4	NPAT	NPB	NPBWR1	NPBWR2
NPC1	NPC1L1	NPC2	NPDC1	NPEPPS
NPFF	NPFFR1	NPFFR2	NPHP1	NPHP3
NPHP4	NPHS1	NPHS2	NPIP	NPIPL1
NPIPL2	NPL	NPLOC4	NPM1	NPM2
NPM3	NPNT	NPPA	NPPB	NPPC
NPR1	NPR2	NPR3	NPS	NPSR1
NPTN	NPTX1	NPTX2	NPTXR	NPVF
NPW	NPY	NPY1R	NPY2R	NPY5R
NPY6R	NP_001073948_1	NQ01	NQ02	NR0B1
NR0B2	NR1D1	NR1D2	NR1H2	NR1H3
NR1H4	NR1I2	NR1I3	NR2C1	NR2C2
NR2C2AP	NR2E1	NR2E3	NR2F1	NR2F2
NR2F6	NR3C1	NR3C2	NR4A1	NR4A2
NR4A3	NR5A1	NR5A2	NR6A1	NRAP
NRARP	NRAS	NRBF2	NRBP1	NRBP2
NRCAM	NRD1	NRF1	NRG1	NRG2
NRG3	NRG4	NRGN	NRIP1	NRIP2
NRIP3	NRK	NRL	NRM	NRN1
NRN1L	NRP1	NRP2	NRSN1	NRSN2
NRTN	NRXN1	NRXN2	NRXN3	NR_002168_1
NR_002217_1	NR_002453_4	NR_002730_1	NR_002733_1	NR_002781_1
NR_002938_2	NR_003034_1	NR_003148_2	NR_003276_1	NSA2
NSD1	NSDHL	NSF	NSFL1C	NSL1
NSMAF	NSMCE1	NSMCE2	NSMCE4A	NSUN2
NSUN3	NSUN4	NSUN5	NSUN5P1	NSUN5P2
NSUN6	NSUN7	NT5C	NT5C1A	NT5C1B
NT5C2	NT5C3	NT5C3L	NT5DC1	NT5DC2
NT5DC3	NT5E	NT5M	NTAN1	NTF3
NTF4	NTHL1	NTM	NTN1	NTN3
NTN4	NTN5	NTNG1	NTNG2	NTRK1
NTRK2	NTRK3	NTS	NTSR1	NTSR2
NUAK1	NUAK2	NUB1	NUBP1	NUBP2
NUBPL	NUCB1	NUCB2	NUCKS1	NUDC
NUDCD1	NUDCD2	NUDCD3	NUDT1	NUDT10
NUDT11	NUDT12	NUDT13	NUDT14	NUDT15
NUDT16	NUDT16L1	NUDT17	NUDT19	NUDT2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
NUDT21	NUDT22	NUDT3	NUDT4	NUDT5
NUDT6	NUDT7	NUDT8	NUDT9	NUF2
NUFI P 1	NUFI P2	NUMA1	NUMB	NUMBL
NUP1 07	NUP1 33	NUP1 53	NUP1 55	NUP1 60
NUP1 88	NUP205	NUP21 0	NUP21 0L	NUP21 4
NUP35	NUP37	NUP43	NUP50	NUP54
NUP62	NUP62CL	NUP85	NUP88	NUP93
NUP98	NUPL1	NUPL2	NUPR1	NUS1
NUTF2	NVL	NWD1	NXF1	NXF2
NXF2B	NXF3	NXF4	NXF5	NXN
NXNL1	NXNL2	NXPH1	NXPH2	NXPH3
NXPH4	NXT1	NXT2	NYNRIN	NYX
000434 _HUMAN	O 10D4 _HUMAN	O 10J6_HUMA N	052L2 _HUMA N	05AK3 _HUM AN
060374 _HUMAN	060384 _HUMAN	06041 1_HUM AN	075863 _HUM AN	09501 4_HU MAN
095431 _HUMAN	OAF	OAS1	OAS2	OAS3
OASL	OAT	OAZ1	OBFC1	OBFC2A
OBFC2B	OBP2A	OBP2B	OBSCN	OBSCN _EN ST00000359 599
OBSL1	OC90	OC90 _ENSTOO 000262283	OCA2	OCEL1
OCIAD1	OCIAD2	OCLN	OCM	OCM2
OCRL	ODAM	ODC1	ODF1	ODF2
ODF2L	ODF3	ODF3B	ODF3L1	ODF3L2
ODF4	ODZ1	ODZ2	OFCC1	OFD1
OG DH	OG DHL	OG FOD1	OGFOD2	OG FR
OG FRL1	OGG1	OGN	OGT	OGT _ENSTO 000037371 9
O IP5	OIT3	OLA1	OLAH	OLFM1
OLFM2	OLFM3	OLFM4	OLFML1	OLFML2A
OLFML2B	OLFML3	OLIG1	OLIG2	OLIG3
OLR1	OMA1	OMD	OMG	ONECUT1
ONECUT2	OPA1	OPA3	OPALIN	OPCML
OPHN1	OPLAH	OPN1 LW	OPN1 MW	OPN1 MW2
OPN1 SW	OPN3	OPN4	OPN5	OPRD1
OPRK1	OPRL1	OPRM1	OPTC	OPTN
OR1 0A2	OR1 0A3	OR1 0A4	OR1 0A5	OR1 0A6
OR1 0A7	OR1 0AD1	OR1 0AG1	OR1 0C1	OR1 0G2
OR1 0G3	OR1 0G4	OR1 0G6	OR1 0G7	OR1 0G8
OR1 0G9	OR1 0H1	OR1 0H2	OR1 0H3	OR1 0H4
OR1 0H5	OR1 0J1	OR1 0J3	OR1 0J5	OR1 0K1
OR1 0K2	OR1 0P1	OR1 0Q1	OR1 0R2	OR1 0R3P
OR1 0S1	OR1 0T2	OR1 0V1	OR1 0W1	OR1 0X1
OR1 0Z1	OR1 1A 1	OR1 1G2	OR1 1H 1	OR1 1H 12
OR1 1H4	OR1 1H6	OR1 1L 1	OR1 2D2	OR1 2D3
OR1 3A1	OR1 3C2	OR1 3C3	OR1 3C4	OR1 3C5
OR1 3C8	OR1 3C9	OR1 3D1	OR1 3F1	OR1 3G 1
OR1 3H1	OR1 3J1	OR1 4A1 6	OR1 4C36	OR1 4I1
OR1 4J1	OR1 A 1	OR1 A2	OR1 B 1	OR1 C 1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
OR1 D2	OR1 D4	OR1 E 1	OR1 E2	OR1 F 1
OR1 G 1	OR1 I1	OR1 J 1	OR1 J2	OR1 J4
OR1 K 1	OR1 L 1	OR1 L3	OR1 L4	OR1 L6
OR1 L8	OR1 M 1	OR1 N 1	OR1 N2	OR1 Q 1
OR1 S 1	OR1 S2	OR2A1 2	OR2A1 4	OR2A2
OR2A25	OR2A4	OR2A5	OR2AE1	OR2AG1
OR2AG2	OR2AJ1	OR2AK2	OR2AP1	OR2AT4
OR2B1 1	OR2B2	OR2B3P	OR2B6	OR2C1
OR2C3	OR2D2	OR2D3	OR2F1	OR2F2
OR2G2	OR2G3	OR2G6	OR2H1	OR2H2
OR2J1	OR2J2	OR2J3	OR2J3 _HUMA N	OR2K2
OR2L1 3	OR2L1 P	OR2L2	OR2L3	OR2L8
OR2M1 P	OR2M2	OR2M3	OR2M4	OR2M5
OR2M7	OR2S2	OR2T1	OR2T1 0	OR2T1 1
OR2T1 2	OR2T2	OR2T27	OR2T3	OR2T33
OR2T34	OR2T35	OR2T4	OR2T5	OR2T6
OR2T8	OR2V2	OR2W1	OR2W3	OR2W5
OR2Y1	OR2Z1	OR3A1	OR3A3	OR3A4
OR4A1 3P	OR4A1 5	OR4A1 6	OR4A47	OR4A5
OR4B1	OR4C1 1	OR4C1 2	OR4C1 3	OR4C1 5
OR4C1 6	OR4C3	OR4C46	OR4C5 _HUMA N	OR4C6
OR4D1	OR4D1 0	OR4D1 1	OR4D2	OR4D5
OR4D6	OR4D9	OR4E2	OR4F1 5	OR4F1 6
OR4F1 7	OR4F21	OR4F29	OR4F3	OR4F4
OR4F5	OR4F6	OR4K1	OR4K1 3	OR4K1 4
OR4K1 5	OR4K1 7	OR4K2	OR4K5	OR4L1
OR4M1	OR4M2	OR4N2	OR4N4	OR4N5
OR4P4	OR4Q3	OR4S1	OR4S2	OR4X1
OR4X2	OR51 A2	OR51 A4	OR51 A7	OR51 B2
OR51 B4	OR51 B5	OR51 B6	OR51 D 1	OR51 E 1
OR51 E2	OR51 F 1	OR51 F2	OR51 G 1	OR51 G2
OR51 H 1P	OR51 I1	OR51 I2	OR51 J 1	OR51 L 1
OR51 M 1	OR51 Q 1	OR51 S 1	OR51 T 1	OR51 V 1
OR52A1	OR52A4	OR52A5	OR52B4	OR52B6
OR52D1	OR52E2	OR52E4	OR52E6	OR52E8
OR52H1	OR52I 1	OR52I2	OR52J3	OR52K1
OR52K2	OR52L1	OR52M1	OR52N1	OR52N2
OR52N4	OR52N5	OR52R1	OR52W1	OR56A1
OR56A3	OR56A4	OR56B1	OR56B4	OR5A1
OR5A2	OR5AC2	OR5AK2	OR5AN1	OR5AP2
OR5AR1	OR5AS1	OR5AU1	OR5AX1	OR5B1 2
OR5B1 7	OR5B2	OR5B21	OR5B3	OR5C1
OR5D1 3	OR5D1 4	OR5D1 6	OR5D1 8	OR5D3P
OR5E1 P	OR5F1	OR5H1	OR5H1 4	OR5H1 5
OR5H2	OR5H6	OR5I 1	OR5J2	OR5K1
OR5K2	OR5K3	OR5K4	OR5L1	OR5L2
OR5M1	OR5M3	OR5M8	OR5M9	OR5P2
OR5P3	OR5R1	OR5T1	OR5T2	OR5T3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
OR5V1	OR5W2	OR6A2	OR6B1	OR6B3
OR6C1	OR6C2	OR6C3	OR6C4	OR6C6
OR6C65	OR6C68	OR6C70	OR6C74	OR6C75
OR6C76	OR6F1	OR6J1 _HUMAN	OR6K2	OR6K3
OR6K6	OR6M1	OR6N1	OR6N2	OR6P1
OR6Q1	OR6S1	OR6T1	OR6W1 P	OR6X1
OR6Y1	OR7A1 0	OR7A1 7	OR7A5	OR7C1
OR7C2	OR7D2	OR7D4	OR7E24	OR7E5P
OR7G 1	OR7G2	OR7G3	OR8A1	OR8B1 2
OR8B2	OR8B3	OR8B4	OR8B8	OR8D1
OR8D2	OR8D4	OR8H1	OR8H2	OR8H3
OR8I2	OR8J1	OR8J3	OR8K1	OR8K3
OR8K5	OR8S1	OR8U1	OR9A2	OR9A4
OR9G 1	OR9G4	OR9I 1	OR9K2	OR9Q1
OR9Q2	ORAM	ORAI2	ORAI3	ORAOV1
ORC1 L	ORC2L	ORC3L	ORC4L	ORC5L
ORC6L	ORM1	ORM2	ORMDL1	ORMDL2
ORMDL3	OS9	OSBP	OSBP2	OSBPL1 0
OSBPL1 0_ENST00000396556	OSBPL1 1	OSBPL1 A	OSBPL2	OSBPL3
OSBPL5	OSBPL6	OSBPL7	OSBPL8	OSBPL9
OSCAR	OSCP1	OSGEP	OSG IN1	OSGIN2
OSM	OSMR	OSR1	OSR2	OSTC
OSTCL	OSTF1	OSTM1	OSTN	OSTalpha
OSTbeta	OTC	OTOA	OTOF	OTOF _ENST00000361 394
OTOG	OTOP1	OTOP2	OTOP3	OTOR
OTOS	OTP	OTUB1	OTUB2	OTUD1
OTUD3	OTUD4	OTUD5	OTUD5 _ENST00000453548	OTUD6A
OTUD7A	OTUD7B	OTX1	OTX2	OVCH1
OVCH2	OVGP1	OVOL1	OVOL2	OXA1 L
OXCT1	OXCT2	OXER1	OXGR1	OXNAD1
OXR1	OXSM	OXSR1	OXT	OXTR
P1 17	P2RX1	P2RX2	P2RX3	P2RX4
P2RX5	P2RX7	P2RXL1	P2RY1	P2RY1 0
P2RY1 1	P2RY1 2	P2RY1 3	P2RY1 4	P2RY2
P2RY4	P2RY6	P2RY8	P461 _HUMAN	P4HA1
P4HA2	P4HA3	P4HB	P4HTM	P78389 _HUMAN
P78561 _HUMAN	PA2G4	PAAF1	PABPC1	PABPC1 L
PABPC1 L2A	PABPC1 L2B	PABPC3	PABPC4	PABPC5
PABPCP2	PABPN1	PACRG	PACRG L	PACS1
PACS2	PACSIN 1	PACSIN2	PACSIN3	PADI 1
PADI2	PADI3	PADI4	PADI6	PAEP
PAF1	PAFAH1 B 1	PAFAH1 B2	PAFAH1 B3	PAFAH2
PAG1	PAG E 1	PAG E2	PAG E2B	PAG E3
PAG E4	PAG E5	PAH	PAICS	PAI P 1
PAI P2	PAI P2B	PAK1	PAK1 IP 1	PAK2
PAK3	PAK4	PAK6	PAK7	PALB2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PALLD	PALM	PALM2	PALM2-AKAP2	PALMD
PAM	PAMR1	PAN2	PAN3	PANK1
PANK2	PANK3	PANK4	PANX1	PANX2
PANX3	PAOX	PAOX_ENST00000357296	PAP2D	PAPD4
PAPD5	PAPD5_ENSTOO000436909	PAPD7	PAPLN	PAPOLA
PAPOLB	PAPOLG	PAPPA	PAPPA2	PAPSS1
PAPSS2	PAQR3	PAQR4	PAQR5	PAQR6
PAQR7	PAQR8	PAQR9	PARD3	PARD3B
PARD6A	PARD6B	PARD6G	PARG	PARK2
PARK7	PARL	PARP1	PARP10	PARP11
PARP12	PARP14	PARP15	PARP16	PARP2
PARP3	PARP4	PARP6	PARP8	PARP9
PARS2	PARVA	PARVB	PARVG	PASD1
PASK	PATE1	PATE2	PATZ1	PAWR
PAX1	PAX2	PAX3	PAX4	PAX5
PAX6	PAX7	PAX8	PAX9	PAXIP1
PBK	PBLD	PBRM1	PBX1	PBX2
PBX3	PBX4	PBXIP1	PC	PCBD1
PCBD2	PCBP1	PCBP2	PCBP3	PCBP4
PCCA	PCCB	PCDH1	PCDH10	PCDH11X
PCDH11Y	PCDH12	PCDH15	PCDH17	PCDH18
PCDH19	PCDH19_NM_020766_1	PCDH20	PCDH24	PCDH7
PCDH8	PCDH9	PCDHA1	PCDHA10	PCDHA10_ENST00000505235
PCDHA11	PCDHA13	PCDHA2	PCDHA3	PCDHA4
PCDHA5	PCDHA6	PCDHA7	PCDHA8	PCDHA9
PCDHAC1	PCDHAC2	PCDHB1	PCDHB10	PCDHB11
PCDHB12	PCDHB13	PCDHB14	PCDHB15	PCDHB16
PCDHB18	PCDHB2	PCDHB3	PCDHB4	PCDHB5
PCDHB6	PCDHB7	PCDHB8	PCDHGA1	PCDHGA12
PCDHGA12_ENST00000252085	PCDHGA2	PCDHGA3	PCDHGA6	PCDHGB7
PCDHGC3	PCDHGC3_ENST000003081 77	PCDHGC4	PCDHGC5	PCDHGC5_ENST00000252087
PCF11	PCGF1	PCGF2	PCGF3	PCGF5
PCGF6	PCID2	PCIF1	PCK1	PCK2
PCM1	PCMT1	PCMTD1	PCMTD2	PCNA
PCNP	PCNT	PCNX	PCNXL2	PCNXL3
PCOLCE	PCOLCE2	PCP2	PCP4	PCQAP
PCSK1	PCSK1N	PCSK2	PCSK4	PCSK5
PCSK5_ENSTOO000376767	PCSK7	PCSK9	PCTP	PCYOX1
PCYOX1L	PCYT1A	PCYT1B	PCYT2	PDAP1
PDC	PDCD1	PDCD10	PDCD11	PDCD11LG2
PDCD2	PDCD2L	PDCD4	PDCD5	PDCD6
PDCD6IP	PDCD7	PDCD8	PDCL	PDCL3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PDDC1	PDE1 0A	PDE1 1A	PDE1 2	PDE1 A
PDE1 B	PDE1 C	PDE2A	PDE3A	PDE3B
PDE4A	PDE4B	PDE4B _ENST 00000423207	PDE4C	PDE4D
PDE4DI P	PDE5A	PDE6A	PDE6B	PDE6C
PDE6D	PDE6G	PDE6H	PDE7A	PDE7B
PDE8A	PDE8B	PDE9A	PDGFA	PDG FB
PDG FC	PDG FD	PDG FRA	PDGFRB	PDG FRL
PDHA1	PDHA2	PDHB	PDHX	PDIA2
PDIA3	PDIA4	PDIA5	PDIA6	PDIK1 L
PDILT	PDK1	PDK2	PDK3	PDK4
PDLIM1	PDLIM2	PDLIM3	PDLIM4	PDLIM5
PDLIM7	PDP1	PDP2	PDPK1	PDPN
PDPR	PDRG 1	PDS5B	PDSS1	PDSS2
PDX1	PDXDC1	PDXDC2	PDXK	PDXP
PDYN	PDZD1 1	PDZD2	PDZD3	PDZD4
PDZD7	PDZD8	PDZK1	PDZK1 IP 1	PDZRN3
PDZRN4	PEA1 5	PEAR1	PEBP1	PEBP4
PECI	PECR	PEF1	PEG 10	PEG3
PELI 1	PELI2	PELI3	PELO	PELP1
PEMT	PENK	PEPD	PER1	PER2
PER3	PERP	PES1	PET1 12L	PEX1
PEX1 0	PEX1 1A	PEX1 1B	PEX1 1G	PEX1 2
PEX1 3	PEX1 4	PEX1 6	PEX1 9	PEX2
PEX26	PEX3	PEX5	PEX5L	PEX6
PEX7	PF4	PF4V1	PFAS	PFDN1
PFDN2	PFDN4	PFDN5	PFDN6	PFKFB1
PFKFB2	PFKFB3	PFKFB4	PFKL	PFKM
PFKP	PFN1	PFN2	PFN3	PFN4
PGA3	PGA4	PGA5	PGAM1	PGAM1 _HU MAN
PGAM2	PGAM4	PGAM5	PGAP1	PGAP3
PGBD1	PGBD2	PGBD3	PGBD4	PGBD5
PGC	PGCP	PG D	PGF	PGGT1 B
PGK1	PGK2	PGLS	PGLYRP1	PGLYRP2
PGLYRP3	PGLYRP4	PGM1	PGM2	PGM2L1
PGM3	PGM5	PG P	PGPEP1	PG R
PG RMC1	PG RMC2	PGS1	PHACTR2	PHACTR3
PHACTR4	PHAX	PHB	PHC1	PHC1 B
PHC2	PHC3	PHEX	PHF1	PHF1 0
PHF1 1	PHF1 2	PHF1 3	PHF1 4	PHF1 5
PHF1 6	PHF1 7	PHF1 9	PHF2	PHF20
PHF20L1	PHF21 A	PHF21 B	PHF23	PHF3
PHF5A	PHF6	PHF7	PHF8	PHG DH
PHI P	PHKA1	PHKA2	PHKB	PHKG 1
PHKG2	PHLDA1	PHLDA2	PHLDA3	PHLDB1
PHLDB2	PHLDB3	PHLPP	PHLPP2	PHOSPH01
PH0SPH02	PH0X2A	PH0X2B	PHPT1	PHTF1
PHYH	PHYHD1	PHYHI P	PHYHIPL	PI15
PI16	PI3	PI4K2A	PI4K2B	PI4KA

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PI4KAP2	PI4KB	PIAS1	PIAS2	PIAS3
PIAS4	PIBF1	PICALM	PICK1	PID1
PIF1	PIGA	PIGB	PIGC	PIGF
PIGG	PIGH	PIGK	PIGL	PIGM
PIGN	PIGO	PIGP	PIGQ	PIGR
PIGS	PIGT	PIGU	PIGV	PIGW
PIGX	PIGZ	PIH1D1	PIH1D2	PIK3AP1
PIK3C2A	PIK3C2B	PIK3C2G	PIK3C3	PIK3CA
PIK3CB	PIK3CD	PIK3CG	PIK3IP1	PIK3R1
PIK3R2	PIK3R3	PIK3R4	PIK3R5	PIKFYVE
PILRA	PILRB	PIM1	PIM2	PIM3
PIN1	PIN4	PINK1	PINX1	PION
PIP	PIP4K2A	PIP4K2B	PIP4K2C	PIP5K1A
PIP5K1B	PIP5K1C	PIP5KL1	PIPOX	PIR
PISD	PITPNA	PITPNB	PITPNC1	PITPNM1
PITPNM2	PITPNM3	PITRM1	PITX1	PITX2
PITX3	PIWIL1	PIWIL2	PIWIL3	PIWIL4
PJA1	PJA2	PKD1	PKD1L1	PKD1L2
PKD1L2_ENSTO0000360678	PKD1L3	PKD2	PKD2L1	PKD2L2
PKDREJ	PKHD1	PKHD1L1	PKIA	PKIB
PKIG	PKLR	PKM2	PKMYT1	PKN1
PKN2	PKN3	PKNOX1	PKNOX2	PKP1
PKP2	PKP3	PKP4	PLA1A	PLA2G10
PLA2G12A	PLA2G12B	PLA2G15	PLA2G16	PLA2G1B
PLA2G2A	PLA2G2C	PLA2G2D	PLA2G2E	PLA2G2F
PLA2G3	PLA2G4A	PLA2G4C	PLA2G4D	PLA2G4F
PLA2G5	PLA2G6	PLA2G7	PLA2R1	PLAA
PLAC1	PLAC1L	PLAC8	PLAC8L1	PLAC9
PLAG1	PLAGL1	PLAGL2	PLAT	PLAU
PLAUR	PLB1	PLBD1	PLBD2	PLCB1
PLCB2	PLCB3	PLCB4	PLCD1	PLCD3
PLCD4	PLCE1	PLCG1	PLCG2	PLCH1
PLCH2	PLCL1	PLCL2	PLCXD1	PLCXD2
PLCXD3	PLCZ1	PLD1	PLD2	PLD3
PLD4	PLD5	PLD6	PLDN	PLEC
PLEK	PLEK2	PLEKHA1	PLEKHA3	PLEKHA4
PLEKHA5	PLEKHA5_ENST00000429027	PLEKHA6	PLEKHA7	PLEKHA8
PLEKHA9	PLEKHB1	PLEKHB2	PLEKHF1	PLEKHF2
PLEKHG1	PLEKHG2	PLEKHG3	PLEKHG4	PLEKHG4B
PLEKHG4B_ENST00000283426	PLEKHG5	PLEKHG6	PLEKHG7	PLEKHH1
PLEKHH2	PLEKHH3	PLEKHJ1	PLEKHM1	PLEKHN1
PLEKH01	PLEKH02	PLG	PLGLB1	PLGLB2
PLIN1	PLIN2	PLIN3	PLIN4	PLIN5
PLK1	PLK2	PLK3	PLK4	PLLP
PLN	PLOD1	PLOD2	PLOD3	PLP1
PLP2	PLRG1	PLS1	PLS3	PLSCR1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PLSCR2	PLSCR3	PLSCR3_ENST00000324822	PLSCR4	PLTP
PLUNC	PLVAP	PLXDC1	PLXDC2	PLXNA1
PLXNA2	PLXNA3	PLXNA4	PLXNB1	PLXNB2
PLXNB3	PLXNC1	PLXND1	PM20D1	PM20D2
PMAIP1	PMCH	PMEPA1	PMF1	PMFBP1
PML	PMM1	PMM2	PMP2	PMP22
PMPCA	PMPCB	PMS1	PMS2	PMS2L1
PMS2L11	PMS2L3	PMS2L4	PMS2L5	PMVK
PNCK	PNKD	PNKP	PNLDC1	PNLIP
PNLIPRP1	PNLIPRP2	PNLIPRP3	PNMA1	PNMA2
PNMA3	PNMA5	PNMA6A	PNMAL1	PNMAL2
PNMT	PNN	PN01	PNOC	PNP
PNPLA1	PNPLA2	PNPLA3	PNPLA4	PNPLA5
PNPLA6	PNPLA7	PNPLA8	PNPO	PNPT1
PNRC1	PNRC2	PODN	PODNL1	PODXL
P0DXL2	POF1B	POFUT1	POFUT2	POGK
POGZ	POL3S	POLA1	POLA2	POLB
POLD1	POLD2	POLD3	POLD4	POLDIP3
POLE	POLE2	POLE3	POLE4	POLG
POLG2	POLH	POLI	POLK	POLL
POLM	POLN	POLO	POLR1A	POLR1B
POLR1C	POLR1D	POLR1E	POLR2A	POLR2B
POLR2C	POLR2D	POLR2E	POLR2F	POLR2G
POLR2H	POLR2I	POLR2J	POLR2J2	POLR2K
POLR2L	POLR3A	POLR3B	POLR3C	POLR3D
POLR3E	POLR3F	POLR3G	POLR3GL	POLR3H
POLR3K	POLRMT	POM121	POM121L3	POMC
POMGNT1	POMP	POMT1	POMT2	POMZP3
PON1	PON2	PON3	POP1	POP4
POP5	POP7	POPDC2	POPDC3	POR
PORCN	POSTN	POT1	POT14_HUMAN	POTE2_HUMAN
POTEA	POTEB	POTED	POTEF	POTEG
POU1F1	POU2AF1	POU2F1	POU2F2	POU2F3
POU3F1	POU3F2	POU3F3	POU3F4	POU4F1
POU4F2	POU4F3	POU5F1	POU6F1	POU6F2
PPA1	PPA2	PPAN	PPAN-P2RY11	PPAP2A
PPAP2B	PPAP2C	PPAPDC1A	PPAPDC2	PPAPDC3
PPARA	PPARD	PPARG	PPARGC1A	PPARGC1B
PPAT	PPBP	PPCDC	PPCS	PPDPF
PPEF1	PPEF2	PPFIA1	PPFIA2	PPFIA3
PPFIA4	PPFIBP1	PPFIBP2	PPHLN1	PPIA
PPIAL4A	PPIAL4G	PPIA_HUMAN	PPIB	PPIC
PPID	PPIE	PPIF	PPIG	PPIH
PPIL1	PPIL2	PPIL3	PPIL4	PPIL5
PPIL6	PPIP5K1	PPIP5K2	PPL	PPM1A
PPM1B	PPM1D	PPM1E	PPM1F	PPM1G
PPM1H	PPM1J	PPM1K	PPM1L	PPOX
PPP1CA	PPP1CB	PPP1CC	PPP1R10	PPP1R11

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PPP1 R12A	PPP1 R12B	PPP1 R12C	PPP1 R13B	PPP1 R13L
PPP1 R14A	PPP1 R14B	PPP1 R14C	PPP1 R14D	PPP1 R15A
PPP1 R15B	PPP1 R16A	PPP1 R16B	PPP1 R1A	PPP1 R1B
PPP1 R1C	PPP1 R2	PPP1 R2P9	PPP1 R3A	PPP1 R3B
PPP1 R3C	PPP1 R3D	PPP1 R3E	PPP1 R3F	PPP1 R3G
PPP1 R7	PPP1 R8	PPP1 R9A	PPP1 R9B	PPP2CA
PPP2CB	PPP2R1 A	PPP2R1 B	PPP2R2A	PPP2R2B
PPP2R2C	PPP2R2D	PPP2R3A	PPP2R3B	PPP2R3C
PPP2R4	PPP2R5A	PPP2R5B	PPP2R5C	PPP2R5D
PPP2R5E	PPP3CA	PPP3CB	PPP3CC	PPP3R1
PPP3R2	PPP4C	PPP4R1	PPP4R1 L	PPP4R2
PPP4R4	PPP5C	PPP6C	PPPDE1	PPPDE2
PPRC1	PPT1	PPT2	PPTC7	PPWD1
PPY	PPYR1	PQBP1	PQLC1	PQLC2
PQLC3	PRAF2	PRAME	PRAMEF1	PRAMEF1 0
PRAMEF1 2	PRAMEF1 3	PRAMEF1 4	PRAMEF1 6	PRAMEF1 7
PRAMEF1 8	PRAMEF1 9	PRAMEF2	PRAMEF20	PRAMEF21
PRAMEF22	PRAMEF3	PRAMEF4	PRAMEF5	PRAMEF6
PRAMEF7	PRAMEF8	PRAMEF9	PRAMEL	PRAP1
PRB1	PRB2	PRB4	PRC1	PRCC
PRCC _ENSTOOO 00353233	PRCD	PRCP	PRDM1	PRDM1 0
PRDM1 1	PRDM1 2	PRDM1 3	PRDM1 4	PRDM1 5
PRDM1 6	PRDM2	PRDM4	PRDM5	PRDM7
PRDM8	PRDM9	PRDX1	PRDX2	PRDX3
PRDX4	PRDX5	PRDX6	PREB	PRELI D1
PRELI D2	PRELP	PREP	PREPL	PREX1
PREX2	PRF1	PRG-3	PRG2	PRG3
PRG4	PRH2	PRIC285	PRICKLE1	PRICKLE2
PRICKLE3	PRICKLE4	PRIM2	PRIMA1	PRKAA1
PRKAA2	PRKAA2 _ENSTO 0000371 244	PRKAB1	PRKAB2	PRKACA
PRKACB	PRKACB _ENSTO 0000370685	PRKACG	PRKAG 1	PRKAG2
PRKAG3	PRKAR1 A	PRKAR1 B	PRKAR2A	PRKAR2B
PRKCA	PRKCB	PRKCD	PRKCDBP	PRKCE
PRKCG	PRKCH	PRKCI	PRKCQ	PRKCSH
PRKCZ	PRKD1	PRKD1 _ENST 00000331 968	PRKD2	PRKD3
PRKDC	PRKG 1	PRKG2	PRKRA	PRKRI P1
PRKRI R	PRKX	PRKY	PRL	PRLH
PRLHR	PRLR	PRM1	PRM2	PRMT1
PRMT1 0	PRMT2	PRMT3	PRMT5	PRMT6
PRMT7	PRMT8	PRND	PRNP	PRO1 073
PROC	PROCA1	PROCR	PRODH	PRODH2
PROK1	PROK2	PROKR1	PROKR2	PROL1
PROM1	PROM2	PROP1	PROS1	PROSC
PROX1	PROX2	PROZ	PRPF1 8	PRPF1 9
PRPF3	PRPF31	PRPF38A	PRPF38B	PRPF39

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PRPF4	PRPF40A	PRPF40B	PRPF4B	PRPF4B _ENST00000337659
PRPF6	PRPF8	PRPH	PRPH2	PRPS1
PRPS2	PRPSAP1	PRPSAP2	PRR1 1	PRR1 2
PRR1 3	PRR1 4	PRR1 5	PRR1 5L	PRR1 6
PRR1 8	PRR1 9	PRR20A	PRR21	PRR22
PRR23B	PRR23C	PRR25	PRR3	PRR4
PRR5	PRR5-ARHGAP8	PRR5L	PRR5 _ENSTOO0004321 86	PRR7
PRR8	PRRC1	PRRG 1	PRRG2	PRRG3
PRRG4	PRRT1	PRRT2	PRRT3	PRRX1
PRRX2	PRSS1	PRSS1 2	PRSS1 6	PRSS2
PRSS21	PRSS22	PRSS23	PRSS27	PRSS3
PRSS33	PRSS35	PRSS36	PRSS37	PRSS38
PRSS42	PRSS50	PRSS7	PRSSL1	PRTFDC1
PRTG	PRTN3	PRUN E	PRUNE2	PRUN E2_ENST00000376718
PRX	PRY	PRY2	PSAP	PSAPL1
PSAT1	PSD	PSD2	PSD3	PSD4
PSD_ENSTOOOO0020673	PSEN1	PSEN2	PSEN EN	PSG1
PSG1 _ENST0000031 2439	PSG2	PSG3	PSG4	PSG5
PSG6	PSG8	PSG9	PSI P 1	PSI P 1_ENST00000380733
PSKH1	PSKH2	PSMA1	PSMA2	PSMA3
PSMA4	PSMA5	PSMA6	PSMA7	PSMA8
PSMB1	PSMB1 0	PSMB2	PSMB3	PSMB4
PSMB5	PSMB6	PSMB7	PSMB8	PSMB9
PSMC1	PSMC2	PSMC3	PSMC3I P	PSMC4
PSMC5	PSMC6	PSMD1	PSMD1 0	PSMD1 1
PSMD1 2	PSMD1 3	PSMD1 3_ENST00000431 206	PSMD2	PSMD3
PSMD4	PSMD5	PSMD6	PSMD7	PSMD8
PSMD9	PSME1	PSME2	PSME3	PSME4
PSMF1	PSMG1	PSMG2	PSMG3	PSORS1 C 1
PSORS1 C2	PSPC1	PSPH	PSPN	PSRC1
PSTK	PSTPI P2	PTAFR	PTAR1	PTBP1
PTBP2	PTCD1	PTCD2	PTCD3	PTCH1
PTCH1 _ENSTOO000331 920	PTCH2	PTCHD1	PTCHD2	PTCHD3
PTCRA	PTDSS1	PTDSS2	PTEN	PTER
PTF1 A	PTG DR	PTG DS	PTGER1	PTG ER2
PTG ER3	PTG ER4	PTG ES	PTGES2	PTG ES3
PTG FR	PTG FRN	PTG FR_ENST00000370758	PTGI R	PTG IS
PTG R 1	PTGS1	PTGS2	PTH	PTH1 R
PTH2	PTH2R	PTHLH	PTK2	PTK2B

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
PTK2B_ENSTOO 000397497	PTK6	PTK7	PTMA	PTMS
PTN	PTOV1	PTP4A1	PTP4A2	PTP4A3
PTPDC1	PTPLA	PTPLAD1	PTPLAD2	PTPLB
PTPMT1	PTPN1	PTPN1 1	PTPN1 2	PTPN1 3
PTPN1 4	PTPN1 8	PTPN2	PTPN20A	PTPN20B
PTPN21	PTPN22	PTPN23	PTPN3	PTPN4
PTPN5	PTPN6	PTPN7	PTPN9	PTPRA
PTPRB	PTPRB_ENSTOO 00033441 4	PTPRC	PTPRCAP	PTPRD
PTPRE	PTPRF	PTPRG	PTPRH	PTPRJ
PTPRK	PTPRM	PTPRN	PTPRN2	PTPRO
PTPRR	PTPRS	PTPRT	PTPRU	PTPRZ1
PTRF	PTRH1	PTRH2	PTS	PTTG1
PTTG1 IP	PTX3	PUM1	PUM2	PURA
PURB	PURG	PURG_ENSTO 0000475541	PUS1	PUS1 0
PUS3	PUS7	PUS7L	PUSL1	PVALB
PVR	PVRIG	PVRL1	PVRL2	PVRL3
PVRL4	PW P 1	PW P2	PWWP2A	PWWP2B
PXDN	PXDNL	PXK	PXMP2	PXMP4
PXN	PXT1	PYCARD	PYCR1	PYCR2
PYCRL	PYDC1	PYGB	PYGL	PYGM
PYG01	PYG02	PYHIN1	PYROXD1	PYROXD2
PYY	PYY3	PZP	ProSAPi PI	QOVFXO_HU MAN
Q 13034_HUMAN	Q 13209_HUMAN	Q 15202_HUM AN	Q 16370_HUM AN	Q 1A5X8_HU MAN
Q2M2F3_HUMA N	Q2QD04_HUMA N	Q2VIK4_HUMA N	Q2VIK8_HUMA N	Q2VIL1_HU MAN
Q3SX88_HUMA N	Q3ZCN4_HUMA N	Q49A61_HUM AN	Q49AQ9_HUM AN	Q4G0P5_HU MAN
Q4G0S1_HUMA N	Q4G 129_HUMA N	Q4G 197_HUM AN	Q4TT42_HUM AN	Q4VXG5_HU MAN
Q4VXZ3_HUMA N	Q5I0X0_HUMAN	Q5JSM7_HUM AN	Q5JUV9_HUM AN	Q5JV89_HU MAN
Q5JX50_HUMAN	Q5JXA8_HUMA N	Q5JY96_HUM AN	Q5JYU7_HUM AN	Q5SWJ0_HU MAN
Q5T344_HUMAN	Q5T669_HUMAN	Q5T6S7_HUM AN	Q5T740_HUM AN	Q5T7C0_HU MAN
Q5T909_HUMAN	Q5TBE2_HUMA N	Q5TFB2_HUM AN	Q5VVH2_HUM AN	Q5VZ27_HU MAN
Q5VZ43_HUMAN	Q5W1 B9_HUMA N	Q69YG7_HUM AN	Q69YJ1_HUM AN	Q6AI01_HU MAN
Q6AI40_HUMAN	Q6GMT2_HUMA N	Q6I955_HUMA N	Q6IPT3_HUMA N	Q6NSH2_HU MAN
Q6NUR6_HUMA N	Q6NZ63_HUMA N	Q6P094_HUM AN	Q6P462_HUM AN	Q6PEB8_HU MAN
Q6RG F6_HUMA N	Q6TXQ4_HUMA N	Q6UXU0_HUM AN	Q6VEP2_HUM AN	Q6YL47_HU MAN

