(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
24 June 2010 (24.06.2010)

PCT

(10) International Publication Number
WO 2010/069008 A1

(51) International Patent Classification:
C12N 5/074 (2010.01)

(21) International Application Number:
PCT/AU2009/001665

(22) International Filing Date:
21 December 2009 (21.12.2009)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
2008906529 19 December 2008 (19.12.2008) AU

(71) Applicants *(for all designated States except US)*: **GRIFFITH UNIVERSITY** [AU/AU]; 170 Kessels Road, Nathan, Queensland 4111 (AU). **THE UNIVERSITY OF QUEENSLAND** [AU/AU]; St Lucia, Queensland 4072 (AU).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **BROWNE, Catherine** [AU/AU]; 170 Kessels Road, Nathan, Queensland 4111 (AU). **MACKAY-SIM, Alan** [AU/AU]; 170 Kessels Road, Nathan, Queensland 4111 (AU).

(74) Agent: **FISHER ADAMS KELLY**; Level 29 Comalco Place, 12 Creek Street, Brisbane, Queensland 4000 (AU).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

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

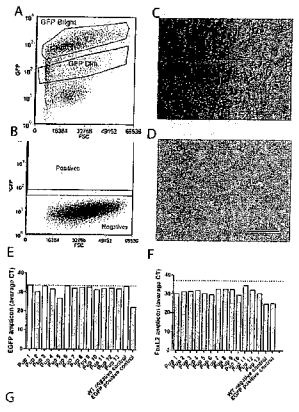
Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

(54) **Title**: A GERMLINE COMPETENT CELL DERIVED FROM ADULT TISSUE

Figure 1



Experiment date	Blastocysts transplanted	Cell type	Cell state	Cells per blastocyst	Number offspring	Number chimeras	Mouse age
9/05/2007	28	EGFP-dim	Fresh	15-18	13	9	P14
7/11/2007	30	EGFP-dim	Thawed	20-25	5	0	P14
2/05/2008	14	EGFP-neg	Fresh	15-18	14	7	E16.5
7/05/2008	41	EGFP-neg	Thawed	15-18	15	9	E16.5
12/09/2008	20	EGFP-neg	Thawed	15-18	10	6	P14
3/10/2008	20	EGFP-neg	Thawed	1	15	15	E13.5
31/10/2008	14	EGFP-neg	Thawed	1	4	4	P14

(57) **Abstract**: An adult mammalian stem cell is provided which is pluripotent and non-teratogenic in immune deficient animals. The mammalian stem cell is obtainable by culturing olfactory epithelium in the presence of one or more of FGF2, FGF9, SCF, LIF, TGF- β2 and BMP-4. The mammalian stem cell expresses low levels of Sox2 and Oct4 mRNA and higher levels of SP1 and ANP32A mRNA. The mammalian stem cell expresses one or more proteins such as OCT-3./4, SOX2, NANOG, KLF4, MVH, KIT, NESTIN and also selected CD antigens. The mammalian stem cell may be useful in compositions and methods for treating diseases or conditions responsive to cell-based therapies, including but not limited spinal repair, heart muscle regeneration, skin repair, bone-marrow transplantation and repair of neural degeneration. The mammalian stem cell and non-human mammals generated therefrom may be useful in drug screening, disease modelling and identifying cell differentiation pathways.

WO 2010/069008 A1

TITLE

A GERMLINE COMPETENT CELL DERIVED FROM ADULT TISSUE

FIELD

THIS INVENTION relates to pluripotent mammalian cells and to methods of isolating, culturing and using same.

BACKGROUND

Pluripotent cells are cells that have the potential to differentiate into all cell types found in an adult organism, except for certain placental tissue and umbilicus. These cells naturally occur in the inner cell mass of an embryo and they differentiate to form three embryonic germ layers: ectoderm, endoderm and mesoderm. It is from these three germ layers that all adult tissues in a human are formed. There is considerable interest in using pluripotent cells in drug development and discovery, gene therapy and cell and tissue therapy. There has been clinical application of these cells in *in vitro* fertilisation and tissue and cellular regeneration and replacement therapies.

Pluripotent cells known to date may be classified into 3 groups. The first of these includes cells derived predominantly from embryonic tissue such as: (i) embryonic stem cells (ESCs), which are derived by long-term culture of cells from the inner cell mass of a blastocyst (Thomson *et al.* 1998 *Science* **282**:1145-1147); and (ii) embryonic germ cells (EG cells), which are derived from migratory primordial germ cells found in the region of the hind gut in transit to the genitalgonadal ridge in E8.5 - E9.5 mouse foetuses (Shamblott *et al.* 1998 *PNAS USA* **10**:13726-31). EG cells of a late embryo have many of the properties of ESCs. The primordial germ cells in an embryo develop into stem cells that in an adult generate the gametes. These cells are generally derived from embryos (created naturally or via cloning), fetal tissue or via the mixing of nucleus and cytoplasm of multiple species. Reprogramming of somatic cells to cells exhibiting pluripotent properties has been achieved by nuclear transplantation of a somatic nucleus into an enucleated egg. There are ethical issues that arise from the derivation of these cells.

A second group includes those cells obtained by introducing defined transcription factors into somatic cells. Cells formed by expression of a combination of transcription factors (*e.g* SOX2, OCT-3/4, NANOG and KLF4) expressed from a

retrovirus or other compounds are referred to as "induced pluripotent stem cells" or "iPS cells" (Takahashi & Yamanaka, 2006, *Cell* **126**:663-676).

Until recently, adult stem cells have been thought not to be pluripotent although recent studies have cast some doubt on this thinking. In this context some adult stem cells are thought to represent a third class of pluripotent cells.

The *in vivo* developmental potency of a given cell may be determined by assessing for germline competency or, for teratoma formation in an immune deficient animal.

A "germline competent" cell is capable of giving rise to functional gametes. One form of assessing germline competence includes injecting a candidate cell into a blastocyst and determining whether F1 derived from an intercross involving a founder derived from the blastocyst contains the genetic complement of the candidate cell. Germline competency is a defining feature of all pluripotent cells.

The capacity to form a teratoma – a tumour containing tissue that is characteristic of endodermal, ectodermal and mesodermal lineages– is also understood to indicate that the candidate cell has pluripotency *in vivo*. All pluripotent cells known to date – ESCs, EG cells and iPS cells – have this defining property. It is generally understood that teratoma formation occurs as a consequence of a "reprogramming" of the cell during culture to differentiate when placed in an environment in the absence of LIF. That is, the differentiation is a function of the cell itself, rather than stimuli from the tissue environment in which it is placed. As an example, inner cell mass cells generally do not form teratomas whereas ESCs do.

Teratoma formation is generally understood to be a significant limitation to the use of all pluripotent cells identified to date in clinical applications. More particularly, it is generally understood that there is a significant risk that pluripotent cells identified to date will cause teratomas or other forms of neoplasia or unregulated cell or tissue growth if used in clinical applications.

SUMMARY

The present invention is broadly directed to a mammalian pluripotent stem cell that is obtainable from adult cells and/or tissues. A preferred advantage of the mammalian pluripotent stem cell is that it does not form teratomas.

In one aspect, there is provided an isolated mammalian cell having the developmental potency of an embryonic stem cell (ESC), characterised in that the isolated mammalian cell does not form a teratoma when provided in an immune deficient animal.

Suitably, the isolated mammalian cell is a germline competent, pluripotent stem cell.

The isolated mammalian cell may be further characterized by a presence, absence, relatively high or relatively low level of expression of one or more genes or proteins set forth in Tables 1-12.

In particular embodiments, the invention provides:

(i) an isolated human cell designated Human XY pOS-17 deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121602;

(ii) an isolated mouse cell designated B6 Rosa26-EGFP XY Pos deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121601; and/or

(i) an isolated rat cell designated SD Rat XY pOS deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121603.

In another aspect, the invention provides a method of producing a mammalian cell, said method including the step of culturing a one or more cells or tissues obtained from a mammal in a medium including one or more of FGF9, FGF2, SCF and LIF, to thereby produce the isolated mammalian cell.

In one particular embodiment, the method includes culturing neurospheres or a neurosphere-like cellular mass in a medium comprising one or more of FGF2, FGF9, SCF and/or leukaemia inhibitory factor (LIF).

In a particular embodiment of this aspect relating to human cells, the medium includes one or more of FGF2, FGF9, SCF, LIF, TGF-β2 and/or BMP-4.

In further embodiments, the method includes: (a) forming a neurosphere or a neurosphere-like cellular mass; and (b) isolating the mammalian cell from the neurosphere or neurosphere-like cellular mass, thereby providing the isolating mammalian cell.

Preferably, the one or more cells or tissues, inclusive of the neurosphere or a neurosphere-like cellular mass, are obtainable from adult olfactory epithelium.

This aspect of the invention also provides an isolated mammalian cell obtainable by the method of this aspect.

In yet another aspect, there is provided a method of producing a differentiated mammalian cell, said method including the step of culturing the isolated mammalian cell of any of the aforementioned aspects under conditions which facilitate the production of the differentiated cell.

This aspect of the invention also provides a differentiated cell obtainable by the method of this aspect.

In one particular embodiment of the aforementioned aspects, there is provided an isolated mammalian cell, or differentiated cell, transformed or transfected with an isolated nucleic acid.

Preferably, the isolated nucleic acid is, or is provided in, a genetic construct.

In one particular embodiment, the isolated nucleic acid encodes a therapeutic agent.

In a further aspect there is provided a composition comprising an isolated mammalian cell according to the aforementioned aspects and/or a cell differentiated therefrom; and a suitable carrier, diluent or excipient.

In another further aspect there is provided a method of treatment of a disease or condition in a mammal, said method including the step of administering an isolated mammalian cell according to the aforementioned aspects and/or a cell differentiated therefrom to said mammal to thereby treat said disease or condition.

In yet another further aspect there is provided an isolated mammalian cell according to the aforementioned aspects and/or a cell differentiated therefrom for use in treating a disease or condition mammal.

In a yet still further aspect there is provided a method of producing a non-human mammal, said method including the steps of:

(i) delivering one or more isolated mammalian cells of the aforementioned aspects to a blastocyst of a non-human mammal; and

(ii) producing one or more progeny from said blastocyst.

Suitably, the one or more progeny comprise one or more cells or tissues that have a genetic complement of the one or more isolated mammalian cells delivered at step (i).

Preferably, the method further includes the step of implanting or otherwise transferring the blastocyst produced at step (i) to a female non-human mammal.

In one embodiment, one or more isolated mammalian cells delivered at step (i) are genetically modified, wherein the progeny produced at step (ii) are genetically modified.

This aspect of the invention also includes a genetically-modified non-human mammal obtainable by the method of this aspect.

In a still yet another further aspect, the invention provides a method of identifying, designing, screening or otherwise producing a compound having a desired activity, said method including the step of: (i) contacting a candidate compound with an isolated mammalian cell of any of the aforementioned aspects, or a cell differentiated therefrom; or (ii) administering a candidate molecule to a non-human mammal produced according to the method of the aforementioned aspect, to thereby produce a compound having said activity.

Non-limiting examples of activities include cell growth and/or differentiation, anti-tumour activity, pro- or anti-apoptotic activity, neuropharmacological activity; regulation of metabolism; hormonal activity; gene regulatory activity; cell cycle regulation and immunoregulatory activity,

In particular embodiments of each of the aforementioned aspects, the mammal is a preferably human, rat or mouse.

Preferably, in aspects relating to non-human mammal, the non-human mammal is a rat or a mouse.

As used herein, except where the context requires otherwise, the term "comprise" and variations of the term, such as "comprising", "comprises" and "comprised", are not intended to exclude further additives, components, integers or steps.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1: Pluripotent adult stem cells were derived from adult olfactory mucosa. Cells from adult, Rosa-EGFP mouse olfactory mucosa were grown as neurospheres,

dissociated and cultured for 48 hours as an adherent monolayer of expanded neurospheres in the presence of EGF and FGF2 for 2 days. The cells were then trypsinised and grown in POSE medium on mouse stromal feeder layers for 2 weeks (**A**) or 3 weeks (**B**) after which they were sorted on the basis of EGFP fluorescence, Y-axis, and forward scatter (X-axis (**A, B**). Prior to sorting, EGFP-negative cells were of similar undifferentiated phenotype (**C**). After sorting they were small and round (**D**). Scale bar = 100 μm. **E**: qPCR genotyping identified the EGFP amplicon in tail-tip DNA from 9 out of 13 live born offspring created from blastocyst injection of EGFP-dim cells (First experiment in **G**). Controls were DNA from non-transgenic mouse (WT negative control) and Rosa-EGFP mouse (EGFP-positive control). **F**: qPCR Control for FoxL2 amplicon from the same DNA samples. **G**: Summary Table of 67 separate blastocyst injections using EGFP-dim and EGFP-negative cells and different numbers of cells injected.

Figure 2: EGFP was detected in many tissues in chimeric mice and throughout the tissues of progeny of germ-line chimeras. Immunochemistry detects EGFP in chimeric mouse generated from blastocyst injection of a single pOS cell (**A-C**). Small green dots are autofluorescence in blood cells which are also seen in controls (**D-I**). **D-F**: Negative control, adjacent section without primary antibody. **G-I**: Negative control, wild-type non-EGFP mouse with primary antibody. Images A-I are confocal, taken on the same settings, from similar regions of the embryo: **A, D, G**, head region showing brain (b); **B, E, H**, mid-region showing lung (lu), skin (sk), dorsal root ganglia (drg); **C, F, I**, lower region showing liver (li), spinal cord (sc), stomach (st). All images show EGFP, autofluorescence, and DAPI-labelled nuclei. Bar (in I) = 200 μm. **J-O**: Fluorescence immunochemistry detects EGFP in transgenic offspring of chimeric founder (Pup 11 in Fig. 1E, F) (**J**). Autofluorescence only is detected in Negative Controls: no primary antibody on adjacent section (**L**) and non EGFP mouse with primary antibody (**N**). K, M, O are the same sections as J, L, N, imaged for DAPI-labelled nuclei. Bars = 1mm (J, K) and 2 mm (L-O).

Figure 3: pOS cells express genes associated with pluripotency. A recent study identified 300 genes (the "PluriNet") associated with pluripotency in embryonic stem cells, induced pluripotent stem cells and embryonic carcinoma cells[15]. 273 probes on the mouse Illumina array map to 265 PluriNet members. **A**: Graph of expression of 166 PluriNet genes in different populations of olfactory cells: Reference (dissociated

neurosphere cells prior to pOS cell culture and selection), Bright (EGFP-bright cells negatively selected from pOS cell cultures), Dim (EGFP-dim, pOS cells selected for initial blastocyst injections), Negative (EGFP-negative cells selected for blastocyst injections). Y-axis shows log normalised intensity for each gene: Grey shows genes not detected or reduced in Negative pOS cells. Lighter shading shows genes expressed in Negative pOS cells but neither reduced or enriched. Darker shading shows genes enriched in Negative pOS cells.

B: Relative expression in pOS cells of the chromatin modification subnetwork of PluriNet. Genes are shown that are significantly repressed or enriched in Negative pOS cells compared to Reference cells ($p<0.01$). Low or no expression of two of the key pluripotency genes *Nanog* and *Oct4* are also associated with low levels of expression of protein-partners and adjacent network members. The chromatin targets *Myc*, *Klf4/5*, *HDAC1* are induced in pOS cells, as are the cell cycle subnetworks associated with PluriNet.

C: Immunofluorescence for key pluripotency proteins. Left column: antibodies against: Sox2 (top line), Oct4 (2nd line), Nanog (3rd line) and Klf4 (bottom line). Middle column: the same cells imaged for D APIDAP-label led nuclei. Right column: merged images of other columns. *Sox2*, *Oct4*, and *Nanog* mRNAs were below detection thresholds on the microarray but their proteins were detected in about 10% of cells.

Figure 4: F1, F2 offspring of F0 chimaeras.

Detection of pOS cell-derived EGFP expression in first and second generation offspring of chimaeric founder mice. On each slide the first column shows sections from the wild-type control reacted for anti-EGFP immunochemistry, the second column shows sections from the animals listed but without primary antibody, and the third column shows sections from the animals listed with primary antibody. Nuclei stained with DAPI. Endogenous EGFP expression visualised using a rabbit anti-EGFP primary antibody and an Alexa-488-conjugated goat anti-rabbit antibody. Each foetus is imaged using darkfield (DF), DAPI-labelled nuclei and EGFP filters, using an Olympus BX-51 fluorescent microscope and DP Manager software.

Key to nomenclature:

WT6 – Wild-type, non-transgenic control

Fo11, Fo2, Fo10, Fo13 – Chimaeric founders 11, 10, 13 and 2, respectively.

Fo11/F11 – 1st generation pup #1 bred from chimaeric founder #11.

Fo11/F12 - 1st generation pup #2 bred from chimaeric founder #11.

Fo11/F13 – 1st generation pup #3 bred from chimaeric founder #11.

Fo11/F14 – 1st generation pup #4 bred from chimaeric founder #11.

Fo11/F16 – 1st generation pup #6 bred from chimaeric founder #11.

F02/F11/F21 – 2nd generation pup #1 bred from 1st generation Tg mouse #1, descended from chimaeric founder 2.

F02/F11/F22 - 2nd generation pup #2 bred from 1st generation Tg mouse #1, descended from chimaeric founder 2.

F02/F11/F23 - 2nd generation pup #3 bred from 1st generation Tg mouse #1, descended from chimaeric founder 2.

F02/F11/F24 - 2nd generation pup #4 bred from 1st generation Tg mouse #1, descended from chimaeric founder 2.

F02/F11/F25 - 2nd generation pup #5 bred from 1st generation Tg mouse #1, descended from chimaeric founder 2.

F02/F11/F26 - 2nd generation pup #6 bred from 1st generation Tg mouse #1, descended from chimaeric founder 2.

Fo10/F11 – 1st generation pup #1 bred from chimaeric founder #10.

Fo10/F13 – 1st generation pup #3 bred from chimaeric founder #10.

Fo13/F11 – 1st generation pup #1 bred from chimaeric founder #13.

Fo13/F13 – 1st generation pup #3 bred from chimaeric founder #13.

Figure 5: EGFP immunochemistry in chimeric embryo SC14 after injection of a single pOS cell into a blastocyst. **A, C, E, G**: EGFP immunoreactivity in different tissues. **B, D, F, H**: Negative control – nearby sections without primary antibody showing autofluorescence, predominantly in blood cells. **A, B**: Sections through limb bud (lb). **C, D**: Sections through head showing developing brain (b). **E, F**: Sections through liver (i) and lung (lu). **G, H**: Sections through spinal cord (sc) and dorsal root ganglion (drg). All images are composites of two images at different excitation and emission wavelengths: green (for EGFP), and red (for autofluorescence). All images show autofluorescent blood cells. Photomicrographs were taken on a Zeiss Axio Imager Z1 epi-fluorescence microscope at the same exposures and assembled in Adobe photoshop and Adobe Illustrator without adjustment. Scale bar = 200 μm.

Figure 6: qPCR for pluripotency gene expression in pOS cells. Positive controls (lighter shaded bars) indicate gene expression in primordial germ cells (PGCs) from E11.5 embryos. Gene expression in pOS cells (darker shaded bars) and PGCs is expressed relative to the internal control, 18S ribosomal RNA sub-unit.

Figure 7: **A**: Mouse pOS cells; **B**: human pOS cells; and **C**: rat pOS cells.

Figure 8: Injection of 1 pOS cell into one blastocyst is sufficient to generate male and female chimaeric founder (Fo) mice and F1 offspring. PCR detection of an EGFP amplicon was performed using DNA obtained from F1 progeny of an Fo2 female.

Figure 9: Expression of OCT-3/4, SOX2, NANOG and NESTIN in murine ES cells and pOS cells. Representative flow cytometry analysis of cell number (count) vs fluorescence intensity. The unshaded histogram shows the binding profile of anti-Oct4, anti-Sox2 and anti-Nestin. The shaded histogram shows the binding of the isotype-matched control antibody. The % of positive cells and the normalized mean fluorescence intensity (nMFI= MFI_{marker}/MFIisotype) is shown for each marker.

Figure 10: Bar graph showing comparison of Sox2 and Oct4 expression by murine pOS cells, murine ES cells and murine embryonic fibroblast (MEF) cells.

DETAILED DESCRIPTION

The inventors have produced an isolated mammalian cell obtainable or derivable from adult mammalian tissue. The isolated mammalian cell has germline competency, and therefore is by definition, a pluripotent stem cell. As exemplified herein the genetic complement of the isolated mammalian cell is inherited in F1 progeny formed from a founder mammal produced from a blastocyst into which the cell has been injected or otherwise delivered.

Further, as exemplified herein, the genetic complement of the cell can be identified in tissues derived from ectodermal, endodermal and mesodermal lineages of mammals produced from a blastocyst into which the cell is delivered.

Surprisingly, as exemplified herein the inventors have observed that the isolated mammalian cell is unable to form a teratoma when provided in an immune deficient animal. Further none of the founders, F1 or progeny derived therefrom to date have been found to have neoplastic or other uncontrolled cell or tissue growth. The finding suggests that the culture methodology and/or conditions that the

inventors designed to produce the isolated mammalian cell of the invention are unlike those for derivation of ESCs and EG cells in that they do not appear to reprogram the cell of the invention for teratoma formation. It will be understood that having produced a isolated mammalian cell capable of self renewal, that cell can then be produced by a variety of processes including those described further herein.

For the purposes of this invention, by "isolated" is meant material (*e.g.* cells) that has been removed from its natural state or otherwise been subjected to human manipulation. Isolated material may be partly, substantially or essentially free from components that normally accompany it in its natural state, or may be manipulated so as to be in an artificial state together with components that normally accompany it in its natural state. The term "isolated" also includes "enriched" or "purified", which in the context of cells, means that the frequency or proportion of cells after enrichment or purification is greater than before enrichment or purification.

Thus in one aspect there is provided an isolated mammalian cell having the developmental potency of an embryonic stem cell (ESC), the cell being characterised in that the cell does not form a teratoma when provided in an immune deficient animal.

In certain embodiments, the isolated mammalian cell is of human, mouse or rat origin.

An isolated mammalian cell having the developmental potency of an ESC is typically one that is capable of differentiating to form tissues derived from mesodermal, endodermal and ectodermal lineages. Typically the cell is also capable of self renewing proliferation.

An isolated mammalian cell having the developmental potency of an ESC is not a totipotent cell. An ESC does not form extra embryonic tissues. In contrast to a pluripotent cell, a "totipotent cell" is defined as a cell that may differentiate into an entire organism. A totipotent cell has the capability to develop into a complete embryo including extra-embryonic cell types. In this context, a "pluripotent cell" is generally understood as meaning a cell that may differentiate into all cell types that constitute an organism. A pluripotent cell cannot develop into any extra-embryonic cell types.

Other cells that have the developmental potency of an ESC include embryonic germ cells (EG cells) and induced pluripotent stem cells (iPS cells). However, these cells form a teratoma when provided in an immune deficient animal.

It will therefore be appreciated that in one embodiment, the invention provides a pluripotent stem cell, that does not form a teratoma when provided in an immune deficient animal. Suitably, the pluripotent stem cell is obtainable, derivable or otherwise produced from adult tissue.

A teratoma is generally understood as meaning a malignant tumour that contains tissues derived from all three embryonic layers (mesoderm, endoderm and ectoderm) including bone, muscle, cartilage, nerve, tooth buds and various glands.

Prior to the invention, teratoma formation in an immune deficient, or immune compromised animal such as a SCID mouse had been regarded as a defining characteristic of pluripotency. Assays for teratoma formation generally involve the injection of candidate pluripotent cells into such an animal and examination of the animal after a period in which a teratoma or related tumour would be expected to have formed without any other cell growth stimuli. The isolated mammalian cell according to the invention is characterised in that it does not form a teratoma under these assay conditions.

In certain embodiments the isolated mammalian cell retains an undifferentiated phenotype when provided in an immune deficient animal. For example, the cell may not differentiate in the immune deficient animal. In these embodiments, after injection into an immune deficient animal the cell may retain capacity for self renewal. For example, the isolated mammalian cell may retain the developmental potency of an ES, EG or iPS cell.

In another embodiment, the cell may retain the phenotype of a multipotent stem cell.

A "multipotent cell" is generally understood as meaning a cell that can develop into several cell types. A multipotent cell does not have the capability to develop into a complete embryo nor does it have the capacity to develop into all cell types that constitute an organism.

In other embodiments the cell may differentiate in the immune deficient animal to form tissue and cellular elements of the tissue in which it is placed. In other

embodiments the cell may migrate to another site in the immune deficient animal or undergo cell death.

It will also be appreciated from the foregoing that the inventors have produced a germline competent cell. A germline competent cell is a cell that when injected into a blastocyst can give rise to germ cells. These germ cells can then give rise to progeny.

It will therefore be appreciated that in one embodiment, the invention provides a germline competent cell, that does not form a teratoma when provided in an immune deficient animal. Suitably, the germline competent cell is obtainable, derivable or otherwise produced from adult tissue.

The isolated mammalian cell hereinbefore described is obtainable, derivable or otherwise produced from adult cells or tissues. Non-limiting examples include bone marrow, central nervous system tissue, neural tissue, skin, gut, pancreas, muscle, brain, heart, adipose, olfactory mucosa or other mucosa or epithelia.

Typically the tissue is olfactory mucosa.

It will also be appreciated that isolated mammalian cells of the invention may be characterized by levels of gene expression. Levels of gene expression may be relative levels of gene expression compared to a Reference cell, or may be detected as the presence or absence of expression of a particular gene. Typically, although not exclusively, this may be through detection and/or measurement of RNA expression. This may be by transcriptome analysis or by mRNA expression profile analysis, for example. Suitable techniques for analysis of gene expression are provided in the Examples herein, inclusive of microarray analysis, RT-PCR, northern blotting and other techniques known in the art.

The inventors have determined the protein-coding transcriptome of the isolated mammalian cell of the invention. The inventors have compared the transcriptome with PluriNet genes – a regulatory network of genes that is shared by pluripotent ES cells, embryonal carcinomas and iPS cells – to identify genes in the isolated mammalian cell of the invention that are also expressed in these pluripotent cells. Surprisingly the inventors have found that certain genes that have been observed as being associated with pluripotency in these pluripotent cells are not actively transcribed in the isolated mammalian cells of the invention. These are Sox

2, Oct3/4, all of which appear to have little or no transcription, and Nanog which appears to have very little transcription.

While not wishing to be bound by hypothesis, the inventors recognise that the unique differences in mRNA expression profile of the isolated mammalian cell of the invention as compared with known pluripotent cells may mean that the isolated mammalian cell of the invention is incapable of forming teratoma because it does not have expression of certain genes that are observed in known pluripotent cells. By extension it is recognised that the invention identifies the genes that are transcribed in known pluripotent cells but not in the isolated mammalian cell of the invention as being tumourigenic genes that are not necessary for germline competency.

In one embodiment, the isolated mammalian cell according to the invention does not contain, or contains relatively low amounts of Sox 2 or Oct3/4 mRNA.

Typically the isolated mammalian cell does not contain, or contains relatively low amounts of one or more of SET, ZFP42, HMGB1 or ARID38 mRNA.

Typically the isolated mammalian cell does not contain, or contains relatively low amounts of one or more of the mRNAs shown in Table 3 herein.

Typically the cell does not contain, or contains relatively low amounts of DNMT3b, HDAC2 and Nanog mRNA.

In embodiments where the isolated mammalian cell, or a population of said cells, does not contain, or contains relatively low amounts of one or more mRNAs, it will be understood that the isolated mammalian cell does not contain a detectable level of the mRNA, or contains an amount that is significantly lower than in a Reference cell or cell population. Accordingly, the isolated mammalian cell or population of said cells preferably contains a relative amount or abundance of said mRNA that is less than 50%, less than 40%, less than 30%, less than 20%, less than 15%, less than 10%, less than 5%, less than 2% or less than 1% of that of a Reference cell or cell population.

A preferred Reference cell is a neurosphere-derived cell.

A preferred method of mRNA quantification is quantitative PCR.

In another embodiment, the isolated mammalian cell may contain SP1 and/or ANP32A mRNA.

Typically the isolated mammalian cell may contain one or more mRNAs shown in Table 2 herein.

Typically the cell may contain one or more of Myc, HMGA1, SMARCAD1, SMARCC1, PTMA, MCM6, PCNA, HDAC1, KLF5, KLF4, BTBD14B, HoxA5, FoxA1, Meis1 and/or EN1 mRNA. These mRNAs are enriched in the isolated mammalian cell of the invention as compared with Reference cells (described further herein) from which they are derived. Although not wishing to be bound by theory, it is possible that culture conditions exemplified herein effectively direct the emergence and/or phenotype of the isolated mammalian cell of the invention.

In one embodiment, the isolated mammalian cell may express one or more genes at a level at least 2-fold, at least 3-fold, at least 5-fold, at least 10-fold or at least 20-fold greater than that of a Reference cell or cell population.

For example, the cell may contain one or more mRNAs shown in Table 1 herein, wherein the Reference cell is, or derived from, expanded neurospheres.

In other particular embodiments, the isolated mammalian cell has a profile of mRNA expression substantially as shown in Table 4 or Table 5 herein.

In yet another particular embodiment, an isolated human cell of the invention is characterized by a presence, absence, relatively high or relatively low level of expression of one or more genes (*e.g* mRNAs) set forth in any one of Tables 9-12. As will described in more detail in the Examples and is evident from Tables 9-12, microarray analysis of genes expressed in human cells of the invention has revealed that certain genes are expressed at higher or lower levels human cells compared to neurosphere-derived cells from which the cells were cultured. It is also evident that exposure to growth factors such as FGF-2, FGF9, leukaemia inhibitory factor (LIF), SCF, BMP-4 and/or TGFβ2 modulates gene expression in human cells.

It will also be appreciated that isolated mammalian cells of the invention may be characterized by protein expression.

Protein expression can be determined using the techniques in the Examples herein and other standard protein chemistry and serology techniques such as western blotting, 2D gel electrophoresis (e.g. SDS-PAGE and isoelectric focussing), mass spectrometry, immunohistochemistry and immunofluorescence (*e.g* by flow cytometric analysis).

In one embodiment, the isolated mammalian cell expresses one or more of the proteins set forth in Table 6, or preferably the proteins expressed by at least 20% of isolated mammalian cells listed in Table 7 and/or wherein mean fluorescence is

greater than 5000 units. Referring to Table 6, particular examples of proteins expressed by said isolated mammalian cell, wherein mean fluorescence is greater than 18000 units include: CD13; CD16/32; CD23; CD34; CD28; CD38; CD40; CD45; CD61; CD69; CD95; CD117; CD122; CD124; CD201 and/or CD309.

In another embodiment, the isolated mammalian cell expresses one or more of OCT-3/4, SOX2 , NANOG, KLF4, MVH, KIT and NESTIN. Typically, OCT-3/4 and SOX2 proteins appear to be less abundant than in a Reference cell such as an ES cell.

The isolated mammalian cell of the invention may include a label for detection of the cell. GFP is one example. The label may be passed on to subsequent generations so as to monitor the development and cellular fate of the progeny.

Typically the isolated mammalian cell of the invention has a diameter of about 6 to 12 micron, preferably 8 to 10 micron and defines a spherical shape in suspension culture. The diameter of the cell can be determined by microscopy or other standard methods in the art. The adherent mammalian cell defines an elongated shape, with a morphology that resembles a fibrocyte or mesenchymal cell, with variable dimensions.

An isolated mammalian cell according to the invention may be provided, produced, cultured or obtained by any of a number of processes. Advantageously, these processes do not require the use of embryonic tissues, nor do they require genetic manipulation or modification of cells or tissues.

In one embodiment, an isolated mammalian cell according to the invention is provided by culturing the one or more cells or tissues in conditions for promoting cell proliferation and self renewal. These conditions prevent the cell from differentiating. In another embodiment, the isolated mammalian cell is provided by a process including culturing one or more cells or tissues in a medium containing factors for inducing plasticity and/or inhibiting differentiation and/or for inducing proliferation.

Generally the sample is a sample of adult tissue, examples including bone marrow, central nervous system tissue, neural tissue, skin, gut, pancreas, muscle, brain, heart, adipose, olfactory mucosa or other mucosa or epithelia.

Preferably, the tissue is olfactory mucosa. Particularly preferred examples of olfactory mucosa and methods for isolation are discussed in the Examples below.

Isolated mammalian cells may be cultured "directly" from primary olfactory mucosa or from neurospheres or a neurosphere-like cellular mass which is derived from primary olfactory mucosa.

In certain embodiments, the isolated mammalian cell is provided by a process including culturing neurospheres or a neurosphere-like cellular mass in a medium containing factors for inducing plasticity and/or inhibiting differentiation and/or for inducing proliferation, thereby providing the isolated mammalian cell.

A "neurosphere" is generally known in the art as a heterogenous mixture of sometimes free floating cells generated by neural stem cells *in vitro*. Neurospheres are understood to form because daughter neural stem cells remain attached to their mothers through many rounds of cell division. They may also form by aggregation in which some aggregates are clonal whereas others are not.

A "neurosphere -like cellular mass" is generally understood as meaning a cellular mass that has the physical characteristics of a neurosphere. However the mass is generally not just derived from a neural stem cell. A neurosphere is a heterogenous mass that contains multipotent cells (typically less than 0.5 – 1 % of total cells) plus proliferating progenation and precursom, plus differentiating progeny (neurons and glia). Prior to the invention a neurosphere-like cellular mass was understood to be multipotent normally giving rise to neurons or glia, and not to contain pluripotent cells.

In one embodiment the neurosphere or neurosphere-like cellular mass is formed by the process discussed in Murrell *et al.* 2005 Dev. Dynamics **233:** 496.

In another embodiment, the cell is provided by a process including:

(a) forming a neurosphere or neurosphere-like cellular mass from a sample of tissue; and

(b) obtaining the cell from the neurosphere or neurosphere-like cellular mass, thereby providing the cell.

Examples of a medium containing factors for inducing plasticity and/or inhibiting differentiation and/or for inducing proliferation are described further herein. Typically the factors that are used in the cell culture are FGF2, FGF9, leukaemia inhibitory factor (LIF) and SCF or homologues thereof that retain the functional activity of these molecules. In one embodiment SCF is provided in a form wherein it is attached to, or otherwise expressed by, a feeder layer of cells.

In certain embodiments, the cell obtained from the neurosphere or neurosphere-like cellular mass or tissue sample is cultured on a feeder layer and exposed to a gelatin coated surface. Examples of these culture conditions are described further herein.

Preferably, the cell is provided by a process including the following steps:

(a) forming a neurosphere or neurosphere-like mass from a sample of tissue;

(b) dissociating cells that form part of the neurosphere or neurosphere-like mass;

(c) culturing the dissociated cells on a feeder layer in a culture medium comprising one or more of the group selected from FGF2, LIF, FGF9 and/or SCF or homologues thereof; and

(d) harvesting cultured cells produced at step (c).

Preferably, the culture medium is POSE medium.

Preferably, the cells are cultured in step (c) for greater than 7 days. More preferably, the cells are cultured for greater than 16 days.

In specific embodiments relating to isolated human cells of the invention, the medium may further comprise one or more of TGFβ2 or BMP4.

In one particular embodiment relating to isolated human cells of the invention, the medium comprises FGF2, LIF, FGF9, SCF, TGFβ2 and BMP4. As shown in Table 8, various combinations of some or all of FGF2, LIF, FGF9, SCF, TGFβ2 and BMP4 may be used. It is also noted that feeder cells expressing SCF (column I in Table 8) may support cell culture in the absence of any of the other factors.

In some embodiments, the RNA and/or expressed protein is analysed for expression of genes that are required for pluripotency of cells. The resulting gene expression profile can be compared to the PluriNet database to determine the genes expressed in common with those in the PluriNet database. The analysis provides information in regard to the pluripotentiality of the cells by providing information in relation to the ability of cells to form teratomas and to undergo differentiation in culture along specific differentiation pathways.

It will also be appreciated that isolated mammalian cells of the invention may be propagated and differentiated into one or more cells or tissues of interest. Differentiation may be facilitated by culture of isolated mammalian cells of the

invention in suitable growth and/or differentiation factors, as are well known in the art. Non-limiting examples of such growth and/or differentiation factors include NGF, colony stimulating factors, EGF, FGF, VEGF, HGF, IGFs and the like.

By way of example only, isolated mammalian cells of the invention may be differentiated into particular cell or tissue types such as neural cells, glia, epithelial cells such as skin and corneal cells, bone marrow cells or more differentiated cell types of the lymphoid or myeloid lineages, hepatic cells, pancreatic islet cells, cardiomyocytes and other muscle cell types and endothelial cells such as vascular endothelium, although without limitation thereto. In particular, isolated mammalian cells of the invention may be differentiated into cells or tissues known to be affected in a disease or disorder. Examples of such diseases are schizophrenia, Parkinson's disease, motor neurone disease, hereditary spastic paraplegia, MELAS mitochondrial mutational disorder and Alzheimer's disease.

In certain embodiments, differentiated cells and tissues may be useful for autologous or non-autologous cell or tissue transplantation for the treatment of a disease or condition responsive to such treatment.

In certain other embodiments, these differentiated cells may be useful for identifying or screening compounds for a desired activity, such as by drug screening and identification, toxicology, pharmacological testing and the like. Accordingly the desired activity may biological, pharmacological or any other desired activity. By way of example only, desired activities may include cell growth and/or differentiation activity, anti-tumour activity, pro- or anti-apoptotic activity, neuropharmacological activity; activity in regulation of metabolism; hormonal activity; gene regulatory activity; cell cycle regulation and immunoregulatory activity.

For example candidate drug (*i.e.* any suitable compound) could be screened using these differentiated cells to test their toxicological or teratogenic effect. For example if a drug is being developed for treating cancer, isolated mammalian cells of the invention cells may be differentiated into corresponding normal cells.

A candidate drug or other compound may then be applied to the differentiated cells (*i.e* normal or non-cancerous) cells to determine which drugs or compounds that act on the cancer cell line, but not on normal cells. In this manner, the drug or other compound may be added to the cancer cell line and the differentiated cells to select a

drug or compound and/or dose suitable for killing the cancer cell line, but not the normal cells. In another example, isolated mammalian cells of the invention may be propagated and differentiated into a specific type of neuron (with a specific neurotransmitter profile) or glia and then drug effects and gene expression assessed.

Differentiated cells may then be screened using nucleic acid expression profiling or protein expression profiling to identify nucleic acids or proteins that may be used to investigate a cause of the disorder or could be used for clinical diagnosis.

Nucleic acid and protein profiling is known in the art and may include methods such as an array, microarray and protein binding assays (*e.*g. ELISA and Western blot). The arrays may be nucleic acid arrays or protein arrays. A reference expression profile may be determined by profiling expression of a number of selected nucleic acids or proteins from one or more representative normal or diseased individuals (*i.e.* individuals having a disorder). A particular reference expression profile may be correlated with normal or diseased condition.

In one embodiment, isolated mammalian cells of the invention may be propagated from a patient presenting with a particular disease, such as those mentioned above, and a nucleic acid or protein expression profile determined. This patient expression profile may be compared with a reference expression profile of an unaffected control. Such a comparison may determine a nucleic acid or protein profile correlated with a particular disease. A reference expression profile of a diseased condition may be determined once an expression profile is known that correlates with a diseased condition.

In embodiments where isolated mammalian cells of a patient are differentiated into cells of interest that are associated with a particular disease (*e.g.* neurons, glia), nucleic acid or protein expression of these differentiated cells may then be compared with a reference expression profile, *e.g.* a control or known profile correlated with a diseased condition.

Comparing an expression profile of a diseased condition with a normal control may reveal a biochemical pathway associated with the diseased condition. Such a finding may lead to a diagnostic test for that disease and may aid in defining a cause of the disease.

The reference nucleic acid or protein expression profile may comprise a variety of cell types or tissue types. The reference profiles may be purchased

commercially. In general, a reference profile may comprise a "control sample" from normal tissues of developmental stages of interest, such as those available commercially or the control sample may originate from cells of a particular disorder. For example, in schizophrenia a change in gene expression is observed in post-mortem brain. A similar change in gene expression may be assessed in cells available from a skin biopsy. A comparison may be made between fibroblast cell from skin, olfactory tissue biopsies and isolated and propagated olfactory stem cells. All these samples may be compared with commercially available reference profile (s) or a unique reference profile may be discovered which may be compared with future samples for research or diagnostic purposes.

When assessing genetic fingerprints of disease it may not be necessary to differentiate the isolated mammalian cells of the invention uniformly into a specific cell type and a heterogeneous population of neurons and glia that are reproducibly presented in control and disease cultures may be sufficient to compare gene expression. Alternatively, if a particular neuron type is suspected to be affected in a disease the isolated mammalian cells may be differentiated into a single cell type.

The method described above does not require assaying for a previously known nucleic acid or protein. As will be appreciated by a person skilled in the art, a comparison between expressed nucleic acids or proteins of a test cell and a known normal and/or diseased cell may provide information in relation to the test cell being normal or diseased (i. e. associated with a disorder).

It will be appreciated that toxicity or teratogenicity of a drug or other compound may be assessed as described above. Toxicity or teratogenicity of a compound may be determined by abnormal or a change in behavior of the isolated mammalian cell and/or differentiated cell therefrom. For example, abnormal or changed behaviour may include a change when compared with control non-disease cultures or control non-compound exposed cultures. Such changes include: cell death rate, cell division rate, proliferation rate, differentiation fate or abnormal differentiation, a change in morphology (perhaps due to cytoskeletal deficits), a changes in nuclear repair mechanisms such as in response to ionising radiation or a change in gene expression or protein expression. A person skilled in the art would be able to consider other changes in cell behaviour.

In one embodiment, there is provided an isolated mammalian cell of the invention, or a cell differentiated therefrom as hereinbefore described, transformed or transfected with an isolated nucleic acid, referred to herein as a "genetically-modified cell of the invention".

In one preferred embodiment, the isolated nucleic acid encodes a therapeutic agent, such as a therapeutic protein or therapeutic nucleic acid. Examples of therapeutic nucleic acids include RNA molecules, as wil be described in more detail hereinafter.

In one particular embodiment, the isolated nucleic acid is, or is provided in, a genetic construct, such as an expression vector or construct.

Suitably, the genetic construct comprises said isolated nucleic acid operably linked or connected to one or more additional nucleotide sequences. In certain embodiments additional nucleotide sequences may be regulatory sequences that facilitate and/or control expression of said nucleic acid. Non-limiting examples include promoters, enhancers, repressors, polyadenylation sequences, introns and/or splice donor/acceptor sequences, although without limitation thereto.

Promoters operable in mammalian cells are well known the art. The promoter may be constitutive, regulatable (*i.e* inducible or repressible), tissue specific or subject to other desired functional constraints or influences on promoter activity. By way of example only, the promoter may be any promoter useful for mammalian expression, including but not limited to a CMV promoter, an SV40 promoter, an elongation factor α promoter (*e.g.* pEF-BOS), a crystallin promoter (*e.g.* αA crystallin, β2 crystallin) or a hybrid promoter (*e.g.* SRα), for example.

Other embodiments of additional nucleotide sequences may be selection marker sequences to facilitate selection of stable transformants/transfectants (*e.g* by providing resistance to neomycin, geneticin *etc.,* or susceptibility to gangcyclovir, for example). Yet further additional nucleotide sequences may include sequences that facilitate homologous recombination, inclusive of gene "knock out" or "knock in" sequences such as *Cre*, *loxP* and/or FLP recombinase sequences.

Isolated mammalian cells of the invention, or differentiated cells, may be transfected or transformed with a genetic construct, such as an expression vector or construct comprising a nucleic acid of interest. It will be appreciated that any suitable means for delivering a nucleic acid into a cell may be used, for example transfection

or transformation such as by electroporation, calcium phosphate precipitation, cationic lipid delivery, DEAE dextran or other methods known in the art.

The construct or vector may be integrated into the genome of the isolated mammalian cell, or alternatively may be maintained extra-chromosomally.

The nucleic acid may encode a protein or another molecule such as an RNA molecule, such as a therapeutic protein or RNA (*e.g.* an interfering RNA, microRNA, snoRNA, piRNA, ncRNA or a ribozyme). These RNA molecules may have a role in cellular activities including tumour suppression, regulation of transcription and/or of translation and/or regulation of the cell cycle, or of regulation of apoptosis.

Proteins encoded by the nucleic acid may be hormones, cytokines, growth factors, neurotransmitters, enzymes, antibodies, immunogenic and/or antigenic proteins, although without limitation thereto. The protein may be a gene regulatory protein such as a transcription factor, repressor or other DNA-binding protein, or a protein that induces epigenetic changes in chromatin structure. Examples include but are not restricted to: histone modifiers (acetylases, deacetylases, DNA methyltransferases).

In some embodiments, the nucleic acid may correspond to an "endogenous nucleic acid" normally expressed by the cell, or a fragment thereof, or may be homologous to an endogenous nucleic acid.

By way of example only, the construct or vector may comprise an endogenous nucleic acid that corresponds to a defective or mutated nucleic acid of a recipient. Accordingly, expression of the nucleic acid and/or encoded protein may treat a disease present in the recipient caused by the mutated or otherwise defective endogenous nucleic acid of the recipient.

Genetically modified cells of the invention may be suitable for delivering therapeutic agents to a mammal to thereby treat a disease or condition.

In one particular example, the nucleic acid may enable said genetically modified cell of the invention to express a secreted protein such as a hormone, growth factor or cytokine, or biologically active fragment thereof. Expression of these proteins may have therapeutic benefit. By way of example only, these include: insulin for treating diabetes; thyroxine for treating hypothyroidism; and/or treatment of the nervous system such as by expressing dopamine or GDNF for Parkinson's

Disease or acetylcholine to treat Alzheimer disease. In brain and spinal cord regeneration other growth factors might be useful such as BDNF, NGF, NT3.

Accordingly, in other aspects the invention provides compositions, methods and/or uses of one or more isolated mammalian cell according to the invention, and/or one or more cells differentiated therefrom, for treating a disease or condition in a mammal. Such treatments may be prophylactic or therapeutic, as required.

In one particular embodiment there is provided a composition, methods and/or uses of an isolated mammalian cell according to the invention, and/or one or more cells differentiated therefrom, for autologous or non-autologous cell transplantation for the treatment of a disease or condition.

Compositions of the invention may comprise one or more of said cells together with a carrier, diluent, excipient or preservative.

Preferably, the composition is a pharmaceutical composition. The pharmaceutical composition suitably comprises a pharmaceutically-acceptable carrier, diluent or excipient. By "pharmaceutically-acceptable carrier, diluent or excipient" is meant a solid or liquid filler, medium, diluent or encapsulating substance that may be safely administered to a mammal, such as a human.. Depending upon the particular route of administration, a variety of carriers, well known in the art may be used. These carriers may be selected from a group including sugars, starches, phosphate buffered solutions, emulsifiers and isotonic saline.

Any suitable route of administration may be employed for providing a patient with the pharmaceutical composition of the invention. For example, intravenous, intra-articular, intra-muscular, intra-dermal, subcutaneous, intraperitoneal, surgically implanted and the like may be employed.

In a preferred form, the pharmaceutical composition is administrable to a specific site by surgical implantation. Non-limiting examples include compositions administrable at a site of a spinal injury, as bone marrow for reconstitution in immune compromised patients, as heart muscle for regeneration in cardiac patients, as pancreatic β cells for diabetics, or as neural tissue for treating brain injury or degeneration. For example, cells may be administered into either the caudate nucleus or the substantia nigra for dopamine neuron replacement in treating Parkinson's disease patients.

A predetermined dosage form includes dispersions, suspensions, injections, solutions and the like. Dosage forms may also include implants, matrices, microcapsules, prostheses, gels, controlled-delivery devices, osmotic pumps and the like.

Pharmaceutical compositions of the present invention suitable for administration may be presented as discrete units such as vials containing a pre-determined amount of one or more cells of the invention, as a solution or a suspension in an aqueous liquid or a non-aqueous liquid. Such compositions may be prepared by any of the methods of pharmacy, but all methods include the step of bringing into association one or more cells as described above with the carrier which constitutes one or more necessary ingredients.

It may be possible to treat several diseases using cells of the present invention. For example, stem cells obtained from a biopsy of human donor having the CCR5 allele may confer resistance to HIV infection (Samson et al., 1996, Nature 382 722, incorporated herein by reference). Cells may be transplanted into a patient infected with HIV to prevent or reduce progression of AIDS. Alternatively, cells may be transplanted into a non-infected patient to confer immunity or resistance to HIV infection. Similar methods may be used to genetically modify a cell propagated in accordance with the methods of the invention such that the propagated cells express any nucleic acid of interest. Using the cells of the invention, several diseases may potentially be treated, for example, nerve injury, spinal injury, schizophrenia, Parkinson's disease, Alzheimer's disease, bipolar disorder, mitochondrial disorders, epilepsy, diabetes, kidney failure, neuro-degenerative diseases, plastic anemia, immune-deficiency diseases, autoimmune diseases, cancers including lymphomas and leukemias, sickle cell anemia and osteoporosis deficiency in expression of a protein.

The cells of the invention may be useful for treating genetic defects. For example, U. S. Pat. No. 5,760, 012 (incorporated herein by reference), describes methods to genetically modify hematopoietic stem cells in patients afflicted with hemoglobinopathies such as sickle cell anemia, beta-thalassemia, or Gaucher's Disease. Methods of treating sickle cell anemia are disclosed by Cole-Strauss, A., et al., 1996, Science, 273 1386, incorporated herein by reference.

In particular embodiments, genetically modified cells of the invention may express an antibody or an antigen. For example, the genetically modified cell of the invention may be differentiated into a "dendritic cell" (DC) for use in dendritic cell therapy. DC's are antigen presenting cells capable of initiating an antigen-specific T-cell response in an animal. DC's may be isolated from various locations of an animal's body, including peripheral blood, however, it may be difficult and laborious to isolate and propagate DC's from blood. Alternatively, DC precursors may be propagated. For example, a DC precursor may be propagated and expanded in accordance with the methods of the present invention so that a suitable number of cells may be cultured for use in dendritic cell therapy. A isolated mammalian cell may be differentiated into a predetermined stage of development suitable for dendritic cell therapy.

"Dendritic cell therapy" refers to therapeutic cancer vaccines or cellular vaccines used for tumour immunotherapy as a method for treating cancer. Dendritic cell therapy typically involves isolating DC from a patient (or isolating propagating the DC precursor), culturing the isolated DC in the presence of a tumour-associated antigen or transfecting the isolated DC with a nucleic acid encoding a tumour-associated antigen ("antigen loading or pulsing"), and administering the antigen loaded or transfected DC's to the patient. Methods for loading or pulsing dendritic cells with an antigen are described in (Meidenbauer *et al*, 2001, Biol Chem **4** 507; Rains, *et al*, 2001, Hepatogastroenterology **38** 347; Nestle, 2000, Oncogene **56** 6673; Gilboa & Lyerly, 1998, Cancer Immunotherapy **46** 82).

By way of example, US Patent 5,788, 963, describes methods and compositions for use of human dendritic cells to activate T-cells for immunotherapeutic responses against primary and metastatic prostate cancer. In one embodiment isolated DC are exposed in vitro to a prostate cancer antigen before administration to a patient.

Isolated mammalian cells may be used with a patient undergoing high dose chemotherapy and/or radiation therapy. Prior to chemotherapy, a neural tissue biopsy may be performed on a patient and the stem cells expanded in vitro in accordance with the invention and stored. The stem cells may be genetically modified or not after biopsy. The cells may later be infused into the patient after the chemotherapy treatment.

Isolated mammalian cells of the invention may undergo spontaneous or induced immortalisation *in vitro*. The resulting immortalised, clonal or non-clonal cells may be useful as a cell line that may be genetically manipulated or not. The cell line may be placed in conditions that induce or do not induce, lineage commitment *in vitro* or *in vivo* and/or undergo cell differentiation or not, *in vitro* or *in vivo*.

Isolated mammalian cells of the invention can be used for basic research to understand the fundamental biology of development, including genes, growth factors and nutrients, which direct cellular and tissue formation. Examples of typical methods that may be used with cells prepared in accordance with the present invention are well known in the art.

Accordingly, one particular aspect of the invention provides a method of producing a non-human mammal, said method including the steps of:

(a) delivering one or more isolated mammalian cells of the invention to a blastocyst of a non-human mammal; and

(b) producing one or more progeny from said blastocyst.

Suitably, the one or more progeny comprise one or more cells or tissues that have a genetic complement of the one or more isolated mammalian cells delivered at step (i).

Preferably, the method further includes the step of implanting or otherwise transferring the blastocyst produced at step (i) to a female non-human mammal.

Suitably, the one or more progeny comprise one or more cells or tissues that have a genetic complement of the one or more isolated mammalian cells delivered at step (i).

It will be appreciated that "progeny" include and encompass immediate offspring and the progeny of subsequent generations.

One particular embodiment includes producing a genetically-modified non-human mammal. For example, one or more genetically-modified mammalian cells, as hereinbefore described, may be delivered to the blastocyst of the non-human mammal at step (i). Subsequent "transgenic" progeny may be bred which include the genetic modification of the cell delivered at step (i).

A non-human mammal (*e.g.* a mouse or rat) produced according to the invention, inclusive of genetically-modified non-human mammals, may be useful for drug screening, analysis of developmental gene expression and identification of

candidate molecules having a desired biological activity, such as by high-throughput screening, although without limitation thereto. The desired biological activity may include cell growth and/or differentiation, anti-tumour activity, pro- or anti-apoptotic activity, cell cycle regulation and immunoregulatory activity, although without limitation thereto.

Isolated mammalian cells of the invention may be used with a known animal model of disease to assess cell replacement therapy.

These animal models include: (A) neurobiology and disorders thereof, in all of its manifestations, including: Alzheimer's disease, Amyotrophic lateral sclerosis, Huntington's disease research tools for neurobiology, spinal cord injury, spinal cord disease, multiple sclerosis, cerebral palsy, muscular atrophy, (B) cardiovascular biology and disorders thereof, in all of its manifestations including myocardial infarction, stroke, ischemia, (C) epilepsy in all of its manifestations, (D) reproduction and disorders thereof, in all of its manifestations, (E) endocrinology and disorders thereof, in all of its manifestations, including Diabetes Mellitus Type I and Type II, (F) sensorineural development and function and disorders thereof, in all of its manifestations, (G) immune deficiency in all of its manifestations, (L) inflammation in all of its manifestations, (H) vital organ development and function and disorders thereof, in all of its manifestations, (I) dermatology and disorders thereof in all of its manifestations, (J) lung and respiratory tract development and function and disorders thereof, in all of its manifestations, (K) apoptosis and disorders thereof, in all of its manifestations, (L) cancer in all of its manifestations, (M) cell biology and disorders thereof, in all of its manifestations, (N) developmental biology and disorders thereof, in all of its manifestations, (O) haematology and disorders thereof, in all of its manifestations, (P) rodent/human gene homologs / orthologs, and mutants thereof, in all of their manifestations, (Q) metabolism and disorders thereof, in all of its manifestations.

The following non-limiting examples illustrate the isolated mammalian cells, compositions and methods of the invention. These examples should not be construed as limiting: the examples are included for the purposes of illustration only. The pluripotent olfactory stem "pOS" cell discussed in the Examples will be understood to represent an exemplification of the isolated mammalian cell of the invention.

EXAMPLES

Production and characterization of a murine pluripotent olfactory stem "pOS" cell

Generation of murine pOS cells

Olfactory mucosa was dissected from adult, transgenic Rosa-EGFP mice (Quah *et al.*, 2008, Proceedings of the National Academy of Sciences of the United States of America **105**, 4259) and the cells grown in serum-free medium with EGF and FGF2 to form neurospheres in order to select for a cell population that includes a multipotent, neural stem cell (Murrell *et al.*, 2005, Dev Dyn **233**, 496; Murrell *et al.*, 2008, Stem cells (Dayton, Ohio) **26**, 2183)

Neurosphere-derived cells were dissociated and grown on a feeder layer of mouse stromal cells expressing a membrane-associated form of mouse Stem Cell Factor (SCF; Matsui *et al.*, 1992, Cell **70** 841) in a medium containing FGF2, SCF, FGF9, and Leukemia Inhibitory Factor (LIF). After 2 weeks, fluorescence-activated cell sorting (FACS) of these cultures revealed three populations of cells based on their EGFP expression: bright, dim and negative (Fig. 1A). After a further week, EGFP expression was lost completely (Fig. 1B). Prior to FACS these EGFP-negative cells were relatively homogeneous and non-differentiated in appearance (Fig. 1C) and after sorting they were small and round and about 10 μM in diameter (Fig. 1D). EGFP-dim and EGFP-negative cells (pOS cells) were selected for blastocyst injection; some were frozen and stored beforehand (Fig. 1G). The EGFP-bright cells were of mixed, more complex morphologies and were not selected for blastocyst injection.

Generation of chimeric mice from pOS cells and of F1 from chimerics

pOS cells were injected into syngeneic C57BL/6 blastocysts (3.5 d.p.c.) which were then implanted in pseudo-pregnant CD-1 females. Chimeric embryos and neonates were identified by the presence in their tissues of the EGFP transgene identified using qPCR or PCR of DNA from tissue samples of tail, limb-bud or liver (Fig. 1E, F; Supplementary Fig. 1). Chimeric mice were generated in 5 out of 6 series of blastocyst injections (Fig. 1G). In the initial experiments EGFP-dim cells were selected and 15-18 or 20-25 cells were injected into each blastocyst. This produced 18 live born pups, 9 of which were chimeras (Fig. 1G). Six of these chimeric founders (3F, 3M) were bred with wild-type C57BL/6J mice to test for germ-line transmission. Of these, 3 females and 2 males were transgenic, producing 41

offspring, 26 of which were transgenic, identified by qPCR of DNA (Fig. 1E and 1F) or immunochemistry of tissues (Fig. 2J-N). A transgenic male offspring of a chimeric female founder was bred to produce a second generation of 11 pups, 7 of which were transgenic. Transgenic offspring expressed EGFP throughout their tissues (Figure 2J and Figure 4).

For the next series of experiments, a new population of pOS cells was generated from a second culture preparation. This time, culturing for an extra week produced EGFP-negative pOS cells (Fig. 1B-D), 15-18 of which were injected per blastocyst, producing 39 offspring; 22 were chimeric (Fig. 1G). pOS cells were able to be frozen and thawed. The proportion of chimeras was similar whether the pOS cells were taken from fresh cultures or thawed from frozen aliquots of those same cultures (Fig. 1G). Taken together these results demonstrate that the pOS cells robustly and repeatedly gave rise to chimeric mice after blastocyst injection. Significantly, we demonstrated germline chimerism in 5 of these chimeras of both sexes and demonstrated passage of the EGFP transgene through two subsequent generations.

As a more stringent test of pluripotency, we injected blastocysts with single pOS cells (Fig. 1G). This generated 15 chimeras from a total of 15 embryos (Fig. 1G), identified by qPCR for the EGFP transgene in fetal limb bud samples. The tissues of chimeric animals were demonstrably chimeric for the EGFP transgene identified immunochemically at 13.5 d.p.c. Organs from all embryonic germ layers were EGFP-positive in some embryos (Fig. 2A-C; Fig. 5). Negative controls included EGFP-containing tissues without primary antibody (Fig. 2D-F) and wild-type, non-EGFP tissues processed for immunochemistry with the primary antibody (Fig. 2G-I). These single pOS cells were previously frozen, stored and thawed before blastocyst injection (Fig. 1G). These results revealed that the progeny of a single cell are capable of proliferation and contributing to multiple tissues of all germ layers in the chimeric offspring.

Assessment of chimerics and F1 for abnormalities and tumours

There were no abnormalities observed in any of the chimeric embryos and the live born chimeric pups were healthy and otherwise indistinguishable from their non-chimeric littermates. None of the 48 chimeras had any obvious tumours. Adult

chimeric mice and their offspring were healthy and fertile. Thirteen chimeras were maintained until 14 months old without evidence of any tumours. Independent veterinary pathology analysis revealed no pathologies in any mice except those associated with normal ageing in this strain. Similarly, no tumours were observed in pathological analysis of the first and second generation offspring of the chimeric mice at 6 -12 months of age (n = 10). These results demonstrate that germline chimerism of pOS cells is not associated with the unrestrained growth associated with tumour formation in chimeras or their offspring.

Assessment of teratomas formation by murine pOS cells

The developmental potency of stem cells is often evaluated by their ability to form teratomas when injected into immune deficient mice. Pluripotency demonstrated by teratoma formation is taken as a marker for pluripotency (Okita *et al.*, 2007, Nature **448** 313; Takahashi *et al.*, 2007, Cell **131** 861; Thomson *et al.*, 1998, Science **282** 1145). The ability of pOS cells to form teratomas was assessed by subcutaneous injection of 100,000 cells into each of two sites per mouse (n=3). The injected pOS cells were from the same batch that produced chimeric mice. None of the 6 injection sites showed any tumours or teratomas during the 4 month period of observation. Independent veterinary post-mortem and pathological inspection revealed no tumours in any part of the body. These results suggest that pluripotency defined by teratoma formation and germline chimerism can be dissociated.

Gene expression in murine pOS cells

Several genes are thought to be essential for pluripotency in embryonic stem cells (ES cells). These include *Nanog*, *Oct3/4*, *Sox2*, *Myc*, and *KlfF4* (Yamanaka, 2007 Cell stem cell **1** 39). Remarkably, retroviral insertion of the latter 4 genes was able to induce pluripotency in adult fibroblasts (Takahashi & Yamanaka, 2006, Cell **126** 663). These "induced pluripotent stem cells" (iPS cells) are germline competent (Okita *et al.*, 2007 *supra*) and were recently generated without viral vectors (Okita *et al.*, 2008, Science **322** 949).

Preliminary analysis of pOS cells indicated that they did not express *Oct3/4* or *Sox2*, although they robustly expressed *Myc* and *Klf4* and only very low levels of *Nanog* (Fig. 6). It was therefore of interest to compare the transcriptome of pOS cells

with other pluripotent cells, to seek a deeper understanding to the lack of expression of such "essential" pluripotency genes as *Oct3/4* and *Sox2*(Kim *et al.*, 2008, Nature **454** 646). Whole transcriptome analysis was undertaken to compare cells at different stages of pOS cell generation: neurosphere-derived cells (Reference cells), EGFP-dim and EGFP-bright (FACS selected but not injected). Overall, the EGFP-bright cells were more similar in gene expression to the Reference cells, with an increasing trend to homogeneity of expression in EGFP-dim and EGFP-negative pOS cells (Fig. 3A).

Comparison of gene expression in the different cell populations generated a list of genes whose expression was increased in the pOS cell population compared to the Reference population (Table 1). A recent study (Muller *et al.*, 2008, Nature **455** 401) compared the transcriptome of 150 pluripotent and non-pluripotent cell lines to define a regulatory network of genes that is shared by pluripotent human cells (ES cells, embryonal carcinomas and iPS cells). This "pluripotency network" (PluriNet) included *Nanog* and the iPS genes as well as many genes regulated by *Oct3/4 and Sox2*, but also included many genes outside these better studied regulatory pathways. The existence of a "pluripotency network" of gene regulation (rather than just a few regulatory genes) may help explain how pOS cells are pluripotent by one measure (germline chimerism) but not another (teratoma and tumour formation). This was tested by comparing the list of genes enriched in pOS cells (Table 1) and the list of genes in the pluripotency network (Muller *et al.*, 2008, *supra*) to derive a list of PluriNet genes expressed in pOS cells (Table 2). Of the 299 PluriNet genes, 273 were represented on the mouse array, of which 166 were detected in pOS cells, and 49 were significantly enriched ($p<0.01$) in the pOS cells compared to the original neurosphere population (Reference cells). Taking into account the number of probes on the microarray (24,620), the number of genes expressed by the pOS cells (7,475) and the number of mouse genes in the pluripotency network (273), the probability of finding 166 PluriNet genes expressed by pOS cells by chance was very small ($p=1.11e-25$, Fisher's exact test). This demonstrates that, while pOS cells share a significant number of pluripotency genes with other pluripotent cells, they do not share the full complement, just as they do not share the full phenotype that includes teratoma and tumour formation.

The gene expression analysis confirmed the preliminary qPCR analysis in detecting mRNAs for *Klf4* and *Myc*, but not *Oct3/4* and *Sox2*, genes thought central for pluripotency in iPS cells (Kim *et al.*, 2008, *supra*). *Nanog* mRNA was detected at low levels in EGFP-dim pOS cells but not in EGFP-negative pOS cells. Notably, OCT-3/4, SOX2 and NANOG proteins were detected *in vitro* by immunofluroescence in some clusters of pOS cells (Fig. 3C), indicating that a minority of cells (10%) retained these proteins while their mRNA was undetectable in the pOS cell population (Fig. 3C). Therefore, the high rate of chimerism (66%) after blastocyst injection of single pOS cells indicates that ongoing expression of *Nanog*, *Sox2* and *Oct3/4* may not be required for pluripotency and germline competence, although they may initiate the process. Alternatively, these genes may be induced in pOS cells after they are injected into blastocysts and are exposed to the local milieu. This seems paradoxical given their importance for pluripotency in iPS cells but it is consistent with their transient induction of pluripotency in iPS cells without on-going expression (Okita *et al.*, 2008). We examined this hypothesis indirectly by investigating the expression of genes that are connected to a sub-network of the PluriNet in which *Oct3/4*, *Sox2* and *Nanog* are responsible for chromatin modification (Fig. 3B). Low or absent expression of *Oct3/4*, *Sox2* and *Nanog* were linked with low levels of expression of protein-partners and adjacent network members in pOS cells whereas the chromatin modifiers *Myc*, *Klf4/5*, *HDAC1* and their partners were induced in pOS cells, as were the cell cycle sub-networks associated with PluriNet (Muller *et al.*, 2008, *supra*).

Murine pOS Cell culture

Olfactory neurosphere cultures were prepared from olfactory mucosa (Murrell *et al.*, 2005, *supra*) from adult male Rosa-EGFP transgenic (Quah *et al.*, 2008, *supra*). Neurospheres were grown for 7-8 d in a serum-free medium containing EGF and FGF2 then harvested by trypsin digestion and grown for a further 2 d as single cells. They were then dissociated and plated in flasks, pre-coated with a solution gelatin, and seeded with a confluent monolayer of freshly-thawed, immortalised, *Sl/Sl4*-mSCF220 mouse stromal cells that were mitotically inactivated. The cells were grown at 37C and 5% CO_2 in humidified air in pOS enrichment (POSE) medium. After 8 d the cells were harvested by trypsin digestion and grown

for 2 passages on gelatin-coated flasks without feeders, and harvested at 70-80% confluence by trypsin digestion. Trypsin was inactivated by the addition of surplus POSE medium. pOS cells were analysed and sorted using a BD FACSVantage SE DiVa Cell Sorter according to levels of EGFP fluorescence.

Blastocyst injection, embryo transfer and detection of EGFP in chimeras and transgenic offspring

Blastocysts were harvested at 3.5 days *post coitus* (dpc) after mating wild type, adult C57BL/6J females and males. Single or multiple GFP-dim or GFP-negative populations of pOS cells, selected by FACS were injected into blastocysts after which they were placed within the oviduct (0.5 dpc,) or the anterior uterine horn (2.5 dpc) of pseudopregnant CD-1 female mice, that were mated with vasectomised CD-1 males (Nagy *et al.*, *Manipulating the mouse embryo: a laboratory manual*, 3rd ed. (Cold spring Harbor Laboratory Press, Cold Spring Harbor, 2003)). Chimerism was detected in embryos harvested at 13.5 or 16.5 dpc and in neonatal pups by analysing DNA from tail, foetal liver or limb bud tissue, using quantitative, real-time polymerase chain reaction (qPCR). Some chimeric pups were grown to adulthood and mated with adult C57BL/6J mice to test for germ-line transmission of the EGFP transgene to produce transgenic offspring. These were identified by detection of EGFP using qPCR genotyping. Chimeric and transgenic embryos were also analysed for EGFP protein expression using immunofluorescence.

Teratoma formation

In three animals 100,000 pOS cells were injected subcutaneously at two sites in immune deficient NOD.CB17-*Prkdc*^{scid} mice. Mice were examined weekly and underwent a detailed post-mortem 4 months later.

Gene expression profiling

Cells were analysed for their gene expression at different stages of the culture process: reference cells, prior to growing in POSE medium (dissociated neurosphere-derived cells grown in FGF2 and EGF); after 8 d in POSE medium, prior to FACS sorting; after FACS sorting as EGFP-bright and EGFP-negative. Purified RNA was hybridized to the Illumina Mouse-Ref8 v1.1 BeadChip (Illumina, Inc.). Genes were

identified that were enriched in the pOS cells (EGFP-negative) compared to the reference cells using a a series of stringent statistical criteria (see Example 23). For comparative purposes with human-mouse translation tables were built using Orthology tables at NIH DAVID (http://david.abcc.ncifcrf.gov/; Dennis *et al.*, 2003, Genome biology **4** P3).

Mice

Donor mice were adult male Rosa-EGFP Tg (EGFP-Tg) mice, 15 weeks old. The mice were generated by crossing a Rosa26 stop/flox-EGFP mouse (kindly provided by Martyn Goulding, Department of Neurobiology, Salk Institute, University of California at San Diego, La Jolla, CA) with a generalized Cre recombinase-expressing mouse *TNAP* Cre, to activate expression of EGFP (Clarke *et al.*, 2000, Science **288** 1660). Blastocysts were obtained from naturally-mated adult female C57Bl6J mice, 7-12 weeks of age. Outbred wild type CD-1, inbred, wild type C57BL/6J and immune deficient NOD.CB17-*Prkdc*^{scid} mice were purchased from the Animal Resources Centre, Canning Vale, Western Australia. All mice were maintained in specific pathogen free barrier conditions at all times. All experiments were performed with approval of the Animal Ethics Committees of Griffith University and the University of Queensland in accordance with the guidelines and recommendations of the National Health and Medical Research Council of Australia.

Olfactory mucosa cultures

For each experiment five mice were killed with CO_2 and olfactory neurosphere cultures were prepared as described previously (Murrell *et al.*, 2005, Dev Dyn **233**, 496). The olfactory mucosa was removed from the nasal septum and placed in ice cold Dulbecco's modified Eagle's medium /HAM F12 (DMEM/F12 ; GIBCO- Invitrogen) supplemented with 10% Foetal Bovine Serum (Bovogen, Australia) and 50 U/ml penicillin and 50 µg/ml streptomycin (GIBCO-Invitrogen). After washing twice in Hank's buffered salt solution (HBSS; GIBCO-Invitrogen), the olfactory mucosa was incubated with Dispase II (2.4U/ml; Roche) for 45 minutes. The olfactory epithelium was isolated from lamina propria under the dissection microscope and both tissues were washed separately in HBSS. The lamina propria was further digested with Collagenase I (Sigma-Aldrich) for 10 minutes and

gently triturated. The cells were washed with HBSS. In the mean time, the olfactory epithelium was gently triturated to break sheets of tissue into cells and washed with HBSS. The cell pellets resuspended in DMEM/F12 supplement with 10% FBS and 50U/ml Penicillin and 50µg/ml streptomycin and cultured together in a 6-well tissue culture plate (Nunc) in 5% CO_2 at 37°C. The cells were passaged using 0.25% trypsin n 0.02% EDTA (GIBCO-Invitrogen) and seeded onto poly-L-lysine (0.85µg/cm^2; Sigma) coated 6-well tissue culture plates (Nunc) in DMEM/F12 supplemented with Insulin, Transferrin and Sodium Selenite (ITS; GIBCO-Invitrogen), 50 ng/ml Epidermal Growth Factor (EGF; Chemicon) and 25 ng/ml Fibroblast Growth Factor 2 (FGF2; Chemicon) to generate neurospheres. After 7-8 days, the neurospheres were collected. They were incubated with 1ml of TrypLE (GIBCO-Invitrogen) for 10 minutes to dissociate the spheres. The cells were washed once in DMEM/F12 and cultured in DMEM/F12 supplemented with ITS, 50ng/ml EGF and 25ng/ml FGF2 for 48 hours before culturing in POSE medium (see below).

Enrichment of pOS cells from adherent neurospheres

Medium was aspirated from cultures containing confluent neurospheres. Cells were detached from the poly-L-lysine substratum by digestion with 0.25% trypsin-EDTA in HBSS (5 mins; 37C; 5% CO_2 in humidified air). Trypsin was inactivated by the addition of surplus pOS enrichment (POSE) medium (Dulbecco's modifed Eagle's medium containing 4.5 g L-glucose/mL (Invitrogen), and supplemented with 20% (v/v) heat-inactivated (56C; 30 mins) foetal bovine serum (Cambrex), 2 mM Glutamax-1 (Invitrogen), 20 units penicillin/mL: 20 ug streptomycin /mL (Invitrogen), 50 ug gentamicin/mL (Invitrogen), 30 uM adenosine (Sigma-Aldrich), 30 uM cytidine (Sigma-Aldrich), 30 uM guanosine (Sigma-Aldrich), 10 uM thymidine (Sigma-Aldrich), 30 uM uridine (Sigma-Aldrich), 1,000 units ESGRO murine Leukemia Inhibitory Factor (LIF)/mL (Millipore), 40 ng recombinant murine Stem Cell Factor (SCF)/mL (Millipore), 20 ng recombinant human FGF2/mL (Millipore), 25 ng recombinant human FGF9/mL (Sigma-Aldrich), and 0.1 mM 2-mercaptoethanol (Sigma-Aldrich)). Cell clumps were disaggregated by gentle, repeated pipetting. Cell suspensions were transferred to polypropylene tubes and centrifuged (1,000 x g; 5 mins; 4C). Medium was aspirated. Cell pellets were dislodged by gently tapping the tubes. Cells were resuspended in fresh POSE

medium and plated at 40% - 50% confluence in ventilated tissue culture-grade flasks, pre-coated with a solution of 0.1% (w/v) gelatin type A (Sigma-Aldrich), and seeded with a confluent monolayer of freshly-thawed, immortalised, *Sl/Sl4*-mSCF220 mouse stromal cells (a kind gift from Prof. B. Hogan, Duke University), that were mitotically inactivated by incubation in 10 μg Mitomycin C (Sigma-Aldrich M-4287) / mL POSE medium, minus LIF, SCF, FGF2 and FGF9, (3 hrs; 37C; 5% CO_2 in humidified air). Culture medium was replaced daily. Cells were passaged every two days and seeded into sterile flasks, pre-coated with gelatin and seeded with freshly-thawed, mitotically-inactivated feeders.

The culture medium caused feeders to detach from the gelatin substratum, and so were replenished every passage (every 2 days). When sufficient pOS cells were generated for blastocyst injections or tumour studies, pOS cells were pre-plated onto gelatin without feeders for 2 passages. Short-term culture without feeders did not appear to compromise pluripotency, as indicated by FACS, microarray, and qPCR data.

FACS analysis and sorting

Cells were pre-plated for 2 passages on 0.1% (w/v) gelatin-coated flasks without feeders, and harvested at 70-80% confluence by trypsin digestion. Trypsin was inactivated by the addition of surplus POSE medium. Between $5x10^5$ and $1x10^6$ cells were deposited into each 5 mL, polystyrene round-bottomed tube (Becton Dickinson BD352054), and centrifuged (1,000 x g; 5 mins; 4C). Supernatants were aspirated and cells washed once in PBS containing 2% (v/v) heat-inactivated FBS (1,000 x g; 5 mins; 4C). Cells were resuspended in 0.5 mL – 1 mL PBS/2% FBS and maintained on ice when not in use. Cells were analysed and sorted using a BD FACSVantage SE DiVa Cell Sorter. EGFP fluorescence was detected using a Coherent Innova 70C argon laser at 488 nm wavelength.

Blastocyst injection and embryo transfer

Wild type, adult C57BL/6J females (7-12 weeks of age), in oestrus, were naturally mated with adult C57BL/6J males (8-24 weeks of age). The morning after the mice were paired, females were examined for the presence of a copulatory plug. Noon on the day of the plug was designated 0.5 days *post coitus* (dpc). At 3.5 dpc,

plug-positive females were euthanased by cervical dislocation or CO_2 overdose. Uterine horns were resected and blastocysts harvested by flushing with FHM (Specialty Media). Blastocysts were transferred to a dish containing KSOM-AA medium (Specialty Media) and incubated for 2-3 hrs (37C; 5% CO2 in humidified air). Immediately before microinjection into blastocysts, pOS cells were harvested and FACS-sorted. EGFP-dim or EGFP-negative populations were collected in PBS/2% FBS, washed, resuspended in POSE medium and placed on ice prior to blastocyst injection.

Blastocysts were removed from the incubator, transferred to a dish containing FHM medium and pOS cells. The dish was placed on a cooling stage set to 14C attached to a DM-IRB inverted microscope (Leica) fitted with DIC objectives and microinjectors (Narishige). Single or multiple pOS cells were injected into each blastocyst, as described elsewhere. Following microinjection, blastocysts were washed through KSOM medium and incubated in KSOM medium (37C ; 5% CO2 in humidified air) for 1 hr or until blastocysts re-expanded. Blastocysts were placed within the oviduct (0.5 dpc,) or the anterior uterine horn (2.5 dpc) of pseudopregnant CD-1 female mice, that were mated with vasectomised CD-1 males. CD-1 females were placed under general anaesthesia during embryo transfers, as described in Nagy *et al.*[3].

DNA isolation and QPCR genotyping

Tail, foetal liver or limb bud tissue was digested in a solution containing 50 mM Tris-HCl (pH 7.6) (Sigma-Aldrich), 100 mM Na_2EDTA (Sigma-Aldrich), 100 mM NaCl (Sigma-Aldrich), 1% (w/v) sodium dodecyl sulfate (Sigma-Aldrich) and 0.4 mg Proteinase K (Roche) / mL. Tissue was incubated at 55C for 16 hours. Genomic DNA was then extracted by the addition of 0.5 vol. of Tris-buffered phenol (Fluka) biopsies plus 0.5 vol. chloroform:isoamyl alcohol (24:1) (Fluka). The organic and aqueous phases were mixed thoroughly by inversion, then centrifuged (12,000 x g; 15 mins; room temp.). The upper, aqueous phase minus the interface, was transferred to a clean tube. An equal volume of chloroform:isoamyl alcohol (24:1) was added to the aqueous solution, mixed by inversion, and centrifuged as before. The upper, aqueous phase was transferred to a clean tube and residual isoamyl alcohol allowed to evaporate. An equal volume of isopropanol was added to each

tube, shaken thoroughly, and centrifuged (12,000 x g; 20 mins; room temp.). The supernatant was aspirated. Nucleic acid was rinsed with 70% EtOH and centrifuged for 5 mins. Ethanol was aspirated and residual moisture evaporated by incubating tubes at 37C for 10 mins. DNA was resuspended in TE buffer (10 mM Tris-HCl (pH 7.6): 1 mM EDTA), incubated at 37C for 1 hr, and then stored at 4C. QPCR forward and reverse primers (Sigma-Aldrich) were designed to anneal within the same exon

FoxL2 FP 5'GCTACCCCGAGCCCGAAGAC3' (SEQ ID NO:1)

FoxL2 RP 5'GTGTTGTCCCGCCTCCCTTG3' (SEQ ID NO:2)

EGFP FP 5'CTGAGCAAAGACCCCAACGA3' (SEQ ID NO:3)

EGFP RP 5'TCGTCCATGCCGAGAGTGA3' (SEQ ID NO:4)

Reactions were performed in 25 uL volumes, in the following conditions: Stage 1: 50C; 2 mins (1 cycle); Stage 2: 95C; 10 mins (1 cycle); Stage 3: 95C; 15 secs; 60C; 1 min (40 cycles). Reactions contained 5 uL genomic DNA, diluted 1:10 in 10 mM Tris (pH 7.6): 1 mM EDTA, 0.15 uM forward and reverse primers, 1x SYBR Green PCR Mastermix (Applied Biosystems). Volumes were adjusted to 25 uL with MilliQ water. For each primer pair, a "no template" control reaction was included, as a test of primer specificity and to ensure the water was not contaminated with gDNA. QPCR reactions were undertaken in 96-well plates, in an ABI Prism Detection System 7000 plate reader. Analyses were performed using ABI Prism SDS software (Applied Biosystems).

Non-denaturing polyacrylamide gel electrophoresis

QPCR amplicons were electrophoresed through a 12% non-denaturing polyacrylamide gel, prepared according to *Sambrook et al.* Molecular Cloning: A Laboratory Manual 2nd Ed. (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989).

Teratoma assay

FACS-sorted pOS (GFP negative) and GFP-bright cells were each resuspended in sterile PBS at a concentration of 10^6 cells/mL. 0.1 mL (10^5) pOS cells was injected subcutaneously at the right shoulder and hip of 3 male NOD/SCID

mie (5 wks of age), The same mice were injected at the contralateral sites with 0.1 mL PBS. A second group of 3 NOD/SCID males (5 wks of age) was injected s.c. at the right shoulder and hip with 0.1 mL (3×10^3) GFP-bright cells, and with 0.1 mL PBS at the contralateral sites. Mice were maintained for 4 months, then euthanased prior to full histopathological analysis by an independent veterinary pathologist (Institute for Medical and Veterinary Science, Adelaide, S.A.).

Histology of embryos

Pregnant females (12.5-16.5 dpc) were euthanased by cervical dislocation. Foetuses were resected and placed in pre-chilled petri dishes containing sterile PBS, maintained on ice. Foetuses were euthanased by hypothermia. Foetuses were transferred to a dissecting microscope, to remove extra-embryonic structures. A small piece of tissue (e.g. tail or hindlimb) was removed from each foetus for DNA extraction and determination of genotype.

Whole foetuses were fixed in Bouin's solution (Sigma-Aldrich) and incubated on a rocking platform at room temperature for 24 hrs. Surplus fixative was decanted and diluted by washing foetuses in several changes of 70% (v/v) ethanol over a period of 2-3 days. Foetuses were processed overnight (Leica tissue processor), and embedded in Paraplast Extra embedding wax (Lomb Scientific). 7-10 um thickness saggital sections (Jung Biocut 2035 microtome (Leica)) were dried onto Menzel-Glaser Superfrost™ Plus glass microscope slides (Lomb Scientific) and dried at room temperature.

Immunofluorescent detection of EGFP

Sections were immersed in two changes of xylene (20 mins each; room temp.), then rehydrated through an ethanol series (100%, 100%, 95%, 80%, 70%, 50%, 30%), and finally, through two changes of MilliQ water. Sections were immersed in each solution for 3 mins and then in antigen unmasking solution (Vector Laboratories H-3300), prepared according to the manufacturer's instruction and brought to boiling point immediately before slides were boiled for a further 5 mins in a microwave. Slides were cooled to room temperature in the antigen retrieval solution, submerged in MilliQ water (10 mins; room temp.), then PBTX (PBS containing 0.1% (v/v) Triton X-100), (10 mins; room temp.). Surplus PBTX was

drained from the slides before they were overlaid with blocking solution (PBTX containing 10% (v/v) heat-inactivated horse serum), sealed within a humidified chamber, and incubated overnight at 4C. Excess blocking solution was drained from the slides before they were overlaid with either fresh blocking solution, or, with the primary rabbit anti-EGFP polyclonal antibody (Invitrogen A6455), diluted 1:200 in blocking solution. Slides were sealed within a humidified chamber and incubated overnight at 4C. Slides were drained, immersed in PBTX, blocked for 30 mins at room temp., then overlaid with an Alexa 488-goat anti-rabbit IgG_{H+L} secondary antibody (Invitrogen A11008), diluted 1:200 in blocking solution. Slides were sealed within a light-resistant humidified chamber and incubated at room temp. for 1 hr. Slides were rinsed with PBTX, and overlaid with DAPI (4'-6'-Diamidino-2-phenylindole dihydrochloride (2.5 ng/mL) (Sigma-Aldrich)), for 5 mins at room temp. in a light-resistant, humidified chamber. Slides were rinsed with PBTX, mounted with 70% (v/v) glycerol: 30% (v/v) PBS, and sealed with coverslips. Slides were stored at 4C in the dark when not in use. Sections were photographed using either an Olympus BX-51 fluorescent microscope with DP Controller and DP Manager imaging software or an Olympus FV1000 Confocal Microscope system. Figures were compiled in Adobe Photoshop 7.0 and Adobe Illustrator 10.0 (Adobe Systems Incorporated).

RNA isolation and qRT-PCR genotyping

Total RNA was extracted from cells using an SV Total RNA Isolation System (Promega), with manufacturer's instructions. Total RNA was reverse transcribed using a Superscript III First Strand Synthesis System (Invitrogen) with manufacturer's instructions. QRT-PCR amplification of cDNA was performed in 25 uL reaction volumes, using a dissociation temperature of 60C. Reactions contained 5 uL cDNA (diluted 1:5 in MilliQ water), 0.15 uM forward and reverse primers, and 1X SYBR Green PCR Mastermix (Applied Biosystems). Volumes were adjusted to 25 uL with MilliQ water. For each primer pair, a "no template" control reaction was included, as a test of primer specificity and to ensure the water was not contaminated with cDNA. To guard against amplification of genomic DNA contaminants, forward and reverse primers (Sigma-Aldrich) were designed to span an intron.

18S rRNA 5' GATCCATTGGAGGGCAAGTCT3' (SEQ ID NO:5)
18S rRNA 3' CCAAGATCCAACTACGAGCTTTTT3' (SEQ ID NO:6)

Oct-3/4 FP 5' TGCGGAGGGATGGCATACTG3' (SEQ ID NO:7)
Oct-*3/4* RP 5' GCACAGGGCTCAGAGGAGGTTC3' (SEQ ID NO:8)

Stra8 FP 5' CCTAAGGAAGGCAGTTTACTCCCAGTC3' (SEQ ID NO:9)
Stra8 RP 5' GCAGGTTGAAGGATGCTTTGAGC3' (SEQ ID NO:10)

Mvh FP 5' AAGCAGAGGGTTTTCCAAGC3' (SEQ ID NO:11)
Mvh RP 5' GCCTGATGCTTCTGAATCG3' (SEQ ID NO:12)

LIFR FP 5' GACTGGTCGCAATCCACTG3' (SEQ ID NO:13)
LIFR RP 5' GTCGGATCATGAGGAGCAAC3' (SEQ ID NO:14)

Sox2 FP 5' AGGGTGGGGAAAGGAGATT3' (SEQ ID NO:15)
Sox2 RP 5' CGTCGCCAGCCTCTTACTT3' (SEQ ID NO:16)

Ifitm3 (Fragilis1) FP 5' GTCGGTGCCTGACCATGT3' (SEQ ID NO:17)
Ifitm3 (Fragilis1) RP 5' CATCTTCCGATCCCTAGACTTC3' (SEQ ID NO:18)

Nanog FP 5' AGCCTCCAGCAGATGCAA3' (SEQ ID NO:19)
Nanog RP 5' GGTTTTGAAACCAGGTCTTAACC3' (SEQ ID NO:20)

c-Kit FP 5' GGTTGTCCAACTTATTGAGAAGC3' (SEQ ID NO:21)
c-*Kit RP* 5' GCAGTTTGCCAAGTTGGAGT3' (SEQ ID NO:22)

Klf4 FP 5' CGGGAAGGGAGAAGACACT3' (SEQ ID NO:23)
Klf4 RP 5' GAGTTCCTCACGCCAACG3' (SEQ ID NO:24)

Cdh1 FP 5' CAGAAGGCGCTGTTCCAG3' (SEQ ID NO:25)
Cdh1 RP 5' GTTGACGTCATCGTCTGCAT3' (SEQ ID NO:26)

Reactions were performed in 25 uL volumes, in the following conditions: Stage 1: 50C; 2 mins (1 cycle); Stage 2: 95C; 10 mins (1 cycle); Stage 3: 95C; 15 secs; 60C; 1 min (40 cycles). Reactions contained 5 uL cDNA, diluted 1:5 in MilliQ water, 0.15 uM forward and reverse primers, 1x SYBR Green PCR Mastermix (Applied Biosystems). Volumes were adjusted to 25 uL with MilliQ water. For each primer pair, a "no template" control reaction was included, as a test of primer specificity and to ensure the water was not contaminated with gDNA.

QRT-PCR reactions were undertaken in 96-well plates, in an ABI Prism Detection System 7000 plate reader. Analyses were performed using ABI Prism SDS software (Applied Biosystems).

RNA extraction, labelling and microarray hybridization

Total RNA was isolated by RNaqueous Micro column (Ambion). Quality was checked with an Agilent 2100 Bioanalyser (RNA Pico chips). 50ng of RNA was biotin labelled using a Illumina® TotalPrep™ Amplification Kits (Ambion, Inc) with a 14 hour in vitro transcription. 750ng of cRNA was hybridized to Illumina Mouse-Ref8 v1.1 BeadChip (Illumina, Inc.). Slides were then scanned on an Illumina Beadstation and bead summarization was performed using BeadStudio Version 3.1.7 (Illumina, Inc). After summarization raw data was exported from BeadStudio with no additional processing.

Data normalisation and filtering

The data exported from BeadStudio was imported into R/BioConductor using the readBead function from the BeadExplorer package (http://bioconductor.org/packages/1.9/bioc/vignettes/BeadExplorer/inst/doc/BeadHelp.pdf). Background adjustment and quantile normalization[5] was performed using algorithms within the Affymetrix package (http://bioconductor.org/packages/1.8/bioc/vignettes/affy/inst/doc/affy.pdf) (function: bg.adjust and normalize.quantiles). The normalized data was exported out off R/BioConductor using write.beadData function for further analysis in Genespring GX 7.3.1. software (Agilent Technologies). Genes were initially filtered using Illumina® detection p-value of 0.99 and a floor of 100FU. Genes enriched in the pOS (EGFP-negative) state compared to the reference cells were identified using a

Welch parametric t-test, p-value cutoff 0.01, multiple testing correction: Benjamini and Hochberg False Discovery Rate. This restriction tested 8,511 genes. Genes were further described as differentially expressed using a volcano plot fold difference of 2 with a P-value < 0.01. Human-mouse translation tables were built for the Loring dataset using Orthology tables at NIH DAVID (http://david.abcc.ncifcrf.gov/).

Immunochemistry

Cultures of pOS cells plated onto gelatin without feeders on glass coverslips, were cultured for two days, then incubated for 30 minutes in HBSS prior to fixation in modified Zamboni's fixative (2% paraformaldehyde and 0.2% picric acid in 0.1M phosphate buffer, pH 7.2) from 5 to 30 minutes. The adherent cells were stored in PBS azide (PBS containing 0.1% sodium azide) at 4°C until immunofluorescence processing.

The specimens were rinsed in PBS triton (0.1M PBS and 0.1% Triton-X-100 [TX-100]) and permeabilised in DMSO (100%) for 10 minutes, then rinsed in PBS triton for 5 min before being blocked with 10% donkey serum (Sigma Chemical Corporation)) in PBS triton. DMSO was omitted for cell-surface immunostaining. The specimens were incubated with primary antibodies diluted in block buffer over night, at room temperature. The primary antibodies used in single and multiple labelling are listed in Table 1. The specimens were incubated for 30 minutes in block buffer before being incubated for 3 hours with the secondary antibodies diluted in block buffer, followed by washing. The secondary antibodies were donkey anti-rabbit, anti-goat or anti-mouse antibodies (Invitrogen) conjugated with Alexa-488 (green), 594 (red), or 647 (far red). The coverslips with adherent cells were mounted on glass slides using Vectashield DAPI (4'6-diamidino-2-phenylindole·2HCl, Vector Labs) mounting media which labels cell nuclei. No cross-reactivity occurred between the primary and secondary antisera combinations. Control experiments showed omission of either primary antisera abolished visible labelling with the appropriate secondary antibody/fluorophore combination.

The specimens were imaged on an Axio Imager Z1 epi-fluorescence microscope using 10X and 20X Plan-Apochromatic objectives and an oil immersion 63X Plan-Apochromatic objective. Images were captured on an Axiocam Mrm

camera using AxioVision software. Figures were compiled in Adobe Photoshop 7.0 and Adobe Illustrator 10.0 (Adobe Systems Incorporated).

Production of pOS cells in vitro

Cells obtained as previously described were resuspended in fresh POSE medium and plated at 30% - 40% confluence in ventilated tissue culture-grade flasks, pre-coated with a solution of 0.1% (w/v) gelatin type A (Sigma-Aldrich), and seeded with a confluent monolayer of freshly-thawed, immortalised, *Sl/Sl4*-mSCF220 mouse stromal cells that were mitotically inactivated by incubation in 10 µg Mitomycin C (Sigma-Aldrich M-4287) / mL POSE medium, minus LIF, SCF, FGF2 and FGF9, (3 hrs; 37C; 5% CO2 in humidified air). POSE culture medium is replaced daily. Cells are passaged every 2 – 3 days and seeded into sterile flasks, pre-coated with gelatin and seeded with freshly-thawed, mitotically-inactivated feeders. The cells may be passaged up to 10 times or more without loss of developmental potency.

Cryopreservation of pOS cells

pOS cells are harvested by trypsin digestion (3 mins; 37C; 5% CO2 in humidified air). Trypsin is inactivated by the addition of surplus pOS cell enrichment medium. The cell suspension is transferred to polypropylene centrifuge tubes. Cells are pelleted (1,000 x g; 5-8 mins; 4C or room temp). The supernatant is aspirated and discarded. Cells are resuspended in 90% (v/v) FBS; 10% (v/v) cell culture-tested DMSO, dispensed into cryovials. The cryovials are placed on dry ice for 15 mins then stored for 24 hrs at -80C before transfer to LN2 (preferably vapour phase) for long-term storage.

Culturing of thawed pOS cells

pOS cells are removed from the LN2 source and placed on dry ice. Cells are then thawed rapidly by immersion of the cryovial in a 37C waterbath. The cell suspension is diluted in surplus pOS cell enrichment medium and centrifuged (1,000 x g; 5-8 mins; 4C or room temp). The supernatant is aspirated and discarded. The cell pellet is resusupended gently in fresh pOS cell enrichment medium then plated into TC-grade plastic, pre-coated with gelatin and containing a confluent monolayer of feeders.

EXAMPLE 2

Further characterization of murine pOS cells

Cell culture protocol

Cell source

For each experiment five mice were killed with CO2 and olfactory neurosphere cultures were prepared as described previously (Murrell *et al.*, 2005, Dev Dyn **233**, 496). The olfactory mucosa was removed from the nasal septum and placed in ice cold Dulbecco's modified Eagle's medium /HAM F12 (DMEM/F12 ; GIBCO-Invitrogen) supplemented with 10% Foetal Bovine Serum (Bovogen, Australia) and 50 U/ml penicillin and 50 μg/ml streptomycin (GIBCO- Invitrogen). After washing twice in Hank's buffered salt solution (HBSS; GIBCO-Invitrogen), the olfactory mucosa was incubated with Dispase II (2.4U/ml; Roche) for 45 minutes. The olfactory epithelium was isolated from lamina propria under the dissection microscope and both tissues were washed separately in HBSS. The lamina propria was further digested with Collagenase I (Sigma-Aldrich) for 10 minutes and gently triturated. The cells were washed with HBSS. In the mean time, the olfactory epithelium was gently triturated to break sheets of tissue into cells and washed with HBSS. The cell pellets resuspended in DMEM/F12 supplement with 10% FBS and 50U/ml Penicillin and 50μg/ml streptomycin and cultured together in a 6-well tissue culture plate (Nunc) in 5% CO2 at 37°C.

Alternatively, expanded neurospheres were cultured as a monolayer from disrupted neurospheres that are in turn, derived from primary olfactory mucosal cells (olfactory epithelium + lamina propria), as described in Murrell et al., 2005, *supra.* Briefly, cells were passaged using 0.25% trypsin in 0.02% EDTA (GIBCO-Invitrogen) and seeded onto poly-L-lysine (0.85μg/cm2; Sigma) coated 6-well tissue culture plates (Nunc) in DMEM/F12 supplemented with Insulin, Transferrin and Sodium Selenite (ITS; GIBCO-Invitrogen), 50 ng/ml Epidermal Growth Factor (EGF; Chemicon) and 25 ng/ml Fibroblast Growth Factor 2 (FGF2; Chemicon) to generate neurospheres. After 7-8 days, the neurospheres were collected. They were incubated with 1ml of TrypLE (GIBCO-Invitrogen) for 10 minutes to dissociate the spheres. The cells were washed once in

DMEM/F12 and cultured in DMEM/F12 supplemented with ITS, 50ng/ml EGF and 25ng/ml FGF2 for 48 hours before culturing in pOS cell enrichment medium.

pOS cell enrichment medium

DMEM containing 4.5 g glucose/L; 20% (v/v) heat-inactivated (56C; 30 mins) foetal bovine serum; 2 mM Glutamax-1 or 2 mM L-glutamine; 1 mM Na pyruvate; 0.1 mM non-essential amino acids; 30 μM adenosine; 30 μM guanosine; 30 μM cytidine; 30 μM uridine; 10 μM thymidine; 50 U penicillin/mL; 50 μg streptomycin/mL; 50 μg gentamicin/mL; 0.1 mM beta-mercaptoethanol.

Mouse pOS cells

Mouse pOS cells were cultured on mitotically-inactivated Sl/Sl4 mSCF220 stromal feeders, in pOS cell enrichment medium supplemented wtih 1 or more of: 1,000 units ESGRO murine LIF/mL; 40 ng recombinant murine Stem Cell Factor/mL; 20 ng recombinant human FGF-2/mL; 25 ng recombinant human FGF9/mL.

Cell manipulation

Medium was aspirated. Primary cells or their expanded neurosphere derivatives, were flooded with a solution of 0.25% trypsin/EDTA in HBSS. Cells are detached by incubation in the trypsin solution (3-5 mins; 37C; 5% CO2 in humidified air). Trypsin is inactivated by the addition of surplus pOS cell enrichment medium. A uniform cell suspension was generated by gentle pipetting. The cells were then seeded into a tissue culture-grade flask / dish / multi-well plate, pre-coated with 0.1% (w/v) gelatin (type A from porcine skin) and containing a confluent monolayer of mitotically-inactivated Sl/Sl4 stromal cells, expressing a truncated, surface membrane-bound form of murine Stem Cell Factor.

pOS cells are cultivated on feeders in pOS cell enrichment medium (37C; 5% CO2 in humidified air). Medium is replaced daily. Cells are passaged every 2-3 days at 60-70% confluency and are seeded into new flasks, pre-coated with gelatin and containing new feeders at a dilution of 1:5 – 1:10. pOS cells may be cultivated on gelatin in the absence of feeders for a short period without detectable changes to their phenotype.

Depending on the species and strain, the attainment of a stable, homogeneous population of pOS cells occurs as early as three weeks following initiation of culture of primary cells or expanded neurospheres in pOS cell enrichment medium.

Generation of mouse pOS cells

Cells were cultivated on feeders, and in the presence of one or more of: LIF, SCF, FGF-2, FGF9. Mouse pOS cells that are derived from primary cells, exhibited a stable and homogeneous phenotype that is very similar to that shown by murine pOS cells that are derived from expanded neurospheres.

An example of an isolated mouse cell designated B6 Rosa26-EGFP XY pOS was deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121601

CD antigen expression by murine pOS cells

Murine pOS cells were produced as hereinbefore described and analysed for expression of CD antigens, intracellular OCT-3/4 and SCA-1 by flow cytometry. CD (cluster of differentiation) antigens are proteins expressed on the cell surface that are antigenic. Mouse pOS cells were plated into a 96-well plate format. Each well was coated with one antibody, reactive against one species-specific CD or other antigen. All antigens tested are shown in Table 6. Table 7 provides a ranking of expression levels according to mean fluorescence intensity. Highest mean expression levels (>18,000 MFI units) were identified for CD13; CD16/32; CD23; CD34; CD28; CD38; CD40; CD45; CD61; CD69; CD95; CD117; CD122; CD124; CD201; and CD309.

Demonstration of pluripotency *in vivo*

GFP-dim or GFP-negative pOS cells from C57BL/6J *ROSA26-EGFP/ROSA26-EGFP* mice (see Figure. 1), were collected by fluorescence-activated cell sorting (FACS), and injected into wild type C57BL/6J pre-implantation-stage mouse blastocysts. PCR analysis of EFGP expression was performed using one or both of two sets of primers and cycling conditions:

Protocol 1

Forward primer 5' CGA CGT AAA CGG CCA CAA GTT CA 3'(SEQ ID NO:27)
Reverse primer 5' GCT TTA CTT GTA CAG CTC GTC CAT 3' (SEQ ID NO:28)
under the following PCR cycling conditions: 95°C 3 mins; 41 cycles of: 95°C 15 secs; 65°C for 15 secs, 72°C for 1 min; followed by one cycle of 72°C for 3 mins; followed by one cycle of 25°C for 5 mins and pause at 8°C. This generated a 661 bp product from the EGFP template.

Protocol 2

Forward primer 5' CCT GAA GTT CAT CTG CAC CA 3' (SEQ ID NO: 29)
Reverse primer 5' CCG TCC TCC TTG AAG TCG 3' (SEQ ID NO: 30)
under the following PCR cycling conditions: 95°C 10 mins; 41 cycles of: 95°C 15 secs; 65°C 30 secs; 72°C 50 secs; followed by one cycle of 72 °C 2 mins and pause at 8°C. This generated a 273 bp product from the EGFP template.

Injection of 1 pOS cell into one blastocyst was sufficient to generate chimaeric founder (Fo) mice, and to colonise tissues of endo-, meso- and ectodermal origin, plus the germ cells. All transgenic mice (Fo, F1, F2) were viable, fertile and remained tumour-free, even after 14 months. The pOS cell-derived EGFP transgene was confirmed in tissues of founder (Fo) mice, and in their F1 and F2 offspring, by qPCR and also by PCR (Figure 8) and Southern analysis. These data show conclusively that pOS cell-derived gDNA contributes to all three embryonal germ layers plus sperm and oocytes.

Protein expression by murine pOS cells

Immunophenotypic analysis of pOS cells was performed on GFP negative cells grown at 37C and 5% CO2 in humidified air in pOS enrichment (POSE) medium, treated with trypsin and then fixed in 4% paraformaldehyde for 10 min at room temperature (RT). Approximately 1 x 10^5 cells were washed twice with HBSS and incubated 30 min at RT in 0.2 ml PBS/ 1% BSA/ 1% NGS (normal goat serum)/ 0.1% Triton-X 100 together with the following antibodies: anti-human/mouse SOX2 Allophycocyanin (APC)-conjugated (IC2018A, R&D), anti-human NESTIN phycoerythrin-conjugated (IC1259P, R&D), rabbit anti-OCT4 (AB3209, Chemicon), rabbit anti-human-NANOG (AB9220, Millipore), rabbit anti-KLF4 (AB4138, Millipore) and anti-MYC (9402, Cell Signalling Technology). All antibodies and

their isotype controls were diluted according to the manufacturer's instructions, or were determined empirically. Cells were washed twice in PBS/1%BSA and incubated 30 min RT with goat anti-rabbit Alexa-488 (A11078, Invitrogen). After two washes the cells were resuspended in 200 µL of PBS and analysed by flow cytometry (BD FACSAria flow cytometer). Isotype-matched controls were run in parallel for all antibodies. Results shown correspond to a representative flow cytometry histogram chosen from the analysis of 3 independent experiments. For each marker the mean fluorescence intensity (MFI) was normalized to the MFI of the corresponding isotype control. The % of positive cells was calculated as the staining observed above the isotype control.

The level of expression of the pluripotentiality markers OCT-3/4 and SOX2, KLF4, c-MYC, NANOG and a neuronal stem cell marker (NESTIN) were analysed in murine ES cells and pOS cells (Figure 9). OCT-3/4 and SOX2 expression were also compared between MEF, mouse ES cells and mouse pOS cells, as summarized in Figure 10. OCT-3/4-positive staining was observed in all cell types but the level of expression was greater in the ES cells (48.6 vs 25.1). In both cases the staining was considered moderate to high. In addition, SOX2 staining was moderate to high in ES cells and was low to moderate in 47% of pOS cells. NESTIN was positive in only 5% of the ESC with very low levels of expression and in 23% of the pOS cells with low to moderate levels of expression. KLF4, c-MYC and NANOG expression was clearly detected. The MFI of each of these proteins was similar in mouse ES cells and mouse pOS cells. This suggests that these factors may be active in the maintenance of pluripotency in pOS cells.

Immunohistochemistry

Expression of SOX2 and OCT-3/4, NANOG, KLF4, MVH, KIT and NESTIN proteins was compared between murine ES cells and pOS cells. Cells were fixed in Zamboni's solution (13.33% (w/v) paraformaldehyde in phosphate-buffered saturated picric acid, (pH 7.3) 5 mins; room temp.), washed *in situ* with three changes of PBS then permeabilised with PBS containing 0.1% (v/v) Triton X-100. Nucleic acid was visualised with DAPI stain. Antibodies were Alexa-conjugated, except for anti-SOX2, which was an APC conjugate. All antibodies were used at a 1:200 dilution together with a 1:200 diluted isotype control. Mouse pOS cells

expressed low but detectable levels of SOX2 and OCT-3/4, whereas NANOG, KLF4, MVH, KIT and NESTIN proteins were expressed more abundantly.

Murine pOS cells were also analysed for CD117 and AP-2γ expression Mouse anti-mouse AP-2γ Ab was used at a 1:200 dilution with a rabbit anti-mouse Alexa 594 secondary Ab at a 1:200 dilution. Rat anti-mouse CD117 Ab was used at a 1:50 dilution with a donkey anti-rat Alexa 594 secondary Ab at a 1:200 dilution. Secondary antibody controls were used at the same dilution. AP-2γ is a transcription factor and downstream target of *Prdm1*. AP-2γ mediates the suppression of somatic differentiation and the reacquisition of pluripotency (Weber, S. *et al.* Biol Reprod 2009 [PMID: 19776388]). CD117 is a regulator of gametogenesis, mast cell development, haematopoiesis and melanogenesis. Loss of function mutations in CD117 results in dose-dependent anaemia, hypopigmentation, infertility and survival. Gain of function mutations in CD117 are associated with a range of neoplasms, including acute myelogenous leukaemia, gastrointestinal stromal tumours and mastocytomas (Roskoski, 2005, Biochem Biophys Res Commun; **337**: 1-13). Both AP-2γ and CD117 were expressed abundantly by pOS cells, suggesting a role for these factors in the maintenance of pOS cell pluripotency.

NOD-SCID tumour assay

1-1.5 million pOS cells were injected beneath the capsule of the left testis of immune-deficient NOD-SCID adult mice (n=8), to test whether pOS cells were similar to mouse ES cells in their capacity to form teratoma in this tissue. None of the mice developed a teratoma. Instead, each mouse developed a slow-growing fibrosarcoma that infiltrated the abdominal wall anterior to the left (injected) testis. Within the testis, there was extensive proliferation of the injected pOS cells, which compromised the blood supply. This led to a loss of integrity of the testis cords, and impaired spermatogenesis. Typically, the fibrosarcoma was evident on palpation, 3 months after injection of the pOS cells.

Testis morphology

Fixed testis sections (3 um thickness) of left (injected) and right (uninjected) testes, harvested from NOD-SCID male mouse at 3 months after injection of 1-1.5 x 10e6 pOS cells beneath the capsule of the left testis.

Fibrosarcoma

A 3 μm section of fibrosarcoma, resected from left abdominal wall, anterior to left testis. The tumour mass comprised fibrocytes of mesenchymal origin. The morphology of the injected pOS cells was the same as that of the cells making up the bulk of the fibrosarcoma. These observations suggest that the fibrosarcoma originated from the injected pOS cells. The sub-capsular niche failed to elicit teratoma formation from pOS cells. This phenomenon distinguishes pOS cells from ES cells.

EXAMPLE 3

Production and characterization of a human pluripotent olfactory stem "pOS" cell

Cell culture protocol

Cell source

Cells were obtained from expanded neurospheres cultured as a monolayer from disrupted neurospheres that are in turn, derived from primary olfactory mucosal cells (olfactory epithelium + lamina propria), as hereinbefore described. It is anticipated that cells may be obtained from expanded primary adult human olfactory mucosal cells (olfactory epithelium + lamina propria).

Human pOS cells

Human cells were cultured on mitotically-inactivated Sl/Sl4 hSCF220 stromal feeders, in pOS cell enrichment medium supplemented with one or more of: 1,000 units glycosylated human LIF/mL; 40 ng recombinant human Stem Cell Factor/mL; 20 ng recombinant human FGF-2/mL; 25 ng recombinant human FGF9/mL; 5 ng recombinant human TGF-β2/mL; 10 ng recombinant human BMP-4/mL.

Table 8 shows all of the growth factor combinations tested that have yielded human pOS cells from expanded neurospheres.

The attainment of a stable, homogeneous population of human pOS cells occurs as early as three weeks following initiation of culture expanded neurospheres in pOS cell enrichment medium.

An example of a human pOS cell is shown in Figure 7B.

An example of a human pOS cell human XY pOS-17 was deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121602.

pOS cells represent a new member of the pluripotent stem cell family with significant potential clinical application. Unlike other pluripotent stem cells, pOS cells do not form teratomas or tumours after transplantation and they could provide a source of autologous or non-autologous human stem cells for therapy. Human olfactory mucosa is safely accessible via biopsy through the external naris and multipotent olfactory neurosphere-derived cells. These may provide a source of human pOS cells.

Illumina Microarray analyses of pOS cell transcriptomes

Microarray analysis of human pOS cell gene expression. Human pOS cell cultures were initiated from expanded human neurospheres in flasks pre-coated with 0.1% (w/v) gelatin and seeded with a confluent monolayer of mitotically-inactivated Sl/Sl4-hSCF220 feeders. The cells were cultured in POSE medium, either without added growth factors, or supplemented with the six growth factors (LIF, SCF, FGF-2, FGF9, TGFβ2, as indicated in Table 8.

In Tables 9-12, the following code is used. "XS" refers to expanded neurospheres; "no GF's" refers to an absence of growth factors **(Cate did these cultures include feeders?)** "6 GF's" refers to culture in the presence of LIF, FGF-2, FGF9, SCF, BMP-4 and TGF-β2.

Table 9 shows a ranked, fold change in expression of genes compared between pOS cells cultured with or without a combination of LIF, FGF-2, FGF9, SCF, BMP-4 and TGF-β2 and expanded neurospheres from which the pOS cells were derived.

Table 10 shows a ranked, fold increase or induction in expression of genes in pOS cells cultured with a combination of LIF, FGF-2, FGF9, SCF, BMP-4 and TGF-β2 compared to expanded neurospheres from which the pOS cells were derived.

Table 11 shows fold decrease in expression of genes compared between pOS cells cultured with or without a combination of LIF, FGF-2, FGF9, SCF, BMP-4 and TGF-β2 and expanded neurospheres from which the pOS cells were derived.

Table 12 shows a ranked, fold difference in expression of genes compared between pOS cells cultured with and without a combination of LIF, FGF-2, FGF9, SCF, BMP-4 and TGF-β2.

Analysis of these data using Ingenuity™ software shows that human pOS cells cultured with or without added growth factors, exhibit an increase in expression of transcripts that encode chromatin modifying proteins, including transcriptional repressors, histone proteins, histone modifying enzymes, and the Ubiquitin pathway. This is coordinated with the down regulation of expression of the interferon signalling pathways that are mediated by SRC, STAT5 and IRF1/7. AKT is implicated as a central coordinator of these events.

PluriNet gene expression in human neurospheres

The expressed PluriNet genes in human neurospheres from which a human isolated mammalian cell may be derived are shown in Table 5. These genes were expressed in neurospheres before transfer to the POSE medium, and not because of the POSE medium.

EXAMPLE 4

Production and characterization of a rat pluripotent olfactory stem "pOS" cell

Cell source

Cells were obtained from expanded primary adult rat olfactory mucosal cells (olfactory epithelium + lamina propria), as hereinbefore described. It is anticipated that cells may be obtainable from expanded neurospheres cultured as a monolayer from disrupted neurospheres that are in turn, derived from primary rat olfactory mucosal cells (olfactory epithelium + lamina propria)

pOS cell enrichment medium

DMEM containing 4.5 g glucose/L; 20% (v/v) heat-inactivated (56C; 30 mins) foetal bovine serum; 2 mM Glutamax-1 or 2 mM L-glutamine; 1 mM Na

pyruvate; 0.1 mM non-essential amino acids; 30 uM adenosine; 30 uM guanosine; 30 uM cytidine; 30 uM uridine; 10 uM thymidine; 50 U penicillin/mL; 50 ug streptomycin/mL; 50 μg gentamicin/mL; 0.1 mM beta-mercaptoethanol.

Rat pOS cells

Rat pOS cells are cultured on mitotically-inactivated Sl/Sl4 mSCF220 stromal feeders, in pOS cell enrichment medium supplemented with 1 or more of: 1,000 units ESGRO murine or rat LIF/mL; 40 ng recombinant murine or rat Stem Cell Factor/mL; 20 ng recombinant human FGF-2/mL; 25 ng recombinant human FGF9/mL.

Cell manipulation

Medium was aspirated. Primary cells or their expanded neurosphere derivatives, were flooded with a solution of 0.25% trypsin/EDTA in HBSS. Cells are detached by incubation in the trypsin solution (3-5 mins; 37C; 5% CO2 in humidified air). Trypsin is inactivated by the addition of surplus pOS cell enrichment medium. A uniform cell suspension was generated by gentle pipetting. The cells were then seeded into a tissue culture-grade flask / dish / multi-well plate, pre-coated with 0.1% (w/v) gelatin (type A from porcine skin) and containing a confluent monolayer of mitotically-inactivated Sl/Sl4 stromal cells, expressing a truncated, surface membrane-bound form of murine Stem Cell Factor.

pOS cells are cultivated on feeders in pOS cell enrichment medium (37C; 5% CO2 in humidified air). Medium is replaced daily. Cells are passaged every 2-3 days at 60-70% confluency and are seeded into new flasks, pre-coated with gelatin and containing new feeders at a dilution of 1:5 – 1:10. pOS cells may be cultivated on gelatin in the absence of feeders for a short period without detectable changes to their phenotype.

The attainment of a stable, homogeneous population of human pOS cells occurs as early as three weeks following initiation of culture of primary cells or expanded neurospheres in pOS cell enrichment medium. An example of a rat pOS cell is shown in Figure 7C.

An example of a isolated rat cell designated SD Rat XY pOS was deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121603.

Throughout the specification the aim has been to describe the preferred embodiments of the invention without limiting the invention to any one embodiment or specific collection of features. It will therefore be appreciated by those of skill in the art that, in light of the instant disclosure, various modifications and changes can be made in the particular embodiments exemplified without departing from the scope of the present invention.

All computer programs, algorithms, patent and scientific literature referred to herein is incorporated herein by reference.

Table 1

Pluripotent genes enriched in pOS cells
2-fold compared to
Reference

Genbank	RefSeq	Symbol_I
NM_008569	NM_008569.1	Anapc1
NM_013470	NM_013470.1	Anxa3
NM_009689	NM_009689.1	Birc5
NM_025788	NM_025788.2	Btbd14b
NM_172301	NM_172301.2	Ccnb1
XM_131801	XM_131801.1	Cda
NM_011991	NM_011991.1	Cops3
XM_128714	XM_128714.3	Ddx11
NM_027148	NM_027148.2	Exosc8
NM_007999	NM_007999.2	Fen1
XM_130877	XM_130877.3	Gmps
NM_010325	NM_010325.1	Got2
NM_008228	NM_008228.1	Hdac1
NM_146165	NM_146165.1	Jtv1
XM_130821	XM_130821.1	Kpna2
NM_010693	NM_010693.1	Lck
NM_026309	NM_026309.1	Lsm3
NM_025349	NM_025349.1	Lsm7
NM_008567	NM_008567.1	Mcm6
NM_008628	NM_008628.1	Msh2
NM_010830	NM_010830.1	Msh6
NM_008652	NM_008652.2	Mybl2
NM_010849	NM_010849.2	Myc
NM_053089	NM_053089.2	Narg1
NM_024193	NM_024193.1	Nol5a
NM_053086	NM_053086.1	Nolc1
NM_019716	NM_019716.1	Orc6l
NM_011045	NM_011045.1	Pcna
NM_011072	NM_011072.2	Pfn1
NM_007905	NM_007905.1	Phc1
NM_024250	NM_024250.3	Phf10
NM_016966	NM_016966	Phgdh
NM_026398	NM_026398.2	Pop5
NM_031868	NM_031868.1	Ppp1ca
NM_133948	NM_133948.2	Psip1
XM_132528	XM_132528.3	Rfc3
NM_145480	NM_145480	Rfc4
XM_132348	XM_132348.2	Rfc5
NM_026014	NM_026014.3	Ris2
NM_026653	NM_026653.1	Rpa1

NM_026632	NM_026632.1	Rpa3
NM_011358	NM_011358.1	Sfrs2
NM_025656	NM_025656.1	Sip1
NM_031196	NM_031196.1	Slc19a1
NM_017407	NM_017407.1	Spag5
NM_178652	NM_178652.1	Supt3h
NM_011552	NM_011552.1	Tcof1
NM_011605	NM_011605.1	Tmpo
NM_024187	NM_024187	U2af1

Table 2

Plurinet genes detected in pOS cells

Genbank	RefSeq	Symbol_I
NM_019816	NM_019816.1	Aatf
NM_008569	NM_008569.1	Anapc1
NM_009672	NM_009672.2	Anp32a
NM_007585	NM_007585.2	Anxa2
NM_013470	NM_013470.1	Anxa3
NM_009687	NM_009687	Apex1
NM_026195	NM_026195.1	Atic
XM_181344	XM_181344.3	Aurkb
NM_057171	NM_057171.1	Bat3
NM_025392	NM_025392.1	Bccip
NM_009689	NM_009689.1	Birc5
NM_007550	NM_007550	Blm
NM_025788	NM_025788.2	Btbd14b
NM_009773	NM_009773	Bub1b
NM_009811	NM_009811.2	Casp6
NM_146089	NM_146089.1	Ccdc5
NM_172301	NM_172301.2	Ccnb1
NM_007631	NM_007631.1	Ccnd1
NM_007633	NM_007633.1	Ccne1
XM_131801	XM_131801.1	Cda
NM_009862	NM_009862.1	Cdc45l
NM_009863	NM_009863.1	Cdc7
NM_013733	NM_013733.2	Chaf1a
NM_016706	NM_016706.1	Coil
NM_011991	NM_011991.1	Cops3
NM_012002	NM_012002.1	Cops6
NM_007829	NM_007829.1	Daxx
XM_128714	XM_128714.3	Ddx11
NM_053272	NM_053272.1	Dhcr24
NM_007858	NM_007858.1	Diap1
NM_023479	NM_023479.1	Elac2
NM_011729	NM_011729	Ercc5
XM_284543	XM_284543.2	Exosc7
NM_027148	NM_027148.2	Exosc8
NM_007991	NM_007991.2	Fbl
NM_007999	NM_007999.2	Fen1
NM_057172	NM_057172.1	Fubp1
NM_139149	NM_139149.1	Fus
NM_007836	NM_007836.1	Gadd45a
NM_026053	NM_026053.1	Gemin6
NM_027189	NM_027189.1	Gemin7
XM_130877	XM_130877.3	Gmps
NM_010325	NM_010325.1	Got2
NM_022011	NM_022011.2	Gtf2h2
NM_008228	NM_008228.1	Hdac1

NM_008229	NM_008229.1	Hdac2
NM_016660	NM_016660.1	Hmga1
NM_010448	NM_010448.2	Hnrpab
NM_025279	NM_025279.1	Hnrpk
NM_013559	NM_013559.1	Hsp105
NM_008301	NM_008301.2	Hspa2
NM_031165	NM_031165.3	Hspa8
NM_010477	NM_010477.2	Hspd1
NM_008303	NM_008303.2	Hspe1
NM_146165	NM_146165.1	Jtv1
XM_130821	XM_130821.1	Kpna2
NM_008379	NM_008379.2	Kpnb1
NM_010693	NM_010693.1	Lck
NM_026309	NM_026309.1	Lsm3
NM_015816	NM_015816.1	Lsm4
NM_025349	NM_025349.1	Lsm7
NM_027290	NM_027290.1	Mcm10
NM_008564	NM_008564.1	Mcm2
NM_008563	NM_008563.1	Mcm3
NM_008566	NM_008566.1	Mcm5
NM_008567	NM_008567.1	Mcm6
NM_019939	NM_019939.1	Mpp6
NM_018736	NM_018736.2	Mre11a
NM_011885	NM_011885.2	Mrps12
NM_008628	NM_008628.1	Msh2
NM_010830	NM_010830.1	Msh6
NM_013602	NM_013602.2	Mt1
NM_138745	NM_138745	Mthfd1
NM_016776	NM_016776.2	Mybbp1a
NM_008652	NM_008652.2	Mybl2
NM_010849	NM_010849.2	Myc
NM_177619	NM_177619.2	Myst2
NM_053089	NM_053089.2	Narg1
NM_010880	NM_010880.2	Ncl
NM_008704	NM_008704.2	Nme1
NM_024193	NM_024193.1	Nol5a
NM_026578	NM_026578.1	Nola1
NM_053086	NM_053086.1	Nolc1
NM_008726	NM_008726.2	Nppb
NM_008743	NM_008743.1	Nthl1
NM_008637	NM_008637.1	Nudt1
NM_016714	NM_016714.2	Nup50
NM_001014425	NM_001014425.1	Orc1l
NM_019716	NM_019716.1	Orc6l
NM_011119	NM_011119.1	Pa2g4
NM_008778	NM_008778.1	Pak3
NM_008783	NM_008783.1	Pbx1
NM_011045	NM_011045.1	Pcna
NM_029231	NM_029231.2	Pelp1
NM_011072	NM_011072.2	Pfn1
NM_007905	NM_007905.1	Phc1
NM_024250	NM_024250.3	Phf10
NM_016966	NM_016966	Phgdh

NM_177262	NM_177262.3	Pkn1
NM_011636	NM_011636.1	Plscr1
NM_025928	NM_025928.1	Pmf1
NM_011131	NM_011131.2	Pold1
NM_008894	NM_008894.1	Pold2
NM_015810	NM_015810	Polg2
NM_026398	NM_026398.2	Pop5
NM_028753	NM_028753.1	Pop7
NM_145610	NM_145610	Ppan
NM_026352	NM_026352.2	Ppid
NM_031868	NM_031868.1	Ppp1ca
NM_011170	NM_011170.1	Prnp
NM_133948	NM_133948.2	Psip1
NM_011192	NM_011192.2	Psme3
NM_008972	NM_008972.1	Ptma
NM_011223	NM_011223.1	Pxn
NM_009015	NM_009015.2	Rad54l
NM_011237	NM_011237.1	Rad9
NM_026557	NM_026557.2	Rchy1
NM_058214	NM_058214.1	Recql4
XM_132528	XM_132528.3	Rfc3
NM_145480	NM_145480	Rfc4
XM_132348	XM_132348.2	Rfc5
NM_026014	NM_026014.3	Ris2
NM_026653	NM_026653.1	Rpa1
NM_011284	NM_011284.2	Rpa2
NM_026632	NM_026632.1	Rpa3
NM_009085	NM_009085.1	Rpo1-1
NM_009087	NM_009087.1	Rpo1-3
NM_009087	NM_009087.1	Rpo1-3
NM_019685	NM_019685.1	Ruvbl1
NM_173374	NM_173374.2	Sfrs1
NM_011358	NM_011358.1	Sfrs2
NM_013663	NM_013663.3	Sfrs3
NM_025656	NM_025656.1	Sip1
NM_019812	NM_019812.1	Sirt1
NM_031196	NM_031196.1	Slc19a1
XM_132597	XM_132597.3	Smarcad1
NM_009211	NM_009211.1	Smarcc1
NM_011420	NM_011420.1	Smn1
NM_015782	NM_015782.2	Snrpa
NM_009225	NM_009225.1	Snrpb
NM_009226	NM_009226.2	Snrpd1
		Snrpf
NM_009896	NM_009896.1	Socs1
NM_017407	NM_017407.1	Spag5
NM_021448	NM_021448.1	Statip1
NM_152220	NM_152220.1	Stx3
NM_011503	NM_011503.2	Stxbp2
NM_009460	NM_009460.1	Sumo1
NM_178652	NM_178652.1	Supt3h
NM_019666	NM_019666.1	Syncrip
NM_009319	NM_009319	Tarbp2

NM_011552	NM_011552.1	Tcof1
NM_011605	NM_011605.1	Tmpo
NM_028109	NM_028109.2	Tpx2
NM_011588	NM_011588.1	Trim28
XM_127444	XM_127444.3	Trip13
NM_011640	NM_011640.1	Trp53
NM_009446	NM_009446.1	Tuba3
NM_024187	NM_024187	U2af1
NM_011676	NM_011676.2	Unc119
NM_016794	NM_016794.2	Vamp8
NM_021499	NM_021499.1	Wdr8
XM_128102	XM_128102.2	Wdyhv1
NM_020570	NM_020570.2	Xrcc2
NM_177643	NM_177643.2	Zfp281
NM_024215	NM_024215.1	Zpf593

Table 3

Plurinet_orthology list
median normalised pOS cells Rosa Mus
Hand edited on Tue Nov 04 15:21:21 EST 2008
Genes present in [pluri_2] or [Plurinet]

pOS cells		
Raw fluorescence	**Genbank**	**Symbol_l**
99.05	NM_020567	Gmnn
95.54	NM_007415	Adprt1
86.11	NM_001025378	Orc2l
85.65	NM_010068	Dnmt3b
82.52	NM_011237	Rad9
80.64	NM_011677	Ung
77.45	NM_010829	Msh3
72.34	NM_009406	Tnni3
70.94	NM_013672	Sp1
70.50	XM_358372	Ctbp2
62.10	NM_009828	Ccna2
59.30	NM_007523	Bak1
58.45	NM_175400	Sephs1
56.42	NM_211138	Pcyt1b
53.18	NM_007691	Chek1
52.77	NM_009387	Tk1
48.63	NM_146203	Zpf764
48.36	NM_013545	Hcph
45.41	NM_172612	Rnd1
38.48	NM_080850	Pask
36.40	NM_011237	Rad9
35.78	NM_177309	4933421E11Rik
35.37	NM_133188	Dazap1
34.89	NM_016681	Chek2
34.39	NM_021451	Pmaip1
33.69	NM_010049	Dhfr
33.15	NM_019869	Rbm14
32.31	NM_019689	Arid3b
32.16	NM_133250	Mutyh
31.71	NM_145938	Rpp40
30.44	NM_031181	Siglecl1
30.15	NM_030152	Nol3
29.25	NM_009696	Apoe
29.01	NM_011237	Rad9
28.76	NM_009882	Cebpz
27.23	NM_181730	Rpo1-3
27.10	NM_009499	Vasp
24.01	NM_008565	Mcm4
23.58	NM_011634	Traip
22.51	NM_144848	Eppk1
22.34	NM_009227	Snrpe
21.46	NM_013902	Fkbp3
21.15	NM_019551	Ttrap
20.65	NM_009860	Cdc25c

19.95	NM_011151	Ppm1b	
19.44	NM_011968	Psma6	
16.96	NM_177309	4933421E11Rik	
16.91	NM_025513	Exosc3	
16.85	NM_013633	Pou5f1	**Oct3/4**
16.58	NM_008110	Gdf9	
15.48	NM_008722	Npm1	
14.53	NM_007659	Cdc2a	
14.48	NM_007546	Biklk	
12.80	XM_132755	**Nanog**	
12.62	NM_018789	Mllt7	
12.18	NM_009261	Strbp	
12.09	NM_009516	Wee1	
11.81	NM_033174	Snurf	
9.77	NM_010908	Nfkbib	
9.49	NM_009556	Zfp42	
9.20	NM_015817	Ppap2c	
9.14	NM_025415	Cks2	
9.02	NM_019512	Tcerg1	
8.86	NM_009741	Bcl2	
8.60	NM_015733	Casp9	
8.44	NM_019733	Rbpms	
8.07	NM_009401	Tnfrsf8	
8.04	NM_009988	Cxadr	
7.82	NM_175303	Sall4	
7.69	NM_173762	Cenpe	
7.58	NM_019393	Exosc9	
7.09	NM_178616	Psmd11	
7.00	NM_008034	Folr1	
6.92	NM_013632	Pnp	
6.84	XM_125954	Erbb3	
6.71	NM_011184	Psma3	
6.70	NM_013773	Tcl1b1	
6.65	NM_010346	Grb7	
6.33	NM_008891	Pnn	
6.28	NM_010848	Myb	
6.22	NM_009606	Acta1	
6.19	XM_358869	Dppa2	
6.09	NM_013670	Snrpn	
5.95	NM_023871	Set	
5.88	NM_010773	Mbd2	
5.74	NM_008831	Phb	
5.70	NM_007858	Diap1	
5.57	NM_025520	Lsm5	
5.47	NM_024285	Bves	
5.42	NM_010439	Hmgb1	
5.32	NM_010768	Matk	
5.04	NM_175749	Nup153	
4.99	NM_029977	Polq	
4.96	NM_021099	Kit	
4.91	NM_007630	Ccnb2	
4.90	NM_011504	Stxbp3	
4.63	NM_016859	Bysl	

4.62	NM_009874	Cdk7
4.45	NM_144841	Otx2
4.44	NM_010849	Myc
4.44	NM_009533	Xrcc5
4.41	NM_011562	Tdgf1
4.35	NM_015765	Hspa14
4.19	NM_012012	Exo1
4.13	NM_011721	Wrn
4.11	NM_013552	Hmmr
4.04	NM_009278	Ssb

Table 4

Plurinet_orthology list
median normalised pOS cells Rosa Mus
Hand edited on Tue Nov 04 15:21:21 EST 2008
Genes present in [pluri_2] or [Plurinet]

pOS cells Raw fluorescence	Genbank	Symbol_I
29811.32	NM_013602	Mt1
27477.97	NM_007585	Anxa2
24153.31	NM_031165	Hspa8
18331.27	NM_010448	Hnrpab
16224.09	NM_008704	Nme1
13468.14	NM_016660	Hmga1
10018.97	NM_009226	Snrpd1
9426.97	NM_013470	Anxa3
8829.10	NM_011072	Pfn1
7622.83	NM_031868	Ppp1ca
7592.03	NM_011991	Cops3
7257.88	NM_026653	Rpa1
7014.66	NM_008972	Ptma
6694.12	NM_025349	Lsm7
6551.64	NM_003095	Snrpf
6369.04	NM_173374	Sfrs1
5751.13	NM_008566	Mcm5
5555.94	NM_026352	Ppid
5361.51	NM_019716	Orc6l
4772.94	NM_012002	Cops6
4352.20	NM_011588	Trim28
4023.31	NM_007991	Fbl
4000.61	NM_007999	Fen1
3572.81	NM_009087	Rpo1-3
3358.59	NM_026578	Nola1
3103.30	NM_011170	Prnp
3095.99	XM_284543	Exosc7
2791.05	NM_010830	Msh6
2650.19	NM_008564	Mcm2
2617.83	NM_009087	Rpo1-3
2433.70	NM_011640	Trp53
2270.74	NM_007631	Ccnd1
2201.13	NM_013559	Hsp105
2186.59	NM_024193	Nol5a
2126.41	NM_024250	Phf10
2097.10	NM_008894	Pold2
2050.14	NM_026014	Ris2
2029.67	NM_024187	U2af1
2009.90	NM_172301	Ccnb1
1993.73	XM_130821	Kpna2
1985.69	NM_009225	Snrpb
1977.14	NM_026632	Rpa3
1957.23	NM_021448	Statip1

1901.50	NM_008228	Hdac1
1898.49	NM_008567	Mcm6
1756.42	NM_146165	Jtv1
1745.35	NM_022011	Gtf2h2
1738.24	NM_026398	Pop5
1734.67	NM_008303	Hspe1
1641.33	NM_015816	Lsm4
1608.78	NM_011420	Smn1
1606.76	NM_009863	Cdc7
1600.43	NM_009687	Apex1
1576.08	NM_011192	Psme3
1520.74	NM_011119	Pa2g4
1482.60	NM_178652	Supt3h
1477.52	NM_007905	Phc1
1473.17	NM_009689	Birc5
1467.90	NM_008229	Hdac2
1382.04	XM_181344	Aurkb
1363.66	NM_017407	Spag5
1285.07	NM_011885	Mrps12
1246.03	NM_026309	Lsm3
1222.51	NM_008569	Anapc1
1210.59	NM_139149	Fus
1201.31	NM_009015	Rad54l
1192.71	NM_010477	Hspd1
1190.14	NM_008379	Kpnb1
1151.51	XM_132348	Rfc5
1108.94	NM_015782	Snrpa
1101.00	NM_011552	Tcof1
1024.67	NM_011131	Pold1
1023.60	NM_027148	Exosc8
1020.94	NM_019816	Aatf
1010.47	NM_011284	Rpa2
1006.28	NM_008301	Hspa2
996.12	NM_016794	Vamp8
962.63	NM_011636	Plscr1
945.55	XM_128714	Ddx11
941.83	NM_057171	Bat3
919.60	NM_019685	Ruvbl1
866.90	NM_009773	Bub1b
815.01	NM_009085	Rpo1-1
803.10	NM_011503	Stxbp2
803.01	NM_145610	Ppan
781.07	NM_013733	Chaf1a
779.94	NM_133948	Psip1
776.72	NM_009811	Casp6
772.82	NM_008778	Pak3
740.43	NM_007550	Blm
736.75	NM_011045	Pcna
728.94	NM_026053	Gemin6
691.73	NM_138745	Mthfd1
663.02	NM_010325	Got2
631.26	NM_026195	Atic
598.45	NM_031196	Slc19a1

587.05	NM_009672	Anp32a
566.58	NM_146089	Ccdc5
554.79	XM_132528	Rfc3
542.08	NM_007633	Ccne1
536.25	NM_013663	Sfrs3
530.06	XM_131801	Cda
524.49	NM_016966	Phgdh
520.38	NM_021499	Wdr8
505.62	NM_026557	Rchy1
483.21	NM_025279	Hnrpk
471.06	NM_058214	Recql4
461.21	NM_152220	Stx3
457.60	XM_130877	Gmps
454.00	NM_008743	Nthl1
447.49	NM_057172	Fubp1
446.36	NM_010880	Ncl
438.57	NM_025928	Pmf1
425.69	NM_053089	Narg1
421.40	NM_008563	Mcm3
416.25	XM_132597	Smarcad1
401.23	NM_007829	Daxx
386.03	NM_177619	Myst2
385.98	NM_011605	Tmpo
383.80	NM_027290	Mcm10
382.31	NM_007836	Gadd45a
375.83	NM_029231	Pelp1
361.17	NM_028753	Pop7
338.41	NM_016714	Nup50
315.28	NM_008783	Pbx1
298.22	NM_025392	Bccip
277.04	NM_011237	Rad9
262.70	NM_019939	Mpp6
254.26	NM_009460	Sumo1
252.15	NM_025788	Btbd14b
250.56	XM_128102	Wdyhv1
242.98	NM_010693	Lck
242.81	NM_008637	Nudt1
234.69	NM_001014425	Orc1l
233.99	NM_177643	Zfp281
230.51	NM_009862	Cdc45l
227.98	NM_008628	Msh2
226.60	NM_177262	Pkn1
224.27	NM_023479	Elac2
219.76	NM_019666	Syncrip
215.06	NM_009446	Tuba3
214.19	NM_053086	Nolc1
210.39	NM_019812	Sirt1
201.09	NM_009896	Socs1
200.60	NM_015810	Polg2
200.14	NM_007858	Diap1
191.39	NM_025656	Sip1
185.13	NM_011729	Ercc5
176.18	NM_145480	Rfc4

153.43	NM_018736	Mre11a
149.41	NM_027189	Gemin7
147.74	NM_010849	Myc
147.22	NM_008652	Mybl2
146.06	NM_020570	Xrcc2
145.15	NM_009319	Tarbp2
140.04	NM_008726	Nppb
139.50	NM_024215	Zpf593
138.25	NM_011676	Unc119
133.36	NM_053272	Dhcr24
124.42	NM_016706	Coil
110.33	NM_028109	Tpx2
110.12	XM_127444	Trip13
106.53	NM_011358	Sfrs2
103.29	NM_009211	Smarcc1
103.20	NM_011223	Pxn
101.97	NM_016776	Mybbp1a
99.05	NM_020567	Gmnn
95.54	NM_007415	Adprt1
86.11	NM_001025378	Orc2l
85.65	NM_010068	Dnmt3b
82.52	NM_011237	Rad9
80.64	NM_011677	Ung
77.45	NM_010829	Msh3
72.34	NM_009406	Tnni3
70.94	NM_013672	Sp1
70.50	XM_358372	Ctbp2
62.10	NM_009828	Ccna2
59.30	NM_007523	Bak1
58.45	NM_175400	Sephs1
56.42	NM_211138	Pcyt1b
53.18	NM_007691	Chek1
52.77	NM_009387	Tk1
48.63	NM_146203	Zpf764
48.36	NM_013545	Hcph
45.41	NM_172612	Rnd1
38.48	NM_080850	Pask
36.40	NM_011237	Rad9
35.78	NM_177309	4933421E11Rik
35.37	NM_133188	Dazap1
34.89	NM_016681	Chek2
34.39	NM_021451	Pmaip1
33.69	NM_010049	Dhfr
33.15	NM_019869	Rbm14
32.31	NM_019689	Arid3b
32.16	NM_133250	Mutyh
31.71	NM_145938	Rpp40
30.44	NM_031181	Siglecl1
30.15	NM_030152	Nol3
29.25	NM_009696	Apoe
29.01	NM_011237	Rad9
28.76	NM_009882	Cebpz
27.23	NM_181730	Rpo1-3

27.10	NM_009499	Vasp	
24.01	NM_008565	Mcm4	
23.58	NM_011634	Traip	
22.51	NM_144848	Eppk1	
22.34	NM_009227	Snrpe	
21.46	NM_013902	Fkbp3	
21.15	NM_019551	Ttrap	
20.65	NM_009860	Cdc25c	
19.95	NM_011151	Ppm1b	
19.44	NM_011968	Psma6	
16.96	NM_177309	4933421E11Rik	
16.91	NM_025513	Exosc3	
16.85	NM_013633	Pou5f1	**Oct3/4**
16.58	NM_008110	Gdf9	
15.48	NM_008722	Npm1	
14.53	NM_007659	Cdc2a	
14.48	NM_007546	Biklk	
12.80	XM_132755	**Nanog**	
12.62	NM_018789	Mllt7	
12.18	NM_009261	Strbp	
12.09	NM_009516	Wee1	
11.81	NM_033174	Snurf	
9.77	NM_010908	Nfkbib	
9.49	NM_009556	Zfp42	
9.20	NM_015817	Ppap2c	
9.14	NM_025415	Cks2	
9.02	NM_019512	Tcerg1	
8.86	NM_009741	Bcl2	
8.60	NM_015733	Casp9	
8.44	NM_019733	Rbpms	
8.07	NM_009401	Tnfrsf8	
8.04	NM_009988	Cxadr	
7.82	NM_175303	Sall4	
7.69	NM_173762	Cenpe	
7.58	NM_019393	Exosc9	
7.09	NM_178616	Psmd11	
7.00	NM_008034	Folr1	
6.92	NM_013632	Pnp	
6.84	XM_125954	Erbb3	
6.71	NM_011184	Psma3	
6.70	NM_013773	Tcl1b1	
6.65	NM_010346	Grb7	
6.33	NM_008891	Pnn	
6.28	NM_010848	Myb	
6.22	NM_009606	Acta1	
6.19	XM_358869	Dppa2	
6.09	NM_013670	Snrpn	
5.95	NM_023871	Set	
5.88	NM_010773	Mbd2	
5.74	NM_008831	Phb	
5.70	NM_007858	Diap1	
5.57	NM_025520	Lsm5	
5.47	NM_024285	Bves	

5.42	NM_010439	Hmgb1
5.32	NM_010768	Matk
5.04	NM_175749	Nup153
4.99	NM_029977	Polq
4.96	NM_021099	Kit
4.91	NM_007630	Ccnb2
4.90	NM_011504	Stxbp3
4.63	NM_016859	Bysl
4.62	NM_009874	Cdk7
4.45	NM_144841	Otx2
4.44	NM_010849	Myc
4.44	NM_009533	Xrcc5
4.41	NM_011562	Tdgf1
4.35	NM_015765	Hspa14
4.19	NM_012012	Exo1
4.13	NM_011721	Wrn
4.11	NM_013552	Hmmr
4.04	NM_009278	Ssb

Table 5

List of genes detected in pOS cells and in neurosphere-derived cells generated from human olfactory mucosa (equivalent to the Reference cells in the pOS transcriptome analysis)

These are genes shared by pOS cells and human neurosphere-derived cells that are also present in the PluriNet, the network of 300 genes common to a set of human pluripotent cell types - ES, iPS, EC.
Reference: F. J. Muller, L. C. Laurent, D. Kostka et al., Nature 455 (7211), 401 (2008).

Gene Common Names	Synonyms	Genbank
16E1BP	16E1BP	NM_004237
A1; RFC37; MGC27291	A1; RFC37; MGC27291	NM_181573
ABBP1; FLJ40338	ABBP1; FLJ40338	NM_031266
ABBP1; FLJ40338	ABBP1; FLJ40338	NM_004499
ANX3	ANX3	NM_005139
APC1; MCPR; TSG24	TSG24; MCPR; APC1	NM_022662
APE; APX; APE1; APEN; APEX; HAP1; REF1; REF-1	APEX; REF1; APE1; HAP1; APE; APX; REF-1; APEN	NM_080649
ASF; SF2; SF2p33; SRp30a; MGC5228	SF2; SF2p33; MGC5228; ASF; SRp30a	NM_001078166
ATLD; HNGS1; MRE11; MRE11B	MRE11B; MRE11; ATLD; HNGS1	NM_005591
AWD; GAAD; NM23; NDPKA; NM23-H1	NDPKA; NM23-H1; NM23; AWD; GAAD	NM_000269
AWD; GAAD; NM23; NDPKA; NM23-H1	NDPKA; NM23-H1; NM23; AWD; GAAD	NM_198175
BCL1; PRAD1; U21B31; D11S287E	PRAD1; D11S287E; BCL1; U21B31	NM_053056
BM28; CCNL1; CDCL1; cdc19; D3S3194; MITOTIN; KIAA0030; MGC10606	MGC10606; CCNL1; MITOTIN; CDCL1; KIAA0030; D3S3194; BM28; cdc19	NM_004526
CDC2; POLD	CDC2; POLD	NM_002691
CDC46; MGC5315; P1-CDC46	MGC5315; CDC46; P1-CDC46	NM_006739
CJD; GSS; PrP; ASCR; PRIP; PrPc; CD230; MGC26679; PrP27-30; PrP33-35C	CD230; PrP33-35C; ASCR; PrP27-30; GSS; CJD; PRIP; PrPc; PrP; MGC26679	NM_001080121
CLN80; p80-coilin	p80-coilin; CLN80	NM_004645
c-Myc	c-Myc	NM_002467
CNA43; PRO2249; MGC126776	PRO2249; CNA43; MGC126776	NM_018518
COD; SNRPB1; snRNP-B; SmB/SmB'	snRNP-B; SNRPB1; COD; SmB/SmB'	NM_003091
COD; SNRPB1; snRNP-B; SmB/SmB'	snRNP-B; SNRPB1; COD; SmB/SmB'	NM_003091
CPN10; GROES; HSP10	CPN10; GROES; HSP10	NM_002157
CPN60; GROEL; HSP60; HSP65; SPG13; HuCHA60	HuCHA60; GROEL; HSP60; SPG13; CPN60; HSP65	NM_002156
CPN60; GROEL; HSP60; HSP65; SPG13; HuCHA60	HuCHA60; GROEL; HSP60; SPG13; CPN60; HSP65	NM_002156

CSBP; TUNP; HNRNPK; FLJ41122	CSBP; TUNP; FLJ41122; HNRNPK	NM_031263
CSN6; MOV34-34KD	MOV34-34KD; CSN6	NM_006833
CYPD; CYP-40; MGC33096	MGC33096; CYPD; CYP-40	NM_005038
DAP6; BING2; MGC126245; MGC126246	MGC126246; BING2; MGC126245; DAP6	NM_001350
DBK; PKN; PAK1; PRK1; PRKCL1; MGC46204	PRKCL1; PAK1; PKN; DBK; PRK1; MGC46204	NM_213560
DDIT1; GADD45	GADD45; DDIT1	NM_001924
DED; CHE1; CHE-1	CHE1; CHE-1; DED	NM_012138
DIL2; p100; DIL-2; HCTP4; FLS353; HCA519; REPP86; C20orf1; C20orf2; GD:C20orf1	GD:C20orf1; HCTP4; C20orf1; FLS353; DIL-2; HCA519; DIL2; p100; REPP86; C20orf2	NM_012112
DRF1; DFNA1; LFHL1; hDIA1; FLJ25265	LFHL1; hDIA1; DFNA1; FLJ25265; DRF1	NM_005219
DUP; RIS2	DUP; RIS2	NM_030928
EBP1; HG4-1; p38-2G4	p38-2G4; HG4-1; EBP1	NM_006191
EDB; VAMP5	VAMP5; EDB	NM_003761
EDR1; HPH1; RAE28	HPH1; EDR1; RAE28	NM_004426
ELC2; HPC2; FLJ10530; FLJ36693; FLJ42848	ELC2; FLJ10530; FLJ36693; HPC2; FLJ42848	NM_018127
FBP; FUBP	FBP; FUBP	NM_003902
FIB; FLRN; RNU3IP1	RNU3IP1; FLRN; FIB	NM_001436
FLJ16691	FLJ16691	NM_002859
FLJ20430; MGC99569	FLJ20430; MGC99569	NM_017818
FLJ23459	FLJ23459	NM_024775
FLJ40994	FLJ40994	NM_002080
G3; D6S52E	BAG-6; G3; D6S52E; BAG6	NM_080702
Ga19; NATH; TBDN100	Ga19; NAT1; NATH; TBDN100	NM_057175
GAR1	GAR1	NM_018983
GAR1	GAR1	NM_032993
GEMIN2; SIP1-delta	GEMIN2; SIP1-delta	NM_001009182
GTBP; HSAP; HNPCC5	HSAP; GTBP; HNPCC5	NM_000179
H2-ALPHA		NM_207312
HCC5; P1.h; RLFB; MGC1157; P1-MCM3	RLFB; HCC5; P1-MCM3; MGC1157; P1.h	NM_002388
HD1; RPD3; GON-10; RPD3L1; DKFZp686H12203	GON-10; DKFZp686H12203; HD1; RPD3; RPD3L1	NM_004964
HEI-C; HsT1461; FLJ21094; FLJ40084	FLJ40084; HEI-C; FLJ21094; HsT1461	NM_138443
HERMES	HERMES	NM_006867
HERMES	HERMES	NM_001008710
HMX3; MNAR; P160	P160; HMX3; MNAR	NM_014389
HP55; POLB; PEOA4; POLGB; MTPOLB	POLB; POLGB; HP55; MTPOLB; PEOA4	NM_007215
HRG4	HRG4	NM_054035
HRI; KIAA1369	KIAA1369; HRI	NM_014413
Hsk1; CDC7L1; HsCDC7; huCDC7; MGC117361; MGC126237; MGC126238	MGC126237; CDC7L1; huCDC7; MGC126238; HsCDC7; Hsk1; MGC117361	NM_003503

HSP105; HSP105A; HSP105B; KIAA0201; NY-CO-25; DKFZp686M05240	HSP105B; DKFZp686M05240; HSP105; HSP105A; NY-CO-25; KIAA0201	NM_006644
HSSB; RF-A; RP-A; REPA1; RPA70	RPA70; REPA1; RF-A; HSSB; RP-A	NM_002945
IMB1; IPOB; Impnb; NTF97; MGC2155; MGC2156; MGC2157	IPOB; NTF97; MGC2157; Impnb; MGC2155; IMB1; MGC2156	NM_002265
JAB; CIS1; SSI1; TIP3; CISH1; SSI-1; SOCS-1	SSI-1; CISH1; SSI1; CIS1; JAB; TIP3; SOCS-1	NM_003745
JTV1; P38; AIMP2; PRO0992	AIMP2; PRO0992; P38	NM_006303
KAP1; TF1B; RNF96; TIF1B; FLJ29029	FLJ29029; TIF1B; RNF96; TF1B; KAP1	NM_005762
Ki; PA28G; REG-GAMMA; PA28-gamma	PA28-gamma; PA28G; Ki; REG-GAMMA	NM_005789
KIAA0018; SELADIN1; Nbla03646; seladin-1	Nbla03646; seladin-1; SELADIN1; KIAA0018	NM_014762
LANP; MAPM; PP32; PHAP1; PHAPI; I1PP2A; C15orf1; MGC119787; MGC150373	C15orf1; PP32; PHAPI; MGC150373; PHAP1; I1PP2A; LANP; MAPM; MGC119787	NM_006305
LAP1; HSC54; HSC70; HSC71; HSP71; HSP73; NIP71; HSPA10; MGC29929; MGC131511	MGC131511; HSC54; HSPA10; MGC29929; HSC70; HSP71; HSP73; LAP1; HSC71; NIP71	NM_153201
LAP1; HSC54; HSC70; HSC71; HSP71; HSP73; NIP71; HSPA10; MGC29929; MGC131511	MGC131511; HSC54; HSPA10; MGC29929; HSC70; HSP71; HSP73; LAP1; HSC71; NIP71	NM_006597
MAP126; DEEPEST; hMAP126	hMAP126; DEEPEST; MAP126	NM_006461
MCH2	MCH2	NM_001226
MF1; RAD2; FEN-1	RAD2; FEN-1; MF1	NM_004111
MGC126627; DKFZp686B09108	DKFZp686B09108; MGC126627	NM_002585
MGC8367	MGC8367	NM_182649
MMTRA1B	MMTRA1B	NM_021105
MTH1	MTH1	NM_198950
MTHFC; MTHFD	MTHFC; MTHFD	NM_005956
NME1-NME2; NME2	NME2	NM_001018136
NOP56	NOP56	NM_006392
NPAP60; NPAP60L; MGC39961	NPAP60; MGC39961; NPAP60L	NM_007172
NTH1; OCTS3	NTH1; OCTS3	NM_002528
ORC6	ORC6	NM_014321
P130; NOPP130; NOPP140; KIAA0035; NS5ATP13	P130; NOPP140; KIAA0035; NOPP130; NS5ATP13	NM_004741
P160; PAP2; FLJ37886	P160; PAP2; FLJ37886	NM_014520
P36; ANX2; LIP2; LPC2; CAL1H; LPC2D; ANX2L4; PAP-IV	P36; LPC2D; ANX2L4; ANX2; PAP-IV; CAL1H; LIP2; LPC2	NM_001002857
p52; p75; PAIP; DFS70; LEDGF; PSIP2; MGC74712	MGC74712; PAIP; LEDGF; p75; PSIP2; p52; DFS70	NM_033222

p52; p75; PAIP; DFS70; LEDGF; PSIP2; MGC74712	MGC74712; PAIP; LEDGF; p75; PSIP2; p52; DFS70	NM_021144
p53; LFS1; TRP53	TRP53; p53; LFS1	NM_000546
p8; EAP1; RRP42; Rrp42p; hRrp42p; FLJ26543; KIAA0116	hRrp42p; FLJ26543; Rrp42p; KIAA0116; p8; EAP1; RRP42	NM_015004
p9; CIP3; EAP2; OIP2; RRP43; Rrp43p; bA421P11.3; RP11-421P11.3	Rrp43p; EAP2; RRP43; RP11-421P11.3; CIP3; bA421P11.3; OIP2; p9	NM_181503
PDG; PGD; PGAD; PGDH; SERA; 3PGDH; 3-PGDH; MGC3017	PGD; 3-PGDH; PGDH; PDG; SERA; PGAD; MGC3017; 3PGDH	NM_006623
PFN1		NM_005022
PMF1		NM_007221
PP-1A; PPP1A; MGC1674; MGC15877	PP-1A; MGC15877; MGC1674; PPP1A	NM_001008709
pp68; NSAP1; HNRPQ1; GRY-RBP; dJ3J17.2; RP1-3J17.2	dJ3J17.2; pp68; RP1-3J17.2; HNRPQ1; hnRNP-Q; NSAP1; GRY-RBP	NM_006372
puf; NDPKB; NM23B; NM23-H2; MGC111212	NME2	NM_001018136
PURH; AICAR; AICARFT; IMPCHASE	PURH; AICARFT; AICAR; IMPCHASE	NM_004044
RAD9	RAD9	NM_004584
REPA2; RPA32	REPA2; RPA32	NM_002946
REPA3	REPA3	NM_002947
RN; FP793; U2AF35; U2AFBP; RNU2AF1; DKFZp313J1712	DKFZp313J1712; U2AFBP; U2AF35; RN; RNU2AF1; FP793	NM_001025203
RPA5; RPA39; RPA40; RPAC1; RP3-337H4.4	RPAC1; RPA40; RPA5; RPA39; RP3-337H4.4	NM_203290
RPA5; RPA39; RPA40; RPAC1; RP3-337H4.4	RPAC1; RPA40; RPA5; RPA39; RP3-337H4.4	NM_203290
RPA9; RPA16; RPAC2; POLR1C; RPO1-3; MGC9850; FLJ20616	MGC9850; RPAC2; RPA16; RPA9; POLR1C; FLJ20616; RPO1-3	NM_152705
RPA9; RPA16; RPAC2; POLR1C; RPO1-3; MGC9850; FLJ20616	MGC9850; RPAC2; RPA16; RPA9; POLR1C; FLJ20616; RPO1-3	NM_015972
RPD3; YAF1	YAF1; RPD3	NM_001527
RPP2; RPP20; 0610037N12Rik	0610037N12Rik; RPP20; RPP2	NM_005837
RPP2; RPP20; HSPC004	HSPC004; RPP20; RPP2	NM_198202
RPS12; RPMS12; RPSM12; MPR-S12; MT-RPS12	MPR-S12; MT-RPS12; RPS12; RPSM12; RPMS12	NM_033362
Rsc8; SRG3; SWI3; BAF155; CRACC1	BAF155; CRACC1; SWI3; Rsc8; SRG3	NM_003074
RVB1; ECP54; TIP49; NMP238; TIP49A	ECP54; RVB1; NMP238; TIP49; TIP49A	NM_003707
SC35; PR264; SC-35; SFRS2A; SRp30b	PR264; SRp30b; SC35; SFRS2A; SC-35	NM_003016
SGN3	SGN3	NM_003653
SIR2L1	SIR2L1	NM_012238