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
Q6ZMS4_HUMAN	Q6ZNB5_HUMAN	Q6ZNL0_HUMAN	Q6ZNV0_HUMAN	Q6ZQP8_HUMAN
Q6ZQU9_HUMAN	Q6ZRG5_HUMAN	Q6ZRP8_HUMAN	Q6ZRU5_HUMAN	Q6ZSP4_HUMAN
Q6ZSU1_HUMAN	Q6ZSY1_HUMAN	Q6ZTY5_HUMAN	Q6ZU04_HUMAN	Q6ZU24_HUMAN
Q6ZUD9_HUMAN	Q6ZUG5_HUMAN	Q6ZUQ5_HUMAN	Q6ZUR4_HUMAN	Q6ZUS2_HUMAN
Q6ZV46_HUMAN	Q6ZV65_HUMAN	Q6ZV72_HUMAN	Q6ZVE3_HUMAN	Q6ZVS6_HUMAN
Q6ZW54_HUMAN	Q6ZWB7_HUMAN	Q6ZWC0_HUMAN	Q71RG6_HUMAN	Q75L30_HUMAN
Q75MH1_HUMAN	Q75MM1_HUMAN	Q76B61_HUMAN	Q7M4M3_HUMAN	Q7Z2M6_HUMAN
Q7Z2Q7_HUMAN	Q7Z2S2_HUMAN	Q7Z3M5_HUMAN	Q7Z4Q0_HUMAN	Q7Z4S1_HUMAN
Q7Z5Z2_HUMAN	Q7Z7K7_HUMAN	Q86TT0_HUMAN	Q86TU9_HUMAN	Q86U10_HUMAN
Q86U47_HUMAN	Q86U89_HUMAN	Q86V52_HUMAN	Q86V94_HUMAN	Q86VG7_HUMAN
Q86X61_HUMAN	Q86XG0_HUMAN	Q86Y87	Q86YR2_HUMAN	Q86YX8_HUMAN
Q8IVE0_HUMAN	Q8IVF9_HUMAN	Q8IVN4_HUMAN	Q8IVR1_HUMAN	Q8IXE5_HUMAN
Q8IXE7_HUMAN	Q8IXV1_HUMAN	Q8MH63_HUMAN	Q8N0U1_HUMAN	Q8N0W1_HUMAN
Q8N164_HUMAN	Q8N1B8_HUMAN	Q8N1G8_HUMAN	Q8N1I6_HUMAN	Q8N1L4_HUMAN
Q8N1R6_HUMAN	Q8N1T0_HUMAN	Q8N1X6_HUMAN	Q8N214_HUMAN	Q8N266_HUMAN
Q8N2D2_HUMAN	Q8N2E2_HUMAN	Q8N2W8_HUMAN	Q8N3U1_HUMAN	Q8N4W5_HUMAN
Q8N5Q1_HUMAN	Q8N642_HUMAN	Q8N646_HUMAN	Q8N6L5_HUMAN	Q8N6V7_HUMAN
Q8N6X1_HUMAN	Q8N6X9_HUMAN	Q8N799_HUMAN	Q8N7D3_HUMAN	Q8N7N0_HUMAN
Q8N7N2_HUMAN	Q8N7P5_HUMAN	Q8N7Q6_HUMAN	Q8N7Z9_HUMAN	Q8N800_HUMAN
Q8N811_HUMAN	Q8N822_HUMAN	Q8N843_HUMAN	Q8N849_HUMAN	Q8N867_HUMAN
Q8N8C5_HUMAN	Q8N8C9_HUMAN	Q8N8F0_HUMAN	Q8N8H9_HUMAN	Q8N8K0_HUMAN
Q8N8P5_HUMAN	Q8N8S3_HUMAN	Q8N8S4_HUMAN	Q8N950_HUMAN	Q8N997_HUMAN
Q8N9F6_HUMAN	Q8N9G5_HUMAN	Q8N9G9_HUMAN	Q8N9H1_HUMAN	Q8N9I1_HUMAN
Q8N9J4_HUMAN	Q8N9K3_HUMAN	Q8N9Z1_HUMAN	Q8N9Z5_HUMAN	Q8NA17_HUMAN
Q8NA34_HUMAN	Q8NAG9_HUMAN	Q8NAP4_HUMAN	Q8NAP5_HUMAN	Q8NAQ8_HUMAN

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
Q8NAT4_HUMAN	Q8NAV9_HUMAN	Q8NAZ9_HUMAN	Q8NB20_HUMAN	Q8NB83_HUMAN
Q8NBE0_HUMAN	Q8NCA1_HUMAN	Q8NCK2_HUMAN	Q8NEQ2_HUMAN	Q8NFX8_HUMAN
Q8NGC8_HUMAN	Q8NGD7_HUMAN	Q8NGE6_HUMAN	Q8NGF2_HUMAN	Q8NGG1_HUMAN
Q8NGK8_HUMAN	Q8NGM0_HUMAN	Q8NGM4_HUMAN	Q8NGM6_HUMAN	Q8NGP1_HUMAN
Q8NGP5_HUMAN	Q8NGP7_HUMAN	Q8NGQ7_HUMAN	Q8NGY4_HUMAN	Q8NH06_HUMAN
Q8NH08_HUMAN	Q8NH11_HUMAN	Q8NH32_HUMAN	Q8NH33_HUMAN	Q8NH46_HUMAN
Q8NH47_HUMAN	Q8NH58_HUMAN	Q8NH68_HUMAN	Q8NH71_HUMAN	Q8NH75_HUMAN
Q8NH77_HUMAN	Q8NH80_HUMAN	Q8NH82_HUMAN	Q8NH88_HUMAN	Q8NH95_HUMAN
Q8NH98_HUMAN	Q8NHA6_HUMAN	Q8NHB0_HUMAN	Q8NHB3_HUMAN	Q8NHB5_HUMAN
Q8NHC0_HUMAN	Q8NHC1_HUMAN	Q8NHC2_HUMAN	Q8TAF5_HUMAN	Q8TBR1_HUMAN
Q8TCI8_HUMAN	Q8TDK1_HUMAN	Q8TDP9_HUMAN	Q8TE05_HUMAN	Q8WM95_HUMAN
Q8WTY6_HUMAN	Q8WYW5_HUMAN	Q8WYX1_HUMAN	Q8WZ27_HUMAN	Q8WZ91
Q96AM0_HUMAN	Q96CK5_HUMAN	Q96DR3_HUMAN	Q96HF5_HUMAN	Q96HZ0_HUMAN
Q96IP2_HUMAN	Q96K91_HUMAN	Q96M56_HUMAN	Q96M66_HUMAN	Q96M92_HUMAN
Q96MC4_HUMAN	Q96MT0_HUMAN	Q96MZ3_HUMAN	Q96NE0_HUMAN	Q96NP5_HUMAN
Q96PS2_HUMAN	Q96PS6_HUMAN	Q96QE0_HUMAN	Q96RF1_HUMAN	Q96RI3_HUMAN
Q96RW6_HUMAN	Q96RY6_HUMAN	Q96RY9_HUMAN	Q99543-2	Q9BRP9_HUMAN
Q9BSD4_HUMAN	Q9BSM8_HUMAN	Q9BSY8_HUMAN	Q9BVW6_HUMAN	Q9BVX4_HUMAN
Q9BZU6_HUMAN	Q9C0K3_HUMAN	Q9GZQ9_HUMAN	Q9H2C7_HUMAN	Q9H354_HUMAN
Q9H4I0_HUMAN	Q9H521_HUMAN	Q9H5Q3_HUMAN	Q9H614_HUMAN	Q9H693_HUMAN
Q9H6A9_HUMAN	Q9H6K5_HUMAN	Q9H6S2_HUMAN	Q9H6Z8_HUMAN	Q9H8C5_HUMAN
Q9H8D1_HUMAN	Q9H960_HUMAN	Q9HAB5_HUMAN	Q9HAC4_HUMAN	Q9HAD2_HUMAN
Q9HAJ0_HUMAN	Q9HAZ8_HUMAN	Q9HBS9_HUMAN	Q9NQ39_HUMAN	Q9NRE4_HUMAN
Q9NRE7_HUMAN	Q9NSI3_HUMAN	Q9NSQ0_HUMAN	Q9NT31_HUMAN	Q9NU36_HUMAN
Q9NW32_HUMAN	Q9NWP0_HUMAN	Q9NYD3_HUMAN	Q9NYS9_HUMAN	Q9NZ01-2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
Q9P0C7_HUMAN	Q9P143_HUMAN	Q9P147_HUMAN	Q9P156_HUMAN	Q9P184_HUMAN
Q9P1D0_HUMAN	Q9P1G6_HUMAN	Q9P1L5_HUMAN	Q9P1M5_HUMAN	Q9P2A3_HUMAN
Q9UHU1_HUMAN	Q9UHU9_HUMAN	Q9UI72_HUMAN	Q9UJN8_HUMAN	Q9UK71_HUMAN
Q9Y6V0-3	QARS	QDPR	QKI	QPCT
QPCTL	QPRT	QRFP	QRFPR	QRICH1
QRICH2	QRSL1	QSER1	QS0X1	QS0X2
QTRT1	QTRTD1	R3HCC1	R3HDM1	R3HDM2
R3HDML	RAB10	RAB11A	RAB11B	RAB11FIP1
RAB11FIP2	RAB11FIP3	RAB11FIP4	RAB11FIP5	RAB12
RAB13	RAB14	RAB15	RAB17	RAB18
RAB19	RAB19B	RAB1A	RAB1B	RAB20
RAB21	RAB22A	RAB23	RAB24	RAB25
RAB26	RAB27A	RAB27B	RAB28	RAB2A
RAB2B	RAB30	RAB31	RAB32	RAB33A
RAB33B	RAB34	RAB35	RAB36	RAB37
RAB38	RAB39	RAB39B	RAB3A	RAB3B
RAB3C	RAB3D	RAB3GAP1	RAB3GAP2	RAB3IL1
RAB3IP	RAB40A	RAB40AL	RAB40B	RAB40C
RAB41	RAB42	RAB43	RAB44	RAB4A
RAB4B	RAB5A	RAB5B	RAB5C	RAB6A
RAB6B	RAB6C	RAB7A	RAB7L1	RAB8A
RAB8B	RAB9A	RAB9B	RABACI	RABEP1
RABEP2	RABEPK	RABGAP1	RABGAP1L	RABGEF1
RABGGTB	RABIF	RABL2A	RABL2B	RABL3
RABL4	RABL5	RAC1	RAC1P4	RAC2
RAC3	RACGAP1	RAD1	RAD17	RAD18
RAD21	RAD23A	RAD23B	RAD50	RAD51
RAD51AP1	RAD51AP2	RAD51C	RAD51L1	RAD51L3
RAD52	RAD54B	RAD54L	RAD54L2	RAD9A
RAD9B	RADIL	RAE1	RAET1E	RAET1G
RAET1L	RAF1	RAG1	RAG1AP1	RAG2
RAGE	RAM	RAM4	RAM6	RAI2
RALA	RALB	RALBP1	RALGAPA1	RALGAPB
RALGDS	RALGPS1	RALGPS2	RALY	RAMP1
RAMP2	RAMP3	RAN	RANBP1	RANBP10
RANBP17	RANBP2	RANBP3	RANBP3L	RANBP6
RANBP9	RANGAP1	RANGRF	RAP1A	RAP1B
RAP1GAP	RAP1GAP_ENST00000374761	RAP1GDS1	RAP2A	RAP2B
RAP2C	RAPGEF1	RAPGEF2	RAPGEF3	RAPGEF4
RAPGEF5	RAPGEF5_ENST00000344041	RAPGEF6	RAPGEFL1	RAPH1
RAPSN	RARA	RARB	RARG	RARRES1
RARRES2	RARRES3	RARS	RARS2	RASA1
RASA2	RASA3	RASA4	RASAL1	RASAL2
RASD1	RASD2	RASEF	RASGEF1A	RASGEF1B
RASGEF1C	RASGRF1	RASGRF2	RASGRP1	RASGRP2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
RASGRP3	RASGRP4	RASIP1	RASL10A	RASL10B
RASL11A	RASL11B	RASL12	RASL2_HUMAN	RASSF1
RASSF2	RASSF3	RASSF4	RASSF5	RASSF5_ENST00000304534
RASSF6	RASSF7	RASSF8	RAVER1	RAVER2
RAX	RAX2	RB1	RB1CC1	RBAK
RBBP4	RBBP5	RBBP6	RBBP7	RBBP8
RBBP9	RBCK1	RBKS	RBL1	RBL2
RBM10	RBM12	RBM12B	RBM14	RBM15
RBM15B	RBM16	RBM17	RBM18	RBM19
RBM22	RBM23	RBM24	RBM25	RBM26
RBM27	RBM28	RBM3	RBM34	RBM34_ENST00000408888
RBM39	RBM4	RBM41	RBM42	RBM43
RBM45	RBM46	RBM47	RBM4B	RBM5
RBM6	RBM7	RBM8A	RBM9	RBMS1
RBMS2	RBMS3	RBMX	RBMX2	RBMXL2
RBMY1A1	RBMY1B	RBMY1D	RBMY1E	RBMY1F
RBMY1J	RBP1	RBP2	RBP3	RBP4
RBP5	RBP7	RBPJ	RBPJL	RBPMS
RBPMS2	RBX1	RC3H1	RC3H2	RCAN1
RCAN2	RCAN3	RCBTB1	RCBTB2	RCC1
RCC2	RCCD1	RCE1	RCHY1	RCL1
RCN1	RCN2	RCN3	RC0R1	RC0R2
RCOR3	RCSD1	RCVRN	RD3	RDBP
RDH10	RDH11	RDH12	RDH13	RDH14
RDH16	RDH5	RDH8	RDM1	RDX
REC8	RECK	RECQL	RECQL4	RECQL5
REEP1	REEP2	REEP4	REEP5	REEP6
REEP6_ENSTOO000395484	REG1A	REG1B	REG3A	REG3G
REG4	REL	RELA	RELB	RELL1
RELL2	RELN	RELT	REM1	REM2
REN	RENBP	RENBP_ENST00000393700	REP15	REPIN1
REPS1	REPS2	RER1	RERE	RERG
RERGL	RESP18	REST	RET	RETN
RETNLB	RETSAT	REV1	REV3L	REX01
REX02	REX04	RFC1	RFC2	RFC3
RFC4	RFC5	RFESD	RFFL	RFK
RFNG	RFPL1	RFPL2	RFPL3	RFPL4A
RFPL4B	RFT1	RFTN1	RFTN2	RFWD2
RFWD3	RFX1	RFX2	RFX3	RFX4
RFX5	RFX6	RFX7	RFXANK	RFXAP
RG9MTD1	RG9MTD2	RG9MTD3	RGAG1	RGAG4
RGL1	RGL2	RGL3	RGL3_ENSTOO000380456	RGL4
RGMA	RGN	RGPD2	RGPD5	RGPD6

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
RGPD7	RGR	RGS1	RGS1 0	RGS1 1
RGS1 2	RGS1 3	RGS1 4	RGS1 6	RGS1 7
RGS1 8	RGS1 9	RGS2	RGS20	RGS21
RGS22	RGS3	RGS4	RGS5	RGS6
RGS7	RGS7BP	RGS8	RGS9	RGS9BP
RGSL1	RGSL2	RHAG	RHBDD1	RHBDD2
RHBDD3	RHBDF1	RHBDF2	RHBDL1	RHBDL2
RHBDL3	RHBG	RHCE	RHCG	RHD
RHEB	RHEBL1	RHO	RHOA	RHOB
RHOBTB1	RHOBTB2	RHOBTB3	RHOC	RHOD
RHOF	RHOG	RHOH	RHOJ	RHOQ
RHOT1	RHOT2	RHOU	RHOV	RHOXF1
RHOXF2	RHOXF2B	RHPN1	RHPN2	RIBC1
RIBC2	RIC3	RIC8A	RIC8B	RICTOR
RIF1	RILP	RILPL2	RIMBP2	RIMKLA
RIMS1	RIMS2	RIMS2_ENSTO 0000436393	RIMS3	RIMS4
RIN1	RIN2	RIN3	RING1	RINL
RINT1	RIOK1	RIOK2	RIOK3	RIPK1
RIPK2	RIPK3	RIPK4	RIPPLY1	RIPPLY2
RIT1	RIT2	RL17_HUMAN	RL41_HUMAN	RLBP1
RLBP1L1	RLF	RLIM	RLN1	RLN2
RLN3	RLTPR	RLTPR_ENST 00000334583	RMI1	RMND1
RMND5A	RMND5B	RNASE1	RNASE10	RNASE11
RNASE12	RNASE13	RNASE2	RNASE3	RNASE4
RNASE6	RNASE7	RNASE8	RNASE9	RNASEH1
RNASEH2A	RNASEH2B	RNASEH2C	RNASEK	RNASEL
RNASEN	RNASET2	RND1	RND2	RND3
RNF10	RNF103	RNF11	RNF111	RNF112
RNF113A	RNF113B	RNF114	RNF115	RNF121
RNF122	RNF123	RNF125	RNF126	RNF128
RNF13	RNF130	RNF133	RNF134	RNF135
RNF138	RNF139	RNF14	RNF141	RNF144A
RNF144B	RNF145	RNF146	RNF148	RNF149
RNF150	RNF151	RNF152	RNF157	RNF160
RNF165	RNF166	RNF167	RNF168	RNF169
RNF17	RNF170	RNF180	RNF181	RNF182
RNF183	RNF185	RNF186	RNF187	RNF19A
RNF19B	RNF2	RNF20	RNF207	RNF208
RNF212	RNF213	RNF214	RNF215	RNF216
RNF217	RNF219	RNF220	RNF222	RNF24
RNF25	RNF26	RNF31	RNF32	RNF34
RNF38	RNF39	RNF4	RNF40	RNF41
RNF43	RNF44	RNF5	RNF6	RNF7
RNF8	RNFT1	RNGTT	RNH1	RNLS
RNMT	RNMTL1	RNPEP	RNPEPL1	RNPS1
ROBLD3	ROB01	ROB01_ENST 00000305299	ROB02	ROB03
ROB04	ROCK1	ROCK2	ROD1	ROGDI

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ROM1	ROM01	ROPN1	ROPN1 B	ROPN1 L
ROR1	ROR2	RORA	RORB	RORC
ROS1	RP1	RP1-19N1_1	RP1-210 18_1_NEW	RP1-241 P17_4
RP1-3211 0.10	RP1 1-274K13_2	RP1 1-45B20_2	RP1 1-5291 10_4	RP1 1-551 L14.1
RP1 1-9816_3	RP1 3-218H24_1	RP1 3-36C9_1	RP1 L1	RP2
RP3-364I1_1	RP3-402G1_1_5	RP3-527F8_2	RP4-545K1 5_3	RP4-765F1 3_3
RP5-1 1391 1_4	RP6-149D1 7_1	RP9	RPA1	RPA2
RPA2_ENSTOOO0031 3433	RPA3	RPA4	RPAIN	RPAP1
RPAP2	RPAP3	RPE	RPE65	RPF1
RPF2	RPG R	RPGRI P1	RPG RIP1L	RPH3A
RPH3AL	RPIA	RPL1 0	RPL1 0A	RPL1 0AP3
RPL1 0L	RPL1 1	RPL1 2	RPL1 3	RPL1 3A
RPL1 3AP25	RPL1 4	RPL1 4P5	RPL1 5	RPL1 7P39
RPL1 8	RPL1 8A	RPL1 9	RPL21	RPL21 P128
RPL21 P20	RPL21 P44	RPL22	RPL23	RPL23A
RPL23AP82	RPL24	RPL26	RPL26L1	RPL27
RPL27A	RPL27AP6	RPL28	RPL29	RPL29P1 2
RPL3	RPL30	RPL31	RPL32	RPL32P3
RPL32P36	RPL34	RPL35	RPL35A	RPL35P1
RPL36	RPL36A	RPL36AL	RPL36P1 4	RPL37
RPL37A	RPL38	RPL39	RPL39L	RPL3L
RPL4	RPL41	RPL5	RPL6	RPL7
RPL7A	RPL7L1	RPL8	RPL9	RPL9P7
RPLPO	RPLP1	RPLP1 P3	RPLP2	RPN1
RPN2	RPP1 4	RPP21	RPP25	RPP30
RPP38	RPP40	RPRD1 A	RPRD1 B	RPRM
RPRML	RPS1 0	RPS1 1	RPS1 2	RPS1 3
RPS1 4	RPS1 5	RPS1 5A	RPS1 5P4	RPS1 6
RPS1 7	RPS1 8	RPS1 9	RPS1 9BP1	RPS2
RPS20	RPS20P1 4	RPS21	RPS23	RPS24
RPS25	RPS26	RPS26P1 1	RPS26P3	RPS27
RPS27A	RPS27AP1 7	RPS27L	RPS28	RPS29
RPS2P55	RPS3	RPS3A	RPS3AP6	RPS4X
RPS4Y1	RPS4Y2	RPS5	RPS6	RPS6KA1
RPS6KA2	RPS6KA3	RPS6KA4	RPS6KA5	RPS6KA6
RPS6KB1	RPS6KB2	RPS6KC1	RPS6KL1	RPS6P1
RPS7	RPS7P4	RPS8	RPS9	RPSA
RPTN	RPTOR	RPUSD1	RPUSD2	RPUSD3
RPUSD4	RQCD1	RRAD	RRAGA	RRAGB
RRAGC	RRAG D	RRAS	RRAS2	RRBP1
RREB1	RRH	RRM1	RRM2	RRM2B
RRN3	RRP1	RRP1 2	RRP1 5	RRP1 B
RRP7A	RRP8	RRP9	RRS1	RS1
RSAD1	RSAD2	RSBN1	RSBN1 L	RSC1 A1
RSF1	RSL1 D1	RSL24D1	RSPH1	

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
RSPH1 0B	RSPH1 0B2	RSPH3	RSPH4A	RSPH6A
RSPH9	RSP01	RSP02	RSP03	RSP04
RSPRY1	RSRC1	RSRC2	RSU1	RTBDN
RTCD1	RTDR1	RTEL1	RTF1	RTKN
RTKN2	RTN1	RTN2	RTN3	RTN4
RTN4IP1	RTN4R	RTN4RL2	RTP1	RTP2
RTP3	RTP4	RTTN	RUFY1	RUFY2
RUFY3	RUNDC1	RUNDC2A	RUNDC2B	RUNDC3B
RUNX1	RUNX1 T 1	RUNX1 T 1_ENST00000265814	RUNX2	RUNX3
RUSC1	RUSC2	RUVBL1	RUVBL2	RWDD1
RWDD2A	RWDD2B	RWDD3	RWDD4A	RXFP1
RXFP2	RXFP3	RXFP4	RXRA	RXRB
RXRG	RYK	RYR1	RYR2	RYR3
S 100A1	S 100A1 0	S 100A1 1	S 100A1 2	S 100A1 3
S 100A1 4	S 100A1 6	S 100A2	S100A3	S 100A4
S 100A5	S 100A6	S 100A7	S 100A7A	S 100A7L2
S 100A8	S 100A9	S 100B	S 100G	S 100P
S 100PBP	S 100Z	S 1 PR1	S 1 PR2	S 1 PR3
S 1 PR4	S 1 PR5	SAA1	SAA2	SAA3P
SAA4	SAAL1	SAC3D1	SACM1 L	SACS
SAE1	SAFB	SAFB2	SAG E 1	SALL1
SALL2	SALL3	SALL4	SAMD1 0	SAMD1 1
SAMD1 2	SAMD1 3	SAMD1 4	SAMD3	SAMD4A
SAMD4B	SAMD5	SAMD7	SAMD8	SAMD8_ENST00000372690
SAMD9	SAMD9L	SAMHD1	SAMM50	SAMSN 1
SAP1 30	SAP1 8	SAP30	SAP30BP	SAP30L
SAPS1	SAPS2	SAPS3	SAR1 A	SAR1 B
SARDH	SARNP	SARS	SARS2	SART1
SART3	SASH1	SASH3	SASS6	SAT1
SAT2	SATB1	SATB2	SATL1	SAV1
SBDS	SBF1	SBF2	SBK1	SBK2
SBN01	SBSN	SC4MOL	SC5DL	SC65
SCAF1	SCAI	SCAMP2	SCAMP3	SCAMP4
SCAND1	SCAND3	SCAP	SCAPER	SCARA3
SCARA5	SCARB1	SCARB2	SCARF1	SCARF2
SCCPDH	SCD	SCD5	SCEL	SCFD1
SCFD2	SCG2	SCG3	SCGB1 A 1	SCGB1 C 1
SCGB1 D 1	SCGB1 D2	SCGB1 D4	SCGB2A1	SCGB2A2
SCGB3A1	SCGB3A2	SCGBL	SCGN	SCHI P 1
SCLT1	SCLY	SCMH1	SCML1	SCML2
SCML4	SCN1 0A	SCN1 1A	SCN1 A	SCN1 B
SCN2A	SCN2B	SCN3A	SCN3B	SCN4A
SCN4B	SCN5A	SCN7A	SCN9A	SCNM1
SCNN1 A	SCNN1 B	SCNN1 D	SCNN1 G	SC01
SC02	SCOC	SCP2	SCPEP1	SCRG 1
SCRIB	SCRN1	SCRN2	SCRN3	SCRT1
SCRT2	SCTR	SCUBE1	SCUBE2	SCUBE3

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SCXB	SCYL1	SCYL2	SCYL3	SDAD1
SDC1	SDC2	SDC3	SDC4	SDCBP
SDCBP2	SDCCAG 1	SDCCAG3	SDCCAG3L	SDCCAG8
SDF2	SDF2L1	SDF4	SDHA	SDHAF1
SDHAF2	SDHB	SDHC	SDHD	SDK1
SDPR	SDR1 6C5	SDR42E1	SDR9C7	SDS
SDSL	SEC1 1B	SEC1 1C	SEC1 3	SEC1 4L1
SEC1 4L2	SEC1 4L3	SEC1 4L4	SEC1 6B	SEC22A
SEC22C	SEC23A	SEC23B	SEC23I P	SEC24A
SEC24B	SEC24C	SEC24D	SEC31 A	SEC31 B
SEC61 A 1	SEC61 A2	SEC61 B	SEC61 G	SEC62
SEC63	SECISBP2	SECISBP2L	SECTM1	SEH1 L
SEL1 L	SEL1 L2	SELE	SELENBP1	SELI
SELL	SELM	SELP	SELPLG	SELV
SEMA3A	SEMA3B	SEMA3C	SEMA3D	SEMA3E
SEMA3F	SEMA3G	SEMA4A	SEMA4B	SEMA4C
SEMA4D	SEMA4F	SEMA4G	SEMA5A	SEMA5B
SEMA6A	SEMA6B	SEMA6C	SEMA6D	SEMA7A
SEMG1	SEMG2	SENP1	SEN P2	SENP3
SENP5	SENP6	SENP7	SEN P8	15-Sep
SEPHS1	SEPHS2	SEPN1	SEPP1	SEPSECS
01-Sep	10-Sep	11-Sep	12-Sep	02-Sep
03-Sep	04-Sep	05-Sep	06-Sep	08-Sep
09-Sep	SEPX1	SERAC1	SERBP1	SERF1 A
SERF1 B	SERF2	SERG EF	SERHL	SERHL2
SERINC1	SERINC2	SERINC3	SERINC4	SERP1
SERP1 _ENSTOO 000491 660	SERP2	SERPINA1	SERPINA1 0	SERPINA1 1
SERPINA1 2	SERPINA1 3	SERPINA2	SERPINA3	SERPINA4
SERPINA5	SERPINA6	SERPINA7	SERPINA9	SERPINA9 _ ENST000003 37425
SERPINB1	SERPINB1 0	SERPINB1 1	SERPINB1 2	SERPINB1 3
SERPINB2	SERPINB3	SERPINB4	SERPINB5	SERPINB6
SERPINB7	SERPINB8	SERPINB9	SERPINC1	SERPIND1
SERPIN E 1	SERPIN E2	SERPINF1	SERPINF2	SERPING 1
SERPINH 1	SERPINI 1	SERPINI2	SERTAD1	SERTAD2
SERTAD3	SERTAD4	SESN1	SESN2	SESN3
SESTD1	SET	SETBP1	SETD1 A	SETD1 B
SETD2	SETD2 _ENSTOO 000409792	SETD3	SETD4	SETD5
SETD6	SETD7	SETD8	SETDB1	SETDB2
SETMAR	SETX	SEZ6	SEZ6L	SEZ6L2
SF1	SF3A1	SF3A2	SF3A3	SF3B1
SF3B1 4	SF3B2	SF3B3	SF3B4	SF3B5
SF4	SFI1	SFMBT1	SFMBT2	SFN
SFPQ	SFRP1	SFRP2	SFRP4	SFRP5
SFRS1	SFRS1 1	SFRS1 2	SFRS1 2IP 1	SFRS1 3B
SFRS1 4	SFRS1 5	SFRS1 6	SFRS1 7A	SFRS1 8
SFRS2	SFRS2IP	SFRS3	SFRS4	SFRS5
SFRS6	SFRS7	SFRS8	SFRS9	SFT2D1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SFT2D2	SFT2D3	SFTA2	SFTPA1 B	SFTPA2
SFTPA2B	SFTPB	SFTPC	SFTPD	SFXN1
SFXN2	SFXN3	SFXN4	SFXN5	SG223 _HUM AN
SG269 _HUMAN	SGCA	SGCB	SGCE	SGCG
SGCZ	SG EF	SG IP1	SGK1	SGK2
SGK3	SGMS1	SGMS2	SGOL1	SGOL2
SG PL1	SG PP1	SG PP2	SGSH	SGSM1
SGSM2	SGSM3	SGTA	SGTB	SH2B1
SH2B3	SH2D1 A	SH2D1 B	SH2D2A	SH2D3A
SH2D3C	SH2D4A	SH2D4B	SH2D5	SH2D6
SH3BG R	SH3BG RL	SH3BG RL2	SH3BGRL3	SH3BP1
SH3BP2	SH3BP4	SH3BP5	SH3BP5L	SH3D1 9
SH3D20	SH3GL1	SH3GL2	SH3GL3	SH3GLB1
SH3GLB2	SH3KBP1	SH3PXD2A	SH3PXD2B	SH3RF1
SH3RF2	SH3TC1	SH3TC2	SH3YL1	SHANK1
SHANK2	SHANK3	SHARPIN	SHB	SHBG
SHC1	SHC1 _ENSTOOO 004481 16	SHC2	SHC3	SHC4
SHCBP1	SHD	SHE	SHF	SHFM1
SHH	SHISA2	SHIS A3	SHISA4	SHISA5
SHKBP1	SHMT1	SHMT2	SHOC2	SHOX
SHOX2	SHPK	SHPRH	SHQ1	SHROOM1
SHROOM2	SHROOM3	SHROOM4	SI	SIAE
SIAH1	SIAH1 L	SIAH2	SIAH3	SIDT1
SIDT2	SIGI RR	SIGLEC1	SIGLEC1 0	SIGLEC1 1
SIGLEC1 2	SIGLEC1 2_ENS T00000439889	SIGLEC1 4	SIGLEC1 5	SIGLEC5
SIGLEC6	SIGLEC7	SIGLEC8	SIGLEC9	SIGMAR1
SIK1	SIK2	SIK3	SIKE1	SIL1
SILV	SIM1	SIM2	SIN3A	SIN3B
SIP 1	SIPA1	SIPA1 L 1	SIPA1 L2	SIPA1 L3
SIRPA	SIRPB1	SIRPB2	SIRPD	SIRPG
SIRT1	SIRT2	SIRT3	SIRT4	SIRT5
SIRT6	SIRT7	SIT1	SIVA1	SIX1
SIX2	SIX3	SIX4	SIX5	SIX6
SK681	SKA1	SKA3	SKAP1	SKAP2
SKI	SKIL	SKI P	SKIV2L	SKIV2L2
SKP1	SKP2	SLA	SLA2	SLAIN1
SLAMF1	SLAMF6	SLAMF7	SLAMF8	SLAMF9
SLBP	SLC1 0A1	SLC1 0A2	SLC1 0A3	SLC1 0A4
SLC1 0A5	SLC1 0A6	SLC1 0A7	SLC1 1A 1	SLC1 1A2
SLC1 2A1	SLC1 2A2	SLC1 2A3	SLC1 2A4	SLC1 2A5
SLC1 2A6	SLC1 2A7	SLC1 2A8	SLC1 2A9	SLC1 3A1
SLC1 3A2	SLC1 3A3	SLC1 3A4	SLC1 3A5	SLC1 4A1
SLC1 4A2	SLC1 5A1	SLC1 5A2	SLC1 5A3	SLC1 5A4
SLC1 6A1	SLC1 6A1 0	SLC1 6A1 1	SLC1 6A1 2	SLC1 6A1 3
SLC1 6A1 4	SLC1 6A2	SLC1 6A3	SLC1 6A4	SLC1 6A5
SLC1 6A6	SLC1 6A7	SLC1 6A8	SLC1 6A9	SLC1 7A1
SLC1 7A2	SLC1 7A3	SLC1 7A4	SLC1 7A5	SLC1 7A6

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SLC1 7A7	SLC1 7A8	SLC1 7A9	SLC1 8A1	SLC1 8A2
SLC1 8A3	SLC1 9A1	SLC1 9A2	SLC1 9A3	SLC1 A 1
SLC1 A2	SLC1 A3	SLC1 A4	SLC1 A5	SLC1 A6
SLC1 A7	SLC20A1	SLC20A2	SLC22A1	SLC22A1 0
SLC22A1 1	SLC22A1 2	SLC22A1 3	SLC22A1 4	SLC22A1 5
SLC22A1 6	SLC22A1 7	SLC22A1 8	SLC22A2	SLC22A20
SLC22A23	SLC22A25	SLC22A3	SLC22A4	SLC22A5
SLC22A6	SLC22A7	SLC22A8	SLC22A9	SLC23A1
SLC23A2	SLC23A3	SLC24A2	SLC24A3	SLC24A4
SLC24A5	SLC24A6	SLC25A1	SLC25A1 0	SLC25A1 1
SLC25A1 2	SLC25A1 3	SLC25A1 4	SLC25A1 5	SLC25A1 6
SLC25A1 7	SLC25A1 8	SLC25A1 9	SLC25A2	SLC25A20
SLC25A21	SLC25A22	SLC25A23	SLC25A24	SLC25A25
SLC25A27	SLC25A28	SLC25A29	SLC25A3	SLC25A30
SLC25A31	SLC25A32	SLC25A33	SLC25A34	SLC25A35
SLC25A36	SLC25A37	SLC25A38	SLC25A39	SLC25A4
SLC25A40	SLC25A42	SLC25A43	SLC25A44	SLC25A45
SLC25A46	SLC25A5	SLC25A6	SLC26A1	SLC26A1 0
SLC26A1 1	SLC26A2	SLC26A3	SLC26A4	SLC26A5
SLC26A6	SLC26A7	SLC26A8	SLC26A9	SLC27A1
SLC27A2	SLC27A3	SLC27A4	SLC27A5	SLC27A6
SLC28A1	SLC28A2	SLC28A3	SLC29A1	SLC29A2
SLC29A3	SLC29A4	SLC2A1	SLC2A1 0	SLC2A1 1
SLC2A1 2	SLC2A1 3	SLC2A1 4	SLC2A2	SLC2A3
SLC2A4	SLC2A4RG	SLC2A5	SLC2A6	SLC2A7
SLC2A8	SLC2A9	SLC30A1	SLC30A1 0	SLC30A2
SLC30A3	SLC30A4	SLC30A5	SLC30A6	SLC30A7
SLC30A8	SLC30A9	SLC31 A 1	SLC31 A2	SLC32A1
SLC33A1	SLC34A1	SLC34A2	SLC34A3	SLC35A1
SLC35A2	SLC35A3	SLC35A4	SLC35A5	SLC35B1
SLC35B2	SLC35B3	SLC35B4	SLC35C1	SLC35C2
SLC35D1	SLC35D2	SLC35D3	SLC35E1	SLC35E2
SLC35E3	SLC35E4	SLC35F1	SLC35F2	SLC35F3
SLC35F5	SLC36A1	SLC36A2	SLC36A3	SLC36A4
SLC37A1	SLC37A2	SLC37A3	SLC37A4	SLC38A1
SLC38A1 0	SLC38A1 1	SLC38A2	SLC38A3	SLC38A4
SLC38A5	SLC38A6	SLC38A7	SLC38A8	SLC38A9
SLC39A1	SLC39A1 0	SLC39A1 1	SLC39A1 2	SLC39A1 3
SLC39A1 4	SLC39A2	SLC39A3	SLC39A4	SLC39A5
SLC39A6	SLC39A7	SLC39A8	SLC39A9	SLC3A1
SLC3A2	SLC40A1	SLC41 A 1	SLC41 A2	SLC41 A3
SLC43A1	SLC43A2	SLC43A3	SLC44A1	SLC44A2
SLC44A3	SLC44A4	SLC44A5	SLC45A1	SLC45A2
SLC45A3	SLC45A4	SLC46A2	SLC46A3	SLC47A1
SLC47A2	SLC48A1	SLC4A1	SLC4A1 0	SLC4A1 1
SLC4A1 AP	SLC4A2	SLC4A3	SLC4A4	SLC4A5
SLC4A7	SLC4A8	SLC4A9	SLC4A9_ENST00000506757	SLC5A1
SLC5A1 0	SLC5A1 1	SLC5A1 2	SLC5A2	SLC5A3
SLC5A4	SLC5A5	SLC5A6	SLC5A7	SLC5A8