SMA; SMN; SMA1; SMA2; SMA3; SMA4; SMA@; SMNT; BCD541; T-BCD541	SMNT; SMA2; SMN; SMA3; SMA@; SMA; BCD541; T-BCD541; SMA4; SMA1	NM_000344
SMD1; SNRPD; HsT2456	SNRPD; HsT2456; SMD1	NM_006938
SMN; SM-D; RT-LI; HCERN3; SNRNP-N; SNURF-SNRPN		NM_005678
SMN; SM-D; RT-LI; HCERN3; SNRNP-N; SNURF-SNRPN	SNURF-SNRPN; HCERN3; SMN; RT-LI; SM-D; SNRNP-N	NM_022806
SMX4; USS2; YLR438C	USS2; YLR438C; SMX4	NM_014463
SNRPN	SNURF-SNRPN; HCERN3; SMN; RT-LI; SM-D; SNRNP-N	NM_022806
SPS; SELD; SPS1; MGC4980	MGC4980; SELD; SPS; SPS1	NM_012247
SPT3; SPT3L	SPT3L; SPT3	NM_181356
SPT3; SPT3L	SPT3L; SPT3	NM_181356
SRp20	SRp20	NM_003017
SSF; SSF1; SSF2; BXDC3; MGC14226; MGC45852	MGC14226; SSF2; SSF1; BXDC3; SSF; MGC45852	NM_020230
SSK1; BUBR1; Bub1A; MAD3L; hBUBR1; BUB1beta	Bub1A; hBUBR1; MAD3L; BUB1beta; SSK1; BUBR1	NM_001211
StIP; SHINC-2; STATIP1; FLJ10879	SHINC-2; ELP2; StIP; FLJ10879; STATIP1	NM_018255
STX3A	STX3A	NM_004177
TOK-1	TOK-1	NM_078468
TOK-1	TOK-1	NM_016567
TOK-1	TOK-1	NM_016567
TP; LAP2; CMD1T; PRO0868; MGC61508	MGC61508; PRO0868; CMD1T; TP; LAP2	NM_003276
TRBP; TRBP1; TRBP2	TRBP1; TRBP; TRBP2	NM_134323
U1A	U1A	NM_004596
UNC18B; Hunc18b; UNC18-2; pp10122; MUNC18-2	pp10122; UNC18B; MUNC18-2; UNC18-2; Hunc18b	NM_006949
VAM1; p55T; PALS2; VAM-1	p55T; PALS2; VAM-1; VAM1	NM_016447
WDR50; CGI-48	WDR50; CGI-48	NM_016001
XAP135; FLJ10975; MGC111009	XAP135; FLJ10975; MGC111009	NM_018288
XPG; UVDR; XPGC; COFS3; ERCM2	XPG; ERCM2; UVDR; XPGC; COFS3	NM_000123
YER112W	YER112W	NM_012321
YNL147W	YNL147W	NM_016199
ZBP-99; ZNP-99; FLJ12859; FLJ14378	FLJ12859; ZNP-99; ZBP-99; FLJ14378	NM_012482
ZT86	ZT86	NM_015871

TABLE 6

Protein	P1 #Events	P1 % Parent	P1 PE (575/26) -A Mean	P2 #Events	P2 %Parent	P2 PE (575/26) -A Mean
CD1d	3079	95.5	140	2	0.1	588
No ab	2762	95.5	150	1	0	826
No ab	2021	95.2	30	0	0	
CD2	2896	94.8	85	1	0	792
CD3	3030	95	110	14	0.5	11526
CD4	3478	95	108	3	0.1	4152
CD5	3723	95.2	170	17	0.5	608
CD8a	4063	94.5	139	19	0.5	2239
CD11a	3485	95.6	148	18	0.5	6197
CD11b	3869	94.6	152	9	0.2	926
CD11c	3377	94.7	72	7	0.2	7269
CD13	3939	94.8	1752	307	7.8	20839
CD14	3685	95.7	184	28	0.8	6879
CD16/32	3806	95.7	496	53	1.4	26987
CD18	2522	94.5	58	12	0.5	2824
CD19	3612	95.2	119	3	0.1	1602
CD23	3386	94.7	173	21	0.6	21510
CD24	3577	92	6003	3015	84.3	7098
CD25	4367	95.1	256	148	3.4	3078
CD27	4007	95.4	160	33	0.8	2942
CD28	4184	95.1	576	51	1.2	38652
CD29	4292	95.1	738	2942	68.5	927
CD30	3414	93.6	100	80	2.3	828
CD31	4673	94.8	98	10	0.2	1211
CD34	3963	95.4	275	63	1.6	13697
CD38	4084	94.9	711	34	0.8	70226
CD40	3990	95.2	191	9	0.2	34346
CD41	3639	94.3	467	106	2.9	18510
CD43	3825	94.6	213	56	1.5	8182
CD44	3622	94.8	2428	2292	63.3	3633
CD45	4012	94.4	323	79	2	10254
CD48	4222	96.1	191	21	0.5	11203
CD49b	3782	95.2	131	5	0.1	794
CD49d	4420	95.5	147	16	0.4	1422
CD49e	4378	95.1	235	85	1.9	3211
CD51	4566	95.2	265	128	2.8	2339
CD54	4018	96	124	3	0.1	1085
CD55	3836	95.3	246	29	0.8	15442
CD61	4298	95.6	170	9	0.2	23642
CD62E	3944	95.1	156	20	0.5	7473
CD62L	4068	94.5	124	7	0.2	3984
CD69	2994	94.7	211	17	0.6	31004
CD71	3382	94.8	2895	2302	68.1	4106
CD73	4015	94.6	836	596	14.8	4757
CD80	4058	95.2	158	48	1.2	1638
CD81	4467	95.8	11050	3089	69.2	15869
CD86	3849	94.9	316	129	3.4	6131
CD90	4273	95.4	190	42	1	6482
CD90.2	4201	95.2	104	6	0.1	1449
CD93	4129	95.5	154	21	0.5	7079
CD95	2183	94.5	290	22	1	23639
CD103	3752	95.6	147	20	0.5	8488
CD105	2573	93.9	531	110	4.3	9072
CD117	2742	95.6	146	10	0.4	20683
CD120b	3859	95.3	155	13	0.3	773
CD121a	4211	95.5	147	9	0.2	8728
CD121b	3867	94.5	235	34	0.9	15088
CD122	3034	94.8	199	9	0.3	25478
CD124	3809	95.8	217	12	0.3	23626
CD126	4988	95.7	252	36	0.7	19941

Protein	P1 #Events	P1 % Parent	P1 PE (575/26) -A Mean	P2 #Events	P2 %Parent	P2 PE (575/26) -A Mean
CD127	4236	95.9	425	75	1.8	17669
CD131	4270	95.9	176	17	0.4	11002
CD132	3927	95.5	120	16	0.4	3241
CD133	4377	95.5	172	68	1.6	5428
CD135	1899	94.7	163	25	1.3	2843
CD137	2867	95.7	67	18	0.6	3345
CD138	3688	95.3	187	51	1.4	3620
CD140a	4272	95.5	127	11	0.3	3494
CD140b	4301	95.9	127	20	0.5	2678
CD150	4567	94.9	139	4	0.1	10829
CD152	4620	95.4	347	70	1.5	16101
CD153	4467	95.3	249	86	1.9	6674
CD166	4226	95.2	1038	272	6.4	13867
CD178	4024	95.2	210	25	0.6	14600
CD184	3962	95.4	211	43	1.1	13840
CD201	2538	95.4	5484	666	26.2	20381
CD202	2947	95.7	307	81	2.7	8919
CD212	2709	95.3	86	11	0.4	7440
CD273	4434	95.5	301	49	1.1	18034
CD274	4462	95.8	271	111	2.5	7659
CD284	4629	95.8	222	66	1.4	7447
CD309	3834	95.3	320	37	1	28476
Oct3/4 interna	3820	94.9	271	147	3.8	4247
Sca-1	3101	96.2	2236	1102	35.5	5931
CD45	4369	95.8	273	44	1	15082
CD45	4101	95.1	169	8	0.2	19338
Sca-1	4356	95.2	537	978	22.5	1716
Sca-1	3193	95.6	905	1184	37.1	2047

Table 7

Antigen expression levels Mean fluorescence intensity (MFI)	**% total cell population expressing antigen**	**Antigen**	**Cell lineage(s) marked**
> 5,000 units	< 20%	CD3, CD11a, CD11c, CD13, CD14, CD16/32, CD23, CD28, **CD34, CD38**, CD40, CD41, CD43, CD45, CD48, CD55, CD61, CD62E, CD69, CD86, CD90, CD93, CD103, CD105, CD117, CD121a, CD121b, CD122, CD124, CD126, CD127, CD131, **CD133**, CD150, CD152, CD153, CD166, CD178, CD184, CD202, CD212, CD273, CD274, CD284, CD309, Sca-1	Thymocytes, T, NK, B, granulocytes, monocytes, macrophages, dendritic cells, myeloid, endothelial, neutrophils, mast cells, platelets, haematopoietic precursors, capillary endothelial cells, BM, mast cells, yolk sac subsets, foetal liver subsets, BM (including stroma), cardiomyocytes, thymic epithelium, megakaryocytes, oestrogen-stimulated uterus, neurons, intraepithelial lymphocytes, haematopoietic stem and progenitor cells, neural crest-derived melanocytes, primordial germ cells, **fibroblasts, brain, pancreas, cardiac endothelium, developing oocytes, epidermis, dermis, vaginal basal epithelium, brain,** plasma cells, leukocytes, pro-B, pro-T cells, primitive cells (haematopoietic progenitors, neural, endothelial stem cells), **retina, retinoblastoma**, developing epithelium (apical surface), testis, stem cells, endothelial cells from early development, angiogenic precursor cells, hemangioblasts

Variable	> 20%	CD24, CD29, CD44, CD71, CD81, CD95, CD201	Leukocytes, fibroblasts, endothelial cells, epithelial cells, broad memory cells, proliferating cells, reticulocytes, erythroid precursors, T, B, NK, thymocytes, dendritic cells, neuroblastomas, melanoma, activated lymphocytes, endothelial & stem cell subset
< 5,000 units	< 20%	CD1d, CD2, CD4, CD5, CD8a, CD11b, CD18, CD19, CD25, CD27, CD30, CD31, CD49b, CD49d, CD49e, CD51, CD54, CD62L, CD73, CD80, CD90.2, CD120b, CD132, CD135, CD137, CD138, CD140a, CD140b, OCT-3/4	Leukocytes, intestinal epithelium, thymocytes, T-, pre-T cells, NK cells, B-, pre-B-cells, myeloid cells, erythrocytes, dendritic cells, activated B-, T-cells, monocytes, macrophages, plateletes, granulocytes, endothelial cells, LAK cells, megakaryocytes, osteoblasts, melanoma, resting lymphocytes, pancreatic β cells, TNF-R-expressing cells (broad), haematopoietic progenitors, myeloid & primitive B progenitors, epithelial cells, plasma cells, neurons, fibroblasts, smooth muscle, glial cells, chondrocytes, mouse ES, EC, EG cells, primordial germ cells

Table 8

Growth factor combinations used in cultures of human expanded neurospheres (XS)

	A	B	C	D	E	F	G	H	I
None									+
LIF	+	+	+	+					
FGF-2	+	+	+	+	+	+	+	+	
FGF9	+	+	+	+	+	+	+	+	
SCF	+	+	+	+	+	+	+	+	
BMP4		+		+		+		+	
TGFβ2			+	+			+	+	

TABLE 9

Fold change	Raw XS	pOS + 6 GFs	pOS +no GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
18.94	8.083271	149.43094	137.69762	MYB	c-myb_CDS; Cmyb; c-myb; efg	NM_005375	Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA.	AGCAACATGCTTGGTAATTTGGCATC	ILMN_1788778	GTGTTTGCAACTGGGGAGACAGAAACTGTGGTTGATAGCCAGTCACTGCC
13.6	27.009567	368.9726	411.55597	STRBP	DKFZp434N214; FLJ14223; SPNR; FLJ14984; MGC21529; MGC3405; FLJ11307	NM_018387	Homo sapiens spermatid perinuclear RNA binding protein (STRBP), mRNA.	CTCGGAGTGGCAGACTGACAACTGTGAGACATGCACTTGCTACGAAACAG	ILMN_1699243	CTGCTTTGTTGTAACACAGAGTACTGCCTGGTTCCTGATGCAGTCACTGA
13.16	223.60178	2991.606	3160.0894	PIAS2	SIZ2; MIZ1; miz; ZMIZ4; PIASX-ALPHA; MGC102682; PIASX-BETA	NM_004671	Homo sapiens protein inhibitor of activated STAT, 2 (PIAS2), transcript variant beta, mRNA.	TCACCAGCCCTGAGATTGAGGCCCCATACACCAGTGAAGAGGAGCAGGAG	ILMN_1696151	CAGCCATCTTCTGTAAGGGTGCCCAGTGTGACTTCGGTTGATCCTGCTGC
11.85	130.38095	1541.7976	2045.5476	MTHFD1	MTHFC; MTHFD	NM_005956	Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (MTHFD1), mRNA.			CTTAGTAGGAACGATGAGCACAATGCCTGGACTCCCCACCCGGCCCTGTT
7.891	11.5048275	87.94775	94.547646	ORC1L	HSORC1; ORC1; PARC1	NM_004153	Homo sapiens origin recognition complex, subunit 1-like (yeast) (ORC1L), mRNA.			ACCATGGCCGTGTGTTCTCACCTGGGCTCCTGTCGCCTCCTGCTTGTGGA
7.555	425.65594	2938.7725	2542.1892	CCNA2	CCN1; CCNA	NM_001237	Homo sapiens cyclin A2 (CCNA2), mRNA.			CCTTGTCTCATGGACCTTCACCAGACCTACCTCAAAGCACCACAGCATGC
7.313	121.860115	879.07263	412.32263	PMAIP1	APR; NOXA	NM_021127	Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA.	GGGTACTTGTAGGAATACAATGAGGAGCTTGAATGCCACCTTCTGACATG	ILMN_1696079	CAGCCTAGAGGCAGCTATTTTACCATCTGGTATTTATGGTCTAATTTGTA
7.235	78.25325	562.4393	587.91846	PSMD11	S9; p44.5; MGC3844	NM_002815	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA.	GAAGCCGGTGGGGCCTTCGGAAAGAGAGAGCAGGCTGAAGAGGAACGATA	ILMN_1727332	GGGATTTTGGACCAGGGGGAGGGTGTCCTGATTATTTTCGATGAACCCCC
6.793	261.34763	1780.4309	1733.2686	NUP153	HNUP153; N153	NM_005124	Homo sapiens nucleoporin 153kDa (NUP153), mRNA.	CTTGAGTGTCTTGCTGAGGGTTACTGTATCTAGCAGGTGATGGAGCTTGG	ILMN_1750412	CACTGATTTGACATAGTCTGGCTGTACCCAGGAATGGAGCCTGCACGGTG
6.264	1704.756	10732.556	12162.406	SNRPB	snRNP-B; COD; SNRPB1; SmB/SmB'	NM_003091	Homo sapiens small nuclear ribonucleoprotein polypeptides B and B1 (SNRPB), transcript variant 2, mRNA.			CCACCAAGGCCCTAGACTCATCTTGGCCCTCCTCAGCTCCCTGCCTGTTT
5.948	74.83727	416.01013	386.0393	RFC3	RFC38; MGC5276	NM_002915	Homo sapiens replication factor C (activator 1) 3, 38kDa (RFC3), transcript variant 1, mRNA.			GCCGTCACCCCAAAAAGTTCCCTCCATATCCCTTTGCAGTCAGTTCATCC
5.931	37.361214	208.47678	193.4226	SPAG5	hMAP126; DEEPEST; MAP126	NM_006461	Homo sapiens sperm associated antigen 5 (SPAG5), mRNA.			GCAGGCCCAGGAAGAACAGCATCAGGAAGTCCAGAAGGCAAAAGAAGCAG
5.796	18.767662	102.79762	116.77678	CDC25C	CDC25	NM_001790	Homo sapiens cell division cycle 25 homolog C (S. pombe) (CDC25C), transcript variant 1, mRNA.	GAATTACTACAAAACTCCCATCGCGTCGTGGAGGAGTACTTTGTGGCCCC	ILMN_1809034	GTAGCCCAGCACAGCTTCTTTGTAGCACTCCGAATGGTTTGGACCGTGGC

Fold change	Raw XS	pOS + 6 GFs	pOS +no GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.671	84.88533	395.4768	230.7143	HMGB1	DKFZp686A04236; HMG3; SBP-1; HMG1	NM_002128	Homo sapiens high-mobility group box 1 (HMGB1), mRNA.	TCAAAGCAAGAAGGGAGCGCTGA GGCATGAAGCCCTGGGGAAACTGG CAG	ILMN_1722798	GCTGTGCAAAGGTTGAGAGCTATTGCT GATTAGTTACCACAGTTCTGATG
4.248	160.83095	660.8726	627.5893	RFC5	MGC1155; RFC36	NM_007370	Homo sapiens replication factor C (activator 1) 5, 36.5kDa (RFC5), transcript variant 1, mRNA.			AAACGCACTTGTTTTCATGCAGGAGCGG GGCAAGTAAGGTTGAGCCTGAC
3.943	1914.006	7546.6226	7308.8643	SFRS1	SF2; SF2p33; MGC5228; ASF; SRp30a	NM_001078166	Homo sapiens splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1), transcript variant 2, mRNA.			GGAGCAAAGCGAGGACCTGGAGATAA ACGCTGGAGCAATCTCCTTGGAAG
3.933	4656.456	18040.09	20689.965	SFRS2	PR264; SC-35; SRp30b; SC35; SFRS2A	NM_003016	Homo sapiens splicing factor, arginine/serine-rich 2 (SFRS2), mRNA.	GGGGCCTCAAAAGAGACACCAGCA ACTGGGCCTTGAGAACTTCCATTTT T	ILMN_1699091	CCCGATTGCTCCTGTGTAAAGATGCCTT GTCGTGCAGAAACAAATGGCTG
3.856	408.7893	1510.435	1314.7144	GMNN	Gem; RP3-369A17.3	NM_015895	Homo sapiens geminin, DNA replication inhibitor (GMNN), mRNA.			GAGGATTCTCTAGTGGAAGACTCAGAA ATTGGCACGTGTGCTGAAGGAAC
3.743	312.9226	1212.6143	1435.406	BAT3	G3; D6S52E	NM_080703	Homo sapiens HLA-B associated transcript 3 (BAT3), transcript variant 3, mRNA.			CGAGAGCCTGAGCCGGGACCTGGAGGC ACCAGAGGTTCAGGAGAGCTACA
3.11	149.56429	465.1643	444.64758	ITGB3BP	TAP20; HSU37139; CENPR; CENP-R; NRIF3	NM_014288	Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA.			CAGGACTTCCTCACAAAGCATCACGTCA TCTTGACAGCTATGAATTCCTT
2.949	310.98096	911.8059	1073.7227	GEMIN6	FLJ23459	NM_024775	Homo sapiens gem (nuclear organelle) associated protein 6 (GEMIN6), mRNA.	GGGGATGGTGGTCTTTGCCTTTGCC ACTATCACGCCTCTCATGTTCACAG	ILMN_1673681	AGGGAGACGCTCCAAGGACTCTCTGTG TGGCTGGGGTCCTGACTATAGAC
2.906	304.1476	883.85596	915.2976	KPNA2	SRP1alpha; RCH1; QIP2; IPOA1	NM_002266	Homo sapiens karyopherin alpha 2 (RAG cohort 1, importin alpha 1) (KPNA2), mRNA. XM_001133262 XM_001133265 XM_001133267 XM_001133271			AGCATCCTGTAAATAAACATTCAAGTCC ACCCTTTTCTTGACTTCAAAAA
2.658	2342.406	6170.3643	7377.0146	PRNP	CD230; PrP33-35C; ASCR; PrP27 30; GSS; CJD; PRIP; PrPc; PrP; MGC26679	NM_183079	Homo sapiens prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerstmann-Strausler-Scheinker syndrome, fatal familial insomnia) (PRNP), transcript variant 2, mRNA.	CCTAGGCCTCATAATATTAAGGACT CCTTCAGTGGGCCTTCAACTTCTGG	ILMN_1676905	CAGCCCGCTGGAGCATGAGCTCTGTGT GTACCGAGAACTGGGGTGATGTT
2.607	306.97263	786.57263	652.2101	CHEK1	CHK1	NM_001274	Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA.			GATCGGACCATCGGCTCTGGGGAATCCT GGTGAATATAGTGCTGCTATGT
2.569	117.37262	301.45596	220.89345	STX3	STX3A	NM_004177	Homo sapiens syntaxin 3 (STX3), mRNA.			GGCCGGTCACAATCCAGCACTCAGACA GAGCCAAGGCAATATCCTCTTGC
2.565	24.084644	61.679188	81.160286	FUBP1	FBP; FUBP	NM_003902	Homo sapiens far upstream element (FUSE) binding protein 1 (FUBP1), mRNA.			CACTGGCATGTTTTTCCCCCCTTGCAGTA TAGTGGTAGATTGGAGGATCT
2.539	182.68094	457.98096	468.56012	HSPA14	HSP70-4; HSP70L1; MGC131990	NM_016299	Homo sapiens heat shock 70kDa protein 14 (HSPA14), transcript variant 1, mRNA.			GGACTCCTTTGCCAGCTCGAAGACAACA CACATTGCAAGCCCCTGGAAGC
2.524	80.48529	203.1726	193.96011	CCDC5	FLJ40084; HEI-C; FLJ21094; HsT1461	NM_138443	Homo sapiens coiled-coil domain containing 5 (spindle associated) (CCDC5), mRNA.			TAGTAAAGTGGCGGGAGCCGCAGCTAT GGAGCCGCAGGAGGAGAGAGAAA

Fold change	Raw XS	pOS + 6 GFs	pOS +no GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.46	112.38095	276.43512	263.29346	TCERG1	MGC133200; TAF2S; CA150	NM_006706	Homo sapiens transcription elongation regulator 1 (TCERG1), transcript variant 1, mRNA.	CTTCCGTCTGTGGATAATGGGAGGATCTATGCCCCTCTTTTCAGAGCAGG	ILMN_1707529	CCACCCCCACCTCCCACAGCATCGGAGCCCACGAGACGATCAACAAAATA
2.212	5153.373	11402.705	12874.855	HSP90AB1	HSP90-BETA; HSPC2; HSP90B; FLJ26984; D6S182; HSPCB	NM_007355	Homo sapiens heat shock protein 90kDa alpha (cytosolic), class B member 1 (HSP90AB1), mRNA.	CCAGTGGATCGACATAACCGACGTGCAGCCTGGGAACTACATCCTCAAGG	ILMN_1734950	AATGCTGCAGTTCCTGATGAGATCCCCCCTCTCGAGGGCGATGAGGATGC
2.129	1815.0059	3899.4229	4183.381	HSPE1	HSP10; CPN10; GROES	NM_002157	Homo sapiens heat shock 10kDa protein 1 (chaperonin 10) (HSPE1), mRNA.	GGCCAGACAGAGTTGAATGCAAGCAATCCAGAAGAAGTGTTACAGCTGGC	ILMN_1759084	CCGAGTATTGGTTGAAAGGAGTGCTGCTGAAACTGTAACCAAAGGAGGCA
2.021	390.19763	789.4143	805.756	BXDC2	BRIX; FLJ11100	NM_018321	Homo sapiens brix domain containing 2 (BXDC2), mRNA.			CCACATGATCCCACTGCAGATGTTTTTGTAACACCAGCTGAGGAGAAACC
2.003	598.4143	1196.4435	1251.6143	EXOSC3	RP11-3J10.8; RRP40; MGC723; hRrp40p; MGC15120; p10; Rrp40p; bA3J10.7; CGI-102	NM_016042	Homo sapiens exosome component 3 (EXOSC3), transcript variant 1, mRNA.	GGGGACTGGGGATGTGGGAGGGAGCAGACAGGAGGAATCATGTCAGGCCT	ILMN_1655639	CAGGTCAGTTGAGGCAAAAAACTATGGGTTTTTTCAGGTGAACCTCCCCC
1.994	1063.6226	2120.3977	1893.3726	HSPH1	HSP105B; DKFZp686M05240; HSP105; HSP105A; NY-CO-25; KIAA0201	NM_006644	Homo sapiens heat shock 105kDa/110kDa protein 1 (HSPH1), mRNA.	AAGAGATGCCTGGGCGTCACCATGCCACAGCTACCCACTTGTTGCCACCA	ILMN_1654156	CCTGCCAAGGTAGTTTTCTTGCATTTTGCTCTCCATTCAGCATGTGTGTG
1.991	252.15596	502.88513	533.98926	POP7	0610037N12Rik; RPP20; RPP2	NM_005837	Homo sapiens processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae) (POP7), mRNA.	CACAGGGAGCCAGTGAGGTCCCAGTAGTCTAAAACAGTTCATGTGTTCAC	ILMN_1765480	CCAATACCTCCACCGTGGAGCTTGTTGATGAGCTGGAGCCAGAGACCGAC
1.951	449.8351	877.7018	797.3684	PRMT5	SKB1; HRMT1L5; IBP72; SKB1Hs; JBP1	NM_001039619	Homo sapiens protein arginine methyltransferase 5 (PRMT5), transcript variant 2, mRNA.			GGTGCAGTACATCTATGGGCTGTGATTCCCCTTGCCCATCAGAGAGGAGC
1.946	824.2726	1602.881	1524.1143	STK39	DCHT; PASK; SPAK; DKFZp686K05124	NM_013233	Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA.	GCCCAAGGGAGGTTAAAGTGGTGGCCAAAGGATTTTGTAGTGCCAATGGG	ILMN_1812463	CAAGGAGGTGGGCTCCCAGGATGGTACCATTGCTCTTTCCTAGCTAACCC
1.943	245.96844	482.19763	511.6018	RNMTL1	FLJ10581; HC90	NM_018146	Homo sapiens RNA methyltransferase like 1 (RNMTL1), mRNA.	GATCGGCCCTGAACCCACAAAGGACTCCTCGCTCCTTCAAGCCTCCACCA	ILMN_1729402	TCGCCAAGCACCAGCTATAGGTCACAGCCACATCACTCACAGCTGATCAC
1.936	10038.306	19423.48	21466.848	HSPA8	MGC131511; HSC54; HSPA10; MGC29929; HSC70; HSP71; HSP73; LAP1; HSC71; NIP71	NM_006597	Homo sapiens heat shock 70kDa protein 8 (HSPA8), transcript variant 1, mRNA.	GCAAAACACCACCCAAAGTACCAGAATGGGGAATGGAGTGAGGAACAAGT	ILMN_1763843	CTGGAGAAAGTTTGCAACCCCATCATCACCAAGCTGTACCAGAGTGCAGG
1.928	700.70593	1353.2393	1158.4642	EXOSC8	CIP3; Rrp43p; EAP2; bA421P11.3; RRP43; OIP2; RP11-421P11.3; p9	NM_181503	Homo sapiens exosome component 8 (EXOSC8), mRNA.			GGCAAACTCTGTTGTCTTCACAAACCAGGTGGAAGTGGGCTAACTGGAGC
1.884	349.53513	659.881	745.61426	POP5	HSPC004; RPP20; RPP2	NM_198202	Homo sapiens processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae) (POP5), transcript variant 3, mRNA.	CTCCTGCTGTGAGAACAAGTGGATGTCCCTCTCCCCGCCCTCCTGCTGAA	ILMN_1802872	GCAGAAGCAATGGAGTGAACCTCTGCTCCCCACACAGCTGGCTACACTGC
1.875	48.73645	90.54347	100.376945	ARL4A	ARL4	NM_001037164	Homo sapiens ADP-ribosylation factor-like 4A (ARL4A), transcript variant 3, mRNA.	GTGAAGCTGGCCCACACCTATCAAAGCCCCCTGCTCTACTGTGACCTGGA	ILMN_1668814	TCCTCTGCCATCGCCCACGCCTCCCTGGTGCCAGGGAACAGGTATCAGCG
1.796	91.647675	163.63512	132.34761	LSM6	YDR378C	NM_007080	Homo sapiens LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM6), mRNA.	CAGGGAGCCATGACCCAGGGACCTTCACACTCCCCCATGTTTGTTACTTG	ILMN_1684721	CATCAGTACACAGAAGAGACGGATGTGAAGACACCAAGAGAGCAACGCTT

Fold change	Raw XS	pOS + 6 GFs	pOS +no GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.434	1390.4976	604.15594	552.4643	CDK7	p39MO15; CDKN7; CAK1; STK1	NM_001799	Homo sapiens cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) (CDK7), mRNA.			GGGCCAACACCTGGATGTCAGCTGCCA AGACCAAACTGTCCAGTGGAAAC
0.346	975.53925	336.21844	460.68097	SNRPN	SNURF-SNRPN; HCERN3; SMN; RT-LI; SM-D; SNRNP-N	NM_022805	Homo sapiens small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 2, mRNA.	CTCTGTTCACTCCACTGAATGCAAC CCATATAGTTTCTTGCACAAGGTGC	ILMN_1729617	GGTCCACCTCCCCCAGGAATGCGTCCAC CAAGACCTTAGCATACTGTTGA
0.288	3396.6475	959.64764	896.5851	PXDN	D2S448E; D2S448; VPO; MG50; KIAA0230; PXN; PRG2	NM_012293	Homo sapiens peroxidasin homolog (Drosophila) (PXDN), mRNA. XM_935183 XM_935184 XM_936786 XM_942966 XM_942982 XM_942986 XM_942994 XM_943000	CCGTGGGAGTACAAAAGTGGAGTG TGGCCTGAGTAATGCATTATGGGT GG	ILMN_1705892	GTGCGGTCTGGGCCAGTCACAAGGAAT TGTGTTGTCTAAGCCAAAGGGGG
0.272	693.72266	191.78928	122.20595	SOCS1	SSI-1; CISH1; SSI1; CIS1; JAB; TIP3; SOCS-1	NM_003745	Homo sapiens suppressor of cytokine signaling 1 (SOCS1), mRNA.	TGACTAGAGGCAGAGCCCGAGTAG AAACAGGTCTGAACGGATGGAACT GC	ILMN_1808018	CTCCTGGTGCTCCCTCTGGGTCCCCCTG GTTGTTGTAGCAGCTTAACTGT
0.114	250.81845	31.627804	83.18938	TP53	p53; TRP53; LFS1	NM_000546	Homo sapiens tumor protein p53 (TP53), mRNA.			CTGTGAAATGCTGGCATTTGCACCTACC TCACAGAGTGCATTGTGAGGGT
0.0421	349.69763	17.690117	102.4527	KLF4	GKLF; EZF	NM_004235	Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA.			TGGTGCTTGGTGAGTCTTGGTTCTAAAG GTACCAAACAAGGAAGCCAAAG

TABLE 10

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
33.46367237	12.910944	432.0476	102.84102	103.84102		NM_198391	Homo sapiens fibronectin leucine rich transmembrane protein 3 (FLRT3), transcript variant 2, mRNA.			AGTGCATTGTACGCCCTTTGGCCAGT CTTGTATGTGCCTTGATCCAACGC
26.94332874	10.906446	293.85596	35.249313	36.249313	Hek6; EPHT2; NET; FLJ37986; ELK	NM_004441	Homo sapiens EPH receptor B1 (EPHB1), mRNA.	GACAGTGTGGGGAAGTGTC CCTGTGATCTTGGCAGTGGA ACATGCAAGGC	ILMN_1779794	CAGACAGGAAACAGGTGAGTGGTTTG AATTGGATGCAGTGTGGGCCATCC
25.98898971	10.28856	267.38928	140.40182	141.40182		XM_001132419	PREDICTED: Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA.			ATGGTGCATTCTGTAACCATGGAGTCT TCTGTTTCCTGGGGGAAAGGGGC
23.59394326	44.6775	1054.1184	47.015976	48.015976	SgV; 7B2; P7B2; SGNE1	NM_003020	Homo sapiens secretogranin V (7B2 protein) (SCG5), mRNA.			AGAAGGCTGTACTCAAGAGGAGGAGC TGACACATTTCACTTGGCTGCGTC
15.23240794	98.13929	1494.8977	1370.0643	1371.0643	PTBLP; nPTB; nPTB7; PTB; nPTB8; nPTB6; FLJ34897; MIBP; nPTB5; brPTB	NM_021190	Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), mRNA.	GCTGTGGATTACATCTTGTG TGTGTCAGAGAAACTGCAGA GAACCTGGAG	ILMN_1712360	GTGGCAGTTTTCTAAAACTGACAACCA GGTGGGACCAAAGTTTATGTGCC
13.03930798	6.671953	86.99765	35.163696	36.163696	KIAA1580; NGL1; NGL 1	NM_020929	Homo sapiens leucine rich repeat containing 4C (LRRC4C), mRNA.			TTACGGGAGACACACCCATGGAAAGC CACCTGCCCATGCCTGCTATCGAG
10.91868321	5.6919904	62.14904	22.580227	23.580227	HOVO1	NM_004561	Homo sapiens ovo-like 1(Drosophila) (OVOL1), mRNA.			GCCAAACCCCACCTGAAGCAGAACCA CTTTGGCCTCCCCTGCCCAAAATG
10.27813522	36.069866	370.73096	155.53513	156.53513	STMP; PCANAP1; STAMP1; IPCA1; IPCA 1	NM_152999	Homo sapiens six transmembrane epithelial antigen of the prostate 2 (STEAP2), mRNA.			GTGTTGGCCAGTGAGATGAAGTCTCC TCAAAGGAAGGCAGCATGTGTCCT
10.19431299	6.5091376	66.356186	49.971592	50.971592	vig1; cig33; 2510004L01Rik; cig5	NM_080657	Homo sapiens radical S-adenosyl methionine domain containing 2 (RSAD2), mRNA.			CGCTGGAACCTTGGGCAAGGAAGAAT GTGAGCAAGAGTAGAGAGAGTGCC
10.12510993	7.253701	73.44452	15.674002	16.674002	ABC37; FLJ36852; SUR2; CMD1O	NM_020297	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2B, mRNA.			CGAGTACACACTATTCTGACGGCAGA CCTGGTTATTGTGATGAAGCGAGG
8.991019535	94.28131	847.6851	609.6226	610.6226	MKP3; PYST1	NM_022652	Homo sapiens dual specificity phosphatase 6 (DUSP6), transcript variant 2, mRNA.			GTTGTCGCAAAGGGGATAATCTGGGA AAGACACCAAATCATGGGCTCACT
8.60146103	31.612083	271.9101	81.1853	82.1853	KIAA0032	NM_014606	Homo sapiens hect domain and RLD 3 (HERC3), mRNA.	GAATGGCAGGACCCTGAGTT GATGAGAGACGTGGAAGCA GCCACAGGGCA	ILMN_1729827	TCACCTTCCTCTGTACACTTGGAAATG CCTCTGGCTTGTTGCAGCCCTCC
8.574296039	34.590996	296.59344	363.56427	364.56427	UKp68; FLJ11806; MGC26892; NY-REN-37	NM_024824	Homo sapiens zinc finger CCCH-type containing 14 (ZC3H14), transcript variant 1, mRNA.	GTAGCAGAAGAGGAGGAGT GGCTACACAAACAAGCTGAG GCACGAAGAGC	ILMN_1812523	GATGGTGTCCCCAGCCCCCCAGGATA CATGTCAGATCAAGAGGAGGACAT

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
8.040458133	7.3495235	59.093536	81.198135	82.198135	bA301J7.3; ANX8	NM_001040084	Homo sapiens annexin A8 (ANXA8), mRNA. XM_931361 XM_931369 XM_931374 XM_931375 XM_931378 XM_931383 XM_931388 XM_931391 XM_931399 XM_931404 XM_931411	GGCCATCCCAAAGCTATTCT GGGGGCAACAGAGGTGAAA CTACTGGGCCA	ILMN_1744914	GGCCCTTATGTACCCGCCATACAGATA CGAAGCCAAGGAGCTGCATGACG
7.844616811	24.109648	189.13095	381.7976	382.7976	p53BP2; ASPP2; 53BP2; PPP1R13A; BBP	NM_005426	Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), transcript variant 2, mRNA.	CTCCTGGATAGTTCCAAACA TCTTCCTTGTGGCAGGTTTC CTGGCTGAGC	ILMN_1724487	CATCATGTTGGCCAGGATGGTCTCGA TCTCCTGACCTTGTGATCCGCCTG
7.644057119	11.707075	89.48955	46.772972	47.772972	ABC37; FLJ36852; SUR2; CMD1O	NM_020298	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2A-delta-14, mRNA.	AGACGTTCGGGGCAGGGTG GGAGTGGGTATGGAGATGC AATTTGGGACTG	ILMN_1664896	CCTGGAGGTCTAGATGCGGTTGTCAC TGAAGGTGGGGAGAATTTTAGCGT
7.025617547	40.647335	285.57263	330.38095	331.38095	PRKACN1	NM_006823	Homo sapiens protein kinase (cAMP dependent, catalytic) inhibitor alpha (PKIA), transcript variant 6, mRNA.			CTCCTTGCAATCATGTGGACACCAATC ACAAAAGTAAAGCCCTGGTGTTG
6.812500653	261.34763	1780.4309	1733.2686	1734.2686	HNUP153; N153	NM_005124	Homo sapiens nucleoporin 153kDa (NUP153), mRNA.	CTTGAGTGTCTTGCTGAGGG TTACTGTATCTAGCAGGTGA TGGAGCTTGG	ILMN_1750412	CACTGATTTGACATAGTCTGGCTGTAC CCAGGAATGGAGCCTGCACGGTG
6.501949884	116.73512	759.0059	494.1601	495.1601	FLJ21474; MGC119474; FLJ32076; MGC119477; KIAA1034	NM_015265	Homo sapiens SATB homeobox 2 (SATB2), mRNA.	CTCCCAGCCATCTCCTCTTC CCTAAGGCCTCTGTCTCCAT AGCTCTGGTT	ILMN_1804993	GCAGTGGTTCTAAGTGAATCTGTGGG CATTTTAGCCTGTGGTCTTGCCAG
6.33186362	11.402901	72.201614	229.13097	230.13097	AEP; LGMN1; PRSC1	NM_001008530	Homo sapiens legumain (LGMN), transcript variant 2, mRNA.	CCCAGCAGGGCCAGGTCGG AAGGTGATTGAATACAAAAG CACCAGGGACC	ILMN_1804444	TGGCACAATCTTGGCTCACTGCAACCT CTGCCTCCCGGGTTCAAGCAATT
5.766845981	9.651041	55.656067	68.971115	69.971115	KF; DKFZp686F03259	NM_001010982	Homo sapiens arylformamidase (AFMID), mRNA.	TCCCCACTCTAAGCACTGCC TCCCCTACTCCCCGCATCTT TGGGGAATCG	ILMN_1739605	GGCGTGAGCCACTGCGCCCGGCCAG AATGGCATTATATTTAAATAGTTCA
5.258358801	187.26012	984.6809	764.9143	765.9143	NY-SAR-105; C11orf14	NM_020645	Homo sapiens nuclear receptor interacting protein 3 (NRIP3), mRNA.			GCCAAGACTCCCATGCTGCCTCATTTG TATTCAAGCCTTTAACAGGAGGG
5.108507008	34.76181	177.58095	183.65594	184.65594	PRO2463; KIAA0410	NM_014089	Homo sapiens nucleoporin like 1 (NUPL1), transcript variant 1, mRNA.	ATTACTGTACATAGAGAGAC AGGTGGGCATTTTTGGGCTA CCTGGTTCGT	ILMN_1735930	GTTACTACTGGACCCACTCCTTTCAGC ACCATGCCAAACGCAGCAGCCGT
4.964831302	57.59127	285.93094	193.49762	194.49762	FLJ10545; C6orf139; CENP-Q	NM_018132	Homo sapiens centromere protein Q (CENPQ), mRNA.	CAAGTCTCAAGAGACACTTA ATTCAGATGACTTGGATGCC ACTGACAAAC	ILMN_1720955	GCCAATGGCTTACAGTTTCTGTCTGGT CATCTGGAACTTGAAAAATCCTC
4.863801288	16.468401	80.09903	98.07051	99.07051	RCC1-l; CHC1	NM_001269	Homo sapiens regulator of chromosome condensation 1 (RCC1), transcript variant 3, mRNA.			AGCGCCGGAGTTCCTTGTGGCCGACG TGCACCAAGGACAGGAAGATGTCA
4.622106413	11.189314	51.7182	76.05653	77.05653	H3/c; H3FC; H3.1	NM_003531	Homo sapiens histone cluster 1, H3c (HIST1H3C), mRNA.	GTCCAGATGAGAGCAGAGAT ACAGTGAGAAATTATGTGAT CTGTGTGTTG	ILMN_1742324	TGGGACTCTTCGAAGACACCAATCTGT GCGCTATTCACGCTAAACGCGTC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.283732806	1594.6309	6830.9727	8530.181	8531.181	PEO2; ANT1; PEO3; T1; ANT	NM_001151	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 (SLC25A4), nuclear gene encoding mitochondrial protein, mRNA.			GTGCCTGGTCCAATGTGCTGAGAGGC ATGGGCGGTGCTTTTGTATTGGTG
4.135770497	2150.4392	8893.723	10224.697	10225.697	RDJ2; DNAJ; DJA2; DNJ3; HIRIP4; PRO3015; CPR3	NM_005880	Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 2 (DNAJA2), mRNA.			AAAAAATGGGCTTTGCACACAATGGGT TTGGAGCTGACTGGGAACAATGG
3.978921515	206.03094	819.78094	1007.14764	1008.14764	p40; PRKM2; MAPK2; PRKM1; p38; p41; ERK; ERT1; P42MAPK; p41mapk; ERK2	NM_138957	Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 2, mRNA.			GTAGAACAGGCTCTGGCCCACCCATA TCTGGAGCAGTATTACGACCCGAG
3.866772299	1923.5309	7437.856	3208.2976	3209.2976	MGC48949; RAL	NM_005402	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA.	CACCTGTAATCCGACTGTAA GCTCATCACCTTGGGAGGC CACTGTAGGAG	ILMN_1669201	GCTTTGAGACCTTTCCTCTCCTGGGTA CTGAGGTGCTATGAAGCCAACTG
3.772072238	294.78094	1111.935	1178.1309	1179.1309	Seh1; SEH1A; SEC13L; SEH1B	NM_001013437	Homo sapiens SEH1-like (S. cerevisiae) (SEH1L), transcript variant 1, mRNA.	CCTACTCATCCAAGACCCAG CTTCATTGTCTCCATCTCTG GGAAGCCTGC	ILMN_1717195	ATGCTGACACTGCCAACCTCCAGTATC CTCACCCTCGCAGACGATATCTC
3.762270598	579.65594	2180.8225	2545.3892	2546.3892	C5orf6	NM_016605	Homo sapiens family with sequence similarity 53, member C (FAM53C), mRNA.			GCCCTTCACTCCCACCTGCTGCCAAA GTCCCTGTGCTAATGGGATTACAA
3.761254149	163.11429	613.5143	584.7726	585.7726	FLJ14724; FLJ10430; NEOT2; FLJ90456	NM_018092	Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 2 (NETO2), mRNA.	GGCAATACCTGATGTCAGTC ACAGGCATCCAACTCATGAC AAGAGATACC	ILMN_1811050	GTTCACATCAGTGGCTTTGTATGCAAA TATGCTGTGTTGGACCTGGACGC
3.3885441	40.57228	137.48096	104.75186	105.75186	MGC130009; SPR-1; HF1B; MGC130008	NM_003112	Homo sapiens Sp4 transcription factor (SP4), mRNA.	AATGCACCTCATTCTTCCCT GGCCTCTTTCCCACCCACAG CCCCCAGAGG	ILMN_1732323	ATGCATGTCACTAAGTTGTCATCCCAC ATAAATTGATGTGCAGCATAGGG
3.373783841	23.652443	79.79823	72.15463	73.15463	ANKS4A; SANS; FLJ33924	NM_173477	Homo sapiens Usher syndrome 1G (autosomal recessive) (USH1G), mRNA.	TGGATAGTTTTTTGCCCTATT GAATCATTCAGTTGGTGTAC AAACATGCC	ILMN_1799843	TGCCTGCCACCGCCATCTGGAGCCCA CCACAGCTCTTCTCCCTGTTCTCT
3.309017321	25.25606	83.57274	22.341427	23.341427	FLJ31718; ABLL; ARG; FLJ22224; FLJ41441	NM_005158	Homo sapiens v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene) (ABL2), transcript variant a, mRNA.			CACTTTGCTGCCTGTGCACTGAGGCC TCAGAATCTGCTCTACCCGACTTA
3.22653257	716.98926	2313.3892	2875.356	2876.356	M11S1; p137GPI; GPIP137; GPIAP1; caprin-1	NM_005898	Homo sapiens cell cycle associated protein 1 (CAPRIN1), transcript variant 1, mRNA.	ACATGCCCCGAGTGCGGAA GAGGATTTACAAGGAGCTAT GTGAGTGCCGG	ILMN_1675501	CGGGGCCCTGCCAATGGATTCAGAGG AGGATATGATGGTTACCGCCCTTC
2.907064608	247.11845	718.3893	282.2393	283.2393	FLJ33845; KIAA1720	NM_030645	Homo sapiens SH3-binding domain protein 5-like (SH3BP5L), mRNA.	GAAACCCCTGTCCCCAGTCA GAGATAACATCCAACTAACT CCAGAAGCGG	ILMN_1673721	AGATCTGGGTGCCTTGGGAGAACCAG TCCTTCCTTTTGACCCACCCCAGG
2.883793461	1257.1685	3625.4143	4412.081	4413.081	DKFZp761N202	NM_001032293	Homo sapiens zinc finger protein 207 (ZNF207), transcript variant 2, mRNA.	GCACCACTGCGTCAATTCCC CAGGCTCCTATTTCTGTCAC TGCCAAGTTG	ILMN_1737503	CCCAGCTGTGGACCACTGCCTGAAAG GTTTGTACAGATGCATGCCACAGT
2.867175551	178.42679	511.58093	497.9018	498.9018	MGC13170	NM_199250	Homo sapiens chromosome 19 open reading frame 48 (C19orf48), mRNA.			CCACACACCCAGGAGAAGGTGGATAA GTGGGCTACCAAGGGCTTCCTGCA

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.766789751	29.96322	82.90193	69.49157	70.49157	TPC; MCPHA; DNC; MUP1	NM_021734	Homo sapiens solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 (SLC25A19), nuclear gene encoding mitochondrial protein, mRNA.			ACACTCCTGGTCTGGATGGGGCTGCT GCTTGAGTGCAGAGGGCTGCGGTA
2.757929189	26.5355	73.18303	32.136074	33.136074	MGC120612; ARL2L1; DKFZp761H079; MGC120611; DKFZp686M2074; DKFZp686L2472; DKFZp686E2075	NM_144996	Homo sapiens ADP-ribosylation factor-like 13B (ARL13B), transcript variant 2, mRNA.	GAGCGGGCAAAGGAAATGT GACAAGGAGAAGAAAGAAGA CACACTTGGGC	ILMN_1680379	CTTGGAGTTTGTACATGGGACTTAGCA ACCACACTGAGTGAGGTAAAAGC
2.724976168	1270.9644	3463.3477	3396.0977	3397.0977	DAR; ATP2B; MGC45367; DD; SERCA2	NM_170665	Homo sapiens ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2), transcript variant 1, mRNA.			GCTGAACGTGACCCAGTGGCTGATGG TGCTGAAAATCTCCTTGCCCGTGA
2.705198935	9985.873	27013.773	29913.398	29914.398	MGC110998; HNRPE2; hnRNP-E2	NM_005016	Homo sapiens poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA.			CCACCCATGATCCATCTGTGTAGTTTC TGAACAGTCAGCGATTCCAGGTT
2.694008456	58.268852	156.97678	225.90594	226.90594	ED3; EDA3	NM_145861	Homo sapiens EDAR-associated death domain (EDARADD), transcript variant A, mRNA.			GCAACATTTGTAGGGGCCGCTGCTAG TTAGCTACCCTTGCCCACCGCCGT
2.690585215	213.33095	573.9851	480.01013	481.01013	FLJ25291	NM_033211	Homo sapiens chromosome 5 open reading frame 30 (C5orf30), mRNA.	CGGAGCACGGAAGCACACA CAAGCTCTTTATGAATTCTG CTCTCCATCAG	ILMN_1810593	AGGAAACACAACTGGTTACCTATGAGA CCTGTTCTGTCCGTGTGCCTACG
2.667056556	29.329708	78.22399	54.512367	55.512367	MGC125642; SG2NA	NM_003162	Homo sapiens striatin, calmodulin binding protein (STRN), mRNA.			ATAGCCCAAAGAGTATGGTTAACTTCA CGCAGCTGCTTTTGCAGAAGCAC
2.568366967	117.37262	301.45596	220.89345	221.89345	STX3A	NM_004177	Homo sapiens syntaxin 3 (STX3), mRNA.			GGCCGGTCACAATCCAGCACTCAGAC AGAGCCAAGGCAATATCCTCTTGC
2.557956172	42.49556	108.70178	124.77261	125.77261		NM_022353	Homo sapiens O-sialoglycoprotein endopeptidase-like 1 (OSGEPL1), mRNA.	TGTACTGTGCTAGTGACTGG AGGCCCTGCTACTGCAAATA TAAAACCTAA	ILMN_1666904	CGTGCTGGCTTGGGCATTTTACATGA CATAGAAGGCATCCGCTATGAACC
2.547248747	71.61555	182.42262	113.04346	114.04346	Gpnat1; GNPNAT; FLJ10607	NM_198066	Homo sapiens glucosamine-phosphate N-acetyltransferase 1 (GNPNAT1), mRNA.	CCACTAGCCCCTTACCCAGA GTGGCCCACAGGAAACAGC CTGCACCATTT	ILMN_1699599	GGTGATCTTAGATTTGATGAAGCACAG TATGCAGGTAGGCCTAATGGGGG
2.545708766	187.31429	476.84763	593.8976	594.8976	MGC3394; USP16; USP23	NM_012475	Homo sapiens ubiquitin specific peptidase 21 (USP21), transcript variant 1, mRNA.	ACATGTCCTGGGTGACATGG GATGTGACTTTCGGGTGTCG GGGCAGCATG	ILMN_1717702	CGGAGAATGCCCCAGTGTGTGACCGA TGTCGGCAGAAAACTCGAAGTACC
2.538535884	49.395973	125.39345	67.78848	68.78848	ZNF372	NM_016353	Homo sapiens zinc finger, DHHC-type containing 2 (ZDHHC2), mRNA.	TGTCAGGACGCGGAAAGCA GGGAGGCAAGGCCCGCGCT AAGGCCAAGTCG	ILMN_1747589	GGACAGGATTCGATTAAGTATTCCCTC TTGTCAAACTGGAAGCTAGGGGA
2.524344511	80.48529	203.1726	193.96011	194.96011	FLJ40084; HEI-C; FLJ21094; HsT1461	NM_138443	Homo sapiens coiled-coil domain containing 5 (spindle associated) (CCDC5), mRNA.			TAGTAAAGTGGCGGGAGCCGCAGCTA TGGAGCCGCAGGAGGAGAGAGAAA
2.479860984	409.16846	1014.6809	1091.781	1092.781	Npn3; SRX1; C20orf139; YKL086W; dJ850E9.2	NM_080725	Homo sapiens sulfiredoxin 1 homolog (S. cerevisiae) (SRXN1), mRNA.	GGCCAAAGGAGCAGCTGTG GAAGTGAACCTAAACACAAT GACAAGTGTGG	ILMN_1721926	GGCAGGCCTTGTTCTCACTGCCCTCT AAGGGAACTTGGTCACTCGGCACT

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.475289645	188.62679	466.90594	332.88928	333.88928	FRMD4; KIAA1294; bA295P9.4; FLJ10210	NM_018027	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA.	GGCAGGAACCACCTTCCTCC AAGATCCTCACTATGGCAAC TGTGGACCCC	ILMN_1762170	CCCCATCCAGGTGCTATCAGATGACC AGTTACTGCTTAGTTAACTAGGTG
2.475199096	63.72792	157.73929	148.22263	149.22263	DKFZP547N043; PRO4323; DDDL1880; dJ876B10.3; RP5-876B10.3	NM_001010984	Homo sapiens chromosome 1 open reading frame 124 (C1orf124), transcript variant 2, mRNA.	TACCAGACTCCGACACAATG GGCCACCACCAGTGTGACA GCAGGACATCC	ILMN_1804419	GGGTGCTACATTCACTCTTGCCTTAGG TATACTGTAACCCAGGTTCTGCC
2.451653597	761.8726	1867.8477	1582.4226	1583.4226	MGC3331; MSSP-1; MSSP; YC1; SCR2; MSSP-3; MGC15146; MSSP-2	NM_002897	Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA.			TAGTCCGACTTCACCCATGGTGTTCTG TGCTTGCAGTGCGAGTGTTGCTG
2.43551012	127.45178	310.4101	218.01428	219.01428	MGC22671; bA355M14.1; POP3	NM_022361	Homo sapiens popeye domain containing 3 (POPDC3), mRNA.	TCTTAACCAGCTGAGGGAGC TTGTACAACACCTTATGTATG CTGGTTGGG	ILMN_1805148	CAGCCTGAGGGTGGGTTGCTACTGTC CACATAGGCATTTCCGGAATTCAC
2.4025985	54.894432	131.88928	112.2518	113.2518	BGGI; GGTI	NM_005023	Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B), mRNA.			GTAGGGGGATTTGCCAAGTGGCCAGA CAGTCATCCAGATGCTTTGCATGC
2.400318237	40.988365	98.38512	98.49486	99.49486	FLJ10846	NM_018241	Homo sapiens transmembrane protein 34 (TMEM34), mRNA.	GTAGAACAGGCTCTGGCCCA CCCATATCTGGAGCAGTATT ACGACCCGAG	ILMN_1767320	ACCTAGGATGGGGTTTCTCTAATTGCT AATCACAACCCCACTGGGTCATG
2.393387444	1211.5768	2899.7727	3621.2559	3622.2559	ALR; ALDR1; MGC1380; MGC12529	NM_006066	Homo sapiens aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1), transcript variant 1, mRNA.			ATCTTGCTCAGGTGGCAGGTCCAGCG GAAAGTGATCTGCATCCCCAAAAG
2.384570378	403.44345	962.0393	1094.1726	1095.1726	HLC14-06-P; dJ794I6.3; ITPase; C20orf37	NM_033453	Homo sapiens inosine triphosphatase (nucleoside triphosphate pyrophosphatase) (ITPA), transcript variant 1, mRNA.			AGAGGCTGCCAGGACTTTGGCTGGGA CCCCTGCTTTCAGCCTGATGGATA
2.347559778	64.37612	151.12679	94.044495	95.044495	MGC163279; IRE1; IRE1P; FLJ30999; MGC163277	NM_152461	Homo sapiens endoplasmic reticulum to nucleus signalling 1 (ERN1), transcript variant 2, mRNA.			ACTGACATGTGTGTGCCTGAGTGCCA GCCACCGTGTGAACTCTTTGGAGG
2.3319628	273.35596	637.45593	452.7851	453.7851	MGC2599	NM_001014380	Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), transcript variant 2, mRNA.	AACGCCCCGGGCAAAGGGT CTTTTGCAGCTTTTGCAGAC GGGCAAGAAGC	ILMN_1753550	TCATATGATGGTACGGCAGCAGGGAG TGGCCCCCAGTTAACATGGCTGTG
2.298844153	327.18512	752.1476	472.37262	473.37262	HDGF2; CGI-142	NM_016073	Homo sapiens hepatoma-derived growth factor, related protein 3 (HDGFRP3), mRNA.	AGGCAAACACAACTCTTGAC TGCCCTCCCACCCTCCTACC TGTTCAGTAC	ILMN_1764617	TAAAGCTGGAATCAGCAACAGCCCTAT GGGAAACCAGACAAAGCATTGAC
2.284190884	45.755493	104.51428	86.25282	87.25282	YGL047W; GLT28D1; MDS031	NM_018466	Homo sapiens asparagine-linked glycosylation 13 homolog (S. cerevisiae) (ALG13), mRNA.			AGGACTTACTATTGTTTTTTAAGGATCT CCTCTCACAGTGGTAATGAAAC
2.267744374	130.13928	295.12262	254.40594	255.40594	MGC102835; HNRNPA1	NM_031157	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRNPA1), transcript variant 2, mRNA.			TTATGGAGGAGGCGGCCCTGGTTACT CTGGAGGAAGCAGAGGCTATGGAA
2.258477032	41.58118	93.91014	76.44257	77.44257	FLJ12673; PRMT9; UG063H01; MGC44383; FBX11; VIT1	NM_018693	Homo sapiens F-box protein 11 (FBXO11), transcript variant 2, mRNA.	TCCCCCCAGTCATATCTCAT GATTTCCACAGTTGTTGTATT GGTGTGGAG	ILMN_1808636	CAATACTTTTCCTTTTGTAGCCACTTTG AGTCTGCAGTTGTCAGTAAGCC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.226506517	106.15178	236.34763	171.78094	172.78094		NM_144710	Homo sapiens septin 10 (SEPT10), transcript variant 1, mRNA.	CGCCTGGCCTATTGAAGGTT TTTAATCTTCAGAGTTTCGAC TTTATCAAC	ILMN_1658713	GCACTGACTTGACCCCACAAGTGGAA AATTCCCCACCCGACACCTTTGCT
2.223727465	164.94345	366.78928	256.31427	257.31427	MGC99481	NM_138353	Homo sapiens hypothetical protein BC002926 (LOC90379), mRNA.			AGGGCAGCCTCTGTTGGCCTGAGGGT CTGGACGCTTTTTATTTATGCCTA
2.157742534	217.96011	470.3018	481.2976	482.2976	GSE1	NM_014615	Homo sapiens KIAA0182 (KIAA0182), mRNA.	GCTCAAGGAAAGATAAAGCT GGGCGGAAGGAGGTGTGCG TGGCTTCTGGG	ILMN_1700681	CCGGTGCCTCGGTCACTCTGGGGGCA GTTTAGATGCTGTGAAATTAAACC
2.153210771	31.19235	67.163704	39.281055	40.281055	MGC21830	NM_182563	Homo sapiens chromosome 16 open reading frame 79 (C16orf79), mRNA.	TTTTCTATCAACAATTGGGAA ATGCTTATACATGTAAATATG AAAATGTT	ILMN_1673815	AGCAGAGGGGCCCCGGAGACAGCGG CTGATTTATCTCTGCATCGACATCT
2.144857526	110.555954	237.12677	228.32262	229.32262	RP4-796F18.1; TERE1	NM_013319	Homo sapiens UbiA prenyltransferase domain containing 1 (UBIAD1), mRNA.	AAGCTGGGTTGTGTACTTTC TGGTGACACTCCTGGGCTCC TCCCCATCCC	ILMN_1793033	GGAATGTGATTTGGCAGTCAGGGTAC TAAGCATGGGTGGGAACTCCTGCC
2.134165271	196.23096	418.7893	206.35178	207.35178	CDHH	NM_001257	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA.	CAGTGGAGAACCAAGCCCC ATGGCCTCAGAATTTCCCCC CAGTTCCCCAA	ILMN_1700770	AGTGACAGCTTGTGGCTTTTTATTAGA GCTCGCCACGAACTAGGGTAAGG
2.094395317	142.86429	299.2143	304.97263	305.97263	MGC150539; FLJ21869	NM_001071775	Homo sapiens similar to RIKEN cDNA 2410129H14 (LOC440145), mRNA.			CCAGAAGCTTTATCATCGGTTATTAAG GAGCTTCGCAAGGCTACTGAAGC
2.092095105	66.35977	138.83095	71.15883	72.15883	COD1; CORDX1; XLRP3; RP15; CRD; orf15; PCDX; RP3	NM_001023582	Homo sapiens retinitis pigmentosa GTPase regulator (RPGR), transcript variant B, mRNA.	CTGAAACTCCCTTGTGTTCC TTCTGTGAAGAAGCCCTGTT CTCGTTGCCC	ILMN_1753613	GATGCCGACCAGAACCACATGAGTCA GAATCATCAGAATATCCCACCAAC
2.075133114	127.13928	263.83093	363.34763	364.34763	FLJ16691	NM_002859	Homo sapiens paxillin (PXN), mRNA.	AGCGAGGCACCCTTACTGG CTTACCTCCTCATGGCAGCC TACTCTCCTTG	ILMN_1725560	ATGACCAGAAAGGGGCCACCGGGGTC TAATGGTGACAGTCCAAACCACTC
2.074732756	32.976276	68.41696	48.57859	49.57859	MGC45293	NM_198088	Homo sapiens zinc finger protein 200 (ZNF200), transcript variant 3, mRNA.			ACTGTACCCGGCATGAGAAAACCCAC TCAGCCTGTAAGACCCGAAAGCAG
2.050050516	41.88808	85.87268	104.83512	105.83512	PZF; FKSG11; ZNF757	NM_053023	Homo sapiens zinc finger protein 91 homolog (mouse) (ZFP91), mRNA.	CATGTATCGGAACTTAGAAC TGGTGGGCGCGGTGGCTCT TGCCTGTAATC	ILMN_1661519	GAAGAAGGACAGCGTAGTGGCACACA AGGCAAAAAGCCACCCTGAGGTGC
2.038574951	45.404335	92.56014	75.18869	76.18869	MRL3; RPML3	NM_007208	Homo sapiens mitochondrial ribosomal protein L3 (MRPL3), nuclear gene encoding mitochondrial protein, mRNA.			GTGAAATAGTGGTTGTGGAACAGTAG AAAACCATATGGGGACTATAGTGC
2.010135763	48.944515	98.38512	102.126785	103.126785	FLJ25078	NM_152485	Homo sapiens chromosome 1 open reading frame 74 (C1orf74), mRNA.	CACTCTATGGGAAACTCTTC AGCACCTACCTGCGCCCCC CACACACCTCT	ILMN_1674759	TATACCTGCTCTATGTGGGTGCTGCAT GCTAGGAAAGTAGGGCTGGGGGC
1.991629516	131.62679	262.1518	182.15594	183.15594	DKFZp686M1969; FLJ90492; DKFZp686O2342; DKFZp686O22167; DKFZp686C0968; SMILE	NM_181783	Homo sapiens transmembrane and tetratricopeptide repeat containing 3 (TMTC3), mRNA.	TTCCATACTGCAAGGGCAAC GTCATACCCCACACCTACTG TGACCACATG	ILMN_1770442	CTGATACCAGTGGGAGTTGGTCTTGA TCTAGGAGATTCTGTTAAGCATCC
1.990849952	164.5893	327.6726	246.74762	247.74762	MGC75174; DKFZp686L13217; MGC117277	NM_032239	Homo sapiens La ribonucleoprotein domain family, member 2 (LARP2), transcript variant 3, mRNA.	GGAAAGGCTGCTCTTGCTCT CCCTCCCAGGGCTTGAGGC TCCCTATACTT	ILMN_1697081	TTCTCTGCAGGGTAGGTAAGATAGGT CAGTCAAGTTGGTAATGCCTGTCC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.96831009	246.58511	485.35596	362.12262	363.12262	CAP2; PI8	NM_002640	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), transcript variant 1, mRNA.	GCTGCTGCCCACACCGCGT CGACGCCTTCACTGCCATCC CCGCTGTCCTT	ILMN_1738473	AGGAGCTGAGCATGGTCATTCTGCTT CCCGATGACAACACGGACCTCGCC
1.967603512	1415.4559	2785.056	2346.2144	2347.2144	NAP57; NOLA4; XAP101; dyskerin; DKC	NM_001363	Homo sapiens dyskeratosis congenita 1, dyskerin (DKC1), mRNA.	GGGGAGGAAGACACCTCAT ATCAGCCCTCAAAGGCTCCC CTCACTGTCTC	ILMN_1686587	GTACAGTGCTCACCTAAATCCATCTGA CTACTTGTTCCTGTGCCCTCTTG
1.960293978	541.2101	1060.9309	1005.88513	1006.88513	KIAA0507; CGI-115; MGC22291	NM_016052	Homo sapiens ribosomal RNA processing 15 homolog (S. cerevisiae) (RRP15), mRNA.	GCTAATAGCCTAACTGCAGA GGAACTGAGTGGATGGGGT AGCTGCTGTAT	ILMN_1790008	CTGCTTGACCAGCGAGATGTGCATTTT GCCAGGATCATATTGGTCATGTC
1.95255194	69.454895	135.61429	132.41846	133.41846	SPD; BDE; HOX4I; BDSD	NM_000523	Homo sapiens homeobox D13 (HOXD13), mRNA.	GTGCGACCTCGATCTGTCCC AAGCATTCATGTTCCCTCAC CAGCTGTAGT	ILMN_1757336	CCAGGTTGGCCACAGACAGCTTAGAA GCCATTCGGTTGTCTCCAAAAGGC
1.951163437	449.8351	877.7018	797.3684	798.3684	SKB1; HRMT1L5; IBP72; SKB1Hs; JBP1	NM_001039619	Homo sapiens protein arginine methyltransferase 5 (PRMT5), transcript variant 2, mRNA.			GGTGCAGTACATCTATGGGCTGTGAT TCCCCTTGCCCATCAGAGAGGAGC
1.936256195	922.0143	1785.2559	2437.2893	2438.2893	HP10481	NM_014254	Homo sapiens transmembrane protein 5 (TMEM5), mRNA.			GAGGCTTGCTCCTATGGCTCCATTCCT GTGGTGGAAGACGTGATGACAGC
1.931251388	700.70593	1353.2393	1158.4642	1159.4642	CIP3; Rrp43p; EAP2; bA421P11.3; RRP43; OIP2; RP11-421P11.3; p9	NM_181503	Homo sapiens exosome component 8 (EXOSC8), mRNA.			GGCAAACTCTGTTGTCTTCACAAACCA GGTGGAAGTGGGCTAACTGGAGC
1.919072538	73.619385	141.28094	88.88519	89.88519	MGC29949; HSPK36	NM_152720	Homo sapiens NIMA (never in mitosis gene a)-related kinase 3 (NEK3), transcript variant 2, mRNA.			CAAGGGAGAAGGTATAGTGGAATGAG TGTGAGCATCGGGCTTTGCAGTCC
1.915002084	118.84762	227.59344	141.51428	142.51428	ACATN; AT-1; AT1	NM_004733	Homo sapiens solute carrier family 33 (acetyl-CoA transporter), member 1 (SLC33A1), mRNA.			CTGACCAAAGCATGTTTTAAGCTGCAA TGCAGTAGTCACGGGTGGTAACC
1.90775658	66.10607	126.11429	81.873	82.873	FLJ23251Uba5; Uba5; FLJ23251	NM_198329	Homo sapiens ubiquitin-activating enzyme E1-domain containing 1 (UBE1DC1), transcript variant 2, mRNA.	GTGATTGGGAATGGATGGG GGACAGTGAGGAGGACACA CCAGCCCATTAG	ILMN_1798690	GTTTGGAGACTCATAAATACCATGCAG GTGTAACCACTGCCAATAGGCTG
1.884910481	4094.1895	7717.1807	7593.0645	7594.0645	MGC117317; SMG	NM_003096	Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA.	ACCCCCGCGCTCCACCTGC AGTGTTTCTGCCCTGTAAAT AGGACCAGTCT	ILMN_1659599	GGCTGTTCAGCAGAGAAACCCATGTC CTCTCTCCATAGGGCCTGTTTTAC
1.881696537	533.70593	1004.2726	951.4435	952.4435	KIAA1646; dA59H18.3; hCERK; dA59H18.2; FLJ23239; MGC131878; LK4; FLJ21430; DKFZp434E0211	NM_022766	Homo sapiens ceramide kinase (CERK), transcript variant 1, mRNA.	TGCATTTGTTTATGTAATTTC AGGAGGAATACTGAACATCT GAGTCCTGG	ILMN_1791466	GCTCTGATTTCCGGGGCAGCCTTTCA GATGCGGCAGACATACAACACCTG
1.872783601	108.09762	202.44345	193.83511	194.83511	RA-GEF-2; DKFZp686I15116; DKFZp667N084; PDZGEF2; PDZ-GEF2; KIA001LB	NM_016340	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 6 (RAPGEF6), mRNA.	CTCTCGCTTGCTCTCTCTCA CCATGTGACACACTGGCTCC CCTTCACCTT	ILMN_1718309	TTCTGCAGCATGCCTCCCCCACATCTC ATAGCACCAGGTTGTGTCTGACC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.872208993	48.69568	91.16849	113.97262	114.97262	MGC126288	NM_005708	Homo sapiens glypican 6 (GPC6), mRNA.	GAGAGAGACCCGTTTCCTTT CAGGGATGTGGACAGGGTA AGGGCAGCAAG	ILMN_1787922	ACCGGGTGCCAGACTGAACTGCTTCC TCTTTCCTTCAGCTATCTGTGGGG
1.867771311	5084.048	9495.839	6432.231	6433.231	P28; GSTTLp28; DKFZp686H13163	NM_004832	Homo sapiens glutathione S-transferase omega 1 (GSTO1), mRNA.	GGGACTTCCCTTGACTGGGT TGTGTTTCTTTTCCTGCCTCA GCCCAGCTC	ILMN_1796288	GACTGGCAAGGTTTCCTAGAGCTCTA CTTACAGAACAGCCCTGAGGCCTG
1.813808153	604.73926	1096.881	1164.2726	1165.2726	MBDIN; ATPBD1A; NTPBP	NM_007266	Homo sapiens XPA binding protein 1, GTPase (XAB1), mRNA.	GCGGTGTCAGCCTTTTCTTC AGAGCATTTGTTTGACTGAC TTCCAAAGCA	ILMN_1682910	GCCTCTACTCCCCCAGCTTCTTGCTCT TGACCCTGCACTGTAAGTTGCCC
1.792543021	123.78928	221.89761	162.55594	163.55594	CG-8; FLJ20457	NM_017832	Homo sapiens chromosome 9 open reading frame 6 (C9orf6), mRNA.	TGCAAGGGACAGGGGGCCT GACTACCCAGTCTTTGACTT GTATCCTCTCC	ILMN_1749006	CTTCTGTCCCCCTTATGCCAACAAGAT GGCCTTCCCCTCTGAAACAAAGT
1.790955641	5437.798	9738.855	9947.848	9948.848	PP1; IOPPP; MGC111556; PP; SID6 8061	NM_021129	Homo sapiens pyrophosphatase (inorganic) 1 (PPA1), mRNA.	GCCTTTATGGGTGATCCAGG GAAGATTGGTTTTGCTGATC AGATTCCACC	ILMN_1745529	GAGAGCCCCTTCAAGTGTGATCCTGA TGCTGCCAGAGCCATTGTGGATGC
1.763483907	1092.3392	1926.3226	1893.5892	1894.5892	Sth1p; SNF2L2; SWI2; FLJ36757; SNF2; BAF190; MGC74511; BRM; hBRM; SNF2LA; hSNF2a	NM_003070	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transcript variant 1, mRNA.			CTTTGCTTTCTTTGCACAATGTCTTTG GTTGCAAGTCATAAGCCTGAGGC
1.748632897	1028.9644	1799.281	1572.7935	1573.7935		NM_020814	Homo sapiens membrane-associated ring finger (C3HC4) 4 (MARCH4), mRNA.			CCTGCCAGGGAAGGCCACTGGGTGTT CACCTGCAAAGTTTCTGGTTGTCA
1.74507554	48.55436	84.731026	47.989887	48.989887	ZNF-U69274; FLJ13426; MGC133303	NM_014415	Homo sapiens zinc finger and BTB domain containing 11 (ZBTB11), mRNA.	CAGATACAACTACGGGGTTG TGGAGAGCTTCACAGTGCAG CGGCGAGTCC	ILMN_1752592	CAGCTGTGTGGCTGACTTTCAATTTTA AGACGTGAATTGACATACAGCCC
1.742671384	86.19772	150.2143	185.10596	186.10596	FLJ32746	NM_001082968	Homo sapiens target of myb1-like 2 (chicken) (TOM1L2), transcript variant 3, mRNA.	AGGGACCGCTTGGAGCAGT TAGAAAGGAAGCGGGAGCG GGAGCGCAAGAT	ILMN_1711078	TGGCACGCTGCTGAGACGACACTACC AATAAACCAAACTGCCACGCACAC
1.720888068	73.981735	127.314285	100.72284	101.72284	MGC:3310; RNF85	NM_004620	Homo sapiens TNF receptor-associated factor 6 (TRAF6), transcript variant 2, mRNA.			TATTAGTGCGCTGTGAGGTCTCCACC CGCTTTGACATGGGTAGCCTTCGG
1.707359521	57.62902	98.393456	90.772705	91.772705	KIAA1454; Zfp291; FLJ31533; ZNF291; MSTP063; FLJ31953	NM_020843	Homo sapiens S phase cyclin A-associated protein in the ER (SCAPER), mRNA.			CCAAGACTATCTTGAGCTGGCTAACAG ATTTCCTCAGCAGGCCTGGGAAG
1.700776303	89.585144	152.36429	149.66846	150.66846	FLJ25412; PDZK8; bA129M16.2; FLJ34427	NM_173791	Homo sapiens PDZ domain containing 8 (PDZD8), mRNA.			CCTCGTATGCACTCTGGCCTGCTTCTC CAGTTACTTGCTTGTGTAAGAAC
1.697950579	127.468445	216.43512	153.05594	154.05594	MGC10084; 9830169G11Rik	NM_153702	Homo sapiens ELMO/CED-12 domain containing 2 (ELMOD2), mRNA.			CCCCTCTGTAGAGTCATGCGAACTACA GTTTGGAACTTGGGACTTAGCCC
1.685436394	80.50197	135.68095	109.73095	110.73095		NM_206840	Homo sapiens nuclear VCP-like (NVL), transcript variant 2, mRNA.	GCTGGGCACTATGCTAAGCA CTTTGGGAGCAAGAACCTCC TACCTTCCAG	ILMN_1690887	CCATCAAGCCGGCAGAGAATCCCCCA CACGCTCTGAAGGACCCACTTTCA
1.670884956	183.43929	306.50595	297.05594	298.05594	MGC45714; C17orf32	NM_152464	Homo sapiens transmembrane protein 199 (TMEM199), mRNA.	CCGCCTCATTTGCGCCTTGC AGCACTGCTGGACCAGGTTA CAAGATGTTC	ILMN_1723398	GAGAAAGATGGGTTGCTAGAGGATGG TAGAACTGGAAGCAAGGCAGCTAC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.667052451	6136.8477	10230.447	10951.897	10952.897	EEF1B; EF1B; EEF1B1	NM_001959	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA.			GTGTCCAGCCCACCGCCTGCCGACTT GTGTCATGCCCTACGTTGGTATAA
1.660709729	1879.8977	3121.9644	2067.4644	2068.4644	GIG10; MIG18; CIN85	NM_031892	Homo sapiens SH3-domain kinase binding protein 1 (SH3KBP1), transcript variant 1, mRNA.			CTTTTGCTTCAGGCTAAGAGCTGCCTC GCTCTTTGTCCCCCCATTAGGAT
1.658087645	5699.873	9450.889	6218.006	6219.006	CL-20; EMP-1; TMP	NM_001423	Homo sapiens epithelial membrane protein 1 (EMP1), mRNA.			GAGGGCAAGCCACCAAATTACCTAGG CTGAGGTTAGAGAGATTGGCCAGC
1.65688212	234.19345	388.03094	314.5976	315.5976		NM_181575	Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA.	TCCCCCGGCGGAGCCAACC CTCACTGATGGGAGCCCTG GGGTCATCTGTG	ILMN_1658427	TACGCAAGAAGGAGATTCACAGAGAG ACGAGCCCAGGAGGCTGACTGAGC
1.65582243	47.22109	78.18974	32.8719	33.8719	FLJ12552	NM_022832	Homo sapiens ubiquitin specific peptidase 46 (USP46), mRNA.	GAATGGGTGTCATTGGACAG GATGGTCTGCTTTTTAAAGT GACTCTGGGC	ILMN_1734194	GGTGTGGGAGATGTGAGACCATTCTG AGGTCAGCGATAGCCCAAAGGCTC
1.639011209	703.6393	1153.2727	1093.6434	1094.6434	KIAA0011; TFIIIC-BETA; TFIIIC110	NM_001521	Homo sapiens general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), transcript variant 1, mRNA.	CATTCCCTACTCTCTAAGGC CAAAATATCCTGAGCAAGGC TGGCAACCCC	ILMN_1739374	CCACAGACACCCTACCGATAGAACAG TGGCTCAGATCTTACTTGCTCCTG
1.633660764	330.74347	540.32263	366.09763	367.09763	C1orf22	NM_025191	Homo sapiens ER degradation enhancer, mannosidase alpha-like 3 (EDEM3), mRNA.	CGCCTGGCAACCAAGTATCA TACCGTTCCACTGCCACCAA AAGGAAGGGT	ILMN_1766851	GGGGGGTAGAATTTAGTAAATATTCCA GCCGGTCGTTTTATGCACAAGGC
1.631528726	96.67679	157.73096	172.63928	173.63928		NM_001035267	Homo sapiens ribosomal protein L41 (RPL41), transcript variant 2, mRNA.			ACCCGGCGCTCCATTAAATAGCCGTA GACGGAACTTCGCCTTTCTCTCGG
1.627355291	106.33928	173.05179	161.53513	162.53513	TNRC2; PACIP1; CAGF29; PAXIP1L; CAGF28; PTIP; FLJ41049	NM_007349	Homo sapiens PAX interacting (with transcription-activation domain) protein 1 (PAXIP1), mRNA.	ACAGTCAGTGATGGTGGAGA TGGAAGCAGCAGTGAGGAA ATTAGGATTCC	ILMN_1699317	CCTTCACATGCTCTTGTTTTCCAGCTG CTTTCCTGGGGGATCAGACTGTG
1.610462167	385.1726	620.3059	408.06427	409.06427	MAN1	NM_014319	Homo sapiens LEM domain containing 3 (LEMD3), mRNA.	CCACCATGCCCAGCCTGAAT GATGAATTTATGTGAACACA AAGCCCTCTG	ILMN_1702244	TACCTGAAACTGTTAAGCCGACCAAGA TCCCTCCCTGCAAGACAGATGGG
1.608048834	842.95593	1355.5143	1014.90173	1015.90173	DKFZP434F2021	NM_001025072	Homo sapiens chromosome 3 open reading frame 17 (C3orf17), transcript variant 2, mRNA.			CATATAAGCCCTGGGTCGGGGGGTAA CTGTGGGGATCACTGCCTGAGACA
1.597832961	184.2976	294.47678	323.28928	324.28928	rjd10; c367G8.3; RPL2B; RPL23AL	NM_001045548	Homo sapiens similar to C367G8.3 (novel protein similar to RPL23A (60S ribosomal protein L23A)) (LOC441743), mRNA.			CACAAGATGGCGCTGAAAGCAAAGAA GGAAGCTCCTGCCTCTCCTGAAGC
1.594984055	234.96428	374.76428	355.78094	356.78094		NM_138797	Homo sapiens ankyrin repeat domain 54 (ANKRD54), mRNA.			AACAGAAGAGCAGGTGACGGGAGAGG AGGTTGGAGGTGTAGCGATGGAGC
1.594308848	118.35178	188.68929	164.88512	165.88512	TRM61; FLJ40452; GCD14; Gcd14p	NM_152307	Homo sapiens chromosome 14 open reading frame 172 (C14orf172), mRNA.	ACTCCAGCCCGCAGCACATT TCCGCTGTCCGTCAGTAATT GTGTCCTCTC	ILMN_1722056	TCTGACAGCCTCAAGGAAGGAGCAGT GCCTGTGTCAGCCATGGGGCCCTT

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.584040743	75.68573	119.88928	88.48572	89.48572	MRTF-B; DKFZp686J1745; FLJ31823; FLJ45623; NPD001	NM_014048	Homo sapiens MKL/myocardin-like 2 (MKL2), mRNA.	GGGTGCGATCCTTTGCTGTA AACTGGAGAGACCAGTCCCA AACAGAGGGG	ILMN_1778734	GGAGAAAGATACCAATCTACAGAGCC CTGCTTGTTGAAGCACTAGTTTAA
1.574749569	107.59761	169.43929	133.7768	134.7768	alkB; hABH; ALKBH; ABH	NM_006020	Homo sapiens alkB, alkylation repair homolog 1 (E. coli) (ALKBH1), mRNA.			AGTCAGTCCAAGGAGGTATGTTCTTCC ACAACAGCCTTCTCAGCCTCTGC
1.557231407	1698.2476	2644.5645	2982.7642	2983.7642	OEBT; MGC120398; OBTP; C6orf49	NM_013397	Homo sapiens prickle homolog 4 (Drosophila) (PRICKLE4), mRNA.			GGCACCTCAGCCAGGGGTGTAGCCAA GTAGACAAATGGAATCCTGTGCTG
1.548102347	86.29766	133.59761	107.564285	108.564285	MGC10999; RP11-575L7.5	NM_032307	Homo sapiens chromosome 9 open reading frame 64 (C9orf64), mRNA.			GCCACAGTCACGCCACTGCATTCTATC CTGGGCAACAGATGGAGACCTTG
1.538701406	665.48926	1023.98926	874.3976	875.3976	PMSCL2; PM-Scl; PM/Scl-100; PMSCL; RRP6; p4; Rrp6p; p2; p3	NM_002685	Homo sapiens exosome component 10 (EXOSC10), transcript variant 2, mRNA.			CAGTTTGATCCAAATAAACAGACCCCG TCTGGCAAGAAATGCATTGCAGC
1.536818035	6375.639	9798.197	3647.7725	3648.7725	PAI; PAI-1; PAI1; PLANH1	NM_000602	Homo sapiens serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1 (SERPINE1), mRNA.			GGAGCAGAAATGCAAGGGGCTGCATG ACCTACCAGGACAGAACTTTCCCC
1.528886574	85.935165	131.38512	133.49344	134.49344	AD026; RP11-552M11.7; A3AR; bA552M11.5	NM_000677	Homo sapiens adenosine A3 receptor (ADORA3), transcript variant 2, mRNA.	GCAGCGAGAGCTCACGGAA TTCCTCTCGTGCCAAAAGGA AACCCAGTTGG	ILMN_1795139	CCTTCAGATTCCCCATCAACAAACACT TGAGGGCCTGTATGCCTGGGCCA
1.525588651	89.11431	135.95178	86.68529	87.68529	KIAA1339; P71; P51; ZER6	NM_170686	Homo sapiens zinc finger protein 398 (ZNF398), transcript variant 1, mRNA.	TTGTCCCTTTCGCTTCCACG TCCAAACCCCTTTAAGAAGG ATGAATGGGC	ILMN_1665416	CCAGACAAGATAGGAAAGGGGAAACC CCAGAAACGTGCTCTTCATCTGTC
1.525142048	2072.5977	3161.0059	3450.331	3451.331	BRMS2; MRPS4; C15orf12; FLJ10968; DKFZp586L0118	NM_018285	Homo sapiens IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (IMP3), mRNA.	GTCAGAATCACAAAGACAGA GTGGTGGTTGGCAGGGGCT GCAGGAAGGGG	ILMN_1717064	CTGGAAATCCCCACGCCCTGTTTCCCT TTATCGTCTTGTGGTTGGACTGG
1.509572477	780.3518	1177.9976	1046.0559	1047.0559	PMSCL2; PM-Scl; PM/Scl-100; PMSCL; RRP6; p4; Rrp6p; p2; p3	NM_001001998	Homo sapiens exosome component 10 (EXOSC10), transcript variant 1, mRNA.	AGGAGAGAGGTTTGAGTTCT GGGTATCCTCCCTTTCTGTA ACAGCCTCAA	ILMN_1685472	GACAGAGGCTTCAGGTACAACTGGCC ACAGAGATAGTCCTGGAAGACACG
1.50041281	7813.531	11723.522	9620.764	9621.764	SSS1	NM_001012456	Homo sapiens Sec61 gamma subunit (SEC61G), transcript variant 2, mRNA.			GCTACGTGTCCCTGGCATTTTAGGTGT CGGTTGGGCAGTCATGGATCAGG
1.495692183	370.6518	554.381	345.40594	346.40594	FLJ33201; FLJ12788; MGC120200	NM_022492	Homo sapiens tetratricopeptide repeat domain 31 (TTC31), mRNA.	GAGGCAGCATCCCGCGGCG CTGACGGTCCTGGGGAGAG CATGGCGCCGAG	ILMN_1701937	GCTGCCCTGTGGGTCTTGCTCAATAC TGTTCATACCTGGAGAGAGAAGGT
1.494423027	738.6893	1103.9143	942.0226	943.0226	ZNF376; FLJ21952	NM_022494	Homo sapiens zinc finger, DHHC-type containing 6 (ZDHHC6), mRNA.			GCCTACTCTGGTTAAGATGTTCTTTTC CTCAAAGGTGCCCTAGTGCCATG
1.483318581	7551.456	11201.215	11606.256	11607.256	IPOB; NTF97; MGC2157; Impnb; MGC2155; IMB1; MGC2156	NM_002265	Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA.	GGCTCGAAAGGCAAGAGCC CAGCATCGGTTTTCAGAACA CCTACATCTGG	ILMN_1805998	TCAGAATTGGCAGCACAAAGAAAACG CCCTCTCCTGACTTGTATTGTGGC
1.46030923	3156.031	4608.7812	4809.0894	4810.0894	YAF1; RPD3	NM_001527	Homo sapiens histone deacetylase 2 (HDAC2), mRNA.	GATGCCTTCTGGATCTTAAG CCAGTTGTCAGTGGAGGTCC TCAGGGCTGC	ILMN_1739496	AGGAACCAAATCAGAACAGCTCAGCAA CCCCTGAATTTGACAGTCTCACC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.458695475	484.38095	706.5643	851.9976	852.9976	SFRSK1	NM_003137	Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA.	GCTAAAGAATAAGACCTTGC TTGAGAAGGCTGACCTGGAC CCCTCCCTGG	ILMN_1659985	GGCAGCTGTAGATCTTGATCTTCCAG GTACCCCATGTACCTTTATTGAGC
1.449864221	169.93094	246.37679	217.87262	218.87262	FLJ38932; PAT4	NM_152313	Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 4 (SLC36A4), mRNA.			AGCTCTCTCCAGATCATCCCTGTGAAT GCCAAAGTAAACTTTATGTACAG
1.435618909	1416.2893	2033.2517	1844.6643	1845.6643	hYSAH1; YSA1H	NM_014142	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 5 (NUDT5), mRNA.	GATATGGTGCCCTGTGTATC CCAGAGATGCTAGAAAACTG TTCTTTGCTC	ILMN_1676448	GCCGAAAACGCAAGGCCGAAGCCAAA GCCAGGGGATGGAGAGTTTGTGGA
1.425244024	84.87268	120.96428	94.90597	95.90597	FLJ13703; KIAA0795	NM_025010	Homo sapiens kelch-like 18 (Drosophila) (KLHL18), mRNA.	CCGTTCAGTGTGGCCTGAAA ACACCATGTGTGCCAAGTTC CAGTTCACGC	ILMN_1814397	AACAAGGAGATAGGGTAGACATTGTAC TCAGTGGGCCTTGGGGCCTAGCC
1.424574845	240.73096	342.93927	311.48096	312.48096	MGC42237; FLJ44612; DRB1	NM_152945	Homo sapiens RNA binding motif protein 45 (RBM45), mRNA.	AAGATGCTGAGTGTCTGCAC TGCTCCACTTGTCCCCCCGC TCTCTCCTCA	ILMN_1697800	CCTGATAGTCTGTGTACAGCATTGTTT TGTCTGGGAAGCAGGGATTGCTG
1.422574271	386.91428	550.4143	574.20593	575.20593	dJ520B18.2; FARS1; HSPC320; PheRS	NM_006567	Homo sapiens phenylalanyl-tRNA synthetase 2, mitochondrial (FARS2), nuclear gene encoding mitochondrial protein, mRNA.			ACATCCAAAGACGCACAAGACCAGCC ACTGCTACCGCATCACGTACCGCC
1.415799115	154.9226	219.33928	202.85596	203.85596	Zfp105; HF.10; HF10	NM_003420	Homo sapiens zinc finger protein 35 (ZNF35), mRNA.			CTAGTCTCCATGGCCAAGCACTCAAG GATTGATGGACACCACACACCAGC
1.405395262	741.2726	1041.781	1135.9727	1136.9727	L13mt; L13; RPML13; RPL13	NM_014078	Homo sapiens mitochondrial ribosomal protein L13 (MRPL13), nuclear gene encoding mitochondrial protein, mRNA.	TGGCATCGTCCCTGAAACGT GGATTGATGGCCCCAAAGAC ACATCAGTGG	ILMN_1695576	CTGCTACAGTTCAGCACCTGTTTTATG TGCCGAATCACTGTGGGGAAAGG
1.391650292	230.53094	320.81845	331.38095	332.38095	FLJ22086; TIP39; bK445C9.6	NM_012143	Homo sapiens tuftelin interacting protein 11 (TFIP11), transcript variant 2, mRNA.	GCCCCAGGATTAAGATGGAT GCCTTAAGCGATGGCCCAG GGGTGCTTGGT	ILMN_1746682	GGCATTGGCGTGGCCGCTAGCTCTGT GCCCATGAACTTTAAGGACCTCAT
1.389486973	5486.298	7623.1396	7028.6978	7029.6978	ALURBP; MGC110981	NM_003133	Homo sapiens signal recognition particle 9kDa (SRP9), mRNA.			TGACACCCCTGCCCATTTTCTGTCTTT AATTAACCAAGGTGTTAGGTGTG
1.383296551	193.01846	267.00177	270.74762	271.74762	CGI-204; MGC45403; NCM1	NM_177988	Homo sapiens mitochondrial ribosomal protein L47 (MRPL47), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.			CACCTGCTACCTTAGAGTGTGAAGGT GATGGTAACTGCCACAGCAAAGGC
1.38100461	428.2976	591.48096	695.9976	696.9976	MGC75122; MGC43001; MGC117398; CSTF-77	NM_001326	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa (CSTF3), transcript variant 1, mRNA.	CCACAGTGTGTGGCGCTGAT GGAGATGTCAGAACCGAGAA CACTTAACCT	ILMN_1658149	GTGGCAGAACCACATTTTGTTCCCTCT TCAAGGGTGTCTTGTATGTGCCG
1.378241891	942.36426	1298.8059	1112.56	1113.56	GPCR41; PAR1; D15Ertd747e; GPCR	NM_024531	Homo sapiens G protein-coupled receptor 172A (GPR172A), mRNA.			AGGCCCGCACACCGGTACACTCGTGG ACACCTACACACTCCATAGGAGAT
1.3737574	404.1726	555.2351	477.35596	478.35596	FEM1A; EUROIMAGE686608; KIAA1785; EUROIMAGE783647	NM_020177	Homo sapiens fem-1 homolog c (C. elegans) (FEM1C), mRNA.	AGACCATTTCTGCAGTTTGC CCAAACCTCTACTGTTTGGG ACAGTAAGCC	ILMN_1773643	GCCCTTATGTGTCACTAAACAACTAGT TTCTCTCCCTTTTGTCAGTTCCC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.368173048	344.85596	471.82263	441.62262	442.62262	MGC3251; MENTHO	NM_032016	Homo sapiens STARD3 N-terminal like (STARD3NL), mRNA.	GATGCACAGAGGACACAGAA GGACTTGGCAGCAGGGTGA TGACCTGATCA	ILMN_1684943	GAGTCTCCCTGTCGACAGTAAAGTTGA AATGGTGACGTCCACTGCTGGCT
1.361593065	647.68933	881.8893	810.01843	811.01843	DPH2L2	NM_001384	Homo sapiens DPH2 homolog (S. cerevisiae) (DPH2), transcript variant 1, mRNA.			CAAGTGTTCAGACAGCCACATGAGGG GACAGTGCAGCTACAGGATATGCC
1.360511622	1834.1184	2495.3394	2266.306	2267.306	MGC997; DXS8237E; KIAA0122; ZRANB5; GPATC9; GPATCH9; MGC1132	NM_152856	Homo sapiens RNA binding motif protein 10 (RBM10), transcript variant 2, mRNA.			GAGGTGGTGACTTTTGTTGGAAAATTG GGCTGGGATCACGTCCTGTTTTG
1.349210351	993.98096	1341.0894	1257.6477	1258.6477	AAC-11; AAC11; API5L1	NM_006595	Homo sapiens apoptosis inhibitor 5 (API5), mRNA.	TGCCACCAGACCAACACCCC CAGACTTCCCCACCTTCAGC CACCATCAGA	ILMN_1784477	GACCAGCTAATCTGGACCTCAGAGATA GATCAGCCAGTGGCCCAAAGCCA
1.336476004	146.09761	195.25595	83.60916	84.60916	POPDC1; MGC42413; POP1; HBVES	NM_147147	Homo sapiens blood vessel epicardial substance (BVES), transcript variant 5, mRNA.			TCACTGCTTCGGTTCTGCTCATCAGG GGACACGCTCCCTTACTCATGGCA
1.325465401	468.0476	620.3809	589.4976	590.4976		NM_004077	Homo sapiens citrate synthase (CS), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GGCTGTTCAGCAGAGAAACC CATGTCCTCTCTCCATAGGG CCTGTTTTAC	ILMN_1683562	CCTCAGGCAGAGGATGTTCTGGACCT CCCCCTCTTGGTCCCTACTAGAGA
1.303330702	349.9893	456.1518	345.26013	346.26013	OLF44; HNOEL-iso	NM_020190	Homo sapiens olfactomedin-like 3 (OLFML3), mRNA.	GGAGCTTGCCTCCTTTGAAT GACCTAGAGCACAGGGAGG AACTTGTCCAT	ILMN_1813840	AGAGCCCGAAGAGTCAAAACCCTCAA TGTTCCCTCCTGCTCTCCTGCCCC
1.302543959	33132.957	43157.133	40647.273	40648.273	MIG12; TB10	NM_021103	Homo sapiens thymosin beta 10 (TMSB10), mRNA.			AAGAACACCCTGCCGACCAAAGAGAC CATTGAGCAGGAGAAGCGGAGTGA
1.276538656	191.88095	244.94345	243.31012	244.31012	EIF-2B; EIF2Bepsilon; CACH; LVWM; CLE	NM_003907	Homo sapiens eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa (EIF2B5), mRNA.	ATGAAAGAGGACGCGAAAG GGAAGAGCGAGGAGGAGCT GGCCGAGTGCTT	ILMN_1693428	GAGGAGCTAAGCAGGCCCGGCAGTTG GAGGAAGGCCAGAGGAACAGCTTT
1.274209653	350.00595	445.98096	417.4726	418.4726	UBE2G; UBC7; E217K	NM_003342	Homo sapiens ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast) (UBE2G1), mRNA.	GATGTATGGTATCTCCCTTT GCCAAGCCATCCTGGATGAA ACCAAAGGAG	ILMN_1681783	TTGATATGCCCACTCACCCTCGACGAA TCTGCCCGCTTTGGGCTGTGGTG
1.266100965	2267.4976	2870.8809	3155.4727	3156.4727	HSPC108; SLP-2	NM_013442	Homo sapiens stomatin (EPB72)-like 2 (STOML2), mRNA.			TGATCGAGTCAAGATGAGTTAGTGGA GCTGGGCTTGGCCAGGGAGTCTGG
1.261682069	2544.1812	3209.9478	2657.3892	2658.3892	MGC131709; BBF2H7; MGC71006	NM_194071	Homo sapiens cAMP responsive element binding protein 3-like 2 (CREB3L2), mRNA.	TCGGTCCTGCTGGAGGCCA CGGGTGCCACACACTCGGT CCCGACATGATG	ILMN_1703108	AACCAGGGGTTTTAGCTCTGTTCTCTG CTCCCATCCTTCGCTCACCAGCT
1.25638015	1311.756	1648.0642	1680.6976	1681.6976	FLJ10294; HSPC128	NM_014167	Homo sapiens coiled-coil domain containing 59 (CCDC59), mRNA.	GTCCGCCCTGCTGCGTCTGT TCGTCAGCTGAGTTCCTTGT GAATCTCTGT	ILMN_1695792	ATCTGCTGCCTATTAGGTTCTTCTGTG ACATGTGCCTCCCAGCAGTGAAC
1.253228219	1473.506	1846.6393	1602.5559	1603.5559	LBP-1B; LBP1A; LBP1B; LBP-1a; DKFZp686L1745	NM_014517	Homo sapiens upstream binding protein 1 (LBP-1a) (UBP1), mRNA.			CCTTTGCTTTCGTGTGACCACATGTTT TCTGTACCAGTCACTGGGGAAAG
1.253200211	289.23096	362.4643	373.37262	374.37262	FLJ10766; KIAA0483; Fbx28	NM_015176	Homo sapiens F-box protein 28 (FBXO28), mRNA.	GTCATCTCCGTAGCCCTCCC AGTTGTGCCTCCTGCACATT GATGAGTGCC	ILMN_1805930	CCGTCCACCGTGACATGGTTATGCAT CCTTTAGATTAACCTCACCAAATG

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.249480053	46.24128	57.777557	50.697205	51.697205	DRP; DRP1; DMDL; FLJ23678	NM_007124	Homo sapiens utrophin (UTRN), mRNA.			ACCGCACGACACCAGCACGGATCTCA CGGAGGTCATGGAGCAGATTCACA
1.238598163	766.0893	948.8768	1120.9392	1121.9392	CPSF; CPSF73; CPSF-73	NM_016207	Homo sapiens cleavage and polyadenylation specific factor 3, 73kDa (CPSF3), mRNA.			AGCGTCACAGTGGACGGGAAAACTGC CAACCTTAACTTGGAGACACGGAC
1.235616826	114.89345	141.96428	151.82678	152.82678	ZNF450; BIF1; PATZ2	NM_014797	Homo sapiens zinc finger and BTB domain containing 24 (ZBTB24), mRNA.	TTATTGGGCAGGGGGAGGG GGAGGGCACAGGCAAGAAG AGATTCACAGTG	ILMN_1693975	TGGGGCTCCTGAAACACCTCGTTTTGA AGGTGAATCTTTGGTTTTCTCCC
1.195219843	472.33093	564.5393	611.381	612.381	CCTG; TRIC5; TCP-1-gamma; PIG48; CCT-gamma	NM_001008800	Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), transcript variant 3, mRNA.			GCCAGGAACACTGTGGACGTCTTTGT TCAGAAGGGATCAGGTTGGGGGGC
1.187472386	3265.5476	3877.7476	3548.9644	3549.9644	MGC117372; HUM3CL	NM_005102	Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), transcript variant 1, mRNA.	AGACTTCCCTACTGAGCCAC CTTCTCTGCCACGAACCGGT CGGGCTAGGA	ILMN_1777663	AGTGTGTGTCCTCTGAGGTGCTTGAG AAAGTGTACACTGCAGAACTGCCC
1.183482704	1738.856	2057.906	2062.0977	2063.0977	FLJ26680; cC1qR; RO; SSA	NM_004343	Homo sapiens calreticulin (CALR), mRNA.			CCCTCCAACCTGGGGGGCAGTGGTGT GGAGAAGCCACAGGCCTGAGATTT
1.177628734	1999.3477	2354.4893	2349.7227	2350.7227	SF3a66; SAP62; PRPF11; PRP11	NM_007165	Homo sapiens splicing factor 3a, subunit 2, 66kDa (SF3A2), mRNA.			TTTTGTACTGCCCCCCGCTCATTAAAC AGCCTCCCCCAGCCCTGAGTGCA
1.175472196	249.73096	293.5518	251.81429	252.81429	FLJ20232; dJ1104E15.3; HSU79252	NM_019008	Homo sapiens Smith-Magenis syndrome chromosome region, candidate 7-like (SMCR7L), mRNA.	CCCAAGGGTCTCAAGCCTGC AAGTCCAGAAGGTGACAAAC CCAGGAGCAC	ILMN_1805979	GGCAGCTTAGCCCTGAGGCCCAGAGA CCTGCTGTCCTTTTTCTCCTTGAG
1.174074865	965.58093	1133.6643	1090.3351	1091.3351	MGC33424	NM_153705	Homo sapiens KDEL (Lys-Asp-Glu-Leu) containing 2 (KDELC2), mRNA.			CAGCAGCCTTAATCTACATAATTCTTC ATCTCGCCAATTCAGCCGCAGCC
1.124498103	947.73926	1065.731	965.77673	966.77673	CGI-128	NM_016062	Homo sapiens family with sequence similarity 96, member B (FAM96B), mRNA.	GAAGGGCATGGGGTGCAGC TAGAACAGTGTAGGTTCCCT CAATAACCCCT	ILMN_1673215	TTGGAGGTTGTGAATCAGTGCCTGTC AGCCCGCTCCTGAGCCTGGCCTTT
1.10832817	1066.9727	1182.5559	1354.3726	1355.3726	MGC142259; CSIG; L12; PBK1; DKFZP564M182; MGC138433	NM_015659	Homo sapiens ribosomal L1 domain containing 1 (RSL1D1), mRNA.			CCTCAATGCTGCCTCCAGAGCTTTTTG GAAATACTCAGATCCTGGCCGCC
1.033414285	858.4143	887.0976	988.98096	989.98096	XT2; XT-II; xylT-II	NM_022167	Homo sapiens xylosyltransferase II (XYLT2), mRNA.	GGACAGAGTCCCCAAGGTTC CTGTTGTTGCCTCCTTCCTA AGCCTCATAT	ILMN_1681236	CCAGGTGTGCACTGGAAGTGAGGTCA CATGAGCAGCGTGGGAAGAAGACT
0.954120553	252.56429	240.97678	200.74344	201.74344	ZNHIT5; DKFZP564B1023; RP11-92G12.2	NM_001031725	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 59 (DDX59), transcript variant 1, mRNA.			CTGGGATATTGCAAAACGAGTAAAGCC CACAGGATCCATTCTTCCCCCTC
0.893938756	1137.4727	1016.83093	747.38513	748.38513	hsyn16; SYN16; MGC90328	NM_001001433	Homo sapiens syntaxin 16 (STX16), transcript variant 1, mRNA.			GTGCTGGCTGGGCCATGCTTGTGAAG TGATGTGTGTCTCTGATTTAACGG
0.823093297	25317.39	20838.574	24803.848	24804.848		NM_001035258	Homo sapiens ribosomal protein L38 (RPL38), transcript variant 2, mRNA.			TCAAGGACTTCCTGCTCACAGCCCGA CGAAAGGATGCCAAATCTGTCAAG

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.807618512	3140.981	2536.7144	2924.3643	2925.3643	CGI-119; ZPRO; S1R; GAAP	NM_016056	Homo sapiens transmembrane BAX inhibitor motif containing 4 (TMBIM4), mRNA.			GGAGTTGGTCTTAGCCGCTGCAGGAG CCCTTCTTTTCTGTGGATTCATCA
0.797878712	1856.8059	1481.5059	1359.1143	1360.1143	TCFL2; LZTR-1; MGC21205	NM_006767	Homo sapiens leucine-zipper-like transcription regulator 1 (LZTR1), mRNA.	CTGGCTAAACAACCTGACAA ACTGTGGCCAGGGGAACCG ACACAACCCTC	ILMN_1735495	GAGGGGCCTACCCAGAAGCCTCCTTG AACCAGTCTGCAACCCTGCTCTAT
0.795990745	10373.098	8256.89	9004.189	9005.189	MGC87783; H3.3A; H3F3; MGC87782	NM_002107	Homo sapiens H3 histone, family 3A (H3F3A), mRNA.	TATTTAGGGCAATAAGCAGC ATTGGCCTGGAGTGCCAGA GCGTCACCTCC	ILMN_1675190	TACAGGCCTGGTACTGTGGCGCTCCG TGAAATTAGACGTTATCAGAAGTC
0.79299651	1603.7976	1271.8059	1353.9476	1354.9476	CLC-7; CLC7; FLJ39644; FLJ26686; OPTA2; FLJ46423	NM_001287	Homo sapiens chloride channel 7 (CLCN7), mRNA.			CCTCACAGGGCCCCAAGGTGTCCGAG TGTGTTGGGTCTGAACGCGAAATA
0.789297602	473.45593	373.69763	381.56427	382.56427	BM-019; GL010; ACP33; MAST	NM_016630	Homo sapiens spastic paraplegia 21 (autosomal recessive, Mast syndrome) (SPG21), mRNA. XM_945612 XM_945613 XM_945615 XM_945617 XM_945619 XM_945622			CCCCGAAGTATCAGGTGTCCTCTCATA TTCCTGCCCCCTGTCAGTGGAAC
0.775008601	370.68097	287.28094	146.64345	147.64345	MGC4400	NM_032679	Homo sapiens zinc finger protein 577 (ZNF577), mRNA.			TAAATTAACCTACCTGGCCAGGCACAG TGGCTCACACCTGTAATCTCAGC
0.769703812	1537.0059	1183.0393	1408.5393	1409.5393	NAG-2; NAG2; TETRASPAN; TM4SF7; TSPAN-4	NM_001025235	Homo sapiens tetraspanin 4 (TSPAN4), transcript variant 3, mRNA.			CCCTCACCTACATTCCATAGTGGGCC CGTGGGGCTCCTGGTGCATCTTAA
0.760310871	19342.062	14705.98	10281.739	10282.739	L5; p15(PAF); OEATC1; OEATC-1; NS5ATP9	NM_001029989	Homo sapiens KIAA0101 (KIAA0101), transcript variant 2, mRNA.			TACTCGGGAGGCTGAGGCAGGAGAAT GGCGTGAACCCGGGAAGTGGAGCT
0.750959019	5899.4644	4430.256	4142.164	4143.164	FLJ36146; DKFZp586A1420; MGC157720; ES/130; MGC157721; ES130; hES	NM_001042576	Homo sapiens ribosome binding protein 1 homolog 180kDa (dog) (RRBP1), transcript variant 1, mRNA.	GGTATGTCTGCCCATTTATT GCCGCTCTCTTTTCTGGAGG AGCGAACCGG	ILMN_1657141	CTCACCCCTAGACGTTGCCAACCAGA ACTGACGTGTGACCTCCTGGGTGT
0.743692001	242.83928	180.59763	162.20178	163.20178		XM_941392	PREDICTED: Homo sapiens CDC-like kinase 2, transcript variant 3 (CLK2), mRNA.	GTCTACACCCAGGTGCTAAG CTACACAGACTGGATTCAGA GAACCCTGGC	ILMN_1770765	GGGATATCAGTCGGTGACGATCAGGC CCTGGGCCCCCCTGCATCTTTTAT
0.743498453	261.56427	194.47263	302.69345	303.69345	T-STAR; SLM-2; SLM2; Etle; TSTAR; etoile; SALP	NM_006558	Homo sapiens KH domain containing, RNA binding, signal transduction associated 3 (KHDRBS3), mRNA.	GTCCCTGCTCCTCATGTTTC TGGTTTGGTGAGTCCTTTGT GCCACCACCC	ILMN_1731648	GCACCCCAGCCCAAAGTGGTGCTGAT TACTATGATTACGGACATGGACTC
0.741511578	1184.7726	878.5226	975.0143	976.0143	MGC138220; FLJ11838; RP11-163G10.1; MGC117357	NM_001077447	Homo sapiens phosphopantothenoylcysteine synthetase (PPCS), transcript variant 2, mRNA.			AGAAAGGGAAAAGGCAGTGGTGTGTA GGCAAATATGGTTTGGCATTTGTC
0.738420452	961.3393	709.8726	738.0393	739.0393	ARFL1	NM_001177	Homo sapiens ADP-ribosylation factor-like 1 (ARL1), mRNA.			GGTCCTTGTCTAGCAGGAGACAACTG CACAGGTATACTACCAGCGTTTGG
0.735434369	265.43512	195.21011	200.2143	201.2143	FLJ36175; WDSAM1; UBOX6	NM_152528	Homo sapiens WD repeat, sterile alpha motif and U-box domain containing 1 (WDSUB1), mRNA.			CGTACAAGTCCCATGACAAATCTTGTT CTTCCTTCAGCGGTACTTACACC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.729058698	431.44345	314.5476	478.35596	479.35596	STRF2; FLJ12666; RP11-781D11.2	NM_024595	Homo sapiens chromosome 1 open reading frame 108 (C1orf108), mRNA.	CTATGTTGACGCTAGCCTGC ACAGACACTTGGGTCTATGA GAGCACAGTG	ILMN_1680225	CGGAAAGTCAACCTCACTCCTCAGCA CTCACAGCACCTAGCTCTCCAGGT
0.720670392	548.45593	395.25595	419.04346	420.04346	MGC14098; GSHS	NM_000178	Homo sapiens glutathione synthetase (GSS), mRNA.	GTAGTGAGCACAGGAGTCTT GGGACGAGGCCTAGACTTG ATCAGTGTCAG	ILMN_1665414	CCTGTGTGAGGGCACAACCAGGCCAC GGGACCTTCTATCCTCTGTATTTG
0.718805088	1765.7976	1269.2643	1095.8976	1096.8976	NCE2; MGC18120	NM_080678	Homo sapiens ubiquitin-conjugating enzyme E2F (putative) (UBE2F), mRNA.			CCCCTGGATTGCCCCAGTCCTGTGAC CATGTTGCCCTGAAGAAGACCATC
0.716882816	512.2143	367.19763	399.26428	400.26428	KIAA0199	NM_012235	Homo sapiens SREBF chaperone (SCAP), mRNA.	GCCCTTCTGCACAGGAGAG CAAGGCACTTGCAGTAGTGA TCTATGCCAGC	ILMN_1712365	AATGCACTGAACCTGGACTTGGGGGA AAGAGCCGAGTATCTTCCAGCCGC
0.715837275	277.30597	198.50595	195.62677	196.62677	PSK1; TAO1; TAO2; MAP3K17; KIAA0881; PSK	NM_016151	Homo sapiens TAO kinase 2 (TAOK2), transcript variant 2, mRNA.	ACCTGGAGTTTAATACAGTG AGCTCTAGCAAGGGAGGCG CTGCCTTTTGT	ILMN_1665276	CTGTGTTCTCCTGGCGCTCCTCCCCT AAGTTATTGCTGTTCGCCCGCTGT
0.713232468	2130.1226	1519.2726	1440.781	1441.781	DKFZp686D1664; NPC-A-13; DKFZp686O24200	NM_001537	Homo sapiens heat shock factor binding protein 1 (HSBP1), mRNA.	CGATGACAAGGGAGACCATC CCCCACCCCCGGAGTCCAA AATACAGAGTT	ILMN_1800172	GACCATCCGAAACCTGCGTCCCTGGT GATGTTCTCAAGCCTCGGAAGTGG
0.713215071	617.1726	440.1768	486.5976	487.5976	FLJ12270; MGC11230; FP977	NM_030581	Homo sapiens WD repeat domain 59 (WDR59), mRNA.	TTGGGGCTGAATCTCCAGGC CTCACGAGGTCCCCTGTGG GGATGCTGCTA	ILMN_1774387	CTCTTGATGCCAGTGCAGAGACCAGA GTCAGATGCCCGAGGACAGTGGGT
0.696526199	3212.331	2237.4727	1963.606	1964.606	KIAA0905; HSPC334; MGC90305; ABP125; SEC31L1; HSPC275; DKFZp686N07171; ABP130	NM_014933	Homo sapiens SEC31 homolog A (S. cerevisiae) (SEC31A), transcript variant 1, mRNA.	TGCAGCTCCAGGAAGTCCCC GCAATGTCTCACGTTGTCTT TGACCAGTGG	ILMN_1808919	CCCAGGCCAATAAGCTGGGTGTCTAA AAGGACAGCTTCTCTTCCACTCAA
0.695965815	1107.7976	770.98926	460.1643	461.1643	KIAA1202	NM_020717	Homo sapiens shroom family member 4 (SHROOM4), mRNA.			CGAAAATGTTATTAAGAAAACAGTTCC GGCCGGGCATGGTGGCTCACGCC
0.695942333	1255.1892	873.5393	753.0476	754.0476	MSTP011; A6RP; PTK9L; A6r	NM_007284	Homo sapiens twinfilin, actin-binding protein, homolog 2 (Drosophila) (TWF2), mRNA.			ACCGGGCTGGCATTTTGTGACCCTTC CCTGTTGCTGTCCCTGCATCTCGT
0.695047898	699.6726	486.30597	315.9893	316.9893		NM_197964	Homo sapiens hypothetical protein HSPC268 (HSPC268), mRNA.	CCTTCTGGAAGCTCAATTAT CACGAGCACATGGTGGAAAA CGTGGGCCGG	ILMN_1766219	TAAAAGTAGTACAAGCCTTAGCCAGGC ACGGTGGCTCACGCCTGTAATCC
0.694099559	134.28928	93.21013	114.96428	115.96428	MGC34222; PMS7	NM_174930	Homo sapiens postmeiotic segregation increased 2-like 5 (PMS2L5), mRNA.			AACTTCGAAGGCTTAATGATGTCACCA TTTCTACCTGCCACGTATCGGCG
0.689090901	41520.11	28611.13	27673.639	27674.639	LDH-M; PIG19; LDH1	NM_005566	Homo sapiens lactate dehydrogenase A (LDHA), mRNA.	CTTGGTCGCTGGCTGCGCT CCACCCGATTCTCGGGATCA TTGGACCGTTT	ILMN_1655171	CTGGTTAGTGTGAAATAGTTCTGCCAC CTCTGACGCACCACTGCCAATGC
0.688778796	1238.7227	853.20593	984.5059	985.5059	MGC52424	NM_001042462	Homo sapiens trafficking protein particle complex 5 (TRAPPC5), transcript variant 3, mRNA.	GCCAAACTTCCATTGGTCAG GTAATTCAGGAGGGTGGGG AGGACCGGCTA	ILMN_1655504	ACAAGCTGGAGCAGGCCAACGATGAC GCGCGCACCTTCTACATCATCGAG
0.688702581	1969.981	1356.731	1614.856	1615.856	RAH; RAB39	NM_031934	Homo sapiens RAB34, member RAS oncogene family (RAB34), mRNA.	AACCATGCCATCATTCAGAC GCTGCTCAACTCCATGGCAC CAGACGCGGC	ILMN_1803881	GCTTGACCCCTGGACATTTGCACTGA CTTTATCCAGACCAAAGAGCTGCC
0.683115186	1852.0269	1265.1477	1274.9019	1275.9019	HSPA1; HSP70-1; HSPA1B; HSP72	NM_005345	Homo sapiens heat shock 70kDa protein 1A (HSPA1A), mRNA.	GCCATCCGAGTTACTCATGA GACCAGTGCCCATGAAGGTC AGACTGAGGC	ILMN_1660111	GGAGCTTCAAGACTTTGCATTTCCTAG TATTTCTGTTTGTCAGTTCTCAA

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.680743776	241.86429	164.64761	173.04346	174.04346	CLAPA1; AP2-ALPHA; ADTAA	NM_130787	Homo sapiens adaptor-related protein complex 2, alpha 1 subunit (AP2A1), transcript variant 2, mRNA.	TGACTTGAGTCCACAAGGAC ACAAACACCTGAGTAGCTGG GCAGCCCTTG	ILMN_1730347	CAAAGCCAACCACCCCATGGACGCAG AAGTTACTAAGGCCAAGCTTCTGG
0.679783151	941.08093	639.73096	871.11426	872.11426	NICE-4; FLJ42300; KIAA0144	NM_014847	Homo sapiens ubiquitin associated protein 2-like (UBAP2L), mRNA.			TGCTATGGGCCCTGCACTTCCTTTGCT TCCTCCTGTTCACCCTGGTGGTG
0.678646611	846.71844	574.6226	654.08093	655.08093	MGC138220; FLJ11838; RP11-163G10.1; MGC117357	NM_024664	Homo sapiens phosphopantothenoylcysteine synthetase (PPCS), transcript variant 1, mRNA.			AATATTGGTTGAATGCCTATGTATGTC AGGCCCTGTGCTGAGCCATGAGG
0.67428617	118.59762	79.968735	92.844215	93.844215	D1S155E; FLJ26882; UNR; DKFZp779B0247; DKFZp779J1455; RP5-1000E10.3	NM_001007553	Homo sapiens cold shock domain containing E1, RNA-binding (CSDE1), transcript variant 1, mRNA.			GATGACAAGGGTCAGCTCAGGGGATG TGGGGGAGGGCGGTTTTATCTTCC
0.670159098	618.1643	414.26843	412.20178	413.20178	WIPI-3; WIPI3	NM_019613	Homo sapiens WDR45-like (WDR45L), mRNA.	AAGGAGACAGTGCCATCCAT GGAAACGGGAGACCTCTGT GCCGACACCGC	ILMN_1708529	GCCTGTGGTCTTCTCCGTACCCGCAA CGTGGTCATCTGTGCCCGTGACGT
0.668414993	232.30595	155.27678	253.38095	254.38095	FLJ11218	NM_001031709	Homo sapiens chromosome 10 open reading frame 59 (C10orf59), transcript variant 1, mRNA.	ATTCACATTGAAGAGGACTC CTTAAAAGCCGATTTGCATG TGTGAAAGCC	ILMN_1770266	TCCTCACACCTTGCACCTTCCCTACTT TTCTGAATTGCTATGACTACTCC
0.666797486	291.16428	194.14761	148.34763	149.34763	MGC150640; KIAA1610; MGC131940; ER1; MI-ER1; DKFZp781G0451; RP5-944N15.1; MGC150641; hMI-ER1	NM_020948	Homo sapiens mesoderm induction early response 1 homolog (Xenopus laevis) (MIER1), transcript variant 1, mRNA.			TTGCACTACTTTTTCAGTGGTTCTTGG TCCCCTTTACCACATCTTGGGTG
0.659985386	93.18513	61.500824	106.89761	107.89761	SMD3	NM_004175	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3), mRNA.	GTGAGGCACACATGATTGAT GGGTATGGGGCCATGAAGA CCTTGAAGAGC	ILMN_1705984	TGGCCAGTTGCAGGTTAAGCCCCAGA AAAGTTCACCTTGGAGAAGCTCCG
0.659205502	3652.3477	2407.6477	3276.9644	3277.9644	HGPS; EMD2; FPLD; LDP1; LMNC; FPL; LFP; CDCD1; LGMD1B; IDC; CMT2B1; PRO1; LMN1; CMD1A; CDDC	NM_005572	Homo sapiens lamin A/C (LMNA), transcript variant 2, mRNA.	CCCATGGTCATCCTCCAGAA CCTGGCCAAAAAGGAAGACC TCAGAAGCGT	ILMN_1737416	ACAGAACACCTGGGGCTGCGGGAACA GCCTGCGTACGGCTCTCATCAACT
0.656178854	2361.789	1549.756	1024.2393	1025.2393	CFR-1; FLJ23319; MG160; FLJ23967; MG-160; ESL-1	NM_012201	Homo sapiens golgi apparatus protein 1 (GLG1), mRNA.			GGCAGTCCAGCCTGACCTTTCTGCAC ACTCCAGACAAACTTCCCAGACAA
0.655548829	383.7143	251.54346	308.50177	309.50177	D6S82E; NG26	NM_021160	Homo sapiens HLA-B associated transcript 5 (BAT5), mRNA.			TCTGGCTCGGAAGCATCTGCACAACTT TGAGGCCACTCACTGCACCCCAC
0.655021957	222.27261	145.59344	174.99762	175.99762	VRF; VEGFL	NM_003377	Homo sapiens vascular endothelial growth factor B (VEGFB), mRNA.	ACCTGGTTCCCTCCAAACCT CCCAGCCACTCGGGCTTGTA ACTGTCTGAG	ILMN_1785336	GGACAGAGTTGGAAGAGGAGACTGGG AGGCAGCAAGAGGGGTCACATACC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.653797115	5355.289	3501.2725	2528.2559	2529.2559	CDA1; codanin; PRO1295; CDA-I; CDAI	NM_138477	Homo sapiens congenital dyserythropoietic anemia, type I (CDAN1), mRNA.	CCTGGGGATTGGGTGCCAT CTCTCTAGGGGTAACACAAA GGGCAAGAGGT	ILMN_1704368	AGGTCGCACCACTGCACTCCAGTCTG GGTAACAGAGCGAGACTTTCTAGA
0.641932594	4376.481	2809.4058	2482.9727	2483.9727	FLJ34583	NM_198276	Homo sapiens transmembrane protein 17 (TMEM17), mRNA.			GTCTATATTTGTAAACCAAGAGACCGG CTGGGTGTGGTGGCTCACGCCTG
0.637953454	173.38928	110.61429	90.1103	91.1103	FLJ13902; FLJ40957; C114	NM_024653	Homo sapiens PRKR interacting protein 1 (IL11 inducible) (PRKRIP1), mRNA.			GTGTAGATTGCCCCGGCCCCTCTCTG AGCCCTGTAGCATCTGTGATAGCT
0.637815401	116.88095	74.54847	42.310047	43.310047		NM_001013701	Homo sapiens hypothetical gene supported by AK096951; BC066547 (LOC440157), mRNA.	CCAGGGGCCTGTCAGTCTG AATGGTTGTCCTGACCAGTA ACCCAAGCCTA	ILMN_1704599	GAGGATCCCTTGAGCCCAGAGGTTCG AGACTAGCCTGGGCAACACAGTCA
0.633892417	1184.7727	751.01843	971.9768	972.9768	MYLE	NM_014015	Homo sapiens dexamethasone-induced transcript (DEXI), mRNA.			CGCTCCTTCATTTCAGGTTACTCGTTC TTCAGCAAGTTGGCAAAACAGAC
0.629083546	814.2893	512.256	581.36426	582.36426	ATP6N1; VPP1; DKFZp781J1951; Stv1; a1; ATP6N1A; Vph1	NM_005177	Homo sapiens ATPase, H+ transporting, lysosomal V0 subunit a1 (ATP6V0A1), mRNA.			GCCCTGGTGTCCTGGGTTTTCGTGAT GATCTTTGCTCTGTTTCCAGTGGG
0.628646639	1408.2727	885.3059	843.1101	844.1101	TLX; MCP; TRA2.10; MGC26544; MIC10	NM_172358	Homo sapiens CD46 molecule, complement regulatory protein (CD46), transcript variant m, mRNA.			ACTCAGGCAGATCTCAGCCCTCTACT GAGTCCCTTAGCCAAGCAGTTTCT
0.625982959	683.13513	427.63095	513.96844	514.96844		NM_001025603	Homo sapiens regulatory factor X, 5 (influences HLA class II expression) (RFX5), transcript variant 2, mRNA.	GCAGAAAAACGCCTTAGCAG CCTGTGTGAGGCTCGGAGT AGTGGAGAAGA	ILMN_1699859	GCTAGTTCTGTGGTCAGGCGGCACCA ATGAGAAAGGAATGCAGACCCTCC
0.624969577	166.36429	103.97262	196.85596	197.85596	EBF3-S; RP3; EBF3; EB3	NM_012326	Homo sapiens microtubule-associated protein, RP/EB family, member 3 (MAPRE3), mRNA.	GCCAAATGGCAACACCACGT CTAAAGCAGTTTCACAGCAT GGTCCCCTAC	ILMN_1720606	ACTCCCTCCAGCAGCCTGGTTCACCA CACAAACTCTGCCTGGACCCCATT
0.623495322	1176.0809	733.28094	530.756	531.756		NM_000745	Homo sapiens cholinergic receptor, nicotinic, alpha 5 (CHRNA5), mRNA.	TCCGCAGACGCTATTGCCAG GTGCTCAATGCTGTTCGCAT CATCCAGGCT	ILMN_1786570	GCTTGATATAATAATTACTTAATGTGG CCGGGCACGGTGGCTCACACCTG
0.618258746	200.85596	124.180954	84.3134	85.3134	RP3-465N24.4; NPD014; DJ465N24.2.1	NM_020317	Homo sapiens chromosome 1 open reading frame 63 (C1orf63), mRNA.			TGCAGATATGAGAGATAGCACAGATG GACCAAAGGTTATGCACAGGTGGG
0.616715692	5876.556	3624.1643	2863.539	2864.539	FLJ23633; FLJ23807; FLJ23701; L-RAP; ERAP2	NM_022350	Homo sapiens leukocyte-derived arginine aminopeptidase (LRAP), mRNA.			ACTTAAATGGTCAATAGAAAAAGTAGG CTGGGCGCGGTGGCTCACGCCTG
0.614935049	551.7143	339.26846	455.96008	456.96008	FLJ29018; SBBI54	NM_138334	Homo sapiens Josephin domain containing 2 (JOSD2), mRNA.	TGGGTACCCCAAAAAGTGGA ACTGCTGGATCACATGGTAC TTCTAACTTT	ILMN_1739814	CCTGTGCGAGGTGCTGCTGGTAGTGA CCAAGGAGGTGGAGGAGAAGGGCA
0.614405166	424.03094	260.5268	282.41846	283.41846	MPS2; SIDS	NM_000202	Homo sapiens iduronate 2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA.			ATGTGCTCCCTTCCAGCTGGTGAGAG GAGGAGTTAGAGCTGGTCGTTTTG
0.614169196	1707.4518	1048.6643	614.0393	615.0393	FLJ20731; FKBP22	NM_017946	Homo sapiens FK506 binding protein 14, 22 kDa (FKBP14), mRNA.			TTCTGTCTCATCAAAAACTGAAGTTAG CTGGGTGTGGTGGCTCATGCCTG

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.613405945	123.73928	75.90241	73.33264	74.33264	HZF3; MGC126498	NM_003415	Homo sapiens zinc finger protein 268 (ZNF268), mRNA.			TGCCTTTGCCTCTCCATGACGCAATTC CTGTGCGACATACGTAGCGGCCG
0.609596043	786.85596	479.66428	601.9018	602.9018	FLJ32495; CFBP	NM_138401	Homo sapiens family with sequence similarity 125, member A (FAM125A), mRNA.			TGCCGGGCAGGGCTGGAGCTGGACA GAAGCCAGTGCCTTTAAGTCATTTG
0.608990266	2008.3477	1223.0642	1361.0143	1362.0143	TST1; TPC; PTC; H4; D10S170; FLJ32286	NM_005436	Homo sapiens coiled-coil domain containing 6 (CCDC6), mRNA.	ATCCCCGACTCGGAAAGCAA TCTGGATCAGAACTGTTTGT CTCGCTGCAG	ILMN_1676254	AGAGGAGAGCCAAGCGCTAGCATGCC TTTTGCCTCTGCATATCTGTGCAC
0.608267583	6260.0977	3807.8145	3339.6477	3340.6477	DKFZp686K23158; FSGS1; FSGS	NM_004924	Homo sapiens actinin, alpha 4 (ACTN4), mRNA.	GTCTGCATTTTGGAGAGTCC ACACCACGGACCAGGTTTTC CCCCAAGGCT	ILMN_1692742	AGGAGATGGCCCCAACAAGCACCCCG CTTTTGCAGCAGAGGAGCTGAGTT
0.606244039	4381.331	2656.1558	2775.5728	2776.5728		NM_001605	Homo sapiens alanyl-tRNA synthetase (AARS), mRNA.			AGATAACGGCTCTCCAGACCTGAGCT TTCCGCGTCAGCAAGTAGGAATCG
0.605624937	2001.3309	1212.0559	1096.9727	1097.9727	FinGER3; dJ337H4.3; KLIP1; DKFZP566C243; RP3-337H4.3; C6orf109	NM_015388	Homo sapiens Yip1 domain family, member 3 (YIPF3), mRNA.	GGACTTCCCGGAGGAGGAC TACGGGTTGGACGAGATATG ACACCTAAGGA	ILMN_1790953	TGCAGCCAATGCAGAAAATGGGTCAG CTCCTTTGAGAACCCCTCCCCACC
0.602429387	2519.6895	1517.935	1158.231	1159.231	MGC138210; SKRP1; DUSP17; TS-DSP1	NM_080876	Homo sapiens dual specificity phosphatase 19 (DUSP19), mRNA.	TCACGGTGGGGGAGGAATG TGAGCTGGAGACAATGACAG GGGAGAAAGTC	ILMN_1772328	CTGAATTAAAAAATCTGTTGGTGGCCG GGCGCAGTGGCTCATGCCTGTGG
0.5993542	153.71011	92.1268	161.57262	162.57262	TAPL; KIAA1520; EST122234	NM_019624	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 9 (ABCB9), transcript variant 2, mRNA.			AGCCCAGGATCTGGCTTTGCCAGAGG TTGCAACATGTTGAGAGAACCCGG
0.593829582	917.03094	544.5601	615.4435	616.4435	MGC5442; C7orf21; SB144	NM_031434	Homo sapiens transmembrane and ubiquitin-like domain containing 1 (TMUB1), mRNA.			TTAGTGTTCTGCCGGAGGACCCAGCC GCCTCCAATCCCTGACAGCTCCTT
0.586090963	178.31012	104.50595	124.91429	125.91429	SAC3; RP1-249I4.1; hSac3; dJ249I4.1; KIAA0274	NM_014845	Homo sapiens FIG4 homolog (S. cerevisiae) (FIG4), mRNA.			GATCTTCCAAGCCCACATCCAGGCCA GCCAAGGTATCATGCAGCCCCTAG
0.580051095	392.88513	227.89345	321.34763	322.34763	GLUTX1; GLUT8	NM_014580	Homo sapiens solute carrier family 2, (facilitated glucose transporter) member 8 (SLC2A8), mRNA.			GGATCTTTGTCTTCTGGCTGGAGGTG CTTTTGGAGGTTGGGTGCTGGGCA
0.575832958	206.00179	118.62262	107.99762	108.99762	C20orf81; bA12M19.1; FLJ22376; DKFZp547L054	NM_022760	Homo sapiens family with sequence similarity 113, member A (FAM113A), mRNA.	CCATCCTTGCCCTGGCAGCT GTGGTGGTCATTATAAGCAT GGTCCTCCTG	ILMN_1750312	CACTCAGAGAGACTGATCCACACATAC AAACTGGACAGACGGCCTCCTGC
0.574010549	730.39764	419.25595	482.72263	483.72263	MGC141937; FBH1; Fbx18; MGC131916; FLJ14590; MGC141935	NM_178150	Homo sapiens F-box protein, helicase, 18 (FBXO18), transcript variant 2, mRNA.			CTTGCCTCCCCTCTGGATGTATCTGGT CAGGGAAGTGGGGGATGTTCTTT
0.57042723	751.82263	428.8601	429.18927	430.18927	FLJ22678; CSS2	NM_024536	Homo sapiens chondroitin polymerizing factor (CHPF), mRNA.	GCCTCTTCCCAGATGGCAAT CTGTCCTATCTCTGTGCTGG AAGATGCTAG	ILMN_1767113	CCCCCTGACGCTGCTGATTCGGGCTG TGGCCTCCACGTATTTATGCAGTA
0.563404601	343.44345	193.49762	275.41428	276.41428	FAM108A2; C1orf47	NM_001080422	Homo sapiens family with sequence similarity 108, member A3 (FAM108A3), mRNA.	CCTACTGGGAGGTGGGACC CCTTTCATTTTCAGTTTTGCT CATCTAGGGA	ILMN_1746171	GTGCCTGGTGCCAGGTACACGGTCCT CTTCTCGCACGGCAATGCCGTGGA

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.561836648	164.86429	92.6268	164.73929	165.73929	ERGIC32; MGC14345; KIAA1181; ERGIC-32	NM_020462	Homo sapiens endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (ERGIC1), transcript variant 2, mRNA.			CTGCGAGTTGGTTGGGCTTGACATTC AGGATGAGATGGGCAGGCACGAAG
0.557679737	1056.531	589.20593	431.0101	432.0101	CSIF; IL-10; IL10A; MGC126451; TGIF; MGC126450	NM_000572	Homo sapiens interleukin 10 (IL10), mRNA.	GCTCAGCGGCTATGACCAG GTGCTCCACGAAGACGAAAC CACGAACCGCA	ILMN_1800381	GGAAGTTGCAGTGAGCTGATATCATG CCCCTGTACTCCAGCCTGGGTGAC
0.556429571	2500.1475	1391.156	1254.2101	1255.2101	DIA1; B5R	NM_000398	Homo sapiens cytochrome b5 reductase 3 (CYB5R3), transcript variant M, mRNA.			GGGCCCTCCCAGAACCTCAGCATTTC CTTCCAGCCCATCCAAACACTGAG
0.555538632	6851.0645	3806.031	3956.5435	3957.5435	ALURBP; MGC14326	NM_003134	Homo sapiens signal recognition particle 14kDa (homologous Alu RNA binding protein) (SRP14), mRNA.	CCCCGTATGCAACCCTTGCC TCAGAATTCCTTCAGAGAGA GGTGACTGTC	ILMN_1744817	AGCAGTTCCTGACGGAGCTGACCAGA CTTTTCCAGAAGTGCCGGACGTCG
0.551728253	337.63928	186.28513	276.76428	277.76428	KOX30	NM_001005368	Homo sapiens zinc finger protein 32 (ZNF32), transcript variant 2, mRNA.			CTGTACCCAGTGCAGGAAGAGTTTCC ACACCAGGGGGAATTGTATTCTGC
0.55133506	538.1893	296.72263	327.87262	328.87262	MGC16770	NM_020673	Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA.			GCCTGGTTACCTGTCATGGAATGCTG CAGTGGTGGTTTGCCAAGCTTCTG
0.550581367	2773.806	1527.2059	967.83514	968.83514	MGC150473; MGC150472; DMC1H; HsLim15; dJ199H16.1; LIM15	NM_007068	Homo sapiens DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast) (DMC1), mRNA.	GCCAGGACAGCCCTCCCAG CCATGAATCCTTACTCAGCT ACCTCGGGTTG	ILMN_1758529	CAAGTGCAGTGGCATGTGCTTGTAATC CCAGCTACTCTGGAGGCTGAGGC
0.545161734	3203.9226	1746.656	2032.0977	2033.0977	KAR	NM_016142	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 12 (HSD17B12), mRNA.			TGCAGCAAGAAGATTGGTCTTTACCTA GGCTGTGTTTCCTAAGCTCTGAG
0.539813908	784.1393	423.2893	567.631	568.631	EMLP; HLC-10; EMP; PIG5	NM_005882	Homo sapiens macrophage erythroblast attacher (MAEA), transcript variant 2, mRNA.			TCCGCCCATGATGCTGCCCAACGGCT ACGTCTACGGCTACAATTCTCTGC
0.538308076	608.5226	327.57263	518.3976	519.3976	MGC125857; AMP; MGC125856; DKFZp686D13177; MGC129961	NM_000485	Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, mRNA.	CTCAGGGATGTGACTGAGG CCCAGGAGGGACCTGTGAG GGTCTGTTTACA	ILMN_1760628	TCCCTGGAGTACGGGAAGGCTGAGCT GGAGATTCAGAAAGACGCCCTGGA
0.533381597	149.26428	79.61482	133.55595	134.55595	SEC15L1; SEC15L3; EXOC6A; Sec15p; DKFZp761I2124; FLJ1125; FLJ11251; SEC15L; MGC33397	NM_019053	Homo sapiens exocyst complex component 6 (EXOC6), transcript variant 1, mRNA.	CGGAGCCCCTACGGCTTTA GGCATGGAGCCAGCGTCAA CTACGATGACTA	ILMN_1676822	GTGCGAGGGTAGATGGTTCCTGCACA CAGAAGTTACCACAGGGGTCAGGT
0.53099092	499.8393	265.41013	311.9643	312.9643	MGC138424; MGC138422	NM_001752	Homo sapiens catalase (CAT), mRNA.			ACATTTAATACAGCAGTGTCATCAGAA GATAACTTGAGCACCGTCATGGC
0.529289963	15775.848	8349.998	9824.389	9825.389	NRAGE; DLXIN-1	NM_001005332	Homo sapiens melanoma antigen family D, 1 (MAGED1), transcript variant 3, mRNA.	TACAATAGGACTGTTTACTG CCCACCTCCGCCTGCCAGC CCACCCCAGCC	ILMN_1716957	CAGCCAGTGCCAACTTCGCTGCCAAC TTTGGTGCCATTGGTTTCTTCTGG
0.528694471	3634.3726	1921.4727	1301.1892	1302.1892	O-Fuc-T; O-FUT; FUT12; O-FucT-1; MGC2482; KIAA0180	NM_015352	Homo sapiens protein O-fucosyltransferase 1 (POFUT1), transcript variant 1, mRNA.			AATAATAGCCAGGCGTGGTGGCACAT GCCTGTATTCCCAGCTGCTTGGGA

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.526894405	110.09762	58.00982	141.35178	142.35178	DKFZp686F2182; MGC126529; DPDE4; PDE4B5; PDEIVB	NM_002600	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), transcript variant a, mRNA.	GGTGCTTTGGCCCTAATAGC ACTGGACAACACCACGACCA CATGGAAACA	ILMN_1670807	TTCTTCTGAATGCTCCCGAACTACTGA CTTTGAAGAGGTAGCCTCCTGCC
0.524752801	307.15594	161.18094	144.58511	145.58511	MGC125648; FLJ20367; FLJ20154; OPAL1	NM_001083913	Homo sapiens chromosome 10 open reading frame 26 (C10orf26), transcript variant 1, mRNA.			GCAGTCCCCTGTGTTTGCCAGAGATA CTGTGCTCGAAGTAGAGGTTTTAC
0.516537309	811.98096	419.41846	559.55597	560.55597		NM_001001660	Homo sapiens LYR motif containing 5 (LYRM5), mRNA.			ATGTATGGAGTCATTACTTCTGACCTT GAAATAGCCTGCTGGTGACTGGC
0.512576384	35501.062	18197.006	19623.04	19624.04		NR_002202	Homo sapiens ferritin, heavy polypeptide-like 7 (FTHL7) on chromosome 13.	GTGCCACCTCCTGTCTACTC ATTGTTGCATGAGCCCTGTC TGCCAGCCCA	ILMN_1796490	GGCCGCCATAAACCGCCAGATCAACC TGGAGCTCTACGCCTCCTACGTTT
0.495481585	207.74762	102.93512	109.180954	110.180954	TFAP2; AP-2; AP2TF; AP-2alpha	NM_003220	Homo sapiens transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha) (TFAP2A), transcript variant 1, mRNA.	CTGCTCGGCCCCCAGCCCA CCCAGCCAAAAATACAGCTG GGCTGAAACCT	ILMN_1659660	GGTGCGAGACCGAGAGGGGCATATCC GTTCACGCCGATCCATGAAAATGC
0.49209589	991.19763	487.76428	508.57678	509.57678	NR1B1; RAR	NM_000964	Homo sapiens retinoic acid receptor, alpha (RARA), transcript variant 1, mRNA.	AGCTACTTTTCCAGTAGTTT GCCACTTTCTCCGAGGTAGT TTGGCTGCTC	ILMN_1751615	CCTGGAGCCCGTGGGTGCACCTGTTA CTGTTGGGCTTTCCACTGAGATCT
0.487674688	216.96011	105.805954	168.73929	169.73929	SIR2L5	NM_012241	Homo sapiens sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae) (SIRT5), transcript variant 1, mRNA.	TCTTCGGGTCCTTTTTCCTC TCTTCAGCGTGGGGCGCCC ACAATTTGCGC	ILMN_1701930	GGCCACACGCAGAGGAGAAATGGTCT TATGGGTGGTGAGCTGAGTACTGA
0.486387667	1643.5059	799.381	840.6476	841.6476	MGC16353	NM_138774	Homo sapiens chromosome 19 open reading frame 22 (C19orf22), mRNA.			CAGCCTGACTCCTGCCTGATAGCTCC TGTGTCCCCATGCTGGTCCTCCTG
0.484681646	1640.2643	795.006	1096.5977	1097.5977	CCNG	NM_199246	Homo sapiens cyclin G1 (CCNG1), transcript variant 2, mRNA.			GCTGCTGAAGTAGTGTTTAGGATCCTC CATGGCAGTTAGTGAATGTAAGA
0.48418884	654.9393	317.1143	264.78094	265.78094	ARA9; FKBP16; XAP2; SMTPHN; FKBP37	NM_003977	Homo sapiens aryl hydrocarbon receptor interacting protein (AIP), mRNA.	TAGGAATCTATGATGCTGAT GGTGATGGAGATTTTGATGT GGATGATGCC	ILMN_1693771	TTCTCCCATTGACAGGAGCACTTGGC CCTGCCTTACCTGCCAAGCCCACT
0.484066151	844.7143	408.8976	324.02264	325.02264	MGC133309; FLJ35755; DKFZp434N1928; IL-17RD; SEF; IL17RLM	NM_001080973	Homo sapiens interleukin 17 receptor D (IL17RD), transcript variant 1, mRNA.			ATTAATCAGGCGTGGTTGTGTGTGCCT GTAATCCCAGCTACTCGAGAGGC
0.483801807	1547.0559	748.46844	1009.97266	1010.97266	beta2i; MGC1665; LMP10; MECL1	NM_002801	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10), mRNA.			ACCCTGGAGCTAGTGGAGGAAACTGT GCAGGCTATGGAGGTGGAGTAAGC
0.483740768	1925.1309	931.2643	641.9309	642.9309		NR_002220	Homo sapiens double homeobox A pseudogene 3 (DUXAP3) on chromosome 10.	GAATTGGGCAGCTCATGCTT GAGACCCAATCTCCATGATG ACCTACAAGC	ILMN_1792922	TGTGGTGGCATGTGCCTGTAATCCCA GCTACTCTGGAAGCTGAGGTAGGG
0.47954595	3787.206	1816.1393	2138.2559	2139.2559	FLJ34709; AXLLG; AXSF; DKFZp666G247	NM_000820	Homo sapiens growth arrest-specific 6 (GAS6), mRNA.	GATTGCAGGGTCCGCCTTCT CAAACCCCACTTCCTGGACC ACATCATCCA	ILMN_1705433	GCTGAGAGCTGGGCTTTCCTCTGTGA CCATCCCGGCCTGTAACATATCTG

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.47589945	3110.456	1480.2643	1591.8477	1592.8477	PRDX6; AOEB166; MGC142285; B166; PRXV; PLP; MGC117264; SBBI10; ACR1; PMP20; MGC142283	NM_012094	Homo sapiens peroxiredoxin 5 (PRDX5), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	TCCCACTCCGCCACCTCCGT CCACACCTCGGTCTGATGG GCGAGAAATAT	ILMN_1715110	GGCCAAGGGAGTCCAGGTGGTGGCC TGTCTGAGTGTTAATGATGCCTTTG
0.474428932	626.73096	297.3393	421.2726	422.2726	RNUT1; Snurportin1; KPNBL	NM_001042588	Homo sapiens snurportin 1 (SNUPN), transcript variant 3, mRNA.			CCCAAGTTGAAGGGTTCTTCCCATAGC CCAGACCACCCTGGATGCCTCAT
0.47056792	412.50177	194.1101	271.18097	272.18097	GDE1; 363E6.2	NM_016641	Homo sapiens glycerophosphodiester phosphodiesterase 1 (GDE1), mRNA.	GAGTGGGGCTTCATGACCAT GTGCATCAGAATTGCCTGGA GTGTGCACTG	ILMN_1797903	GCTTACCGCTTCTCACCTTTCAACCCC ATCTGTGGCCTTTGTCCAGGCCC
0.465124943	366.22263	170.33928	234.43929	235.43929	MAP-1; PNMA4	NM_022151	Homo sapiens modulator of apoptosis 1 (MOAP1), mRNA.	AAACAACCCTGAGCCCAGG GCCAACCCCTACGGAACACC ACTACTTTACC	ILMN_1662383	GTGCAGTGCTCTGAGGGGACAGACAA GGCTTGGGTGTATATGCCAACCAG
0.462923758	201.98096	93.501785	72.96098	73.96098	FLJ39091; PGR-2; PGR2; DKFZp686P10120	NM_152444	Homo sapiens zinc binding alcohol dehydrogenase, domain containing 1 (ZADH1), mRNA.	ACGATTGCCAGCCGCCCGC GTACACCTACAACAACATCA CCTGTGCCAGC	ILMN_1673488	ACAGCCGGGCCTGATGTCTCAAGCCT GTAATCCTAGCACTTTGGGAGGCA
0.453864618	467.58093	212.21844	207.84761	208.84761	FLJ13222; TEX27	NM_021943	Homo sapiens zinc finger, AN1-type domain 3 (ZFAND3), mRNA.			TTTACCACTGCTGTCAAGCCACAGCCC TTGGCCACCATACGGGCCATCCT
0.452037606	549.23926	248.2768	237.39761	238.39761	MLVAR; PIT-2; GLVR2; Glvr-2	NM_006749	Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA.	CCGTGTGAGCCAGTCCAGG AGGGTGTAAGTTCTGAATGG TTCCTTGCTGA	ILMN_1687501	TCTGAGGCCCACACAAAGCTGGACAC CCCCAGGCTCTACTCCATCCCATT
0.450345985	1302.7893	586.70593	731.45593	732.45593		NM_005780	Homo sapiens lipoma HMGIC fusion partner (LHFP), mRNA.			TCCCCACACACGCCTATGCACAAACGT GGATTATCGCACAGACTGGGAGG
0.443868574	759.6226	337.1726	268.13095	269.13095	CRP2; LMO5; SmLIM	NM_001321	Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA.	TGCACGGCTCCAGCTCAGC CCATTGAGCCAATAACTGCT GCTCCCAGTGG	ILMN_1798138	GAGCTGGAAAGCCCTGGCACAAAAAC TGTTTCCGATGTGCAAAGTGTGGG
0.438254685	1219.7476	534.5601	602.4643	603.4643	FLJ10420; RP4-798A10.1	NM_018090	Homo sapiens NECAP endocytosis associated 2 (NECAP2), mRNA.			TGTTGTCATGGAGCTGTGGGAGTTGG CACTCTGTCTGCTGGTGGCCCTCT
0.437917295	2858.706	1251.8768	2207.2644	2208.2644	PAST1; PAST; HPAST1; FLJ42622; FLJ44618; H-PAST	NM_006795	Homo sapiens EH-domain containing 1 (EHD1), mRNA.	TGGACGCGTCCAGCCAGAC CCAAGGGGCTGGGGGCCCT GCTGGAGTGATT	ILMN_1768427	CACTCCATACAGTATTAGGTGAGGATG GATGCGGGCGCTGTCCTTGCCGG
0.434473309	1076.7101	467.8018	505.81012	506.81012	PIP5Kgamma; PIP5K-GAMMA; KIAA0589	NM_012398	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, gamma (PIP5K1C), mRNA.	TGTCCAGAGGGGGTTCTGC CCCTTGTGAAGGCCCATTCC TGGCACTTAGA	ILMN_1745365	TGGTGCGTGACAATCCAAAGCGCCGA GACGAGGGTGCTGTGTCCCTCAAA
0.431694425	520.4726	224.68512	543.631	544.631	FLJ23617	NM_138809	Homo sapiens carboxymethylenebutenolidase homolog (Pseudomonas) (CMBL), mRNA.			GGACCAGCTGACAGGTCAAGTGTGGC CTTTTCTGGTCTTTGAACACATCA
0.429060045	712.2976	305.61844	508.85178	509.85178	BRCC45; BRCC4	NM_199191	Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, mRNA.	GTACGTTGGTGCCCGCTGCT GTCTAATGCCCTGGAGCCTC CCTGGCCCCC	ILMN_1693060	CCTGCCTCTGTTTTTCCCTCGAGACCA GCCAACTCTCACATTTCAGTCCG

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.41871783	323.32263	135.38095	41.610107	42.610107		NM_001050	Homo sapiens somatostatin receptor 2 (SSTR2), mRNA.	GGTGAGCCCACCAGTGAGG ATTACTGATGTGGACAGTTG ATGGGGTTTGT	ILMN_1787680	TGTAAATTAGTCGGGCGTGGTGTCAC GTGCCTGTAATCCTAGCTGCTCGG
0.417857496	2284.206	954.4726	1457.656	1458.656	FBL1; MGC1366; FBXL1; FLB1	NM_032637	Homo sapiens S-phase kinase-associated protein 2 (p45) (SKP2), transcript variant 2, mRNA.	CCCATCTTCCTGCTATAAAT GTGGGTGTGATGGCTGGAT CTGGGGCAGCC	ILMN_1764577	AGTGACAAGAGCTGGGGTTAGGATCC GGTTGGACTCTGACATCGGATGCC
0.417701378	183.51012	76.65243	182.24762	183.24762	HUS; MGC88246; HF1; FH; ARMD4; ARMS1; HF; CFHL3; FHL1; HF2	NM_001014975	Homo sapiens complement factor H (CFH), transcript variant 2, mRNA.			GGATCACATTCATTGCACACAAGATGG ATGGTCGCCAGCAGTACCATGCC
0.401038578	265.01428	106.28095	118.180954	119.180954	PWDMP; KIAA1638; FLJ23127; ORF26	NM_025132	Homo sapiens WD repeat domain 19 (WDR19), mRNA.	GCTGTGGAACAATCAGCCCA TCTCTTTGTGACCTGGAGCA GTCAGAGGGC	ILMN_1680367	ACCTCTCCAGGTCGGCACTTTCCACTT CTGTACGGTGGCAAAACGATGAC
0.397927384	96.29762	38.31946	59.494514	60.494514	FLJ00001; C9orf28	NM_033446	Homo sapiens family with sequence similarity 125, member B (FAM125B), transcript variant 1, mRNA.	CAGTTCTCACTCTCTTAAATG GTACCTCAAAAAGCTGGAGC CTCTCTGCC	ILMN_1661833	ACCAGAGACGGCTTTGTTCTCCCAGC TAAGGCCGTGGAGCTGCTGTGTGA
0.377937991	1215.2393	459.2851	651.85596	652.85596	RP1; EB1; EB2	NM_014268	Homo sapiens microtubule-associated protein, RP/EB family, member 2 (MAPRE2), mRNA.	TATCAATTCTGCTGTGTTCC CTGGCCTGCAGGGAGGTCC CCACAACCACG	ILMN_1743784	CCCTCTTTAACACAAGGGCCCTCCTTG TCATTGACCTTAGCTAAACCATG
0.377634922	373.4143	141.01428	162.47263	163.47263	MGC125831; DKFZp686J07229; MGC125832	NM_001002034	Homo sapiens family with sequence similarity 109, member B (FAM109B), mRNA.	GAATAGTCTCACTGTCCCCC GTTTGCCTCCACGAGCCTGC TGTTTCCAGG	ILMN_1709247	AGAGACACCCCCTCCCAAACACATAAA ACTTGCCCCTTCCTAGCCTCGGC
0.377383484	2100.885	792.8393	922.5476	923.5476	ADPRT3; ADPRTL3; pADPRT-3; ADPRTL2; IRT1; hPARP-3	NM_005485	Homo sapiens poly (ADP-ribose) polymerase family, member 3 (PARP3), transcript variant 2, mRNA.	TGAGGTCAACGGCAGAGACT TATCCAGAGCAACTCATGAC CAGGCTGTGG	ILMN_1742949	CTGTGCCTGGCTTATTTCACTCAGCAT AATGTGCACCGGGTTCACCCATG
0.364462925	1032.0143	376.13095	242.88095	243.88095	RNF49; MALT2; API2; HIAP1; AIP1; MIHC; HAIP1; CIAP2	NM_182962	Homo sapiens baculoviral IAP repeat-containing 3 (BIRC3), transcript variant 2, mRNA.			GTGGTGGTATGTGCCTGTAGTCCCAG GCTGAGGCAAGAGAATTACTTGAG
0.360290889	560.90594	202.0893	311.45593	312.45593	UB1; CEP3; FLJ46903; BORG2	NM_006449	Homo sapiens CDC42 effector protein (Rho GTPase binding) 3 (CDC42EP3), mRNA.			CCATGACTCTCCAGTGTTTTTTCTGTT GGACCACACCCGTCACAGTTCAC
0.35363462	328.2393	116.07678	98.50185	99.50185	ATP-BL	NM_004913	Homo sapiens chromosome 16 open reading frame 7 (C16orf7), mRNA.	GGAGATGGTGTGTCCTGAAC AGTGTAGCTCAGGTCAGCTT GAACTTTCCA	ILMN_1788786	CTCACCTTGGCTGTGGGCTGTGAACA TTCCGGGACCCTGGGCATCTTATC
0.350496348	494.26846	173.23929	225.4226	226.4226	CAP50; ANX11	NM_001157	Homo sapiens annexin A11 (ANXA11), transcript variant a, mRNA.	AAGCGGGGAGAGGGTACAC AATGGGTATCTAATAAATACT TAAGAGGTGG	ILMN_1808732	GCCAAAACTTGTTTCCACATTAAGAGT CAGCCAGCTCTGGAATGGTCTGG
0.348155907	411.6143	143.30595	230.57262	231.57262	PHS; PCD; DCOH; PCBD	NM_000281	Homo sapiens pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (PCBD1), mRNA.			GTGGGATGTGCCAGTGTCCCCACCAA CACCAGGAATTTAGACCTTTTCCC
0.344702664	1001.33923	345.1643	234.30179	235.30179	FP1572; 447AA	NM_001856	Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA.			CCATGCCGATGGAGCAGCAGTACCCA CCCATGAAAACCATGAAGGGGCCT

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.344648808	975.53925	336.21844	460.68097	461.68097	SNURF-SNRPN; HCERN3; SMN; RT-LI; SM-D; SNRNP-N	NM_022805	Homo sapiens small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 2, mRNA.	CTCTGTTCACTCCACTGAAT GCAACCCATATAGTTTCTTG CACAAGGTGC	ILMN_1729617	GGTCCACCTCCCCCAGGAATGCGTCC ACCAAGACCTTAGCATACTGTTGA
0.324503107	348.73096	113.16428	161.70178	162.70178	RAB7L; DKFZp686P1051	NM_003929	Homo sapiens RAB7, member RAS oncogene family-like 1 (RAB7L1), mRNA.	GCTGGGGCCCGGGGATCTA ATTGTTTAGAGAGCCCCAAA AGTGGCTCAGA	ILMN_1669753	GCAAGTGACATCAGCTGGCTGTGATG CTTCGAAATAGGTCTGCTCCTCAC
0.321629554	335.49762	107.90595	188.44762	189.44762	FBL2; FBL3; DKFZP564P0622	NM_012157	Homo sapiens F-box and leucine-rich repeat protein 2 (FBXL2), mRNA.			GCTCGGAGTCTGTGTTGCCTGATTGG AAAGTAGAAGCTCTGGTGTATGCT
0.320342906	854.0643	273.59344	407.7726	408.7726	AGU; ASRG; GA	NM_000027	Homo sapiens aspartylglucosaminidase (AGA), mRNA.			CTCTCTGTATGACAACTCTACAGAAGT TGTGCGCGTGCTTTCTCAGCAGC
0.319156288	744.2726	237.53928	353.62262	354.62262	FGFR5; FHFR	NM_021923	Homo sapiens fibroblast growth factor receptor-like 1 (FGFRL1), transcript variant 3, mRNA.	CCAGGGCGGTTCCAAACTCT AAACCGTTCCCACCGTCAGG GAGACCTACA	ILMN_1775956	AATGATGGAAGGAAGACTGGGTTGCA GGGACTGTGGTCTCTCCTGGGGCC
0.314364607	354.98096	111.59345	265.4226	266.4226	THIF; EST01027; VDUP1; HHCPA78	NM_006472	Homo sapiens thioredoxin interacting protein (TXNIP), mRNA.	TGCATCCGACACCCACCCCC TCTTTGTGTACTTCAGTCTTG GAGTTTGGA	ILMN_1698297	CAGCCATAGCACTTTGTTCACTGTCCT GTGTCAGAGCACTGAGCTCCACC
0.313860666	167.36844	52.53037	91.239296	92.239296	MGC5179; ZC3HDC5L; FLJ12623; KIAA0734; ZC3H5L; C16orf28; FLJ23360	NM_023076	Homo sapiens unkempt homolog (Drosophila)-like (UNKL), transcript variant 1, mRNA.	ACTAGGAGGAAGGGGGCAG AGAGAGTTATGACCCCGAGA GGGCGCACAGA	ILMN_1734660	TCTGTGCGCCTGCGCCTCGGAGAGCA AGTGAAGGAGCATCATGGGTTTTG
0.312664152	4711.5977	1473.1477	1180.2144	1181.2144	MGC40146; SEPM	NM_080430	Homo sapiens selenoprotein M (SELM), mRNA.			GAATACTTCTCTTGCTGAGAGCCGATG CCCGTCCCCGGGCCAGCAGGGAT
0.31251618	288.16428	90.056	124.21011	125.21011	AVSD2; CIRRIN; DKFZP566D213	NM_001031717	Homo sapiens cysteine-rich with EGF-like domains 1 (CRELD1), transcript variant 1, mRNA.			GGTGGCTGCTAGAGCTTTGGCCCCTG CTTAGGATTAGGTGGTCCTCACAG
0.309020538	507.9143	156.95595	176.47263	177.47263	CREG	NM_003851	Homo sapiens cellular repressor of E1A-stimulated genes 1 (CREG1), mRNA.	AGCAAGTGCCTCGGCCCAG TCTTCCTGTATTTATGTGGAA GGCGGCGGCT	ILMN_1701629	CCAGCTTCAGCCAGGGACAAAATCCC CTCCCAAACCACTCTCCACAGCTT
0.303648113	1026.0977	311.57263	410.0393	411.0393	DKFZp686I10125; MLCK108; FLJ12216; MSTP083; KRP; MLCK210; smMLCK; MLCK; MYLK1	NM_053032	Homo sapiens myosin light chain kinase (MYLK), transcript variant 8, mRNA.			AGAGCTGGAGAACTCCATGTACTTTG GAATCTCCTCCAAGATAGCCAGAG
0.303183999	179.93095	54.552185	97.264465	98.264465	MGC138864; FLJ34766; MGC138863; RNF154	NM_178502	Homo sapiens deltex 3 homolog (Drosophila) (DTX3), mRNA.			AAGGGAGGGTCTCTTGATTCCTAACC GCCCCCACATACTGCTCCACCGCT
0.285947305	309.60596	88.53099	120.62262	121.62262	MGC131937; FLJ21478; NOD26; NOD9; CLR11.3; NOD5; DLNB26; MGC21025	NM_170722	Homo sapiens NLR family member X1 (NLRX1), transcript variant 2, mRNA.			GGATGCCCTCACATTGGTGCTTTCTCC TCATCCTCATGCCCCCTTTGCCA