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SLC5A9	SLC6A1	SLC6A1 1	SLC6A1 2	SLC6A1 3
SLC6A1 4	SLC6A1 5	SLC6A1 6	SLC6A1 7	SLC6A1 8
SLC6A1 9	SLC6A2	SLC6A20	SLC6A3	SLC6A4
SLC6A5	SLC6A6	SLC6A7	SLC6A8	SLC6A9
SLC7A1	SLC7A1 0	SLC7A1 1	SLC7A1 3	SLC7A1 4
SLC7A2	SLC7A3	SLC7A4	SLC7A5	SLC7A6
SLC7A60S	SLC7A7	SLC7A8	SLC7A9	SLC8A1
SLC8A2	SLC8A3	SLC9A1	SLC9A1 0	SLC9A1 1
SLC9A2	SLC9A3	SLC9A3R1	SLC9A3R2	SLC9A4
SLC9A5	SLC9A6	SLC9A7	SLC9A8	SLC9A9
SLC01 A2	SLC01 B1	SLC01 B3	SLC01 C1	SLC02A1
SLC02B1	SLC03A1	SLC04A1	SLC04C1	SLC05A1
SLC06A1	SLFN1 1	SLFN1 2	SLFN1 3	SLFN1 4
SLFN5	SLFNL1	SLIT1	SLIT2	SLIT3
SLITRK1	SLITRK2	SLITRK3	SLITRK4	SLITRK5
SLITRK6	SLK	SLMAP	SLM01	SLM02
SLN	SLPI	SLTM	SLU7	SLURP1
SMAD1	SMAD2	SMAD3	SMAD4	SMAD5
SMAD50S	SMAD6	SMAD7	SMAD9	SMAP1
SMAP2	SMARCA1	SMARCA2	SMARCA4	SMARCA5
SMARCAD1	SMARCAL1	SMARCB1	SMARCC1	SMARCC2
SMARCD1	SMARCD2	SMARCD3	SMARCE1	SMC1 A
SMC1 B	SMC2	SMC2L1	SMC3	SMC4
SMC5	SMC6	SMCHD1	SMCP	SMCR7
SMCR7L	SMCR8	SMEK1	SMEK1 _ENST 0000041 7249	SMEK2
SMG1	SMG5	SMG6	SMG7	SMN1
SMN2	SMNDC1	SMO	SMOC1	SMOC2
SMOX	SMPD1	SMPD2	SMPD3	SMPD4
SMPDL3A	SMPDL3B	SMPX	SMR3A	SMR3B
SMS	SMTN	SMTNL2	SMU 1	SMUG1
SMURF1	SMURF2	SMYD1	SMYD2	SMYD3
SMYD4	SMYD5	SNAI 1	SNAI2	SNAI3
SNAP23	SNAP25	SNAP29	SNAP47	SNAPC1
SNAPC2	SNAPC3	SNAPC4	SNAPC5	SNAPIN
SNCA	SNCAI P	SNCB	SNCG	SND1
SNED1	SNF8	SNI P1	SNN	SNPH
SNRK	SNRN P200	SNRN P25	SNRNP27	SNRN P35
SNRN P48	SNRN P70	SNRPA	SNRPA1	SNRPB
SNRPB2	SNRPC	SNRPD1	SNRPD2	SNRPD3
SNRPE	SNRPEL1	SNRPF	SNRPG	SNRPN
SNTA1	SNTB1	SNTB2	SNTG1	SNTG2
SNTN	SNU PN	SNURF	SNW1	SNX1
SNX1 0	SNX1 1	SNX1 2	SNX1 3	SNX1 4
SNX1 5	SNX1 6	SNX1 7	SNX1 8	SNX1 9
SNX2	SNX20	SNX21	SNX22	SNX24
SNX25	SNX27	SNX3	SNX30	SNX31
SNX32	SNX33	SNX4	SNX5	SNX6
SNX7	SNX8	SNX9	SOAT1	SOAT2
SOBP	SOCS1	SOCS2	SOCS3	SOCS4

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SOCS5	SOCS6	SOCS7	SOD1	SOD2
SOD3	SOHLH1	SOHLH2	SOLH	SON
SORBS1	SORBS2	SORBS3	SORCS1	SORCS2
SORCS3	SORD	SORL1	SORT1	SOS1
SOS2	SOST	SOSTDC1	SOX1	SOX1 0
SOX1 1	SOX1 2	SOX1 3	SOX1 4	SOX1 5
SOX1 7	SOX1 8	SOX2	SOX21	SOX3
SOX30	SOX4	SOX5	SOX6	SOX7
SOX8	SOX9	SP1	SP1 00	SP1 10
SP1 40	SP1 40L	SP2	SP3	SP4
SP5	SP6	SP8	SPA1 7	SPACA1
SPACA3	SPACA4	SPACA5	SPACA5B	SPAG1
SPAG1 1A	SPAG1 1B	SPAG1 6	SPAG 17	SPAG4
SPAG5	SPAG6	SPAG7	SPAG8	SPAG9
SPAM1	SPANX-N1	SPANXA1	SPANXA2	SPANXB1
SPANXC	SPANXD	SPANXN1	SPANXN2	SPANXN3
SPANXN4	SPANXN5	SPARC	SPARCL1	SPAST
SPATA1	SPATA1 2	SPATA1 3	SPATA1 6	SPATA1 7
SPATA1 8	SPATA1 9	SPATA2	SPATA20	SPATA21
SPATA22	SPATA2L	SPATA4	SPATA5	SPATA5L1
SPATA6	SPATA7	SPATA8	SPATA9	SPATC1
SPATS1	SPATS2	SPC25	SPCS1	SPCS2
SPDEF	SPDYA	SPDYC	SPDYE1	SPDYE2
SPEF1	SPEF2	SPEF2_ENSTO 0000356031	SPEG	SPEM1
SPEM1_ENSTOO 000323383	SPEN	SPERT	SPESP1	SPFH 1
SPG1 1	SPG20	SPG21	SPG7	SPHAR
SPHK1	SPHK2	SPHKAP	SPI 1	SPIB
SPIC	SPIN1	SPIN2A	SPIN2B	SPIN3
SPIN4	SPINK1	SPINK2	SPINK4	SPINK5
SPINK5L2	SPINK5L3	SPINK6	SPINK7	SPINK9
SPINLW1	SPINLW1_ENST 00000336443	SPINT1	SPINT2	SPINT4
SPI RE1	SPI RE2	SPN	SPNS1	SPNS2
SPNS3	SP01 1	SPOCD1	SPOCK1	SPOCK2
SPOCK3	SPON2	SPOP	SPOPL	SPP1
SPP2	SPPL2A	SPR	SPRED1	SPRED2
SPRED3	SPRN	SPRR1 A	SPRR1 B	SPRR2A
SPRR2B	SPRR2D	SPRR2E	SPRR2F	SPRR2G
SPRR3	SPRR4	SPRY1	SPRY2	SPRY3
SPRY4	SPRYD3	SPRYD4	SPRYD5	SPRYD5_EN ST00000327 733
SPSB1	SPSB2	SPSB3	SPSB4	SPTA1
SPTAN1	SPTB	SPTBN1	SPTBN2	SPTBN4
SPTBN5	SPTLC1	SPTLC2	SPTLC3	SPTY2D1
SPZ1	SQLE	SQRDL	SQSTM1	SR1 40_HUM AN
SRA1	SRBD1	SRC	SRCAP	SRCRB4D
SRD5A1	SRD5A3	SREBF1	SREBF2	SRF

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SRFBP1	SRGAP1	SRGAP2P1	SRGAP3	SRGN
SRI	SRL	SRM	SRMS	SRP1 4
SRP1 9	SRP54	SRP68	SRP72	SRP9
SRP9L1	SRPK1	SRPK2	SRPK3	SRPK3_ENST00000489426
SRPR	SRPRB	SRPX	SRPX2	SRR
SRRD	SRRM1	SRRM2	SRRT	SRXN1
SRY	SS1 8	SS1 8L1	SS1 8L2	SSB
SSBP1	SSBP2	SSBP3	SSBP4	SSFA2
SSH1	SSH2	SSH3	SSNA1	SSPN
SSR1	SSR2	SSR3	SSR4	SSRP1
SSSCA1	SST	SSTR1	SSTR2	SSTR3
SSTR4	SSTR5	SSU72	SSX1	SSX2
SSX2I P	SSX3	SSX4	SSX4B	SSX5
SSX6	SSX7	SSX9	ST1 3	ST1 4
ST1 8	ST20	ST3GAL1	ST3GAL2	ST3GAL3
ST3GAL4	ST3GAL5	ST3GAL6	ST5	ST6GAL1
ST6GAL2	ST6GALNAC1	ST6GALNAC2	ST6GALNAC3	ST6GALNAC4
ST6GALNAC5	ST6GALNAC6	ST7	ST7L	ST8SIA1
ST8SIA2	ST8SIA3	ST8SIA4	ST8SIA5	ST8SIA6
STAB1	STAB2	STAC	STAC2	STAC3
STAG1	STAG2	STAG3	STAG3L1	STAG3L3
STAG3L4	STAM	STAM2	STAM BP	STAMBPL1
STAP1	STAP2	STAR	STARD1 0	STARD1 3
STARD3	STARD3NL	STARD4	STARD5	STARD6
STARD7	STARD8	STARD8_ENST00000252336	STARD9	STAT1
STAT2	STAT3	STAT4	STAT5A	STAT5B
STAT6	STATH	STAU1	STAU2	STBD1
STC1	STC2	STEAP1	STEAP2	STEAP3
STEAP4	STIL	STIM1	STIM2	STI P 1
STK1 0	STK1 1	STK1 1IP	STK1 6	STK1 7A
STK1 7B	STK1 9	STK24	STK25	STK3
STK31	STK32A	STK32B	STK32C	STK33
STK35	STK36	STK38	STK38L	STK39
STK4	STK40	STMN1	STMN2	STMN3
STMN4	STOM	STOML1	STOML2	STOML3
ST0N1	STON1 - GTF2A1 L	STON2	STOX1	STOX2
STRA1 3	STRA6	STRA8	STRADA	STRADB
STRAP	STRBP	STRC	STRN	STRN3
STRN4	STS	STT3A	STT3B	STUB1
STX1 0	STX1 1	STX1 2	STX1 6	STX1 7
STX1 8	STX1 9	STX1 A	STX1 B	STX2
STX3	STX4	STX5	STX6	STX7
STX8	STXBP1	STXBP2	STXBP3	STXBP4
STXBP5	STXBP5L	STXBP6	STYK1	STYX
STYXL1	SUB1	SUCLA2	SUCLG1	SUCLG2
SUCNR1	SUDS3	SUFU	SUGT1	SULF1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
SULF2	SULT1A1	SULT1A2	SULT1A3	SULT1A4
SULT1B1	SULT1C2	SULT1C3	SULT1C4	SULT1E1
SULT2A1	SULT2B1	SULT4A1	SULT6B1	SUMF1
SUMF2	SUMO1	SUMO1P1	SUMO2	SUMO3
SUMO4	SUN1	SUN2	SUN3	SUN5
SUOX	SUPT16H	SUPT3H	SUPT4H1	SUPT5H
SUPT6H	SUPT7L	SUPV3L1	SURF1	SURF2
SURF4	SURF5	SURF6	SUSD1	SUSD2
SUSD3	SUSD4	SUSD5	SUV39H1	SUV39H2
SUV420H1	SUV420H2	SUZ12	SUZ12P	SV2A
SV2B	SV2C	SVEP1	SVIL	SVIP
SVOPL	SWAP70	SYAP1	SYCE1	SYCE2
SYCN	SYCP1	SYCP2	SYCP2L	SYCP3
SYDE1	SYDE2	SYF2	SYK	SYMPK
SYN1	SYN2	SYN3	SYNC	SYNCRIP
SYNE1	SYNE1_ENST00000265368	SYNE2	SYNGAP1	SYNGAP1_ENST00000293748
SYNGR1	SYNGR2	SYNGR3	SYNGR4	SYNJ1
SYNJ2	SYNJ2BP	SYNM	SYNPO	SYNPO2
SYNPO2L	SYNRG	SYP	SYPL1	SYPL2
SYP_ENST00000263233	SYS1	SYT1	SYT10	SYT11
SYT12	SYT13	SYT14	SYT14L	SYT15
SYT15_ENST00000374328	SYT16	SYT17	SYT2	SYT3
SYT4	SYT5	SYT6	SYT7	SYT8
SYT9	SYTL1	SYTL2	SYTL3	SYTL4
SYTL5	SYVN1	SgK069	SgK085	SgK110
SgK223	SgK269	SgK424	SgK493	SgK494
SgK495	T	T183B_HUMAN	TAAR1	TAAR2
TAAR5	TAAR6	TAAR8	TAB1	TAB2
TAB3	TAC1	TAC3	TAC4	TACC1
TACC2	TACC3	TACO1	TACR1	TACR2
TACR3	TACSTD2	TADA1	TADA2A	TADA2B
TADA3L	TAF1	TAF10	TAF11	TAF12
TAF13	TAF15	TAF1A	TAF1B	TAF1C
TAF1D	TAF1L	TAF2	TAF3	TAF4
TAF4B	TAF5	TAF5L	TAF6	TAF6L
TAF7	TAF7L	TAF8	TAF9	TAF9B
TAGAP	TAGLN	TAGLN2	TAGLN3	TAL1
TAL2	TALDO1	TANC1	TANK	TAOK1
TAOK2	TAOK3	TAP1	TAP2	TAP2_ENST00000458336
TAPBP	TAPBPL	TAPT1	TARBP1	TARBP2
TARDBP	TARS	TARS2	TARSL2	TAS1R1
TAS1R2	TAS1R3	TAS2R1	TAS2R10	TAS2R13
TAS2R14	TAS2R16	TAS2R19	TAS2R20	TAS2R3
TAS2R38	TAS2R4	TAS2R41	TAS2R42	TAS2R5
TAS2R50	TAS2R60	TAS2R7	TAS2R8	TAS2R9

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
TASP1	TAT	TATDN1	TATDN2	TATDN3
TAX1 BP1	TAX1 BP3	TAZ	TBC1 D 1	TBC1 D 10A
TBC1 D 10C	TBC1 D 12	TBC1 D 13	TBC1 D 14	TBC1 D 15
TBC1 D 16	TBC1 D 17	TBC1 D 19	TBC1 D2	TBC1 D20
TBC1 D21	TBC1 D22A	TBC1 D22B	TBC1 D23	TBC1 D24
TBC1 D25	TBC1 D26	TBC1 D28	TBC1 D29	TBC1 D2B
TBC1 D3	TBC1 D30	TBC1 D3B	TBC1 D3C	TBC1 D3E
TBC1 D3F	TBC1 D3G	TBC1 D3H	TBC1 D3P2	TBC1 D4
TBC1 D5	TBC1 D7	TBC1 D8B	TBC1 D9B	TBCA
TBCB	TBCC	TBCCD1	TBCD	TBCE
TBCEL	TBCK	TBK1	TBKBP1	TBL1 X
TBL1 XR1	TBL1 Y	TBL2	TBL3	TBP
TBPL1	TBPL2	TBR1	TBRG1	TBRG4
TBX1	TBX1 0	TBX1 5	TBX1 8	TBX1 9
TBX2	TBX20	TBX21	TBX22	TBX3
TBX4	TBX5	TBX6	TBXA2R	TBXAS1
TC2N	TCAP	TCEA1	TCEA2	TCEAL1
TCEAL2	TCEAL3	TCEAL4	TCEAL5	TCEAL6
TCEAL7	TCEAL8	TCEANC	TCEB1	TCEB2
TCEB3	TCEB3B	TCEB3C	TCERG1	TCERG 1L
TCF1 2	TCF1 5	TCF1 9	TCF20	TCF21
TCF23	TCF25	TCF3	TCF4	TCF7
TCF7L1	TCF7L2	TCFL5	TCHH	TCHHL1
TCHP	TCIRG 1	TCL1 A	TCL1 B	TCL6
TCN1	TCN2	TC0F1	TCP1	TCP1 0
TCP1 0L	TCP1 1	TCP1 1L 1	TCP1 1L2	TCTA
TCTE1	TCTE3	TCTEX1 D 1	TCTEX1 D2	TCTEX1 D4
TCTN1	TCTN2	TCTN3	TDG	TDGF1
TDH	TD02	TDP1	TDRD1	TDRD1 0
TDRD3	TDRD5	TDRD6	TDRD7	TDRD9
TDRKH	TEAD1	TEAD2	TEAD4	TEC
TECPR1	TECPR2	TECR	TECRL	TECTA
TECTB	TEDDM1	TEF	TEK	TEKT1
TEKT2	TEKT3	TEKT4	TEKT5	TEL02
TENC1	TEP1	TEPP	TERF1	TERF2
TERF2IP	TERT	TES	TESC	TESK1
TESK2	TET1	TET2	TEX1 0	TEX1 0 1
TEX1 1	TEX1 2	TEX1 3A	TEX1 3B	TEX1 4
TEX1 5	TEX1 9	TEX2	TEX261	TEX264
TEX28	TEX9	TF	TFAM	TFAP2A
TFAP2B	TFAP2C	TFAP2D	TFAP2E	TFAP4
TFB1 M	TFB2M	TFCP2	TFCP2L1	TFDP1
TFDP2	TFDP3	TFE3	TFEB	TFEC
TFF1	TFF2	TFF3	TFG	TFI P 1 1
TFPI	TFPI2	TFPT	TFR2	TFRC
TFSM1 _HUMAN	TG	TGDS	TGFA	TGFB1
TGFB1 I1	TGFB2	TGFB3	TGFBI	TGFBR1
TGFBR2	TGFBR3	TGFBRAP1	TGIF1	TGI F2
TGI F2LX	TGI F2LY	TGM1	TGM2	TGM3
TGM4	TGM5	TGM6	TGM7	TG0LN2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
TGS1	TH	TH1L	THADA	THAP1
THAP10	THAP11	THAP2	THAP3	THAP4
THAP5	THAP6	THAP7	THAP8	THAP9
THBD	THBS1	THBS2	THBS3	THBS4
THEG	THEM4	THEM5	THEMIS	THG1L
THNSL1	THNSL2	THOC1	THOC2	THOC3
THOC4	THOC5	THOC6	THOC7	THOP1
THPO	THRA	THRAP3	THRB	THRSP
THSD1	THSD4	THSD7A	THSD7B	THTPA
THUMPD1	THUMPD2	THUMPD3	THY1	THYN1
TIA1	TIAF1	TIAL1	TIAM1	TIAM2
TICAM1	TICAM2	TIE1	TIF1	TIFA
TIFAB	TIGD1	TIGD2	TIGD3	TIGD4
TIGD5	TIGD6	TIGD7	TIGIT	TIMD4
TIMELESS	TIMM10	TIMM13	TIMM17A	TIMM17B
TIMM22	TIMM23	TIMM44	TIMM50	TIMM8A
TIMM8B	TIMM9	TIMP1	TIMP2	TIMP3
TIMP4	TINAG	TINAGL1	TINF2	TIPARP
TIPIN	TIPRL	TIRAP	TJAP1	TJP1
TJP2	TJP3	TK1	TK2	TKT
TKTL1	TKTL2	TLCD1	TLCD2	TLE1
TLE3	TLE4	TLE6	TLK1	TLK2
TLL1	TLL2	TLN1	TLN2	TLR1
TLR10	TLR2	TLR3	TLR4	TLR5
TLR6	TLR7	TLR8	TLR9	TLX1
TLX2	TLX3	TM2D1	TM2D2	TM2D3
TM4SF1	TM4SF18	TM4SF19	TM4SF2	TM4SF20
TM4SF5	TM6SF1	TM6SF2	TM7SF2	TM7SF3
TM7SF4	TM9SF1	TM9SF2	TM9SF3	TM9SF4
TMBIM1	TMBIM4	TMBIM6	TMC1	TMC2
TMC3	TMC4	TMC5	TMC6	TMC7
TMC8	TMCC1	TMCC2	TMCC3	TMC01
TMC02	TMC03	TMC04	TMC05A	TMC06
TMC07	TMED1	TMED10	TMED2	TMED3
TMED4	TMED5	TMED6	TMED7	TMED8
TMED9	TMEFF1	TMEFF2	TMEM100	TMEM101
TMEM102	TMEM104	TMEM105	TMEM106A	TMEM106B
TMEM106C	TMEM107	TMEM108	TMEM109	TMEM11
TMEM110	TMEM111	TMEM115	TMEM116	TMEM117
TMEM119	TMEM120B	TMEM121	TMEM123	TMEM125
TMEM126A	TMEM126B	TMEM127	TMEM128	TMEM129
TMEM130	TMEM131	TMEM132A	TMEM132B	TMEM132C
TMEM132D	TMEM132E	TMEM133	TMEM134	TMEM135
TMEM136	TMEM138	TMEM139	TMEM140	TMEM141
TMEM143	TMEM144	TMEM145	TMEM146	TMEM147
TMEM149	TMEM14A	TMEM14B	TMEM14C	TMEM150A
TMEM150B	TMEM151A	TMEM154	TMEM155	TMEM156
TMEM159	TMEM160	TMEM161A	TMEM161B	TMEM163
TMEM164	TMEM165	TMEM167A	TMEM167B	TMEM168
TMEM169	TMEM17	TMEM170A	TMEM170B	TMEM171

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
TMEM1 73	TMEM1 74	TMEM1 75	TMEM1 76A	TMEM1 76B
TMEM1 77	TMEM1 78	TMEM1 79	TMEM1 79B	TMEM1 8
TMEM1 80	TMEM1 8 1	TMEM1 82	TMEM1 83A	TMEM1 84A
TMEM1 84B	TMEM1 84C	TMEM1 85A	TMEM1 85B	TMEM1 86
TMEM1 87	TMEM1 89	TMEM1 89-UBE2V1	TMEM1 9	TMEM1 90
TMEM1 92	TMEM194A	TMEM1 95	TMEM1 96	TMEM1 98
TMEM1 99	TMEM2	TMEM20	TMEM200A	TMEM200B
TMEM201	TMEM202	TMEM203	TMEM204	TMEM205
TMEM206	TMEM207	TMEM209	TMEM21 1	TMEM21 4
TMEM21 5	TMEM21 7	TMEM21 8	TMEM21 9	TMEM22
TMEM220	TMEM222	TMEM225	TMEM229B	TMEM25
TMEM26	TMEM27	TMEM30A	TMEM30B	TMEM31
TMEM33	TMEM35	TMEM37	TMEM38A	TMEM38B
TMEM39A	TMEM39B	TMEM40	TMEM41 A	TMEM41 B
TMEM42	TMEM43	TMEM44	TMEM45A	TMEM45B
TMEM47	TMEM48	TMEM49	TMEM5	TMEM50A
TMEM50B	TMEM51	TMEM52	TMEM53	TMEM54
TMEM55A	TMEM55B	TMEM56	TMEM57	TMEM59
TMEM59L	TMEM60	TMEM61	TMEM62	TMEM63A
TMEM63B	TMEM64	TMEM65	TMEM66	TMEM67
TMEM68	TMEM69	TMEM70	TMEM71	TMEM72
TMEM74	TMEM78	TMEM79	TMEM80	TMEM81
TMEM82	TMEM85	TMEM86A	TMEM86B	TMEM87A
TMEM87B	TMEM88	TMEM89	TMEM8A	TMEM8B
TMEM8C	TMEM9	TMEM90A	TMEM90B	TMEM91
TMEM92	TMEM93	TMEM95	TMEM97	TMEM98
TMEM99	TMEM9B	TMF1	TMIE	TMIGD1
TMIGD2	TMLHE	TMOD1	TMOD2	TMOD3
TMOD4	TMPO	TMPO_ENSTO0000266732	TMPPE	TMPRSS1 1A
TMPRSS1 1B	TMPRSS1 1D	TMPRSS1 1E	TMPRSS1 1E2	TMPRSS1 1F
TMPRSS1 3	TMPRSS2	TMPRSS2_ENST000003321 49	TMPRSS3	TMPRSS4
TMPRSS6	TMPRSS7	TMPRSS9	TMSB1 0	TMSB1 5A
TMSB1 5B	TMSB4X	TMSB4Y	TMSL2	TMSL3
TMTC1	TMTC2	TMTC3	TMTC4	TMUB1
TMUB2	TMX1	TMX2	TMX3	TMX4
TNAP	TNC	TNF	TNFAI P 1	TNFAIP2
TNFAIP3	TNFAIP6	TNFAIP8L1	TNFAI P8L2	TNFAIP8L3
TNFRSF1 0A	TNFRSF1 0B	TNFRSF1 0C	TNFRSF1 0D	TNFRSF1 1A
TNFRSF1 1B	TNFRSF1 2A	TNFRSF1 3B	TNFRSF1 3C	TNFRSF1 4
TNFRSF1 7	TNFRSF1 8	TNFRSF1 9	TNFRSF1 A	TNFRSF1 B
TNFRSF21	TNFRSF25	TNFRSF4	TNFRSF6B	TNFRSF8
TNFRSF9	TNFSF1 0	TNFSF1 1	TNFSF1 2	TNFSF1 2-TNFSF1 3
TNFSF1 3	TNFSF1 3B	TNFSF1 4	TNFSF1 5	TNFSF1 8
TNFSF4	TNFSF8	TNFSF9	TNIK	TNIP1
TNIP2	TNIP3	TNK1	TNK2	TNK2_ENST00000381 9 16

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
TNKS	TNKS1 BP1	TNKS2	TNMD	TNN
TNNC1	TNNC2	TNNI1	TNNI2	TNNI3
TNNI3K	TNNT1	TNNT2	TNNT3	TNP1
TNP01	TNP02	TNP03	TNR	TNRC1 8
TNRC6A	TNRC6B	TNS1	TNS3	TNS4
TNXB	TNXB _ENSTOOO 00375247	TOB1	TOB2	TOB2P1
TOE1	TOLLI P	TOM1	TOM1 L 1	TOM1 L2
TOMM20	TOMM20L	TOMM22	TOMM34	TOMM40
TOMM40L	TOMM5	TOMM7	TOMM70A	TOP1
TOP1 MT	TOP2A	TOP2B	TOP3A	TOP3B
TOP3B _ENSTOO 0003571 79	TOPBP1	TOPORS	TOR1 A	TOR1 AIP1
TOR1 AIP2	TOR1 B	TOR2A	TOR3A	TOX
TOX2	TOX3	TOX4	TP53	TP53AI P 1
TP53BP1	TP53BP2	TP53I 11	TP53I1 3	TP53I3
TP53INP1	TP53INP2	TP53RK	TP53TG1	TP53TG5
TP63	TP73	TPBG	TPCN1	TPCN2
TPD52	TPD52L1	TPD52L2	TPD52L3	TPH1
TPH2	TPI 1	TPK1	TPM1	TPM2
TPM3	TPM4	TPM4 _ENSTOO 000344824	TPMT	TPO
TPP1	TPP2	TPPP	TPPP2	TPPP3
TPR	TPRA1	TPRG 1	TPRG1 L	TPRKB
TPRX1	TPRXL	TPSAB1	TPSD1	TPSG1
TPST1	TPST2	TPT1	TPTE	TPTE2
TPX2	TRA2A	TRA2B	TRABD	TRAD
TRADD	TRAF1	TRAF2	TRAF3	TRAF3IP1
TRAF3IP2	TRAF3IP3	TRAF4	TRAF5	TRAF6
TRAF7	TRAFD1	TRAI P	TRAK1	TRAK2
TRAM1	TRAM1 L 1	TRAM2	TRANK1	TRAP1
TRAPPC1	TRAPPC1 0	TRAPPC2	TRAPPC2L	TRAPPC3
TRAPPC4	TRAPPC5	TRAPPC6A	TRAPPC6B	TRAPPC9
TRAT1	TRDMT1	TRDN	TREM1	TREM2
TREML1	TREML2	TREML4	TRERF1	TREX1
TREX2	TRH	TRHDE	TRHR	TRIAP1
TRIB1	TRIB2	TRIB3	TRIM1 0	TRIM1 1
TRIM1 3	TRIM1 4	TRIM1 5	TRIM1 6	TRIM1 6L
TRIM1 7	TRIM2	TRIM21	TRIM22	TRIM23
TRIM24	TRIM25	TRIM26	TRIM27	TRIM28
TRIM29	TRIM3	TRIM31	TRIM32	TRIM33
TRIM34	TRIM35	TRIM36	TRIM37	TRIM38
TRIM39	TRIM4	TRIM40	TRIM41	TRIM42
TRIM43	TRIM44	TRIM45	TRIM46	TRIM47
TRIM48	TRIM49	TRIM5	TRIM50	TRIM52
TRIM54	TRIM55	TRIM56	TRIM58	TRIM59
TRIM6	TRIM6-TRIM34	TRIM60	TRIM61	TRIM62
TRIM63	TRIM64C	TRIM65	TRIM66	TRIM67
TRIM68	TRIM69	TRIM7	TRIM71	TRIM72
TRIM73	TRIM74	TRIM8	TRIM9	TRIML1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
TRIML2	TRIO	TRIOBP	TRIOBP _ENST 00000344404	TRIP1 0
TRIP1 1	TRIP1 2	TRIP1 3	TRI P4	TRIP6
TRIT1	TRMT1	TRMT1 1	TRMT1 12	TRMT1 2
TRMT2A	TRMT2B	TRMT5	TRMT6	TRMT61 A
TRMT61 B	TRMU	TRNAU1 AP	TRNP1	TRNT1
TRO	TROAP	TROVE2	TRPA1	TRPC1
TRPC3	TRPC4	TRPC4AP	TRPC5	TRPC6
TRPM1	TRPM2	TRPM3	TRPM4	TRPM5
TRPM6	TRPM7	TRPM8	TRPS1	TRPT1
TRPV2	TRPV3	TRPV4	TRPV5	TRPV6
TRRAP	TRUB1	TRUB2	TRYX3	TSC1
TSC2	TSC22D1	TSC22D2	TSC22D3	TSC22D4
TSC2 _ENSTOOO 0021 9476	TSEN1 5	TSEN2	TSEN34	TSEN54
TSFM	TSG 10 1	TSGA1 0	TSGA1 0IP	TSGA1 3
TSGA1 4	TSHB	TSHR	TSHZ1	TSHZ2
TSHZ3	TSKS	TSKU	TSLP	TSN
TSNARE1	TSNAX	TSNAXIP1	TSPAN1	TSPAN1 1
TSPAN1 2	TSPAN1 3	TSPAN1 4	TSPAN1 5	TSPAN1 6
TSPAN1 7	TSPAN1 8	TSPAN2	TSPAN3	TSPAN31
TSPAN32	TSPAN33	TSPAN4	TSPAN5	TSPAN6
TSPAN7	TSPAN8	TSPAN9	TSPO	TSP02
TSPY2	TSPY3	TSPYL1	TSPYL2	TSPYL5
TSPYL6	TSR1	TSR2	TSSC1	TSSC4
TSSK1 B	TSSK2	TSSK3	TSSK4	TSSK6
TST	TSTA3	TSTD2	TTBK1	TTBK2
TTC1	TTC1 2	TTC1 3	TTC1 4	TTC1 5
TTC1 6	TTC1 7	TTC1 8	TTC1 9	TTC21 A
TTC21 B	TTC22	TTC23	TTC26	TTC27
TTC29	TTC3	TTC30A	TTC31	TTC32
TTC33	TTC35	TTC36	TTC37	TTC38
TTC39A	TTC39B	TTC39C	TTC3L	TTC4
TTC5	TTC6	TTC7A	TTC7B	TTC8
TTC9B	TTC9C	TTF1	TTF2	TTK
TTL	TTLL1	TTLL1 0	TTLL1 1	TTLL1 2
TTLL1 3	TTLL2	TTLL3	TTLL4	TTLL5
TTLL6	TTLL6 _ENSTOOO 00393382	TTLL7	TTLL9	TTN
TTN _ENSTOOOOO 3561 27	TTN _ENST0000 0360870	TTPA	TTPAL	TTR
TTRAP	TTYH1	TTYH2	TTYH3	TUB
TUBA1 A	TUBA1 B	TUBA1 C	TUBA3C	TUBA3D
TUBA3E	TUBA4A	TUBA4A _ENS T00000392088	TUBA8	TUBAL3
TUBB	TUBB1	TUBB2A	TUBB2B	TUBB2C
TUBB3	TUBB4	TUBB4Q	TUBB6	TUBB8
TUBD1	TUBE1	TUBG 1	TUBG2	TUBGCP2
TUBGCP3	TUBGCP4	TUBGCP5	TUBGCP6	TUFM
TUFT1	TULP1	TULP2	TULP3	TULP4

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
TUSC1	TUSC2	TUSC3	TUSC4	TUSC5
TUT1	TWF1	TWF2	TWIST1	TWISTNB
TWSG1	TXK	TXLNA	TXLNB	TXN
TXN2	TXNDC1 1	TXNDC1 2	TXNDC1 5	TXNDC1 6
TXNDC1 7	TXNDC2	TXNDC3	TXNDC5	TXNDC6
TXNDC8	TXNDC9	TXNI P	TXNL1	TXNL2
TXNL4A	TXNL4B	TXNRD1	TXNRD2	TXNRD3IT1
TYK2	TYMP	TYMS	TYR	TYR03
TYROBP	TYRP1	TYSND1	TYW 1	TYW3
U258_HUMAN	U2AF1	U2AF1 L4	U2AF2	U2D3L _HUM AN
U464_HUMAN	U66061 _1	U66061 _1_EN ST0000039039 6	UACA	UAP1
UAP1 L 1	UBA1	UBA2	UBA3	UBA5
UBA52	UBA6	UBA7	UBAC1	UBAC2
UBAP1	UBAP2	UBAP2L	UBASH3A	UBASH3B
UBB	UBC	UBD	UBE2A	UBE2B
UBE2C	UBE2CBP	UBE2D1	UBE2D2	UBE2D3
UBE2D4	UBE2E1	UBE2E2	UBE2E3	UBE2F
UBE2G 1	UBE2G2	UBE2H	UBE2I	UBE2J1
UBE2J2	UBE2K	UBE2L3	UBE2L6	UBE2M
UBE2N	UBE2NL	UBE20	UBE2Q1	UBE2Q2
UBE2R2	UBE2S	UBE2T	UBE2U	UBE2V1
UBE2V2	UBE3A	UBE3B	UBE3C	UBE4A
UBE4B	UBFD1	UBIAD1	UBL3	UBL4A
UBL4B	UBL5	UBL7	UBLCP1	UBN1
UBN2	UBOX5	UBP1	UBQLN1	UBQLN2
UBQLN3	UBQLN4	UBQLNL	UBR1	UBR2
UBR3	UBR3 _ENSTOOO 00272793	UBR4	UBR5	UBR7
UBTD1	UBTD2	UBTF	UBXN1	UBXN1 0
UBXN1 1	UBXN2A	UBXN2B	UBXN4	UBXN6
UBXN7	UBXN8	UCHL1	UCHL3	UCHL5
UCK1	UCK2	UCKL1	UCMA	UCN
UCN2	UCN3	UCP1	UCP2	UCP3
UEVLD	UFC1	UFD1 L	UFM1	UFSP1
UFSP2	UGCG	UGDH	UGGT1	UGGT2
UGP2	UGT1 A 1	UGT1 A 10	UGT1 A3	UGT1 A4
UGT1 A5	UGT1 A6	UGT1 A7	UGT1 A8	UGT1 A9
UGT2A1	UGT2A3	UGT2B1 1	UGT2B1 5	UGT2B1 7
UGT2B28	UGT2B4	UGT2B7	UGT3A1	UGT3A2
UGT8	UHMK1	UHRF1	UHRF1 BP1	UHRF1 BP1 L
UHRF2	UIMC1	ULBP1	ULBP2	ULBP3
ULK1	ULK2	ULK3	ULK4	UMOD
UMODL1	UMPS	UNC1 19	UNC1 19B	UNC1 3B
UNC1 3D	UNC45A	UNC45B	UNC50	UNC5A
UNC5B	UNC5C	UNC5CL	UNC5D	UNC80
UNC93A	UNC93B6	UNCX	UNG	UNG _ENSTO 0000242576
UNK	UNKL	UNQ1 887	UNQ3045	UNQ9391

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
UPB1	UPF1	UPF2	UPF3A	UPF3B
UPK1 A	UPK1 B	UPK2	UPK3A	UPK3B
UPP1	UPP2	UPRT	UQCC	UQCR1 1
UQCRB	UQCRC1	UQCRC2	UQCRFS1	UQCRH
UQCRQ	URB2	URGCP	URM1	UROC1
UROD	UROS	URP2	USF1	USF2
USH1 C	USH1 G	USH2A	USHBP1	USMG5
USMG5P1	US01	USP1	USP1 0	USP1 1
USP1 2	USP1 3	USP1 4	USP1 5	USP1 6
USP1 7L2	USP1 8	USP1 9	USP2	USP20
USP21	USP22	USP24	USP25	USP26
USP27X	USP28	USP29	USP3	USP30
USP31	USP32	USP33	USP34	USP35
USP35_ENSTOO 00026331 1	USP36	USP37	USP38	USP39
USP4	USP41	USP42	USP43	USP44
USP45	USP46	USP47	USP48	USP49
USP5	USP50	USP51	USP53	USP54
USP54_ENSTOO 00040801 9	USP6	USP6NL	USP7	USP8
USP9X	USP9Y	USPL1	UST	UTF1
UTP1 1L	UTP1 4A	UTP1 4C	UTP1 5	UTP1 8
UTP20	UTP23	UTP3	UTP6	UTRN
UTS2	UTS2D	UTS2R	UTY	UVRAG
UXT	VAC 14	VAMP1	VAMP2	VAMP3
VAMP4	VAMP5	VAMP7	VAMP8	VANGL1
VANGL2	VAPA	VAPB	VARS	VARS2
VASH1	VASH2	VASN	VASP	VAT1
VAT1 L	VAV1	VAV2	VAV3	VAX1
VAX2	VBP1	VCAM1	VCAN	VCL
VCP	VCPI P 1	vex	VCX2	VCX3A
VCY	VCY1 B	VDAC1	VDAC2	VDAC3
VDAC4	VDR	VEGFA	VEG FB	VEGFC
VENTX	VEPH1	VEZF1	VGF	VGLL1
VGLL2	VGLL3	VGLL4	VHL	VHLL
VIL1	VILL	VIM	VIP	V IPAR
V IPR1	V IPR2	VIT	VKORC1	VKORC1 L 1
VLDLR	VMA21	VMAC	VM01	VN1 R 1
VN1 R2	VN1 R4	VN2R1 P	VNN1	VNN2
VNN3	VPRBP	VPREB1	VPREB3	VPS1 1
VPS1 3A	VPS1 3B	VPS1 3C	VPS1 3D	VPS1 6
VPS1 8	VPS24	VPS25	VPS26A	VPS26B
VPS28	VPS29	VPS33A	VPS33B	VPS35
VPS36	VPS37A	VPS37B	VPS37C	VPS37D
VPS39	VPS41	VPS45	VPS4B	VPS52
VPS53	VPS54	VPS72	VPS8	VRK1
VRK2	VRK3	VSIG 1	VSIG2	VSIG4
VSIG7	VSIG8	VSNL1	VSTM1	VSTM2B
VSTM2L	VSX1	VSX2	VTA1	VTCN1
VTI 1A	VTI 1B	VTN	VWA1	VWA2

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
VWA3A	VWA3B	VWA5A	VWC2	VWCE
VWDE	VWF	WAC	WAPAL	WARS
WARS2	WAS	WASF1	WASF2	WASF3
WASF4	WASL	WBP1	WBP1 1	WBP2
WBP2NL	WBP4	WBP5	WBSCR1 6	WBSCR1 7
WBSCR22	WBSCR27	WBSCR28	WDFY1	WDFY2
WDFY3	WDFY4	WDHD1	WDR1 1	WDR1 2
WDR1 3	WDR1 6	WDR1 7	WDR1 8	WDR1 9
WDR20	WDR23	WDR24	WDR25	WDR26
WDR27	WDR27 _ENSTOO 000333572	WDR3	WDR31	WDR33
WDR34	WDR35	WDR36	WDR37	WDR38
WDR4	WDR41	WDR43	WDR44	WDR44 _ENS T000004353 84
WDR45	WDR45L	WDR46	WDR47	WDR48
WDR49	WDR5	WDR51 A	WDR51 B	WDR52
WDR52 _ENSTOO 000393845	WDR53	WDR54	WDR55	WDR57
WDR59	WDR5B	WDR6	WDR60	WDR61
WDR62	WDR63	WDR64	WDR65	WDR66
WDR67	WDR69	WDR7	WDR70	WDR72
WDR73	WDR75	WDR76	WDR77	WDR78
WDR8	WDR81	WDR82	WDR82 _ENST 00000296490	WDR83
WDR85	WDR88	WDR89	WDR90	WDR91
WDR92	WDR93	WDSUB1	WDTC1	WDYHV1
WEE1	WEE2	WFDC1	WFDC1 0A	WFDC1 0B
WFDC1 1	WFDC1 2	WFDC1 3	WFDC2	WFDC3
WFDC5	WFDC6	WFDC8	WFDC9	WFIKKN1
WFIKKN2	WFS1	WHAMM _ENS T00000234505	WHSC1	WHSC1 L 1
WHSC2	WIF1	WIPF1	WIPF2	WIPF3
WIPI1	WIPI2	WISP1	WISP2	WISP3
WIT1	WIZ	WLS	WNK1	WNK2
WNK3	WNK4	WNT1	WNT1 0A	WNT1 0B
WNT1 1	WNT1 6	WNT2	WNT2B	WNT3
WNT3A	WNT4	WNT5A	WNT5B	WNT6
WNT7A	WNT7B	WNT8A	WNT8B	WNT9A
WNT9B	WRAP53	WRB	WRN	WRNIP1
WSB1	WSB2	WSCD1	WSCD2	WT1
WTAP	WTIP	WWC1	WWC2	WWC3
WWOX	WWP1	WWP2	WWTR1	XAB1
XAB2	XAF1	XAG E 1C	XAGE1 D	XAG E2
XAG E3	XAG E5	XBP1	XCL1	XCL2
XCR1	XDH	XG	XIAP	XIRP1
XIRP2	XIRP2 _ENSTOOO 00409728	XK	XKR3	XKR4
XKR5	XKR6	XKR7	XKR8	XKR9
XKRX	XPA	XPC	XPNPEP1	XPNPEP2
XPNPEP3	XP01	XP04	XP05	XP06

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
XP07	XPOT	XPR1	XRCC1	XRCC2
XRCC3	XRCC4	XRCC5	XRCC6	XRCC6BP1
XRN1	XRN2	XRRA1	XXyac-YX1 55B6_1	XYLB
XYLT1	XYLT2	YAF2	YAP1	YARS
YARS2	YBX1	YBX2	YDJC	YEATS2
YEATS4	YES1	YIF1A	YIF1 B	YIPF1
YIPF2	YIPF3	YIPF4	YIPF5	YIPF6
YJEFN3	YKT6	YLPM1	YME1 L1	YOD1
YPEL1	YPEL2	YPEL3	YPEL4	YPEL5
YRDC	YSK4	YSK4_ENSTOO 000375845	YTHDC1	YTHDC2
YTHDF1	YTHDF2	YV009_HUMA N	YWHAB	YWHAE
YWHAG	YWHAH	YWHAQ	YWHAZ	YY1
YY1 AP1	YY2	ZACN	ZADH1	ZADH2
ZAK	ZAN	ZAP70	ZAR1	ZAR1 L
ZBBX	ZBBX_ENSTOOO 00455345	ZBED1	ZBED2	ZBED3
ZBED4	ZBP1	ZBTB1	ZBTB1 0	ZBTB1 1
ZBTB1 2	ZBTB1 6	ZBTB1 7	ZBTB2	ZBTB20
ZBTB22	ZBTB24	ZBTB25	ZBTB26	ZBTB3
ZBTB32	ZBTB33	ZBTB34	ZBTB37	ZBTB38
ZBTB39	ZBTB4	ZBTB40	ZBTB41	ZBTB43
ZBTB44	ZBTB45	ZBTB46	ZBTB48	ZBTB49
ZBTB5	ZBTB6	ZBTB7A	ZBTB7B	ZBTB7C
ZBTB8A	ZBTB8B_ENSTO 0000291 374	ZBTB80S	ZBTB9	ZC3H1 0
ZC3H1 1A	ZC3H1 2A	ZC3H1 2B	ZC3H1 2B_ENS T00000338957	ZC3H1 2C
ZC3H1 3	ZC3H1 4	ZC3H1 5	ZC3H1 8	ZC3H3
ZC3H4	ZC3H6	ZC3H7A	ZC3H7B	ZC3H8
ZC3HAV1	ZC3HAV1 L	ZC3HC1	ZC4H2	ZCCHC1 0
ZCCHC1 1	ZCCHC1 2	ZCCHC1 3	ZCCHC1 4	ZCCHC1 6
ZCCHC1 7	ZCCHC24	ZCCHC3	ZCCHC4	ZCCHC5
ZCCHC6	ZCCHC7	ZCCHC8	ZCCHC9	ZCRB1
ZCWPW1	ZCWPW2	ZDHHC1	ZDHHC1 1	ZDHHC1 1_E NST0000042 4784
ZDHHC1 2	ZDHHC1 3	ZDHHC1 4	ZDHHC1 5	ZDHHC1 6
ZDHHC1 8	ZDHHC1 9	ZDHHC21	ZDHHC23	ZDHHC24
ZDHHC3	ZDHHC4	ZDHHC5	ZDHHC6	ZDHHC7
ZDHHC8	ZDHHC9	ZEB1	ZEB2	ZER1
ZFAND1	ZFAND2A	ZFAND2B	ZFAND3	ZFAND5
ZFAND6	ZFAT	ZFC3H1	ZFHX3	ZFHX4
ZFP1	ZFP1 06	ZFP1 12	ZFP1 4	ZFP1 6 1
ZFP2	ZFP28	ZFP3	ZFP30	ZFP36
ZFP36L1	ZFP36L2	ZFP37	ZFP41	ZFP42
ZFP57	ZFP64	ZFP64_ENSTO 0000361 387	ZFP82	ZFP90
ZFP91	ZFP91 -CNTF	ZFP92	ZFPL1	ZFPM1

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ZFPM2	ZFR	ZFR2	ZFX	ZFY
ZFYVE1	ZFYVE1 6	ZFYVE1 9	ZFYVE20	ZFYVE21
ZFYVE26	ZFYVE27	ZFYVE28	ZFYVE9	ZG16B
ZGPAT	ZHX1	ZHX2	ZHX3	ZIC1
ZIC2	ZIC3	ZIC4	ZIC5	ZIK1
ZIM2	ZIM3	ZKSCAN1	ZKSCAN2	ZKSCAN3
ZKSCAN4	ZKSCAN5	ZMAT1	ZMAT2	ZMAT3
ZMAT4	ZMAT5	ZMIZ1	ZMIZ2	ZMPSTE24
ZMYM1	ZMYM2	ZMYM3	ZMYM4	ZMYM5
ZMYM6	ZMYND1 0	ZMYND1 1	ZMYND1 2	ZMYND1 5
ZMYND1 7	ZMYND1 9	ZMYND8	ZNF1 0	ZNF1 00
ZNF1 01	ZNF1 07	ZNF1 0_ENSTO 0000228289	ZNF1 14	ZNF1 17
ZNF1 2	ZNF1 21	ZNF1 23	ZNF1 24	ZNF1 31
ZNF1 32	ZNF1 33	ZNF1 34	ZNF1 35	ZNF1 36
ZNF1 38	ZNF1 4	ZNF1 40	ZNF1 41	ZNF1 42
ZNF1 43	ZNF1 46	ZNF1 48	ZNF1 54	ZNF1 55
ZNF1 57	ZNF1 6	ZNF1 60	ZNF1 65	ZNF1 67
ZNF1 69	ZNF1 7	ZNF1 74	ZNF1 75	ZNF1 77
ZNF1 8	ZNF1 80	ZNF1 81	ZNF1 82	ZNF1 84
ZNF1 85	ZNF1 89	ZNF1 9	ZNF1 92	ZNF1 93
ZNF1 95	ZNF1 97	ZNF1 98	ZNF2	ZNF20
ZNF200	ZNF202	ZNF205	ZNF207	ZNF21 1
ZNF21 2	ZNF21 3	ZNF21 4	ZNF21 5	ZNF21 7
ZNF21 9	ZNF22	ZNF221	ZNF222	ZNF223
ZNF224	ZNF227	ZNF229	ZNF23	ZNF230
ZNF232	ZNF233	ZNF235	ZNF236	ZNF238
ZNF239	ZNF24	ZNF248	ZNF25	ZNF251
ZNF253	ZNF254	ZNF256	ZNF257	ZNF257_ENST00000435820
ZNF259	ZNF26	ZNF260	ZNF263	ZNF264
ZNF266	ZNF267	ZNF271	ZNF273	ZNF274
ZNF275	ZNF276	ZNF277	ZNF278	ZNF28
ZNF280A	ZNF280B	ZNF280C	ZNF280D	ZNF281
ZNF282	ZNF283	ZNF285A	ZNF286A	ZNF287
ZNF292	ZNF295	ZNF296	ZNF3	ZNF30
ZNF300	ZNF304	ZNF31 1	ZNF31 7	ZNF31 8
ZNF31 9	ZNF32	ZNF320	ZNF321	ZNF322A
ZNF322B	ZNF323	ZNF324	ZNF324B	ZNF326
ZNF329	ZNF330	ZNF331	ZNF333	ZNF334
ZNF335	ZNF337	ZNF33A	ZNF33B	ZNF34
ZNF341	ZNF343	ZNF345	ZNF346	ZNF347
ZNF35	ZNF350	ZNF354A	ZNF354B	ZNF354C
ZNF358	ZNF362	ZNF365	ZNF366	ZNF367
ZNF37A	ZNF382	ZNF383	ZNF384	ZNF385
ZNF385A	ZNF385B	ZNF385C	ZNF385D	ZNF391
ZNF394	ZNF395	ZNF396	ZNF397	ZNF3970S
ZNF398	ZNF407	ZNF408	ZNF41	ZNF41 0
ZNF41 4	ZNF41 4_ENSTO 0000393927	ZNF41 5	ZNF41 6	ZNF41 7

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ZNF41 8	ZNF41 9	ZNF420	ZNF423	ZNF425
ZNF426	ZNF428	ZNF429	ZNF43	ZNF430
ZNF431	ZNF432	ZNF432_ENST00000354939	ZNF434	ZNF436
ZNF438	ZNF439	ZNF440	ZNF441	ZNF442
ZNF443	ZNF444	ZNF445	ZNF446	ZNF449
ZNF45	ZNF451	ZNF454	ZNF460	ZNF462
ZNF467	ZNF468	ZNF470	ZNF471	ZNF473
ZNF474	ZNF479	ZNF48	ZNF480	ZNF483
ZNF484	ZNF485	ZNF486	ZNF488	ZNF490
ZNF491	ZNF492	ZNF492_ENST00000456783	ZNF493	ZNF496
ZNF497	ZNF498	ZNF500	ZNF501	ZNF502
ZNF503	ZNF506	ZNF507	ZNF51 0	ZNF51 1
ZNF51 2	ZNF51 2B	ZNF51 3	ZNF51 4	ZNF51 6
ZNF51 7	ZNF51 8B	ZNF51 9	ZNF521	ZNF524
ZNF526	ZNF527	ZNF528	ZNF529	ZNF530
ZNF532	ZNF534	ZNF536	ZNF540	ZNF541
ZNF543	ZNF544	ZNF546	ZNF547	ZNF548
ZNF549	ZNF550	ZNF551	ZNF552	ZNF554
ZNF555	ZNF556	ZNF557	ZNF558	ZNF559
ZNF560	ZNF561	ZNF562	ZNF563	ZNF564
ZNF565	ZNF566	ZNF567	ZNF568	ZNF569
ZNF57	ZNF570	ZNF571	ZNF572	ZNF573
ZNF574	ZNF575	ZNF576	ZNF577	ZNF579
ZNF580	ZNF581	ZNF582	ZNF583	ZNF584
ZNF585A	ZNF585B	ZNF586	ZNF587	ZNF589
ZNF592	ZNF593	ZNF594	ZNF596	ZNF597
ZNF599	ZNF600	ZNF605	ZNF606	ZNF607
ZNF608	ZNF609	ZNF61 0	ZNF61 1	ZNF61 3
ZNF61 4	ZNF61 5	ZNF61 6	ZNF61 8	ZNF61 9
ZNF620	ZNF621	ZNF622	ZNF623	ZNF624
ZNF625	ZNF626	ZNF627	ZNF628	ZNF628_ENST00000391718
ZNF630	ZNF638	ZNF639	ZNF641	ZNF642
ZNF643	ZNF644	ZNF645	ZNF646	ZNF648
ZNF649	ZNF652	ZNF653	ZNF654	ZNF655
ZNF658	ZNF658B	ZNF660	ZNF662	ZNF664
ZNF665	ZNF667	ZNF668	ZNF669	ZNF67
ZNF670	ZNF671	ZNF672	ZNF673	ZNF674
ZNF675	ZNF676	ZNF677	ZNF678	ZNF680
ZNF682	ZNF684	ZNF687	ZNF688	ZNF689
ZNF69	ZNF691	ZNF692	ZNF696	ZNF697_ENST00000271263
ZNF699	ZNF7	ZNF70	ZNF700	ZNF701
ZNF703	ZNF704	ZNF705A	ZNF705D	ZNF706
ZNF707	ZNF708	ZNF709	ZNF71	ZNF71 0
ZNF71 1	ZNF71 3	ZNF71 4	ZNF738	ZNF74
ZNF746	ZNF747	ZNF750	ZNF75A	ZNF75D

HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name	HGNC Gene Name
ZNF76	ZNF761	ZNF763	ZNF764	ZNF765
ZNF765_ENSTOO000396408	ZNF767	ZNF768	ZNF77	ZNF770
ZNF772	ZNF773	ZNF774	ZNF775	ZNF776
ZNF777	ZNF780A	ZNF781	ZNF782	ZNF784
ZNF785	ZNF786	ZNF787	ZNF788	ZNF789
ZNF79	ZNF790	ZNF791	ZNF793	ZNF799
ZNF8	ZNF80	ZNF800	ZNF804A	ZNF804B
ZNF81	ZNF81 6A	ZNF821	ZNF826	ZNF827
ZNF828	ZNF829	ZNF83	ZNF830	ZNF831
ZNF833	ZNF834	ZNF835	ZNF836	ZNF837
ZNF839	ZNF84	ZNF841_ENST00000359973	ZNF843	ZNF846
ZNF85	ZNF862	ZNF879	ZNF90	ZNF90_ENST0000041 8063
ZNF91	ZNF91_ENSTOO00030061 9	ZNF92	ZNF93	ZNFX1
ZNHIT1	ZNHIT2	ZNHIT3	ZNHIT6	ZNRD1
ZNRF1	ZNRF2	ZNRF3	ZNRF4	ZP1
ZP2	ZP3	ZP4	ZPBP	ZPBP2
ZPLD1	ZRANB1	ZRANB2	ZRANB3	ZRSR2
ZSCAN 1	ZSCAN 10	ZSCAN 16	ZSCAN1 8	ZSCAN2
ZSCAN20	ZSCAN21	ZSCAN22	ZSCAN23	ZSCAN29
ZSCAN4	ZSCAN5A	ZSWIM1	ZSWIM2	ZSWIM3
ZSWIM4	ZSWIM5	ZSWIM7	ZUFSP	ZW1 0
ZWILCH	ZWINT	ZXDA	ZXDB	ZXDC
ZYG 11B	ZYX	ZZEF1	ZZZ3	dJ341 D 10_1
hCG_1642425	hCG_1644301	hCG_17324	hCG_1757335	hCG_1793639
hCG_2000329	hCG_201 5269	hCG_2023776	hCG_2026038	hCG_38941
mir-223	mir-424			

Table 4 Exemplary transposable elements in GBM microvesicles

Name	GenBank Accession No.
Homo sapiens transposon-derived Buster1 transposase-like protein gene (LOC58486)	[NM_021211]
Human endogenous retrovirus H protease/integrase-derived ORF1, ORF2, and putative envelope protein mRNA, complete cds	[U88896]
Human endogenous retrovirus type C oncovirus sequence	[M74509]
Human endogenous retroviral H protease/integrase-derived ORF1 mRNA, complete cds, and putative envelope protein mRNA, partial cds.	[U88898]
Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence (CBL)	[NM_005188]
Homo sapiens endogenous retroviral sequence K, 6 (ERVK6)	[NM_001007236]
Homo sapiens endogenous retroviral family W, env(C7), member 1 (syncytin) (ERVWE1)	[NM_014590]
Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence b (CBLB)	[NM_170662]
Homo sapiens mRNA containing human endogenous retrovirus H and human endogenous retrovirus E sequences	[AF026246]
Homo sapiens cDNA FLJ11804 fis, clone HEMBA1006272, moderately similar to RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).	[AK021866]
Human DNA/endogenous retroviral long terminal repeat (LTR) junction mRNA, clone lambda-LTR22	[M32220]
ALU8_HUMAN (P39195) Alu subfamily SX sequence contamination warning entry, partial (7%)	[THC2390306]
AA436686 zv59al2.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757918 3' similar to contains Alu repetitive element	[AA436686]
ALU6_HUMAN (P39193) Alu subfamily SP sequence contamination warning entry, partial (19%)	[THC2314369]
ALU1_HUMAN (P39188) Alu subfamily J sequence contamination warning entry, partial (8%)	[THC2320431]
BF476310 naa21a07.xl NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3255444 3' similar to contains Alu repetitive element;contains element MIR MIR repetitive element	[BF476310]

Name	GenBank Accession No.
ALU4_HUMAN (P39191) Alu subfamily SB2 sequence contamination warning entry, partial (4%)	[THC2284657]
LINl_NYCCO (P08548) LINE-1 reverse transcriptase homolog, partial (5%)	[THC2379144]
od56h08.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE: 137 1999 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)	[AA827885]
B28096 line-1 protein ORF2 - human (Homo sapiens), partial (4%)	[THC2281068]
Homo sapiens LINE-1 type transposase domain containing 1 (L1TD1)	[NM_019079]
Q6D545 (Q6D545) Transposase transposon tnl721 (Fragment), partial (12%)	[THC2407148]
Human clone 279131 defective mariner transposon Hsmar2 mRNA sequence	[U92025]
Homo sapiens retrotransposon gag domain containing 4 (RGAG4)	[NM_001024455]
Homo sapiens transposon-derived Buster3 transposase-like (LOC63920)	[NM_022090]
Homo sapiens retrotransposon gag domain containing 1 (RGAG1)	[NM_020769]
Human EST clone 251800 mariner transposon Hsmarl sequence	[U80770]
Homo sapiens SET domain and mariner transposase fusion gene (SETMAR)	[NM_006515]
Homo sapiens tigger transposable element derived 5 (TIGD5)	[NM_032862]
Homo sapiens tigger transposable element derived 1 (TIGD1)	[NM_145702]
Homo sapiens pogo transposable element with KRAB domain (POGK)	[NM_017542]
Homo sapiens pogo transposable element with ZNF domain (POGZ), transcript variant 1	[NM_015100]
Homo sapiens tigger transposable element derived 6 (TIGD6)	[NM_030953]
Homo sapiens piggyBac transposable element derived 4 (PGBD4)	[NM_152595]

Table 5 Human transposable elements.

The list is adapted from Repbase-GIRI. http://www.girinst.org/, accessed January 31, 2011.

Type of Transposon	ID
CR1	CR1_HS
CR1	L3
DNA transposon	LOOPER
DNA transposon	MER105
DNA transposon	MER116
DNA transposon	MER28
DNA transposon	MER45B
DNA transposon	MER45R
DNA transposon	MER53
DNA transposon	MER63A
DNA transposon	MER63B
DNA transposon	MER69C
DNA transposon	MER75
DNA transposon	MER75B
DNA transposon	MER85
DNA transposon	MER91A
DNA transposon	MER91C
DNA transposon	MER99
DNA transposon	ZAPHOD
Endogenous Retrovirus	HERV1_LTR
Endogenous Retrovirus	HERV15I
Endogenous Retrovirus	HERV18
Endogenous Retrovirus	HERV23
Endogenous Retrovirus	HERV30I
Endogenous Retrovirus	HERV38I
Endogenous Retrovirus	HERV39
Endogenous Retrovirus	HERV4_LTR
Endogenous Retrovirus	HERV46I
Endogenous Retrovirus	HERV52I
Endogenous Retrovirus	HERV57I
Endogenous Retrovirus	HERVFH19I
Endogenous Retrovirus	HERVG25
Endogenous Retrovirus	HERVH48I
Endogenous Retrovirus	HERVL_40
Endogenous Retrovirus	HERVP71A_I
Endogenous Retrovirus	HUERS-P2
Endogenous Retrovirus	HUERS-P3B
Endogenous Retrovirus	MER31
Endogenous Retrovirus	MER31_I
Endogenous Retrovirus	MER34B_I
Endogenous Retrovirus	MER41F
Endogenous Retrovirus	MER41I
Endogenous Retrovirus	MER4BI
Endogenous Retrovirus	MER57A_I
Endogenous Retrovirus	MER57I
Endogenous Retrovirus	MER61A
Endogenous Retrovirus	MER84I
Endogenous Retrovirus	PRIMA4_I
Endogenous Retrovirus	PRIMA41
Endogenous Retrovirus	PRIMAXJ
ERV1	HARLEQUIN
ERV1	HERV17
ERV1	HERV19I
ERV1	HERV3
ERV1	HERV35I
ERV1	HERV4_I
ERV1	HERV49I
ERV1	HERV9
ERV1	HERVE
ERV1	HERVI
ERV1	HERVIP10F
ERV1	HERVIP10FH
ERV1	LOR1I
ERV1	LTR06
ERV1	LTR1
ERV1	LTR10B
ERV1	LTR10B2
ERV1	LTR10C
ERV1	LTR10D
ERV1	LTR10F
ERV1	LTR12B
ERV1	LTR12C
ERV1	LTR12D
ERV1	LTR12E
ERV1	LTR15
ERV1	LTR17
ERV1	LTR1B

Type_of Transposon	ID
ERV1	LTR1B1
ERV1	LTR1C
ERV1	LTR1C2
ERV1	LTR1D
ERV1	LTR1E
ERV1	LTR1F
ERV1	LTR2
ERV1	LTR21A
ERV1	LTR21B
ERV1	LTR21C
ERV1	LTR23
ERV1	LTR24
ERV1	LTR24B
ERV1	LTR24C
ERV1	LTR25
ERV1	LTR26
ERV1	LTR26E
ERV1	LTR27
ERV1	LTR2752
ERV1	LTR27B
ERV1	LTR27C
ERV1	LTR27D
ERV1	LTR27E
ERV1	LTR28
ERV1	LTR28B
ERV1	LTR28C
ERV1	LTR29
ERV1	LTR2B
ERV1	LTR2C
ERV1	LTR30
ERV1	LTR31
ERV1	LTR34
ERV1	LTR35
ERV1	LTR35B
ERV1	LTR36
ERV1	LTR37A
ERV1	LTR37B
ERV1	LTR38
ERV1	LTR38A1
ERV1	LTR38B
ERV1	LTR38C

Type_of Transposon	ID
ERV1	LTR39
ERV1	LTR4
ERV1	LTR43
ERV1	LTR43B
ERV1	LTR44
ERV1	LTR45
ERV1	LTR45B
ERV1	LTR45C
ERV1	LTR46
ERV1	LTR48
ERV1	LTR48B
ERV1	LTR49
ERV1	LTR51
ERV1	LTR56
ERV1	LTR58
ERV1	LTR59
ERV1	LTR60
ERV1	LTR60B
ERV1	LTR61
ERV1	LTR64
ERV1	LTR65
ERV1	LTR6A
ERV1	LTR6B
ERV1	LTR70
ERV1	LTR71A
ERV1	LTR71B
ERV1	LTR72
ERV1	LTR72B
ERV1	LTR73
ERV1	LTR76
ERV1	LTR77
ERV1	LTR78B
ERV1	LTR8
ERV1	LTR81AB
ERV1	LTR8A
ERV1	LTR8B
ERV1	LTR9
ERV1	LTR9A1
ERV1	LTR9B
ERV1	LTR9C
ERV1	LTR9D

Type_of Transposon	ID
ERV1	MER101
ERV1	MER101B
ERV1	MER110
ERV1	MER110A
ERV1	MER110I
ERV1	MER21I
ERV1	MER31B
ERV1	MER34
ERV1	MER34B
ERV1	MER34C
ERV1	MER34C2
ERV1	MER39
ERV1	MER39B
ERV1	MER41A
ERV1	MER41B
ERV1	MER41C
ERV1	MER41D
ERV1	MER41G
ERV1	MER48
ERV1	MER49
ERV1	MER4A
ERV1	MER4A1
ERV1	MER4B
ERV1	MER4C
ERV1	MER4CL34
ERV1	MER4D
ERV1	MER4D1
ERV1	MER4E
ERV1	MER4E1
ERV1	MER50
ERV1	MER50B
ERV1	MER50I
ERV1	MER51A
ERV1	MER51B
ERV1	MER51C
ERV1	MER51D
ERV1	MER51E
ERV1	MER52A
ERV1	MER52AI
ERV1	MER52C
ERV1	MER52D

Type_of Transposon	ID
ERV1	MER57A1
ERV1	MER57B2
ERV1	MER57F
ERV1	MER61B
ERV1	MER61C
ERV1	MER65B
ERV1	MER65C
ERV1	MER65D
ERV1	MER66_I
ERV1	MER66A
ERV1	MER66B
ERV1	MER66C
ERV1	MER66D
ERV1	MER67A
ERV1	MER67B
ERV1	MER67C
ERV1	MER67D
ERV1	MER72
ERV1	MER72B
ERV1	MER83
ERV1	MER83AI
ERV1	MER83B
ERV1	MER83BI
ERV1	MER83C
ERV1	MER84
ERV1	MER87
ERV1	MER87B
ERV1	MER89
ERV1	MER89I
ERV1	MER90
ERV1	MER92A
ERV1	MER92B
ERV1	PABL_A
ERV1	PABL_AI
ERV1	PABL_B
ERV1	PABL_BI
ERV1	PRIMA4_LTR
ERV1	PrimLTR79
ERV2	HERVK11DI
ERV2	HERVK11I
ERV2	HERVK13I

Type of Transposon	ID
ERV2	HERVK3I
ERV2	HERVK9I
ERV2	LTR13
ERV2	LTR13A
ERV2	LTR14
ERV2	LTR14A
ERV2	LTR14B
ERV2	LTR14C
ERV2	LTR22A
ERV2	LTR22B
ERV2	LTR22B1
ERV2	LTR22B2
ERV2	LTR22C2
ERV2	LTR22E
ERV2	LTR3
ERV2	LTR3B
ERV2	LTR5
ERV2	LTR5B
ERV2	MER11A
ERV2	MER11C
ERV2	MER11D
ERV2	MER9
ERV2	MER9B
ERV2	RLTR10B
ERV2	RLTR10C
ERV3	ERV3-16A3_I
ERV3	ERV3-16A3_LTR
ERV3	ERVL
ERV3	HERV16
ERV3	HERVL
ERV3	HERVL74
ERV3	LTR16
ERV3	LTR16A1
ERV3	LTR16A2
ERV3	LTR16C
ERV3	LTR16D
ERV3	LTR16E
ERV3	LTR18A
ERV3	LTR18B
ERV3	LTR18C
ERV3	LTR19A

Type of Transposon	ID
ERV3	LTR19B
ERV3	LTR19C
ERV3	LTR32
ERV3	LTR40A
ERV3	LTR40B
ERV3	LTR40C
ERV3	LTR41
ERV3	LTR41B
ERV3	LTR41C
ERV3	LTR42
ERV3	LTR47A
ERV3	LTR47A2
ERV3	LTR47B
ERV3	LTR47B2
ERV3	LTR50
ERV3	LTR52
ERV3	LTR53
ERV3	LTR53B
ERV3	LTR55
ERV3	LTR57
ERV3	LTR62
ERV3	LTR66
ERV3	LTR69
ERV3	LTR75
ERV3	LTR75B
ERV3	LTR77B
ERV3	LTR7A
ERV3	LTR7B
ERV3	LTR7C
ERV3	MER21
ERV3	MER21A
ERV3	MER54_EC
ERV3	MER54A
ERV3	MER54B
ERV3	MER68B
ERV3	MER68C
ERV3	MER70A
ERV3	MER70B
ERV3	MER70C
ERV3	MER73
ERV3	MER74B

Type of Transposon	ID
ERV3	MER74C
ERV3	MER76
ERV3	MER77
ERV3	MER88
ERV3	MLT1G
ERV3	MLT1G1
ERV3	MLT1G2
ERV3	MLT1G3
ERV3	MLT1H
ERV3	MLT1H1
ERV3	MLT1H2
ERV3	MLT1I
ERV3	MLT1K
ERV3	MLT1L
ERV3	MLT1N2
ERV3	MLT2A1
ERV3	MLT2A2
ERV3	MLT2C2
ERV3	MLT2D
ERV3	MSTB
ERV3	MSTD
ERV3	RMER10B
ERV3	THE1A
ERV3	THE1C
ERV3	THE1D
hAT	CHARLIE10
hAT	CHARLIE2A
hAT	CHARLIE2B
hAT	CHARLIE3
hAT	CHARLIE5
hAT	CHARLIE6
hAT	CHARLIE7
hAT	CHARLIE8
hAT	CHARLIE9
hAT	CHESHIRE
hAT	CHESHIRE_A
hAT	CHESHIRE_B
hAT	FORDPREFECT
hAT	FORDPREFECT_A
hAT	MER103B

Type of Transposon	ID
hAT	MER103C
hAT	MER106
hAT	MER106B
hAT	MER107
hAT	MER112
hAT	MER113
hAT	MER113B
hAT	MER117
hAT	MER119
hAT	MER1A
hAT	MER1B
hAT	MER20
hAT	MER20B
hAT	MER30B
hAT	MER33
hAT	MER45
hAT	MER45C
hAT	MER5B
hAT	MER63D
hAT	MER80B
hAT	MER81
hAT	MER94
hAT	MER94B
hAT	MER96
hAT	MER96B
hAT	MER97A
hAT	MER97B
hAT	MER97C
L1	HAL1B
L1	IN25
L1	LI
L1	L1HS
L1	L1M1B_5
L1	L1M2_5
L1	L1M2A_5
L1	L1M2A1_5
L1	L1M2B_5
L1	L1M2C_5
L1	L1M3B_5
L1	L1M3C_5
L1	L1M4B

Type of Transposon	ID
L1	LlM6B_5end
L1	L1MA1
L1	L1MA2
L1	L1MA3
L1	L1MA4
L1	L1MA4A
L1	L1MA5
L1	L1MA5A
L1	L1MA6
L1	L1MA7
L1	L1MA8
L1	L1MA9
L1	L1MB1
L1	L1MB2
L1	L1MB3
L1	L1MB3_5
L1	L1MB4
L1	L1MB5
L1	L1MB8
L1	L1MC1
L1	L1MC2
L1	L1MC4
L1	L1MCA_5
L1	L1MCB_5
L1	L1MCC_5
L1	L1MD1
L1	L1MD2
L1	L1MD3
L1	L1MDB_5
L1	L1ME_0RF2
L1	L1ME1
L1	L1ME2
L1	L1ME3
L1	L1ME3A
L1	L1ME4A
L1	L1MEA_5
L1	L1MEB_5
L1	L1MED_5
L1	L1MEE_5
L1	L1PA10
L1	L1PA11

Type of Transposon	ID
L1	L1PA12
L1	L1PA12_5
L1	L1PA13
L1	L1PA13_5
L1	L1PA14
L1	L1PA14_5
L1	L1PA15
L1	L1PA16
L1	L1PA16_5
L1	L1PA17_5
L1	L1PA2
L1	L1PA3
L1	L1PA4
L1	L1PA5
L1	L1PA6
L1	L1PA7
L1	L1PA7_5
L1	L1PA8
L1	L1PB1
L1	L1PB2
L1	LlPB2c
L1	L1PB3
L1	L1PB4
L1	L1PBA_5
L1	L1PBA1_5
L1	L1PBB_5
L1	L1PREC1
L1	L1PREC2
LTR Retrotransposon	HARLEQUINLTR
LTR Retrotransposon	HERV-K14CI
LTR Retrotransposon	HERV-K14I
LTR Retrotransposon	HUERS-P3
LTR Retrotransposon	LOR1
LTR Retrotransposon	LTR11
LTR Retrotransposon	MER4I
LTR Retrotransposon	MER51I
LTR Retrotransposon	MER52B
LTR Retrotransposon	MER61D
LTR Retrotransposon	MER61E
LTR Retrotransposon	MER61F
LTR Retrotransposon	MER61I

Type of Transposon	ID
LTR Retrotransposon	MER95
LTR Retrotransposon	PTR5
LTR Retrotransposon	THE1_I
Mariner/Tc1	GOLEM_A
Mariner/Tc1	GOLEM_C
Mariner/Tc1	HSMAR1
Mariner/Tc1	HSMAR2
Mariner/Tc1	HSTC2
Mariner/Tc1	KANGA2_A
Mariner/Tc1	MADE1
Mariner/Tc1	MARINER1_EC
Mariner/Tc1	MARNA
Mariner/Tc1	MER44A
Mariner/Tc1	MER44B
Mariner/Tc1	MER44C
Mariner/Tc1	MER6B
Mariner/Tc1	MER8
Mariner/Tc1	TIGGER1
Mariner/Tc1	TIGGER2
Mariner/Tc1	TIGGER5
Mariner/Tc1	TIGGER6B
Mariner/Tc1	TIGGER7
Mariner/Tc1	TIGGER8
Mariner/Tc1	TIGGER9
Mariner/Tc1	ZOMBI_A
Merlin	Merlinl_HS
SINE	SVA
SINE1/7SL	AluYa5
SINE1/7SL	AluYb8
SINE1/7SL	AluYb9
SINE1/7SL	AluYkl3
SINE3/5S	AmnSINEl_HS
Transposable Element	MER54
Transposable Element	TARE

Table 6 Satellite correlated genes. Adapted from Ting et al.(Ting et al., 2011)

Gene Names
A2ML1
ABCA9
ACADSB
ACBD7
ADAMTSL3
ALG11
ANGEL2
ANKRD20A1
API S3
APOL4
APOL6
ATP10B
BNC1
C110RF72
C110RF74
C120RF5
C130RF29
C150RF2
C150RF28
C170RF77
C1ORF130
C10RF69
C10RF84
C210RF82
C3ORF20
C6ORF170
C70RF44
C70RF46
C80RF12
C90RF68
CAGE1
CCBP2
CCDC122
CCDC52
CD3EAP
CDON
CENPM
CES3
CES7
CHRM5
CLCC1
COX 18
CPM
CPSF2
CYP46A1
DBF4B

Gene Names
DCHS2
DDO
DHRS4L2
DKFZP434L187
DKFZP779L1853
DNAH5
DNAH8
DSG3
DUSP19
DZIP3
EEF2K
F2RL3
FAMlllB
FAM122C
FAM22G
FAM75A2
FAM83D
FAT3
FBX015
FBXW10
FCF1
FER
FGF5
FLJ11292
FLJ41649
FLJ43763
FUT1
GALNT13
GBP4
GK5
GLIPR1L2
GPR110
GPR157
GTPBP10
GTSE1
GUSBP1
HERC4
HESRG
HIF3A
HMGA2
HRH4
HUNK
HYDIN
IL12RB1
IP09
KCTD18

Gene Names
KIAA1245
KIAA1257
KIAA1328
KIR3DX1
LEPRE1
LOC147804
LOC349196
LOC440313
LOC441242
LOC441426
LOC642980
LOC643406
LOC649305
LOC91948
LRRC2
LTV1
LYRM2
LYRM7
MCFD2
MED 18
MORC4
MSH5
MTBP
MX2
MYH1
MY03B
MYOM3
NBPF1
NEB
NHEDC1
NIPSNAP3B
NME7
NMNAT1
NUP43
ODF2L
OR11H1
OR11H12
OR4F16
OR4K15
OR7D2
OR7E156P
ORC6L
PCBD2
PDDC1
PGPEP1
PHACTR4

Gene Names
PHTF1
PLA2G2D
PLEKHA5
PRKRIR
PRND
PXMP4
QTRTD1
RASGRP3
REX01L1
RGR
RNF125
SIGLEC10
SIGLEC8
SIRPB1
SLC13A2
SLC14A2
SLC16A12
SLC19A3
SLC1A6
SLC27A1
SLC31A1
SMU1
SP100
STRC
STX17
TAOK1
TCL6
TEX9
TGFB2
TIGD1
TNFRSF19
TRIM43
TRPM3
TTN
ULBP1
USPL1
UTP14C
WDR17
WDR31
XKR9
XRCC2
ZFYVE20
ZMYM1
ZMYND17
ZNF100
ZNF192
ZNF208
ZNF273
ZNF320
ZNF331
ZNF37A
ZNF383

Gene Names
ZNF431
ZNF445
ZNF471
ZNF480
ZNF490
ZNF492
ZNF493
ZNF528
ZNF562
ZNF621
ZNF623
ZNF667
ZNF670
ZNF7
ZNF720
ZNF804B
BC029464
BC082237
BC050580
BC039319
AK096834
BC042893
BC043508
HBET1
NR_003246
LOC643079
BC040190
AK095450
BC036442
DKFZP761G18121
AK092337
KIAA0379
FLJ44076
AX748237
AX747345
AX747165
CR627148
UNQ2963
DKFZP667M2411
AK125319
AK125996
AK026805
AK129982
CR592614
AK095077
BC035989
CR623134
AK026100
RP1-140A9.6
AX747405
NR_002828
NR_003130

Gene Names
BIRC4BP
AK054836
AX747417
AY314745
NR_001318
AX747586
AK125128
AK055694
BC035084
WUGSC:H_DJ0855D2
1.2
CR596262
AX746734
AK024378
BC037952
BC041998
BC008050
NR_003133
AX748369
BC043541
AK131347
FLJ00140
CR620525
AX748243
AX747639
AX746484
CR605783
AK097143
BC052952
AK124179
FLJ16008
BC073807
BC015784
CR592225
BC031280
DKFZP686F19123
AX747440
AK096469
AK124893
AX747721
AK123584
NR_003263
DKFZP762C213
BC094791
CR627394
AK124673
NR_002910
FRABIN
BC069727
BC037884
BX648696
CR627383

Gene Names
BC034569
AX747308
AK123585
BC011779
DKFZP686H1615
BC070093
BX537874
AX748226
CR598144
BC040189
AL832479
NR_002939
AL833449
BC047600
KIAA1031
AK095766
AL832786
BC035181
NR_002220
DQ596646
NM_001001704
AL832797
AK129672
AK123838
AX746771
C20ORF38
AX746989
LOC285382
MGC102966
AK124194
FLJ45337
AK126334
AK057596
NR_003128
AK096077
DERP7
AK098126
BC033330
BC029555
LOCI 29881
AK097527
BX648961
AK096499
AK097777
AK091028
FLJ37953
PTPN1L
AK096196
AK056351
AX746750
LOC440053
BC068605

Gene Names
UNQ9369
PFDN6L
AK125042
AK125489
BC013681
AK056866
AX747590
AX746620
FLJ00310
NM_001042703
AK094618
AX748002
BC041646
AJ617629
AL833139
AK097428
AK056105
MGC13098
AK127557
KIAA1456
BC069809
LOC441108
NM_001039909
AK096291
BX537710
BC041449
NR_002836
CR598129
BC035112
CR613732
DQ597733
AX747172
AK128266
TCAM-1
BC050344
BC047380
AL832439
BC042121
BC041426
C15ORF20
AK125310
DKFZP434P055
KIAA0010
COX18HS
BC038578
AY314748
AK023134
AK131313
BC041865
AX746851
LOC606495
AK127238

Gene Names
LOC441282
BOZF1
AK026825
AK128305
AL713649
DQ573949
AK091996
CR606964
HSKRP1
AX747556
NR_003266
CR749689
BC049371
AX747988
FLJ35848
WHDC1L1
AK126491
AK024841
AX746688
FLJ37357
FLJ44955
BC040631
CR627135
DKFZP451M2119
CR627206
AK127460
BC019672
HERV-HHHL A1_
FUSION
AK057632
FLJ00264
NY-REN-7
AK125288
AF086203
LOC94431
BC043415
AK098333
BC042588
AX747864
AY314747
AK128216
BC044257
AX747062
BX649144
AL137270
PP8961
AK056558
AK094845
AX747742
AK095981
CTRP6
NR_002821

Gene Names
AX746880
AK125817
AK056417
AK026469
AK090984
AK131520
AL833246
AK125832
BC041455
AF380582
AX747658
AX721193
BC047626
FLJ44060
KIAA0982
AK093513
BC038431
BX161428
DKFZP6860248
AK096335
BX640887
BC009626
AY338954
BC036412
NM_001001681
AK056892
DQ573361
BC041466
NR_002210
FLJ33706
KIAA1767

Gene Names
MBL1P1
BC071776
AK127888
NR_002943
AX747340
LOC401252
AX746585
AK091594
AK096412
FLJ34047
AX747756
BC090058
CR611653
AL137733
BX537706
NR_001565
MGC4836
MGC29891
AK098240
AX748249
C1ORF140
AK055868
BC122562
BC041363
BC047625
BC021741
AK056524
BX647358
AK023515
AK125311
AK123891

Gene Names
LOC339809
AK128523
AK094859
PJCG6
AX748371
UNQ3037
AK054880
AK094224
AL833510
KENAE1
BC012110
BC052779
AK097893
BC105727
AK091527
WBSCR23
BC043378
AK056246
LOC401898
AK023856
UNQ1849
BC048997
FLJ36492
KIAA2023
AK054869
CR749689
BC029555
AK024378
NR_002821
DKFZP686F19123

Table 7 Categories of repeated DNA.