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.28578188	1401.6143	400.55597	934.881	935.881	UBCH8; RIG-B; MGC40331	NM_004223	Homo sapiens ubiquitin-conjugating enzyme E2L 6 (UBE2L6), transcript variant 1, mRNA.	AGGAGCTGGAATATGGGGA GTCAGCGAGGACGGTGGGG CCAGGAGCCCTT	ILMN_1659773	CCTCCAGCATTCAGTCCAGGGGGAGC CACGGAAACCATGTTCTTGCTTAA
0.285279011	6349.1562	1811.281	5419.3975	5420.3975	TSA-1; RIGE; RIG-E; SCA2; SCA-2	NM_002346	Homo sapiens lymphocyte antigen 6 complex, locus E (LY6E), mRNA.			CAGGGAGACCGTGTCAGTAGGGATGT GTGCCTGGCTGTGTACGTGGGTGT
0.280661916	419.16428	117.64345	206.49762	207.49762	UGPP	NM_177533	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 14 (NUDT14), mRNA.			CCGGACATCCCCAAGACCCTCGGCGT CATCTTTGGTGTCTCATGGTTCCT
0.280407363	441.34344	123.75595	151.37262	152.37262	PKD; PKCM; PKC-MU; PRKCM	NM_002742	Homo sapiens protein kinase D1 (PRKD1), mRNA.	GAATGCTATCATCCTGCTTG CCTGTCCATTTGTGGAACAG CATCTGGTGA	ILMN_1652826	AGACAATGCACCTAGCTGTGCAAGAC CTAGTGCTCTTAAGCCTAAATGCC
0.278116464	1329.0809	369.63928	333.51428	334.51428	DKFZp686L17253; CGI-40; FLJ90656	NM_001040455	Homo sapiens SID1 transmembrane family, member 2 (SIDT2), mRNA.	AAAGTGATGGCGAGCGACC ACCGAGAGGCGCTGCTGGA CAGGGAGAGCGA	ILMN_1754827	GGGCTGGGAGATGAGGTGGGTCTGG ATCTTTTCTCAGAGCGTCTCCATGC
0.261287789	565.34766	147.71844	307.16846	308.16846	TMS1; MGC10332; ASC; CARD5	NM_013258	Homo sapiens PYD and CARD domain containing (PYCARD), transcript variant 1, mRNA.	CAGAAGGCAACGCTTCTCTT TCTGGTCAAAATGGCTGGTA AGCAGGCCGT	ILMN_1759453	ACGTTGAGTGGCTGCTGGATGCTCTG TACGGGAAGGTCCTGACGGATGAG
0.24709248	1519.6643	375.49762	705.9518	706.9518	RNB6	NM_016337	Homo sapiens Enah/Vasp-like (EVL), mRNA.			CAGCTCCGTCCCCAGCGCTCATGGTG TTGAAACTGTCTGTCATGCACCAC
0.246843604	370.43512	91.43954	198.3393	199.3393	MGC45350; SYN; SLK	NM_153047	Homo sapiens FYN oncogene related to SRC, FGR, YES (FYN), transcript variant 2, mRNA.	CCTCGGGTGGCCAACTTGCT ATCTGGTGGGTGACTTGGG GACTAGAAAGA	ILMN_1715901	CAGCGGAACCGCCCAGGATCAGATTG CATGTGACTCTGAAGCTGACGAAC
0.245369312	427.3393	104.85595	368.05597	369.05597	TP53I2; PIG2	NM_000156	Homo sapiens guanidinoacetate N-methyltransferase (GAMT), transcript variant 1, mRNA.			ACGACACGTACCCACTCTCGGAGGAG ACCTGGCACACACACCAGTTCAAC
0.244972272	6280.1226	1538.4559	2321.8977	2322.8977	FBLN	NM_006486	Homo sapiens fibulin 1 (FBLN1), transcript variant D, mRNA.	GCCCTGGTCCCGAGTGGCG TGGGGACGGGCCATCACTG TATGTATTAAAA	ILMN_1766346	TCACCAGGGGAATGGCTGGGATTTCT CGGCACTCTGCATCATCCATCTTT
0.234412734	472.5893	110.78095	130.08095	131.08095	ADAR2a; ADAR2; DRABA2; DRADA2; ADAR2a-L1; ADAR2a-L2; ADAR2g; ADAR2c; RED1; ADAR2a-L3; ADAR2b; ADAR2d	NM_001112	Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant 1, mRNA.	AGAGGTGTTGGCTGGACCC CTCCTGGCTCCTACAAAGTG GAAATGGCTCG	ILMN_1654960	TACACCACACGTTACAACTGCATGAGC TTCCTCTCGCACAAGACCAGCTG
0.23370653	853.33923	199.43095	306.70593	307.70593	MGC23008	NM_016429	Homo sapiens coatomer protein complex, subunit zeta 2 (COPZ2), mRNA.	GCTGTTTTCAGCCATGTTTC TCTGTGCATCTCCAGTAAGC AGAAGGCTAC	ILMN_1729640	TTCCCCAATCCTGGCAAAAGCCCAAAG ATCCCAGGGTCAGGAGAGACCCC
0.232070062	662.86426	153.83095	422.98096	423.98096		NM_000137	Homo sapiens fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA.			CGGCTCCATGTTGGAACTGTCGTGGA AGGGAACGAAGCCCATAGACCTGG
0.227004272	120.51012	27.356312	80.24065	81.24065		NM_175709	Homo sapiens chromobox homolog 7 (CBX7), mRNA.			CTGGGGGCAGGCGCTGTGCTTCTGTG AGGTGGTTTAGCTTTTGCTTTCGA

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.209537531	11513.798	2412.5728	6394.1807	6395.1807	P35SRJ; MRG1	NM_006079	Homo sapiens Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (CITED2), mRNA.			GTTCTGGATCAGGAAAGTCATACTGTT CACTTTCAAGTTGGCTGTCCCCC
0.202216313	278.56845	56.331085	82.910965	83.910965	NGX6; RP11-112J3.10; MGC120460; NAG-5	NM_016446	Homo sapiens chromosome 9 open reading frame 127 (C9orf127), mRNA.	GCATCAGAAGGAACTGGAAA ACGTGGCACAACCCCCTCAA GCTCCGCACC	ILMN_1659306	TTCCACCACGTTCTCCGAGGGTTTGG GAATGTCTGTGCCTTCACTGTGTC
0.191625889	1202.0476	230.34344	282.57678	283.57678	ST15; hRECK	NM_021111	Homo sapiens reversion-inducing-cysteine-rich protein with kazal motifs (RECK), mRNA.			AAGCTTTCAGAATATGTCAGTGCTGAT GTAGCATGCTTGTTGCAATTGCC
0.191468412	298.43927	57.141693	70.26468	71.26468	AK4; AK3	NM_013410	Homo sapiens adenylate kinase 3-like 1 (AK3L1), nuclear gene encoding mitochondrial protein, transcript variant 6, mRNA.			GGGGTTGAGCAGAATGTTGTACTAGC TGTGCCTGGACTGAGTATAACAGC
0.181433944	753.31433	136.67679	354.2768	355.2768	FLJ23221	NM_024579	Homo sapiens chromosome 1 open reading frame 54 (C1orf54), mRNA.			GAACGATGCCGTGTCCAGTTTGCGAA GTCCTATTCCCCTCCTCCTGTCGC
0.161660748	235.33928	38.045124	148.24762	149.24762	SDS-RS1	NM_138432	Homo sapiens serine dehydratase-like (SDSL), mRNA.	GTCTTGAGGATATGGGAAGC CTAGAGAAACGCAAGCAGAC TGGATTGGGA	ILMN_1804738	GCCCATGGACAGTCCTGTGTCTGGAT GAGGAGGACTCAGTGCTGGCAGAT
0.158183471	439.28094	69.486984	117.69765	118.69765	ACYP; ACYM	NM_138448	Homo sapiens acylphosphatase 2, muscle type (ACYP2), mRNA.			TGGCTGGGTGAAGAATACCAGCAAAG GCACCGTGACAGGCCAAGTGCAGG
0.150562473	960.881	144.67262	289.13928	290.13928		NM_001030001	Homo sapiens ribosomal protein S29 (RPS29), transcript variant 2, mRNA.	CACTGCAGATGCGGTCACCT GACTGACCACCTGGGTTTTC TATTACCAGT	ILMN_1664047	AGAGCAGCCCAGGTGGTCATCAGAGT CACCAATGCCAATGCCAGCCTGCA
0.149965271	562.9226	84.41884	58.469288	59.469288	AM2; FLJ21135; dJ579N16.4	NM_024866	Homo sapiens adrenomedullin 2 (ADM2), mRNA.	GGCCATCTGTGGCTGGAGG GTTCTGAATGTCCTCTCTCC ATGTCAGGCAG	ILMN_1734184	CGCCCTAACAACTTCCCATCCGCTGAC CCCTCCAACGCCATCAATCTCCA
0.14942023	8031.806	1200.1143	2424.0642	2425.0642	ICAP-1alpha; MGC22256; PRO1489; RP11-401M16.1	NM_018584	Homo sapiens calcium/calmodulin-dependent protein kinase II inhibitor 1 (CAMK2N1), mRNA.	AAAGTCGCATCAGAGAGCTG AGGGTAAGACTCAGGTGTCC TGACTCCCAG	ILMN_1661627	TATGACCGACAAGGCACCTCCTGGTG TCTAACTCCCCCAAAGACAATGAG
0.140246942	109.093445	15.300022	68.0383	69.0383	MGC8906; HRASLS4; TIG3; RIG1	NM_004585	Homo sapiens retinoic acid receptor responder (tazarotene induced) 3 (RARRES3), mRNA.			GGCCACGGCGCTTGGAATCCTGGTTG TTGCTGGATGCTCTTTTGCGATTA
0.134345299	430.83093	57.88011	304.4726	305.4726	G0S8	NM_002923	Homo sapiens regulator of G-protein signalling 2, 24kDa (RGS2), mRNA.	TGACTCTTACCCAGCGCATG TCTTTATCAGTGTGTACTCG TGACGATTTG	ILMN_1652434	CTGCAGTGTCCGTTATGAGTGCCAAAA ATCTGTCTTGAAGGCAGCTACAC
0.128826756	748.0476	96.368546	257.38513	258.38513	MGC138902; FLJ31627; MGC138903; RILP; FLJ31937	NM_153026	Homo sapiens prickle homolog 1 (Drosophila) (PRICKLE1), mRNA.			CTGTGCATCTTATTGTGAGGCCAGCTT GTCCCCTCGAACCCTCTTTGGCC
0.126176324	166.93929	21.063786	120.884796	121.884796	PSBG2; PSGGB; CEA; PSG1	NM_031246	Homo sapiens pregnancy specific beta-1-glycoprotein 2 (PSG2), mRNA.	TAAGTAAGTCAGGTCCCTAA GCCCCGTCCCAAGAAGTGA CACAAGTGGCC	ILMN_1765746	CCAACATAGCAGCTGTGATGTCATTTC TGTATTTCAGGAAGACTGGCAGG
0.109503583	2135.3726	233.83095	659.16846	660.16846	PSG9	NM_002780	Homo sapiens pregnancy specific beta-1-glycoprotein 4 (PSG4), transcript variant 1, mRNA.	AATTCCTACTTCACTAACCCT TCCTTATCCTGCCACCTCGC CGGGGGCCA	ILMN_1740104	CCAAAGATGTCAGAACAAGACTCCCCA TCATGATAAGGCTCCCACCCCTC

Fold change	XS	XS+ 6 GFs	pOS +no GFs	pOS +no GFs	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.105854725	6043.756	639.76013	771.506	772.506	FLJ11259	NM_018370	Homo sapiens damage-regulated autophagy modulator (DRAM), mRNA.	CACTGAGAACGCCTGCCAG CTTCCCCATGCCCTCACTTG GTTTGTGTTTT	ILMN_1707232	CTTCTGCCTCACTTCGAGCAGACTTTT GTTCTCGGCGCTCCTCACGATGG
0.104732912	2184.4226	228.78094	507.6976	508.6976	PSG9	NM_002780	Homo sapiens pregnancy specific beta-1-glycoprotein 4 (PSG4), transcript variant 1, mRNA.			GCTAAATGGTCAGAGCCTCCCTGTCA GTCCCAGGGTAAAGCGACCCATTG
0.076132985	476.5976	36.284798	109.51433	110.51433	TSRC1	NM_025008	Homo sapiens ADAMTS-like 4 (ADAMTSL4), transcript variant 2, mRNA.	AGCGTGCGGAGCATCTGAA GTTGCAGTCTTGCGTGTGGA TGGTGCAGCCA	ILMN_1784737	GGGTAACCACGCCCAGGACACCTCAG CCTTTCCAGCATAGCTCAATAAAC
0.067751851	940.68506	63.733154	186.40178	187.40178	FCRN; alpha-chain	NM_004107	Homo sapiens Fc fragment of IgG, receptor, transporter, alpha (FCGRT), mRNA.	AAGACAAGCAGGAGGGTCG ACATGGACTGAAATCACCCT CTGCAGCTGGG	ILMN_1734508	TGTGATTCCAGCCACCGCCTGACCAT CCGCCATTCCGACTGCTAAAAGCG
0.042392629	194.09761	8.228308	306.35596	307.35596	MGC88184	NM_001847	Homo sapiens collagen, type IV, alpha 6 (COL4A6), transcript variant A, mRNA.			CAGATGTGTGCAATGTGGCAAACTGA AGCTGCACAGTGTTGGTTTCCTTG
0.038494152	2721.6726	104.76848	54.837307	55.837307	RTP801; Dig2; REDD1; FLJ20500; RP11-442H21.1; REDD-1	NM_019058	Homo sapiens DNA-damage-inducible transcript 4 (DDIT4), mRNA.			GCTGCGTTTAAGCCTTCCCCCATCGT GTACTGCAGAGTTGAGCTGGCAGG
0.022994124	495.38095	11.390851	79.3989	80.3989	CRABP-II; RBP6	NM_001878	Homo sapiens cellular retinoic acid binding protein 2 (CRABP2), mRNA.	CCCCAGAGATAAAGGCTGCC ATTTTGGGGGTCTGTACTTA TGGCCTGAAA	ILMN_1702691	CCAAGTCAGCAGTCCTAGCCCCAAAC CAGCCCAGAGCAGGGTCTCTCTAA
0.014212892	1171.4476	16.649658	115.31845	116.31845		NM_177964	Homo sapiens hypothetical protein LOC130576 (LOC130576), mRNA.			CCTGGTCAAAGAGAGCTACGTTTGGG CAGTTCTGCAGAGAGGATCCTGGC
0.006603313	12596.923	83.18143	1520.5518	1521.5518	IBP5	NM_000599	Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA.	GGCGGGGGCCGGGCTTGGA ACGATGTACGATACCCTCAT AGTGACCATTA	ILMN_1665095	CACCTGAATGCGGAAGAGCTCGGCTC CCGTTTAGCATTTTGTACTTAAGG

TABLE 11

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
9.658	65.93893	6.566969	7.3681846	WFDC1	PS20	NM_021197	Homo sapiens WAP four-disulfide core domain 1 (WFDC1), mRNA.	GCTGCCTCCCCAGCTC TATCCCAACCTCTCCCA ACTATAAAACTAGGTGC	ILMN_1751028	GCCACTTAACAGCTCTGGGTCC CTGTTTTACCATCCTGGGAGCA AGGCCC
10.53	76.33146	7.2162538	7.288069	PTGFRN	CD9P-1; FPRP; KIAA1436; FLJ11001; SMAP-6; EWI-F; CD315	NM_020440	Homo sapiens prostaglandin F2 receptor negative regulator (PTGFRN), mRNA.			CACCGATGACAACAGAGGAAGA AGGGAACTGGGATTTGGGTAAG TTCTCC
18.42	146.62262	8.171854	7.7511916	C10ORF54	PP2135; GI24; SISP1	NM_022153	Homo sapiens chromosome 10 open reading frame 54 (C10orf54), mRNA.	AAGGTAGGCTGGCAGA TACGTTCGTCAGCTTG CTCCTTTCTGCCCGTG GA	ILMN_1663447	TGTTTGATCCACCCCCTTCCCT GAAAATCCTGGGAGGTTTTATT GCTGCC
39.81	307.39764	6.745281	9.418619	ITGA11	HsT18964	NM_012211	Homo sapiens integrin, alpha 11 (ITGA11), transcript variant 2, mRNA.	TCTATCAACTGCCTGA GAGGACACAATGGGGG AGGGGCTTCGGACCAC AG	ILMN_1768556	CTGTGCAGCCTTGGTGGCAAAT ATCTCATCTGCCGGCCCCCAGG ACAAGT
33.57	198.76428	5.7550135	6.493353	ADAMTS7	DKFZp434H204; ADAM-TS7	NM_014272	Homo sapiens ADAM metallopeptidase with thrombospondin type 1 motif, 7 (ADAMTS7), mRNA.			TGGTGGTGTCCAGCGGCGCCT GGTCAAGTGTGTCAACACCCAG ACAGGGC
29.75	230.40594	7.995535	7.6548815	VAV3	FLJ40431	NM_006113	Homo sapiens vav 3 guanine nucleotide exchange factor (VAV3), transcript variant 1, mRNA.			CTTTGTCTTGCCTGTATGCAGC CCTCGTGTAATACGGTGAATTA GAGTGG
75.37	489.1726	7.4008894	5.9536495	DHRS3	retSDR1; SDR1; Rsdr1; RDH17	NM_004753	Homo sapiens dehydrogenase/reductase (SDR family) member 3 (DHRS3), mRNA.			TGACCCCCACAGGGAGGCAGG AAAACAGCCAGAAGCCACCTTG ACACTTT
14.44	121.297615	7.1823564	9.777615	DAPK1	DAPK; DKFZp781I035	NM_004938	Homo sapiens death-associated protein kinase 1 (DAPK1), mRNA.			GCAGAAGAGGGTGTGTTTGAAA TCATCGGAGTCAGCCAGGAGCT GTCACC
19.58	165.03094	7.0495872	10.288898	CFB	H2-Bf; CFAB; BFD; BF; GBG; PBF2	NM_001710	Homo sapiens complement factor B (CFB), mRNA.	CTAGGGGTTTGGGGTG GGTGACTTAGGGGCGG CTTTTGTGTTCTCCCTC T	ILMN_1805126	GTCCCTATGCTGACCCCAATAC TTGCAGAGGTGATTCTGGCGGC CCCTTG
63.14	556.3143	8.450003	9.812315	C1R		NM_001733	Homo sapiens complement component 1, r subcomponent (C1R), mRNA.	AGTCAACACCTACTATG TACCAGGCACCAGGAA GCCAGAAGCTCAGGGC C	ILMN_1734655	GGCAGCCCCGAAACCTGCCTAA TGGTGACTTCCGTTACACCACC ACAATG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
13.3	115.48929	6.8430586	11.048524	CLEC3B	TN; TNA; DKFZp686H17246	NM_003278	Homo sapiens C-type lectin domain family 3, member B (CLEC3B), mRNA.	GGGGCAACCCCCTTCATTTATCTCGTGAGCGGTATCGGAAGCTCCATTTG	ILMN_1712313	CCCGCATCGCCTACAAGAACTGGGAGACTGAGATCACCGCGCAACCCGAT
5.913	51.319107	8.547511	9.686537	PVRL2	PVRR2; HVEB; PRR2; CD112	NM_001042724	Homo sapiens poliovirus receptor-related 2 (herpesvirus entry mediator B) (PVRL2), transcript variant delta, mRNA.			GATGCTCTGTCCTATAGCAGCCCCTCTGATTCCTACCAGGGCAAAGGCTT
6.699	60.55719	8.341914	10.577591	NFATC4	NFAT3; NF-ATc4	NM_004554	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 (NFATC4), mRNA.	GAGTCTGTTTGCTGTTAATTTCTTTGTGGGGGCAGCAGGAGCCTCTCAGC	ILMN_1727813	TCAGCCCCCTGCCAGAGTCACTGCCCCATAATCACCATGTCAGAAGGGAC
4.236	43.66072	11.3614855	9.471571	DENND3	KIAA0870	NM_014957	Homo sapiens DENN/MADD domain containing 3 (DENND3), mRNA.			GTCTGCATTTTGGAGAGTCCACACCACGGACCAGGTTTTCCCCCAAGGCT
15.99	126.94762	6.540902	10.772864	VIT	MGC70561; DKFZp313L1517; MGC149746	NM_053276	Homo sapiens vitrin (VIT), mRNA.	GGGTAAGAAATGAGCCTAGTCACCAAGAACTCCACCCCCAGAGGAAGTGG	ILMN_1696087	CAGAGCAGGCAGAGCACCAGCAAGTGCTGCTTTACTAACTGACGTGTTGG
14.09	114.62262	5.968002	11.407572	LEPR	OBR; CD295	NM_001003680	Homo sapiens leptin receptor (LEPR), transcript variant 3, mRNA.	AGGCTACGTGGGAGACTCGGCGCTGCAGCTGGAGAGAATCAACGTCTACT	ILMN_1702636	TGGGAAGATGTTCCGAACCCCAAGAATTGTTCCTGGGCACAAGGACTTAA
9.849	94.84346	11.585701	8.145906	C10ORF33	FLJ23849; MGC13047	NM_032709	Homo sapiens chromosome 10 open reading frame 33 (C10orf33), mRNA.			AGAGCATGTGACCCTGAACCAGCTCTGACCCAGGAAGAAGACTCCACCCC
5.438	53.527428	11.897458	8.204365	ADHFE1	HOT; FLJ32430; ADH8; MGC48605; HMFT2263	NM_144650	Homo sapiens alcohol dehydrogenase, iron containing, 1 (ADHFE1), mRNA.	GCGAAACCTGTATCCGGGCCCAACCTGAAAACATCCCAGCCAAGAACTGG	ILMN_1785272	CCAGGCTCGACTTCAGGGGTCAGTGTTCCTGTCCCAAACCCCACACAGAA
6.553	68.69252	8.94445	12.277002	HHLA3		NM_001031693	Homo sapiens HERV-H LTR-associating 3 (HHLA3), transcript variant 1, mRNA.	AACCTGCCACTACATTCTGGTTTACATTAGTTACTTCATGCTGGCTGGGG	ILMN_1715814	ATCTGAGCCTCCCGCAGAGGAATGCAGAATGACGCCACGGCACGCAGGAT
6.055	50.963234	7.4994097	10.732244	RASL11A		NM_206827	Homo sapiens RAS-like, family 11, member A (RASL11A), mRNA.	CAGGTTTCCTGCAGCTCGCTACCTAAGTGTTTCTGTAGGGGAAGGAGCCA	ILMN_1750596	AGAAGAGCCTCCATCATCCCTCGGCCCCGCTCTCCCAACATGCAGGACCT

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
26.1	249.21011	12.398535	7.9340425	ECM2	MGC126355; MGC126356	NM_001393	Homo sapiens extracellular matrix protein 2, female organ and adipocyte specific (ECM2), mRNA.	GCGCCTGGATTCTGCCATTGCGACACATTTTTGTGCCTTTCAGCCCCTGG	ILMN_1715636	GCACCACTGGTCATAGCATCTATCTCCTTTGCCTTAATTTACTGAAATAC
6.938	71.65485	8.428581	12.723093	TBC1D3G		NM_001040282	Homo sapiens TBC1 domain family, member 3G (TBC1D3G), mRNA.			GGCACTGATTCCGACCAGGGCACCCCCTTCAGAGCTAGGGACGAACAGCA
4.982	51.401573	12.797788	8.382192	IL18BP	IL18BPa	NM_173042	Homo sapiens interleukin 18 binding protein (IL18BP), transcript variant A, mRNA.			GCAGCTGCTTCGGATCCACACTGTATCTGTGTCATCCCCACATGGGTCCT
42.71	384.8643	7.101533	12.654845	APOD		NM_001647	Homo sapiens apolipoprotein D (APOD), mRNA.	TAGGGCCTGGGGATTTGGGTCAGTTGTAGTTGCCTCTCCCCCACCCTCTT	ILMN_1690614	CCTGGCCACCGACTATGAGAACTATGCCCTCGTGTATTCCTGTACCTGCA
9.004	77.18435	13.2048435	5.3930697	GATS	DKFZp686B07267	NM_178831	Homo sapiens opposite strand transcription unit to STAG3 (GATS), mRNA.	CGAGAAGCAGATGACAGGCTCAGGCCTTACCAGGGATGCACTTGCCACAT	ILMN_1725633	ACACCTTGTAAGTGTCCCCTCTGGTTTCCTCGGTGGTGGCGCCCTGAACT
5.738	57.957413	9.637452	11.523018	TRAPPC6A	MGC2650; TRS33; HSPC289	NM_024108	Homo sapiens trafficking protein particle complex 6A (TRAPPC6A), mRNA.			AAATTGAGGTGGGGGTGTCAGAGGAGGCAAAGGGGTCCCAGCTGCGGTCA
5.49	57.91084	8.360489	13.403777	YPEL2	DKFZp761C2021; FKSG4	NM_001005404	Homo sapiens yippee-like 2 (Drosophila) (YPEL2), mRNA.			GTATGGAGCTGTTGCGGGTTTGCTCCTTTTTCTTGCTTTGCGTGCTCAGT
10.68	131.00595	11.924184	12.725094	BTG2	PC3; TIS21; MGC126064; MGC126063	NM_006763	Homo sapiens BTG family, member 2 (BTG2), mRNA.			CCAAACACTCTCCCTACCCATTCCTGCCAGCTCTGCCTCCTTTTCAACTC
28.71	330.7101	13.804459	9.680338	ADCY4		NM_139247	Homo sapiens adenylate cyclase 4 (ADCY4), mRNA.			ATGGGCCCTACAGTCCCTGGGCTACACCTGCTACAGCCGGGGTGTCATCA
20.36	222.20178	10.916097	11.747284	UBL4B	FLJ25690	NM_203412	Homo sapiens ubiquitin-like 4B (UBL4B), mRNA.			TCAGCAAAGTCATACACTCCCTGTGGCCAGCGTGAACAGAGCCATGCCCC
7.724	71.55003	5.955261	14.534442	KIAA1217	DKFZP761L0424; RP11-324E23.1; MGC31990; SKT	NM_001098500	Homo sapiens KIAA1217 (KIAA1217), transcript variant 2, mRNA.			GCAAGTGTGGTGCCTTGGATGTGGCCTGTTGGCTCGCTTTCTTCTCTGTG
6.772	66.46344	6.3943424	14.949141	VAV3	FLJ40431	NM_006113	Homo sapiens vav 3 guanine nucleotide exchange factor (VAV3), transcript variant 1, mRNA.	GTGAGATGAAAGAAGAGCCTACTAGTGAGAAGAAGTTGGAGGATGAAGGA	ILMN_1769540	GTTGCATTTCATGGGCCTGGGGGTTTCCTAGCAGAGGATATTGGAGCCCC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
6.142	73.59032	10.961201	14.258721	TFF3	TFI; hP1.B; HITF; ITF	NM_003226	Homo sapiens trefoil factor 3 (intestinal) (TFF3), mRNA.			GCCTGATGTCTTAACGAATAAA GGTCCCATGCTCCACCCGAGGA CAGTTC
19.23	222.83095	8.369144	15.850397	UBA7	UBA7; UBE2; D8; MGC12713; UBA1B	NM_003335	Homo sapiens ubiquitin-like modifier activating enzyme 7 (UBA7), mRNA.	ACTGAGTATGTTCATTG CCACCCCTGTCCTCCC CTGGGCACCCCTCACT T	ILMN_1721178	TCAATGGAGCCCCGGATCCCAA GCCCTGCATTGTAAGCCCACAG TAGGCA
7.985	93.12684	8.389942	16.046589	RASGRP1	V; CALDAG-GEFI; CALDAG-GEFII; MGC129999; RASGRP; MGC129998; hRasGRP1	NM_005739	Homo sapiens RAS guanyl releasing protein 1 (calcium and DAG-regulated) (RASGRP1), mRNA.	GCCGGTGACTGGACAT ATCACCTCTACTTAAAT CCGTCCTGTTTAGCGA C	ILMN_1713124	TCAAGCCTAGTGTAAATTTCTGC ATCTCACACGACTTTAGTTTGGC CAGG
4.261	51.18611	10.705215	14.806075	ARSG	KIAA1001	NM_014960	Homo sapiens arylsulfatase G (ARSG), mRNA.	TCCTCCAGCTGCAAGA AGGGAGCCATGAGCCA GAAGGAGGCCCCTTTC CA	ILMN_1697412	GTTAGCCTTGCATATCCCTTCTG TATCCTGTCCCTCCTCCACGCC GACCC
12.36	107.74762	5.838048	16.430946	LOC388135	MGC131524	NM_001039614	Homo sapiens similar to RIKEN cDNA 6030419C18 gene (LOC388135), mRNA.			CCCTGAACAGACTCGAAGGGTC ACGAGGAACAGCAGCACCCAGA CAGTGT
8.145	98.614334	16.099365	9.638924	JPH2	JP2; JP-2; FLJ40969	NM_020433	Homo sapiens junctophilin 2 (JPH2), transcript variant 1, mRNA.			CAGGCAGCTCTGGGACCTAGGA GTTTGCTTCTGATAGGGTCAGC TTTCCC
4.717	60.206085	15.071852	11.7032585	RNF122	MGC126622; FLJ12526	NM_024787	Homo sapiens ring finger protein 122 (RNF122), mRNA.			CCAGAATGGAAGGGGGTGGGG ATTTTCTGTTCCTCCCTGGAGTG GGTGAG
5.335	58.177677	16.25819	8.359183	RAB33A	RabS10; MGC1488	NM_004794	Homo sapiens RAB33A, member RAS oncogene family (RAB33A), mRNA.	GCAGGGAAAACTGCGG CTGCAAAAATGGTACCT GGCCACTTCGGACAAG G	ILMN_1751345	CCAGGTGCCCTCCAACTTAGCC CTGAAATTTGCTGATGCCCACA ACATGC
42.78	401.95593	6.0140285	17.424347	SERPING1	C1NH; HAE2; C1IN; HAE1; C1INH	NM_001032295	Homo sapiens serpin peptidase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary) (SERPING1), transcript variant 2, mRNA.	GGGCAGAGGTGAAAAA GAAGGAACAACAGCGA GTCCGGATTTAAGGAG GC	ILMN_1685760	TGGGACCAGCAGCACAAGTTCC CTGTCTTCATGGGGCGAGTATA TGACCC
80.7	942.5893	17.46439	8.366522	LBH	MGC163287; MGC104312; DKFZP566J091	NM_030915	Homo sapiens limb bud and heart development homolog (mouse) (LBH), mRNA.			GTCCCTAGACCACTTTGTATGA CCGTTTGCAGTCTGAGCAGGCC AGGGGC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
5.353	80.4065	15.077138	15.606528	MACROD1	LRP16	NM_014067	Homo sapiens MACRO domain containing 1 (MACROD1), mRNA.			ACGCTGCGAGAGTGGCTGGAG CAGCACAAGGACAAGGTGGACC GGCTGAT
30.49	421.83096	15.515303	13.398872	JAM2	VE-JAM; PRO245; JAMB; VEJAM; JAM-B; CD322; C21orf43	NM_021219	Homo sapiens junctional adhesion molecule 2 (JAM2), mRNA.			GCAGCCGTAGTAGTTGTGGCCT TAGTGATTTCCGTTTGTGGCCTT GGTGT
8.468	119.98512	14.805477	14.789437	XAF1	HSXIAPAF1; BIRC4BP	NM_199139	Homo sapiens XIAP associated factor 1 (XAF1), transcript variant 2, mRNA.	TGCTTAAAGGCAGAGC CGCCTGGTTGGTCTCC ACCCTGTGCATTGGGA GC	ILMN_1812489	TCTGGGCCCTACAGCCTGGAGA ACCTGGAGAATCCTACACCCAC AGAACC
10.65	124.21428	18.940153	7.4639544	C22ORF36	MGC131773	NM_207644	Homo sapiens chromosome 22 open reading frame 36 (C22orf36), mRNA.	ACCTCCCTGGATAGCA GGAACTTGACCTGCCA TGTGTGCCCTGCCTTC CT	ILMN_1673555	CAAGCACATGATAGTGGGCGAT GAAGGTCAAGGAGGACTCACAG GCCCCC
4.852	62.587822	11.104998	17.170095	PDZRN3		XM_001133042	PREDICTED: Homo sapiens PDZ domain containing RING finger 3 (PDZRN3), mRNA.			CCACCCAACCCGGTGGTTAACG ATTTAATACATATAACCAAACCG GCAGC
4.064	66.28836	18.013142	15.316745	LRP5	OPS; LR3; EVR4; EVR1; BMND1; HBM; VBCH2; LRP7; OPTA1; OPPG	NM_002335	Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), mRNA.	TAACCTGCCTGTGTCC ATGGCGAACCCTCTAC ATCCTAACCTGCCGGC GA	ILMN_1814487	ACTACCTGGATTTGAACTCGGA CTCAGACCCCTATCCACCCCCA CCCACG
3.16	52.734077	14.074348	19.933693	KATNAL2		XM_001129888	PREDICTED: Homo sapiens katanin p60 subunit A-like 2 (KATNAL2), mRNA.			GAGTTCGAGTCTGTCTGAAACC ACATTTACCCTGACCTGGCCAC AAAGGC
3.062	52.73545	19.961712	15.132526	ZNF521	MGC142208; Evi3; MGC142182; EHZF; DKFZp564D0764	NM_015461	Homo sapiens zinc finger protein 521 (ZNF521), mRNA.			ACTCTGCAGTCTGAACCTGGAG ATTACTGGAATTGTTTTCCAAGA GGAAA
15.54	179.42679	6.74092	20.433655	SMAD6	MADH6; HsT17432; MADH7	NM_005585	Homo sapiens SMAD family member 6 (SMAD6), mRNA.	CACCCGACTTCGCAAC ACTGGGGTTCAGGTGA CTCATAACCATGTTGAG G	ILMN_1805938	CCAGAGACACAGCCCCCACGGA CAAAACCCCCCAGATATCATCTA CCTAG
42.22	584.2893	10.474273	19.82494	RASSF2	DKFZp781O1747; KIAA0168	NM_170773	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), transcript variant 2, mRNA.	GCATCTGGATGGTCAG CTTCATCCTCTCCACAC TGCCCTCCATTGGCTG G	ILMN_1686095	GATGCGTTTACTCATCTAACATA ATCTGACAGGGCCTCAGCAAGG GAGCC
6.942	84.41091	7.695239	20.62691	STAC	FLJ32331; STAC1	NM_003149	Homo sapiens SH3 and cysteine rich domain (STAC), mRNA.			GTTGGGAACTGAGAGGGGATG GCTGCTGGTTTCACAGAAGTTT GGATGCC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.206	57.996643	20.774296	16.05943	ZSCAN2	FLJ20595; ZFP29	NM_181877	Homo sapiens zinc finger and SCAN domain containing 2 (ZSCAN2), transcript variant 1, mRNA.	ACCTGGTCAGCCTAAATCTTCCCAGTCCCGCTGTGGAGCTGTCAGTCACC	ILMN_1721225	ACCTGGAGAGTGAAGACGGGCATGACGGCAGGTGAAGGGGTTTGCTGTGA
4.972	65.51621	15.366575	13.865348	SAMD14	FLJ36890	NM_174920	Homo sapiens sterile alpha motif domain containing 14 (SAMD14), mRNA.	CACTGTCTCAGAGAGGTTTTCCTGTGCTCGCCCTGTTTCTCTCAGGAAGC	ILMN_1751851	TCCCACGCTCTCAGGGGGGACATGCTCTCTCTTACCCTGTCACTTGGTCT
3.022	53.868073	15.24472	21.075993	ZNF248	KIAA0137; bA162G10.3; MGC131882	NM_021045	Homo sapiens zinc finger protein 248 (ZNF248), mRNA.	CGAGCCCAGAGGGATTTTGCCGCTGCTTCCTCTACCCCTGTATTTCACGC	ILMN_1766904	CCAGGTGGGCACAGAGAAGGGTGGAGAGAGAATCTGGGAAGAGAAATGGA
14.62	197.39345	14.988178	14.675433	C1RL	CLSPa; C1RL1; C1RLP; C1r-LP	NM_016546	Homo sapiens complement component 1, r subcomponent-like (C1RL), mRNA.	GGGCTGCCTGAAGACGAAGAGAAAGAGCAAGGTTATTGTTGGCTCAGGCC	ILMN_1779743	TCCCAAAAGGCAGGTGCAATGATGCACACTTATACCCCCAGCCACTCAGG
5.939	106.86429	18.392096	18.46216	GSDML	PRO2521; PP4052	NM_001042471	Homo sapiens gasdermin-like (GSDML), transcript variant 1, mRNA.			TACCAGTCTGTCCTCACTGCCATCGCCACTACCATCCTGTCACCAGTGGG
9.675	116.75597	17.02741	11.109085	PRR5	PP610; FLJ20185	NM_001017530	Homo sapiens proline rich 5 (renal) (PRR5), transcript variant 4, mRNA.	AGTGGAGAGCAAACTTCGAGGACGTACCCTGGAGGAGGTGGTCATGGCAG	ILMN_1776674	GGTTGGAAATACCATCAGCCTTCCTTGCTCGGCCCAGGTCTGTTTCAGGC
2.965	50.72525	16.975222	18.170595	DENND1A	RP11-230L22.3; FLJ38464; KIAA1608; FAM31A	NM_020946	Homo sapiens DENN/MADD domain containing 1A (DENND1A), transcript variant 1, mRNA.			ACTTAGGTGTTTCAGCATAGATTCCAGTTTCGCACCCTGGGCAGACCCCC
3.674	64.24432	16.879091	18.952023	VRK3		NM_016440	Homo sapiens vaccinia related kinase 3 (VRK3), transcript variant 1, mRNA.	CGCATTGGCAATGCCAAAGGAGATGATGCTTTAGAAAAAAGATTTCTTGA	ILMN_1712563	ATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGTG
4.326	81.67314	16.164707	21.941345	PARP10		XM_001127571	PREDICTED: Homo sapiens poly (ADP-ribose) polymerase family, member 10 (PARP10), mRNA.			GATGGCCATAAGGCGGTGTTCGTGGCACGGGTGCTGACTGGCGACTACGG
3.289	55.166992	18.362453	17.14515	CHRNB1	ACHRB; CMS1D; CHRNB; CMS2A; SCCMS	NM_000747	Homo sapiens cholinergic receptor, nicotinic, beta 1 (muscle) (CHRNB1), mRNA.			CTGCAGCATGCCCAGTGCCACGCACAGGTGCTGACCTATAGTAAGTGCTT

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.152	56.17286	18.423567	18.314775	IRF7	IRF7A; IRF-7H	NM_004029	Homo sapiens interferon regulatory factor 7 (IRF7), transcript variant b, mRNA.			GCCTCGGAACTGTGACACCCCC ATCTTCGACTTCAGAGTCTTCTT CCAAG
7.082	117.314285	19.754322	15.800739	MEIS3	DKFZp547H236; MRG2	NM_001009813	Homo sapiens Meis homeobox 3 (MEIS3), transcript variant 2, mRNA.	TCACAGTGATGTCTGC ATTCAACCTGCTGCATT TGGTGACAAAGAGCCA G	ILMN_1779333	TCCAGCTTCAGGACCCCACCTC CAAAGGCCCCTCTGCTCAATGC CTACCT
4.606	79.34465	16.429674	19.515984	TTLL1	C22orf7; HS323M22B	NM_012263	Homo sapiens tubulin tyrosine ligase-like family, member 1 (TTLL1), transcript variant 1, mRNA.	CTACCTCAAGGACAAG ATGCGCAAAGCGGTGG CTGAGGAGCTGGCCAA GT	ILMN_1783728	TCTGTATGATGAAGAATTGGCC CAGGGTGACGGGGCTGACCGG GAGCTGA
6.621	120.70595	19.55054	18.101063	CHAC1	MGC4504	NM_024111	Homo sapiens ChaC, cation transport regulator homolog 1 (E. coli) (CHAC1), mRNA.			GCAGGCTGGATGAGGGATAGTA GGGCATGAGGAGAAGGAGCCC TGTAAGG
6.443	95.71846	10.01433	22.997429	FAM84B	BCMP101; NSE2	NM_174911	Homo sapiens family with sequence similarity 84, member B (FAM84B), mRNA.			GGTGCTTTGGCCCTAATAGCAC TGGACAACACCACGACCACATG GAAACA
8.82	143.93094	23.748478	11.128967	ATHL1	MGC129858; FLJ22635; MGC129859	NM_025092	Homo sapiens ATH1, acid trehalase-like 1 (yeast) (ATHL1), mRNA.	AAAGCCGGTGCAGGCT CTGCTGTCATCGTCAG GACTCCTTGTGGGCTG TG	ILMN_1760049	AATCCCAGGCTCCTCTTGACTC TGGGCAGCTTTAATCAGGTTGG GCAGCC
54.07	618.8476	6.5615797	24.462276	TPD52L1	D53; MGC8556; hD53; TPD52L2	NM_001003397	Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 4, mRNA.			CAGGGCAAAAGGCAACTGCAGC TTTCAGCAACGTTGGAACGGCC ATCAGC
2.39	50.708527	23.337925	20.04875	RAB27A	RAB27; HsT18676; GS2; MGC117246; RAM	NM_004580	Homo sapiens RAB27A, member RAS oncogene family (RAB27A), transcript variant 1, mRNA.	CGTGGAATGGGACAGT GGCTAGAGGTATGGAT GGAGCAAGGTCAAATA TG	ILMN_1740949	GAGGAAAAGATTTAGACATTTCA AGAGCAGGGTTGGCCAGGCGC GGTGGC
10.35	199.09344	24.81089	15.65372	STAT5A	MGF; STAT5	NM_003152	Homo sapiens signal transducer and activator of transcription 5A (STAT5A), mRNA.	GGATGAATGGAGAGGA CAAAGGCAGCTTCTGA CACACCAGCCCCAGGA CC	ILMN_1694539	GCCATGTGCTGCGTGCCTGTGG AATCTGGAGTGAGGGGTAAAAG CTGATC
3.542	69.66217	20.386515	20.305532	GPM6B	MGC17150; MGC54284; M6B	NM_001001995	Homo sapiens glycoprotein M6B (GPM6B), transcript variant 1, mRNA.			TACATGTCCTATCACCTGTTCAT TGTGGCCTGTGCAGGAGCTGGT GCCAC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
9.63	181.51845	16.850765	22.77221	MUC1	PEMT; PUM; PEM; EMA; H23AG; MAM6; CD227	NM_001044390	Homo sapiens mucin 1, cell surface associated (MUC1), transcript variant 5, mRNA.			CCCACCAATTTCTCGGACACTT CTCAGTGTGTGGAAGCTCATGT GGGCCC
6.588	138.19345	20.784874	21.869213	DCN	PGII; DSPG2; CSCD; PGS2; SLRR1B; PG40	NM_001920	Homo sapiens decorin (DCN), transcript variant A1, mRNA.			TCAACCTAGTCACAGAGCAGCA CCTACCCCCTCCTCCTTTCCAC ACCTGC
6.872	116.41428	22.718605	15.230082	TRAF5	MGC:39780; RNF84	NM_004619	Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA.	GGGGGGAGGGAGCTA TTAGAGAAGGATGAGG CAGACCATGTACAGTTA AA	ILMN_1732913	CTGTGGGATTTTCAAAATGCTAA AGACTCACACTGCAGCAATCAT CCCAG
10.75	163.94762	12.319529	23.500063	FAM116B	MGC33692	NM_001001794	Homo sapiens family with sequence similarity 116, member B (FAM116B), mRNA.	CACTGGTGGGATATTTT GGGATGTCAAGGGGTG GAGGCAGAGCACAAGT C	ILMN_1743806	GACTGCAGGCTCCCCTTCCTGC ACCACCATTGTCTCAGCAGTAA AGGCGA
5.539	92.06848	14.408596	22.931309	C16ORF45	FLJ32618	NM_033201	Homo sapiens chromosome 16 open reading frame 45 (C16orf45), mRNA.	TCCCAGCGGGTGCGG GGGGTCCACCAGGCCC TTACACACCGGTCTCT GCT	ILMN_1660816	AGAGTAGATGCTGACCTGGGCA CTCCACCATTCCGGGGCACCAC AGAGAT
2.689	55.805008	23.17091	19.675726	VPS41	HVSP41; hVps41p; HVPS41	NM_014396	Homo sapiens vacuolar protein sorting 41 homolog (S. cerevisiae) (VPS41), transcript variant 1, mRNA.			CTCAGCATTTCCTTATCCCAAGA CTAGTGTGCTTTCTGCTACACT GCTAG
10.96	220.2976	26.52577	15.382851	TCF7L1	TCF-3; TCF3	NM_031283	Homo sapiens transcription factor 7-like 1 (T-cell specific, HMG-box) (TCF7L1), mRNA.	GGAAGATGCCCCGACT TCTTTGGCCAGTGATG GGGAATCAGTGAGTGC TC	ILMN_1669015	CAGTGGAGAAAGCGGTCCTCTG AAATGGTTTCCTCCCAACCCCC GCATTT
7.133	137.04762	13.435646	27.071133	P2RX4	P2X4R; P2X4	NM_002560	Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4), mRNA.			GCAGTCTGTTCTTGGCTGGGTC AACTCTGCTTTTCCCGCAACCT GGGGTT
2.352	58.962425	23.9418	26.401073	CMTM7	CKLFSF7; FLJ30992	NM_138410	Homo sapiens CKLF-like MARVEL transmembrane domain containing 7 (CMTM7), transcript variant 1, mRNA.	CTCCTCCAGCTACCGC AGAGCCCACAAACCCA GGCATCTATCAAAGTC CC	ILMN_1713397	ATTTAATCGGTACCCTGCTCCTC CTCATCGCCTCCATTGTGGCAG CTTCC
22.33	368.8476	12.623283	26.126007	OSR2	FLJ90037	NM_053001	Homo sapiens odd-skipped related 2 (Drosophila) (OSR2), mRNA.	TGGGCTCTCTCGACAC GTTGCTCAGCCAGTCA CTCCTTCCCCTGTGGA TT	ILMN_1692163	CCAAGCACCCCGGGTCTTTACA CAGTCCGCGTCCACAGACTCTG ACGAAG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
25.55	512.7476	27.67228	14.124338	C1QTNF5	LORD; DKFZp586B0621; CTRP5	NM_015645	Homo sapiens C1q and tumor necrosis factor related protein 5 (C1QTNF5), mRNA.			GTCCTGCTGCTGGCAAGGAATG GGAACAGTGGCTGTCTGCGATC AGGTCT
16	268.1768	17.722754	21.687426	RASSF2	DKFZp781O1747; KIAA0168	NM_170774	Homo sapiens Ras association (RalGDS/AF-6) domain family member 2 (RASSF2), transcript variant 2, mRNA.			GCGCCCCCTTCTTCCAGATGTA ATAGAAAGCTCTGCCCTATCAC AAGGGG
9.506	189.03513	27.986189	15.656141	CMAH	CSAH	NR_002174	Homo sapiens cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) (CMAH) on chromosome 6.	CACAGACAAATGGGAT AACACTCATTAATTGGT GGGCGATGGCTCGTGT T	ILMN_1812163	CACCCAACTGGAAGTCATTCCT GATGTGCTGTGAGCAGAATGGG CCTGCG
7.018	144.08096	16.59635	28.731052	CYP2U1	P450TEC	NM_183075	Homo sapiens cytochrome P450, family 2, subfamily U, polypeptide 1 (CYP2U1), mRNA.	GGCTGAAAGAGGCCAA TGCCCCACTGGCAGCA TCTTCACTTCTAAATGC A	ILMN_1781824	CAGTGTGGATTACACTGTACCT TGGGCGGGAGAGTTTGTTCTTG ATATGG
6.887	158.18929	18.014797	29.50241	TBC1D17	FLJ12168	NM_024682	Homo sapiens TBC1 domain family, member 17 (TBC1D17), mRNA.	CAGTGAGCCTTCGCAG ATGCTGGAGATCCTGG GGTTGGTCTGCTTTGT GT	ILMN_1760245	ACATCAACGAGCTGACTATGAA GCTGAGCGTGGAGGACGTGCT GACCCGC
5.937	115.189285	12.80694	29.590256	RTN1	NSP; MGC133250	NM_021136	Homo sapiens reticulon 1 (RTN1), transcript variant 1, mRNA.	GACCGGAAGCAACCCC TTCACAGACACGAGCA CATCGGCAAACCCTAT GA	ILMN_1745994	CGTGGCTAGGCCTTTCCTGCCG AGTGCTCTGATGCAATAGTGGA AATCGC
54.11	1088.906	14.77713	29.676437	C1S		NM_001734	Homo sapiens complement component 1, s subcomponent (C1S), transcript variant 1, mRNA.			ACCCCCCGTGAGGACTAATCCA GATACATCCCACCAGCCTCTCC AAGGGT
5.609	122.46011	29.764801	17.28556	ATF3		NM_001040619	Homo sapiens activating transcription factor 3 (ATF3), transcript variant 4, mRNA.			CTCCCAGCGTTAACACAAAATC CATGGGCAGTATGATGGCAGGT CCTCTG
16.86	227.2351	6.2385783	30.364079	KL		NM_153683	Homo sapiens klotho (KL), transcript variant 2, mRNA.			TCCACCACAGGAATGTATCACA ACTTAACCGTTCCCGTTTGTTAG ACTAG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
5.971	158.66428	28.889027	24.773756	ADAMTSL5	THSD6	NM_213604	Homo sapiens ADAMTS-like 5 (ADAMTSL5), mRNA.	CCCAGGTCGGCCCCTGGAGACTCTGGTTTTTAAGAAATGCACACAGCTAC	ILMN_1804884	GGCACTGTAACGTACCAACGTACCAATTTCCCCTTTTCCCCTGGCTACCA
5.899	113.96428	12.609679	30.544498	HCST	DKFZP586C1522; DAP10; PIK3AP; KAP10	NM_001007469	Homo sapiens hematopoietic cell signal transducer (HCST), transcript variant 2, mRNA.	TCAGACCAAGGGCTCCAAGGAAATACTGCCCACGTCTAGTGCAGGAGCAG	ILMN_1768979	GGGCTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATCCT
4.804	111.243454	24.612354	23.627666	ZNF160	FLJ00032; KR18; DKFZp686B16128; KIAA1611; F11; HZF5; HKr18	NM_198893	Homo sapiens zinc finger protein 160 (ZNF160), transcript variant 2, mRNA.	TGGGAGCCCAGAAGAAATGCTCTTTTGCTTGGAGTTTGTCATCCTACACC	ILMN_1724533	TGGAGATCATTCCATTACACTCCAGCCTGGGCACCAGGAACGAAACTCGT
3.343	78.01481	17.372307	31.80603	Mar-02	HSPC240; RNF172; MARCH-II	NM_001005415	Homo sapiens membrane-associated ring finger (C3HC4) 2 (MARCH2), transcript variant 2, mRNA.			TGTGCCACACGGAGTTTGCAGTGGAGAAACGGCCTCGACCCCTCACAGAG
11.75	266.8393	16.293777	31.814331	LRRC32	GARP; D11S833E	NM_005512	Homo sapiens leucine rich repeat containing 32 (LRRC32), mRNA.	CACACTGCTGGGACATGGCAGGGACTTCACAGTGGGGGTTTTTAGCTGGC	ILMN_1654112	CGCCTGATCTTTGAAAACACTACACAGGGCTGCTGTCACTTCCCAGGGCC
2.273	59.810417	28.253895	25.317493	PPP1R13B	p53BP2-like; p85; KIAA0771; ASPP1	NM_015316	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 13B (PPP1R13B), mRNA.			ATGGCCGCTGCCAGCCCAGACGCTGCTGACGCTGTGTAAATGTGCACAAT
2.828	72.45819	29.512218	23.285923	RHBDF2	RHBDL6; RHBDL5; FLJ22341	NM_001005498	Homo sapiens rhomboid 5 homolog 2 (Drosophila) (RHBDF2), transcript variant 2, mRNA.			TGCTCGAGGCGCATCAGGCCCGTTTTTTACCAGTTTATATCACGGTCTTC
4.071	117.27678	32.026337	25.875755	CBLN3	PRO1486	NM_001039771	Homo sapiens cerebellin 3 precursor (CBLN3), mRNA.			AGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGG
8.288	232.62262	26.618277	29.74316	SARM1	SAMD2; FLJ36296; KIAA0524; SARM	NM_015077	Homo sapiens sterile alpha and TIR motif containing 1 (SARM1), mRNA.	CTGTGCCCCCTGATTTGAGGGTAAGAAGTAGATAATGAGGCCACTGTGGG	ILMN_1748474	AGCTGTGTGACCGGGAGTAGTCACTTAACCTATGTCTCCCCTTCCTCACC
3.21	85.57266	22.355888	32.948074	ACOT8	PTE1; hTE; HNAACTE; PTE-2; PTE2; hACTE-III	NM_005469	Homo sapiens acyl-CoA thioesterase 8 (ACOT8), transcript variant 1, mRNA.	CCTGGGCTCAAGCAGTCCTTCTGCCTTAGCCTCCTAAGTAGCTGAGACTA	ILMN_1665550	TGCTGCTCAGGAGGTCCCCATTGAGATCAAGCCAGTAAACCCATCCCCCC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
9.802	229.82678	25.08123	25.399117	PPP1R14A	CPI-17; CPI17; PPP1INL	NM_033256	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 14A (PPP1R14A), mRNA.	CTAACTTGCTCTGTGAC TTTGACCAAGTCATTTG ACCTCTCTGGGCCCCA	ILMN_1738536	TCTCCCTGCCCCCCGGACGCC GCCCAGCTTGCTTGTGTATAAG TTGTATT
2.736	73.449295	27.890568	27.698284	TMEM91	FLJ27310	NM_001042595	Homo sapiens transmembrane protein 91 (TMEM91), mRNA.	GCCCAGTTTTCTCTGG TGGGTCCAGTGTTTTG TTCCTAGGTGTCTGCT GC	ILMN_1660732	CCACCGCTCTTCGGGCGGCAG CAACCTGAGATTAAACACCAGA CACCCTT
28.62	464.99344	15.042843	27.307652	ITGA11	HsT18964	NM_001004439	Homo sapiens integrin, alpha 11 (ITGA11), mRNA.	GCTGAAGTGCTCACGG CTCACTGCAGTTTCAA GTTCCTGGGCTCAAAG AT	ILMN_1763765	TGATAATGCCCCAAGGACAAGG GGCGTGCCTGGCGCCCAGTGG AGTAATT
4.784	117.76012	26.805578	26.301428	TM7SF2	ANG1; DHCR14A	NM_003273	Homo sapiens transmembrane 7 superfamily member 2 (TM7SF2), mRNA.			TGTCACACCTGCTGCCCTACTT CTACCTCCTCTACTTCACCGCG CTGCTG
3.024	81.65616	30.550749	25.995897	ACAD10	MGC5601	NM_025247	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 10 (ACAD10), mRNA.	GTTTTCCCGTTTTATGT GGGCAATAATGTCAAAT GTGCTATGCAGCCAGG	ILMN_1654583	AGGACCTGGGCGCCTGGGAAA ATGGAATGCAACCCACATTGTA AAGCCAC
7.453	206.9226	22.614029	36.453587	CYP27A1	CYP27; CTX; CP27	NM_000784	Homo sapiens cytochrome P450, family 27, subfamily A, polypeptide 1 (CYP27A1), nuclear gene encoding mitochondrial protein, mRNA.			GGAGACGGGGGAGTTGAAGAG TGTGGCCCGCATTGTCCTGGTT CCCAATA
2.682	88.78516	32.85228	33.7026	ZNF425	MGC150568	NM_001001661	Homo sapiens zinc finger protein 425 (ZNF425), mRNA.	CTCAGCACACACTGCC AGTCTTCCCCAATATCT GTCTCCTCTCAATTCCC	ILMN_1772798	GGAAAGACGTGCCAGTTGTGGA GGAAACATTCACACTGATCTGC TAGTCC
12.52	245.09763	10.877688	36.87484	SSH3	FLJ20515; FLJ10928; SSH-3	NM_017857	Homo sapiens slingshot homolog 3 (Drosophila) (SSH3), mRNA.	TCCAGAATTCCTCCTTC TTGGTGTGTCTGGAGG GTGGGCAAGGCTGGG AG	ILMN_1672635	TGTGACACCACGCCAGATCACA GGGCACCAGGCCAGAGATAGT CTTCTTT
2.873	85.0602	28.811693	32.012035	C9ORF7	D9S2135	NM_017586	Homo sapiens chromosome 9 open reading frame 7 (C9orf7), mRNA.	CCTTCTGGGTGGAGGC TTTCCGACTCCCAATCA TGAAGGCAAGTTAATCT	ILMN_1746632	TGGATCAAGGAAGGCTGCCCCT GTACCCTGTGGGGAAATGGTGG GTGCAT
10.05	276.7393	20.744036	37.367134	THBS3	MGC119564; TSP3; MGC119565	NM_007112	Homo sapiens thrombospondin 3 (THBS3), mRNA.			CAAGGGGTATTACTCAGGCACT AACCCCAGGAAAGATGACAGCA CATTGC
5.486	128.02261	15.996029	37.528507	NPAS2	MGC71151; PASD4; MOP4; FLJ23138	NM_002518	Homo sapiens neuronal PAS domain protein 2 (NPAS2), mRNA.			CTGAGAACTCCAAGTCTGTGAG GGGAGAGGTTTTACAAGCCAGA CAGGCC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.015	90.5268	37.81977	23.868866	OSBPL2	MGC4307; KIAA0772; ORP2; MGC8342; FLJ20223; ORP-2	NM_144498	Homo sapiens oxysterol binding protein-like 2 (OSBPL2), transcript variant 2, mRNA.	GCACACAGCTGGCACC TTCTCCTTATCCTACTG TGGGTCCAACATGGTC C	ILMN_1656724	GGTTGCAAGCTGAGAACATCCA GAGGTGAGACTCAGACACATTG AAAGTG
6.641	210.46011	34.39969	30.88544	LHPP	MGC142189; MGC142191; MGC117251	NM_022126	Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), mRNA.	GTATTGGTGGATCCAG GGATAAATCCCAAACTT CTTAACCCCTAGACCG G	ILMN_1714738	CCAAGGCACACAGGGTACTTTC TGGACCCACTGCTGGACAGACT TGAAGG
2.446	89.122635	35.859634	37.476196	GDPD1	FLJ37451; MGC35046; FLJ27503; GDE4; UGPQ	NM_182569	Homo sapiens glycerophosphodiester phosphodiesterase domain containing 1 (GDPD1), mRNA.	CTGACATGAGTCCAGG GAGAGGCAAGATTGAG CAATAGTCAGTGGCAC CA	ILMN_1804870	AGACTATTGGATACATTTGGCAT TGGGCTGAGTGTGGTGGCTCAT GCCTG
6.993	178.43927	28.587152	28.439234	SPATA18	FLJ32906	NM_145263	Homo sapiens spermatogenesis associated 18 homolog (rat) (SPATA18), mRNA.	TTTTCCTGGCCACAGA GAGATCCACGTGCTGG ACACCGACTACGAGGG CT	ILMN_1761917	GGCACAGGTAGCTCAGTTTATT TGCTTTCTACCCTGCCTGGCCA CTTGCT
11.81	269.88928	28.070717	25.533855	OLFML2B	RP11-227F8.1; MGC51337	NM_015441	Homo sapiens olfactomedin-like 2B (OLFML2B), mRNA.	GGGCCTTTTTGGTGTT GAAGGGAATCAAACTA CATTTGCTGCTTGTGT GC	ILMN_1737320	TGACCAGTAACCACCTTCCTTCA AGCCTTCAGCCCCTCCAGCTCC AAGTC
7.858	270.8976	30.451405	40.298264	SLC27A1	FATP1; ACSVL5; FLJ00336; MGC71751; FATP	NM_198580	Homo sapiens solute carrier family 27 (fatty acid transporter), member 1 (SLC27A1), mRNA.	GGATGGGGAGGATGGT TGCACAACAGTGTGAG TGTACTTAATGCCACTG C	ILMN_1688104	CAGACATCCCTACTGGCTTCGC TGGTGGCTCATCTCGAACATCC ACGCCA
20.22	483.2351	14.831423	42.019188	TPD52L1	D53; MGC8556; hD53; TPD52L2	NM_001003396	Homo sapiens tumor protein D52-like 1 (TPD52L1), transcript variant 3, mRNA.	CTAAGAAGGGAACTTG CCATCAAGATTCCTGTA CCAGGCCCACGGCCGT C	ILMN_1788315	CCCGCTGGGAAAAACCCAGGCC TTGACATTGTTATTCAAATGGCC CCTCC
10.7	263.93097	14.629435	43.67214	SOD3	MGC20077; EC-SOD	NM_003102	Homo sapiens superoxide dismutase 3, extracellular (SOD3), mRNA.	GGCCCAGCATGGCTCA CCTGTCCCGTGGGCTG TGTTTCTTGTTGTTTTT C	ILMN_1663080	ATTTGTACCGAAACACCCCGCT CACGCTGACAGCCTCCTAGGCT CCCTGA
4.875	170.91428	31.700298	40.57979	LOC652968		NM_001037666	Homo sapiens hypothetical protein LOC652968 (LOC652968), mRNA.			CTGTTCTGCTGGGGACCCTCGT TCCGCTCTCTGTATGTAAGCTG CGTGCA
4.327	152.30594	28.618969	44.034157	ASMTL	ASMTLX; ASTML; ASMTLY	NM_004192	Homo sapiens acetylserotonin O-methyltransferase-like (ASMTL), mRNA.	AGAAAGTCCCTGGTCA GGTCTCAGGTAGTGCG GTGTGGCTCAGCTGGG TT	ILMN_1696284	TATGCAGGTGACTGTGTTTGAC CTCCCAGACATTATCGAGCTGG CCGCCC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
23.11	667.97266	44.124336	20.285776	JAG1	CD339; AWS; HJ1; JAGL1; MGC104644; AGS; AHD	NM_000214	Homo sapiens jagged 1 (Alagille syndrome) (JAG1), mRNA.	TGTGGAAGGGGCCTCTGGGTGGCAGCTCTGGGCTTTTGGGTGTTGGACAA	ILMN_1746707	CTGCCACCCTGCTGAGTCTGTTCTGGTAATCGGGGTATAATAGGCTCTGC
2.741	96.58513	36.29148	36.51824	CRY2	FLJ10332; KIAA0658; PHLL2; HCRY2	NM_021117	Homo sapiens cryptochrome 2 (photolyase-like) (CRY2), mRNA.	GCTGCGTTTAAGCCTTCCCCCATCGTGTACTGCAGAGTTGAGCTGGCAGG	ILMN_1661599	TGACCCAAGGGCCAGCATGGGGAAGAGATGGTTGCAGGCAAAATGCACTT
2.038	83.66022	43.581738	38.9263	PLD2		NM_002663	Homo sapiens phospholipase D2 (PLD2), mRNA.	CGGTGCAGGCTTCCTGGATGACAGTTGGGTGATATGTGTCATGTGGCCTA	ILMN_1660841	TCTGCCCCAGGCCCTACTACCCATTGTTCCCTTCCTCTTCCTGCCCTTGA
3.824	167.84763	40.88865	47.202198	PLEKHH3	FLJ21019	NM_024927	Homo sapiens pleckstrin homology domain containing, family H (with MyTH4 domain) member 3 (PLEKHH3), mRNA.			TGGGCCAGGACTGCTCTGAGATTTGAGGGAAACATGGACCCTTTTGGCCC
3.785	129.41428	24.850315	47.346428	FLJ20489		NM_017842	Homo sapiens hypothetical protein FLJ20489 (FLJ20489), mRNA.			CCAGCCCTGCGTTTCCATTCTGCCTTCTCAGAGTGCCCTTGCTGCACCCA
27.22	672.1018	13.574909	47.503815	PLAC9	MGC104710	NM_001012973	Homo sapiens placenta specific 9 (PLAC9), mRNA.			CAGACACATGGCTGTGCAACGCCGTCTAGATGTCATGGAGGAGATGGTAG
7.08	226.55179	43.024178	27.401142	CALCOCO1	KIAA1536; Cocoa; calphoglin; PP13275	NM_020898	Homo sapiens calcium binding and coiled-coil domain 1 (CALCOCO1), mRNA.			GGTTCCTCTTTCTGTTCCCCCATTGACTTCTGTGCCCCACCCTAGCCTTT
3.557	161.81429	42.92425	48.667336	PLCD3	MGC71172	NM_133373	Homo sapiens phospholipase C, delta 3 (PLCD3), mRNA.	CGTGGGGAGAGGGCGTAAATTGTCTTGTGAATGTGTGCTAACCAAAACCC	ILMN_1721127	TCAAAGCAAGAAGGGAGCGCTGAGGCATGAAGCCCTGGGGAAACTGGCAG
2.457	108.76428	43.305183	46.241035	C5ORF33	MGC43298; FLJ30596	NM_153013	Homo sapiens chromosome 5 open reading frame 33 (C5orf33), transcript variant 2, mRNA.	GCATGAGGAACCAGTTGACATGCTGGGTTGTGACTGGCAGCTTTAGCAGC	ILMN_1690963	GAGTCTTGTGGGCTCAGAAGTAAATTCTGTGAAAGCTGGACGGATAGTCG
5.448	211.04346	50.118958	30.000599	ABTB1	BPOZ; PP2259; EF1ABP; MGC20585	NM_172028	Homo sapiens ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1), transcript variant 3, mRNA.	GACCTACCAGGGACAAGCAGGTAAGAGCTGATGTGAGTGTGTGTGATGGG	ILMN_1719433	TCGAGGACCTGCTCGTGTCCATCGGTCTGGACTGTTGAGCCCCTGGCTGG
2.818	112.34761	42.170662	40.07399	INTU	INT; PDZD6; KIAA1284; FLJ41326; PDZK6	NM_015693	Homo sapiens inturned planar cell polarity effector homolog (Drosophila) (INTU), mRNA.	GGTGACGATCAGGCCCTGGGCCCCCCTGCATCTTTTATAGCAGTGGGTGT	ILMN_1811652	ACCTTGTAGCTGTGCTTTCTTGATGCGTAGAAACACGTGCATGGAGGATC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
6.636	199.78513	42.292854	26.857582	RHOJ	ARHJ; TCL; RASL7B; FLJ14445; TC10B; MGC34777	NM_020663	Homo sapiens ras homolog gene family, member J (RHOJ), mRNA.	GCAGACAAAACCTCTT GAAACCCTTCCCCCAT GGCACAAACTCGCCCA TG	ILMN_1657129	GCATGTTTCTACCAAAGCTATTA GAACCAACACGTACCTCTGAAT GCCCG
9.53	330.72678	40.768097	33.457928	DMPK	MDPK; MT-PK; DM1; DM; DMK; DM1PK	NM_001081562	Homo sapiens dystrophia myotonica-protein kinase (DMPK), transcript variant 4, mRNA.			TCCGACTCGCTGACAGGCTACA GGACCCCCAACAACCCCAATCC ACGTTT
5.375	176.56429	30.811539	41.76604	HIST2H2BE	H2BFQ; MGC119804; MGC129733; H2B/q; GL105; MGC129734; H2B; MGC119802; H2B.1	NM_003528	Homo sapiens histone cluster 2, H2be (HIST2H2BE), mRNA.	GAACAAAGTCTCTGGG TCACGTTTTGCCTCATG AACACTGGCTGCAAGT G	ILMN_1797531	CACTTACCACCTCATTTGCTTTT CTGGAGGCCATGCAATATAGGC GGGAC
3.634	154.51428	37.299747	50.115944	SOD2	MNSOD; IPO-B; Mn-SOD	NM_001024466	Homo sapiens superoxide dismutase 2, mitochondrial (SOD2), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA.	GTGTCCAGTATGGCTT TCCAGGCTAATCACTTA GGGCAGAGACCCAGCC T	ILMN_1747047	TACGACTACGGCGCCCTGGAAC CTCACATCAACGCGCAGATCAT GCAGCT
8.931	345.1101	38.96357	41.88762	ENAH	NDPP1; MENA	NM_018212	Homo sapiens enabled homolog (Drosophila) (ENAH), transcript variant 2, mRNA.	CCCCACCACTACCTCC ATGGTTGTTCATTTAGG ATGCTTCTAATTCAGCC	ILMN_1689059	CTGGCCCTGTCACTGTGGTGGA TCAGTGGACCTGCTGAAGTCAC TGGACT
8.859	382.6726	48.843613	39.67196	MYO1D	KIAA0727; myr4	NM_015194	Homo sapiens myosin ID (MYO1D), mRNA.			AGGAGGGCCTGGGTTTGGGTT CTTTCCTCCCAGCCTTTGGATG GTGCCTT
3.16	142.85596	39.241722	52.72283	SGIP1	FLJ43054; DKFZp761D221; FLJ33378; DKFZp686A16142	NM_032291	Homo sapiens SH3-domain GRB2-like (endophilin) interacting protein 1 (SGIP1), mRNA.			ACTCTCAGTTGGCCCCCTACAG CAGTCTGGTGTTGAAGTTTCTTT GAACG
154.5	2744.0977	7.0687838	53.23925	VCAM1	INCAM-100; MGC99561; DKFZp779G2333; CD106	NM_001078	Homo sapiens vascular cell adhesion molecule 1 (VCAM1), transcript variant 1, mRNA.	ATGGATCCCAACTTCTC CCCGGCAGCTCTGCCT CCCTAAGTCTGTGAAG C	ILMN_1798624	TTCACGAAGTTTGTTCATCAGAC TCCTGTGCAACTTTCCCAATGT GGCCT
2.723	120.22261	38.860733	52.06681	TBC1D10A	dJ130H16.2; TBC1D10; dJ130H16.1; EPI64	NM_031937	Homo sapiens TBC1 domain family, member 10A (TBC1D10A), mRNA.	AGCTGCTGTTGCCATC TTGAACAACTCACCAAC CTCCAACCCAGAGCCC C	ILMN_1738819	GGCAGCTAAGGCCTCCAGGGC GGGGTCTCCATATAACTACACG GTTCATG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.973	205.28928	56.788776	47.137867	BBS1	BBS2L2; MGC51114; FLJ23590; MGC126184; MGC126183	NM_024649	Homo sapiens Bardet-Biedl syndrome 1 (BBS1), mRNA.			CTCCCATTCTCTAGTACTGCTCC CCTACCCAGCAGTCACTTCCAG TTCAT
2.445	117.82678	46.58336	51.097603	ZC3H10	FLJ14451; ZC3HDC10	NM_032786	Homo sapiens zinc finger CCCH-type containing 10 (ZC3H10), mRNA.			GGGTCCTAGTTGCTTGGGTTGG ACAATACAGGAATTGCTTCTGG GCCCTG
2.411	115.76428	40.753162	57.77529	DUSP22	JSP1; JKAP; MKPX; VHX	NM_020185	Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA.	TGGATGCCCAGGGGAA GGCATACAGGCCTCAT CCACCAGGCAATAGAC AG	ILMN_1737819	GCCAGGCCTATGTTGGAGGGA GTTAAATACCTGTGCATCCCAG CAGCGGA
6.113	218.80179	25.964321	57.560844	PDE1C	Hcam3	NM_005020	Homo sapiens phosphodiesterase 1C, calmodulin-dependent 70kDa (PDE1C), mRNA.	CCGGTTCTGGGGCGAA AATGCCTGCCCTTCAC ATCGAAGATTTGCCAG AG	ILMN_1782419	GACCTGGCTTTCAAGGCATCTG TCTGGCCTGATGAGAATGGACA TCCTGG
3.074	139.41013	37.46571	57.731255	DOCK6	ZIR1	NM_020812	Homo sapiens dedicator of cytokinesis 6 (DOCK6), mRNA.	GCTATGAGTTTGTGCC TTTGCTGAGGACACTA GAACCTGGCTTGCCTC CC	ILMN_1797731	TCCGAAAGGCAGACCTCTGAGC CCACAAGGACCAAAGCTGTACC TAGAGG
4.22	191.36429	40.603954	54.822678	MAN2B1	LAMAN; MANB	NM_000528	Homo sapiens mannosidase, alpha, class 2B, member 1 (MAN2B1), mRNA.			ACCTGAGCGCCCCCGTTACCTT GAACTTGAGGGACCTGTTCTCC ACCTTC
4.472	206.16013	42.99923	52.20766	C9ORF3	C90RF3; APO; FLJ14675; AP-O	NM_032823	Homo sapiens chromosome 9 open reading frame 3 (C9orf3), mRNA.	GAAGGATACTGGTCTG GATTTGGTTGCTGATG CTCTGGGGGCAGGAGT AG	ILMN_1667907	GGTCCCAGCCAGGCACACACAA AAGGCAGATTCTCGTAAACGCA GCCTCC
6.131	304.56845	49.90547	50.961853	TRO	KIAA1114; MAGE-d3; MAGED3	NM_001039705	Homo sapiens trophinin (TRO), transcript variant 6, mRNA.			TCCCCATGTTTACAGATACCGCT AATAAATTGCAGTAGTCCTTCCC ATGG
15.47	563.0851	23.440025	59.470417	ELN	FLJ38671; SVAS; WS; FLJ43523; WBS	NM_001081754	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), transcript variant 4, mRNA.			ACCCAAGCACCTGAAGCCTCAA AGCTGGATTCGCTCTAGCATCC CTCCTC
4.919	236.74762	47.27073	51.247543	MSRB3	FLJ36866; DKFZp686C1178	NM_001031679	Homo sapiens methionine sulfoxide reductase B3 (MSRB3), transcript variant 2, mRNA.			TCACAGTGATGTCTGCATTCAAC CTGCTGCATTTGGTGACAAAGA GCCAG
2.937	148.84344	49.88272	53.177002	GAB2	KIAA0571	NM_080491	Homo sapiens GRB2-associated binding protein 2 (GAB2), transcript variant 1, mRNA.			CGAGGGGGTCCCCAAGAGATC CAGGCTGTCATGTGATTTATGG TGGCATG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.77	198.69762	57.373505	49.47748	FLJ11286	FLJ40743	NM_018381	Homo sapiens hypothetical protein FLJ11286 (FLJ11286), mRNA.			GAGAAGGAATCTGGACTCCCCA TCCCCCCACCAGGATAAAAGTC CTGACC
5.511	296.7393	51.76651	56.96234	TRPM4	FLJ20041; TRPM4B	NM_017636	Homo sapiens transient receptor potential cation channel, subfamily M, member 4 (TRPM4), mRNA.	GTGTCAGAGGACCTTG ACTGGGTTCATTTTATG TCCAGACATCACCCCT G	ILMN_1669142	GTCCTTGGGGTAACAGGGACCA CAGACCCCTCACCACTCACAGA TTCCTC
8.455	459.9226	63.96224	45.615658	MUC1	PEMT; PUM; PEM; EMA; H23AG; MAM6; CD227	NM_001044391	Homo sapiens mucin 1, cell surface associated (MUC1), transcript variant 6, mRNA.			TAGCGGGGATCCTGAACTGGAC TGAATAAAACGTGGTCTCCCAC TGCGCC
28.4	1193.8059	56.48385	35.517784	P8	COM1	NM_012385	Homo sapiens p8 protein (candidate of metastasis 1) (P8), mRNA.			AGCTGCAGAATTCAGAGAGGAA GAAGCGAGGGGCACGGCGCTG AGACAGA
2.568	141.32262	50.3254	61.736164	CTNNBIP1	MGC15093; ICAT	NM_020248	Homo sapiens catenin, beta interacting protein 1 (CTNNBIP1), transcript variant 1, mRNA.	GAGCCCACCTTTCTTCT TTTTTGCTATTAGATGG GCTTGCTGCTCCCGCC	ILMN_1678684	AGTCAGGTGTCGAGGCCACATT GCTGGCTGCCCCCTCTTTGTAG CTCCTA
2.105	121.930954	65.95953	50.96361	GSTT2		NM_001080843	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA.			TGAGCATCCTGGAACAGGCGGC CAAGAAAACCCTCCCAACACCC TCACCA
5.487	248.57262	49.80632	47.89319	PMP22	CMT1A; GAS-3; DSS; CMT1E; MGC20769; HMSNIA; HNPP; Sp110	NM_153321	Homo sapiens peripheral myelin protein 22 (PMP22), transcript variant 2, mRNA.	ATTTCACTGTGGATATC CCTGAGGCCATGAGGG TGGGAGCCGGCCTGG GC	ILMN_1716999	CCAACGCACCCGAGTTTGTGTT TGAGGCCACCCTGAGGATCGG GACAGCT
2.658	150.61429	51.421036	63.896503	AP2A2	CLAPA2; HYPJ; HIP9; ADTAB	NM_012305	Homo sapiens adaptor-related protein complex 2, alpha 2 subunit (AP2A2), mRNA.	AGCAGCAGAGCGTGCC AGCCGCAGTGTTTGGG AGCCTGAAGGAAGACT GA	ILMN_1771057	TGCACCCCACAATGTCTGCGGC TCTTCTTCCGGCGTGTCGGGCT TTGATC
2.248	134.75595	53.179333	68.48308	KIAA1598	shootin1; shootin-1; MGC40476; DKFZp686A0439	NM_018330	Homo sapiens KIAA1598 (KIAA1598), mRNA.	TGCTGTACTGTGAGCC CCTCCTCACTCTCTACC AACCCTAAACCCTGAG G	ILMN_1668683	TTGCACGTGTGGTAAGCATAGG CTTGAAGAGGTGGGTAGGCAG GTACATG
2.595	163.59344	69.54125	57.88778	PRMT2	HRMT1L1; MGC111373	NM_206962	Homo sapiens protein arginine methyltransferase 2 (PRMT2), transcript variant 1, mRNA.	TAACCAGGAAGGCCAA CAGCTCAGGAGAAGCC ATGTCACTGGGGAGCC AC	ILMN_1714522	GACTGGAAGATGCAGACCTTGG TTCCTGTTAGTGGAAACACTGTA AGGTC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.095	222.73929	42.153183	70.42	ALDH4A1	P5CDh; P5CD; ALDH4; P5CDhL; P5CDhS	NM_170726	Homo sapiens aldehyde dehydrogenase 4 family, member A1 (ALDH4A1), nuclear gene encoding mitochondrial protein, transcript variant P5CDhS, mRNA.	GGATAATCACCCCCTTCATAGTCTTCAGGCTGAGGGAGGTCTGGCAAGCC	ILMN_1675597	GTTCTACTGGTTCTACACTGTGAGGTGGCAATGGGATTTGCTCAGATGCC
13.1	482.53094	33.741356	56.241806	RCAN2	CSP2; ZAKI-4; MCIP2; hRCN2; DSCR1L1; RCN2	NM_005822	Homo sapiens regulator of calcineurin 2 (RCAN2), mRNA.	CCCCTTTGACAAGCTTCCATAGTCTTCAGACACGCACATTGATGGCATCC	ILMN_1721292	AGTGTTGCAAGGGAACCTCCTAGCACTGTGAAAGTCAGAATCGCCTCAGC
5.757	285.10178	47.967438	59.43971	ITGBL1	OSCP; TIED	NM_004791	Homo sapiens integrin, beta-like 1 (with EGF-like repeat domains) (ITGBL1), mRNA.	GCTGTCTGGGGACCCTAAGAGTTTTCTCACCTGTTCAGTCTCATCTAACC	ILMN_1728049	GGGGACAATGAAGACAAGCACACAGGAGGTAGAATATCAGAGTGGGGCTG
2.074	144.2351	69.48305	69.64098	RHBDD3	HS984G1A; C22orf3; PTAG	NM_012265	Homo sapiens rhomboid domain containing 3 (RHBDD3), mRNA.			GTGTCACTGTTGGTTGGAGGACAAGTGGGCACTGAGACCCTGGTGACCCA
7.818	317.10596	22.856537	72.43669	DDEFL1	CENTB6; ACAP4; FLJ20199; UPLC1; ASAP3	NM_017707	Homo sapiens development and differentiation enhancing factor-like 1 (DDEFL1), mRNA.	CTGTTGAGAACTTTTACACTCTGGTGATAAGCACGGCCCTGGACCGGGAG	ILMN_1683942	GTGGTTCCCACAGGAACAGGGTTGTCTTTTGAGCCCCCAGTGTCTGGTTT
4.661	312.53928	67.03815	67.72975	PKD1	PBP	NM_001009944	Homo sapiens polycystic kidney disease 1 (autosomal dominant) (PKD1), transcript variant 1, mRNA.			TAGGTGTGGTGGCGTTATGGCAGCCCGGCTGCTGCTTGGATGCGAGCTTG
15.86	795.1643	42.36229	69.05347	DCN	PGII; DSPG2; CSCD; PGS2; SLRR1B; PG40	NM_133503	Homo sapiens decorin (DCN), transcript variant A2, mRNA.	GGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAATGATGGA	ILMN_1741613	GCTTTGGGAGCAGAGAAGAGGGAGAAAGCAGCATCTTGCCTGGATGAGCC
2.561	157.06427	70.62503	55.88077	WIPI2	FLJ12979; FLJ14217; DKFZP434J154; DKFZp686P02188; Atg21; WIPI-2; CGI-50; FLJ42984	NM_016003	Homo sapiens WD repeat domain, phosphoinositide interacting 2 (WIPI2), transcript variant 2, mRNA.			GGAACCTGGAGTCAAAAAGAACTGCTTCAGTCCCCGCTGTACCGCCTGCC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.026	262.38095	69.67496	61.721268	ALDH2	ALDHI; MGC1806; ALDM; ALDH-E2	NM_000690	Homo sapiens aldehyde dehydrogenase 2 family (mitochondrial) (ALDH2), nuclear gene encoding mitochondrial protein, mRNA.	TAAGGCCCTGCACTGA AAATGCAAGCTCAGGC GCCGGTGGTCGTTGTG AC	ILMN_1653026	GCAAGCTTCCTCCCTCAGCCAT TGATGGAAAGTTCAGCAAGATC AGCAAC
2.547	157.1518	75.25716	52.194458	IQSEC1	KIAA0763	NM_014869	Homo sapiens IQ motif and Sec7 domain 1 (IQSEC1), mRNA.	GGCACCGTGTCCAAGT TTTTAGAACCCTTGTTA GCCAGACCGAGGTGTC C	ILMN_1780036	ACTGTCCCCTTTAGAGATCCCA CCTGTCAGAGCCACAGCTTCGG GGTCCT
2.465	167.78928	67.02692	70.28679	MOSPD3	CDS3	NM_001040097	Homo sapiens motile sperm domain containing 3 (MOSPD3), transcript variant 2, mRNA.	CTGGGAAAGTGCTCGA CTGAGACCTTGGGAGT CTTGGGAAGTCCAATG GG	ILMN_1759848	TCTTCTTGCTGACGGGGATTGT GTCTGTGGCCTTCCTGCTGCTC CCACTC
2.447	150.51845	76.448166	49.482178	LIN7B	LIN-7B; MALS-2; VELI2	NM_022165	Homo sapiens lin-7 homolog B (C. elegans) (LIN7B), mRNA.			CTGTTGTCGGTGAACGGTGTGA GCGTTGAGGGTGAGCAGCATGA GAAGGC
2.721	174.79762	76.540665	55.529587	SIN3B	KIAA0700	NM_015260	Homo sapiens SIN3 homolog B, transcription regulator (yeast) (SIN3B), mRNA.			CTAAGAAGGGAACTTGCCATCA AGATTCCTGTACCAGGCCCACG GCCGTC
8.131	495.98926	71.49109	54.894814	PPFIBP2	Cclp1; MGC42541; DKFZp781K06126	NM_003621	Homo sapiens PTPRF interacting protein, binding protein 2 (liprin beta 2) (PPFIBP2), mRNA.	GTGGGAAAACTATAAA CTCTCTTGTTACAGCCC CGCCACCCCTTGCTGT G	ILMN_1750300	CCACAGTCTTGGCTGAGATCAA AGGGATGAGCAACAGGGACTTC TGCCAC
4.433	266.87262	70.42941	56.191177	SSH1	SSH-1; FLJ38102; KIAA1298	NM_018984	Homo sapiens slingshot homolog 1 (Drosophila) (SSH1), mRNA.	TCGACGGTGATTTGCA GGTGGAGAGTGCTGG GATGGAAGGCCGGGAT ACT	ILMN_1730379	GAGTAGTCCCACGCTGTTGTTG AGCTGACTCTGTGCCCGAATGG TGGTGC
2.325	164.28928	67.259575	75.086975	DUT	dUTPase; FLJ20622	NM_001025248	Homo sapiens deoxyuridine triphosphatase (DUT), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GCAAGAGGGACAGGAG CCCAGAAGAGACACTG AGGACAAGAGATCACA CC	ILMN_1740903	AAATGACTCCCCTCTGCCCTCG CCCCGCGCTCTGCTACCATTTC CTTACG
2.388	153.48096	79.354774	53.128277	RBM33	MGC20460; PRR8; DKFZp434D1319	NM_001008408	Homo sapiens RNA binding motif protein 33 (RBM33), transcript variant 1, mRNA.	GAGCGAGATATGCTCA GAGAGGAGCTGGCTGA CCTGCAGGAGACAGTG AA	ILMN_1749239	CTACCTTGGGGGAATGCCGTTG CCTGTTCCACCCCTTTGTTCACT TCGCG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.473	164.56012	62.344383	73.33541	TUB	rd5	NM_177972	Homo sapiens tubby homolog (mouse) (TUB), transcript variant 2, mRNA.			CCTAGAACGCAACTTAGGATGG CTAGGAAAGGGAAGCCTGACTG CTCGGT
3.648	259.2726	63.360695	80.16894	ADCY6	KIAA0422; DKFZp779F075	NM_020983	Homo sapiens adenylate cyclase 6 (ADCY6), transcript variant 2, mRNA.	GAGCGCTATGCCACCG AAGCGTTGACCTGAAC ATATTAGTGCAATCCAG T	ILMN_1798984	GTGGAGGCCTGGTTTCTGGGTA ATGCCTCCCTTGGGCATCTTCA TGCATC
3.589	223.72263	80.288734	49.720566	LEP	OB; OBS	NM_000230	Homo sapiens leptin (obesity homolog, mouse) (LEP), mRNA.	CAAATATGTCGGGATG ATTGGCGGGGTCCTCA TGGGCCTGCTCTTCGG GA	ILMN_1658003	CGGGAGGCTGAGACAGGAGAA TCGCTTAAACCTGGGAGGCGGA GAGTACA
2.235	157.4226	80.7186	61.42121	SIAH2	hSiah2	NM_005067	Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA.	GCCCACCTCAGCCTCC AGAGTAGCTGGAAATA CAGTGCCACCCAGATA GC	ILMN_1734267	GTGGGAAAGGGTCCAGATTTTA AAGGTGCTTTAAGGTTGCCCTC TGCCGA
3.469	230.02678	82.51982	55.542526	ABTB1	BPOZ; PP2259; EF1ABP; MGC20585	NM_032548	Homo sapiens ankyrin repeat and BTB (POZ) domain containing 1 (ABTB1), transcript variant 1, mRNA.	CAGGACTGTGATGGTA CAGGAAGGGAACGTGG AAAGCGCATACAGGAC CC	ILMN_1655765	CCATTCAGGAAGGGCTGGGGG AGTGTGTGTGGCAATAAAGCTT GAAGGCA
4.098	278.56845	56.331085	82.910965	C9ORF127	NGX6; RP11-112J3.10; MGC120460; NAG-5	NM_016446	Homo sapiens chromosome 9 open reading frame 127 (C9orf127), mRNA.	GCATCAGAAGGAACTG GAAAACGTGGCACAAC CCCCTCAAGCTCCGCA CC	ILMN_1659306	TTCCACCACGTTCTCCGAGGGT TTGGGAATGTCTGTGCCTTCAC TGTGTC
5.329	373.26428	72.789566	69.6468	UST	2OST	NM_005715	Homo sapiens uronyl-2-sulfotransferase (UST), mRNA.			ACTTACAGGGCCTTAATGTTATT TTGTCCCAGCCAACACCCTCTA GGTCC
6.357	488.97263	73.47356	81.71993	YPEL3	MGC10500	NM_031477	Homo sapiens yippee-like 3 (Drosophila) (YPEL3), mRNA.			CTGGCTTGGATCTCGTTTTTAAC CCGTTCCTGCCCCACCTGCCCT ATAGT
2.986	192.31012	86.59468	49.293694	STARD10	SDCCAG28; MGC14401; PCTP2; NY-CO-28; CGI-52	NM_006645	Homo sapiens StAR-related lipid transfer (START) domain containing 10 (STARD10), mRNA.	CCTTCTTCCTCCCAGG AAAGGGGACGTTCAGC TGAGCCGAGTGTGTAT AC	ILMN_1778974	GGCTCCCAAGGCCATGAAGAAG ATGTACAAGGCGTGCCTCAAGT ACCCCG
8.341	562.9226	84.41884	58.469288	ADM2	AM2; FLJ21135; dJ579N16.4	NM_024866	Homo sapiens adrenomedullin 2 (ADM2), mRNA.	GGCCATCTGTGGCTGG AGGGTTCTGAATGTCC TCTCTCCATGTCAGGC AG	ILMN_1734184	CGCCCTAACAACTTCCCATCCG CTGACCCCTCCAACGCCATCAA TCTCCA
4.026	272.66428	67.571045	72.43248	MRAS	RRAS3; M-RAs; FLJ42964; R-RAS3	NM_012219	Homo sapiens muscle RAS oncogene homolog (MRAS), transcript variant 1, mRNA.	CCGCAGCAATCTCCAC AGCCTCCTGGGTCTCA CCCCTTTCATGGGCTC TT	ILMN_1813517	GTGTAGAGTGTGCCCCGTGACA TCCCTCCATCTTCTCCTCCATTA TCATC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.451	174.89761	74.97554	71.6702	SLC35A2	UGALT; UGT2; UGT1; UGT; UGTL; UGAT	NM_005660	Homo sapiens solute carrier family 35 (UDP-galactose transporter), member A2 (SLC35A2), transcript variant 1, mRNA.	CAGGTTGCAATATGAG GACTTCTCTGTCTCCTC TGAAGCCTGGGACACT G	ILMN_1771689	CCCCCCAGCCCCTGCCAGCTCC ACACTATCTCTTAGCTGAGTTTT TGCAA
2.744	197.83511	91.106415	58.268333	CCDC128	MGC111781; FLJ16566	NM_152994	Homo sapiens coiled-coil domain containing 128 (CCDC128), mRNA.			CTCTCTGAGGGAGAGGGAGCC CTCCAAACTTCAGATCCTGTGG GTTTAGT
5.477	462.63513	90.72263	79.574036	CSAD	PCAP; MGC119355; MGC119354; MGC119357; CSD	NM_015989	Homo sapiens cysteine sulfinic acid decarboxylase (CSAD), mRNA.	CATGTCGCTCCGGTCA GATTAGTTGGCTTTGG CCCCTCGACCCTGTGC AG	ILMN_1697787	GCCTTTTTAGGCCACAGTGACC TGCGCAATGTTTATATGCTTTGA CCTAC
2.654	209.8601	68.3605	93.14772	MBOAT5	C3F; OACT5; nessy	NM_005768	Homo sapiens membrane bound O-acyltransferase domain containing 5 (MBOAT5), mRNA.	GCCTCTTTGGAGCATA CCCACTGATGGTGGTT CACAAGCTACCCACGC CC	ILMN_1697872	AGGGGCTCACATCTCCCCTCTG ATTCCCCCATGCACATTGCCTTA TCTCT
2.975	229.37262	72.61534	86.406235	SESN1	SEST1; MGC138241; MGC142129; PA26; RP11-787I22.1	NM_014454	Homo sapiens sestrin 1 (SESN1), mRNA.			CCTGACACTGGAGGGCAGCTGT CTTGTGCATTACTTGTGTTCCCA GCACC
2.099	175.1726	89.26431	79.592186	OS9		NM_006812	Homo sapiens amplified in osteosarcoma (OS9), transcript variant 1, mRNA.	GACTGTCCCCTGGTAC ACATATGCAAGAGACTT TATGCGTAAGAGTGGA G	ILMN_1801236	TGTGGACCTCTCGGGCAACTCT GTGGGTGTGGGGGCCCTGGGT GAATGCT
2.764	206.64761	57.782814	96.00595	GTF2IRD1	hMusTRD1alpha1; WBSCR11; CREAM1; RBAP2; WBSCR12; MUSTRD1; WBS; GTF3	NM_016328	Homo sapiens GTF2I repeat domain containing 1 (GTF2IRD1), transcript variant 1, mRNA.	AGGAGCCTTTCCAGTT ATCTTGAGTTGCAGCT CTGTAGTTTCTTGAGG CC	ILMN_1773906	AACCCGGATTCAGTGGCATCGG CCAACCAGATCTCACTCGTGCA ATGGCC
2.04	174.23929	87.501816	85.19069	ABHD14A	DORZ1; DKFZP564O243	NM_015407	Homo sapiens abhydrolase domain containing 14A (ABHD14A), mRNA.			TGCCTTCCTTGACCATCTACCTT GAACTAACCCACTCCCAGCTCC CAGCC
2.254	188.83096	72.07077	97.98097	DYNC2LI1	D2LIC; CGI-60; LIC3; DKFZP564A033	NM_016008	Homo sapiens dynein, cytoplasmic 2, light intermediate chain 1 (DYNC2LI1), transcript variant 1, mRNA.			CCCATCACAGGTGACACCTTAC GGACGTTTTCTCTTGTTCTCGTT CTGGA
2.754	243.98929	80.02329	98.15179	RNF10	MGC126758; MGC126764; RIE2; KIAA0262	NM_014868	Homo sapiens ring finger protein 10 (RNF10), mRNA.	ACCTGCTTTGCGGTGC AGACCCTCTCAGGAGC AGGAAGACTCAGAGCA AG	ILMN_1727220	GGAAAGCTGTAACTCACGAAGC CCTGAGACCTGCTACCCCTAAG ATCGAG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.189	204.52261	90.085175	97.180954	ZBTB48	pp9964; HKR3	NM_005341	Homo sapiens zinc finger and BTB domain containing 48 (ZBTB48), mRNA.	CTCCTTTCCTGGAGCT GGTTTAGCTGGATATG GGAGGGGGTTTGGCTG CC	ILMN_1757370	AGCCCACTTGGCCCCACCCCTC AATAAACCGTGTGGCTTTGGAC TCTCGT
3.44	318.99347	85.47684	100.89348	BCL3	D19S37; BCL4	NM_005178	Homo sapiens B-cell CLL/lymphoma 3 (BCL3), mRNA.			CTGTCCGGAATGCCACCCACAT CTTCCATTTCCATGTCCCCTCCC AGAGC
2.064	176.05179	89.322975	83.94922	SLC35C2	FLJ37039; BA394O2.1; OVCOV1; MGC39183; CGI-15; C20orf5; MGC32079; MGC20633	NM_0159450	Homo sapiens solute carrier family 35, member C2 (SLC35C2), transcript variant 2, mRNA.	GGGTAGGGGTGGGAA ACTGGCATACTGTGTG TATAGCACTGCCGATT GGC	ILMN_1752954	ATAAATGGTTCACGGTCCACTG GCCGCCTTGTGTTGCTGGAGAC GTGGGG
6.489	527.6893	66.17761	103.19762	SEZ6L2	FLJ90517; PSK-1	NM_201575	Homo sapiens seizure related 6 homolog (mouse)-like 2 (SEZ6L2), transcript variant 2, mRNA.			ATGGCCCTGGAGATCCTACAGT AAATAAACCAGCATCCTGCCGC CCAAAA
5.464	389.15594	90.17309	62.17785	DIXDC1	KIAA1735; CCD1	NM_001037954	Homo sapiens DIX domain containing 1 (DIXDC1), transcript variant 1, mRNA.	GAGTCATTGCATCCTCT ACCAGCTGTTAATCCAT CACTCTGAGGGGGAGG	ILMN_1696702	CTCTTCTTGCTCAGTTCCCTAAA TTAGCTGGGGGGATTGGGATAC TTTAC
6.116	559.73096	89.98132	94.589294	SSPN	SPN1; SPN2; KRAG	NM_005086	Homo sapiens sarcospan (Kras oncogene-associated gene) (SSPN), mRNA.	TGGAGCTGGGGGCCA GAAAGGGGCTGGGTAC CTCTTCTGGTTGCTGA GTG	ILMN_1660321	GGCCTTCCTACACATTAGCTCC AGCTAAAAAGACACATTGGAGA GCTTAG
2.727	237.08095	72.053696	107.42262	TUBG2	MGC131994	NM_016437	Homo sapiens tubulin, gamma 2 (TUBG2), mRNA.	TTCCAGCCTGCCAGTC ATGAATCTCAGACAGC CTGCCACCTATTGCCC TG	ILMN_1666727	CCATGCCTGCTCCCTCTGACCC AGCTTCACCTCATGGACAACCC TTCTTG
3.229	285.1643	100.23931	81.009125	KCTD15	MGC2628; MGC25497	NM_024076	Homo sapiens potassium channel tetramerisation domain containing 15 (KCTD15), mRNA.			GCGGGGCTCCCCAGCCATCAC CATCCTGTGTACAATGGCTGTA GACTTGT
2.322	217.13928	80.01471	108.98929	MOV10	FLJ32791; DKFZp667O1423; gb110; KIAA1631	NM_020963	Homo sapiens Mov10, Moloney leukemia virus 10, homolog (mouse) (MOV10), mRNA.			AGCTCTGAAGACACAGCACCCA GCCTTCTCGCACCAGCCAAGCC TTAACT
6.383	602.57263	88.21452	102.41014	SHRM	MSTP013; KIAA1481	NM_020859	Homo sapiens shroom (SHRM), mRNA.			CCTTCCTGATTGATCTTCTGAGA GCTCGAATGCTGCTGGACACGT ACCCC
7.668	476.5976	36.284798	109.51433	ADAMTSL4	TSRC1	NM_025008	Homo sapiens ADAMTS-like 4 (ADAMTSL4), transcript variant 2, mRNA.	AGCGTGCGGAGCATCT GAAGTTGCAGTCTTGC GTGTGGATGGTGCAGC CA	ILMN_1784737	GGGTAACCACGCCCAGGACACC TCAGCCTTTCCAGCATAGCTCA ATAAAC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.387	403.3018	77.33238	110.485115	IFI35	FLJ21753; IFP35	NM_005533	Homo sapiens interferon-induced protein 35 (IFI35), mRNA.			CCAAGGTTCTCACACTGGCCTG GGCTTGGGTGCCCATATAGGAG GTCTGT
2.111	228.66846	108.73096	108.03095	FBXW4	SHFM3; SHSF3; FBWD4; DAC; FBW4	NM_022039	Homo sapiens F-box and WD repeat domain containing 4 (FBXW4), mRNA.			CCAATAGCCTCCTGGCACCAGC CAGACCTCACCCTTGACCAACC TCTCGG
3.157	302.38928	113.49762	81.59433	LGMN	AEP; LGMN1; PRSC1	NM_001008530	Homo sapiens legumain (LGMN), transcript variant 2, mRNA.	CGGACATCTACCCCTG TTATCATGGAGGGGGT ACAGGAAGAGACTGAC AC	ILMN_1775002	CCCACTGCTTCAACTGGCACTC CCCCACGTACGAGTATGCGTTG AGACAT
2.586	257.38095	91.14419	111.805954	UNC93B1	UNC93B; UNC93; MGC126617	NM_030930	Homo sapiens unc-93 homolog B1 (C. elegans) (UNC93B1), mRNA.			ACGGTCAGGGTCTTCTTGCGAC CCGGCCCGCTCCAGATCCCCAC AGCTCT
2.706	265.40594	103.26435	95.80598	PLEKHF1	APPD; ZFYVE15; PHAFIN1; MGC4090	NM_024310	Homo sapiens pleckstrin homology domain containing, family F (with FYVE domain) member 1 (PLEKHF1), mRNA.	TGACTTCTGTGAGTTTA GACCTGCCCCTCCCAC CCCCACCCTGCCACTA T	ILMN_1698330	GGACTCTGTCCTGTGTCACCTC TCTCCAGGTGTCCAGCTGTCTC ATGCCT
2.531	252.9643	116.17262	86.393814	ZNF419	ZNF419A; FLJ23233	NM_001098495	Homo sapiens zinc finger protein 419 (ZNF419), transcript variant 6, mRNA.			GGCTGTACCCGTCGAATGGAGT TTTGATCTCGCTGAGTTTGGAG TTGGGG
15.82	1280.6267	116.218445	56.03944	GAS1		NM_002048	Homo sapiens growth arrest-specific 1 (GAS1), mRNA.	GTCTTCCACCCCTTGTT CCATCTGCCTGCCAAC CCATCGGAAAGGAATC C	ILMN_1689874	GAATCCATTTGTCATCAGGAATC AAAACCCACAGTCCATTGTGAA GTGTG
2.898	284.69763	110.5643	89.44772	TRADD	MGC11078; Hs.89862	NM_003789	Homo sapiens TNFRSF1A-associated via death domain (TRADD), transcript variant 1, mRNA.			CTATTGCTGAACCCCTGTCCAT CCACGGGACCCTGAAACTCCAC TTGGCC
4.929	439.28094	69.486984	117.69765	ACYP2	ACYP; ACYM	NM_138448	Homo sapiens acylphosphatase 2, muscle type (ACYP2), mRNA.			TGGCTGGGTGAAGAATACCAGC AAAGGCACCGTGACAGGCCAAG TGCAGG
2.989	309.60596	88.53099	120.62262	NLRX1	MGC131937; FLJ21478; NOD26; NOD9; CLR11.3; NOD5; DLNB26; MGC21025	NM_170722	Homo sapiens NLR family member X1 (NLRX1), transcript variant 2, mRNA.			GGATGCCCTCACATTGGTGCTT TCTCCTCATCCTCATGCCCCCTT TGCCA
2.324	246.65594	103.01012	111.901794	IRF1	IRF-1; MAR	NM_002198	Homo sapiens interferon regulatory factor 1 (IRF1), mRNA.	AAGGATGGTCCCAGCT GTGTCAAAAGGAAGCT TGTTTGTAATACGTGTG C	ILMN_1721657	CCTCAACAGGCCCAGGGAGGG AAGTGTGAGCGCCTTGGTATGA CTTAAAA

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.1	328.2393	116.07678	98.50185	C16ORF7	ATP-BL	NM_004913	Homo sapiens chromosome 16 open reading frame 7 (C16orf7), mRNA.	GGAGATGGTGTGTCCTGAACAGTGTAGCTCAGGTCAGCTTGAACTTTCCA	ILMN_1788786	CTCACCTTGGCTGTGGGCTGTGAACATTCCGGGACCCTGGGCATCTTATC
3.566	361.1726	122.70178	85.875336	SPSB3	SSB3; C16orf31	NM_080861	Homo sapiens splA/ryanodine receptor domain and SOCS box containing 3 (SPSB3), mRNA.			TGGAGCCCGCGTTGCTGTTCCCACAGGGCCTCGGTTTTTCCTAACTTGCT
2.041	211.97263	88.83934	123.42678	TRAFD1	FLN29	NM_006700	Homo sapiens TRAF-type zinc finger domain containing 1 (TRAFD1), mRNA.	AACTGGGCCTTGACAAAGTGTAAACCGCATGGATGGGCTTCCCCAAGGAT	ILMN_1704477	CAGTAACGAGGCTTTTGATGTGTTTGAGCTGGAGGTGAGTGGACCGGGGGC
3.306	321.95593	104.46846	96.580414	ST5	HTS1; MGC33090; DENND2B; p126	NM_139157	Homo sapiens suppression of tumorigenicity 5 (ST5), transcript variant 2, mRNA.	ATACCTGTGGCCCCCCACACAACTGAGCCCATGCTGATGGAGTACCCTGA	ILMN_1705266	AAGCCTCCTTCTCAGTAGCAGAGTCCAGTGCCTTGCAGAGCCTGAAGCCT
45.04	1845.156	15.202364	124.79967	TMEM119		NM_181724	Homo sapiens transmembrane protein 119 (TMEM119), mRNA.			GTCTGGCAGCCTGTGTCCACAATATTCGTCAGTCCTCGACAGGGAGCCTG
5.075	548.2976	128.9018	90.460175	TRAF5	MGC:39780; RNF84	NM_004619	Homo sapiens TNF receptor-associated factor 5 (TRAF5), transcript variant 1, mRNA.			CATATCCAAGTTCACTCTGTCTTCCTGAGCAGTGGAAGATCATATTGCTG
2.394	265.01428	106.28095	118.180954	WDR19	PWDMP; KIAA1638; FLJ23127; ORF26	NM_025132	Homo sapiens WD repeat domain 19 (WDR19), mRNA.	GCTGTGGAACAATCAGCCCATCTCTTTGTGACCTGGAGCAGTCAGAGGGC	ILMN_1680367	ACCTCTCCAGGTCGGCACTTTCCACTTCTGTACGGTGGCAAAACGATGAC
3.979	404.81427	83.80601	130.23512	SERGEF	Gnefr; DELGEF	NM_012139	Homo sapiens secretion regulating guanine nucleotide exchange factor (SERGEF), mRNA.	CATGCCACCCTGTTTTCAGCTAAAGCCCAACCTCCTGACCTGTCACCGTG	ILMN_1738742	AAAGCCGGTGCAGGCTCTGCTGTCATCGTCAGGACTCCTTGTGGGCTGTG
2.105	232.64761	130.40594	93.33514	MPDZ	FLJ25909; DKFZp781P216; FLJ34626; MUPP1; FLJ90240	NM_003829	Homo sapiens multiple PDZ domain protein (MPDZ), mRNA.			CCCAACCCCTAGCTCACCTCCTACTGTAAAGAGAATGCACTGGTCCTGAC
2.307	281.5476	122.45595	122.28928	MZF1	MZF1B; ZSCAN6; MZF-1; ZNF42; Zfp98	NM_198055	Homo sapiens myeloid zinc finger 1 (MZF1), transcript variant 2, mRNA.			TGTCCGCCATGGTCAGAACACCTACCTCCCCTGGTTATTGTGAGGCTGGC
5.556	462.86426	53.757637	132.84761	PAX9		NM_006194	Homo sapiens paired box 9 (PAX9), mRNA.			CTCCTGCCCTCCAACCCTTCTGCCTTGAAAGCTGGCTGTACGGACTCACA

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.274	280.37262	113.610115	133.41013	P76		NM_173542	Homo sapiens mannose-6-phosphate protein p76 (P76), mRNA.	AGCTTCTGGGAAGGGAGAGAGGGAGGTCTGCATAAAGAGGGAGTTTTGG	ILMN_1737699	GGCCATCTGTGGCTGGAGGGTTCTGAATGTCCTCTCTCCATGTCAGGCAG
2.02	230.79346	110.20178	121.74762	MAN2C1	MAN6A8; DKFZp686E23167; MANA1; MANA; MGC87979	NM_006715	Homo sapiens mannosidase, alpha, class 2C, member 1 (MAN2C1), mRNA.			TTTTCCGTGTCTTCACCCGCGGTCGTATTGGAGACCGTCAAGCAGGCGGA
2.768	319.1101	106.5435	128.48094	LRSAM1	FLJ31641; RIFLE; TAL	NM_138361	Homo sapiens leucine rich repeat and sterile alpha motif containing 1 (LRSAM1), transcript variant 1, mRNA.	CCCCAGAGCCTGTGGAGATAGAGCCTGTTTGCTGCTTTTTCTTCCCGCTC	ILMN_1752923	CCTGCTCTCCACAACTGTCCCTCCTTACCCCATGTAGCTCGATCCGAAGC
2.176	271.55594	111.430954	139.38928	DUSP22	JSP1; JKAP; MKPX; VHX	NM_020185	Homo sapiens dual specificity phosphatase 22 (DUSP22), mRNA.	TGAGCAACCAAGAGTCCCAGCCCCACCAGTATCTGCTTCTGTAGCCCACG	ILMN_1754035	TTCCCCTTATCCCCACTGCTGTGGAGGTTTCTGTACCTCGCTTGGATGCC
3.79	430.59344	113.06012	119.651794	BAIAP2L1	IRTKS	NM_018842	Homo sapiens BAI1-associated protein 2-like 1 (BAIAP2L1), mRNA.	GTGGCAAGGAAGAAAGTGTTCCGAGCATCGGTGGCTCTAACGCCAACAGC	ILMN_1742260	TCTGCCACGTGCTGACGGTCGGGAAGCTTCAGTGGAGAGGCCTAACTCTA
3.603	452.18927	113.65178	140.62679	PARP3	ADPRTL3; ADPRTL2; ADPRT3; pADPRT-3; IRT1; hPARP-3	NM_001003931	Homo sapiens poly (ADP-ribose) polymerase family, member 3 (PARP3), transcript variant 1, mRNA.	CACATGAACACAGACACGCAGGGAGAAGGCAGCCGTGTGAAGGAGTCGGA	ILMN_1662463	GCAAGGCTGGACTGTGATCTTCAATCATCCTGCCCATCTCTGGTACCCCT
2.628	335.5268	145.43095	114.751785	OSBPL2	MGC4307; KIAA0772; ORP2; MGC8342; FLJ20223; ORP-2	NM_144498	Homo sapiens oxysterol binding protein-like 2 (OSBPL2), transcript variant 2, mRNA.			CCAGAGGTGGAGGAAGAACGGTAGGAAGGCTGATGGCAAAAGCGGCTGTG
3.093	405.07263	115.814285	147.80595	CDC14B	CDC14B3; hCDC14B; Cdc14B1; Cdc14B2	NM_033331	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 2, mRNA.	GCGCTGCCTTTCTTCAGCAACAGACCCTCAAACCAAGAGGAAGCTAGATG	ILMN_1724959	CCGCTGAAACTGCCCTGGAGAGGCTATCTGCTGCTCTTCCATTTACCCAC
3.24	441.34344	123.75595	151.37262	PRKD1	PKD; PKCM; PKC-MU; PRKCM	NM_002742	Homo sapiens protein kinase D1 (PRKD1), mRNA.	GAATGCTATCATCCTGCTTGCCTGTCCATTTGTGGAACAGCATCTGGTGA	ILMN_1652826	AGACAATGCACCTAGCTGTGCAAGACCTAGTGCTCTTAAGCCTAAATGCC
2.163	300.6726	129.91013	149.9851	NAGLU	MPS IIIB; NAG; MPS3B; UFHSD	NM_000263	Homo sapiens N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB) (NAGLU), mRNA.	CCCTCGGCCTTGTCCCGGGATCGCTCCGTCGCACCCACCATGATGGAAGA	ILMN_1690284	TCGCCACCACTGGGCCTTGTTTTCCGCTAATTCCAGGGCAGATTCCAGGG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.26	319.75595	145.64761	138.58511	SLC3A2	CD98HC; 4T2HC; MDU1; NACAE; 4F2HC; CD98; 4F2	NM_001012661	Homo sapiens solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (SLC3A2), transcript variant 1, mRNA.	GGGGACCCCACCTCCCTCCAGGCCTCTTCAGAGAAGACCCAACAGTGACG	ILMN_1742221	AGGGGCTGTAAGTGCCAACATGACTGTGAAGGGCCAGAGTGAAGACCCTG
2.58	346.60596	116.96428	155.25595	MYL5		NM_002477	Homo sapiens myosin, light chain 5, regulatory (MYL5), mRNA.	CTGTACTAGGCCTACTGGGGATCAGAGTTCCCAAGAAAGGAAACCTTTTC	ILMN_1813581	GGCTGACAAGATGACGGCGGAAGAGGTGGACCAGATGTTCCAGTTCGCCT
2.409	317.95178	111.91846	158.85596	ABHD8	FLJ11743; MGC14280; MGC2512	NM_024527	Homo sapiens abhydrolase domain containing 8 (ABHD8), mRNA.			GGGGGGCTGGCGCCACCGAACCTGCACATCTCAACTTGTAACTCAATAAA
2.918	422.82263	131.14345	159.33511	LOC401152		NM_001001701	Homo sapiens HCV F-transactivated protein 1 (LOC401152), mRNA.			GTGGTAGATCACTTGAGGTCAAGAGTTGTGACACCAGCCTGGCCAACCTG
2.407	340.68097	139.39761	146.3393	KIAA0319L	PP791; RP4-765A10.3; KIAA1837; PKD1-like	NM_024874	Homo sapiens KIAA0319-like (KIAA0319L), transcript variant 1, mRNA.	GGAGTTTAGAAGAAGGTCAGAGCCCTGGGCAGTGTTGGGCCAGGCTTTAG	ILMN_1716994	ATGGCCCCGCTGTGGTCCCCTCTCTGTCCCTCCATCTGTATGTGTTCTGT
2.595	348.73096	113.16428	161.70178	RAB7L1	RAB7L; DKFZp686P1051	NM_003929	Homo sapiens RAB7, member RAS oncogene family-like 1 (RAB7L1), mRNA.	GCTGGGGCCCGGGGATCTAATTGTTTAGAGAGCCCCAAAAGTGGCTCAGA	ILMN_1669753	GCAAGTGACATCAGCTGGCTGTGATGCTTCGAAATAGGTCTGCTCCTCAC
3.159	444.1476	161.79346	122.82678	NPIP		NM_006985	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA.	CACCTGCCCCGGGTTTTGGAGAGGATGTGCCCAATAGGCTTGTCGATAAC	ILMN_1806473	CTGGCCCTACCTCACAGCTGAAACTTTAAAAAACAGGATGGGCCACCAGC
3.456	486.26428	119.80595	167.34344	ADCY6	KIAA0422; DKFZp779F075	NM_020983	Homo sapiens adenylate cyclase 6 (ADCY6), transcript variant 2, mRNA.	CAAGCCACGACCAACCAGAGCCCAAACTGCCTGCCACCACGAGCATATCC	ILMN_1736929	GATCAGAGTGGGAAGACCTCAGCCTTGGGTGGCTTGTCTCTGCTTCTTGC
6.263	720.756	85.39186	167.63095	ALDH3B1	FLJ26433; ALDH7; ALDH4	NM_000694	Homo sapiens aldehyde dehydrogenase 3 family, member B1 (ALDH3B1), transcript variant 1, mRNA.	TAGCCCTGATAGTCGGGCAGCTTAGAGGAGTGGGGAGGAGAACTCAGCCT	ILMN_1808530	GCTTGAGAAACCTACATTTGGACAATGAGAGGCTGCTCCTGCGGCCTGCG
2.019	307.15594	161.18094	144.58511	C10ORF26	MGC125648; FLJ20367; FLJ20154; OPAL1	NM_001083913	Homo sapiens chromosome 10 open reading frame 26 (C10orf26), transcript variant 1, mRNA.			GCAGTCCCCTGTGTTTGCCAGAGATACTGTGCTCGAAGTAGAGGTTTTAC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.805	422.33096	134.22263	169.25595	RILPL2	FLJ30380; MGC7036; FLJ32372	NM_145058	Homo sapiens Rab interacting lysosomal protein-like 2 (RILPL2), mRNA.			GATGCCTGGCAAAACCACCTCC CTGTGCCACACAGACACACTAG GCCTGT
13.53	1565.9392	170.59344	76.72356	CDC42EP5	MGC21945; CEP5; Borg3; MGC71153	NM_145057	Homo sapiens CDC42 effector protein (Rho GTPase binding) 5 (CDC42EP5), mRNA.	GTCTTAAGGAGACTGG TAGGAGGAGGCATGGA AACCAAAAGGCCGTGT GT	ILMN_1705685	CTTCCCGCCCGGCACCCCACTT CTGTATACATAAACGGCCAAGG TGTGTG
2.211	353.6726	167.10596	153.86429	ZNF25	DKFZp564C206; KOX19; Zfp9; FLJ31890	NM_145011	Homo sapiens zinc finger protein 25 (ZNF25), mRNA.	GGGGACTGTCTGTCAT GCCTGGAGGCTCTTCG GCACACTTCCCCATCTT T	ILMN_1662417	CCCCAGCAGAGTTGAGTAGTTG TAGCAGACACCACATGCCCTTG AGCCTA
2.363	399.22263	160.07262	178.46428	SUMF1	MGC131853; FGE; AAPA3037; MGC150436	NM_182760	Homo sapiens sulfatase modifying factor 1 (SUMF1), mRNA.			GGGCAGTCATAAGCTCTGTTTC CCCCTCTCCCCAAAGCCTTCAG CGAACG
9	940.68506	63.733154	186.40178	FCGRT	FCRN; alpha-chain	NM_004107	Homo sapiens Fc fragment of IgG, receptor, transporter, alpha (FCGRT), mRNA.	AAGACAAGCAGGAGGG TCGACATGGACTGAAA TCACCCTCTGCAGCTG GG	ILMN_1734508	TGTGATTCCAGCCACCGCCTGA CCATCCGCCATTCCGACTGCTA AAAGCG
4.564	693.72266	191.78928	122.20595	SOCS1	SSI-1; CISH1; SSI1; CIS1; JAB; TIP3; SOCS-1	NM_003745	Homo sapiens suppressor of cytokine signaling 1 (SOCS1), mRNA.	TGACTAGAGGCAGAGC CCGAGTAGAAACAGGT CTGAACGGATGGAACT GC	ILMN_1808018	CTCCTGGTGCTCCCTCTGGGTC CCCCTGGTTGTTGTAGCAGCTT AACTGT
2.17	352.18512	193.18512	136.1101	MAGED2	MAGE-D2; MGC8386; MAGED; JCL-1; BCG1; 11B6; HCA10	NM_201222	Homo sapiens melanoma antigen family D, 2 (MAGED2), transcript variant 3, mRNA.	CATGGACTCCTGCCGA CTCTGGTAGCTGGGAC GCTGGTTTATGGCATC CT	ILMN_1668242	ATCCAGGCGGGAGCAGAAGCTA AAGCCAAAGCCCAAGAGAGTGG CAGTGC
2.463	438.73096	174.28928	182.97263	GRK5	GPRK5	NM_005308	Homo sapiens G protein-coupled receptor kinase 5 (GRK5), mRNA.	GTGCTATCTGTTCAGT GATGCCCTCAGAGCTC TTGCTGTTAGCTGGCA GC	ILMN_1724686	GTGCAGCCACTGTTAAGCCATG TGTTCCAAGGCATTTTAGCGGG GAGGGG
3.557	571.82263	155.27261	176.31012	MIB2	ZZZ5; ZZANK1; FLJ20648; FLJ39787	NM_080875	Homo sapiens mindbomb homolog 2 (Drosophila) (MIB2), mRNA.			TGAAGAAGTGCATCAGGTGCCA GGTGGTCGTCAGCAAGAAACTG CGCCCA
3.118	507.9143	156.95595	176.47263	CREG1	CREG	NM_003851	Homo sapiens cellular repressor of E1A-stimulated genes 1 (CREG1), mRNA.	AGCAAGTGCCTCGGCC CAGTCTTCCTGTATTTA TGTGGAAGGCGGCGG CT	ILMN_1701629	CCAGCTTCAGCCAGGGACAAAA TCCCCTCCCAAACCACTCTCCA CAGCTT
2.051	363.28094	167.44762	190.4643	MTA3	KIAA1266	NM_020744	Homo sapiens metastasis associated 1 family, member 3 (MTA3), mRNA.			GCCAGGCCATGCAGGGAATGC CAGTCCGAAACACTGGGAGTCC AAAGTCT

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.485	437.68097	155.05595	202.24344	RAB13	GIG4	NM_002870	Homo sapiens RAB13, member RAS oncogene family (RAB13), mRNA.	CATCATCAACTTCCAATGTCTGGACAACTCCTTCCTGTTGAGGGTCGAGC	ILMN_1770228	GAGCAGGGGAGAAATAGCAGAGGGGCTTGGAGGGTCACATAGGTAGATGG
15.18	2179.481	103.98166	205.19345	LEPR	OBR; CD295	NM_001003679	Homo sapiens leptin receptor (LEPR), transcript variant 2, mRNA.			TGAATTGAGCTTTTTGCCCACAGATTCTTGATTTGTAGTTGTTTGGCAGG
14.96	1705.1143	137.13104	134.3891	NTN4	FLJ23180; PRO3091	NM_021229	Homo sapiens netrin 4 (NTN4), mRNA.			GCGTGAAGTCTCAGCTTTGAGCTGGAGGCTAGATTCCAAGATGACAGCCA
2.394	460.73096	189.86429	196.46011	UBE2H	UBCH2; E2-20K; UBCH; UBC8	NM_003344	Homo sapiens ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) (UBE2H), transcript variant 1, mRNA.	GAAAGTGAGCGAGGAGTCAGAAACTCAGCCACTGGTTGCCTTGGTAGGCA	ILMN_1704912	GCCTGCTGAACTCGGAGGGGAGTTTGGAGAAATTTTAGACAGCAGCTCTG
3.408	666.21423	188.38095	204.03928	PINK1	FLJ27236; PARK6; BRPK	NM_032409	Homo sapiens PTEN induced putative kinase 1 (PINK1), nuclear gene encoding mitochondrial protein, mRNA.	GGACTGAGGGACCAAGGAAACATGATGGGGGAGGCAGAGAGGGCAAGAGT	ILMN_1711311	CACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATGTCTGATTTGCCACC
2.433	496.62262	218.42679	191.49762	CFLAR	I-FLICE; CASP8AP1; CASH; c-FLIPL; Casper; FLAME1; CLARP; USURPIN; FLIP; c-FLIPR; c-FLIPS; c-FLIP; MRIT; FLAME; FLAME-1	NM_003879	Homo sapiens CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA.	GGGCTGAGAGTATGGGGAAAAGAATCAAGAGACCTGACTGCCGCCAACTC	ILMN_1696827	GTGCCTACGAATAGCCACTGCATACCAACCTGGGCAATATAGCAAGATCC
3.021	633.10596	220.81427	198.44762	TNIP1	KIAA0113; NAF1; ABIN-1; VAN	NM_006058	Homo sapiens TNFAIP3 interacting protein 1 (TNIP1), mRNA.	ACTAAGCCCACCTCCCCTGCTCTCCTTCCCAGCATTGAGCCCTTGGTTGC	ILMN_1666819	TCACAGTAGCCTTGCTGAAGCCATCACAGATGGGAGAAGGCCATGCCAGC
2.169	433.13095	202.2143	200.51845	STK36	FU; DKFZp434N0223; KIAA1278	NM_015690	Homo sapiens serine/threonine kinase 36, fused homolog (Drosophila) (STK36), mRNA.	CAGAAGGCTCAGAAGTCCTGATGTGAGGAGAGGTGCGGGGAGACATTCCA	ILMN_1770610	GGCTCAACCCCTCTTTCAGCTTCTATGTGGTGTTGGAGGTGCTGGTATCG
2.505	494.26846	173.23929	225.4226	ANXA11	CAP50; ANX11	NM_001157	Homo sapiens annexin A11 (ANXA11), transcript variant a, mRNA.	AAGCGGGGAGAGGGTACACAATGGGTATCTAATAAATACTTAAGAGGTGG	ILMN_1808732	GCCAAAACTTGTTTCCACATTAAGAGTCAGCCAGCTCTGGAATGGTCTGG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.185	836.41016	192.93512	208.77261	SRC	SRC1; p60-Src; c-SRC; ASV	NM_198291	Homo sapiens v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC), transcript variant 2, mRNA.	GAGGAGGTGCCTTCTG GGTATCTCTGTGTTGG TGTATCTGTGCCATTG GC	ILMN_1794829	ACCCAAGTCTTCTCCCGTCCATT CCAGTCAAATCTGGGCTCACTC ACCCC
4.198	843.08093	178.36012	226.89343	TCEA2	TFIIS	NM_198723	Homo sapiens transcription elongation factor A (SII), 2 (TCEA2), transcript variant 2, mRNA.	TGGGGACAAGGGCTGC TTCCAGTTCTTGGATG GCGTTCTCCTATCTACC T	ILMN_1732149	CACGTCCTCCGTTGACACAGCT TCTCTGGAGACCCTAGAAGGCG GCATGT
28.85	2740.4976	48.385597	227.03513	ASS1	CTLN1; ASS	NM_054012	Homo sapiens argininosuccinate synthetase 1 (ASS1), transcript variant 2, mRNA.	TCTGCCCCTCCCTGCC CGCGTTTCAGGGCCTC GGTCCATAGAGAACAC CA	ILMN_1789240	CCAGAGCAAGGTCACTGCCAAA TAGACCCGTGTACAATGAGGAG CTGGGG
3.028	547.19763	229.23929	144.09763	SIX5	DMAHP; BOR2	NM_175875	Homo sapiens SIX homeobox 5 (SIX5), mRNA.	TGCTGCTCTTGCACTT GCTGGAATGTACAGGG TGGGCTGGTTGGCCCT AT	ILMN_1813670	GCCCTTGTCCTCATTATCCGGC CCAGACCAAAGATTCCCTCATC CCTGGG
2.24	467.58093	212.21844	207.84761	ZFAND3	FLJ13222; TEX27	NM_021943	Homo sapiens zinc finger, AN1-type domain 3 (ZFAND3), mRNA.			TTTACCACTGCTGTCAAGCCAC AGCCCTTGGCCACCATACGGGC CATCCT
2.443	496.13928	229.11845	183.55179	FAM100A	FLJ32185; FLJ31223; PP11303	NM_145253	Homo sapiens family with sequence similarity 100, member A (FAM100A), mRNA.	GAGGCGCTCAGGGAAA GCTGGACTACTAAAGT GAACTGGATGGCCCAC AC	ILMN_1763347	GCATGTGTGCGCGTGGCCGTG TCTGTGTATTTCTACGTGTGTCG CTCTTC
3.69	675.9309	203.38512	175.56427	SORT1	NT3; Gp95	NM_002959	Homo sapiens sortilin 1 (SORT1), mRNA.	AGGGACACACCCTGAT AGCACAATCTCCTTGG GGCCCTGCCCACCTCC AG	ILMN_1775048	GGTCCCCATGTGCCTGTTGTTC AGCCCTCTCTCTTGTTCCCTTTC TGAGC
2.427	460.96014	151.08511	239.05595	C10ORF32	CYT19; AS3MT; RP11-753C18.6; FLJ40752; DKFZp686B2219; MGC27171	NM_144591	Homo sapiens chromosome 10 open reading frame 32 (C10orf32), mRNA.			GTGGTATCATTATCAGGCCAGC TGCAGCCTCTTGCCTTGACCTG CATTCC
2.952	631.35596	240.37262	191.06429	VGLL4	KIAA0121; VGL-4	NM_014667	Homo sapiens vestigial like 4 (Drosophila) (VGLL4), mRNA.			GCGCTGCCTGCAGTGCGCTCT GACCTTCTCTTCATGTGTGTAAA TCTGTA
2.672	500.6726	240.63095	147.5893	LMOD3	DKFZp313F0135	NM_198271	Homo sapiens leiomodin 3 (fetal) (LMOD3), mRNA.	ACGCCGCTGCTGCTCC GGCTGAGTATCTAGCT TGTCTCCCCGATGGGA TT	ILMN_1709734	CCCTAGAAATTAGAAAATCAAGC TTTGGGCCAGGTGCGGTGGCT CATGCC
3.29	730.2226	204.23929	241.69762	ZFP90	ZNF756; NK10	NM_133458	Homo sapiens zinc finger protein 90 homolog (mouse) (ZFP90), mRNA.	GGCCACACAGCCAAGA AGAGCCCATGCAACTC AGTCCAGGATTTTACTG G	ILMN_1671142	GTCCCAACAGCCATGAACCATG CACTTATGGATACCCAGCCTTTT AGGGC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.681	618.3268	237.06845	225.40594	SPAG7	ACRP; FSA-1; MGC20134	NM_004890	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA.			CTGCTATTAGAGCCCATCCTGG AGCCCCACCTCTGAACCACCTC CTACCA
2.735	600.76013	246.2768	198.28513	STOM	EPB7; EPB72; BND7	NM_004099	Homo sapiens stomatin (STOM), transcript variant 1, mRNA.	GAGGGTTGTCCGTGAT CCACAAGGCATTAGAG CATGGGTGGCATGGAG AA	ILMN_1815205	CTCTGGATGATGCCACTGATGC CTGGGGAATAAAGGTGGAGCGT GTGGAA
2.849	623.10596	198.14345	247.76012	PVRL2	PVRR2; HVEB; PRR2; CD112	NM_001042724	Homo sapiens poliovirus receptor-related 2 (herpesvirus entry mediator B) (PVRL2), transcript variant delta, mRNA.			CAGTCTGTTCAATACCACCTTCG TCTGCACAGTCACCAATGCCGT GGGCA
2.273	549.23926	248.2768	237.39761	SLC20A2	MLVAR; PIT-2; GLVR2; Glvr-2	NM_006749	Homo sapiens solute carrier family 20 (phosphate transporter), member 2 (SLC20A2), mRNA.	CCGTGTGAGCCAGTCC AGGAGGGTGTAAGTTC TGAATGGTTCCTTGCT GA	ILMN_1687501	TCTGAGGCCCACACAAAGCTGG ACACCCCCAGGCTCTACTCCAT CCCATT
3.526	753.7643	214.04346	222.97679	BEXL1		XM_936467	PREDICTED: Homo sapiens brain expressed X-linked-like 1 (BEXL1), mRNA.			AAATGTAGGACCTATCGTCCAG ACTCACAGAGTGGGGCTCCAGA ATCTCC
2.042	454.4226	264.28928	187.93095	ARHGEF17	KIAA0337; P164RHOGEF; p164-RhoGEF; FLJ90019; TEM4	NM_014786	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 17 (ARHGEF17), mRNA.			TCCCACTTGAGAGCAGCCTCTA CCTGACCCCCTGGACCACAGAG AGCCAC
3.021	636.506	192.8601	242.7976	HIST2H2AA3	H2a-615; H2A; H2AFO; HIST2H2AA; H2A/q; H2A/O; H2A.2	NM_003516	Homo sapiens histone cluster 2, H2aa3 (HIST2H2AA3), mRNA.	CGCTACAAAGCAGCCA CTGTGCTTACTGAACG GCCTCCCCCTGTATCG CT	ILMN_1764231	GGCCCGCGTCTCGAAGGGGCA CCTGTGAACTCAAAAGGCTCTTT TCAGAG
25.92	3905.2227	94.69763	269.58093	FHL1	KYO-T; SLIM1; MGC111107; XMPMA; FHL1B; bA535K18.1	NM_001449	Homo sapiens four and a half LIM domains 1 (FHL1), mRNA.			CTAGAGGGGGAGTTGAGCAGG CGCCAGGGCTGTCATCAACATG GATATGA
2.542	649.5143	242.80594	270.2726	VHL	HRCA1; RCA1; VHL1	NM_198156	Homo sapiens von Hippel-Lindau tumor suppressor (VHL), transcript variant 2, mRNA.	GAAGCTGACAATGACT GCATTCAACGGGGCCA TGGCAGGAAAGCTGAC CC	ILMN_1793537	TTCCTGTGCTCAAAAATGAGAGT GACGGCTGGCATGGTGGCTCC CGCCTG
3.563	821.18097	276.24762	189.65594	TRIB3	TRB3; C20orf97; SKIP3; NIPK; SINK	NM_021158	Homo sapiens tribbles homolog 3 (Drosophila) (TRIB3), mRNA.			CATGGGGCTTCTGACCTGAGCA CCAAGGTTGAGGGACAGGATTA GGCAGG
2.251	547.44763	254.1726	236.9226	TESK1		NM_006285	Homo sapiens testis-specific kinase 1 (TESK1), mRNA.	AGTGGTCCATGTCTGT GCTGGCTGGAAGAGG GCTTGCTTAGGGCAGC TTC	ILMN_1706088	AGCCCGTGGTCTCAGGCCTCCA ACTTTGGCCTTCAGGACACCCT GTAAGA

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.944	715.11426	271.8018	224.6518	STK19	RP1; G11; D6S60; HLA-RP1; MGC117388; D6S60E	NM_004197	Homo sapiens serine/threonine kinase 19 (STK19), transcript variant 1, mRNA.	GAGCGTCCTGTTAAGG CACATGCTAACTTCCCA CTCAAGTCTGGCAGCG C	ILMN_1807072	TTGGGAAGGCTTGGGAGCCAG GATGAGTGTCGGGCTCTCGTGT GTGCAAA
2.824	768.33923	256.95593	288.31012	PRMT2	HRMT1L1; MGC111373	NM_001535	Homo sapiens protein arginine methyltransferase 2 (PRMT2), transcript variant 2, mRNA.	CAGCGGAACCGCCCAG GATCAGATTGCATGTG ACTCTGAAGCTGACGA AC	ILMN_1686555	GCACCTGGCTTCTGCACACTCC TGCGAAAGTCGGTGAACATTCA CTCCAC
2.799	807.58093	283.93097	293.7143	ANXA11	CAP50; ANX11	NM_001157	Homo sapiens annexin A11 (ANXA11), transcript variant a, mRNA.			GGTAGCCTGTGCATCTGGTGAG TGTGTCACGAGCTTTGTTACTG CCAAAC
2.142	624.381	292.68512	290.7726	ELMO2	FLJ11656; CED12; CED-12; KIAA1834; ELMO-2	NM_133171	Homo sapiens engulfment and cell motility 2 (ELMO2), transcript variant 1, mRNA.			GCCTCTCTCCCTGGACATACGT TAGCACATTGGCATTCAGTATTG GTGGC
3.476	853.33923	199.43095	306.70593	COPZ2	MGC23008	NM_016429	Homo sapiens coatomer protein complex, subunit zeta 2 (COPZ2), mRNA.	GCTGTTTTCAGCCATGT TTCTCTGTGCATCTCCA GTAAGCAGAAGGCTAC	ILMN_1729640	TTCCCCAATCCTGGCAAAAGCC CAAAGATCCCAGGGTCAGGAGA GACCCC
2.001	581.0643	303.29346	280.71844	SLC3A2	4F2HC; CD98; 4F2; CD98HC; 4T2HC; MDU1; NACAE	NM_001013251	Homo sapiens solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 (SLC3A2), transcript variant 6, mRNA.			TAGGGGTTGAGCCACCATCTGA CCGCAAGCTGCGTCGTGTCGCC GGTTCT
2.268	654.9393	317.1143	264.78094	AIP	ARA9; FKBP16; XAP2; SMTPHN; FKBP37	NM_003977	Homo sapiens aryl hydrocarbon receptor interacting protein (AIP), mRNA.	TAGGAATCTATGATGCT GATGGTGATGGAGATT TTGATGTGGATGATGC C	ILMN_1693771	TTCTCCCATTGACAGGAGCACT TGGCCCTGCCTTACCTGCCAAG CCCACT
3.239	890.6726	235.10178	323.97678	PLD3	HU-K4	NM_001031696	Homo sapiens phospholipase D family, member 3 (PLD3), transcript variant 1, mRNA.	TTCACTGTGGGTTGGG GGAGCTAATTTTAAGCA TGTTCAGTGGCAGCTC C	ILMN_1798187	CCCTGGCCCACCCCCACTTTCC AGGGCAAAAAGGGCCCAGGGT TATAATA
3.814	1068.856	234.06427	335.4018	YEATS2	FLJ13308; KIAA1197; FLJ10201; FLJ12841	NM_018023	Homo sapiens YEATS domain containing 2 (YEATS2), mRNA.			GCAAGTACAGAAGGAATCTATT CTCAGCAGGGCATAGGGCACG CACTGGC
3.978	1000.57263	188.62677	336.06845	PSG9	PSG11	NM_002784	Homo sapiens pregnancy specific beta 1-glycoprotein 9 (PSG9), mRNA.			TCCAACGCATCCCTGCTGATCC AGAATGTCACCCGGAAGGATGC AGGAAC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.538	759.6226	337.1726	268.13095	CSRP2	CRP2; LMO5; SmLIM	NM_001321	Homo sapiens cysteine and glycine-rich protein 2 (CSRP2), mRNA.	TGCACGGCTCCAGCTC AGCCCATTGAGCCAAT AACTGCTGCTCCCAGT GG	ILMN_1798138	GAGCTGGAAAGCCCTGGCACAA AAACTGTTTCCGATGTGCAAAGT GTGGG
2.165	653.006	271.1643	339.8476	RALGDS	RGF; RalGEF; FLJ20922	NM_006266	Homo sapiens ral guanine nucleotide dissociation stimulator (RALGDS), transcript variant 1, mRNA.			AGTGCCATTCACCACTGCGTCC TGGGCTTTACGAGACCATGCAA GACGGG
2.824	883.6893	335.4643	292.15594	NRBP2	pp9320; MGC138699; TRG16; DKFZp434P086	NM_178564	Homo sapiens nuclear receptor binding protein 2 (NRBP2), mRNA.			ACCTCTTTTGTTGGGGAAGGGT GGCATTCTGCTGACCACAGCAC TCCAAC
2.753	859.34766	283.87262	342.95593	PNPLA2	PEDF-R; FP17548; TTS2; TTS-2.2; ATGL; DKFZp667M109; 1110001C14Rik	NM_020376	Homo sapiens patatin-like phospholipase domain containing 2 (PNPLA2), mRNA.	AAAACCACAAGGACCA CCCCCACAAGGAGGAA AGCCACAAGGACCACC CG	ILMN_1740017	TGAGGCCCCGCGCACCTGTGC CTTAATCTTCCCTCCCCTGTGCT GCCCGA
2.459	774.3893	313.3351	320.1143	BRD3	KIAA0043; RING3L; ORFX	NM_007371	Homo sapiens bromodomain containing 3 (BRD3), mRNA.	GGGGTTTGAAGAGGAA GCCAGTTGTGGGAGTC TCTTTGTTACACCCCCT C	ILMN_1792931	GTCAACACGCATTGTCCTTGTC ATTTGGGCCCCGAGCTCTGACC CTCGTG
3.559	1001.33923	345.1643	234.30179	COL16A1	FP1572; 447AA	NM_001856	Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA.			CCATGCCGATGGAGCAGCAGTA CCCACCCATGAAAACCATGAAG GGGCCT
2.661	837.256	285.06427	348.94763	PRMT2	HRMT1L1; MGC111373	NM_001535	Homo sapiens protein arginine methyltransferase 2 (PRMT2), transcript variant 2, mRNA.			TGGCTGGGTCGGAGCTCCATGT TCCTAAGCTAGGTCTAGGTCTA CACTCC
11.73	2466.6475	125.797615	349.2893	CEBPD	C/EBP-delta; NF-IL6-beta; CELF; CRP3	NM_005195	Homo sapiens CCAAT/enhancer binding protein (C/EBP), delta (CEBPD), mRNA.	GGGATCAACTGTACGC CTTTGGTATCTGACCAT AAAGTCTTTTGCTCCGC	ILMN_1656413	CGCCGGGTGCCCGCTGCAGTT TCTTGGGACATAGGAGCGCAAA GAAGCTA
2.604	744.2726	237.53928	353.62262	FGFRL1	FGFR5; FHFR	NM_021923	Homo sapiens fibroblast growth factor receptor-like 1 (FGFRL1), transcript variant 3, mRNA.	CCAGGGCGGTTCCAAA CTCTAAACCGTTCCCAC CGTCAGGGAGACCTAC A	ILMN_1775956	AATGATGGAAGGAAGACTGGGT TGCAGGGACTGTGGTCTCTCCT GGGGCC
2.169	717.6726	334.1643	329.70596	C16ORF68	FLJ12433; MGC2654	NM_024109	Homo sapiens chromosome 16 open reading frame 68 (C16orf68), mRNA.	GGAACTCTGATGCTCT GCGTGGGACCATGCCT GAACTCCCCGAATAAC TG	ILMN_1803197	TTAAAACGCTCTCCCGACTCGC CCACAGATTGAAAAATGCCTGC ACAGCC
3.758	1090.3142	231.14761	362.6101	CTXN1	CTXN; FLJ25968	NM_206833	Homo sapiens cortexin 1 (CTXN1), mRNA.	GGAGAGTGCAGAGAAG GAGATCGGCTTGTGGT TTCACCCTGAGGAACT GG	ILMN_1741133	CCCTCCCATGCCGTTCCACTCC TCCCTGCCTCTGAGCCGAACAT GATAAT

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.582	1050.9642	366.9601	237.54346	KIAA0355		NM_014686	Homo sapiens KIAA0355 (KIAA0355), mRNA.			GACTGTGTGAAGCCGTTTGTGT GGTCTCCATGTAGGTGCTGTGT TCCCGG
2.905	1039.231	361.95593	353.8018	BSDC1	DKFZp686B09139; RP4-811H24.7; FLJ10276	NM_018045	Homo sapiens BSD domain containing 1 (BSDC1), mRNA.	GAGGATGACTCTGAAG AGGAGCAAAGGCAGCT GTTGTTCGAAGACACC TC	ILMN_1788689	CCAATGAGTGAAAGGGATCGTG GGTCAGGGACACCGAGAGAGT GAGGTCA
3.47	1032.0143	376.13095	242.88095	BIRC3	RNF49; MALT2; API2; HIAP1; AIP1; MIHC; HAIP1; CIAP2	NM_182962	Homo sapiens baculoviral IAP repeat-containing 3 (BIRC3), transcript variant 2, mRNA.			GTGGTGGTATGTGCCTGTAGTC CCAGGCTGAGGCAAGAGAATTA CTTGAG
8.442	2346.606	197.9643	380.1726	NCOA7	FLJ45605; dJ187J11.3; ESNA1; Nbla00052; Nbla10993; ERAP140; MGC88425	NM_181782	Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA.	ACAAGGTGCTAAAACA GGTTCACCCCGATACT GGCATCTCATCCAAGG CC	ILMN_1716195	CTGTAGCCTGGGTGTACGTTTC ACTCAAGTTCTCCTACTGAGGA CTCTTG
7.615	2185.9727	217.12262	394.9768	MXD4	MSTP149; MAD4; MST149	NM_006454	Homo sapiens MAX dimerization protein 4 (MXD4), mRNA.	GGGAACGGGTTGTTGG CCAGACAAGTCCCAGA AACTGCCTGCTTTGAA GC	ILMN_1702107	GGCCACCTGTCCACCGTGTGG GCCGTGCTGTGTCCTTATGTCA TTGTAAT
4.596	1496.9309	299.2851	367.4143	PSG6	PSG10	NM_001031850	Homo sapiens pregnancy specific beta 1-glycoprotein 6 (PSG6), transcript variant 2, mRNA.	CCCTGTGCCGTTATTA CCTAGCAACCCTTGCA ATGAAGATGAGCAGAT CC	ILMN_1792434	CTCTATCTGAGTGCCCCAGAAT TGGGAAACTATTCATGAGTATTC ATAGG
3.818	1303.3351	315.18512	379.00177	HLA-F	HLA-5.4; HLAF; HLA-CDA12	NM_018950	Homo sapiens major histocompatibility complex, class I, F (HLA-F), mRNA.	CAGAGCAATCTGCTGC CAATAGAGTTTGGAGG TGGATATTTAGTTTACA G	ILMN_1800253	CTGCAGTCACTGACAGTGCCCA GGGCTCTGGGGTGTCTCTCACA GCTAAT
3.42	1127.0059	267.44763	405.18094	SLC25A23	MGC2615; MCSC2; SCaMC-3; APC2	NM_024103	Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23 (SLC25A23), nuclear gene encoding mitochondrial protein, mRNA.			TCCTTCGACCTCCACTGCGCCC CACCTCCCTGCCTGTGTGTGTT ATTTCA
2.603	854.0643	273.59344	407.7726	AGA	AGU; ASRG; GA	NM_000027	Homo sapiens aspartylglucosaminidase (AGA), mRNA.			CTCTCTGTATGACAACTCTACAG AAGTTGTGCGCGTGCTTTCTCA GCAGC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.703	997.7101	359.00595	383.4268	PLEKHA1	TAPP1	NM_001001974	Homo sapiens pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1 (PLEKHA1), transcript variant 2, mRNA.			ATCCTTGTTCGATAGCATAGGAA AATGTTCTGGTGATTGTCAGGG TCTCC
2.902	1026.0977	311.57263	410.0393	MYLK	DKFZp686I10125; MLCK108; FLJ12216; MSTP083; KRP; MLCK210; smMLCK; MLCK; MYLK1	NM_053032	Homo sapiens myosin light chain kinase (MYLK), transcript variant 8, mRNA.			AGAGCTGGAGAACTCCATGTAC TTTGGAATCTCCTCCAAGATAGC CAGAG
2.289	833.756	387.33093	348.68512	KIAA0913	FLJ34302	NM_015037	Homo sapiens KIAA0913 (KIAA0913), mRNA.	CTGAGGAAGTATCTAG CCTCCGTCCCCCTCGC CTGATCCATGAAGATG GC	ILMN_1809582	CAGGGGGAGTGAAACTTGGCTG GACAGATCATCCTCACTCAGTT CCCTGG
2.236	863.1393	358.21014	417.41846	CHMP4B	CTPP3; SNF7; dJ553F4.4; CHMP4A; Shax1; SNF7-2; C20orf178	NM_176812	Homo sapiens chromatin modifying protein 4B (CHMP4B), mRNA.	AGCTGAAAGTGGGGGT AAAGGTGGAGTAATCT GTGGATTTGTTTCTGTT G	ILMN_1657436	GTGTATTGGCCCTGTGTTTACC ACTCTGGCCCACTCCTCACCCC CTTGCT
2.776	921.35596	258.9268	426.62262	C10ORF56	FLJ90798	NM_153367	Homo sapiens chromosome 10 open reading frame 56 (C10orf56), mRNA.			CCAACGACTAACCCTGAAATGG GGGTGTTCCAGCCTTCAGCGAG ATGGCC
2.061	779.2893	324.7393	439.38928	CYB5R1	B5R.1; NQO3A2; humb5R2	NM_016243	Homo sapiens cytochrome b5 reductase 1 (CYB5R1), mRNA.			GCTGTTTGTGGCAGGAACCCCT GGCTGTGCAAATAAATGGGGCT GAGGCC
2.291	872.4393	329.81427	439.7976	SNRPN	SNURF-SNRPN; HCERN3; SMN; RT-LI; SM-D; SNRNP-N	NM_022806	Homo sapiens small nuclear ribonucleoprotein polypeptide N (SNRPN), transcript variant 3, mRNA.			GCTCCATCTACTCTTTGAAGCTT CTGCCCAGCTTGCATTGTTTCTA GGAG
2.591	961.0893	305.60596	449.05594	GMDS	GMD	NM_001500	Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA.	TCAGTCACATTCGCTTC AGTCCTACGGGCGAGT GGACGGAGGGCTTGCT G	ILMN_1675188	CCTCCAGGGTTTGGGTCGCTTT GCGTTTGTCGAAGCCTCCTCTG AATGGC
6.109	2255.3892	375.15594	378.85178	RPS6KA2	RSK3; S6K-alpha; S6K-alpha2; pp90RSK3; HU-2; RSK; MAPKAPK1C; p90-RSK3	NM_001006932	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 2 (RPS6KA2), transcript variant 2, mRNA.	TTTGTATTTTAAGAGTC TCATGCTCTACCGTTG GAACTAGCCAGATGGC C	ILMN_1683305	GCAGCATCTGTGTCGTTCTACT GAGCACGCTTCTCTGCCTCGCT CCTGAC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4.391	1307.281	459.6601	191.45178	NNMT		NM_006169	Homo sapiens nicotinamide N-methyltransferase (NNMT), mRNA.	TACCCTTCATGAGACCCAACTCTGCCACAGCTCATCCTCGGAGGCAATCC	ILMN_1697975	CAAGGGTCCAGAGAAGGAGGAGAAGTTGAGACAGGCGGTCAAGCAGGTGC
2.496	1077.231	459.38928	405.90594	IL11RA	MGC2146	NM_004512	Homo sapiens interleukin 11 receptor, alpha (IL11RA), transcript variant 1, mRNA.	AGACTACAGCTGGATAGCTGCCCTTTAAGCCTTGGAGATGGGGAGGATCC	ILMN_1801869	TGCATGTATGTAGGTGCCTGGGGAGTGTGTGTGGGTCCTTGGCTCTTGGC
2.178	948.07263	470.87262	403.9226	WDR13	DKFZp779C2057; FLJ20563; MG21	NM_017883	Homo sapiens WD repeat domain 13 (WDR13), mRNA.			CACCTGTGCTTGATGTCAGCTTCAACTGCGACGAGAGCCTACTGGCCTCC
3.634	1399.7144	314.93512	483.68094	GYPC	MGC126191; GE; CD236R; GYPD; CD236; GPC; MGC117309; MGC126192	NM_016815	Homo sapiens glycophorin C (Gerbich blood group) (GYPC), transcript variant 2, mRNA.	GCCCCAGGAGAAGCCCCAGTCCTTGGAAAAGGTGGATGAGAAGTAGCTGG	ILMN_1693961	GGGCAGTGCAGGACAACATCAGCTCACTGGCAGGAAAGTCCTTGTTGAGG
2.336	1028.3392	495.06012	392.50595	CTSA	NGBE; PPCA; GSL; PPGB; GLB2	NM_000308	Homo sapiens cathepsin A (CTSA), mRNA.	CCCTTGATGCTGGGGCATCCGGGTTGGGATGGAGATAGGAGGATCTCAGT	ILMN_1777156	CAAGCAGCCATACTGATGACCACAGCAACCAGCTCCACGGCCTGATGCAG
4.842	2163.9226	437.1643	464.83093	RABGAP1	TBC1D11; RP11-123N4.2; DKFZp586D2123; GAPCENA	NM_012197	Homo sapiens RAB GTPase activating protein 1 (RABGAP1), mRNA.			GACTGAGTTGCGTGTCTGTAAATGTCTGCGCAGGGTGCACATGCTGCGAG
6.518	2184.4226	228.78094	507.6976	PSG4	PSG9	NM_002780	Homo sapiens pregnancy specific beta 1-glycoprotein 4 (PSG4), transcript variant 1, mRNA.			GCTAAATGGTCAGAGCCTCCCTGTCAGTCCCAGGGTAAAGCGACCCATTG
3.57	1616.5642	504.18927	411.81012	LAMB2	LAMS	NM_002292	Homo sapiens laminin, beta 2 (laminin S) (LAMB2), mRNA.	TGCCCTTGCCCCACTCCTGAATGCACCACATGCCTCTGTCTCCCCGCTGA	ILMN_1808415	GGAAGGCACCTATGAGGAAAATGAGCGGGCACTGGAGAGTAAGGCAGCCC
2.024	939.0768	522.9643	415.63095	C3ORF21	FLJ35155	NM_152531	Homo sapiens chromosome 3 open reading frame 21 (C3orf21), mRNA.	GGGTGTGAGGGTCGCGTTCCTGCTGTCTGGACTTTTTCTGTCCCACTGAG	ILMN_1680454	CCTCCTGTACGTAGGCTGCAGACGTGAAAGCCCCAGGGGTCCATTTGTAT
2.878	1355.3726	422.8518	529.2018	C20ORF108	DKFZP434A1114; dJ1167H4.1; 5A3	NM_080821	Homo sapiens chromosome 20 open reading frame 108 (C20orf108), mRNA.			GGGCTTAAATCTCAAACTTTGTTAGGAGTAACAGGAGCGTGCTGAGCGGG
2.225	1076.7101	467.8018	505.81012	PIP5K1C	PIP5Kgamma; PIP5K GAMMA; KIAA0589	NM_012398	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type I, gamma (PIP5K1C), mRNA.	TGTCCAGAGGGGGTTCTGCCCCTTGTGAAGGCCCATTCCTGGCACTTAGA	ILMN_1745365	TGGTGCGTGACAATCCAAAGCGCCGAGACGAGGGTGCTGTGTCCCTCAAA

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.783	1310.7559	411.2143	545.381	TEAD2	ETF; TEF-4; TEF4	NM_003598	Homo sapiens TEA domain family member 2 (TEAD2), mRNA.	GCCTATAAACAGATTGATGCACGTGGTGGGAACCCTGAGCTAGTAGCCTT	ILMN_1692276	AGTGGGTGCTAGGGTCTTGACTTTATCTCCGCTGCACAAGCAGTGTGTTG
2.008	981.66016	536.2476	450.2768	IFNGR1	CD119; IFNGR; FLJ45734	NM_000416	Homo sapiens interferon gamma receptor 1 (IFNGR1), mRNA.	GGCCTGCCAGAGTGTGGTTTGTGGTCCCATTTCAGGGGGAAGATACTTGA	ILMN_1675428	CGGAACATATCCAGTACTCCTGGTTCCTAGGTGAGCAGGTGATGCCCCAG
2.688	1318.6477	480.7268	507.05594	RILPL1	MGC105128; FLJ39378; MGC99793	NM_178314	Homo sapiens Rab interacting lysosomal protein-like 1 (RILPL1), mRNA.	CTGACTTCTGAGCAGGTGAGGAAGCACTACCTGAGTGGGGGACCCGAGGC	ILMN_1743582	CCCACAAACGGAGGCCAGACTTCTGCGTTAACTTCAGTAACACAAGCTTC
6.745	2768.8975	311.96844	558.6268	COL8A1	C3orf7; MGC9568	NM_020351	Homo sapiens collagen, type VIII, alpha 1 (COL8A1), transcript variant 2, mRNA.	GAAGCTGGCGGACATGTATGGAGGTGGTGAAGAGGATTGACTGACCTCGC	ILMN_1769891	CCGTGATGTACACGTACGACGAGTACAAAAAGGGCTTCCTGGACCAGGCA
2.017	1007.4435	561.65594	445.82263	KLHDC2	LCP; HCLP-1	NM_014315	Homo sapiens kelch domain containing 2 (KLHDC2), mRNA.			GCCTATGATCACCTTGCATGGACAGCAATCCTGTAAACATCACAGAGTGG
2.577	1201.631	566.7351	394.51843	MBD4	MED1	NM_003925	Homo sapiens methyl-CpG binding domain protein 4 (MBD4), mRNA.			TTATCGGCTAGGCGTGGTGGTGCATGCCTGTAATCTCGGAAGGCTGAGGC
2.359	1262.0726	490.50177	589.0851	ZNF580		NM_016202	Homo sapiens zinc finger protein 580 (ZNF580), transcript variant 1, mRNA.	TATCTAGGCAGACCCCAGCCAGACCCCCGCCAGACAGACTCCCAACCAGA	ILMN_1770005	CCCCCTTTCTAGCTGTGTGATGTAGACCAAAGTCGTTGCCCCTCCCTGGG
3.454	1572.8394	386.4893	573.9518	SYNC1	SYNC; MGC149626; SYNCOILIN; MGC149625	NM_030786	Homo sapiens syncoilin, intermediate filament 1 (SYNC1), mRNA.			TGGACAACAACTGTCATCTGAAGGACTCTTCTAGAAGCCAGAGACTGGTG
2.154	1219.7476	534.5601	602.4643	NECAP2	FLJ10420; RP4-798A10.1	NM_018090	Homo sapiens NECAP endocytosis associated 2 (NECAP2), mRNA.			TGTTGTCATGGAGCTGTGGGAGTTGGCACTCTGTCTGCTGGTGGCCCTCT
2.172	1101.1726	426.47678	603.31006	TWIST1	TWIST; ACS3; BPES2; SCS; BPES3	NM_000474	Homo sapiens twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) (TWIST1), mRNA.	GTCTTCCCAGTTTCTCCAAGCTGCTTCTGGAATGCAGGTCTGTCGGCTGG	ILMN_1778964	AGACGGGCAGCGGCACCATCCTCACACCTCTGCATTCTGATAGAAGTCTG
2.408	1390.4976	604.15594	552.4643	CDK7	p39MO15; CDKN7; CAK1; STK1	NM_001799	Homo sapiens cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) (CDK7), mRNA.			GGGCCAACACCTGGATGTCAGCTGCCAAGACCAAACTGTCCAGTGGAAAC