Class	Size of repeat	Major chromosomal location(s)
'Megasatellite' DNA (blocks of hundreds of kb in some cases)	several kb	Various locations on selected chromosomes
RS447	4.7 kb	~50–70 copies on 4p15 plus several copies on distal 8p
untitled	2.5 kb	~400 copies on 4q31 and 19q13
untitled	3.0 kb	~50 copies on the X chromosome
Satellite DNA (blocks often from 100 kb to several Mb in length)	5–171 bp	Especially at centromeres
α (alphoid DNA)	171 bp	Centromeric heterochromatin of all chromosomes
β (*Sau3* A family)	68 bp	Centromeric heterochromatin of 1, 9, 13, 14, 15, 21, 22 and Y
Satellite 1 (AT-rich)	25–48 bp	Centromeric heterochromatin of most chromosomes and other heterochromatic regions
Satellites 2 and 3	5 bp	Most, possibly all, chromosomes
Minisatellite DNA (blocks often within the 0.1–20 kb range)	6–64 bp	At or close to telomeres of all chromosomes
telomeric family	6 bp	All telomeres

Class	**Size of repeat**	**Major chromosomal location(s)**
hypervariable family	9-64 bp	All chromosomes, often near telomeres
Microsatellite DNA (blocks often less than 150 bp)	1-4 bp	Dispersed throughout all chromosomes

Table 8 Repeated DNA elements. The list is adapted from Repbase-GIRI. http://www.girinst.org/, accessed January 31, 2011.

Name of Repeat
(AC)n
(AG)n
(AT)n
(C)n
(CAA)n
(CAAA)n
(CAAAA)n
(CAAAAA)n
(CCA)n
(CCCCA)n
(CCCCAA)n
(CCCCCA)n
(CCCGAA)n
(CCCTAA)n
(CCCTCA)n
(CCTA)n
(CG)n
(CGAA)n
(CGGA)n
(CTA)n
(CTCCA)n
(GAA)n
(GAAA)n
(GAAAA)n
(GAAAAA)n
(GACA)n
(GAGACA)n
(GCA)n
(GCC)n
(GCCA)n
(GCCC)n
(GCCCA)n
(GCCCC)n
(GCCCCA)n
(GCCCCC)n
(GCGCA)n
(GCTCA)n
(GGA)n
(GGAA)n
(GGAGA)n
(GGAGAA)n
(GGCA)n
(GGCCC)n
(GGGA)n
(GGGAGA)n
(GGGGA)n
(GGGGGA)n
(TAA)n
(TAAA)n
(TAAAA)n
(TAAAAA)n
(TACA)n
(TACAA)n
(TAGA)n
(TAGAA)n
(TATACA)n
(TCA)n
(TCAA)n
(TCACCA)n
(TCCA)n
(TCCCA)n
(TCTAA)n
(TGAA)n
(TGGAA)n
(TGGCCC)n
(TTAA)n
(TTAAA)n
ACROl
ALR
ALR_
ALRl
ALR2
ALRa
ALRa_
ALRb
BSR
BSRa
>BSRb
>BSRd
>BSRf
>CER
>D20S16
>GGAAT
>GSAT
>GSATII
>GSATX
>HSAT4
>HSAT5
>HSAT6
>HSATI
>HSATII
>LSAU
>MSR1
>REP522
>SAR
>SATR1
>SATR2
>SN5
>SUBTEL_sat
>SUBTEL2_sat
>SVA2
>TAR1

Table 9 Examples of non-coding RNAs in nature.

Non-coding RNA	Abbreviation	Example of function	Reference
Transfer RNA	tRNA	Translation	(Aitken et al., 2010)
Ribosomal RNA	rRNA	Translation	(Aitken et al., 2010)
Signal recognition particle RNA	7SL RNA or SRP RNA	Translocation of proteins across the Endoplasmatic Reticulum	(Gribaldo and Brochier-Armanet, 2006)
Small nuclear RNA	snRNA	Splicing	(Valadkhan, 2010)
Small nucleolar RNA	snoRNA	Guides chemical modifications of other RNAs (like methylation and pseudouridylation).	(Kiss, 2002)
Short Interspersed repetitive elements	SINE	The most common SINE is the Alu element (~10% of the genome). Alu is upregulated in response to stress and binds RNA polymerase II to suppress transcription.	(Mariner et al., 2008)
microRNA	miRNA	Post-transcriptional gene silencing	(Bartel, 2009)
Small interfering RNA	siRNA	Post-transcriptional gene silencing	(Elbashir et al., 2001)
Piwi-interacting RNA	piRNA	Transciptional gene silencing, defense against retrotransposons	(Taft et al., 2010)
Ribonuclease P	RNase P	Ribozyme involved in tRNA maturation	(Guerrier-Takada et al., 1983)
Ribonuclease MRP	RNase MRP	Ribozyme involved in rRNA maturation as well as mitochondrial DNA replication	(Li et al., 2002)
Y RNA	Y RNA	RNA processing, DNA replication	(Lerner et al., 1981)
Telomerase RNA		Telomere synthesis	(Feng et al., 1995)
Antisense RNA	aRNA	Transcriptional attenuation/ mRNA degradation/ mRNA stabilisation/ translation block	(Katayama et al., 2005)
Long ncRNA, large intervening ncRNA (>200 nt)	Long ncRNA, lincRNA	regulation of gene transcription, post-transcriptional regulation, epigenetic regulation	(Kapranov et al., 2007)

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We claim:

1. A method for assaying a biological sample from a subject in aid of diagnosis, prognosis or monitoring of a disease or other medical condition in the subject, comprising the steps of:

    a. obtaining or using a microvesicle fraction from a biological sample from a subject;

    b. extracting nucleic acid from the fraction; and

    c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

    wherein the biomarker is a genetic aberration associated with diagnosis, prognosis, status or stage of a disease or other medical condition, and wherein the genetic aberration is in or corresponds to:

        i. a c-myc gene;

        ii. a transposable element;

        iii. a retrotransposon element;

        iv. a satellite correlated gene;

        v. a repeated DNA element;

        vi. non-coding RNA other than miRNA; or

        vii. a fragment of any of the foregoing.

2. The method of claim 1, wherein the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof.

3. The method of claim 1, wherein the genetic aberration is in or corresponds to a retrotransposon element that is LINE, SINE or HERV, or a fragment thereof.

4. The method of claim 3, wherein the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

5. The method of claim 1, wherein the genetic aberration is in or corresponds to a satellite correlated gene listed in Table 6, or a fragment thereof.

6. The method of claim 1, wherein the genetic aberration is in or corresponds to a repeated DNA element listed in Table 8, or a fragment thereof.

7. The method of claim 1, wherein the genetic aberration is in or corresponds to a non-coding RNA listed in Table 9 (or a fragment thereof), other than miRNA.

8. The method of claim 7, wherein the non-coding RNA is 7SL.

9. A method for assaying a biological sample from a subject in aid of directing treatment of the subject for a disease or other medical condition, comprising the steps of :

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other medical condition, and wherein the genetic aberration is in or corresponds to:

i. a c-myc gene;

ii. a transposable element;

iii. a retrotransposon element;

iv. a satellite correlated gene;

v. a repeated DNA element;

vi. non-coding RNA other than miRNA; or

vii. a fragment of any of the foregoing.

10. The method of claim 9, wherein the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof.

11. The method of claim 9, wherein the genetic aberration is in or corresponds to a retrotransposon element that is LINE, SINE or HERV, or a fragment thereof.

12. The method of claim 11, wherein the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

13. The method of claim 9, wherein the genetic aberration is in or corresponds to a satellite correlated gene listed in Table 6, or a fragment thereof.

14. The method of claim 9, wherein the genetic aberration is in or corresponds to a repeated DNA element listed in Table 8, or a fragment thereof.

15. The method of claim 9, wherein the genetic aberration is in or corresponds to a non-coding RNA listed in Table 9 (or a fragment thereof), other than miRNA.

16. The method of claim 15, wherein the non-coding RNA is 7SL.

17. A method for assaying a biological sample from a subject in aid of a determination of the subject's risk of developing a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid, wherein the biomarker is a genetic aberration associated with a determination of the subject's risk of developing a disease or other medical condition, and wherein the genetic aberration is in or corresponds to:

i. a c-myc gene;

ii. a transposable element;

iii. a retrotransposon element;

iv. a satellite correlated gene;

v. a repeated DNA element;

vi. non-coding RNA other than miRNA; or

vii. a fragment of any of the foregoing.

18. The method of claim 17, wherein the genetic aberration is in or corresponds to a transposable element listed in Table 4 or Table 5, or a fragment thereof.

19. The method of claim 17, wherein the genetic aberration is in or corresponds to a retrotransposon element that is LINE, SINE or HERV, or a fragment thereof.

20. The method of claim 19, wherein the genetic aberration is in or corresponds to a retrotransposon element that is Linel (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment thereof.

21. The method of claim 17, wherein the genetic aberration is in or corresponds to a satellite correlated gene listed in Table 6, or a fragment thereof.

22. The method of claim 17, wherein the genetic aberration is in or corresponds to a repeated DNA element listed in Table 8, or a fragment thereof.

23. The method of claim 17, wherein the genetic aberration is in or corresponds to a non-coding RNA listed in Table 9 (or a fragment thereof), other than miRNA.

24. The method of claim 23, wherein the non-coding RNA is 7SL.

25. A method for assaying a biological sample from a subject in aid of diagnosis, prognosis or monitoring of a disease or other medical condition in the subject, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with diagnosis, prognosis, status or stage of a disease or other medical condition, and wherein the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof.

26. A method for assaying a biological sample from a subject in aid of directing treatment of the subject for a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other medical condition, and wherein the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof

27. A method for assaying a biological sample from a subject in aid of a determination of the subject's risk of developing a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. extracting nucleic acid from the fraction; and

c. detecting the presence or absence of a biomarker in the extracted nucleic acid;

wherein the biomarker is a genetic aberration associated with a determination of the subject's risk of developing a disease or other medical condition, and wherein the genetic aberration is in or corresponds to a cancer gene listed in Table 2 or 3, or a fragment thereof.

28. A method for assaying a biological sample from a subject in aid of diagnosis, prognosis or monitoring of a disease or other medical condition in the subject, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. measuring a polypeptide activity in the fraction; and

c. determining whether the polypeptide activity is higher or lower than a normal or average activity for the polypeptide;

wherein an elevated or lowered activity is associated with diagnosis, prognosis, status or stage of a disease or other medical condition.

29. The method of claim 28, wherein the polypeptide is an enzyme.

30. The method of claim 29, wherein the enzyme is reverse transcriptase.

31. The method of claim 30, wherein step (c) involves determining whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

32. A method for assaying a biological sample from a subject in aid of directing treatment of the subject for a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. measuring a polypeptide activity in the fraction; and

c. determining whether the polypeptide activity is higher or lower than a normal or average activity for the same polypeptide;

wherein an elevated or lowered activity is associated with a disease or other medical condition or with responsiveness to a specific therapy for the disease or other medical condition.

33. The method of claim 32, wherein the polypeptide is an enzyme.

34. The method of claim 33, wherein the enzyme is reverse transcriptase.

35. The method of claim 34, wherein step (c) involves determining whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

36. A method for assaying a biological sample from a subject in aid of a determination of the subject's risk of developing a disease or other medical condition, comprising the steps of:

a. obtaining or using a microvesicle fraction from a biological sample from a subject;

b. measuring a polypeptide activity in the fraction; and

c. determining whether the polypeptide activity is higher or lower than a normal or average activity for the same polypeptide;

wherein an elevated or lowered activity is associated with a subject's risk of developing a disease or other medical condition.

37. The method of claim 36, wherein the polypeptide is an enzyme.

38. The method of claim 37, wherein the enzyme is reverse transcriptase.

39. The method of claim 38, wherein step (c) involves determining whether the reverse transcriptase activity is higher than a normal or average activity for reverse transcriptase.

40. The method of any of claims 1-27, wherein the genetic aberration is:

a. a species of nucleic acid;

b. the level of expression of a nucleic acid;

c. a nucleic acid variant; or

d. a combination of any of the foregoing.

41. The method of any of claims 1-27, wherein the nucleic acid is RNA and the genetic aberration is an expression profile.

42. The method of any of claims 1-27, wherein the fragment contains more than 10 nucleotides.

43. The method of any of claims 1-39, wherein the biological sample is a bodily fluid.

44. The method of claim 43, wherein the bodily fluid is blood, serum, plasma, or urine.

45. The method of any of claims 1-39, wherein the subject is a human subject.

46. The method of claim 45, wherein the disease or other medical condition is brain cancer.

47. The method of claim 46, wherein the brain cancer is medulloblastoma or glioblastoma.

48. The method of claim 45, wherein the disease or other medical condition is melanoma.

49. The method of any of claims 1-27, wherein the step of detecting the presence or absence of a biomarker in the extracted nucleic acid comprises microarray analysis, PCR, quantitative PCR, Digital Gene Expression, or direct sequencing.

50. The method of any of claims 1-39, further comprising the step of enriching the microvesicle fraction for microvesicles originating from a specific cell type.

51. A kit for genetic analysis of a microvesicle fraction obtained from a body fluid sample from a subject, comprising, in a suitable container, one or more reagents capable of hybridizing to or amplifying a nucleic acid corresponding to one or more of the genetic aberrations referenced in any of claims 1-27.

52. An oligonucleotide microarray for genetic analysis of a microvesicle preparation from a body fluid sample from a subject, wherein the oligonucleotides on the array are designed to hybridize to one or more nucleic acids corresponding to one or more of the genetic aberrations referenced in any of claims 1-27.

53. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to a cancer gene listed in Table 2 or 3, or a fragment thereof.

54. The profile of claim 53, wherein the cancer gene is a c-myc gene.

55. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to transposable element from the subject's genome, preferably an element listed in Table 4 or 5, or a fragment of any of the foregoing.

56. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to a retrotransposon element from the subject's genome, preferably LINE, SINE or HERV, more preferably LINE1 (LI), ALU, HERV-H, HERV-K, HERV-K6, HERV-W or HERV-C, or a fragment of any of the foregoing.

57. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to a satellite correlated gene from the subject's genome, preferably a satellite correlated gene listed in Table 6, or a fragment of any of the foregoing.

58. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to an element of repeated DNA from the subject's genome, preferably an element listed in Table 8, or a fragment of any of the foregoing.

59. A profile of microvesicular nucleic acid derived from a bodily fluid sample from a subject, wherein the profile comprises a genetic aberration in or corresponding to non-coding RNA other than miRNA, preferably a species listed in Table 9, or a fragment of any of the foregoing.

60. The profile of claim 59, wherein the non-coding RNA is 7SL.

61. The profile of any of claims 53-60, wherein the genetic aberration is:

a. a species of nucleic acid;

b. the level of expression of a nucleic acid;

c. a nucleic acid variant; or

d. a combination of any of the foregoing.

62. A method of identifying a potential new nucleic acid biomarker associated with a disease or other medical condition, status or stage of disease or other medical condition, a

subject's risk of developing a disease or other medical condition, or a subject's responsiveness to a specific therapy for a disease or other medical condition, comprising the steps of:

(a) obtaining or using a microvesicle fraction from a biological sample from a subject;

(b) extracting nucleic acid from the fraction;

(c) preparing a profile according to any of claims 53-60; and

(d) comparing the profile of step (c) to a control or reference profile and selecting one or more potential new biomarkers based on one or more differences between the profile of step (c) and the control or reference profile.

63. A method of treating a subject having a form of cancer in which cancer cells secrete microvesicles, the method comprising administering to the subject a therapeutically effective amount of a composition comprising:

a. an inhibitor of microvesicle secretion;

b. an inhibitor of a reverse transcriptase;

c. a microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles; or

d. any combination of the forgoing.

64. The method of claim 63, wherein the inhibitor of microvesicle secretion is an inhibitor of RAB GTPase.

65. The method of claim 64, where in the Rab GTPase is Rab 27a, Rab 27b or Rab 35.

66. The method of claim 63, wherein the inhibitor of a reverse transcriptase is a nucleoside analog selected from the group comprising 3'-azido2',3'-dideoxythymidine (AZT), 2',3'-dideoxyinosine (ddl), 2', 3'-didehyro-3 '-deoxythymidine (d4T), nevirapine and efavirenz.

67. The method of claim 63, wherein the inhibitor of a reverse transcriptase is RNAi targeting the reverse transcriptase gene.

68. The method of claim 63, wherein the microvesicle neutralizer is a biological agent that binds microvesicles and destroys the integrity of the microvesicles.

69. A pharmaceutical composition comprising, in a suitable pharmaceutical carrier: (a) an inhibitor of microvesicle secretion, particularly an inhibitor of RAB GTPase, and more particularly Rab 27a, Rab 27b or Rab 35); (b) an inhibitor of reverse transcriptase, particularly a nucleoside analog, more particularly 3'-azido2',3'-dideoxythymidine (AZT), 2',3'-dideoxyinosine (ddl), 2',3'-didehyro-3'-deoxythymidine (d4T), nevirapine, or efavirenz, or an RNAi targeting the reverse transcriptase gene; (c) a microvesicle neutralizer that neutralizes the pro-tumor progression activity of tumor microvesicles, particularly a biological agent that binds microvesicles and destroys the integrity of the microvesicles; or (d) a combination of any of the foregoing.

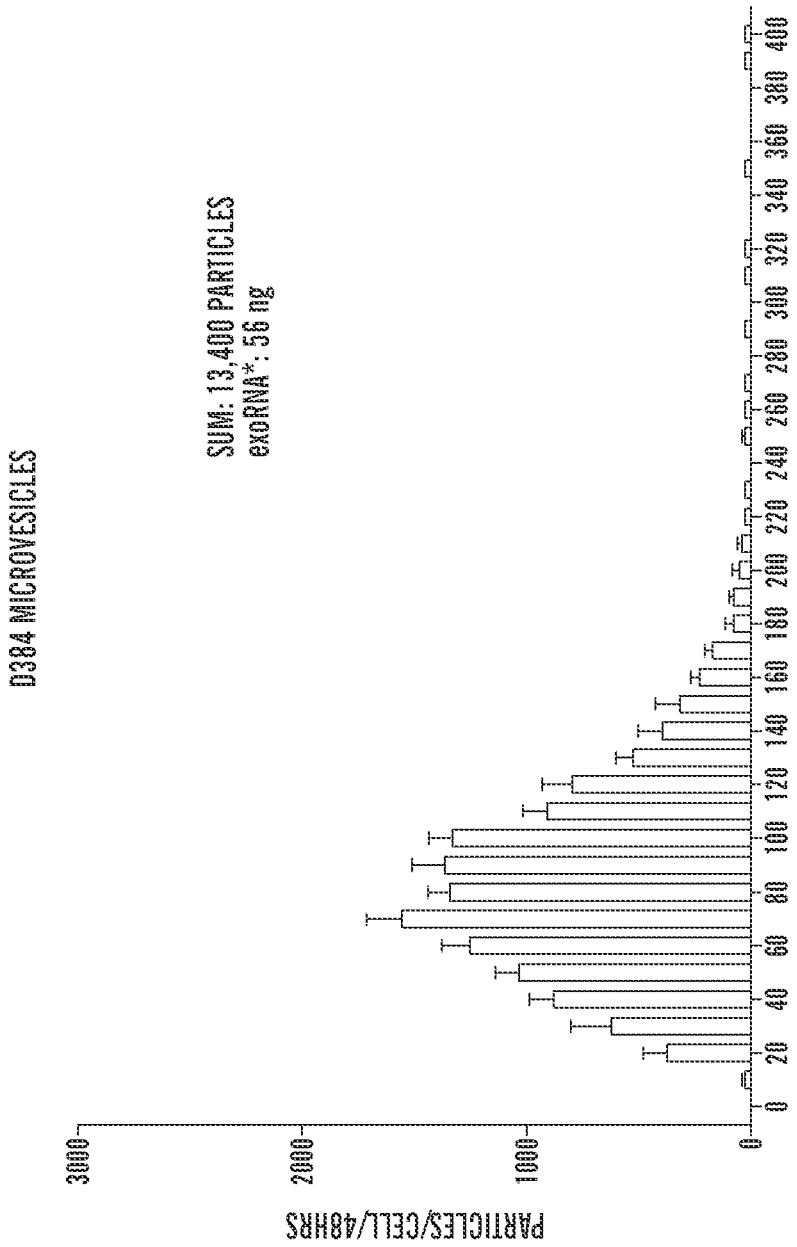
D384 MICROVESICLES
SUM: 13,400 PARTICLES
exoRNA*: 56 ng
PARTICLES/CELL/48HRS
3000
2000
1000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 1

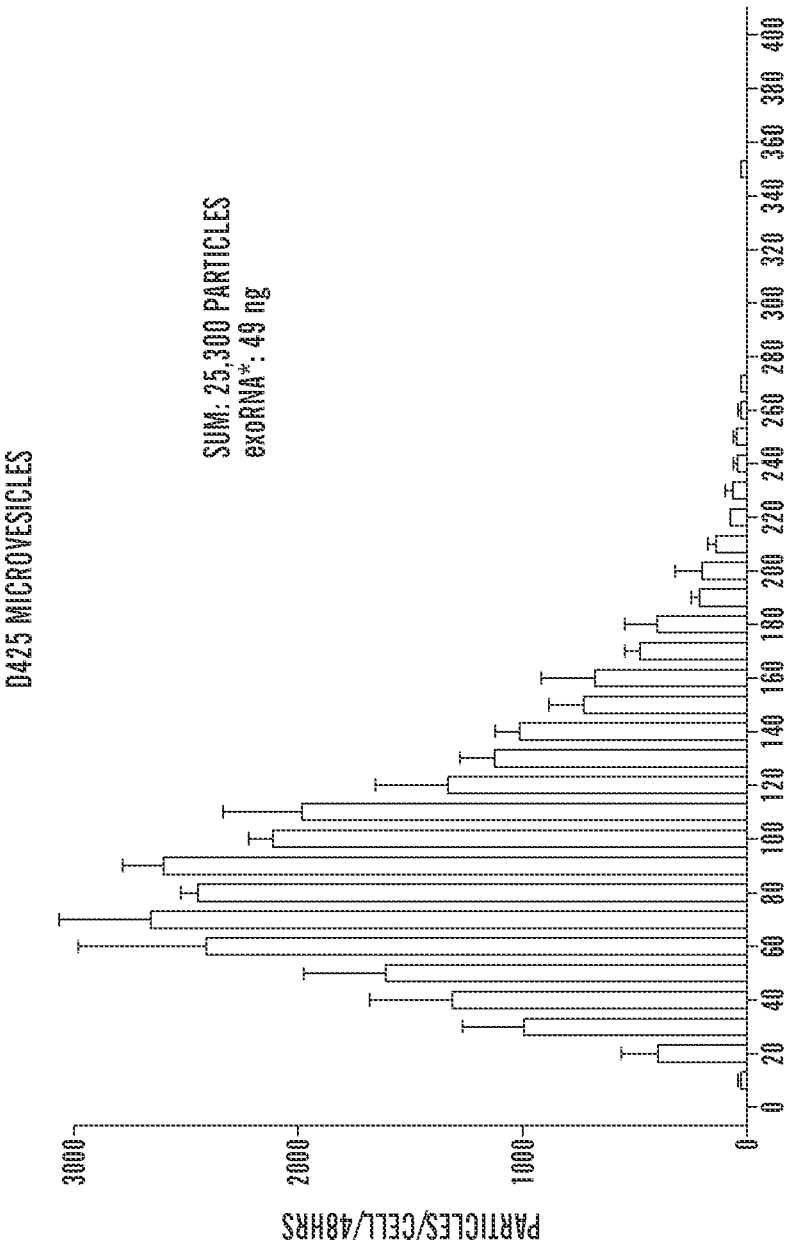
D425 MICROVESICLES
SUM: 25,300 PARTICLES
exoRNA*: 49 ng
PARTICLES/CELL/48HRS
30000
20000
10000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 2

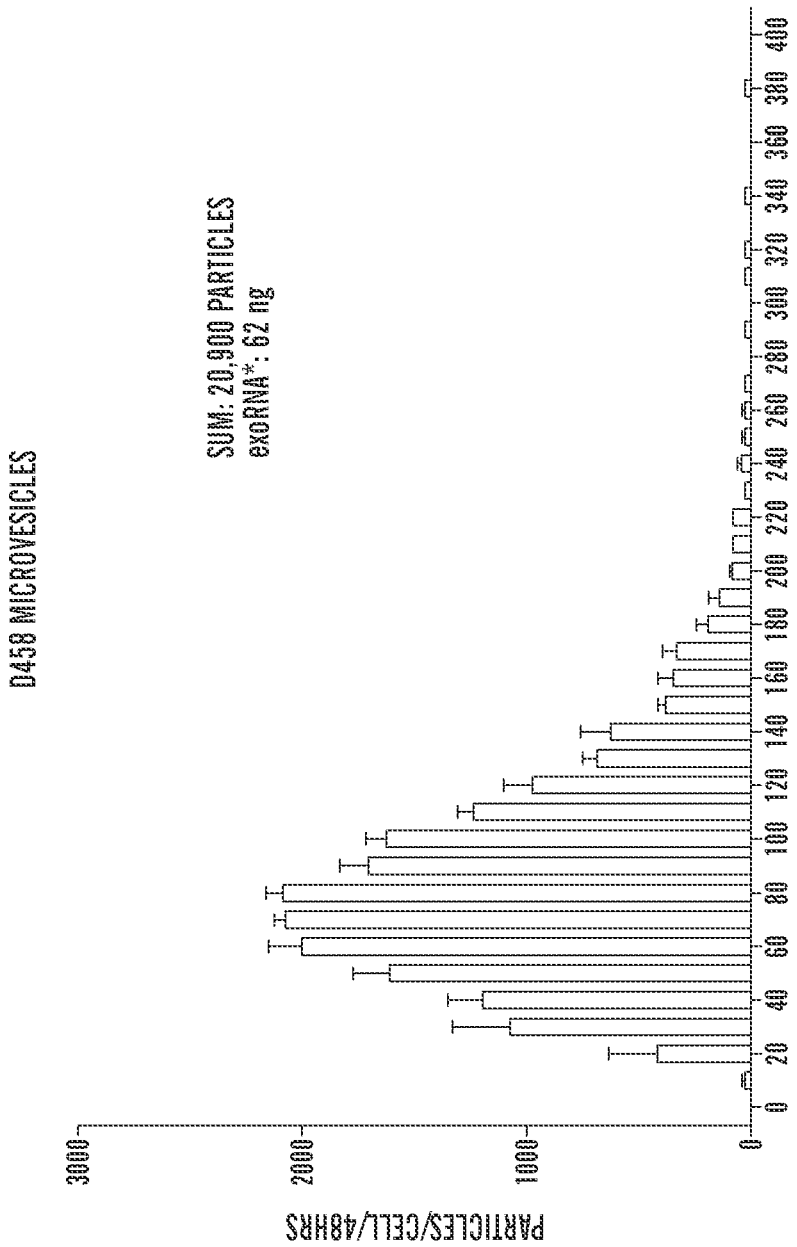
D458 MICROVESICLES
SUM: 20,900 PARTICLES
exoRNA*: 62 ng
PARTICLES/CELL/48HRS
3000
2000
1000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 3

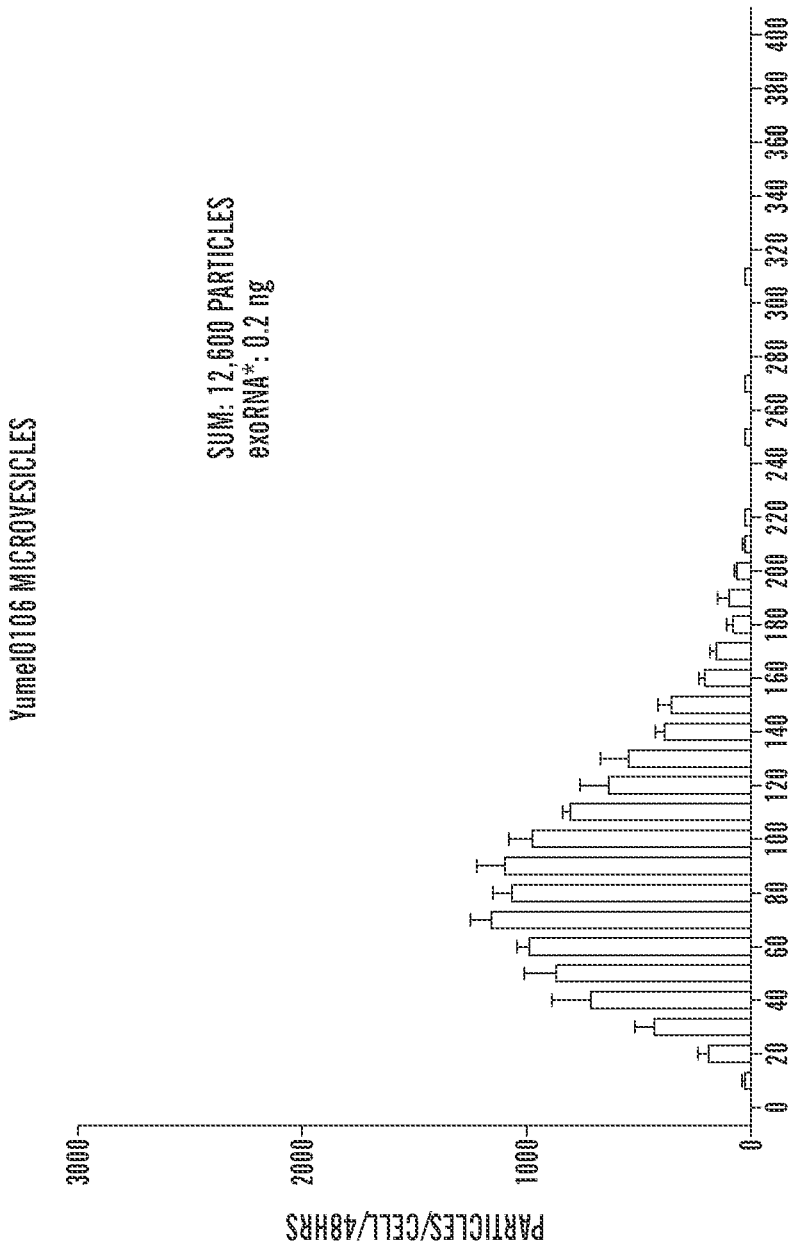
Yumel0106 MICROVESICLES
SUM: 12,600 PARTICLES
exoRNA*: 0.2 ng
PARTICLES/CELL/48HRS
3000
2000
1000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 4

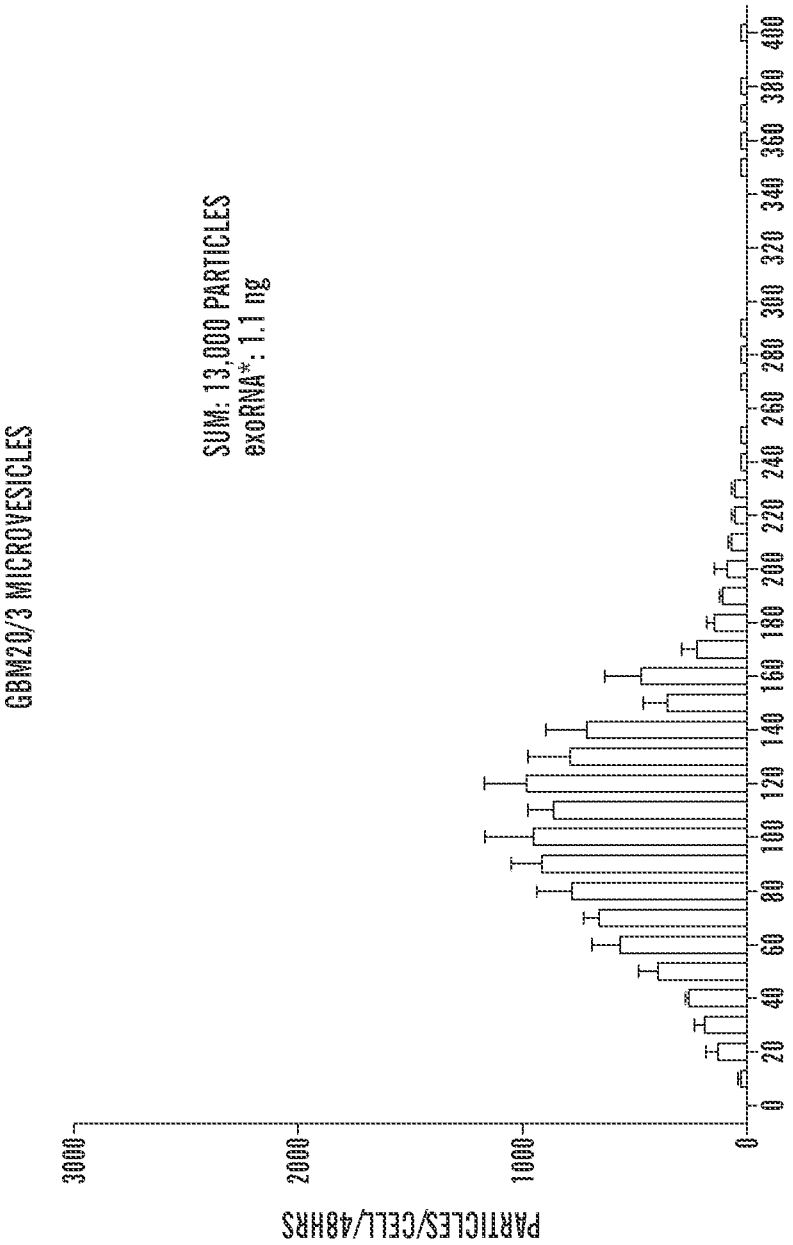
GBM210/3 MICROVESICLES
SUM: 13,000 PARTICLES
exoRNA*: 1.1 ng
PARTICLES/CELL/48HRS
30000
20000
10000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 5