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
6.951	2999.2559	603.381	345.7143	CBS	HIP4	NM_000071	Homo sapiens cystathionine-beta-synthase (CBS), mRNA.			CTCCCGTCTTCCTCCTCCCCTG GCAACTGCTGATCGACTTTGTG TCTCTG
2.371	1298.3643	632.34766	489.2351	SLC35E1	MGC44954; FLJ14251	NM_024881	Homo sapiens solute carrier family 35, member E1 (SLC35E1), mRNA.			TGGGAGGCTGAGGTGGGTGGA TCACTGGAGTTTGAGACCACCC TGGCCAA
2.228	1215.2393	459.2851	651.85596	MAPRE2	RP1; EB1; EB2	NM_014268	Homo sapiens microtubule-associated protein, RP/EB family, member 2 (MAPRE2), mRNA.	TATCAATTCTGCTGTGT TCCCTGGCCTGCAGGG AGGTCCCCACAACCAC G	ILMN_1743784	CCCTCTTTAACACAAGGGCCCT CCTTGTCATTGACCTTAGCTAAA CCATG
2.041	1160.206	631.19763	524.65594	TDP1	FLJ11090; MGC104252	NM_018319	Homo sapiens tyrosyl-DNA phosphodiesterase 1 (TDP1), transcript variant 1, mRNA.			CTGTATTAAAAAGGCAAATCGAA GGCCGGGCGCGGTGACTCACG CCTGTC
2.61	1601.3477	661.8726	570.9351	UBE2E2	UBCH8; FLJ25157	NM_152653	Homo sapiens ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast) (UBE2E2), mRNA.	AAGGCGGCTAGAGAGA AAGGCCAGGTCACCTA CAAAGGGAAGCCCTTC AG	ILMN_1815447	GAGACTCTGTTTATCACTAGCCT TCTGTCCCTCCCGCAGAAGACT GTTGG
2.311	1426.4309	569.69763	669.49347	TAPBP	TAPA; NGS17; TPSN; TPN	NM_003190	Homo sapiens TAP binding protein (tapasin) (TAPBP), transcript variant 1, mRNA.	GGTGAGCCATGGAGCC CCTCTTATCTGGGCCC AACCTCTCCTTAAATAA C	ILMN_1750497	CGCCGCGCGTCCCTCTTGTGC GGTTCACCACAGTTGTATTTAAG TGATCG
3.177	1713.3309	673.5226	433.7893	PPIC	MGC3673; CYPC	NM_000943	Homo sapiens peptidylprolyl isomerase C (cyclophilin C) (PPIC), mRNA.			CCGTCACCCTTTAGTTTGCTTGA ACTTTAGTAAACCACCTGCTTAG GGAC
5.503	2774.3145	695.01013	377.6101	MEG3	PRO2160; FP504; GTL2; prebp1; FLJ31163; FLJ42589; PRO0518	NR_002766	Homo sapiens maternally expressed 3 (MEG3) on chromosome 14. XR_001346-XR_001372			CTAGGGGAGCTGTTGAGCCTTC AGTGTCTGCATGTGGGAAGTGG GCTCCT
2.937	1519.6643	375.49762	705.9518	EVL	RNB6	NM_016337	Homo sapiens Enah/Vasp-like (EVL), mRNA.			CAGCTCCGTCCCCAGCGCTCAT GGTGTTGAAACTGTCTGTCATG CACCAC
2.133	1307.4727	525.86426	714.22266	UBXD1	DKFZp667D109; UBXDC2	NM_025241	Homo sapiens UBX domain containing 1 (UBXD1), mRNA.			TCTGCCCTCCTGACCTTCTCGT GGGACATGGCTGTGCTGGAGG ACATCAA
3.551	2020.6975	444.2768	728.90594	CYBA		NM_000101	Homo sapiens cytochrome b-245, alpha polypeptide (CYBA), mRNA.	CCCATAATACAGGGGG AGCCACTTGGGCAGGA GGCAGGGAGGGGTCC ATT	ILMN_1657571	AATTACTATGTTCGGGCCGTCC TGCATCTCCTGCTCTCGGTGCC CGCCGG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.164	1459.8976	626.531	729.381	PHACTR2	DKFZp686F18175; KIAA0680; C6orf56; MGC176642	NM_001100164	Homo sapiens phosphatase and actin regulator 2 (PHACTR2), transcript variant 1, mRNA.	GGGCTTAACTTTACCTC CTTGAAAATGACATGGA CTTGGGTGGATGGTTC	ILMN_1685521	TGCATGCCCAGGTGTCTGTCTC TGGCTGAGGTTTTGTCTATTTTA CAGTG
6.25	3251.3726	354.35596	768.3393	CXXC5	HSPC195	NM_016463	Homo sapiens CXXC finger 5 (CXXC5), mRNA.			TCTGGCCTTGCTAATGGCAACA GAAGAAAGGGCTTCTTTGCGTG GTCCCC
4.583	3344.4976	773.0893	695.8143	MYL9	LC20; MYRL2; MRLC1; MLC2; MGC3505	NM_006097	Homo sapiens myosin, light chain 9, regulatory (MYL9), transcript variant 1, mRNA.	TGAGCCACGTTATCTC GGCGCTGGTTTCCGAG TACCGCTGAACTGTGG GT	ILMN_1696183	AAGAACCCCACAGACGAATACC TGGAGGGCATGATGAGCGAGG CCCCGGG
7.436	5120.1475	652.6018	747.48096	MAP1LC3A	MAP1ALC3; MAP1BLC3	NM_181509	Homo sapiens microtubule-associated protein 1 light chain 3 alpha (MAP1LC3A), transcript variant 2, mRNA.	ACATGCTTGGGTTGGA GCGCAGCAGTAAACAC CCTGCCCAGTGACCTG GA	ILMN_1744293	CCCCTCGGTCTCCACGTGGTGT ATGGATCTGTGGTCATTGTCCC TCTGCA
6.27	3968.0977	488.99762	853.5768	COL8A1	C3orf7; MGC9568	NM_020351	Homo sapiens collagen, type VIII, alpha 1 (COL8A1), transcript variant 2, mRNA.			GAGACCGGGTGTTCCTCCAGAT GCCCTCAGAACAGGCTGCAGGA CTGTAT
8.825	6043.756	639.76013	771.506	DRAM	FLJ11259	NM_018370	Homo sapiens damage-regulated autophagy modulator (DRAM), mRNA.	CACTGAGAACGCCTGC CAGCTTCCCCATGCCC TCACTTGGTTTGTGTTT T	ILMN_1707232	CTTCTGCCTCACTTCGAGCAGA CTTTTGTTCTCGGCGCTCCTCA CGATGG
9.342	5778.7646	449.89343	870.7643	EPAS1	HLF; ECYT4; HIF2A; MOP2; PASD2	NM_001430	Homo sapiens endothelial PAS domain protein 1 (EPAS1), mRNA.			CCCAGAGCACTTTGCAACTCCC TGGGTAAGAGGGACGACACCTC TGGTTT

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.176	2319.2476	611.23096	871.58923	HLA-A29.1		NM_001080840	Homo sapiens major histocompatibility complex class I HLA-A29.1 (HLA-A29.1), mRNA. XM_001132736 XM_001132742 XM_001132747 XM_001132750 XM_001132753 XM_001132757 XM_001132760 XM_001132769 XM_001132772 XM_001132776 XM_001132779 XM_001132781 XM_001132783 XM_001132785 XM_001132794	GGCGTTGATTTCAACC CTCCTTCACTCTGGCTT CTTCAGGCAACCACGT G	ILMN_1721106	ACGGACGCCCCCAAGACGCATA TGACTCACCACGCTGTCTCTGA CCATGA
5.426	3791.5393	629.6018	810.3393	PALLD	CGI-151; PNCA1; KIAA0992; FLJ22190; SIH002; FLJ38193; FLJ39139	NM_016081	Homo sapiens palladin, cytoskeletal associated protein (PALLD), mRNA.			GCACCGGGTGGCAGATGTTCTA TGCAGTGTGGTTCAAGTTTCTTT GACCG
5.754	3905.2144	523.65594	890.7434	KCTD20	MGC14254; dJ108K11.3; C6orf69	NM_173562	Homo sapiens potassium channel tetramerisation domain containing 20 (KCTD20), mRNA.	CAGCATGTCAGGCCAG GATTATTAGGGAGATTC CTCGAAACTAGTGTGT G	ILMN_1753016	GCCCAGGAAGGTTAGATGTGTT TGCAAATAAGTTGCCCAAAGGG TCCCCC
2.608	1904.4559	576.6476	925.4143	SLC25A1	SLC20A3; CTP	NM_005984	Homo sapiens solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1), nuclear gene encoding mitochondrial protein, mRNA.			GCATTGTGGCTGTCAAATCCAT GTGTCCCCCCTGTGGTCTGTGT GTGACA
2.858	2496.9392	792.84766	969.97266	PGLS	6PGL	NM_012088	Homo sapiens 6-phosphogluconolactonase (PGLS), mRNA.			CCGCCTCCTGACCGTGCCCTTC GAGAAGCATTCCACTTTGTAGC TGGCCA
2.48	2100.885	792.8393	922.5476	PARP3	ADPRT3; ADPRTL3; pADPRT-3; ADPRTL2; IRT1; hPARP-3	NM_005485	Homo sapiens poly (ADP-ribose) polymerase family, member 3 (PARP3), transcript variant 2, mRNA.	TGAGGTCAACGGCAGA GACTTATCCAGAGCAA CTCATGACCAGGCTGT GG	ILMN_1742949	CTGTGCCTGGCTTATTTCACTCA GCATAATGTGCACCGGGTTCAC CCATG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.7	2167.9226	1081.0642	591.46844	SLC7A5	MPE16; CD98; 4F2LC; hLAT1; D16S469E; LAT1; E16	NM_003486	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA.	CTAAGTACGATGTTCAAGTGAGAGCAGCAGTGAGCTCCATGTGCAGAGAG	ILMN_1756455	AGGCTGGACACCCTCTGCCGAGTAATGACGTGTGTGGCTGGGACCTTCTT
7.973	5290.456	805.9435	692.23096	MFGE8	HsT19888; BA46; OAcGD3S; EDIL1	NM_005928	Homo sapiens milk fat globule-EGF factor 8 protein (MFGE8), mRNA.	CCCTGTGGAATTCAACCCCAACTTCGTGGCGCGTATGATACCTAAAGTGG	ILMN_1690802	GGGCCCTCATGCTGGCTTTTCACCCCAGAGGACACAGGCAGCTTCCAAAA
2.707	2653.5728	844.20593	1145.1393	ITFG3	FLJ32603; DKFZP761D0211; gene +108; C16orf9; gs19	NM_032039	Homo sapiens integrin alpha FG-GAP repeat containing 3 (ITFG3), mRNA.			GCTGTGGAATGCGTGTTTGGGTCAGTCTGTGCCCTCTCAGTAGACACTGG
2.103	2163.031	924.2893	1155.9559	RFNG		XM_001132711	PREDICTED: Homo sapiens radical fringe homolog (Drosophila) (RFNG), mRNA.	CAAATGTGCCTTCTCCTCCCAGGAACCGTACTTCAGCTACTCTGGTGCCT	ILMN_1677920	TCTCCGCTCTGACTTGTGGCTCAGGACTACTTTCTGGGTCGTGCTCCTGC
3.236	3082.1143	775.5893	1171.8477	SLC44A2	FLJ44586; DKFZp666A071; PP1292; CTL2	NM_020428	Homo sapiens solute carrier family 44, member 2 (SLC44A2), mRNA.	CCTAGCTGCTCGGGAGGCTGAGGCAGGAGAATCTCTTTCTTAATTGGCCA	ILMN_1772492	GCACACCCCTGCGTGTAACTGCATTCCAACCACTAATAAAGTGCCTATTG
3.775	3839.9893	870.6809	1190.4976	HLA-H	HLAHP	NR_001434	Homo sapiens major histocompatibility complex, class I, H (pseudogene) (HLA-H) on chromosome 6.			GGCAACAGTGCCCAGGGCTCTGATGTGTCTCTCACGGCGTGAAAGTGTGA
2.289	2453.7642	999.8893	1163.4309	TCF25	hKIAA1049; NULP1; PRO2620; Hulp1; FKSG26; KIAA1049	NM_014972	Homo sapiens transcription factor 25 (basic helix-loop-helix) (TCF25), mRNA.			GGGAGTGGGACTGAGCGTCCGCAGAGGTGACCGAAAAGCCGTATGATGAT
2.544	2831.0142	1013.97266	1241.3142	PKD2	PC2; PKD4; APKD2; MGC138468; MGC138466	NM_000297	Homo sapiens polycystic kidney disease 2 (autosomal dominant) (PKD2), mRNA.	GGTTCTGCCTTCCAGTATGAGTATGAGCCACCCTGCACGTCCCTCTGTGC	ILMN_1716480	ATTTGAAGTGCAGCTATTATGTGGTATCCATGTGTATCGACCATGTGCCA
3.719	3454.6143	933.5226	1049.9976	COX7A1	COX7AH; COX7A; COX7AM	NM_001864	Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), mRNA.			ACCGCCCGGAACCGCTTTCAGAACCGAGTGCGCGAGAAACAGAAGCTCTT
4.29	4515.7896	798.22266	1382.156	ARID5B	MRF2; FLJ21150; RP11-341A19.1	NM_032199	Homo sapiens AT rich interactive domain 5B (MRF1-like) (ARID5B), mRNA.	CCCTGGGGAAATTGATGGGTGTGGCAGTGGACCTGTGAAGAGGGAGAATC	ILMN_1674941	GTCCAGTGTTGGCTGTTAGTGTATTTGATATTCTGCCTGTCTCCTCATGG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.673	3480.1892	1332.2101	1281.581	PHPT1	bA216L13.10; CGI-202; PHP14; HSPC141; RP11-216L13.10; DKFZp564M173	NM_014172	Homo sapiens phosphohistidine phosphatase 1 (PHPT1), mRNA.	TGCAGGACAATGCTGCCAGAGGCCTGGTCCTCAGAGCTCACGTAAGCATC	ILMN_1713038	CGGGCGCATCTCCCACCAGAGTCAGGACAAGAAGATTCACGTGTACGGCT
2.474	3212.6895	1162.9644	1448.3684	C10ORF58	MGC4248	NM_032333	Homo sapiens chromosome 10 open reading frame 58 (C10orf58), mRNA.	CTGGATTTCACCTTCTTGCACCTGCCGCGACTGCAGGAGCTTCACCTGCA	ILMN_1762290	GGTGAGCTGAGATCACACCACTGTATTCCAGCCTGGGTGACTGAGACTCT
3.591	4711.5977	1473.1477	1180.2144	SELM	MGC40146; SEPM	NM_080430	Homo sapiens selenoprotein M (SELM), mRNA.			GAATACTTCTCTTGCTGAGAGCCGATGCCCGTCCCCGGGCCAGCAGGGAT
3.454	4553.106	1098.4476	1577.1643	ID2	GIG8; MGC26389; ID2A; ID2H	NM_002166	Homo sapiens inhibitor of DNA binding 2, dominant negative helix loop-helix protein (ID2), mRNA.			GCAGACTTTGCCTTTTTTCAAAGGTGGAGCGTGAATACCAGAAGGATCCA
2.428	3459.831	1402.6101	1463.6809	SRP14P1		NR_003273	Homo sapiens signal recognition particle 14kDa (homologous Alu RNA binding protein) pseudogene 1 (SRP14P1) on chromosome 12.	AGGAGGGCCTGGGTTTGGGTTCTTTCCTCCCAGCCTTTGGATGGTGCCTT	ILMN_1805999	TGCCGGACGTTGGGCAGCGTCTATATCACCTTGAAGAAGTATGATGGTCG
7.95	7588.456	1203.1143	1023.1601	SULF1	SULF-1; FLJ30905; KIAA1077; HSULF-1; FLJ38022; FLJ41750	NM_015170	Homo sapiens sulfatase 1 (SULF1), mRNA.			CCTCACTGAGTCATCAGTACCCTCCTATTCAGCTCCCCAAGATGATGTGT
4.5	5269.0728	834.1726	1621.3143	PGM1		NM_002633	Homo sapiens phosphoglucomutase 1 (PGM1), mRNA.			GCCCTCCTGCATTGCTGCTGCGTGGGTATTTGTCTCCTTAGCCATCAGGT
2.033	3110.456	1480.2643	1591.8477	PRDX5	PRDX6; AOEB166; MGC142285; B166; PRXV; PLP; MGC117264; SBBI10; ACR1; PMP20; MGC142283	NM_012094	Homo sapiens peroxiredoxin 5 (PRDX5), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	TCCCACTCCGCCACCTCCGTCCACACCTCGGTCTGATGGGCGAGAAATAT	ILMN_1715110	GGCCAAGGGAGTCCAGGTGGTGGCCTGTCTGAGTGTTAATGATGCCTTTG
2.051	3227.5562	1429.2142	1735.9976	ZNF428	MGC51082; Zfp428; C19orf37	NM_182498	Homo sapiens zinc finger protein 428 (ZNF428), mRNA.			GATGGGGTACTGCCGGTCTGTGTTGTCTTAGAAGTAGATGTGTGATGGCC
2.114	3389.7144	1465.4893	1770.6726	AES	GRG5; GRG; TLE5; AES-2; ESP1; AES-1	NM_001130	Homo sapiens amino-terminal enhancer of split (AES), transcript variant 2, mRNA.			AGTTCCAGACACCTCCACGCCCACCTGGTCCTCTCCCATCGCCCACAAAA

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.995	6401.539	1677.4559	1535.5059	MYL9	LC20; MYRL2; MRLC1; MLC2; MGC3505	NM_006097	Homo sapiens myosin, light chain 9, regulatory (MYL9), transcript variant 1, mRNA.	CCAGCTGTTGAAAGGATGCTCTCTGCTCGTGCCTCAAACGCTTGGATTCT	ILMN_1682959	CGTGTATCCCCACACAAATGCAAGCTCACCAAGGTCCCCTCTCAGTCCCC
2.059	3439.6978	1887.9392	1482.3976	C12ORF57	C10; GRCC10	NM_138425	Homo sapiens chromosome 12 open reading frame 57 (C12orf57), mRNA.	GGCCAGGGGGGTCTTTCTGCACCTTCATCCTTAATATGTCACAGTTTGTG	ILMN_1800976	TAACGCCTGCAACGACATGGGTAAGATGCTGCAATTCGTGCTGCCCGTGG
2.318	3634.3726	1921.4727	1301.1892	POFUT1	O-Fuc-T; O-FUT; FUT12; O-FucT-1; MGC2482; KIAA0180	NM_015352	Homo sapiens protein O-fucosyltransferase 1 (POFUT1), transcript variant 1, mRNA.			AATAATAGCCAGGCGTGGTGGCACATGCCTGTATTCCCAGCTGCTTGGGA
3.199	6652.139	1966.7476	2218.9143	PAPSS2	SK2; ATPSK2	NM_004670	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthase 2 (PAPSS2), transcript variant 1, mRNA.	CAAGGTTGCCACAGCTCCCACAGCCCTTCCTACAAGCACCTATCATTGGG	ILMN_1748378	TGCCCTGTCTACACCAGACAACACAGGAGCTGGGTCAGATTCCCCTCAGC
2.119	4794.856	2178.4644	2355.781	GLTSCR2	PICT-1; PICT1	NM_015710	Homo sapiens glioma tumor suppressor candidate region gene 2 (GLTSCR2), mRNA.			ACGCAAGTACAAGGTGAAGCTGGTGGAGAAGCGGGCGTTCCGTGAGATCC
4.771	8031.806	1200.1143	2424.0642	CAMK2N1	ICAP-1alpha; MGC22256; PRO1489; RP11-401M16.1	NM_018584	Homo sapiens calcium/calmodulin-dependent protein kinase II inhibitor 1 (CAMK2N1), mRNA.	AAAGTCGCATCAGAGAGCTGAGGGTAAGACTCAGGTGTCCTGACTCCCAG	ILMN_1661627	TATGACCGACAAGGCACCTCCTGGTGTCTAACTCCCCCAAAGACAATGAG
2.425	4818.414	1615.4268	2451.0059	PSME1	PA28A; MGC8628; PA28alpha; REGalpha; IFI5111	NM_006263	Homo sapiens proteasome (prosome, macropain) activator subunit 1 (PA28 alpha) (PSME1), transcript variant 1, mRNA.	GACAGCCACCAGTAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAG	ILMN_1778213	ACCGGGACATCCGGCTGATGGTCATGGAGATCCGCAATGCTTATGCTGTG
4.64	11292.197	1881.5393	3151.906	IGFBP6	IBP6	NM_002178	Homo sapiens insulin-like growth factor binding protein 6 (IGFBP6), mRNA.			GCAACTCCAGACTGAGGTCTACCGAGGGGCTCAAACACTCTACGTGCCCA
2.031	6157.3394	2852.9644	3228.281	CNN3		NM_001839	Homo sapiens calponin 3, acidic (CNN3), mRNA.			GTGGCCTGTGGACATTTAGGCCTGGGTGATGCATTTGCTCTTCCTGTTTG
6.316	16732.38	2903.8477	2475.7393	COL3A1	FLJ34534; EDS4A	NM_000090	Homo sapiens collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA.			TCAACTGCTTGTAAAGGTGCTCCTCTTTTTTCTTGTCATTGCTGGTCAAG

Fold change	XS	pOS+6GF	pOS	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.198	7367.8896	3436.9976	3283.8977	CAPNS1	CDPS; 30K; CANPS; CANP; CAPN4; CALPAIN4	NM_001003962	Homo sapiens calpain, small subunit 1 (CAPNS1), transcript variant 2, mRNA.			TCCCCTGTACCTGTGCCAAGCC TAGCACTTGTGATGCCTCCATG CCCCGA
2.665	10477.322	3785.856	4087.1978	PRDX5	PRDX6; AOEB166; MGC142285; SBBI10; ACR1; MGC142283; B166; PRXV; PLP; MGC117264; PMP20	NM_181652	Homo sapiens peroxiredoxin 5 (PRDX5), nuclear gene encoding mitochondrial protein, transcript variant 3, mRNA.	AGAAGAATTGGTGTTAA AAATGCTTCACCTATAT CTACTTTATTCAACGA	ILMN_1672935	GGTGTCCATCTTTGGGAATCGA CGTCTCAAGAGGTTCTCCATGG TGGTAC
2.105	8538.164	3830.6558	4315.6562	CST3	MGC117328	NM_000099	Homo sapiens cystatin C (CST3), mRNA.	GAAGAGTAACAAGAGT AGACTGGACCAGAAAT CGGAGGGTGGCAAGCA GC	ILMN_1757781	GCCTTGGCAGGGCACAATGACC TTGTCGAAATCCACCTGTCAGG ACGCCT
4.339	19777.998	3910.656	5335.006	IFITM3	1-8U; IP15	NM_021034	Homo sapiens interferon induced transmembrane protein 3 (1-8U) (IFITM3), mRNA.			GATCTTCCAGGCCTATGGATAG ATCAGGAGGCATCACTGAGGCC AGGAGC
2.784	14078.605	4256.6895	6013.5645	GPX4	PHGPx; snPHGPx; snGPx; MCSP	NM_001039847	Homo sapiens glutathione peroxidase 4 (phospholipid hydroperoxidase) (GPX4), transcript variant 2, mRNA.	AGGCTCACTTGCCTTT GGCTTCCTGTTGACTT CTTCCCGACCCAGAAA GC	ILMN_1723843	AGTTCCTCATCGACAAGAACGG CTGCGTGGTGAAGCGCTACGGA CCCATG
2.328	13693.381	6412.4473	5429.256	NUCB1	DKFZp686A15286; NUC; FLJ40471	NM_006184	Homo sapiens nucleobindin 1 (NUCB1), mRNA.			CTGACACTGCTCCGCATCCTGC TGTGTGTCCTGTTCCATGTTCC GGTTCC
2.907	16439.69	4706.2646	6769.831	IFITM2	1-8D	NM_006435	Homo sapiens interferon induced transmembrane protein 2 (1-8D) (IFITM2), mRNA.			TATCTTCCATTCCTCGCCCTGC CCCCAGAGGCCAGGAGCTCTG CCCTTGA

TABLE 12

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
37.51	194.09761	8.228308	306.35596	COL4A6	MGC88184	NM_001847	Homo sapiens collagen, type IV, alpha 6 (COL4A6), transcript variant A, mRNA.			CAGATGTGTGCAATGTGGCAAACTGAAGC TGCACAGTGTTGGTTTCCTTG
35.72	519.71423	8.50958	307.54346	SYTL2	MGC102768; CHR11SYT; SGA72M; KIAA1597; SLP2	NM_206929	Homo sapiens synaptotagmin-like 2 (SYTL2), transcript variant e, mRNA.	GGGTCCCCAGCTTTGCCCCTG GAGGTCTCAATCCTCTCTACAT TCTGAGG	ILMN_1766178	GGGTCTGGTACCCTTGCAGGACCTTTGTA GGTTGTGGGAAAAAGTCGCAG
20.67	157.86429	14.545191	301.20593	PPARG	NR1C3; PPARG1; PPARG2	NM_015869	Homo sapiens peroxisome proliferator-activated receptor gamma (PPARG), transcript variant 2, mRNA.			CCTGAGCCACTGCCAACATTTCCCTTCTT CCAGTTGCACTATTCTGAGGG
20.13	83.92769	15.095779	298.00177	SLC43A3	FOAP-13; EEG1; PRO1659; DKFZp762A227; SEEEG-1	NM_017611	Homo sapiens solute carrier family 43, member 3 (SLC43A3), mRNA.	ACCGGGTGCCAGACTGAACTG CTTCCTCTTTCCTTCAGCTATC TGTGGGG	ILMN_1805216	CCACCACCTTTGAGGACCTCGTGTCCCAA AAGACTTTGCCTATCCCAGCA
17.95	12596.923	83.18143	1520.5518	IGFBP5	IBP5	NM_000599	Homo sapiens insulin-like growth factor binding protein 5 (IGFBP5), mRNA.	GGCGGGGGCCGGGCTTGGAA CGATGTACGATACCCTCATAGT GACCATTA	ILMN_1665095	CACCTGAATGCGGAAGAGCTCGGCTCCC GTTTAGCATTTTGTACTTAAGG
13.17	1200.2893	12.185763	157.73929	GBP2		NM_004120	Homo sapiens guanylate binding protein 2, interferon-inducible (GBP2), mRNA.	AAACACAAGAAGTTCTCGAAAT GGGAGTTTGAAGACCTGGAAT GGGGGAG	ILMN_1798129	GCCTGTCCAGCTCCCTCTCCCCAAGAAAC AACATGAATGAGCAACTTCAG
12.31	464.98096	23.201757	286.02264	CNKSR3	MAGI1; RP11-486M3.1; FLJ31349	NM_173515	Homo sapiens CNKSR family member 3 (CNKSR3), mRNA.	GGGCTTTGATGCCAGCATCCT TGGATCAGTACTGAACTCAGTT CCATCCG	ILMN_1810176	TGCATTTTGACCTGTTCAGTGTCTGTCTT CCAGCACGGTGTGTACACTTC
11.77	20.017391	20.217756	245.25595	C15ORF48	FLJ22645; MGC32925; NMES1; FOAP-11	NM_032413	Homo sapiens chromosome 15 open reading frame 48 (C15orf48), transcript variant 2, mRNA.	GCCTTTCCTCGCTCACCAGGC CAGTCTCAGGGCCTCACCGTA TTTCTACT	ILMN_1800418	GAAGAGTTGCAAAATGTCCAAAGGGTGAC CAAATGACGAGCCCTCGCCTC
11.38	257.87262	12.824924	141.45178	COL4A5	MGC42377; ATS; MGC167109; ASLN; CA54	NM_033380	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), transcript variant 2, mRNA.			AGCTCCAGCTGTGGTGATCGCAGTTCACA GTCAGACGATCCAGATTCCCC
11.29	8.345976	9.320261	107.30597	ANXA10	ANX14	NM_007193	Homo sapiens annexin A10 (ANXA10), mRNA.	GCTTGGACTATAGGTGCATGC CACCATGCCTGGCTAATCTTTT GCAGCGA	ILMN_1771066	ACTGCTTGCCATCTGTGCTGGTGATGCTG AGGACTACTAAAATGAAGAGG
9.797	11.755294	7.983902	79.7632	NOG	SYNS1; SYM1	NM_005450	Homo sapiens noggin (NOG), mRNA.	TCAAACTATTCTCTCCCGGGCT TAACAGCCTCGCAGCCCAGTC ACGGCCT	ILMN_1812702	GGATTCCCATCCAGTACCCCATCATTTCC GAGTGCAAGTGCTCGTGCTAG
7.792	190.57263	14.412636	110.28928	BMP4	BMP2B1; BMP2B; ZYME	NM_130851	Homo sapiens bone morphogenetic protein 4 (BMP4), transcript variant 3, mRNA.	AGACCGGTTCTGGAGACAAAA GGGGCCGCGGCGGCCGGAGC GGGACGGGC	ILMN_1706440	AGTAGAGGGATGTGGGTGCCGCTGAGAT CAGGCAGTCCTTGAGGATAGAC
5.84	60.19111	6.914125	40.297394	CCDC24	RP5-1198O20.2; MGC45441	NM_152499	Homo sapiens coiled-coil domain containing 24 (CCDC24), mRNA.	TGCTTGCTCCCGAATCAGACG CCGGCAGCCAAACTTGTCCCC TCCTGTAG	ILMN_1721440	AGGCCTCCACAAAGGCCTGGCAGACAGA GGTCTCATTCCAGCCTGACTCT
5.511	699.48096	37.82922	206.58095	SMAD3	MADH3; JV15-2; HSPC193; MGC60396; Smad 3; HsT17436; DKFZp686J10186; DKFZP586N0721	NM_005902	Homo sapiens SMAD family member 3 (SMAD3), mRNA.	TTCGATGATCTGCTCACATTCC TGCTCTCTACCTACTTCTTGGT ATTCCG	ILMN_1668498	TGCAACTCGGCTGTTCTGGACTCTGATGT GTGTGGAGGGATGGGGAATAG

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
5.339	73.72434	8.690823	46.073246	KAZALD1	IGFBP-rP10; FKSG40; FKSG28; BONO1; bA108L7.1; FLJ24094; RP11-108L7.10	NM_030929	Homo sapiens Kazal-type serine peptidase inhibitor domain 1 (KAZALD1), mRNA.	GCTCAGAAGCTGGCAAATCTG GCTGTGACTTCAAGCATGCCC CACCAACC	ILMN_1705865	CCTAAGCCCCAGTTGCACCTACTAACTGC AGTCCCTTTTGCTGTCTGCCG
4.767	54.187973	51.743732	246.05594	ST6GALNAC3	SIAT7C; ST6GALNACIII; PRO7177	NM_152996	Homo sapiens ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1, 3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3 (ST6GALNAC3), mRNA.			TCACACCCATAAACATTACTAAGCCCCAG TTCTATCGTTGGAAGGAGTTG
4.705	142.46011	13.921049	65.50559	SYNGR1	MGC:1939	NM_004711	Homo sapiens synaptogyrin 1 (SYNGR1), transcript variant 1a, mRNA.			CAACCAGTGGCAGGTCTCCAAGCCCAAG GACAACCCACTGAACGAAGGGA
4.467	109.093445	15.300022	68.0383	RARRES3	MGC8906; HRASLS4; TIG3; RIG1	NM_004585	Homo sapiens retinoic acid receptor responder (tazarotene induced) 3 (RARRES3), mRNA.			GGCCACGGCGCTTGGAATCCTGGTTGTT GCTGGATGCTCTTTTGCGATTA
4.444	72.60902	14.649551	65.43894	NFIC	CTF5; CTF; NF-I; NFI; MGC20153	NM_005597	Homo sapiens nuclear factor I/C (CCAAT-binding transcription factor) (NFIC), transcript variant 1, mRNA.			AAGCCCCTCCCAAAGCGCCGGCCGACTC GCTGTCTCGCTGGGGACTCTTT
4.066	61.171288	26.945152	110.597626	TMEM171	PRP2	NM_173490	Homo sapiens transmembrane protein 171 (TMEM171), mRNA.			GTCGCTGAGAGTCCTGGAACTAACAGTCT GCTTCCGAATGAAAACCCCCC
4.035	45.226368	37.3899	150.84763	SLC43A3	FOAP-13; PRO1659; DKFZp762A227; SEEEG-1; EEG1	NM_014096	Homo sapiens solute carrier family 43, member 3 (SLC43A3), mRNA.			TGGCTAGAGAACTCACAGCTCTGGGAAAA AGAGGAGCAGACAGGGTTCCC
3.994	4729.881	221.51428	892.23926	CRISPLD2	DKFZP434B044; MGC74865; CRISP11; LCRISP2	NM_031476	Homo sapiens cysteine-rich secretory protein LCCL domain containing 2 (CRISPLD2), mRNA.	GCTCCTCACGGGCGATGGCTG TCTTTTCTTGACTTTGTATCTTC ACTGCC	ILMN_1671281	ACGGCGTTCCTGGCTCTCCTGCCCACAG GATGAACATTTTCGGCTTCCTT
3.93	118.31011	8.852243	34.4825	HLA-DMA	HLADM; RING6; DMA; D6S222E	NM_006120	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA), mRNA.	CACCGATGCCCCCATTTCACG CCTGAGGAAGCGGAGGCTCAG ACGGGCCA	ILMN_1731525	CCAGAGTGGCCTGCCTATCACAACCACAT CCCTTCCCCCCACAAGGCAAT
3.909	32.390465	131.76845	516.86847	AGPAT9	MAG1; AGPAT8; LPAAT-theta; GPAT3; MGC11324	NM_032717	Homo sapiens 1-acylglycerol-3-phosphate O-acyltransferase 9 (AGPAT9), mRNA.	GCGCATGCACCTTCGTCAGTA CGAGCTGCTCTAAGAAGGGAA CCCCCAAA	ILMN_1769191	TCCTTGTTTGAATGCTGTAGATCTGTACC TAGTACCCCTCCCATCTACTG
3.892	16556.098	1475.381	5746.4473	IGFBP4	IBP4; HT29-IGFBP; IGFBP-4; BP-4	NM_001552	Homo sapiens insulin-like growth factor binding protein 4 (IGFBP4), mRNA.			ACCGGGATGAACCTATCCTTCCAGTGGCT CGCTCCCTGTAGCTCTGCCTC
3.783	35.385967	39.3032	150.57262	PTGER4	EP4R; MGC126583; EP4	NM_000958	Homo sapiens prostaglandin E receptor 4 (subtype EP4) (PTGER4), mRNA.	CATGGCCGCCCTACGGAAAAT CACATCCACAGAGGCCAGGGC TACCCAAG	ILMN_1676880	GGGGCACTTAATGGTCACCTTGTAACAGT TTTGTGTAACTCCCAGTGATG
3.744	2289.5225	755.43933	2811.5645	LPAR1	vzg-1; Gpcr26; Mrec1.3; edg-2; rec.1.3; LPA1; LPAR1	NM_057159	Homo sapiens lysophosphatidic acid receptor 1 (LPAR1), transcript variant 2, mRNA.	GGATAAGACCCCAGCAGCCCT GACATTTCTCCTCCACACTCCC CACTCAC	ILMN_1678627	CTTTGTTTGAGGGACTCGTTATCCAGCTC TTGGTAGCCACACCTGCAATG
3.685	100.22262	11.095724	40.722214	CLDN1	SEMP1; ILVASC; CLD1	NM_021101	Homo sapiens claudin 1 (CLDN1), mRNA.	TGAAGAACTCGACTTTATGTGA TCATGGTATTGGTATACATGTG GGGTGG	ILMN_1763730	GTGCTATCTGTTCAGTGATGCCCTCAGAG CTCTTGCTGTTAGCTGGCAGC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
3.526	74.21506	90.10183	316.73096	ERCC1	UV20; COFS4	NM_202001	Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) (ERCC1), transcript variant 1, mRNA.	GGGGAGCCAGGAATGAGGCG GCAGCCGGGCCGTTTGGGCTC AAGACACAC	ILMN_1699854	GATGAGAACGTAGACGCCAGTGGCTCAC TCGCTCCTGGCACCTTCCCTTT
3.497	427.3393	104.85595	368.05597	GAMT	TP53I2; PIG2	NM_000156	Homo sapiens guanidinoacetate N-methyltransferase (GAMT), transcript variant 1, mRNA.			ACGACACGTACCCACTCTCGGAGGAGAC CTGGCACACACACCAGTTCAAC
3.489	60.070377	98.82262	345.51013	FST	FS	NM_006350	Homo sapiens follistatin (FST), transcript variant FST317, mRNA.			TGGCTGTATCAGAGGGCTTTGAAAACATA CACTGAGCTGCTTCTGCGCTG
3.108	1123.1143	1376.9768	4307.6226	FST	FS	NM_013409	Homo sapiens follistatin (FST), transcript variant FST344, mRNA.			AGAGGCCGGTGTTCCCTCTGTGATGAGC TGTGCCCTGACAGTAAGTCGGA
2.993	6349.1562	1811.281	5419.3975	LY6E	TSA-1; RIGE; RIG-E; SCA2; SCA-2	NM_002346	Homo sapiens lymphocyte antigen 6 complex, locus E (LY6E), mRNA.			CAGGGAGACCGTGTCAGTAGGGATGTGT GCCTGGCTGTGTACGTGGGTGT
2.931	633.87256	1092.0476	3189.7642	SLIT2	Slit-2; SLIL3; FLJ14420	NM_004787	Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA.			CTGACGGCTCCTCCTTTGTGGACGAGGTT GAGAAAGTGGTGAAGTGCGGC
2.837	53.823128	18.275572	52.084	SLC46A1	MGC9564; HCP1; PCFT	NM_080669	Homo sapiens solute carrier family 46 (folate transporter), member 1 (SLC46A1), mRNA.	TGTGACTCAGTGACCCGGAGG GCAAGCAGGACTGTGGGTGAC ACCTTGTG	ILMN_1658864	GGGGATGGTGGTCTTTGCCTTTGCCACTA TCACGCCTCTCATGTTCACAG
2.803	441.19345	147.86429	414.63513	PSMB8	RING10; D6S216; MGC1491; LMP7; D6S216E	NM_004159	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) (PSMB8), transcript variant 1, mRNA.	CTCCCTTGGAAGACAGGAGAG ATGACTCCCTTGGAAGACAGA TGACAGCC	ILMN_1707005	AGGTCTCCTCTGGGAGGTCTTGGCCGAC TCAGGGACCTAAGCCACGTTAA
2.758	101.52732	7.983549	21.970535	CXCL16	SRPSOX; CXCLG16; SR-PSOX	NM_022059	Homo sapiens chemokine (C-X-C motif) ligand 16 (CXCL16), mRNA.	GCTCTGAGTGTCCACGGGTGA AGAAGTGAGTGTCCACGGGTG AAGAAGTG	ILMN_1651819	CCATACGGGTTGGTTTCACCTCCTCAGTC CCTTGCCTACCCCAGTGAGAG
2.725	90.85647	296.49762	813.8059	SSTR1	SRIF-2	NM_001049	Homo sapiens somatostatin receptor 1 (SSTR1), mRNA.	GGTTTAAGGTCCCCCACTGCA CACCTTCCTCAAGTCATAGCTG CTTGCAG	ILMN_1694653	GCCAGAGTGTATTACAACAATCTGGAGAT ACTAAATCTGGGGTTCTCAGG
2.67	621.13513	104.63512	278.90594	IL7R	CDW127; CD127; IL-7R-alpha	NM_002185	Homo sapiens interleukin 7 receptor (IL7R), mRNA.			CTGACATTGAACCCAGTTGCTCAGGGTCA GCCCATTCTTACTTCCCTGGG
2.585	38.244774	21.042715	54.5054	HSPA4L	Osp94; APG-1	NM_014278	Homo sapiens heat shock 70kDa protein 4-like (HSPA4L), mRNA.	TGATCAGCTCTGAGGTGCAAC TTCTTCACATACTGTACATACC TGTGACC	ILMN_1724544	GTAACCACGGGGTCCATCTTTTACATCTG GTACACACAACAGACGCTCAG
2.573	158.98929	87.81048	225.97263	ATP8B1	FIC1; PFIC1; PFIC; ATPIC; BRIC	NM_005603	Homo sapiens ATPase, class I, type 8B, member 1 (ATP8B1), mRNA.	TGAGCGACATCCGTGCTGATC ACAATACTGTCCTGCCAGGGC GGCCAAGA	ILMN_1814200	TAAGATCCAGAAGCATCGCAAGCGGTTGA AGGCGGAGGAGCAGTGGCAGC
2.535	180.95178	59.047707	149.91846	C9ORF103	bA522I20.2	NM_001001551	Homo sapiens chromosome 9 open reading frame 103 (C9orf103), mRNA.			CATTGTGCCATCACAAACCTCGTTCCAGC CGCCTTGCCCATACTAGATTC
2.522	64.40842	18.532312	46.545357	ST3GAL5	SIAT9; ST3GalV; SIATGM3S	NM_001042437	Homo sapiens ST3 beta-galactoside alpha-2,3-sialyltransferase 5 (ST3GAL5), transcript variant 2, mRNA.			GGAGAGGGGAGGTCACTCTTTTGATGGT GGCCCTGAACCTCATTCTGGTT

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.48	28.491112	44.3478	110.06845	PEG10	Mart2; KIAA1051; Edr; RGAG3; MEF3L; Mar2; HB-1	NM_001040152	Homo sapiens paternally expressed 10 (PEG10), transcript variant 1, mRNA. XM_940378			CGGAGGGAACTGCAGGGAGACCAACTTA TTTAGAGCGAATTGGACATGGA
2.425	110.09762	58.00982	141.35178	PDE4B	DKFZp686F2182; MGC126529; DPDE4; PDE4B5; PDEIVB	NM_002600	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), transcript variant a, mRNA.	GGTGCTTTGGCCCTAATAGCA CTGGACAACACCACGACCACA TGGAAACA	ILMN_1670807	TTCTTCTGAATGCTCCCGAACTACTGACT TTGAAGAGGTAGCCTCCTGCC
2.379	354.98096	111.59345	265.4226	TXNIP	THIF; EST01027; VDUP1; HHCPA78	NM_006472	Homo sapiens thioredoxin interacting protein (TXNIP), mRNA.	TGCATCCGACACCCACCCCCT CTTTGTGTACTTCAGTCTTGGA GTTTGGA	ILMN_1698297	CAGCCATAGCACTTTGTTCACTGTCCTGT GTCAGAGCACTGAGCTCCACC
2.316	260.45596	115.172615	266.50595	ADAM15	MDC15	NM_003815	Homo sapiens ADAM metallopeptidase domain 15 (ADAM15), transcript variant 2, mRNA.	CCTCTCCCCTCTCCCATTTTGC ACTGTGTGTCGATGCAATCTTC GCTAGC	ILMN_1676526	GGCTTCAAGAGGCGGGCGTGCCCTCTGG AGTCCCCTACCATGACTGAAGG
2.235	1178.006	422.56427	945.8976	FAM20C	RNS; DMP4	NM_020223	Homo sapiens family with sequence similarity 20, member C (FAM20C), mRNA.			CTCAAGGCCAAGCTCACCCCTCAAGTGCT CTCACACTCGGGACCTAATTC
2.194	53.406754	24.186794	52.910774	TRIM62	FLJ16558; FLJ10759	NM_018207	Homo sapiens tripartite motif-containing 62 (TRIM62), mRNA.			CTGCCCAGAGGTGGGAACTGGAGGAGTG GGCTGCAAGACTGAGCCTAAAT
2.176	2374.6143	1651.0226	3580.5142	NR2F2	COUP-TFII; TFCOUP2; MGC117452; COUPTFB; SVP40; ARP1	NM_021005	Homo sapiens nuclear receptor subfamily 2, group F, member 2 (NR2F2), mRNA.	CCTTGAAAGGTGCAGTGGAAA TATTAAGGCAGATACCACTGGA GGGCAGG	ILMN_1809597	CTGTGGAATTTATTGGCAGCCAAGGAATG TGTCCAAGACACATGCTGAGG
2.162	3251.3726	354.35596	768.3393	CXXC5	HSPC195	NM_016463	Homo sapiens CXXC finger 5 (CXXC5), mRNA.			TCTGGCCTTGCTAATGGCAACAGAAGAAA GGGCTTCTTTGCGTGGTCCCC
2.149	60.59512	43.959152	94.39763	PDK3		NM_005391	Homo sapiens pyruvate dehydrogenase kinase, isozyme 3 (PDK3), mRNA.	CCCAGCTTGCTTCCATGGCCA ATCTAAGGGCAGAGAAGAATA AAGTGGAG	ILMN_1756811	ACGCCTGAAGCCGATGATTGGAGCAATC CCAGCAGTGAACCCAGGGATGC
2.138	99.65596	86.69766	185.63095	KCTD14	MGC2376	NM_023930	Homo sapiens potassium channel tetramerisation domain containing 14 (KCTD14), mRNA.	ACCCCTGCTGGCGGATAGCAA GACTCTGTGGAGTTTGTTCAGT GGTACGG	ILMN_1661717	GTAGTAGGTGCTTTCCTGATCCCCTTTGC GAGATGCTGTGGGTGCTAACA
2.138	63.865067	39.669365	84.71434	COG8	FLJ22315; DOR1	NM_032382	Homo sapiens component of oligomeric golgi complex 8 (COG8), mRNA.			GCCCCTCGCCTTTATCCTGCCAAAGAGAG AGACGCTTTTCACCCTGGATG
2.125	338.7726	102.67262	218.37679	PCBD1	PHS; PCD; DCOH; PCBD	NM_000281	Homo sapiens pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (PCBD1), mRNA.	AAGCCCCTGTGAAGGACAACA CCCCTGCTTGGGAGAGAGTCC CATGTCCA	ILMN_1744628	TGCTGCCAAACCTGAGGGCTGTGGGGTG GAATGAGCTGGAAGGCCGTGAT
2.11	119.83096	20.483475	43.27829	ING4	my036; p29ING4; MGC12557	NM_016162	Homo sapiens inhibitor of growth family, member 4 (ING4), mRNA.			GGATTCATCCTGGGAGAGGGGGCAAGGT GGAATGCAGATAACTCACATGT
2.091	87.69475	7.026443	14.716523	SELENBP1	FLJ13813; LPSB; hSP56; SP56; hSBP	NM_003944	Homo sapiens selenium binding protein 1 (SELENBP1), mRNA.	CCCGGCATGCACCTTGTTTCC ATGTTGTCATCCTCCCATGGCT TCCCCTG	ILMN_1691790	GCTCCGCTACCCTGGGGGCGATTGTAGC TCTGACATCTGGATTTGAACTC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2.087	8688.406	5791.289	12071.939	NQO1	NMOR1; NMORI; DHQU; DIA4; DTD; QR1	NM_000903	Homo sapiens NAD(P)H dehydrogenase, quinone 1 (NQO1), transcript variant 1, mRNA.	CCCCTTGCTCCTTGTCTGGCC TAGAAGTGTGGGAAATTCAGG AAAACGAG	ILMN_1758229	GGCACTGGTGGTTTTTGCTCTCGACAGTA TCCACAATAGCTGACGGCTGG
2.081	72.49823	22.777435	47.467953	C19ORF54	FLJ41131; MGC103014	NM_198476	Homo sapiens chromosome 19 open reading frame 54 (C19orf54), mRNA.	CTGGGCTCTATCATATAGACAG GCTTCTGATAGTTTGCAACTGT AAGCAG	ILMN_1726161	GGAGCCTGCCTCTTTCCCAAACTGCTCAT TATCCTGTTACCCCACCCAGC
2.08	42.44354	80.54361	167.60596	RGMB	FLJ90406; MGC86970; DRAGON	NM_173670	Homo sapiens RGM domain family, member B (RGMB), transcript variant 2, mRNA.			AGGTGACTGCCAACAGCCAGCCCAATGT CGAATCCAGAAATGCACCACGG
2.036	473.02264	518.67676	1055.8477	MAPKAPK3	MAPKAP3; 3PK	NM_004635	Homo sapiens mitogen-activated protein kinase-activated protein kinase 3 (MAPKAPK3), mRNA.	ACAAGACTGGCAGAGGCTGGG CAGCCTGGGGCTGATGAAGCA GAGATGTT	ILMN_1678899	CCTAGTTCCTTCCTGGCCCCTCTCTCACT GGCTGGGAAACCCTAGACCAT
2.016	137.04762	13.435646	27.071133	P2RX4	P2X4R; P2X4	NM_002560	Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4), mRNA.			GCAGTCTGTTCTTGGCTGGGTCAACTCTG CTTTTCCCGCAACCTGGGGTT
1.987	247.17262	309.56845	614.68933	C8ORF55	DSCD75	NM_016647	Homo sapiens chromosome 8 open reading frame 55 (C8orf55), mRNA.			AGCACTGCCCGATAGAACACGCCCGCCC TCACTGCTGTTCTTGCCTTACA
1.987	141.7768	83.05623	165.41013	YDJC	MGC133160	NM_001017964	Homo sapiens YdjC homolog (bacterial) (YDJC), mRNA.	CATACGATGCTCCATCAGCCTT ACCTAAAGCTACCAGAAAGGC TTTGGGC	ILMN_1744146	TGGAACCCTCCCTACTCTGACCCCCTACA GACAACCAAGCACTAATCCCC
1.966	118.72261	59.4431	116.92262	DPP3	FLJ11387; FLJ22331; DPPIII	NM_005700	Homo sapiens dipeptidyl-peptidase 3 (DPP3), transcript variant 1, mRNA.	CGCGCTATGCCATCCAGCAGA AATTGAAAGAAGCCCACGACG CCCTGCAC	ILMN_1670595	GACAGGCCCATATGCAGGCCCGGTTTGT GATCCTGAGAGTCTTGCTGGAG
1.965	127.942696	111.51428	218.41428	SCARA3	APC7; MSLR1; MSRL1; CSR; CSR1	NM_016240	Homo sapiens scavenger receptor class A, member 3 (SCARA3), transcript variant 1, mRNA.	TTCCCCCCACTGCTCAGAGAC GGCGAGAACTATGTTGTGCTT CTGGACTC	ILMN_1678730	TCCACCGCCCGCAAGGTTAGGGCATAGA GTTGTCTCCTTCCCAACACGGA
1.933	638.08093	162.9226	315.93927	RBCK1	XAP4; RNF54; ZRANB4; RBCK2; UBCE7IP3; C20orf18	NM_006462	Homo sapiens RanBP-type and C3HC4-type zinc finger containing 1 (RBCK1), transcript variant 1, mRNA.			CCCACCACAACACTCATCTGTCAAACACC AAGCACTCTCAGCCTCCCCGC
1.921	266.9268	63.78645	122.689285	AKNA	RP11-82I1.4; KIAA1968	NM_030767	Homo sapiens AT-hook transcription factor (AKNA), mRNA.	AGCCGGACCCGCCTCCGCATC GGGTTGCGATGCCCTCTGCAT AGTTTCTT	ILMN_1736584	TGGCAGCAGAGGCCTTTCCCTCAGACAA GCTACAAAGTGCCCAGGATGCC
1.919	2346.606	197.9643	380.1726	NCOA7	FLJ45605; dJ187J11.3; ESNA1; Nbla00052; Nbla10993; ERAP140; MGC88425	NM_181782	Homo sapiens nuclear receptor coactivator 7 (NCOA7), mRNA.	ACAAGGTGCTAAAACAGGTTCA CCCCGATACTGGCATCTCATC CAAGGCC	ILMN_1716195	CTGTAGCCTGGGTGTACGTTTCACTCAAG TTCTCCTACTGAGGACTCTTG
1.914	1049.5892	353.98926	678.1935	TNFRSF10B	KILLER/DR5; TRICK2; TRAILR2; TRICK2A; KILLER; TRICKB; ZTNFR9; TRAIL-R2; DR5; TRICK2B; CD262	NM_003842	Homo sapiens tumor necrosis factor receptor superfamily, member 10b (TNFRSF10B), transcript variant 1, mRNA.			TTAGGCTTTGCTATATCCCCAGGCCAAAT AGCATGTGACACAGGACAGCC
1.912	89.5149	51.93021	98.99762	DNAJC19	TIM14; TIMM14	NM_145261	Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 19 (DNAJC19), mRNA.			GAAGATGACAGTCCTTGCTCTCAGGGAG CCCCCACTTTAATGGGAGACTG

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.91	129.41428	24.850315	47.346428	FLJ20489		NM_017842	Homo sapiens hypothetical protein FLJ20489 (FLJ20489), mRNA.			CCAGCCCTGCGTTTCCATTCTGCCTTCTC AGAGTGCCCTTGCTGCACCCA
1.896	222.83095	8.369144	15.850397	UBA7	UBA7; UBE2; D8; MGC12713; UBA1B	NM_003335	Homo sapiens ubiquitin-like modifier activating enzyme 7 (UBA7), mRNA.	ACTGAGTATGTTCATTGCCACC CCTGTCCTCCCCTGGGCACCC CTCACTT	ILMN_1721178	TCAATGGAGCCCCGGATCCCAAGCCCTG CATTGTAAGCCCACAGTAGGCA
1.888	633.59766	425.60596	802.59766	FAM107B	MGC11034; FLJ45505; MGC90261; C10orf45	NM_031453	Homo sapiens family with sequence similarity 107, member B (FAM107B), mRNA.	CCCATGGCAGTCAGGCAAAGT GTTGCCAGGACGTACTGAAAA TCAGCCAG	ILMN_1803609	GGGGCCCTGGTAGGCTCCTTTAGAAGGA CCATTTCTGTTCCTAGAGCTTA
1.871	392.8601	299.3643	560.7351	SVIL	DKFZp686A17191	NM_003174	Homo sapiens supervillin (SVIL), transcript variant 1, mRNA.	GGCGGCAGAATGCCATCAAGT GTGGGTGGCTGAGGAAGCAAG GAGGCTTT	ILMN_1765876	GTTTCCTGCAGCATTAGGTATGACTTGTT CTGAGTACTGCTTCCGGTGCT
1.862	638.8143	204.75595	381.38095	PYGL		NM_002863	Homo sapiens phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI) (PYGL), mRNA.			ATCCAAAGGCCTGGAACACAATGGTACTC AAAAACATAGCTGCCTCGGGG
1.81	96.826454	155.35178	280.8601	TGM2	TGC; TG2	NM_198951	Homo sapiens transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2), transcript variant 2, mRNA.	CCGGGACCACACAGACAGGCT GAGGACGACTTTATGACCAAG AGCTGAAC	ILMN_1700935	AAGGGCGAACCACCTGAACAAACTGGCC GAGAAGGAGGAGACAGGGATGG
1.809	1792.456	823.53516	1490.6477	ADAM15	MDC15	NM_207195	Homo sapiens ADAM metallopeptidase domain 15 (ADAM15), transcript variant 4, mRNA.	GCGCCAGGTTGTCAATGGCCT CATGCTGGGACAGGCCAGGAT TCACGTAA	ILMN_1698185	CGGGATTGAGGAAGGTCCGCACAGCCTG TCTCTGCTCAGTTGCAATAAAC
1.8	537.5601	551.1476	992.11426	ATP6V0E2	ATP6V0E2L; C7orf32	NM_145230	Homo sapiens ATPase, H+ transporting V0 subunit e2 (ATP6V0E2), transcript variant 1, mRNA.			TCTGAGCCTCCGTCGCCCCTCCTGTTGG GTAAGGGTGTTGAGTGTGACTT
1.785	236.5893	151.15594	270.12262	MRPL4	MGC16367; L4mt; MGC2681; CGI-28	NM_146387	Homo sapiens mitochondrial ribosomal protein L4 (MRPL4), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.	TGTGATGCATGTTGTCGCTTTC CCACCCCGGGATCTCCATCTC TCTTCCC	ILMN_1658160	ACTTAACACACGAGGAGATGCCACAGAGC ATCGTGGAGGCCACCTCTAGG
1.781	164.86429	92.6268	164.73929	ERGIC1	ERGIC32; MGC14345; KIAA1181; ERGIC-32	NM_020462	Homo sapiens endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 (ERGIC1), transcript variant 2, mRNA.			CTGCGAGTTGGTTGGGCTTGACATTCAG GATGAGATGGGCAGGCACGAAG
1.765	942.381	289.0476	510.7393	MOCOS	MOS; FLJ20733; HMCS	NM_017947	Homo sapiens molybdenum cofactor sulfurase (MOCOS), mRNA.	GCCAGAAGGCAGAAGGGTAAG AGAGGGCAAGAGTGAGCAAGA GATGGAAG	ILMN_1695087	CAATTGGCTCTTTGCGTTTCCAGGTTTTG GGGCCTTGTCACAGATGCCAG
1.764	887.8393	180.39761	318.30176	MID1	RNF59; OGS1; TRIM18; FXY; OS; XPRF; GBBB1; OSX; BBBG1; ZNFXY	NM_033290	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), transcript variant 3, mRNA.	CAGAGCTGGACGAAGTCTGCT AAGAGAGATGGAGGCTGTGGC GGACTCCT	ILMN_1745389	TTCCCGCTCCCCCATATCAATTTTCCTTTT GTCTCCGGGGCTGAGTAAAT

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.762	641.69763	664.91016	1172.0559	PECI	DRS1; KIAA0536; HCA88; dJ1013A10.3; ACBD2	NM_006117	Homo sapiens peroxisomal D3,D2-enoyl-CoA isomerase (PECI), transcript variant 1, mRNA.	AACGCACCCTCTCTGTGGAGC TCTGACTGGTGTAGCTGGAAA CAAACAGC	ILMN_1678353	GATCTGACTAACTTCACTGATATTCCCCC TGGTGGAGTAGAGGAGAAAGC
1.762	91.47681	65.33559	115.06012	ZNF32	KOX30	NM_006973	Homo sapiens zinc finger protein 32 (ZNF32), transcript variant 1, mRNA.	GAAATGAAGTGGACGGCAGCA ATGAAAAAGCAGCCCTTCTCCC AGCCCCC	ILMN_1707175	CGCTGCTGCGGGCTCGGCGCCGGCCTTT GTCTGCGGGCACGCGCCGCTGC
1.759	92.04765	74.235886	130.62262	NLN	KIAA1226; DKFZp564F123; AGTBP	NM_020726	Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA.			AGGTGTGACCTCTCCTTTGCCTGCATACC TCAAGGCCAGGGGAATATGCC
1.753	153.71011	92.1268	161.57262	ABCB9	TAPL; KIAA1520; EST122234	NM_019624	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 9 (ABCB9), transcript variant 2, mRNA.			AGCCCAGGATCTGGCTTTGCCAGAGGTT GCAACATGTTGAGAGAACCCGG
1.751	339.13095	98.785126	172.81429	ADD3	ADDL	NM_001121	Homo sapiens adducin 3 (gamma) (ADD3), transcript variant 3, mRNA.	ACGTCGTACCTGACGCTGAGC CTGTCATGAGAATGCAACAGG AGCAAACC	ILMN_1652777	GTGAATGTGCCTGAGGAGTCTCGGAACG GAGAAACCAGTCCCCGAACCAA
1.747	1718.5559	5377.7476	9397.739	TMEM158	BBP; DKFZp586E1621; RIS1; p40BBP	NM_015444	Homo sapiens transmembrane protein 158 (TMEM158), mRNA.	GATGCCGACCAGAACCACATG AGTCAGAATCATCAGAATATCC CACCAAC	ILMN_1768097	GAACCTTTTCCAAGTTGATCTATCCAGTG ACGTGGCCTGGTGGGCGTTTC
1.738	93.18513	61.500824	106.89761	SNRPD3	SMD3	NM_004175	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide 18kDa (SNRPD3), mRNA.	GTGAGGCACACATGATTGATG GGTATGGGGCCATGAAGACCT TGAAGAGC	ILMN_1705984	TGGCCAGTTGCAGGTTAAGCCCCAGAAAA GTTCACCTTGGAGAAGCTCCG
1.737	2546.306	931.2893	1616.281	COMMD7	FLJ14987; C20orf92; MGC33315; dJ1085F17.3	NM_001099339	Homo sapiens COMM domain containing 7 (COMMD7), transcript variant 2, mRNA.	AGGGACCATGCTGGGCCTCTG CGCCTCTGTACAACCACTGCT CCGAACTC	ILMN_1815581	CAGAGCCCCCACGGATTTCTGCACACTCT GGGTCTGTGCTGGTGGAACAT
1.666	293.9226	89.589325	149.04346	TMEM98	DKFZP564K1964	NM_015544	Homo sapiens transmembrane protein 98 (TMEM98), transcript variant 1, mRNA.	AGACCTGACTGCCTGGTTCAG CCTCTTCGCTGACCTCGACCC ACTCTCAA	ILMN_1814787	GTGGAGGAACCTAGCACCTGCCATCCTCT TCCCCAATTTGCCACTTCCAG
1.664	712.2976	305.61844	508.85178	BRE	BRCC45; BRCC4	NM_199191	Homo sapiens brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE), transcript variant 3, mRNA.	GTACGTTGGTGCCCGCTGCTG TCTAATGCCCTGGAGCCTCCC TGGCCCCC	ILMN_1693060	CCTGCCTCTGTTTTTCCCTCGAGACCAGC CAACTCTCACATTTCAGTCCG
1.664	198.89761	110.31012	183.7976	UBE2Q1	NICE-5; PRO3094; UBE2Q	NM_017582	Homo sapiens ubiquitin-conjugating enzyme E2Q (putative) 1 (UBE2Q1), mRNA.	GGCTCCCAAGGCCATGAAGAA GATGTACAAGGCGTGCCTCAA GTACCCCG	ILMN_1717052	GGTTTTCAAGGCCTCTGTGGCTTTCTTCT GAACTTACCACCAGCCCTGGC
1.655	128.22261	95.930954	159.00595	RWDD2B	C21orf6; GL011	NM_016940	Homo sapiens RWD domain containing 2B (RWDD2B), mRNA.	GTGCTACAGCAACTGAGACAG CAACCAAGAGGCAAGAAACCT GGGATTGG	ILMN_1732193	CCAGCCATTCCCAACCCCCTTCTCCCTTA CCTGCCTTCACTAAAGAACCC
1.646	921.35596	258.9268	426.62262	C10ORF56	FLJ90798	NM_153367	Homo sapiens chromosome 10 open reading frame 56 (C10orf56), mRNA.			CCAACGACTAACCCTGAAATGGGGGTGTT CCAGCCTTCAGCGAGATGGCC
1.637	321.78094	142.28928	232.70596	GYS1	GYS; GSY	NM_002103	Homo sapiens glycogen synthase 1 (muscle) (GYS1), mRNA.	AGATGGATTATCAAGTGTCAAG TCCAATCTATGACATCAATTAT TATACA	ILMN_1653395	CCACCCCTAACCTGGCTTATTCCCAACTG CTCTGCCCACTGTGAAACCAC
1.637	121.03928	73.67797	120.66846	SDPR	SDR; PS-p68	NM_004657	Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), mRNA.	GTGGGATCGAGACATGTAAGC AGCATCATGGAGGTTTGAAGA TGCCGCAT	ILMN_1725427	GGCCCAGGAAGCAAATCCCCTGCCTTTA GTATGAACCACTATAAGTAACC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.627	656.9643	243.73096	397.08096	MGMT		NM_002412	Homo sapiens O-6-methylguanine-DNA methyltransferase (MGMT), mRNA.	CAGCTAGGTGGGGAAAATTCA CAGGTGGGCTGTCTGTAGAGA GAACTGGC	ILMN_1721525	GCTGGCCGAAACTGAGTATGTGCAGTAG GATGGATGTTTGAGCGACACAC
1.626	258.76428	115.52678	187.88512	C14ORF147	MGC24447	NM_138288	Homo sapiens chromosome 14 open reading frame 147 (C14orf147), mRNA.	TGGGGGAGCAAAGCCTGCAAC AAACGGGAGTGGCTGCTCAGG GGAACATT	ILMN_1692113	GGTGACCTATCCTGGCCCTCTACTCAGAA ACCGGCAATTTGTCTTCACTC
1.624	366.84344	252.21011	410.01013	C3ORF58	MGC33365	NM_173552	Homo sapiens chromosome 3 open reading frame 58 (C3orf58), mRNA.	CACGTTTTCCCATTTGCCCTGT GGCTCACTGTCTTACAATCACT GCTGTG	ILMN_1742789	GCCAGCGGTGATTGCTACTTGAGGTAGTT TTTTACAACTACCATTTCCCC
1.618	1683.5393	717.5601	1160.906	NDUFC1	MGC138266; KFYI; MGC126847; MGC117464	NM_002494	Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa (NDUFC1), mRNA.	GAAAAGCTGTGTCGTGTTCCC TGTGAAACTGAGCAGGTGTGT GTTGGCGC	ILMN_1785424	GGCCCTTCAGTGCGATCAAAGTTCTACGT GCGAGAGCCGCCGAATGCCAA
1.596	268.9226	242.18094	386.88095	C7ORF20	CGI-20	NM_015949	Homo sapiens chromosome 7 open reading frame 20 (C7orf20), mRNA. XM_946081 XM_946082 XM_946083	CTCTCTTCCCTGATCCTTGGAG GAGCCCGAACTGATTCTGGAG CTCTGTG	ILMN_1700428	ACGGGCCTCCGTTTGTGGAGCCGCTGCT TAACTTCATCTGGTTCCTGCTG
1.595	533.94763	180.87262	288.53094	CUL4B	SFM2; DKFZp686F1470; MRXSC; MRXHF2; KIAA0695	NM_001079872	Homo sapiens cullin 4B (CUL4B), transcript variant 2, mRNA.	GCTTCCTGGATGAGAAGAGCG GCAGTTTCGTGAGCGACCTCA GCAGTTAC	ILMN_1652280	GTTAGGAGGAGACTCTTGATGTCACCTTC AGTATCTTGAAAGCGGGTCCC
1.584	16.034212	41.121185	65.198235	ACYP1	ACYPE	NM_203488	Homo sapiens acylphosphatase 1, erythrocyte (common) type (ACYP1), transcript variant 2, mRNA.	CCCCAGAGACGCTCAGCTTGT ATCCATTGACTGGAAGTCTGTC ACGTGGC	ILMN_1728369	GCTGAAACTCACAGCAAGAGCTGTGTTCC AGTTAGCTTTGCTACCAGTTA
1.573	1974.6143	1966.106	3091.0227	MRPL33	C2orf1; RPL33L; MGC23922; MGC111093; MGC13694	NM_004891	Homo sapiens mitochondrial ribosomal protein L33 (MRPL33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	CTCCCCAGGAGGATAGTGCAG AGGACACATCAGGGGCAGAAA TGACATCG	ILMN_1675053	GCGAAGCTGGGACAGGTTTCTGCTTCAA CACCAAGAGAAACCGACTGCGG
1.566	1141.8392	543.11426	850.20593	LPIN1	DKFZp781P1796; KIAA0188	NM_145693	Homo sapiens lipin 1 (LPIN1), mRNA.	GGGCCTCCCTTGACCCCAGTA CGAAGTCTATGCCCTGAATCC CCAGAGTA	ILMN_1697554	ACCCAGTGATGCTGAGGTCATGTGCTGG AATGCTGTATTTGGACCACACA
1.559	171.43927	226.30594	353.00177	SLC37A4	G6PT3; GSD1b; TRG19; PRO0685; G6PT2; GSD1d; GSD1c; MGC15729; G6PT1	NM_001467	Homo sapiens solute carrier family 37 (glucose-6-phosphate transporter), member 4 (SLC37A4), mRNA.	GCATTAGCCTGCATGTTTCTAG GTCTTCTGCCAAGTGCTTTTCT CAGTTG	ILMN_1805645	GACTGCTGTTGCCAATACCTCAGACTCCA GGGAAAGAGAGGAGGCCATCA
1.554	228.64761	139.57262	216.63095	NEK6	SID6-1512	NM_014397	Homo sapiens NIMA (never in mitosis gene a)-related kinase 6 (NEK6), mRNA.	GACAGTTCAGAGGCAGGGACA ACAGATGGGGGTGGCCAAGTG ACAATCGA	ILMN_1763365	GGGCGGCTGCTGTTTCCACACGTGGACT CGGATCTGCTGTGACACCGTCA
1.536	635.55597	848.4768	1302.7935	THOC4	ALY; BEF	NM_005782	Homo sapiens THO complex 4 (THOC4), mRNA.	GTACAAGGCTTCAAAGTACCT GTGTGTGTCCCTCATGGAGCC ACCTGCAG	ILMN_1726415	TGGACATGTCTCTGGACGACATCATTAAA CTGAACCGGAGCCAGCGAGGC
1.535	71.35026	41.92161	64.35622	BCORL1	FLJ11362; B930011H20Rik	NM_021946	Homo sapiens BCL6 co-repressor-like 1 (BCORL1), mRNA.			AGAGAGGAGCTTGGGTTGCTTCCCTGTC CCCGCCCCCTCTGTGGCATTGT

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.534	1790.2726	993.0226	1523.7393	TSEN34	LENG5; SEN34; SEN34L	NM_001077446	Homo sapiens tRNA splicing endonuclease 34 homolog (S. cerevisiae) (TSEN34), transcript variant 2, mRNA.			TGCAGTGAACTCCAGAGACCTAGGGGAT GTGGCTGTGTCGGCAGCAAGAG
1.534	209.58096	443.4018	679.96014	DLEU1	XTP6; MGC22430; DLB1; LEU1; BCMS	NR_002605	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1) on chromosome 13.			GAGACAGAAGATTGAAGCCTTTGCCAGCC ATTCTTTCCCTTTTTGCTTCC
1.53	35.640625	54.819443	83.864365	RWDD1	CGI-24; PTD013	NM_016104	Homo sapiens RWD domain containing 1 (RWDD1), transcript variant 2, mRNA.	GTGGGGACCCTCTTCCTCTAG CACAGTAAAGCTGGCCTCCAG AAACACGG	ILMN_1790574	CCTGTATAGCTCCAGTCCTGTTCATGTTC TCTCTCACCAGCAGTACATCT
1.521	431.44345	314.5476	478.35596	C1ORF108	STRF2; FLJ12666; RP11-781D11.2	NM_024595	Homo sapiens chromosome 1 open reading frame 108 (C1orf108), mRNA.	CTATGTTGACGCTAGCCTGCA CAGACACTTGGGTCTATGAGA GCACAGTG	ILMN_1680225	CGGAAAGTCAACCTCACTCCTCAGCACTC ACAGCACCTAGCTCTCCAGGT
1.515	1127.0059	267.44763	405.18094	SLC25A23	MGC2615; MCSC2; SCaMC-3; APC2	NM_024103	Homo sapiens solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23 (SLC25A23), nuclear gene encoding mitochondrial protein, mRNA.			TCCTTCGACCTCCACTGCGCCCCACCTCC CTGCCTGTGTGTGTTATTTCA
1.502	239.0726	192.56429	289.2351	RPL8		NM_033301	Homo sapiens ribosomal protein L8 (RPL8), transcript variant 2, mRNA.	TTGAGAACTGCTGGACCAGAG CCTTTAGAGCTCTGATAAGGTG TCAACAG	ILMN_1719089	ATGGGCAGTATCCGCCGCCATCCTCTTCC GTGAGGCGCGCTGAGACCCGG
1.494	244.94345	146.84763	219.48096	ANKS1A	ANKS1; KIAA0229; MGC42354	NM_015245	Homo sapiens ankyrin repeat and sterile alpha motif domain containing 1A (ANKS1A), mRNA.	TCCACCCTTCCCCACATCAGTC GGCCTAATCCAAACCTTGAAAG CCTGGC	ILMN_1737642	GCCCAGGCCAGCAGAAAGCAGCTCAGAA GTATTGTTGCTCATGGTGTGGC
1.493	59.252243	38.964825	58.206024	CCDC126	MGC104248; FLJ23031	NM_138771	Homo sapiens coiled-coil domain containing 126 (CCDC126), mRNA.	TTTTCCCCTTCGGTCTTCCACA GCAGTATTATTGTCTTTGTGGA GTTGAC	ILMN_1737462	GGAGGAAGGGACTTTGGAGAATGGAACT CTTGAGGACTTTAGCCAGGTGT
1.486	337.63928	186.28513	276.76428	ZNF32	KOX30	NM_001005368	Homo sapiens zinc finger protein 32 (ZNF32), transcript variant 2, mRNA.			CTGTACCCAGTGCAGGAAGAGTTTCCACA CCAGGGGGAATTGTATTCTGC
1.485	361.06012	227.42679	337.51013	PISD	DJ858B16; DKFZP566G2246; dJ858B16.2; PSSC	NM_014338	Homo sapiens phosphatidylserine decarboxylase (PISD), mRNA.			ATACAGACCTTTGCAGGACCTGATGAGTG ACCCTTCTGGAGCTGGCCAGG
1.479	129.99345	147.02261	217.42679	PGBD3	FLJ90201	NM_170753	Homo sapiens piggyBac transposable element derived 3 (PGBD3), mRNA.	GGCCAGCGGGGCCGAAAGCG GAGTTGGGTTTGCTTATTTTGC TCATTGGA	ILMN_1680113	CCCATGGTCATCCTCCAGAACCTGGCCAA AAAGGAAGACCTCAGAAGCGT
1.476	934.78094	725.73096	1070.5768	LASS6	CerS6; MGC129950; MGC129949	NM_203463	Homo sapiens LAG1 homolog, ceramide synthase 6 (LASS6), mRNA.			CACAGGTCCATGAAAGTTTGGCTTCCTGG TTTGATGTCTGTTGCGTGGCC
1.472	550.65594	517.86426	762.17676	GLRX2	GRX2; bA101E13.1	NM_016066	Homo sapiens glutaredoxin 2 (GLRX2), transcript variant 1, mRNA.			GGAGGTGCAACTGACACTCATAGGCTTCA CAAAGAAGGAAAATTGCTCCC
1.47	961.0893	305.60596	449.05594	GMDS	GMD	NM_001500	Homo sapiens GDP-mannose 4,6-dehydratase (GMDS), mRNA.	TCAGTCACATTCGCTTCAGTCC TACGGGCGAGTGGACGGAGG GCTTGCTG	ILMN_1675188	CCTCCAGGGTTTGGGTCGCTTTGCGTTTG TCGAAGCCTCCTCTGAATGGC
1.463	446.09344	279.33093	408.6476	C11ORF68	P5326; Bles03	NM_031450	Homo sapiens chromosome 11 open reading frame 68 (C11orf68), mRNA.			CCCCTCAGGAGAGAGAAAACTTAGTGCTT CCAGCCCTTCTTGGAGCCTTC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.455	37.62336	63.6984	92.75597	HSPD1	HuCHA60; GROEL; HSP60; SPG13; CPN60; HSP65	NM_002156	Homo sapiens heat shock 60kDa protein 1 (chaperonin) (HSPD1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.			GAGGGGACACGGGCTCATTGCGGTGTGC GCCCTGCACTCTGTCCCTCACT
1.45	1819.406	1078.6726	1564.2727	PSME2	PA28beta; REGbeta; PA28B	NM_002818	Homo sapiens proteasome (prosome, macropain) activator subunit 2 (PA28 beta) (PSME2), mRNA.	GCTCCGAGGTGACCCAGCACA TCACCATCCACTGCCTTAACAT GACCGTG	ILMN_1788377	TGATTTTGGGGTAGCAATCCAGGAGAAG GTGCTGGAGAGGGTGAATGCCG
1.447	312.37262	132.27261	191.20178	MKNK1	MNK1	NM_003684	Homo sapiens MAP kinase interacting serine/threonine kinase 1 (MKNK1), transcript variant 1, mRNA.			ATCGGTGTCTGCTGCTGTGTCCCCAGGT CTTGTGTGGGTGGCACAGATCT
1.446	346.13928	197.68929	286.00177	FIBP	FGFIBP; FIBP-1	NM_198897	Homo sapiens fibroblast growth factor (acidic) intracellular binding protein (FIBP), transcript variant 1, mRNA.	GGATCCGCTCTACTCAGGGGC AACACAAAGCCATTTCCACCTG TGGCTCC	ILMN_1655449	GGCTCCTTGGGAACTGAGACATATCTCAG GGAATGGTGTCTGTGCTCAGC
1.438	16439.69	4706.2646	6769.831	IFITM2	1-8D	NM_006435	Homo sapiens interferon induced transmembrane protein 2 (1-8D) (IFITM2), mRNA.			TATCTTCCATTCCTCGCCCTGCCCCCAGA GGCCAGGAGCTCTGCCCTTGA
1.436	4553.106	1098.4476	1577.1643	ID2	GIG8; MGC26389; ID2A; ID2H	NM_002166	Homo sapiens inhibitor of DNA binding 2, dominant negative helix-loop-helix protein (ID2), mRNA.			GCAGACTTTGCCTTTTTTCAAAGGTGGAG CGTGAATACCAGAAGGATCCA
1.431	279.95178	262.78513	375.84344	CYB5D1	FLJ32499	NM_144607	Homo sapiens cytochrome b5 domain containing 1 (CYB5D1), mRNA.			CATGTCTTGCCTCAGACCCTCACACACTG TCCTCTCTGCCTGCAACACTC
1.428	345.99762	482.79346	689.64343	SPA17	SP17; SP17-1	NM_017425	Homo sapiens sperm autoantigenic protein 17 (SPA17), mRNA.	CCAGGTCAGAAACCATTGTTCA GAAGACCTCCCTGTGAGAGAG TTGCTCC	ILMN_1787552	CTGTCAAAATCCAAGCTGCCTTCCGGGGA CACATAGCCAGAGAGGAGGCA
1.417	119.32678	58.683617	83.13521	RABL2A	MGC117180	NM_013412	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 1, mRNA.			CAAGAAGAGCTTCCTTTAAAGTTCCTATTT CAGCATAAAGAGGCTGTCCT
1.414	1101.1726	426.47678	603.31006	TWIST1	TWIST; ACS3; BPES2; SCS; BPES3	NM_000474	Homo sapiens twist homolog 1 (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) (TWIST1), mRNA.	GTCTTCCCAGTTTCTCCAAGCT GCTTCTGGAATGCAGGTCTGT CGGCTGG	ILMN_1778964	AGACGGGCAGCGGCACCATCCTCACACC TCTGCATTCTGATAGAAGTCTG
1.401	5736.756	6732.0645	9429.206	CALM3	PHKD; PHKD3	NM_005184	Homo sapiens calmodulin 3 (phosphorylase kinase, delta) (CALM3), mRNA.	TTCCACCCCAAGAGAACTCGC GCTCAGTAAACGGGAACATGC CCCCTGCA	ILMN_1699704	CAGCCAAGAGCTGAGGGTAAGGGCAGGT AGGCGTGAGGCTGTGGACATTT
1.4	1447.0894	1686.0977	2360.6143	ERCC1	UV20; COFS4	NM_001983	Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) (ERCC1), transcript variant 2, mRNA.			CCCGGAGGCTGTTTGATGTCCTGCACGA GCCCTTCTTGAAAGTACCCTGA