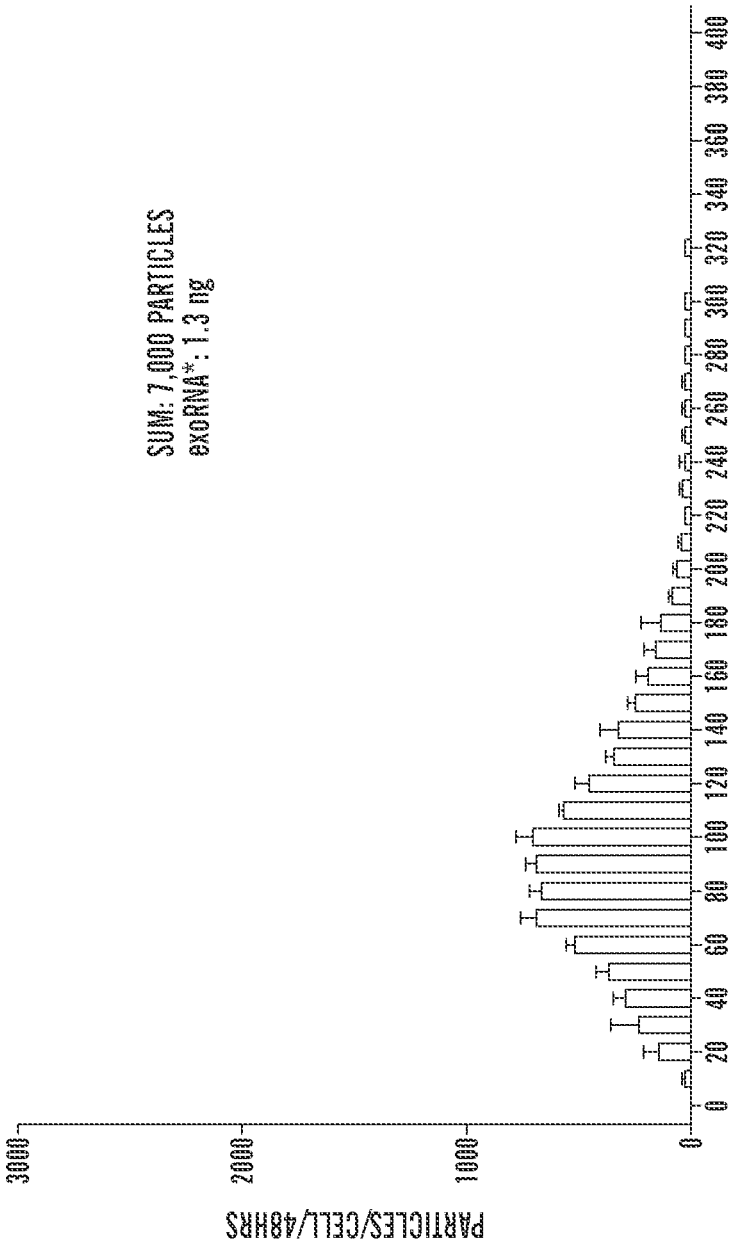
GBM11/5 MICROVESICLES
SUM: 7,000 PARTICLES
exoRNA*: 1.3 ng
PARTICLES/CELL/48HRS
30000
20000
10000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 6

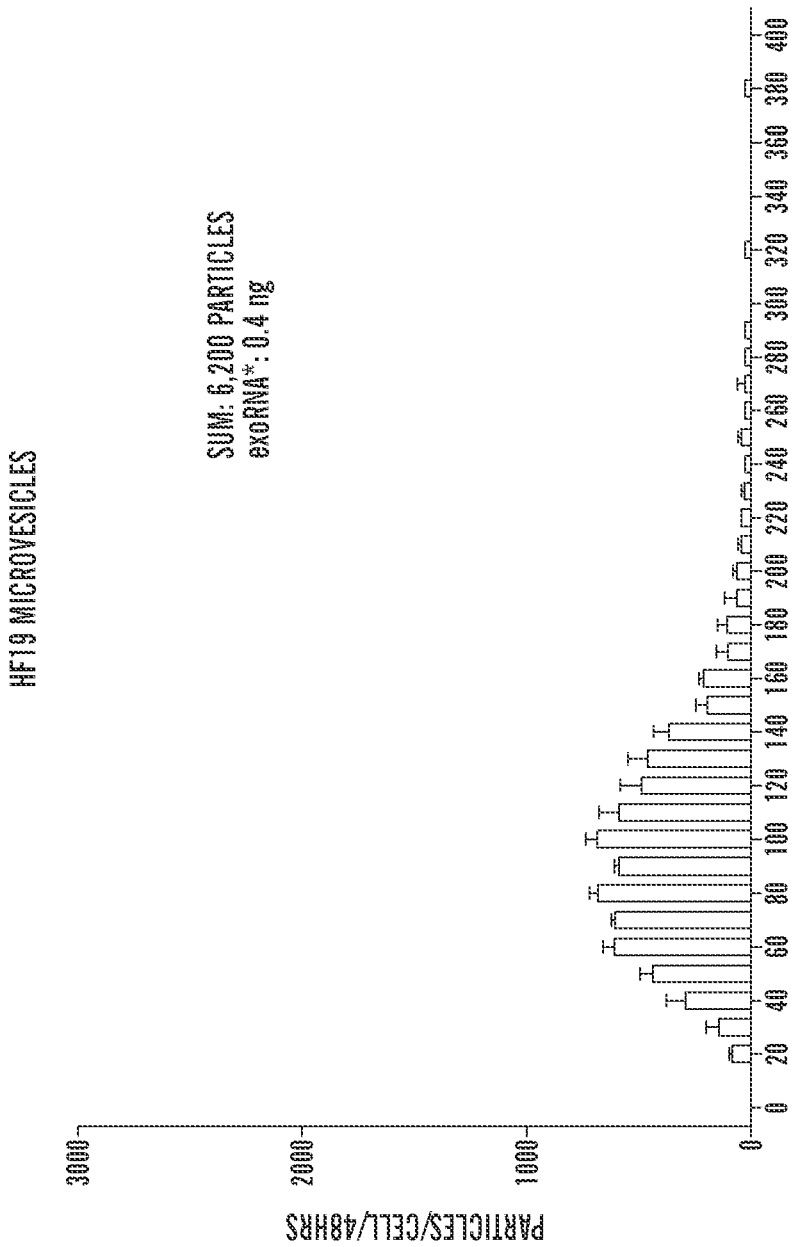
HF19 MICROVESICLES
SUM: 6,200 PARTICLES
exoRNA*: 0.4 ng
PARTICLES/CELL/48HRS
30000
20000
10000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 7

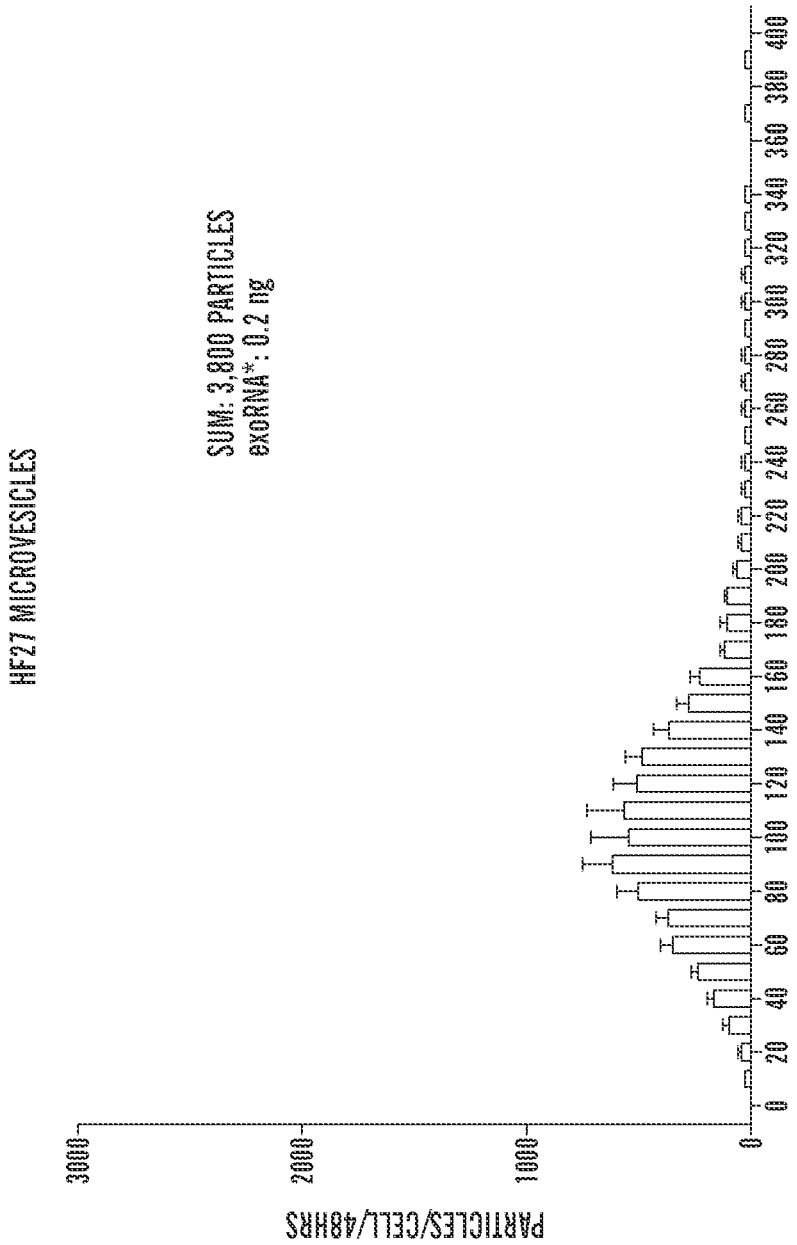
HF27 MICROVESICLES
SUM: 3,800 PARTICLES
exoRNA*: 0.2 ng
PARTICLES/CELL/48HRS
30000
20000
10000
0
0 20 40 60 80 100 120 140 160 180 200 220 240 260 280 300 320 340 360 380 400
DIAMETER (nm)

FIG. 8

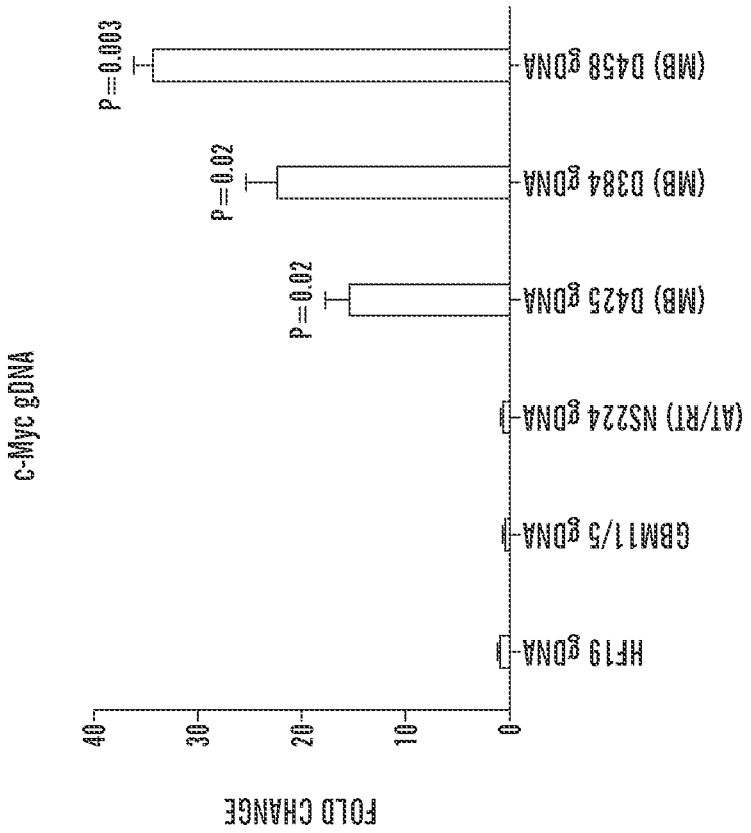
c-Myc gDNA
FOLD CHANGE
40
30
20
10
0
HF19 gDNA
GBM1 1/5 gDNA
(AT/RT) NS224 gDNA
(MB) D425 gDNA
(MB) D384 gDNA
(MB) D458 gDNA
P = 0.02
P = 0.02
P = 0.003

FIG. 9

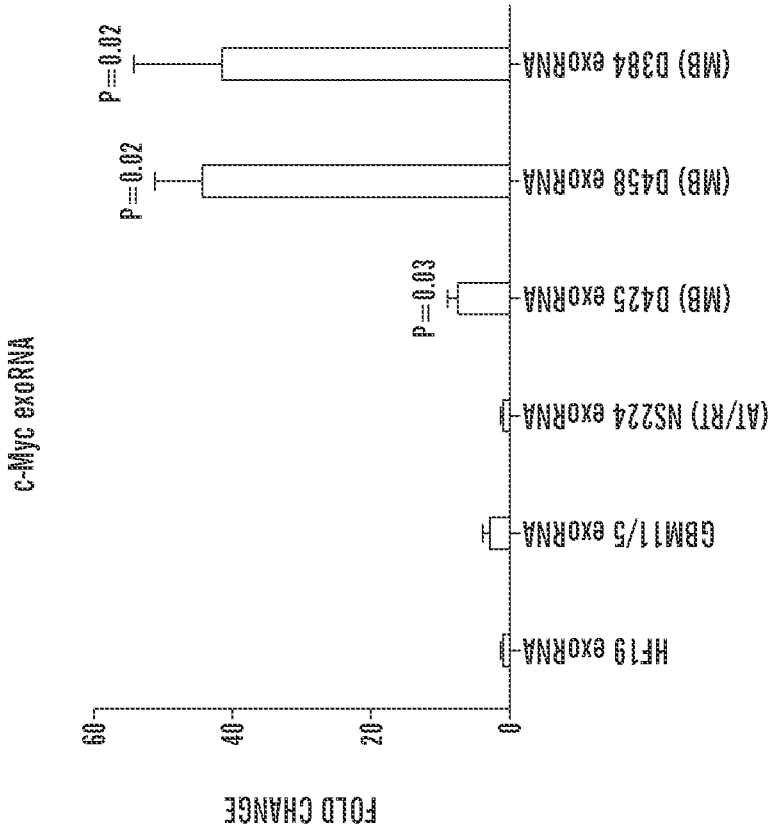
c-Myc exoRNA
FOLD CHANGE
60
40
20
0
HF19 exoRNA
GBM11/5 exoRNA
(AT/RT) NS224 exoRNA
(MB) D425 exoRNA
(MB) D458 exoRNA
(MB) D384 exoRNA
P=0.03
P=0.02
P=0.02

FIG. 10

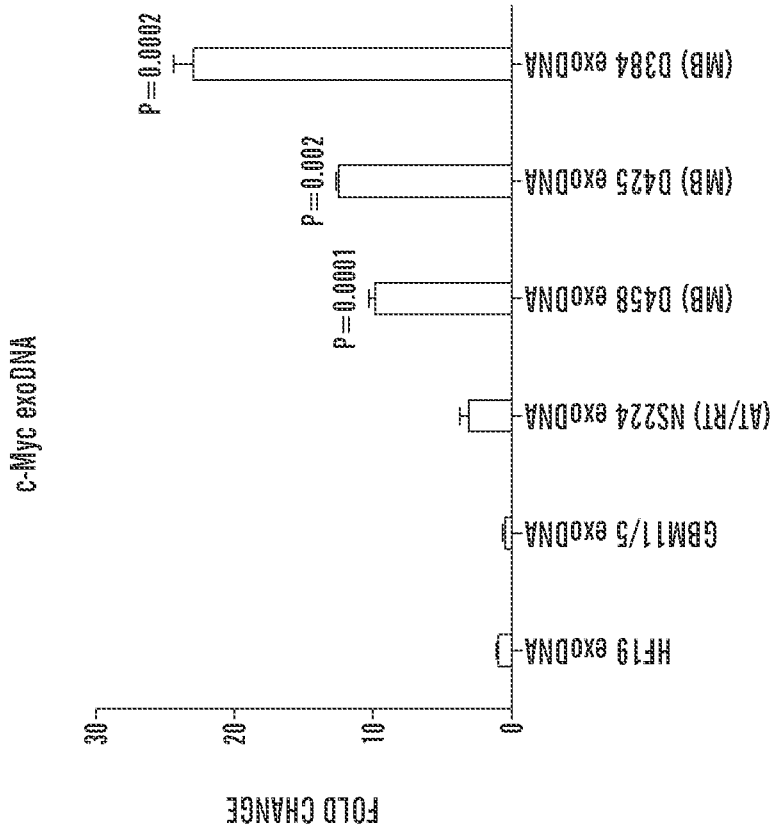
c-Myc exoDNA
FOLD CHANGE
30
20
10
0
HF19 exoDNA
GBM11/5 exoDNA
(AT/RT) NS224 exoDNA
(MB) D458 exoDNA
(MB) D425 exoDNA
(MB) D384 exoDNA
P = 0.0001
P = 0.002
P = 0.0002

FIG. 11

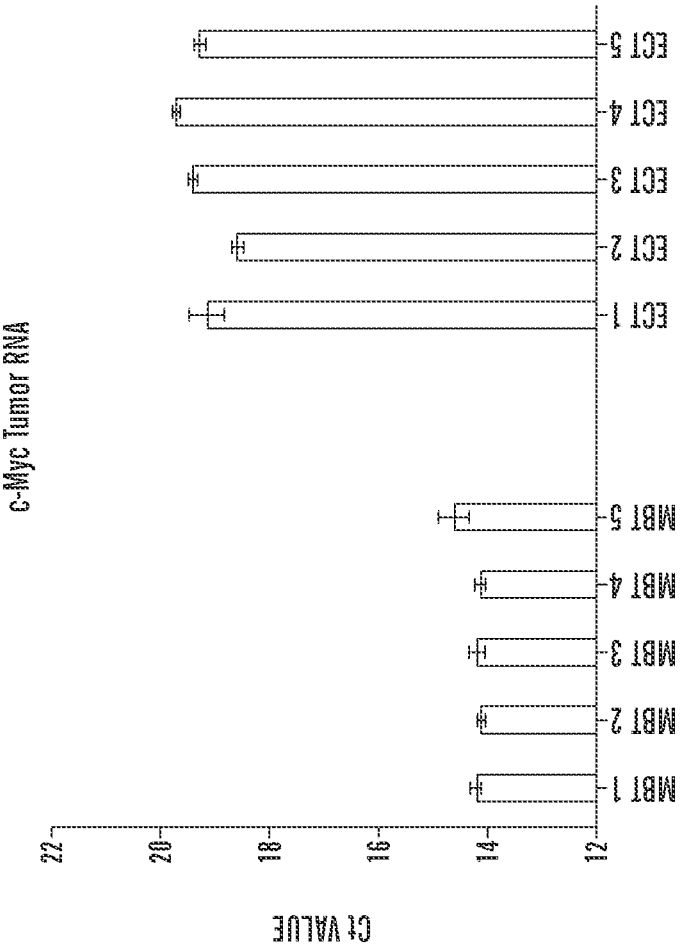
c-Myc Tumor RNA
Ct VALUE
22
20
18
16
14
12
MBT 1
MBT 2
MBT 3
MBT 4
MBT 5
ECT 1
ECT 2
ECT 3
ECT 4
ECT 5

FIG. 12

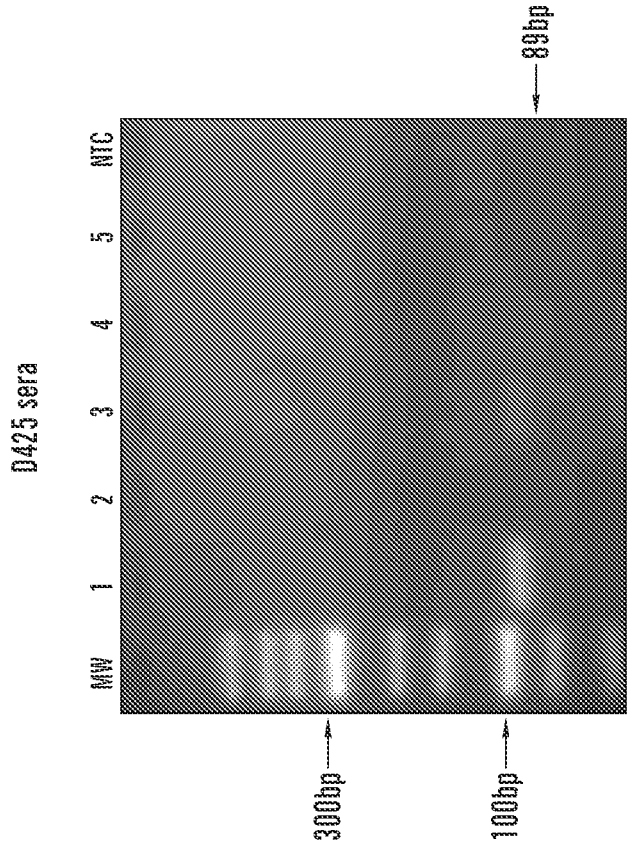

FIG. 13

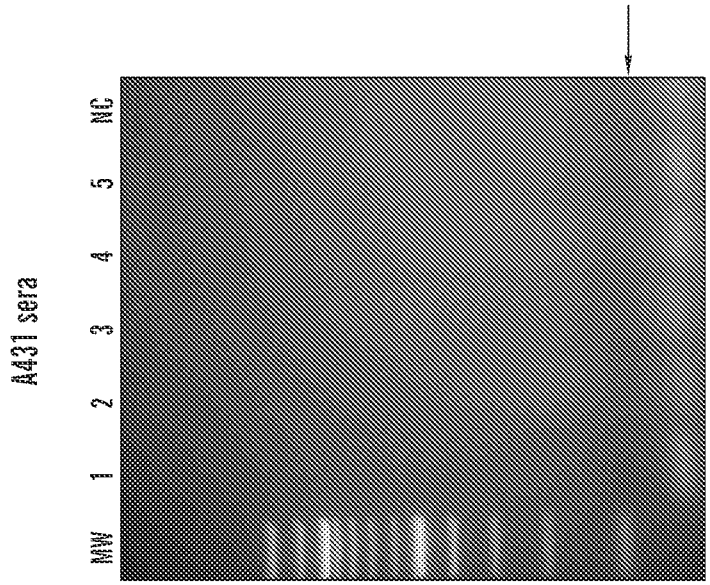

FIG. 14

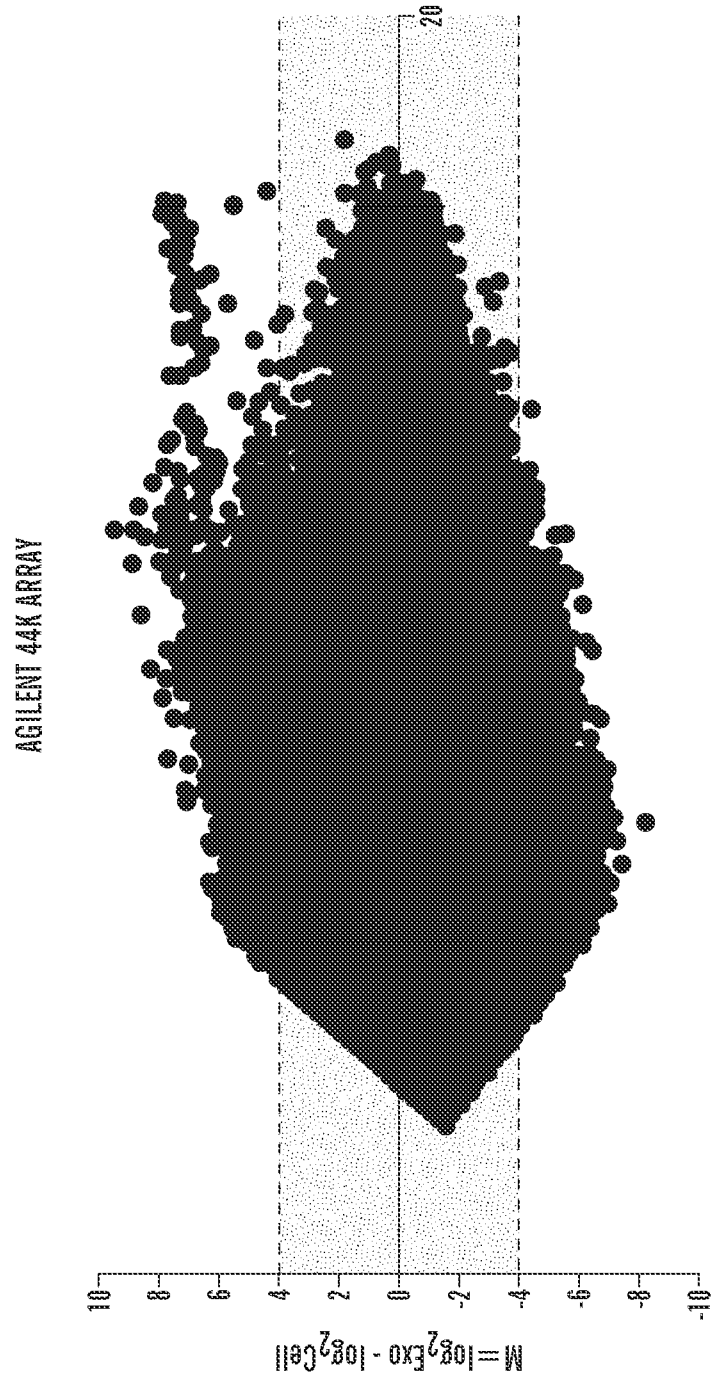
AGILENT 44K ARRAY
M = |log2Exo - log2Cell|
A = 0.5 x (log2Exo + log2Cell)
10
8
6
4
2
0
-2
-4
-6
-8
-10
20

FIG. 15

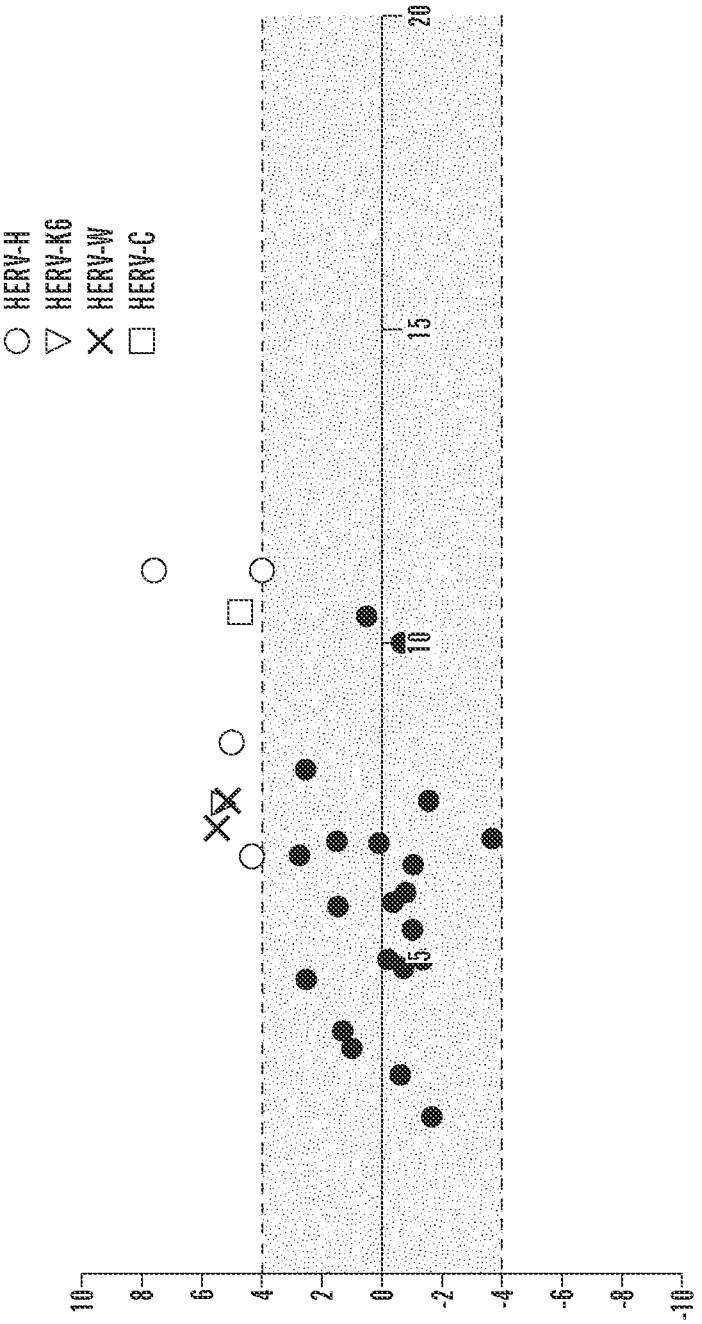

FIG. 16

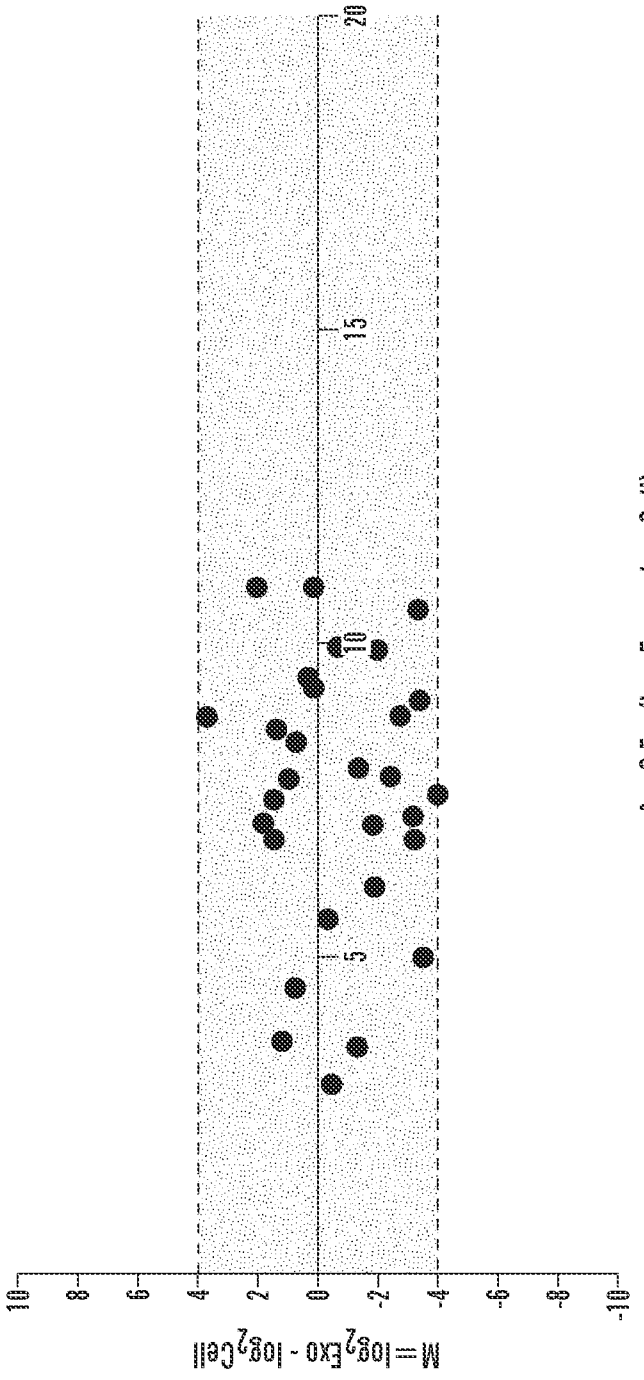
DNA TRANSPOSONS
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
10
8
6
4
2
0
-2
-4
-6
-8
-10
5
10
15
20

FIG. 17

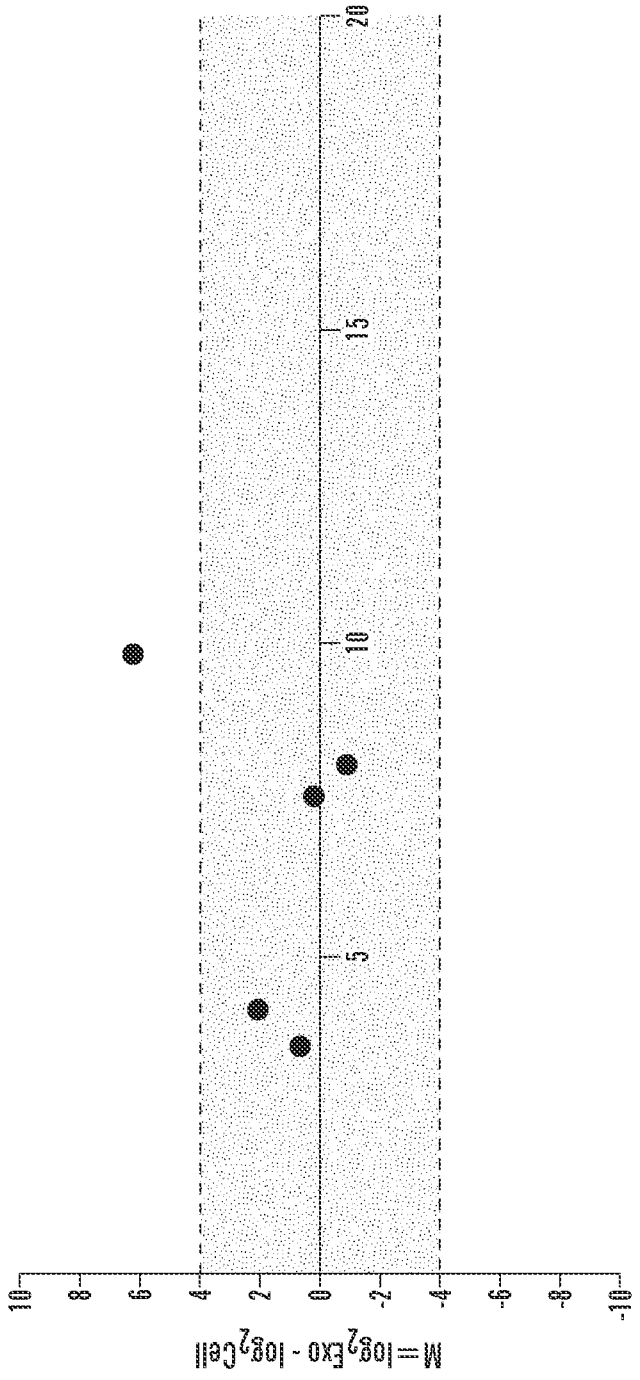
L1
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
10
8
6
4
2
0
-2
-4
-6
-8
-10
20
15
10
5

FIG. 18

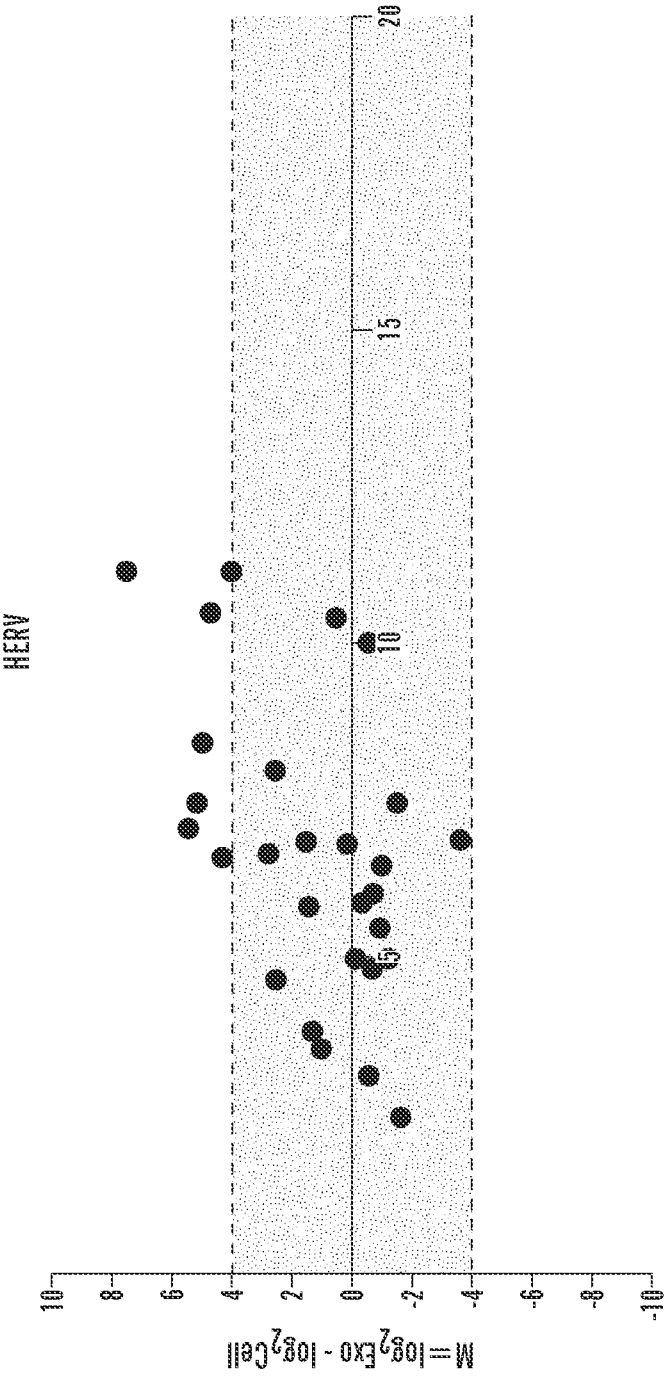
HERV
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
10
8
6
4
2
0
-2
-4
-6
-8
-10
20
15
10
5

FIG. 19

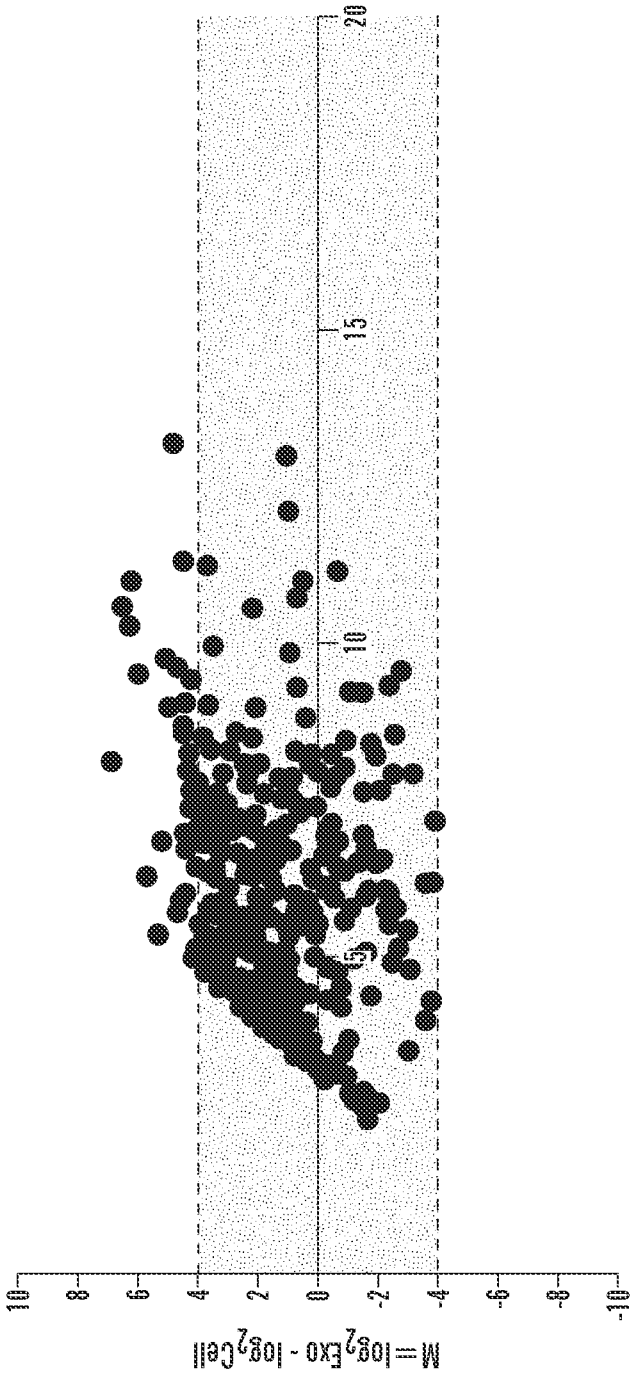
ALU
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
10
8
6
4
2
0
-2
-4
-6
-8
-10
5
10
15
20

FIG. 20

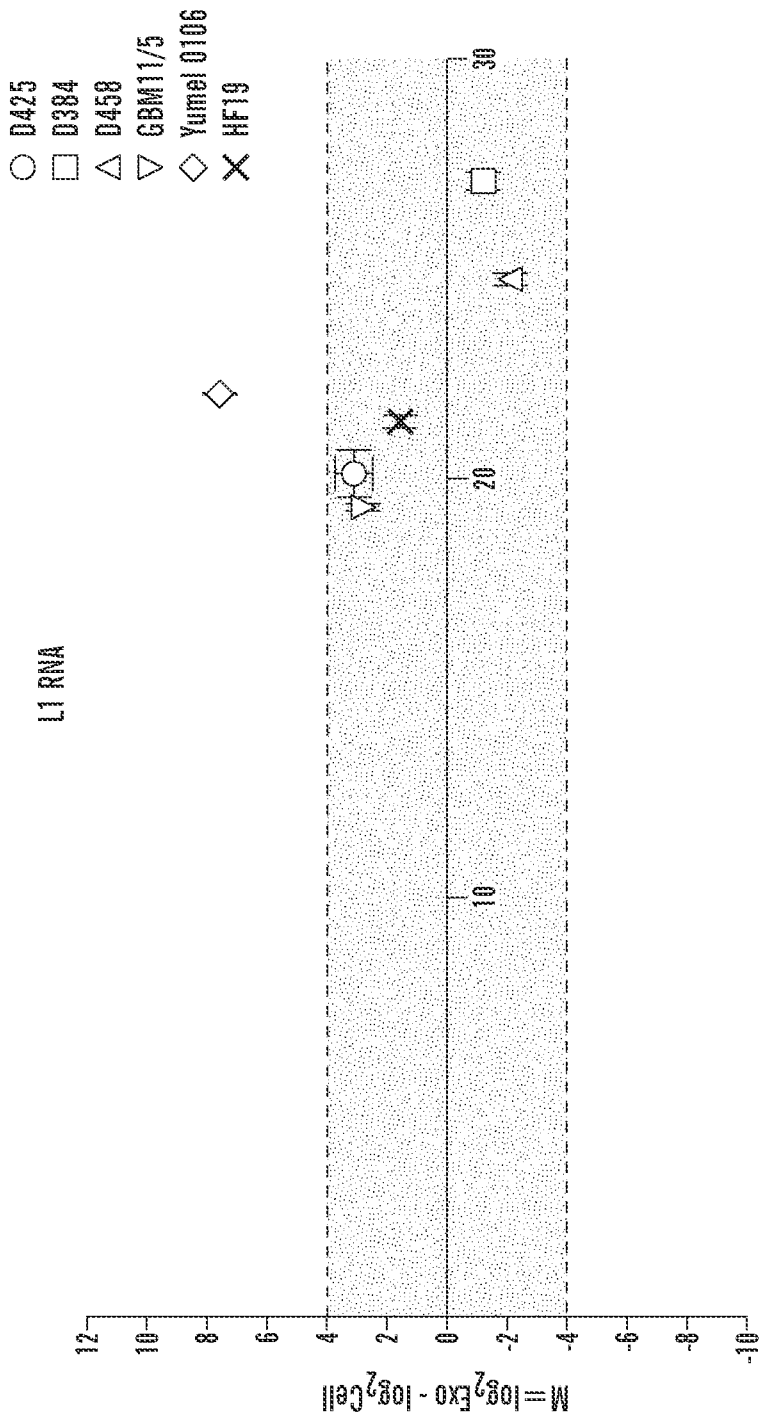
D425
D384
D458
GBM11/5
Yumel 0106
HF19
L1 RNA
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
12
10
8
6
4
2
0
-2
-4
-6
-8
-10
10
20
30

FIG. 21A

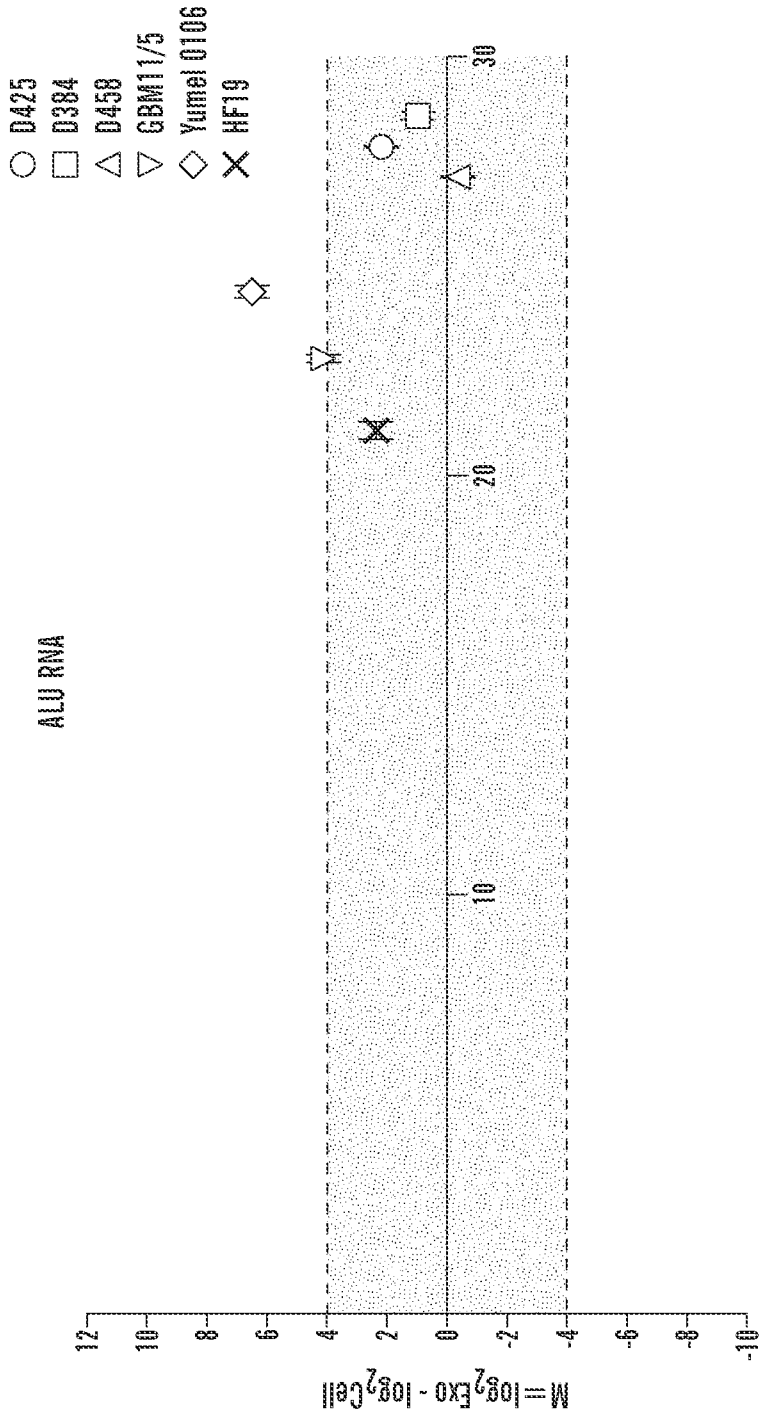
D425
D384
D458
GBM11/5
Yumel 0106
HF19
ALU RNA
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
12
10
8
6
4
2
0
-2
-4
-6
-8
-10
30
20
10

FIG. 21B

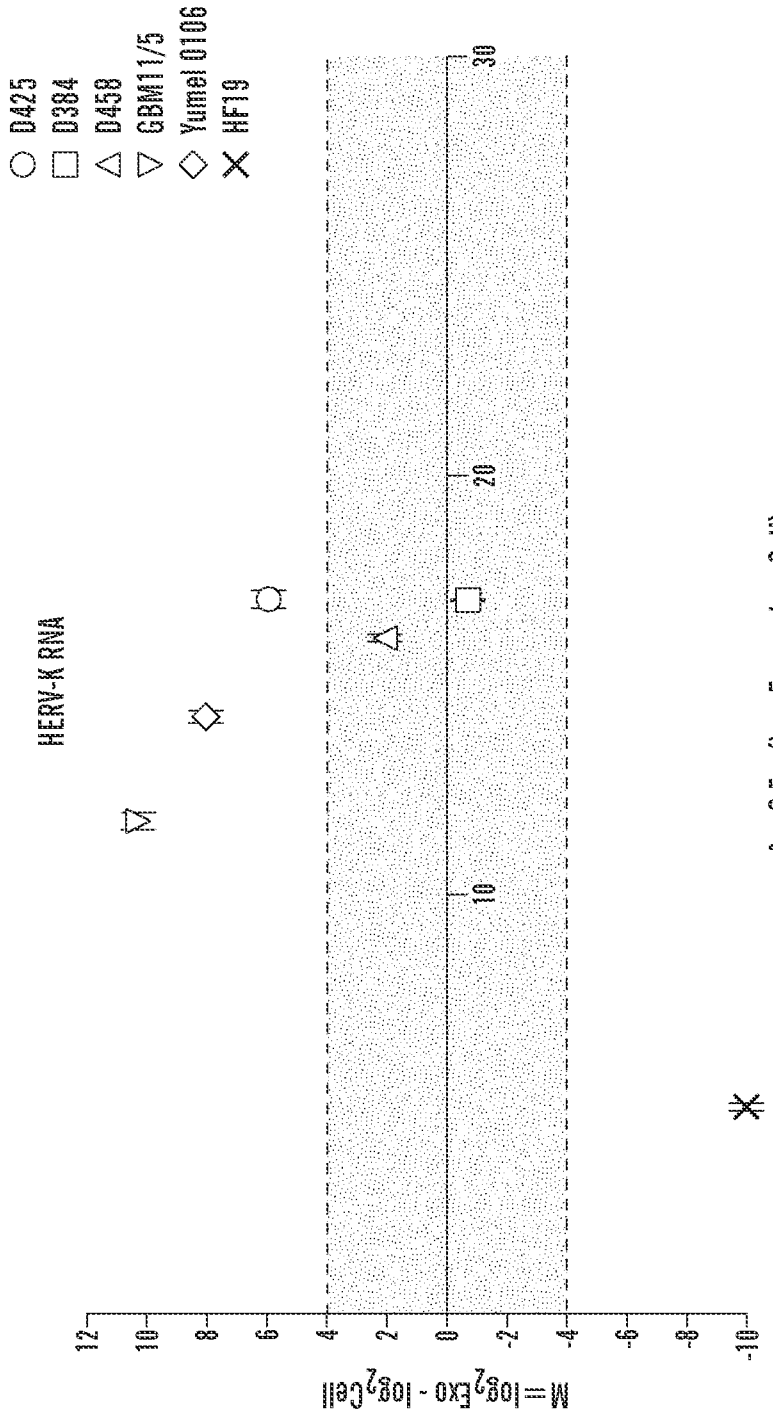
D425
D384
D458
GBM11/5
Yumel 0106
HF19
HERV-K RNA
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
12
10
8
6
4
2
0
-2
-4
-6
-8
-10
10
20
30

FIG. 21C

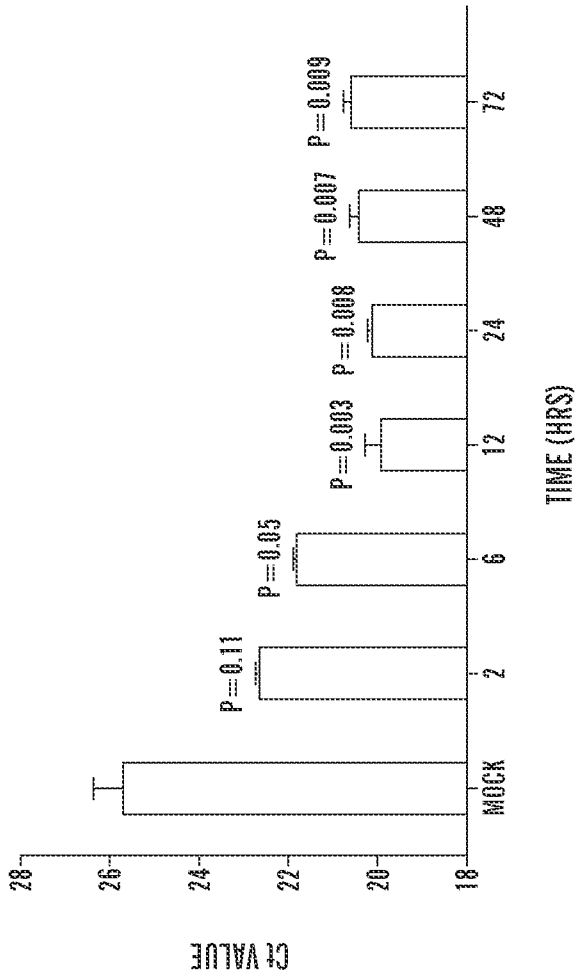
MICROVESICLE TRANSFER OF HERV-K RNA
Ct VALUE
28
26
24
22
20
18
MOCK
2
6
12
24
48
72
TIME (HRS)
P=0.11
P=0.05
P=0.003
P=0.008
P=0.007
P=0.009

FIG. 22

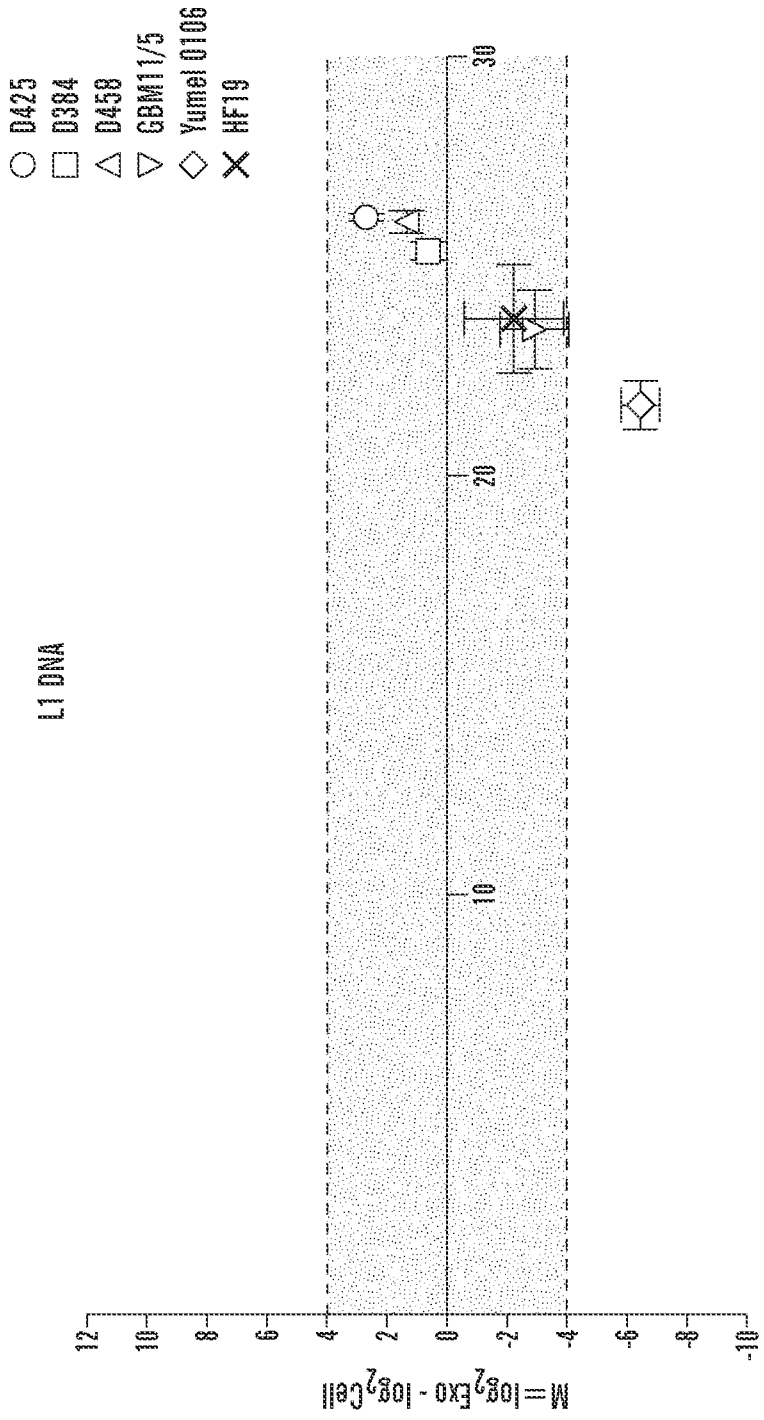
D425
D384
D458
GBM11/5
Yumel 01106
HF19
L1 DNA
A = 0.5 x (log2Exo + log2Cell)
M = log2Exo - log2Cell
12
10
8
6
4
2
0
-2
-4
-6
-8
-10
30
20
10

FIG. 23A

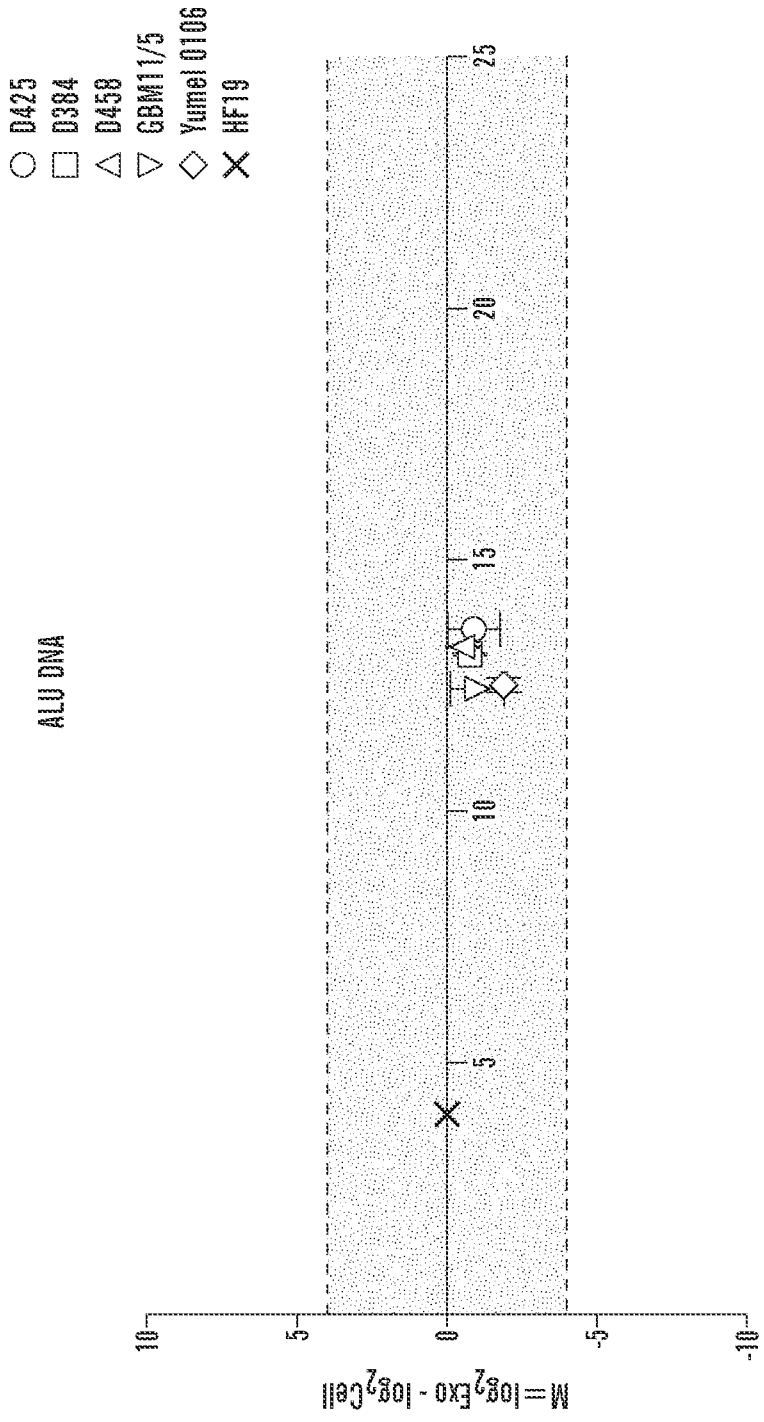
D425
D384
D458
GBM11/5
Yumel 01106
HF19
ALU DNA
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
10
5
0
-5
-10
25
20
15
10
5

FIG. 23B

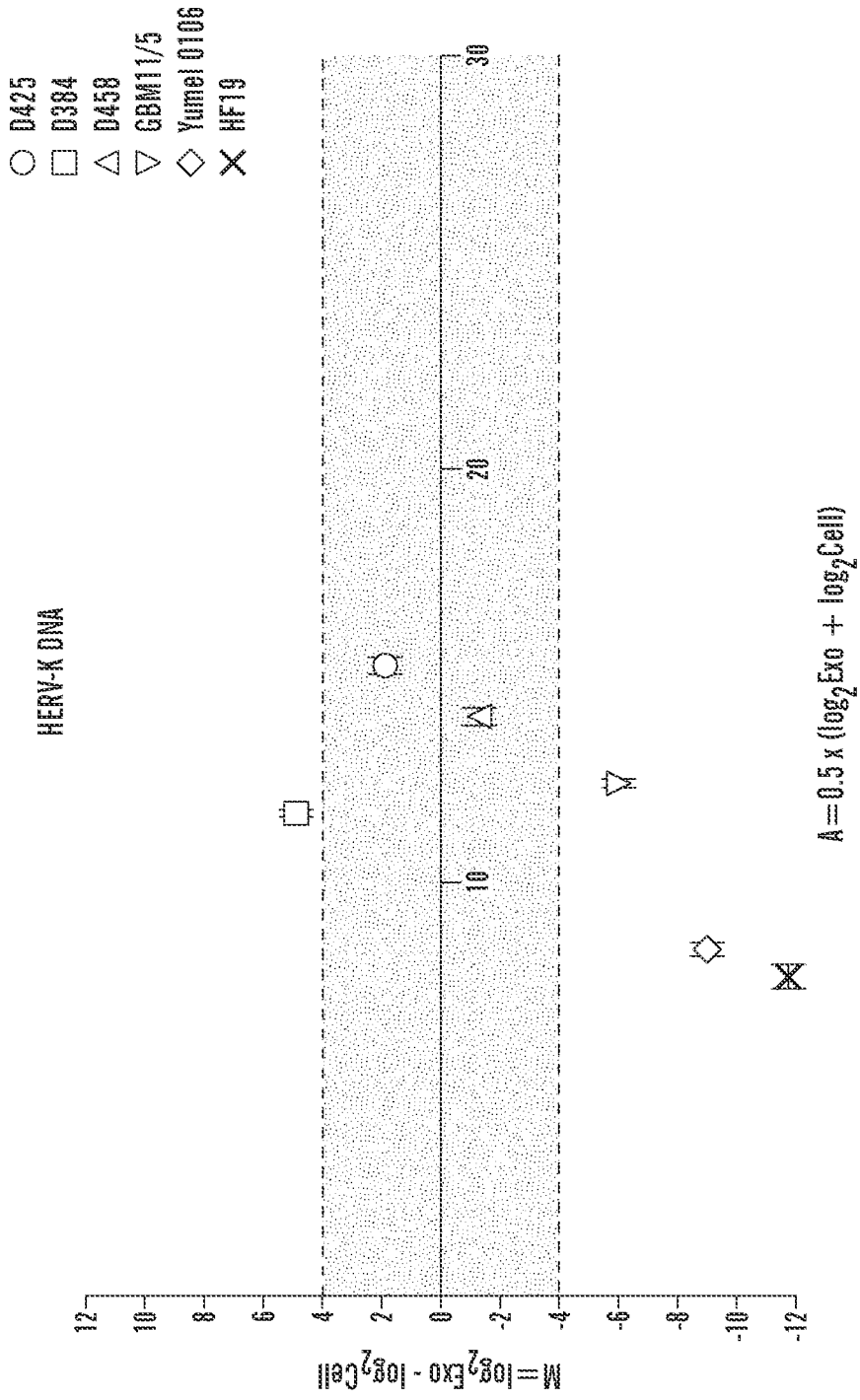
D425
D384
D458
GBM11/5
Yumel 0106
HF19
HERV-K DNA
M = log2Exo - log2Cell
A = 0.5 x (log2Exo + log2Cell)
12
10
8
6
4
2
0
-2
-4
-6
-8
-10
-12
30
20
10

FIG. 23C

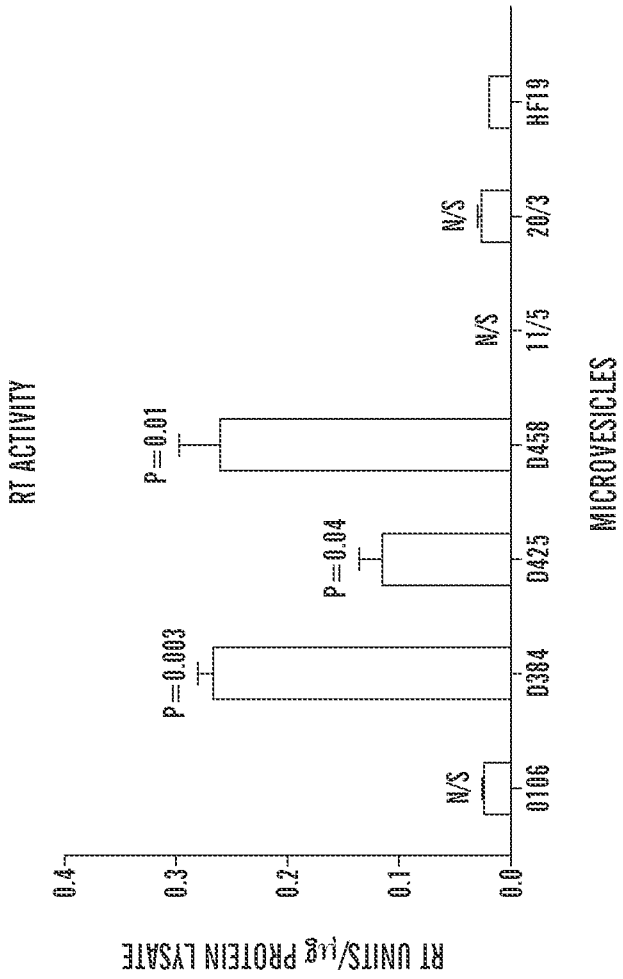
RT ACTIVITY
RT UNITS/μg PROTEIN LYSATE
0.0
0.1
0.2
0.3
0.4
N/S
P=0.003
P=0.04
P=0.01
N/S
N/S
01106
D384
D425
D458
11/5
20/3
HF19
MICROVESICLES

FIG. 24

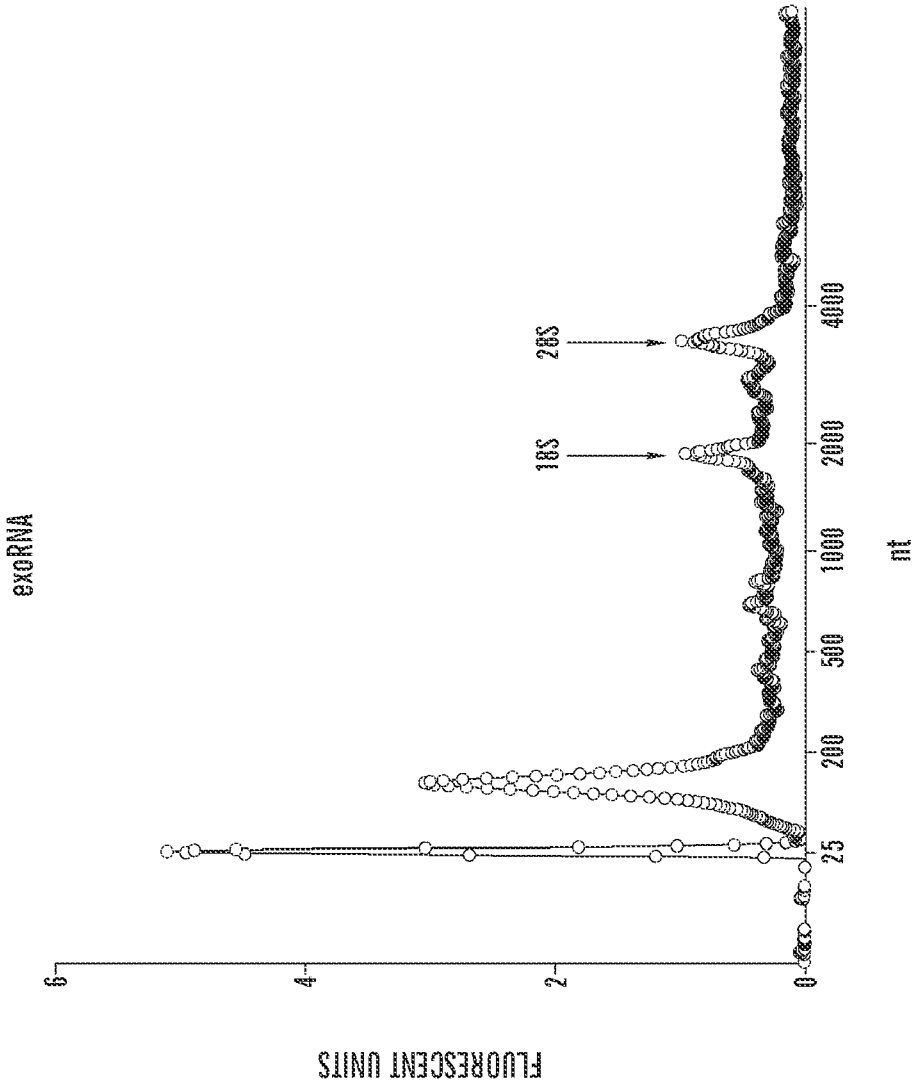
exoRNA
FLUORESCENT UNITS
0
2
4
6
25
200
500
1000
2000
4000
nt
18S
28S

FIG. 25A

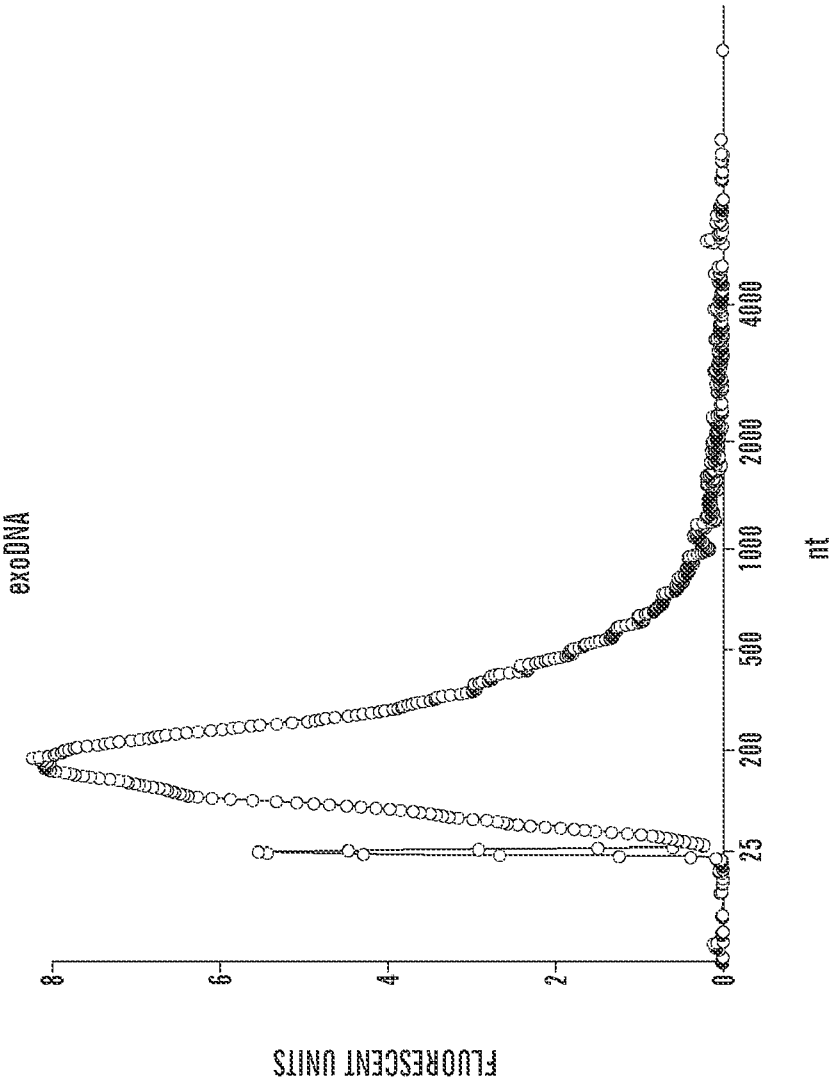

FIG. 25B

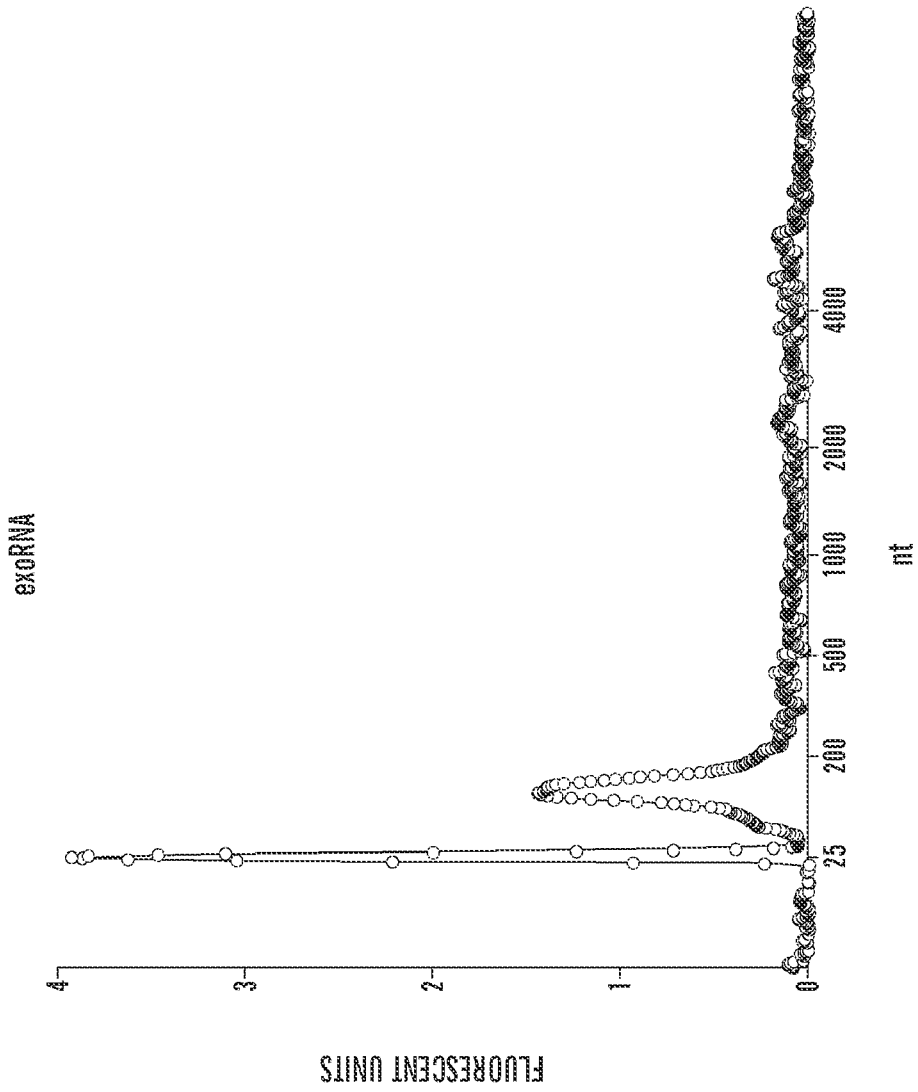

FIG. 25C

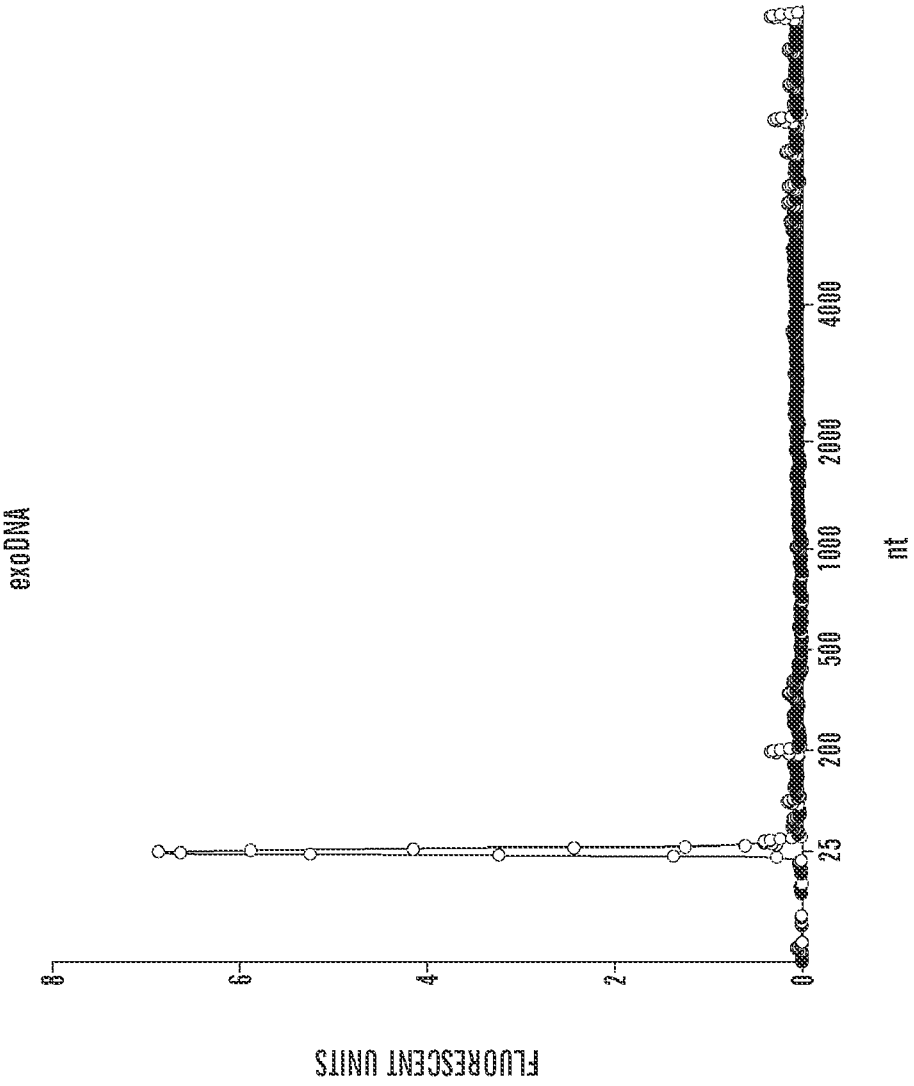

FIG. 25D

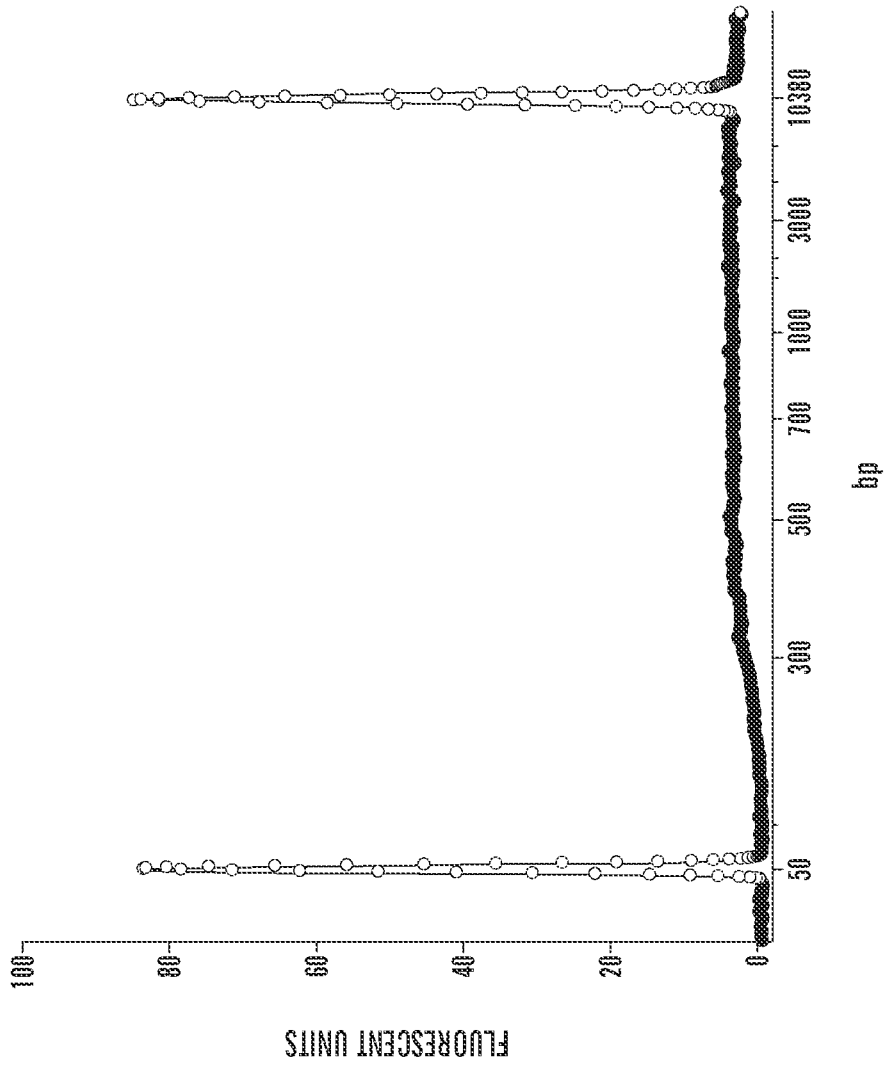
D384 exoDNA
FLUORESCENT UNITS
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
bp

FIG. 26A

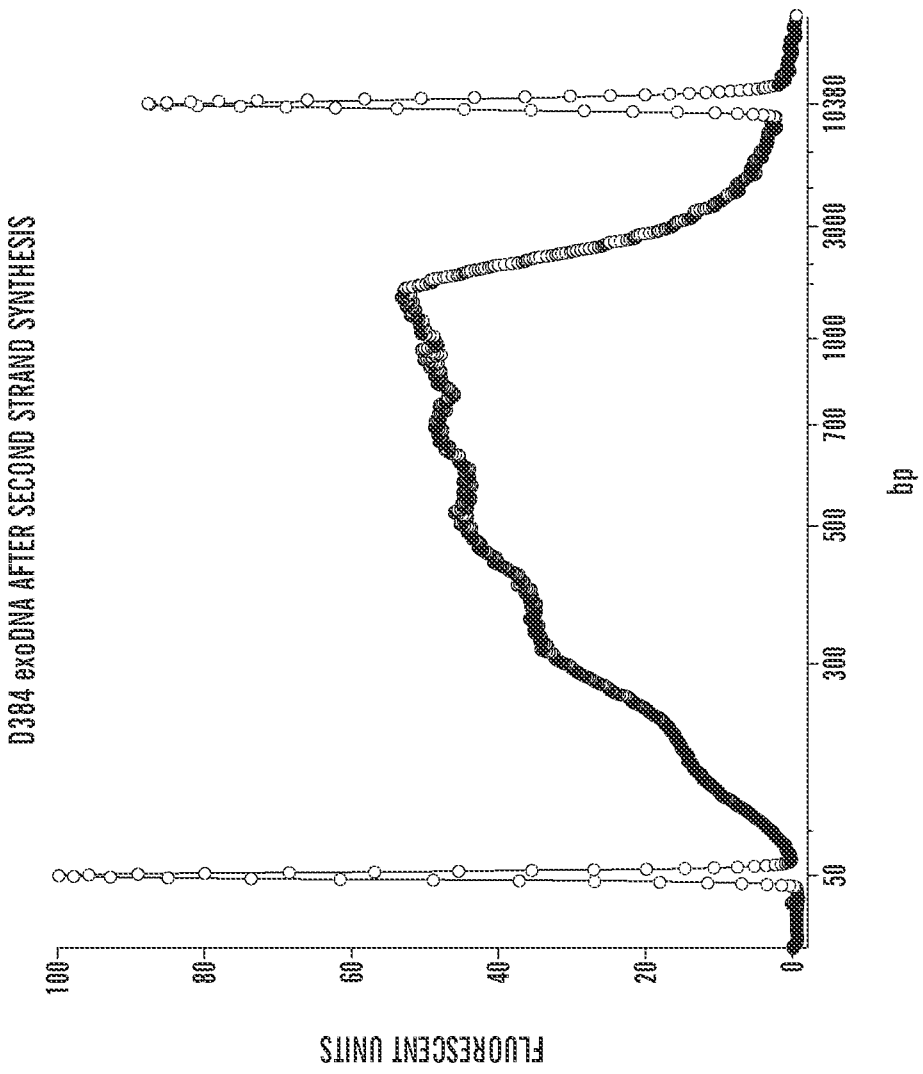
D384 exoDNA AFTER SECOND STRAND SYNTHESIS
FLUORESCENT UNITS
100
80
60
40
20
0
50
300
500
700
1000
3000
10380
bp

FIG. 26B

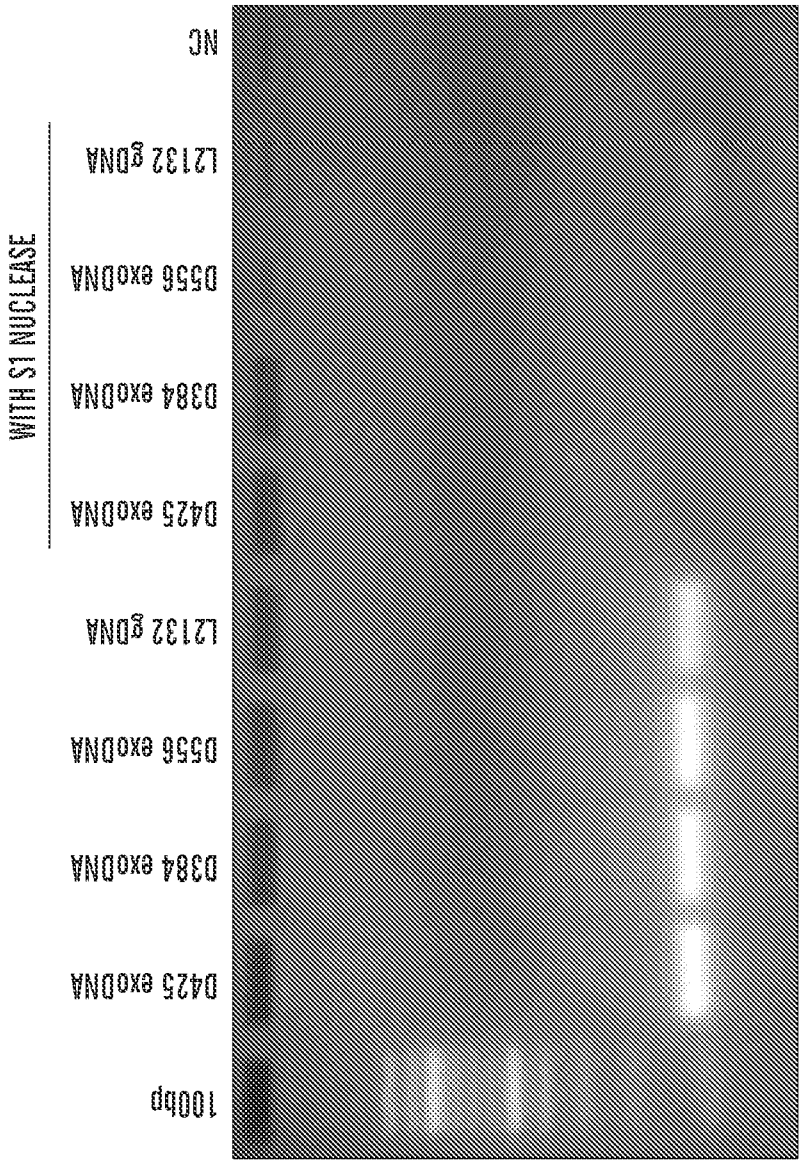
NC
L2132 gDNA
D556 exoDNA
D384 exoDNA
D425 exoDNA
WITH S1 NUCLEASE
L2132 gDNA
D556 exoDNA
D384 exoDNA
D425 exoDNA
100bp

FIG. 27

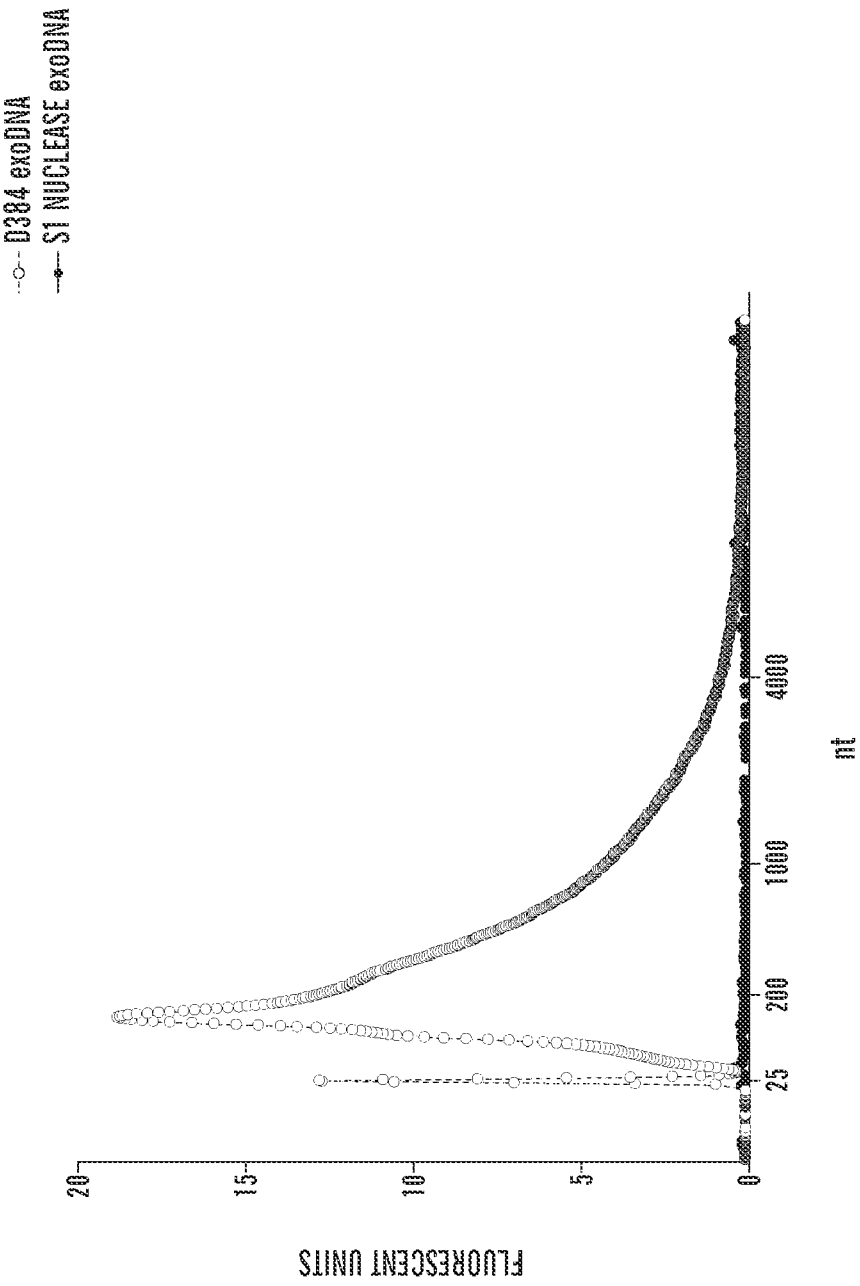
D384 exoDNA
S1 NUCLEASE exoDNA
FLUORESCENT UNITS
20
15
10
5
0
25
200
1000
4000
nt

FIG. 28

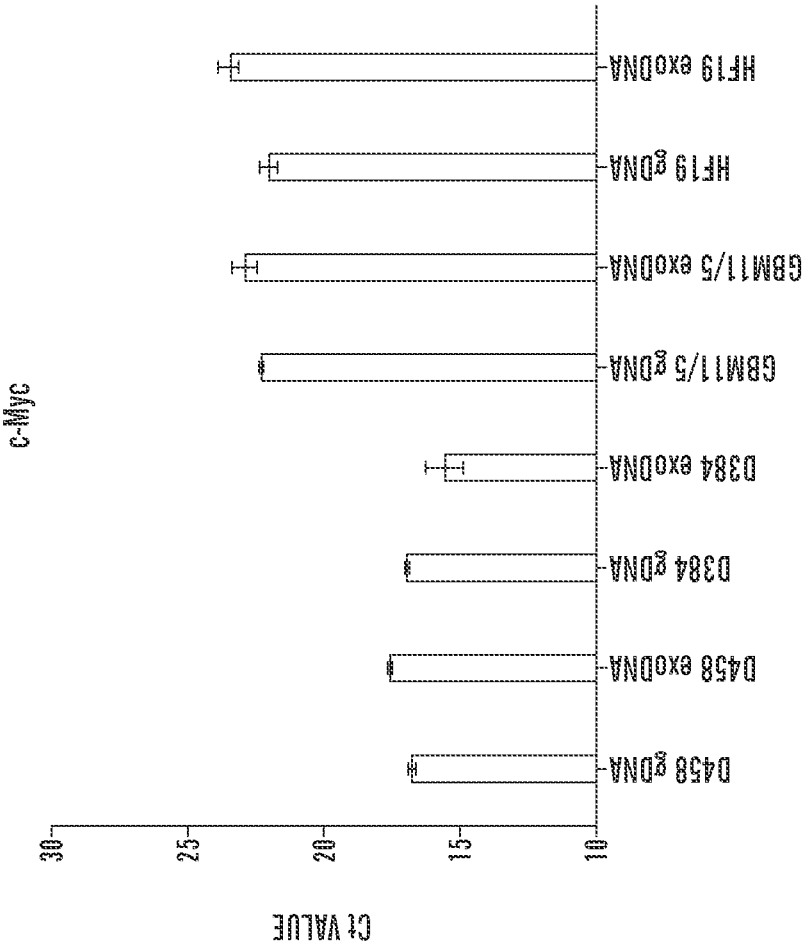
c-Myc
Ct VALUE
30
25
20
15
10
D458 gDNA
D458 exoDNA
D384 gDNA
D384 exoDNA
GBM11/5 gDNA
GBM11/5 exoDNA
HF19 gDNA
HF19 exoDNA

FIG. 29A

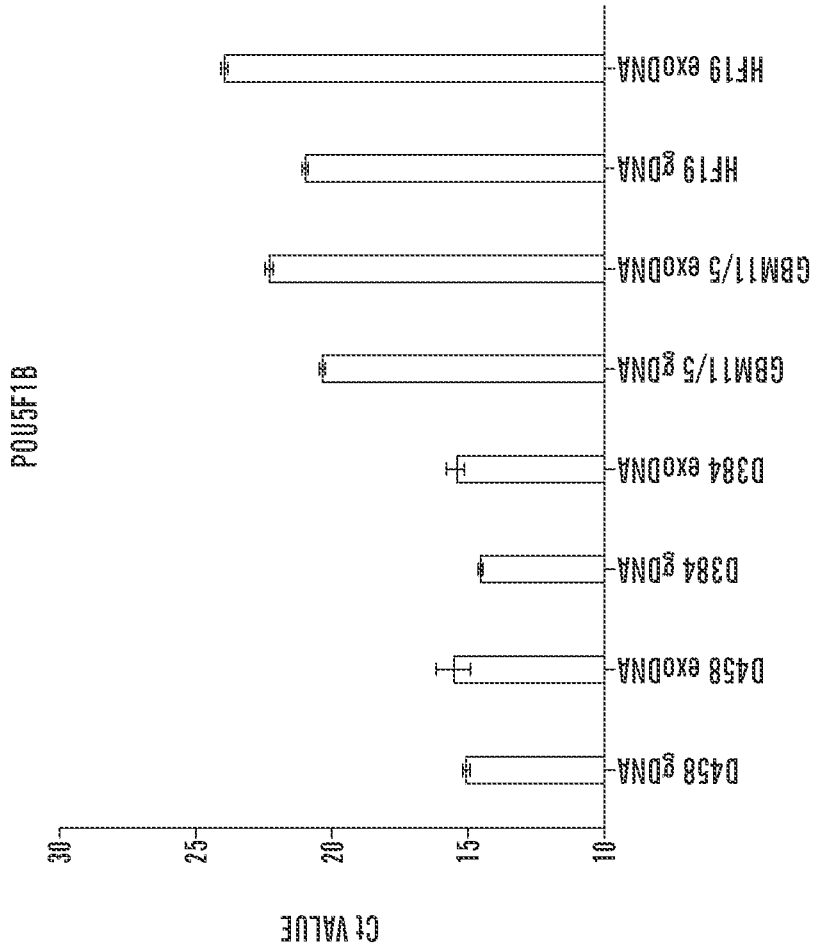
POU5F1B
Ct VALUE
30
25
20
15
10
D458 gDNA
D458 exoDNA
D384 gDNA
D384 exoDNA
GBM11/5 gDNA
GBM11/5 exoDNA
HF19 gDNA
HF19 exoDNA

FIG. 29B

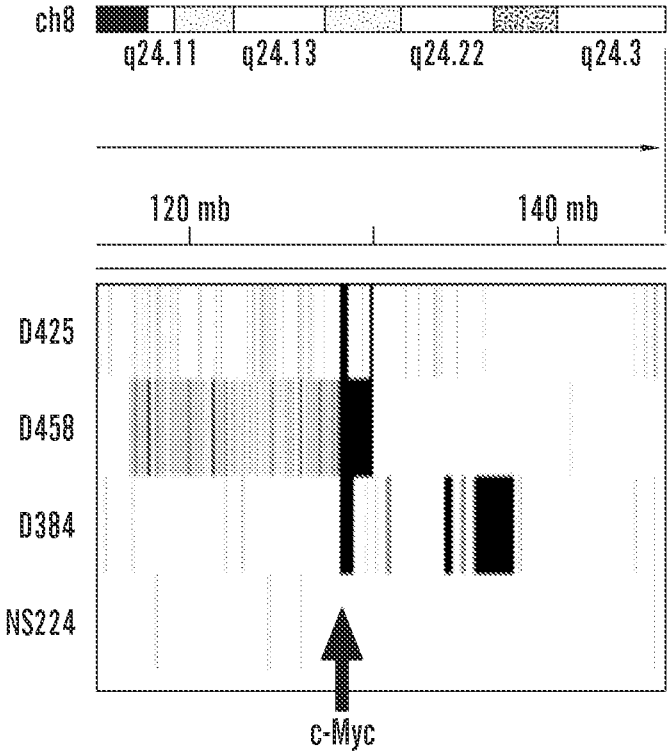
ch8
q24.11
q24.13
q24.22
q24.3
120 mb
140 mb
D425
D458
D384
NS224
c-Myc

FIG. 30

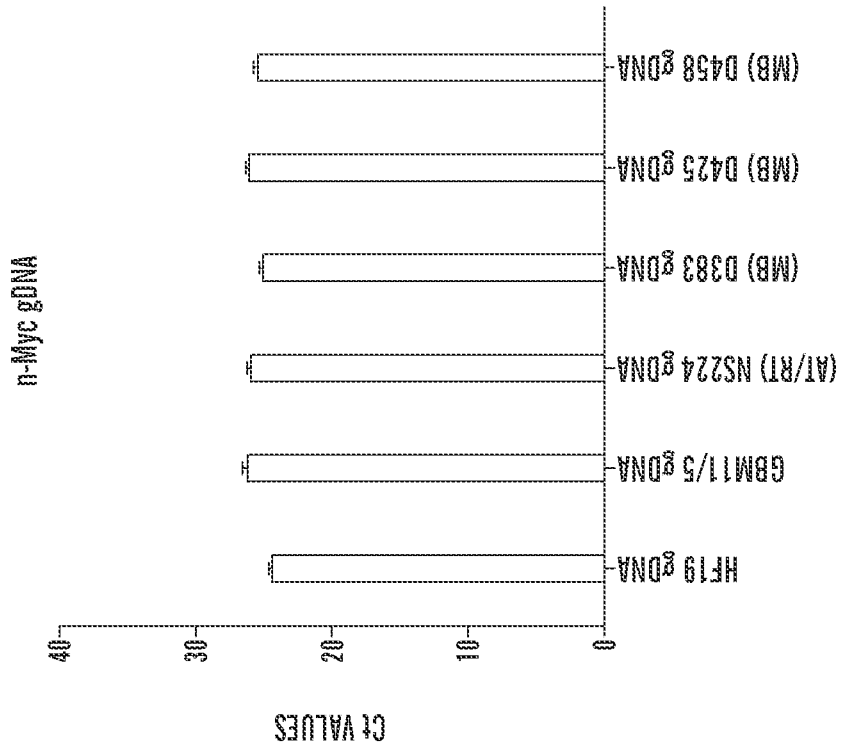
n-Myc gDNA
Ct VALUES
0
10
20
30
40
HF19 gDNA
GBM11/5 gDNA
(AT/RT) NS224 gDNA
(MB) D383 gDNA
(MB) D425 gDNA
(MB) D458 gDNA

FIG. 31A

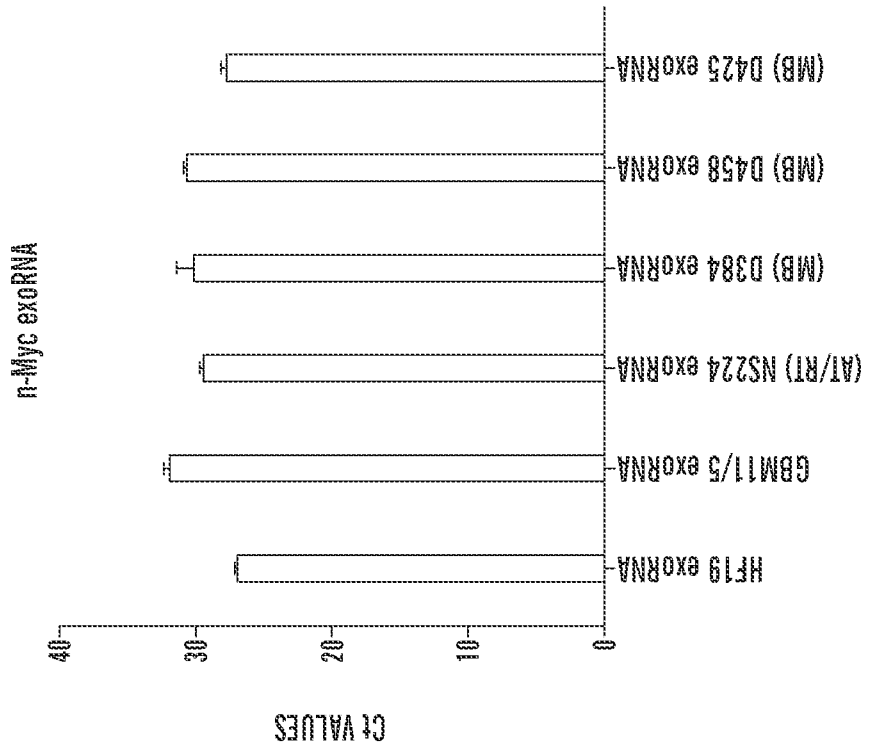
n-Myc exoRNA
Ct VALUES
0
10
20
30
40
HF19 exoRNA
GBM11/5 exoRNA
(AT/RT) NS224 exoRNA
(MB) D384 exoRNA
(MB) D458 exoRNA
(MB) D425 exoRNA

FIG. 31B

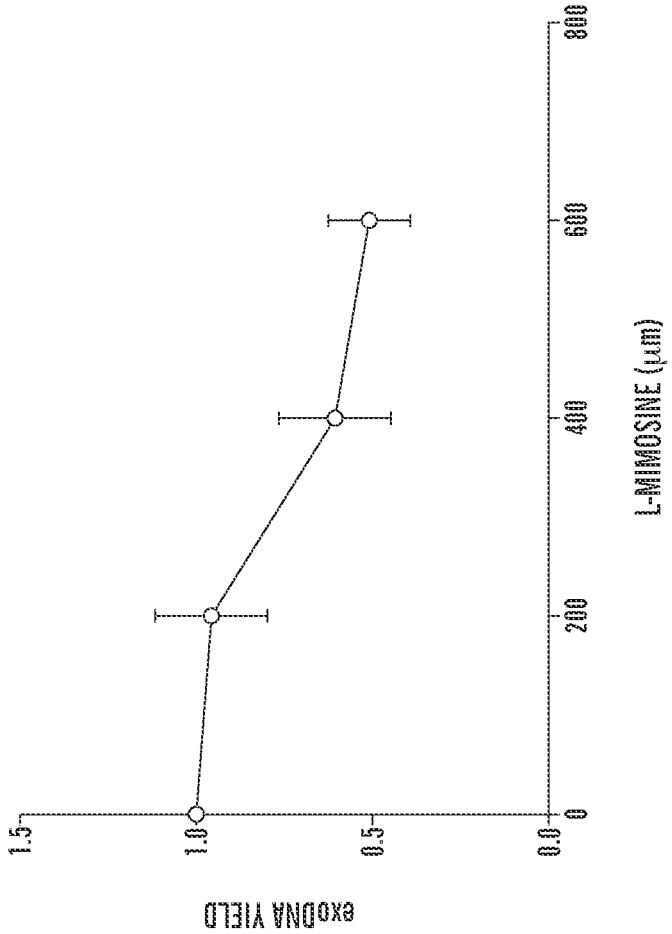

FIG. 32

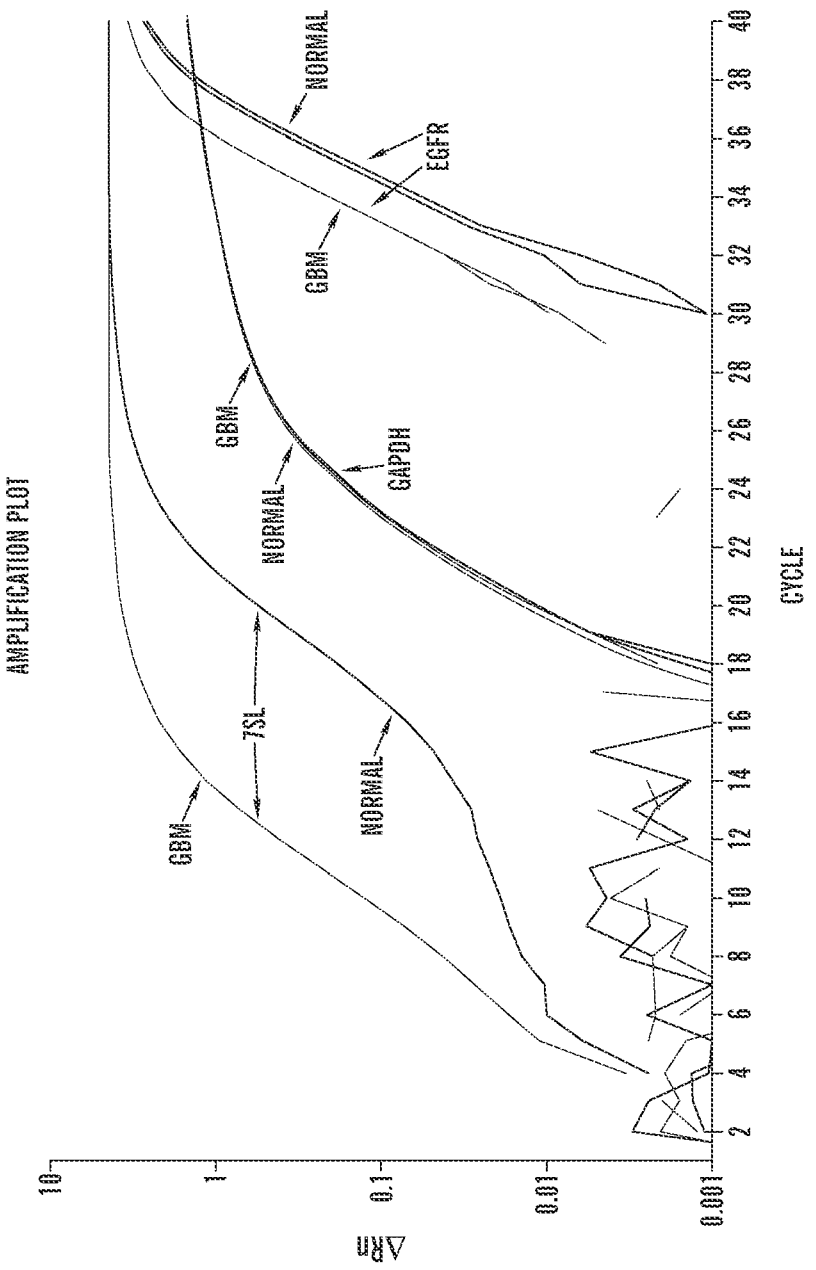
AMPLIFICATION PLOT
ΔRn
10
1
0.1
0.01
0.001
2
4
6
8
10
12
14
16
18
20
22
24
26
28
30
32
34
36
38
40
CYCLE
GBM
TSL
NORMAL
GBM
NORMAL
GAPDH
GBM
EGFR
NORMAL

FIG. 33

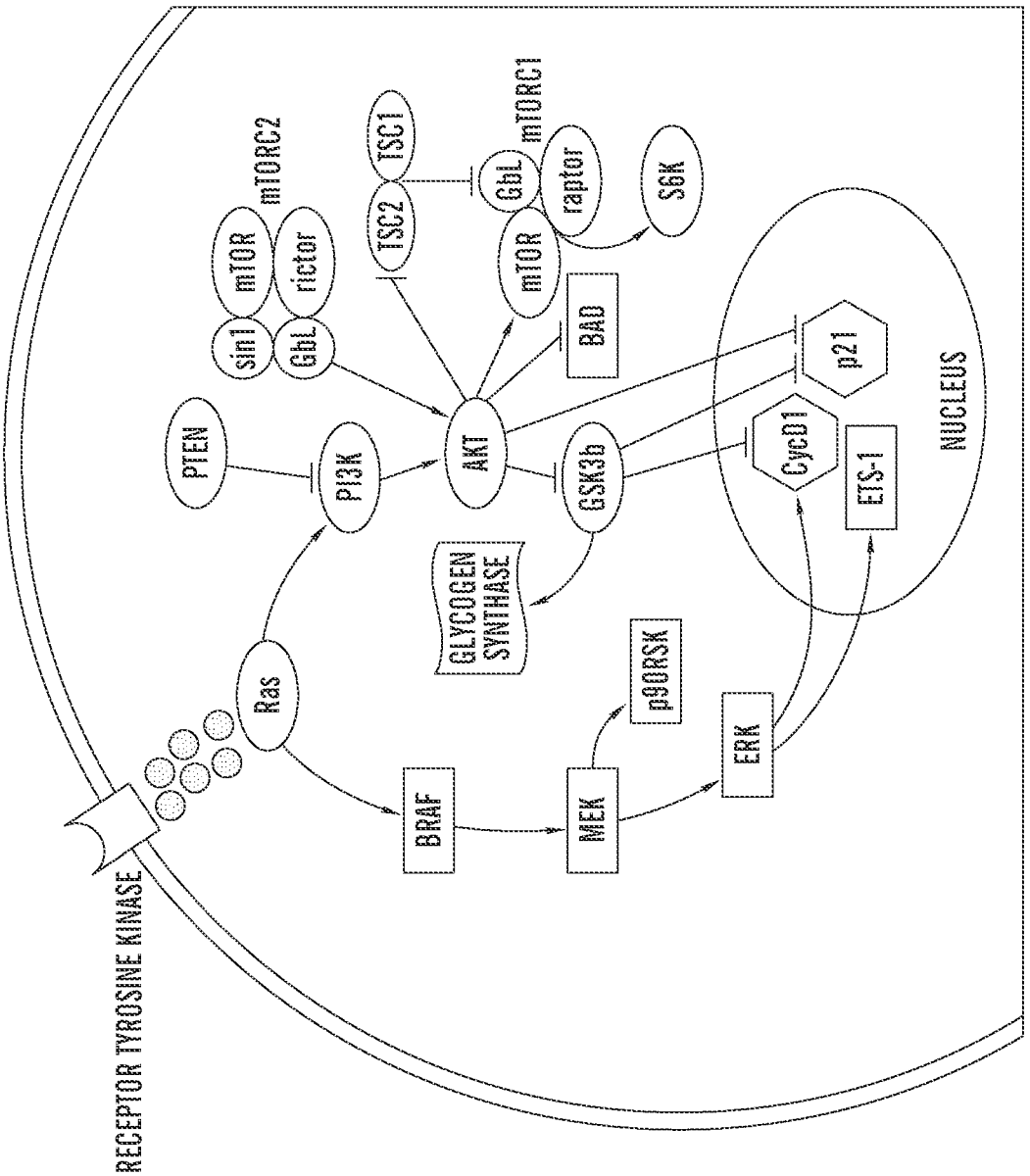
RECEPTOR TYROSINE KINASE
Ras
BRAF
MEK
ERK
p90RSK
PTEN
PI3K
AKT
GSK3b
GLYCOGEN SYNTHASE
sin1
mTOR
mTORC2
GbL
rictor
TSC2
TSC1
GbL
mTOR
raptor
mTORC1
S6K
BAD
p21
CycD1
ETS-1
NUCLEUS

FIG. 34