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1.398	965.07263	766.61426	1071.9518	RPL7A	SURF3; TRUP	NM_000972	Homo sapiens ribosomal protein L7a (RPL7A), mRNA.			CGTAAAATGGGGGTCCCTTACTGCATTAT CAAGGGAAAGGCAAGACTGGG
1.396	1045.5977	645.78094	902.29346	C22ORF16	MGC70831; N27C7-4	NM_213720	Homo sapiens chromosome 22 open reading frame 16 (C22orf16), mRNA.	CTGCGGGCTGCGCGAGTCCC GGGGCGGCGAGTCCCGGCGC TGTCCGCGTC	ILMN_1689380	CACCACTCAGAGTGACCTGTCCCTGTGTG AGGGCTTCAGCGAGGCCCTGA
1.393	519.6893	869.1726	1210.7643	TSPAN5	TSPAN-5; TM4SF9; NET-4	NM_005723	Homo sapiens tetraspanin 5 (TSPAN5), mRNA.	CCCCATGTGCTGCTGAGTGGC CAAGATGATGCCAGGCTGCCC TATACACT	ILMN_1769787	GGCTGTGTGCCCCAGTTTGAGAAGTGGT TGCAGGACAATTTAACCATCGT
1.388	500.72263	575.5559	798.6643	CRYZ	DKFZp779E0834; FLJ41475	NM_001889	Homo sapiens crystallin, zeta (quinone reductase) (CRYZ), mRNA.			CATTATTGGTTGGCTGCCAATGACCCCAT ATGTTCTGTGAGAATAGTAGC
1.386	3457.831	1690.856	2343.1643	NDUFA3	B9	NM_004542	Homo sapiens NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa (NDUFA3), mRNA.	AGCAGGCACCCAGGCTTTAGA GAAGTATAGGGGGCTTCTTCC CTGCTGGG	ILMN_1712755	GAGACAAAGATGGCTGCGAGAGTCGGCG CCTTCCTCAAGAATGCCTGGGA
1.384	634.7976	599.6643	830.4393	ABI2		XM_001126750	PREDICTED: Homo sapiens abl interactor 2 (ABI2), mRNA.			TGGTTGGTATGAGGGAGTTATGAATGGAG TGACTGGGCTTTTTCCTGGGA
1.383	260.62677	184.72678	255.5476	SERP2	bA269C23.1; RP11-269C23.1; C13orf21; MGC35505	NM_001010897	Homo sapiens stress-associated endoplasmic reticulum protein family member 2 (SERP2), mRNA.			TGCTTTTCTGTTGGCAGGATTAGTAGCCA CGCGGGTCGTCCGCAGCAGTG
1.383	72.31564	97.305954	134.5476	PINX1	LPTS; MGC8850; FLJ20565; LPTL	NM_017884	Homo sapiens PIN2-interacting protein 1 (PINX1), mRNA.	GTTCTGCGCGGCGGGGGCCG TACCCGCGGCGGAGCGAGGA GGCGAGAATG	ILMN_1707099	TTCCAAATGAATCCTTCCCAGCCGGGGCC TTCCGACCACTCAGCTGTCAG
1.382	959.3726	373.15594	515.76013	LAYN	FLJ30977; FLJ31092	NM_178834	Homo sapiens layilin (LAYN), mRNA.			ACGACCTCCTGTTGGACCCCCACGTTTTG GCTGTATCCTTTATCCCAGCC
0.72	232.26012	220.22263	158.64346	KIAA0240	DKFZp686P0250	NM_015349	Homo sapiens KIAA0240 (KIAA0240), mRNA.	CATATAAGCCCTGGGTCGGGG GGTAACTGTGGGGATCACTGC CTGAGACA	ILMN_1688372	AGGGAGGCCTTACAGACTGACTTTACTTA AAGAGGACGCGTCACTCGCTG
0.718	1687.981	2604.806	1871.0809	TUBB6	TUBB-5; MGC132410; HsT1601; MGC4083	NM_032525	Homo sapiens tubulin, beta 6 (TUBB6), mRNA.			AGGCTACGTGGGAGACTCGGCGCTGCAG CTGGAGAGAATCAACGTCTACT
0.714	167.8393	233.16428	166.4226	MDFIC	HIC	NM_199072	Homo sapiens MyoD family inhibitor domain containing (MDFIC), mRNA.	CCTAAGCCCCAGTTGCACCTA CTAACTGCAGTCCCTTTTGCTG TCTGCCG	ILMN_1684755	CAGACTCTGAATGCCGACTGTGTGGACTC TCTTCCTCAGACTGTGGGGAC
0.711	454.4226	264.28928	187.93095	ARHGEF17	KIAA0337; P164RHOGEF; p164-RhoGEF; FLJ90019; TEM4	NM_014786	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 17 (ARHGEF17), mRNA.			TCCCACTTGAGAGCAGCCTCTACCTGACC CCCTGGACCACAGAGAGCCAC
0.711	381.03094	274.98096	195.40594	MBD6	KIAA1887	NM_052897	Homo sapiens methyl-CpG binding domain protein 6 (MBD6), mRNA.			GTGATGATGCGACTGAGGATTATGCAACG TGGTCCAACCGGAGCGGCCAG
0.711	48.42914	69.291595	49.202026	IL15	MGC9721; IL-15	NM_172174	Homo sapiens interleukin 15 (IL15), transcript variant 1, mRNA.			GCCCTGAGGGCTGAGTTCTGCACCCAGT CAAGCTCAGGAAGGCCAAGAAA
0.708	361.91846	506.7851	358.82263	CD59	MIN1; MIN2; PROTECTIN; MIN3; 16.3A5; MSK21; MGC2354; EJ16; EL32; EJ30; p18-20; G344; MIC11	NM_000611	Homo sapiens CD59 molecule, complement regulatory protein (CD59), transcript variant 2, mRNA.	GGCAGGAGAAGGGGTGTTCAT AGAAGCAGTGTGCAGGTGAGG CAAAGTGC	ILMN_1655245	CCTCATAGGGACTTTGCCTCCTGACAGCA GTTTATGGGTGTTCATTGTGG

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.706	80.835495	79.464554	56.081486	EXOC5	HSEC10; DKFZp666H126; PRO1912; SEC10P; SEC10L1; SEC10	NM_006544	Homo sapiens exocyst complex component 5 (EXOC5), mRNA.			CACACTCGCCCATTTTCTAAGTGGTTTAG AAGGTTGCAGTCTGCCTCACC
0.705	352.18512	193.18512	136.1101	MAGED2	MAGE-D2; MGC8386; MAGED; JCL-1; BCG1; 11B6; HCA10	NM_201222	Homo sapiens melanoma antigen family D, 2 (MAGED2), transcript variant 3, mRNA.	CATGGACTCCTGCCGACTCTG GTAGCTGGGACGCTGGTTTAT GGCATCCT	ILMN_1668242	ATCCAGGCGGGAGCAGAAGCTAAAGCCA AAGCCCAAGAGAGTGGCAGTGC
0.703	256.43512	300.09344	211.14761	TTC14	DRDL5813; KIAA1980; DKFZp313M1015; FLJ00166; PRO19630	NM_001042601	Homo sapiens tetratricopeptide repeat domain 14 (TTC14), transcript variant 2, mRNA.	CCGCTGAAGCTGTAGGAAGCG CCATTCTTCCCTGTATCTAACT GGGGCTG	ILMN_1767470	ATAGAAGGTGGGAACCAGGTTCTGTGAG GCATTCTACCTCACCAGCAAGC
0.702	706.9226	890.6101	624.6809	BMI1	MGC12685; PCGF4; BMI1; RNF51	NM_005180	Homo sapiens BMI1 polycomb ring finger oncogene (BMI1), mRNA.			TGGTCGAACTTGGTGTGTGTTCATCACCC ATCAGTTATTTGTGAGGGTGT
0.7	800.99347	557.4976	390.1476	RB1CC1	DRAGOU14; FIP200; CC1	NM_001083617	Homo sapiens RB1-inducible coiled-coil 1 (RB1CC1), transcript variant 2, mRNA.	GCTAGAGGCCAGGATTTTGAG ACCAGCTTCGGCAATACGGTG AGACCTTG	ILMN_1657701	CAGTGGATTGGTCATCTGGGTTCTAAAGG GAAGAGTCTGTGCTACTAACC
0.698	99.77262	137.08928	95.714294	SS18L1	MGC78386; MGC26711; LP2261; KIAA0693; CREST	NM_198935	Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 1 (SS18L1), mRNA.			CTGATTTTGTCAGGGTTTTTCTACGTGTA GGCGTGAATAGGGGGCACCCC
0.698	179.66013	199.90178	139.59763	IRF2BP2	MGC72189	NM_182972	Homo sapiens interferon regulatory factor 2 binding protein 2 (IRF2BP2), transcript variant 1, mRNA.	AGGGGCTTTTGTATTTCCTGCC TCTGCCCCACCCCCAAACCTC CTGTATA	ILMN_1667761	CTTTGGGTGGCCTTTGTGGACGGCTCGT AGCTGGAAAGTGTTGATCTGGG
0.697	1128.7893	1130.06	786.98926	SQLE	FLJ30795	NM_003129	Homo sapiens squalene epoxidase (SQLE), mRNA.			GTCAGAACCTTGGATTACAAAACCTCGAG CCCTTCTCAGTAGTGGTGCTG
0.696	31918.273	22501.648	15651.064	BGN	SLRR1A; PG-S1; PGI; DSPG1	NM_001711	Homo sapiens biglycan (BGN), mRNA.	TGATGGCTCCAGAGAACACAC CAGCTATTTATGAGCCTCTGCC CCCAGGC	ILMN_1713029	TCCAGCGCAAGGAGGGGCTGCTTCTGAG GTCGGTGGCTGTCTTTCCATTA
0.694	430.81427	690.15173	479.22678	PRKAA1	MGC57364; AMPK; MGC33776; AMPKa1	NM_206907	Homo sapiens protein kinase, AMP-activated, alpha 1 catalytic subunit (PRKAA1), transcript variant 2, mRNA.			TGATTTCTCACTGAGAGGAACTTTTCTAC CAGGTTGGGGCATATGGGAGC
0.694	1088.0143	1430.856	992.30176	MAPK6	HsT17250; PRKM6; p97MAPK; ERK3; DKFZp686F03189	NM_002748	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA.			TGCCTACCTAGCTGCATCTATAATGTCAG CTTATCCTAAGGCTGTCCACG
0.693	495.8851	671.3143	465.43927	TMEM41B	MGC33897; KIAA0033; MGC57262	NM_015012	Homo sapiens transmembrane protein 41B (TMEM41B), mRNA.	ATGTACGTGGGGGATTCTTGA CTCGGGTTAGTCTCTGGGGAT GCAGAGCC	ILMN_1706644	CACAAGAAGACAAGCATCTGTGGTGCGG AGGCAAGCAGGCTAACTAGGAG
0.693	369.68094	457.56012	317.1518	DYRK1A	HP86; DYRK; DYRK1; MNBH; MNB	NM_130437	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A (DYRK1A), transcript variant 4, mRNA.	GGAGCTGAAGGTCGCCATGAA GAAGACCTTCTTCAGTAAACTC TACCCAG	ILMN_1787434	GCAGAACACCGCGTTTCATTCTATTGGTC AATTCCATGTGGCTGACTAGG
0.692	532.006	2046.4977	1415.7893	AGTR1	AT2R1A; AT2R1B; AT2R1; AT1; AT1B; AGTR1B; AGTR1A; AG2S; HAT1R	NM_000685	Homo sapiens angiotensin II receptor, type 1 (AGTR1), transcript variant 1, mRNA.	GTACAATGTTATCTCTGTGGGA GGAAGGAGGCAGGCTGTGGT GGGACTGG	ILMN_1803110	CAACAGGAGATGAGAGTTCCAGATTGTTC TGTCCAGTTTCCAAAGGGCAG

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.681	108.86432	166.52261	113.51428	DYRK3	DYRK5; hYAK3-2; RED; REDK	NM_003582	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 (DYRK3), transcript variant 1, mRNA.			GCAGTGTATTGCCAAAACTGATTAGCTAG TGGACAGAGATATGCCCAGAG
0.681	275.0476	646.05597	439.69763	MIS12	MTW1; hMis12; MGC2488; 2510025F08Rik; KNTC2AP	NM_024039	Homo sapiens MIS12, MIND kinetochore complex component, homolog (yeast) (MIS12), mRNA.	AGAAGGCCATGACTCTTTAGG TGTGTATGTGTACCTTTCAGCA TCCTAGG	ILMN_1775192	GGAAAGGGGAGAAATAGCAATGGTTGTTC CTAAGGTATTGCTTGCCCTCC
0.677	116.85179	137.83511	93.23512	FAM131A	MGC21688; PRO1378; FLAT715; C3orf40	NM_144635	Homo sapiens family with sequence similarity 131, member A (FAM131A), mRNA.			GGGCCTTGTAGGCTTTGGCAGGTAAGAG GGCCCAAGGTAAGAACGAGAGC
0.677	330.74347	540.32263	366.09763	EDEM3	C1orf22	NM_025191	Homo sapiens ER degradation enhancer, mannosidase alpha-like 3 (EDEM3), mRNA.	CGCCTGGCAACCAAGTATCAT ACCGTTCCACTGCCACCAAAA GGAAGGGT	ILMN_1766851	GGGGGGTAGAATTTAGTAAATATTCCAGC CGGTCGTTTTATGCACAAGGC
0.675	1709.3934	1200.206	810.78094	LDLR	FHC; FH	NM_000527	Homo sapiens low density lipoprotein receptor (familial hypercholesterolemia) (LDLR), mRNA.	CTCAAAGAAGTTACACAGCCTT GGCTGAAGCAAACTGCCTAAA AGGAGCC	ILMN_1689371	GCACGAACTGGACTGTGTGCAACGCTTTT TGGGAGAATGATGTCCCCGTT
0.673	1285.606	1537.5642	1034.3893	PRPSAP1	PAP39	NM_002766	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1), mRNA.			AGGGAAGCTGAGCGCCTGTGGCCCTATT ACTATCCAGTTGGCCTCTCCCA
0.672	25.04816	126.97262	85.306	MESDC1	MGC99595	NM_022566	Homo sapiens mesoderm development candidate 1 (MESDC1), mRNA.			GGTTGTGTTATCACTCCCACCCCCTACCC CAGCCCGTCTTCCGGAATTTC
0.67	462.9643	569.73926	381.9101	TBX3	UMS; XHL; TBX3-ISO	NM_005996	Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA.	TTATTCTCAATACCTGACAGGG GCCCATGGGAATGACTTCAGA AGCATCC	ILMN_1813544	CACCAAAATTGGGGAAGGAGTGCCACTTT CCAGCTCCACTTCAAATTCCT
0.663	1879.8977	3121.9644	2067.4644	SH3KBP1	GIG10; MIG18; CIN85	NM_031892	Homo sapiens SH3-domain kinase binding protein 1 (SH3KBP1), transcript variant 1, mRNA.			CTTTTGCTTCAGGCTAAGAGCTGCCTCGC TCTTTGTCCCCCCATTAGGAT
0.662	47.288147	78.98961	52.356567	PHTF2	DKFZP564F013; FLJ33324; MGC86999	NM_020432	Homo sapiens putative homeodomain transcription factor 2 (PHTF2), mRNA.	GGTGAGAGGAAATGTTGACTG GCCAAAAATATCTTTTTTCCCC CACTGCG	ILMN_1712159	GAAACACTGGGCTGTTTGCACAGCTCCAA CTGTGCATGCTCAAAATGTGC
0.66	200.37262	350.5268	231.18927	TMEM62	FLJ23375	NM_024956	Homo sapiens transmembrane protein 62 (TMEM62), mRNA.			AGGACATCCACAGGGTAGAGGTTGGGTG TGTGTACGGGAGTGTCTGAGGC
0.659	385.1726	620.3059	408.06427	LEMD3	MAN1	NM_014319	Homo sapiens LEM domain containing 3 (LEMD3), mRNA.	CCACCATGCCCAGCCTGAATG ATGAATTTATGTGAACACAAAG CCCTCTG	ILMN_1702244	TACCTGAAACTGTTAAGCCGACCAAGATC CCTCCCTGCAAGACAGATGGG
0.658	5699.873	9450.889	6218.006	EMP1	CL-20; EMP-1; TMP	NM_001423	Homo sapiens epithelial membrane protein 1 (EMP1), mRNA.			GAGGGCAAGCCACCAAATTACCTAGGCT GAGGTTAGAGAGATTGGCCAGC
0.658	157.17679	179.18512	117.780945	SLMO1	FLJ31484; MGC120170; HFL-EDDG1; DKFZp547K106; C18orf43; PRELID3A	NM_006553	Homo sapiens slowmo homolog 1 (Drosophila) (SLMO1), mRNA.			GAGTACAGGAGTCTGGAGTCCGTTGAAG GGTAAAGGCCTCCCGCAAGCTG

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.652	1600.131	4684.081	3053.081	PSMD2	MGC14274; S2; TRAP2; P97	NM_002808	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 (PSMD2), mRNA.	AGTTCCACAGGCTCCCGTCCA GGGGGAGGACTACGGCAAAG GTGTCATCT	ILMN_1668408	CAGTGTTGTTGGCCCACGGGGAACGGGC AGAATTGGCCACTGAGGAGTTT
0.639	2722.081	2993.3228	1912.1226	RFTN1	PIG9; RAFTLIN; KIAA0084; MGC141678; PIB10; MGC44480; MIG2; FLJ23866	NM_015150	Homo sapiens raftlin, lipid raft linker 1 (RFTN1), mRNA.	CTTGTGTTGCAAGGGCAACCT CGTCCATTTTAACTGGCACCTC AGGGATT	ILMN_1702973	CTGGCGAACCTTGGAGAGGGAATGCTGA TTGTCTTGACCAAACCCACAGC
0.637	140.06429	235.46844	149.93512	STAM2	STAM2B; DKFZp564C047; STAM2A; Hbp	NM_005843	Homo sapiens signal transducing adaptor molecule (SH3 domain and ITAM motif) 2 (STAM2), mRNA.	TGCAAGTGCCGCTGTTCGACC CCGACATCACCTCCGACTACC ACAGCCCT	ILMN_1770014	GCATTTAGTCAGTCCCCCAAACAGTCATG CCAACTGTGAAGGAATGTCCC
0.636	595.9226	682.90594	434.20593	SYVN1	KIAA1810; MGC40372; HRD1	NM_032431	Homo sapiens synovial apoptosis inhibitor 1, synoviolin (SYVN1), transcript variant 1, mRNA.	CCCAGTGACGTGGAAGTCATC AGAACCCCACGGTACTTGGAG TACCTCTC	ILMN_1656165	GCCAGACTCCTGGTCTTTCCAGTTTAGAA AAGGCTCTGTGCCAAGGAGGG
0.635	47.66449	44.664005	28.369137	VPS16	hVPS16	NM_022575	Homo sapiens vacuolár protein sorting 16 homolog (S. cerevisiae) (VPS16), transcript variant 1, mRNA.			TGTGTCAGGACCTGCGTGTGCTCAATGCT GTTCGGGACTATCACATCGGG
0.63	67.84902	113.868454	71.69055	CREB3	LZIP; LUMAN; MGC19782; MGC15333	NM_006368	Homo sapiens cAMP responsive element binding protein 3 (CREB3), mRNA.	GAAGCGAAATCGGGCTTCCAC GGCAGCATCTTCAGCTCTTGG GTTTAGCA	ILMN_1653515	ACTCAGGCTAGATATGAGGATATGTGGG GGGTCTCAGCAGGAGCCTGGGG
0.629	55.752842	99.86012	62.83265	HIC2	KIAA1020; ZBTB30; HRG22	NM_015094	Homo sapiens hypermethylated in cancer 2 (HIC2), mRNA.			CTCCTGTACTGGCCACCGCCGCTGTCAC TTGTCACATTGAGTTCATGTCC
0.628	3682.1392	3171.6309	1994.5142	SH3PXD2A	SH3MD1; FISH	NM_014631	Homo sapiens SH3 and PX domains 2A (SH3PXD2A), mRNA.	CTTGCTTCAGTTGAGACCTACG TTTTGGCCAGTCCCAGCAGGA AGATATC	ILMN_1685810	CCCTTGGCCTGCCACTTTCCAGGTGTCCT TTATCACTTTGACGGGACTCT
0.627	327.18512	752.1476	472.37262	HDGFRP3	HDGF2; CGI-142	NM_016073	Homo sapiens hepatoma-derived growth factor, related protein 3 (HDGFRP3), mRNA.	AGGCAAACACAACTCTTGACTG CCCTCCCACCCTCCTACCTGTT CAGTAC	ILMN_1764617	TAAAGCTGGAATCAGCAACAGCCCTATGG GAAACCAGACAAAGCATTGAC
0.626	458.9893	595.7726	373.19763	PURA	PURALPHA; PUR-ALPHA; PUR1	NM_005859	Homo sapiens purine-rich element binding protein A (PURA), mRNA.	GACCACAAAGTTGAAGAATTCA TCAAGTCTATATTTTATTCTGTT CTTAT	ILMN_1669745	CGTGCAGCAATTTCCAGTGAACCTGTACT TGGACATCAGGTAGTGAGTCT
0.624	5217.8145	575.00183	359.09763	PAPPA	DIPLA1; IGFBP-4ase; ASBABP2; PAPPA1; PAPA; PAPP-A	NM_002581	Homo sapiens pregnancy-associated plasma protein A, pappalysin 1 (PAPPA), mRNA.	GGCTGCCAGACAACCAGCCCC CGCCATACATTCTGCACCAACA ATTAAGC	ILMN_1810805	CACAATTCCAATCCTTTTTCTGTACCTCAC GCGCATAAATTTGCTGCTCC
0.623	517.7101	161.73096	100.88095	OPN3	ECPN	NM_014322	Homo sapiens opsin 3 (OPN3), mRNA.			CACCTTCCTGGTCTGTTGGATGCCTTATA TCGTGATCTGCTTCTTGGTGG
0.623	218.58928	276.49762	172.20595	ATAD1	AFDC1; FNP001; FLJ14600	NM_032810	Homo sapiens ATPase family, AAA domain containing 1 (ATAD1), mRNA.	ATGACACTCCTGTGCTTTCTGG GGCTTCTGGCCTCCTATGCAG TCATTCT	ILMN_1706649	CCAGAATTCTGTTATAGGCACCTAACCAC GCAGCATGAGGAAAACGGCAC
0.622	370.6518	554.381	345.40594	TTC31	FLJ33201; FLJ12788; MGC120200	NM_022492	Homo sapiens tetratricopeptide repeat domain 31 (TTC31), mRNA.	GAGGCAGCATCCCGCGGCGC TGACGGTCCTGGGGAGAGCAT GGCGCCGAG	ILMN_1701937	GCTGCCCTGTGGGTCTTGCTCAATACTGT TCATACCTGGAGAGAGAAGGT
0.619	417.33093	399.78094	247.31429	ZNF217	ZABC1	NM_006526	Homo sapiens zinc finger protein 217 (ZNF217), mRNA.			GCTCCTGTGTTACAAGGGAGAACTCATTT GAGATCAGTCTGTTGGCATTG
0.615	179.26428	508.6643	312.66013	PGM2	MSTP006; FLJ10983	NM_018290	Homo sapiens phosphoglucomutase 2 (PGM2), mRNA.	AGAGTCCTGGGGAGCTTCTGT CCACCTGTCCTGCAGAGGAGT CGTTTCCA	ILMN_1661589	GGTCTTACAGCCTTCCAAAATAACTCCAG TTGGGCACCCATGAGCTAGGA

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.614	358.1476	105.91428	65.0433	PCMTD1	FLJ10883	NM_052937	Homo sapiens protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 (PCMTD1), mRNA.	TCCTGATCTCACTGTACACTCC CTTTCCTGGTCTGCTAAGTAGC GGGTGT	ILMN_1726678	TCTAGCATCAGATCAATCCCAAGAATCCA TCAGCAACCTCAGACCAACCC
0.613	228.27261	159.38095	97.768456	FCHSD2	NWK; KIAA0769; SH3MD3	NM_014824	Homo sapiens FCH and double SH3 domains 2 (FCHSD2), mRNA.			AGTGCACAGGTCAGGGCTCGGAGGGAGC CTCTGTGCAGATGTGCTTTCTT
0.613	1715.0059	1300.5642	797.33093	EHBP1	KIAA0903; NACSIN	NM_015252	Homo sapiens EH domain binding protein 1 (EHBP1), mRNA.	ACCACTGAGACCCCAAACCAC CTATCCCCAGTAGATGGCCCT GCCAAGAC	ILMN_1732750	GCCAGAAACAAGCCCTGTGGTTTGAAGGT GAGCTGTGAGGATGGGACTAA
0.609	10410.956	9080.456	5526.0977	LAMC1	LAMB2; MGC87297	NM_002293	Homo sapiens laminin, gamma 1 (formerly LAMB2) (LAMC1), mRNA.	GTGTCATCCTCACTCGGGACG CAGGGACCGTTTTTAAATCACA GGGGCGT	ILMN_1732439	TATGTGCCTTCACTTTAGCTGTTTGCCTTA CTCTACAGCCTTGCTCTCCG
0.607	387.2268	595.7018	361.56427	CAMSAP1L1	MGC150680; KIAA1078; RP11-93N17.1; MGC150681	NM_203459	Homo sapiens calmodulin regulated spectrin-associated protein 1-like 1 (CAMSAP1L1), mRNA.	CTGAGGGGCTGCTCTATGCTG TGTATGCGCCTCTCTGGCATC CGAGACAT	ILMN_1754842	GGTTTCATGGACACTGTTGAGCAATGTAC AGTGTATGGTGTGCTTACCTG
0.605	79.272835	77.33156	46.74492	OR6B1	OR7-9; OR7-3	NM_001005281	Homo sapiens olfactory receptor, family 6, subfamily B, member 1 (OR6B1), mRNA.	GCGGAAGAGGAAGAGCCACC GCCTGTTAAAATAGCCTGGAAA ACTGCGGC	ILMN_1666715	GGCCATTGGCTTTGGCATCTCCCTGGCG AAGATCTACTTCATCTCCTGCC
0.605	1208.2643	1511.2227	913.36426	ACVR1	ALK2; SKR1; FOP; ACTRI; ACVRLK2	NM_001105	Homo sapiens activin A receptor, type I (ACVR1), mRNA.	ATGAAGTACCGAGAGGCTAAA CCCACTGGCCTAAGATCTCAC CAAAGTTC	ILMN_1716790	TTCAGTTCATATGCAGAACGTATTTAGCC ATTACCCACGTGACACCACCG
0.605	1114.5809	1404.7976	849.09766	BCAT1	MECA39; ECA39; PNAS-121; DKFZp686E12175; BCT1	NM_005504	Homo sapiens branched chain aminotransferase 1, cytosolic (BCAT1), mRNA.			GGAGCTGGGGCTCAACCCACTGTTTTTAA GGATTTGCGCTTACTTGTGGC
0.604	77.23142	211.53513	127.91428	C10ORF88	FLJ13490	NM_024942	Homo sapiens chromosome 10 open reading frame 88 (C10orf88), mRNA.	CCTCGAGGACTCTCTGCGTCT CTGGAGACAAGGGCACTACAC GCACTTCA	ILMN_1676689	GAGGCTCTCCATGGAAGGATGAACACATA TGAGTCAAGGGATTGCAATTC
0.602	54.445297	118.55178	71.39479	USP37	KIAA1594; MGC117261	NM_020935	Homo sapiens ubiquitin specific peptidase 37 (USP37), mRNA.			CCTACACTTTGCCTAATTGAGCCACTACC AGGTTTTCTGGCAGCTGTGGC
0.602	527.80597	940.3143	565.34766	GOLPH4	P138; GIMPC; GPP130	NM_014498	Homo sapiens golgi phosphoprotein 4 (GOLPH4), mRNA.	GCTCTGAGACGAATGCTATGG GCTGCAGATGACTTCTTAGAG GATTTGCC	ILMN_1760062	AAACTAATGAGTGTTTGCGTGTGGTGTTT CTATGCGAGCACCCATTCTCA
0.596	447.55597	575.3601	343.01428	KIFAP3	SMAP; Smg-GDS; KAP3; dJ190I16.1; FLJ22818	NM_014970	Homo sapiens kinesin-associated protein 3 (KIFAP3), mRNA.	CCCTGCTGGTGGCTCTGTCCT CTGTTAGGCACCACACTGGTT GGTCAACT	ILMN_1764431	GTTGTTAGCTGCAGATTAACCCCAGCCCC TCTGTCTTCTGTTAAGTACAG
0.594	658.8059	554.6018	329.39343	PHLDB1	FLJ90266; DKFZp686O24210; LL5A; DKFZp686H039; FLJ00141; KIAA0638; MGC111531	NM_015157	Homo sapiens pleckstrin homology-like domain, family B, member 1 (PHLDB1), mRNA.	TGTAGGGCGGGGTGGTGGGC CAAAGTTAGGACACTGCGTAAA ACAGGCCA	ILMN_1723168	ACTAAGCCCACCTCCCCTGCTCTCCTTCC CAGCATTGAGCCCTTGGTTGC
0.593	4523.5894	5314.9727	3154.231	NCOR2	TNRC14; SMRT; TRAC1; SMRTE; TRAC-1; SMRTE-tau; CTG26	NM_006312	Homo sapiens nuclear receptor co-repressor 2 (NCOR2), transcript variant 1, mRNA.	GATGGGGTACTGCCGGTCTGT GTTGTCTTAGAAGTAGATGTGT GATGGCC	ILMN_1652754	CTGCTGCTGTGCTTTTGATCTCTGCTTAC CGTTCAAGAGGCGTGTGCAGG
0.592	2336.0227	249.08511	147.3393	KLF9	BTEB; BTEB1	NM_001206	Homo sapiens Kruppel-like factor 9 (KLF9), mRNA.			GCCCTTCACCATTGTGGAATGATGCCCTG GCTTTAAGGTTTAGCTCCACA

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.59	254.89346	490.5476	289.43927	IKIP	FLJ31051	NM_153687	Homo sapiens IKK interacting protein (IKIP), transcript variant 1, mRNA.			CTGGAGTTAGGAGGGCCTGTGGTAGACA GCGTGAATCATGAAAATAAGCC
0.585	13.217771	103.41846	60.386013	FANCB	FAAP95; FA2; FACB; FAB; FAAP90	NM_152633	Homo sapiens Fanconi anemia, complementation group B (FANCB), transcript variant 2, mRNA.	GCTTCCAGAATTTATAACACAT GAGCCCCCAAAAAGCCGGGAC TGGCAGC	ILMN_1733538	TGCAGAGGTGTGAAGTGAGCAAAGGAAA GAGTAGTGTCGTCGCGGCTGCT
0.584	96.97266	133.5893	78.12309	SENP7	KIAA1707; MGC157730	NM_001077203	Homo sapiens SUMO1/sentrin specific peptidase 7 (SENP7), transcript variant 2, mRNA.			TCGGGGTCAGTTAAGCCTCAGTATTCTTA GCTTTTGTTGATTTTGGCACT
0.582	156.11429	167.43927	97.37263	PHF2	MGC176680; KIAA0662; GRC5; JHDM1E	NM_005392	Homo sapiens PHD finger protein 2 (PHF2), mRNA.			CCATTACCTGGATGTTTTTGTCCACTGGG AGAGGCAGCTTGGTGGAGGCC
0.575	647.7893	564.03094	324.13928	ABL1	JTK7; ABL; p150; bcr/abl; v-abl; c-ABL	NM_005157	Homo sapiens c-abl oncogene 1, receptor tyrosine kinase (ABL1), transcript variant a, mRNA.	ACAGGCGTCCCATGTGAAGCC TGCCCAAGTAACTGTGAAGAC AAACTTTG	ILMN_1758212	CCTGTGGTGGCTCCCCCTCTGCTTCTCG GGGTCCAGTGCATTTTGTTTCT
0.573	96.330956	88.185196	50.41118	ZNF502	FLJ14855; FLJ12515	NM_033210	Homo sapiens zinc finger protein 502 (ZNF502), mRNA.			CCTAGGCTGTTGGTGTACAGAGACCAGA GGAGAGAGACACACTAGGACTA
0.572	864.3726	5135.048	2933.181	HS3ST3A1	3OST3A1; 30ST3A1	NM_006042	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 (HS3ST3A1), mRNA.	GGCCGCCATTGAAGCCACAGG CGCAGTGATCCATTTTGGCAA CGGGAAGT	ILMN_1806647	TGTTCTCACTCCCGCCCCATCTTAATGTA TAACCAACACCAAACACGTGG
0.571	3939.9976	4581.7393	2615.4644	KLF6	GBF; ZF9; ST12; CPBP; BCD1; COPEB; PAC1; DKFZp686N0199	NM_001300	Homo sapiens Kruppel-like factor 6 (KLF6), transcript variant 2, mRNA.			CCCTTCCGAGCGGCGCCTAAGCCTTTGC CGTGAGCATGCACACTGAGAAT
0.568	49.61931	68.60441	38.91951	ANKRD36B	MGC149865; MGC167812; FLJ21281; FLJ90089; MGC149864	NM_025190	Homo sapiens ankyrin repeat domain 36B (ANKRD36B), mRNA.			AAAGGACTGCCCTACATTTGGCCTGTGCC ACTGGCCAACCGGAAATGGTA
0.563	183.46011	220.59761	124.34762	SLC7A6	DKFZp686K15246; KIAA0245; LAT3; LAT-2; y+LAT-2	NM_001076785	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (SLC7A6), transcript variant 2, mRNA.			ACACCAAGGCAGTCAGTTAAGGCAGCTAT GGTTTGGAAAGGCATACGGAC
0.563	5805.014	8462.248	4761.381	TAGLN2	KIAA0120; HA1756	NM_003564	Homo sapiens transgelin 2 (TAGLN2), mRNA.			TGTGTCCTCCGTTCATTCCATGGCTGGGA GTCACTGATGCTGCCTCTGCC
0.563	1405.5642	1805.8976	1016.73096	NCOR2	TNRC14; SMRTE-tau; SMRT; TRAC1; CTG26; SMRTE; TRAC-1	NM_001077261	Homo sapiens nuclear receptor co-repressor 2 (NCOR2), transcript variant 2, mRNA.			CGTTGCCGCAGCGGTGGGAAGGAAAGGC AGATGTAAATGATGTGTTGGTT
0.559	127.95595	73.58258	41.085552	OSMR	OSMRB; MGC75127; MGC150626; MGC150627	NM_003999	Homo sapiens oncostatin M receptor (OSMR), mRNA.			GCAGGATCATGGGAGCATGCTTACCTTCT GCTGTTTGTTCCAGGCTCACC
0.559	562.3059	345.30597	193.00595	MFSD11	FLJ22196; ET; FLJ20226	NM_024311	Homo sapiens major facilitator superfamily domain containing 11 (MFSD11), mRNA.			GCAGAGATGTGTTGGGTTTGGTGGTGCA TGCCTGTGATCCTAGCTGCTGG
0.559	86.278076	63.202793	35.33599	HEXA	TSD; MGC99608	NM_000520	Homo sapiens hexosaminidase A (alpha polypeptide) (HEXA), mRNA.			AGGCTGGAGTCAGTGTCTGCCCCTGAGG TCTTTTAAGTTGAGGGCTGGGA

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.555	75.219696	97.31845	54.024055	TRAF6	MGC:3310; RNF85	NM_145803	Homo sapiens TNF receptor-associated factor 6 (TRAF6), transcript variant 1, mRNA.			CCGCCTTGTGCTAGTGCCCTCGAGAAGA GTTATTGCTCTAGAAAGTTGAG
0.549	57.270725	84.69768	46.47178	ITPR2	IP3R2	NM_002223	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA.	GCCCATTATAGCCTCTGAATTG TCCCTTCCTTGAGTTTGCTAAT GCTTCC	ILMN_1732815	AGCTACTGGTACTCCCCAGCACCACCTCA TACTAAGAATTCCTCACTCTG
0.547	2167.9226	1081.0642	591.46844	SLC7A5	MPE16; CD98; 4F2LC; hLAT1; D16S469E; LAT1; E16	NM_003486	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA.	CTAAGTACGATGTTCAAGTGAG AGCAGCAGTGAGCTCCATGTG CAGAGAG	ILMN_1756455	AGGCTGGACACCCTCTGCCGAGTAATGA CGTGTGTGGCTGGGACCTTCTT
0.546	288.8393	392.26428	214.23096	SNAP23	SNAP23A; SNAP23B; HsT17016	NM_003825	Homo sapiens synaptosomal-associated protein, 23kDa (SNAP23), transcript variant 1, mRNA.	AGGCGGCGAGGCCACCACAC CTGCAGAGCGCTCGGGCTGCC TAGCCGGCA	ILMN_1700037	GCATCTGAACACTTCAAAGCTGTCAGTGT GTATTGGTTTCACCAATAACC
0.545	86.697655	79.68948	43.48703	FAM113B	MGC16044	NM_138371	Homo sapiens family with sequence similarity 113, member B (FAM113B), mRNA.	TGGGAGGATCGCCTGAGCCCA GGGAGGTCAAGGCTGCAGTGA GCAATGAT	ILMN_1713706	ACTTCCTGGGAGTGACCCAGCGTTATTCC TGCCTCCTCACTCCTATTCTC
0.543	299.32263	583.8893	316.55176	ATP1B1	MGC1798; ATP1B	NM_001677	Homo sapiens ATPase, Na+/K+ transporting, beta 1 polypeptide (ATP1B1), transcript variant 1, mRNA.	CTCCCCACCCATTCCTTTAAAT CCGGAGGGGGAAAAAATCCCA AGGTCTG	ILMN_1667831	GCTGTGTCTGAGATCTGGATCTGCCCATC ACTTTGGCTAGTGACAGGGCT
0.543	740.11426	555.86426	301.65594	NCOA3	CAGH16; TNRC14; pCIP; ACTR; AIB-1; CTG26; MGC141848; TRAM-1; TNRC16; AIB1; SRC3; SRC-1; RAC3	NM_181659	Homo sapiens nuclear receptor coactivator 3 (NCOA3), transcript variant 1, mRNA.			CCACATGAAATGACTTATGGGGGATGGTG AGCTGTGACTGCTTTGCTGAC
0.541	49.395973	125.39345	67.78848	ZDHHC2	ZNF372	NM_016353	Homo sapiens zinc finger, DHHC-type containing 2 (ZDHHC2), mRNA.	TGTCAGGACGCGGAAAGCAGG GAGGCAAGGCCCGCGCTAAG GCCAAGTCG	ILMN_1747589	GGACAGGATTCGATTAAGTATTCCCTCTT GTCAAACTGGAAGCTAGGGGA
0.541	1108.7643	3148.3809	1700.0894	ANTXR2	FLJ31074; MGC111533; CMG-2; MGC45856; JHF; CMG2; ISH	NM_058172	Homo sapiens anthrax toxin receptor 2 (ANTXR2), mRNA.	GGATGTGATCCCCTGGATTCC CAAAGCCCAGAAGGAGATTTG CAAGATGC	ILMN_1744701	TGGCGGGCATGTGAGTGCACAAGATGGA AAGAGCGATTGGAGCATCCTGG
0.54	556.88513	423.59344	228.94762	CEBPG	GPE1BP; IG/EBP-1	NM_001806	Homo sapiens CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG), mRNA.			CGTTTCCCAGTCCCCATTAGAGGGCTTGA GACCTTGTACCTGAACAACCC
0.538	1469.9976	1749.1726	940.7143	SNAI2	WS2D; SLUG; SLUGH1; MGC10182	NM_003068	Homo sapiens snail homolog 2 (Drosophila) (SNAI2), mRNA.	GGCCACCATCACAATACTAAG GGGCTCAGATGTGTCTTGTGC CCACCTCT	ILMN_1804445	AGGATTTCCCATAGGAAGAGATCTGCCAG ACGCGAACTCAGGTGCCTTAA
0.536	1517.7976	976.5768	524.19763	ITGAV	CD51; DKFZp686A08142; VNRA; MSK8	NM_002210	Homo sapiens integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) (ITGAV), mRNA.	GGCTGAGATGGTGGACTTCTT CTTGGCCCTCATGGTCATTGC TATTCCTC	ILMN_1683046	AGTCGTTCTTGGAATACCTATGTGCAGCC ACTACCCATCTCAATGTCACC
0.533	107.52678	221.86845	117.89761	KLHL2	ABP-KELCH; MAV; MAYVEN	NM_007246	Homo sapiens kelch-like 2, Mayven (Drosophila) (KLHL2), mRNA.	GTGAGTACTCCACAGTTTACTG GGGGAAAAGGCTTCAGTAAAG CAGAGGC	ILMN_1813100	CCACTTCTGAGGAATGGACCTGGTGTAAC ACACTTGAATATGTGTGATGC
0.532	271.66846	278.70596	148.08095	MEF2D	DKFZp686I1536	NM_005920	Homo sapiens myocyte enhancer factor 2D (MEF2D), mRNA.			TCTTCCTGGGTCCTGGGGCAGGGCGAGT CCAAGTGTGAGGCTGTTGATTT

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.528	789.5018	2990.6978	1580.9976	TMEM200A	TTMC	NM_052913	Homo sapiens transmembrane protein 200A (TMEM200A), mRNA.			TGCCTTGAAGTTTACCTTGTGCTGGAGAG CCTTATGATAACTCCAAAGAC
0.527	2872.831	2411.5227	1270.7393	ANTXR1	ATR; FLJ21776; FLJ11298; TEM8; FLJ10601	NM_032208	Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 1, mRNA.	CCCAGAAGAACCTCAGGAGGT AACCTTGGGCCCTTCCCTGCT ATCCTTTT	ILMN_1796210	ACCATGCTATAGGAGACTGGGCAAAACCT GTACAATGACAACCCTGGAAG
0.523	125.51012	128.36845	66.95981	PNPLA8	IPLA2G; IPLA2(GAMMA); IPLA2-2	NM_015723	Homo sapiens patatin-like phospholipase domain containing 8 (PNPLA8), mRNA.	CACGGCCATTAAAGCTTCCCA CAGACACTGGTCGCTGGGCCT GTGCCAGC	ILMN_1722906	GGTGAAGTTCCAGTCAACCACTTTTTACC CCTGAAATTTCAAGATAATGC
0.522	104.37263	345.06845	180.2351	SLC31A2	hCTR2; CTR2; COPT2	NM_001860	Homo sapiens solute carrier family 31 (copper transporters), member 2 (SLC31A2), mRNA.	GCAGCTGTTGGGATGTGTACA TCGTGAAGCCCACCTGGTGGC CGTGGTTA	ILMN_1692169	TCTTCGTGGCCTCAATGCCCTCCTTTATC CTCATCTTTCTTCTATGCAGA
0.522	65.67034	61.468407	32.002617	LOC401357		NM_001013685	Homo sapiens hypothetical LOC401357 (LOC401357), mRNA.			CTCGGAATCACAGCAGACTCTCCACGCC CAGCTAGCTCTCGCCTCACTGT
0.518	128.05595	329.7768	170.9226	KCNJ8	uKATP-1; KIR6.1	NM_004982	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 8 (KCNJ8), mRNA.	GAGGATGCTACCAGTTTCGGT AGAGTATGATTGCCTCGTTCAA TGTGGCG	ILMN_1682987	GTCGGTGACTCCTGAAGGTTTCCTGGTCC ATCTCATTGCGGCCTGTTGGG
0.512	352.8643	405.3643	206.88512	ARHGAP24	FILGAP; p73RhoGAP; FLJ33877; RC-GAP72; DKFZP564B1162; p73; RCGAP72	NM_031305	Homo sapiens Rho GTPase activating protein 24 (ARHGAP24), transcript variant 2, mRNA.	GGTGATGCCTCGCGTACAGGA TCTGGTTACCTGTGCAGTTGT GAATACCC	ILMN_1703006	GGATTCAGTGAGCCTGCTTTCGCCTGCTG TCTCTGATGGCTCTGGCAAGG
0.506	84.17299	973.19763	493.2893	Mar-03		XM_001127871	PREDICTED: Homo sapiens membrane-associated ring finger (C3HC4) 3 (MARCH3), mRNA.	CCATTTAGTCCCCCATCAGAAC AGAGGTCAGGAATTTAGCTGG GGAGCCT	ILMN_1658815	GGTAGCCTGAGTGGTCTTTTTCATCTCTT TCGCGTCCATTACTCAAGGAG
0.497	7778.756	6459.706	3205.4893	FSTL1	FRP; FSL1	NM_007085	Homo sapiens follistatin-like 1 (FSTL1), mRNA.			ACTAGGTTTGGTTCCTTCAGCCCTCTAAA AGCATAGGGCTTAGCCTGCAG
0.494	12073.348	6545.2393	3242.4727	SPARC	ON	NM_003118	Homo sapiens secreted protein, acidic, cysteine-rich (osteonectin) (SPARC), mRNA.	AGGATTGTCCTGACTCACTAAA GATGCCAGGATATTGGGGCTG AGGGGAG	ILMN_1761580	CGCAGCTCCCCAATCACACTAGCAACATT TCAAGTGCTTGAGAGCCATGC
0.493	196.23096	418.7893	206.35178	CDH13	CDHH	NM_001257	Homo sapiens cadherin 13, H-cadherin (heart) (CDH13), mRNA.	CAGTGGAGAACCAAGCCCCAT GGCCTCAGAATTTCCCCCCAG TTCCCCAA	ILMN_1700770	AGTGACAGCTTGTGGCTTTTTATTAGAGC TCGCCACGAACTAGGGTAAGG
0.492	399.27264	483.23096	237.52261	KLF13	NSLP1; FKLF2; RFLAT-1; BTEB3; RFLAT1	NM_015995	Homo sapiens Kruppel-like factor 13 (KLF13), mRNA.			TTGCTTGTGTGCATGTGTTGGGTGCATGC TTCCGGGTCTCAGCTGCCCCA
0.49	58.259773	170.37262	83.435196	SENP5	MGC27076; FLJ42398	NM_152699	Homo sapiens SUMO1/sentrin specific peptidase 5 (SENP5), mRNA.	GGAGGGCTGGAATCTGTCTTC CCTGACTCGGCTCCTCAGGTC TTTAGCCT	ILMN_1711786	ACATGCCCCGAGTGCGGAAGAGGATTTA CAAGGAGCTATGTGAGTGCCGG
0.488	657.4393	535.54346	261.70596	TMEM16F	MGC104751	NM_001025356	Homo sapiens transmembrane protein 16F (TMEM16F), mRNA.			CCCTGGGGAAATTGATGGGTGTGGCAGT GGACCTGTGAAGAGGGAGAATC
0.488	8510.98	3759.8142	1838.2726	COL5A2	MGC105115	NM_000393	Homo sapiens collagen, type V, alpha 2 (COL5A2), mRNA.	GTTGACATCCAAATCTAGCCAG AGCCCTTCACTGCCATGATAG CTGGGGC	ILMN_1694240	GAGCATCGTTCCAATGCTTGTTCACTGTT CCTCTGTCATACTGTATCTGG
0.473	427.94763	782.4435	369.5226	GOLT1B	GOT1; YMR292W; CGI-141	NM_016072	Homo sapiens golgi transport 1 homolog B (S. cerevisiae) (GOLT1B), mRNA.			GGGTTTGATAATCTCCCAGTCCTTAGTAA AGATTGAGAGAGGCTGGAGCA

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.47	143.93094	23.748478	11.128967	ATHL1	MGC129858; FLJ22635; MGC129859	NM_025092	Homo sapiens ATH1, acid trehalase-like 1 (yeast) (ATHL1), mRNA.	AAAGCCGGTGCAGGCTCTGCT GTCATCGTCAGGACTCCTTGT GGGCTGTG	ILMN_1760049	AATCCCAGGCTCCTCTTGACTCTGGGCAG CTTTAATCAGGTTGGGCAGCC
0.467	1096.481	2733.0562	1277.4559	RASA1	p120RASGAP; CMAVM; RASGAP; DKFZp434N071; CM-AVM; RASA; PKWS; GAP; p120GAP	NM_002890	Homo sapiens RAS p21 protein activator (GTPase activating protein) 1 (RASA1), transcript variant 1, mRNA.			GTGCTACCCCTTTGATTATGCAGACAACC TCATCAGCTGCCTAACTTATC
0.467	678.9976	2688.1726	1252.8643	UCK2	UK; TSA903; UMPK	NM_012474	Homo sapiens uridine-cytidine kinase 2 (UCK2), mRNA.	CTACCCTCATTAACAATTAGCA GGGCACTGGCCAGAGTTTGTA CCCTGTG	ILMN_1703487	TCTCAACGGCTACACCCCTTCACGCAAGA GGCAGGCATCGGAGTCCAGCA
0.46	300.74347	567.7268	261.30597	TPST1		NM_003596	Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), mRNA.	GGCTGGAGCTGGGAGAGGTG CTGAGCTAACAGTGCCAACAA GTGCTCCTT	ILMN_1731064	GCTCTTGATCCCGATTTCATGCACAGCCC TGCAGTAAGGAGCCCAGAAGG
0.456	21859.988	19278.182	8799.223	TPM1	TPM1-alpha; TMSA; HTM-alpha; TPM1-kappa; C15orf13	NM_001018004	Homo sapiens tropomyosin 1 (alpha) (TPM1), transcript variant 3, mRNA.	TAAACACTCACCCCTGTCAGC GTGCGGCTGGGCTCTCAGGAT AAACTCAC	ILMN_1665932	GGAGGCTGAGACTCGGGCTGAGTTTGCG GAGAGGTCAGTAACTAAATTGG
0.456	8407.689	5262.2393	2398.7976	COL5A1		NM_000093	Homo sapiens collagen, type V, alpha 1 (COL5A1), mRNA.			GTTCCAAGGTAAGCCTCGTAAAGGTCATC CCACCATCACCAAAGCCTCCG
0.455	39.23884	67.41689	30.698576	TMEM16H	KIAA1623	NM_020959	Homo sapiens transmembrane protein 16H (TMEM16H), mRNA.	CAAAGAGAATTGTGGCAGATG TTGTGTGTGAACTGTTGTTTCT TTGCCAC	ILMN_1698220	GTCATTCACAGGGGCGGCCGGTCTCCAA AATGCAAAATGCGCTTCAGCCC
0.45	1565.9392	170.59344	76.72356	CDC42EP5	MGC21945; CEP5; Borg3; MGC71153	NM_145057	Homo sapiens CDC42 effector protein (Rho GTPase binding) 5 (CDC42EP5), mRNA.	GTCTTAAGGAGACTGGTAGGA GGAGGCATGGAAACCAAAAGG CCGTGTGT	ILMN_1705685	CTTCCCGCCCGGCACCCCACTTCTGTATA CATAAACGGCCAAGGTGTGTG
0.443	1914.5476	4450.2476	1975.1143	KLF2	LKLF	NM_016270	Homo sapiens Kruppel-like factor 2 (lung) (KLF2), mRNA.	CAGCGGGCTACCCTGGACAAA GTAAAGGTGGAAACTAGGTGA TGTGGCCT	ILMN_1794106	ATTACTGTACATAGAGAGACAGGTGGGCA TTTTTGGGCTACCTGGTTCGT
0.423	266.3018	292.6726	123.93095	PPP1R13L	NKIP1; IASPP; RAI; iASPP gene	NM_006663	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 13 like (PPP1R13L), mRNA.			CAGATCCCGTCCAAAGTGCCTCCCATGCC TACCACCATCATCACATCCCC
0.418	5296.923	5980.431	2503.456	PRRX1	PRX1; PMX1; PHOX1	NM_006902	Homo sapiens paired related homeobox 1 (PRRX1), transcript variant pmx-1a, mRNA.	GTCCAGTTTTGTGTGCTTTACT ACACAGTTTGGTTACAGGACTT CTGTGC	ILMN_1807735	GATGCCTTCTGGATCTTAAGCCAGTTGTC AGTGGAGGTCCTCAGGGCTGC
0.418	163.05595	161.33095	67.1759	BLZF1	JEM1; JEM-1; GOLGIN-45; MGC22497; JEM-1s	NM_003666	Homo sapiens basic leucine zipper nuclear factor 1 (JEM-1) (BLZF1), mRNA.	GCAGTGATCAGGGTCCTGCAA GCAGTGGGGAAGGGGGCCAA GGTATTGGA	ILMN_1812226	GGGTATGTTAGAAAAACAAAAAGGAGGCT GGGCATGGTGGCTCATGCCTC
0.417	1307.281	459.6601	191.45178	NNMT		NM_006169	Homo sapiens nicotinamide N-methyltransferase (NNMT), mRNA.	TACCCTTCATGAGACCCAACTC TGCCACAGCTCATCCTCGGAG GCAATCC	ILMN_1697975	CAAGGGTCCAGAGAAGGAGGAGAAGTTG AGACAGGCGGTCAAGCAGGTGC
0.41	14946.689	14201.84	5822.3057	TPM1	TPM1-alpha; TMSA; HTM-alpha; TPM1-kappa; C15orf13	NM_001018020	Homo sapiens tropomyosin 1 (alpha) (TPM1), transcript variant 7, mRNA.			AGAGATCAAGGTCCTTTCCGACAAGCTGA AGGAGGCTGAGACTCGGGCTG
0.41	77.18435	13.2048435	5.3930697	GATS	DKFZp686B07267	NM_178831	Homo sapiens opposite strand transcription unit to STAG3 (GATS), mRNA.	CGAGAAGCAGATGACAGGCTC AGGCCTTACCAGGGATGCACT TGCCACAT	ILMN_1725633	ACACCTTGTAAGTGTCCCCTCTGGTTTCC TCGGTGGTGGCGCCCTGAACT
0.409	50.64293	53.751915	21.96643	LINS1	FLJ10583; WINS1	NM_001040614	Homo sapiens lines homolog 1 (Drosophila) (LINS1), transcript variant 4, mRNA.			ACACCAGCAAGCAACTAAGGAGATTCAGG ATGCAGCTGGGACAAGCAGGG

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.4	46.980003	102.089294	40.62928	MBOAT2		XM_001129292	PREDICTED: Homo sapiens membrane bound O-acyltransferase domain containing 2 (MBOAT2), mRNA.	CAGCTCTGGAACAATTCCTGTC TGGAGGCCGAGCATGTGGGCA GAAACCT	ILMN_1726328	TGGCCACAGGAGCTGAAAGCAGAAGAGT GGGATTTGATGCCAGGCAGTGG
0.39	439.4643	247.0476	96.17679	ZSWIM4		NM_023072	Homo sapiens zinc finger, SWIM-type containing 4 (ZSWIM4), mRNA.	GCCCCAGATCCCGGGCTTGTG GGACACCTATGAAGATGACAT CTCGGAAA	ILMN_1763520	GAGACTGGGGTGCATCTCCAGAGCCACT CACACCCTCAACCTCGTTTCCT
0.387	199.11429	422.03928	163.39761	C16ORF30	FLJ20898; MGC111564; CLP24	NM_024600	Homo sapiens chromosome 16 open reading frame 30 (C16orf30), mRNA.			TCCAGCTTTCCTGGTTAGCGCAACGCGG CTCCACGACCACACGCACTTCA
0.385	96.677475	131.52261	50.67811	PTPRG	R-PTP-GAMMA; HPTPG; RPTPG; PTPG	NM_002841	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA.	CTATCTCAGTGCCTTCACACAG CCAGCCTGTCCCCGAGTCTCA CCAGTGA	ILMN_1767070	ACAGACTAGCAGGCTACTGGGACCTAAAA AGGTCTGTTAATGTCATGGCC
0.384	12.405609	163.94762	62.987476	C14ORF145	C14orf61	NM_152446	Homo sapiens chromosome 14 open reading frame 145 (C14orf145), mRNA.	AAGCACATTCCTGCCTCAGGG CCTTTGTACCTGTTGTTCCCTC CACCTGG	ILMN_1778382	AGTGTCTAAGAACGTATTCCCTTTACACG CTGATCTCCTAGTGGAGAAGG
0.383	111.435135	96.0518	36.861046	C11ORF75	FN5	NM_020179	Homo sapiens chromosome 11 open reading frame 75 (C11orf75), mRNA.	CATTCAAGAGCTGGCCCCCAA GTATGCAGCGACACACCCCAA AACAGAGC	ILMN_1687291	AGTAGCTCCACCTGAAGAGGGATGGAAC CTCTGGGTCAGGAAACAGCTGG
0.378	120.17262	189.76428	71.86996	ROBO1	FLJ21882; SAX3; MGC131599; DUTT1; MGC133277	NM_133631	Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), transcript variant 2, mRNA.			GTATCAGGTCTGACCCCAGTGGAAAACAA AGCCAAACAAAACTGAACCAC
0.376	125.00597	18.436693	6.951079	GFRA1	MGC23045; GDNFRA; RETL1; GFR-ALPHA-1; RET1L; GDNFR; TRNR1	NM_005264	Homo sapiens GDNF family receptor alpha 1 (GFRA1), transcript variant 1, mRNA.	GATCCTGTCCAGAGGCTTCAG GCATACACGGCCACCGAGCAG GAGATGCA	ILMN_1677542	GGGGCTTCTGTGAAAAACCTGATGCAGT GCTCCATCCAAACTCAGAAGGC
0.374	294.8351	416.32263	155.89761	MALT1	DKFZp434L132; MLT; MLT1	NM_006785	Homo sapiens mucosa associated lymphoid tissue lymphoma translocation gene 1 (MALT1), transcript variant 1, mRNA.	GTTTTGTGGGTCTGCCCTGAG CTGTGCCTGTGTGCTCCAGCC TCTTCCTA	ILMN_1717029	TCCCCTTAAGATTGGGAAGAAGGACAAGG ATGTTCACTCGGCACTACTTC
0.368	5080.606	8171.2974	3005.6309	FRMD6	c14_5320; MGC17921; C14orf31; Willin	NM_152330	Homo sapiens FERM domain containing 6 (FRMD6), mRNA.			TGTCTGTGCTGTCCCTCCTGTGCTGGGTC GCGGATGTGTAGGCAACATTG
0.365	275.20593	377.44345	138.62262	SPSB1	SSB1; SSB-1	NM_025106	Homo sapiens splA/ryanodine receptor domain and SOCS box containing 1 (SPSB1), mRNA.			GTACAGATCCCAGCTTATGGCCTTGACCC AGCCGTCCTCACAGATGCCGG
0.36	692.5226	492.33096	177.57678	NUAK1	KIAA0537; ARK5	NM_014840	Homo sapiens NUAK family, SNF1-like kinase, 1 (NUAK1), mRNA.	GACCCTGCTGCGTCTCCCTTC CAAACTCTGGTGCTGAATAAAC CCTTCTG	ILMN_1789627	GGTTTGAGCCCAGAACAGCCTACAGGGG AAAAACAAGCTGGATAACCACC
0.343	313.78513	82.71024	28.358551	VLDLR	FLJ35024; VLDLRCH	NM_001018056	Homo sapiens very low density lipoprotein receptor (VLDLR), transcript variant 2, mRNA.			GAGGTCTAAACAAATAATACCCCCGTCGG AATGGTAACCGAGCCAGCAGC
0.335	146.63095	276.85178	93.27275	EML1	ELP79; EMAPL; EMAP; HuEMAP; FLJ45033	NM_004434	Homo sapiens echinoderm microtubule associated protein like 1 (EML1), transcript variant 2, mRNA.			GCAGGGTACACAGGCGTTTCCAAGTTTCA GTGACACCGTCCTGCCTAACC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.335	288.49344	687.0476	230.47678	TSHZ3	ZNF537; TSH3; KIAA1474	NM_020856	Homo sapiens teashirt zinc finger homeobox 3 (TSHZ3), mRNA.	CAGCAGAGAGGCCTGTGACAT GGGGCCCTGTACTACTGCCTG GTTCCACA	ILMN_1687035	GACACCGTAACACACTCTGTGCCCTGTTT GGTTGTTGACAATGAAGCACC
0.333	2074.331	2805.5225	931.61426	FRMD6	EX1; c14_5320; MGC17921; C14orf31; Willin	NM_152330	Homo sapiens FERM domain containing 6 (FRMD6), transcript variant 2, mRNA.	GATGGGTCTCCGGTGTCTTTT GCAGCTCACATTGCAGGTGGA TTTGCTGG	ILMN_1685330	AGATGTAGGGTACAGTGGAACATAAGCAG TGTTACCCCTGGCTGGGAGTC
0.331	3653.4644	3020.6392	999.3476	VCAN	DKFZp686K06110; WGN; VERSICAN; PG-M; WGN1; ERVR; CSPG2	NM_004385	Homo sapiens versican (VCAN), mRNA.			CAGCCATAGGTGCAGTTTGCTTCTACATG ATGCTAAAGGCTGCGAATGGG
0.324	588.23096	2998.931	978.32263	HMOX1	HO-1; bK286B10	NM_002133	Homo sapiens heme oxygenase (decycling) 1 (HMOX1), mRNA.			TCAAGTATCCTTGTTGACACGGCCATGAC CACTTTCCCCGTGGGCCATGG
0.312	80.300934	1275.0977	396.09344	FHOD3	Formactin2; FHOS2	NM_025135	Homo sapiens formin homology 2 domain containing 3 (FHOD3), mRNA.	GCACACAGAGCAGGATGCCAT GCTGGTGGACATTGAAGACTT GACCAGAC	ILMN_1794598	GTCACCCCATGGCTTGTGTTGCCTGCTAC GCATTGACTTGGATCTCCAGG
0.304	16.175488	227.96428	69.20842	KBTBD8	TA-KRP; KIAA1842	NM_032505	Homo sapiens kelch repeat and BTB (POZ) domain containing 8 (KBTBD8), mRNA.			TCAATGTTCAGTGCTCAGGTATGTAGTAA GTACTGTAGTCCTGTGGGGGC
0.29	114.12262	103.535126	30.38353	TMEM117	DKFZp434K2435	NM_032256	Homo sapiens transmembrane protein 117 (TMEM117), mRNA.	TTTTCCATCCCAACATTGATGA AGCGTCAGGAACTGTGTGTCT AGATGTA	ILMN_1674633	GCCAACCCTGAGCAAGGGAACTCCTCAAA AAATCATGCAGCGGAACCTTG
0.282	2964.6643	4441.956	1267.0642	GREM1	MGC126660; GREMLIN; PIG2; DAND2; IHG-2; DRM; CKTSF1B1	NM_013372	Homo sapiens gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis) (GREM1), mRNA.	CCTAGCAAGGGCAAGATGAGG CAACTGGAACAGGCCTTGTCA GCCAGAAC	ILMN_1697649	CGGCAAAGAATTATATAGACTATGAGGTA CCTTGCTGTGTAGGAGGATGA
0.28	553.09766	385.24344	106.922615	TSC22D3	hDIP; DIP; DKFZp313A1123; DSIPI; TSC-22R; GILZ	NM_198057	Homo sapiens TSC22 domain family, member 3 (TSC22D3), transcript variant 1, mRNA.			GAAGGATGGTGTCCTACTGTGGATGAGG GATGAACAAGGGGATGGCTTTG
0.279	3438.5476	11067.447	3093.3477	ADAM19	MADDAM; MLTNB; FKSG34	NM_033274	Homo sapiens ADAM metallopeptidase domain 19 (meltrin beta) (ADAM19), transcript variant 2, mRNA.	GGGCGTTGTGTGTGTCGTGAC TTCGTACCTCTCAAGCCCCTCC TTGTACT	ILMN_1679754	TCCAAGCCCACATTTCCAAAGTCACCCCC AACGCGTCCTCTCACACCGTC
0.278	3072.2893	8732.48	2444.731	IER3	IEX-1L; PRG1; IEX1; GLY96; DIF-2; IEX-1; DIF2	NM_003897	Homo sapiens immediate early response 3 (IER3), mRNA.	AGCAGGATGCAGAGTGCTGTT CAAGTTTTCCAGTGGGGTCCC TCAAAGGG	ILMN_1758209	GAGGACGTCCCGGCTGGGATGAAGTCTG GTGGTGGGTCGTAAGTTTAGGA
0.266	168.97678	197.30594	52.520416	ZNF669	FLJ12606	NM_024804	Homo sapiens zinc finger protein 669 (ZNF669), mRNA.			GGCCAAGGCGTGTGGATTGCTTGAGCCC AGGAGTTCATAACCAGCCTGGA
0.26	24477.805	29918.871	7780.639	CTGF	CCN2; MGC102839; IGFBP8; NOV2; HCS24	NM_001901	Homo sapiens connective tissue growth factor (CTGF), mRNA.	TATGCGCCATTTCTGCATTCAC TCTCCCCATCGAAACCAAAGG ACGGGCC	ILMN_1754555	TTGCAAAGGGGAGGCATCAGTGTCCTTG GCAGGCTGATTTCTAGGTAGGA
0.258	4.774254	416.75177	107.33095	IL13RA2	IL-13R; CD213A2; IL13BP	NM_000640	Homo sapiens interleukin 13 receptor, alpha 2 (IL13RA2), mRNA.	GCTCCTAAACCATTGAGCTAG CGATTTCAGACCTAGCAGGGA AGGTGAAG	ILMN_1801262	GTAACCGGTCTGCTTTTGCGTAAGCCAAA CACCTACCCAAAAATGATTCC
0.254	677.83093	244.19762	62.357666	FBXO32	ATROGIN1; MAFbx; Fbx32; MGC33610; FLJ32424	NM_058229	Homo sapiens F-box protein 32 (FBXO32), transcript variant 1, mRNA.	TTGCTCTGTCACCCAGGCTGA AGTGCAGTGGCACAGTCAGGG CCCATTGC	ILMN_1791523	GCTTCCTGGATGAGAAGAGCGGCAGTTT CGTGAGCGACCTCAGCAGTTAC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
0.241	95.83521	112.58095	27.310715	MEX3B	RNF195; DKFZp434J0617; RKHD3; MGC117199; MEX-3B	NM_032246	Homo sapiens mex-3 homolog B (C. elegans) (MEX3B), mRNA.	GTCGGTGACTCCTGAAGGTTT CCTGGTCCATCTCATTGCGGC CTGTTGGG	ILMN_1735779	GAATGTTCGTGGAAGGGCCAGGAGTTCC TGTGAAACCAGGATACTGCAGC
0.239	440.86426	459.14346	109.59345	CTHRC1		NM_138455	Homo sapiens collagen triple helix repeat containing 1 (CTHRC1), mRNA.			CAGATTACCCAAAAGGAGATGCTTCTACT GGATGGAATTCAGTTTCTCGC
0.238	81.14033	266.7976	63.311035	UCN2	SRP; URP; UCN-II; UCNI	NM_033199	Homo sapiens urocortin 2 (UCN2), mRNA.			GAGCTCCAACCAAACTCTGTCCCACTTCA CGCACGGACTGTCCTGGGCAA
0.233	291.38928	787.48926	182.77261	PRDM1	MGC118922; BLIMP1; PRDI-BF1; MGC118925; MGC118924; MGC118923	NM_001198	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1), transcript variant 1, mRNA.			TCTCTTTTCTGCCTCTTACATGTGAATGTT GAGCCCACAATCAACAGTGG
0.198	92.03801	49.356155	9.763102	ZC3H12A	MCPIP; FLJ23231; dJ423B22.1; RP3-423B22.1	NM_025079	Homo sapiens zinc finger CCCH-type containing 12A (ZC3H12A), mRNA.	CAGGTGCCCACACCTCCTGAA GACTTTGCTGTTTTTGCAACTA TGAAGCC	ILMN_1676660	AGGCCTCATCTGTGCTCTCGCTGGGCAC GTGGCTTCATGTCAGTAAGCAA
0.193	40.366806	65.490616	12.475452	FLJ12529	MGC9315; FLJ39024	NM_024811	Homo sapiens pre-mRNA cleavage factor I, 59 kDa subunit (FLJ12529), mRNA.	GCTGCATTCCATACCTCAGTGA AGAAGCCGAAGGATGCTGACA CACAGTG	ILMN_1692121	TTTTCCCCTGTCCCCCAACCCCATCCCCA CCTCCACTTCAGAACATGGCA
0.16	343.35596	202.89761	32.70608	TGFB2	MGC116892; TGF-beta2	NM_003238	Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA.	GCCTGTCGGGCCTCCGATTTC ATCCTCAGACGTAATGCTCACC AACAGCA	ILMN_1684108	CACGAACCCAAAGGGTACAATGCCAACTT CTGTGCTGGAGCATGCCCGTA
0.158	19.908504	58.442833	9.299536	GFRA4		NM_145762	Homo sapiens GDNF family receptor alpha 4 (GFRA4), transcript variant 2, mRNA.	CGCCATCTCATATCATGGACTC CGAAGTAGCCTGTTGCCTCCA AATTTGC	ILMN_1720665	GCCGTGGCGAGGGTGGGGACGGGGCCT CTCTCCGGCTCACCGCCCTCCCG
0.149	258.18927	751.70593	110.3143	PFKFB4		NM_004567	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4), mRNA.	CTGATAGACTTTCCTCTAAAAG CCATTCACTCCAGATTTTACCT GGGGAA	ILMN_1730575	GCTGGCGTGCCCATGTTGCAGATATTTTC CCGAGTTCCCCAGAATGGATG
0.137	320.57678	166.75595	22.763115	TPM1	TPM1-alpha; HTM-alpha; TPM1-kappa; TMSA; C15orf13	NM_001018008	Homo sapiens tropomyosin 1 (alpha) (TPM1), transcript variant 6, mRNA.	CCCCCAAACTGTCTGACTCTGT GTTTCCTGCCCTGAGGAGAGA GGGGTCA	ILMN_1743966	CAGAAGCCCCTGGTTGTCTGAAAGGTATG CTTTACTCAGTCTAATGGTGC
0.136	203.28928	102.697975	13.903629	TSC22D3	hDIP; DIP; DKFZp313A1123; DSIPI; TSC-22R; GILZ	NM_004089	Homo sapiens TSC22 domain family, member 3 (TSC22D3), transcript variant 2, mRNA.	GTGCATTGTGCTCTTTCCAAGT TCAGCAGCAGTTCTATCAGTG GTGCCAC	ILMN_1718961	AGGGCCTAACCAGCCTTGGGAGTATTGA CTGGTCCCTTACCTCTTATGGC
0.134	10.315353	227.28928	29.578827	MMP10	SL-2; STMY2	NM_002425	Homo sapiens matrix metallopeptidase 10 (stromelysin 2) (MMP10), mRNA.	CAGAAGTATGGCCCAGAAGAG CCCTTGCCCCGCCTGTCTGCC CTTGGTGG	ILMN_1657505	CAGTGGATCATCACAGTTTGAGTTTGACC CCAATGCCAGGATGGTGACAC
0.112	9535.772	22431.922	2515.5894	TGFBI	CDGG1; EBMD; CSD3; CSD1; BIGH3; LCD1; CSD2; CDG2; CDB1; CSD	NM_000358	Homo sapiens transforming growth factor, beta-induced, 68kDa (TGFBI), mRNA.			CCAGCCTCATGGGAAGTCCTGGCACAGT TTTTGTAAAGCCCTTGCACAGC
0.0899	7.6926794	130.62262	11.550978	NRG1	HRG; GGF2; HGL; GGF; NDF; HRGA; HRG1; SMDF; ARIA	NM_013962	Homo sapiens neuregulin 1 (NRG1), transcript variant GGF2, mRNA.	TAGAAAGTGTCCCAAAGCAAAT CCCACCAAGACCACCTGAAGG TCTCACC	ILMN_1740449	CTACATCCACCACTGGGACAAGCCATCTT GTAAAATGTGCGGAGAAGGAG
0.0806	43.51835	110.19345	8.816946	COL5A3		NM_015719	Homo sapiens collagen, type V, alpha 3 (COL5A3), mRNA.	GCCCAAGGTAGAGCAGACACT TGAGGAGACCAGCTCAGCAAA CGGAAGAC	ILMN_1730325	GGGACTTCCCTTGACTGGGTTGTGTTTCT TTTCCTGCCTCAGCCCAGCTC

Fold Change	XS No GFs	pOS 6 GFs	pOS No GFs	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
					FLJ42613; FKSG16; RP11-97E23.2		Homo sapiens solute carrier family 46, member 3 (SLC46A3), mRNA.	GCAGCCCCCAGGCCAAAGTGC TTTCTCACACTCCACTGCCCAA TAGTGAC	ILMN_1739887	CTCCTTCCCATCTCATTTCTTACTGCCTTA CGCTCATCCTGAGGTCCACC
0.0573	148.22263	452.90594	26.70903	SLC46A3		NM_181785				
					SgV; 7B2; P7B2; SGNE1	NM_003020	Homo sapiens secretogranin V (7B2 protein) (SCG5), mRNA.			AGAAGGCTGTACTCAAGAGGAGGAGCTG ACACATTTCACTTGGCTGCGTC
0.044	44.6775	1054.1184	47.015976	SCG5						
					THYEX3; HDPR1; DAPPER1; FRODO; DAPPER; DPR1		Homo sapiens dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis) (DACT1), mRNA.			CCTTAAAAGGATTCACAAAAACTTTTGCCA CACTTGGTGCCTAGGCCCTG
0.0303	375.01428	394.06427	11.463751	DACT1		NM_016651				

TABLE 13

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
79.86569	459.32263	387.88928	DTL	DCAF2; CDT2; L2DTL; RAMP	NM_016448	Homo sapiens denticleless homolog (Drosophila) (DTL), mRNA.	GCCATCTGAACATGCTCT CCTGTTGGTGTGTATGT CACTAGGGCAGTGGG	ILMN_1689642	GGAAGCCATAGAATTGCTCTGGTCAAAACCAAG CACACCATAGCCTTAAC
48.371307	81.43953	77.61078	NARG2	BRCC1	NM_024611	Homo sapiens NMDA receptor regulated 2 (NARG2), transcript variant 1, mRNA.	GGAGGAGTGGAAGCTAT TTTGTATGCAACTAGTCA CTGCTGAGGGGTGTC	ILMN_1717935	TGCCTCAGCAAGTTCTGTAGAAAATGAGCCGGC AGTTAGTTCAGCAACTC
482.6768	791.45593	756.3143	ING2	ING1L; p33ING2	NM_001564	Homo sapiens inhibitor of growth family, member 2 (ING2), mRNA.			CGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCA CCTGTTGAGTTTGCAAT
543.64343	1223.231	1132.6226	KIAA1267	MGC102843; DKFZP727C091; DKFZp686P06109	NM_015443	Homo sapiens KIAA1267 (KIAA1267), mRNA.			CCTGCTTTGGAGCTGTGTAATGGCAGCGAAACA TGTAGCTGTCTTTGTTC
670.4976	1036.6393	1001.0143	NXT1	P15; MTR2	NM_013248	Homo sapiens NTF2-like export factor 1 (NXT1), mRNA.	TGGAGTGGCTAAGCAGG TTCGGTTACCTGCCCCC GGCTGACCCCACAACA	ILMN_1801146	TTCTGTTGTTGCGGAGACACTGCAGACTCCACT GTGCCGAGGTTGAACTC
461.6726	1108.5643	1113.9476	LEPREL1	FLJ10718; MLAT4; P3H2	NM_018192	Homo sapiens teprecan-like 1 (LEPREL1), mRNA.			CCATGGCCAGGTTGCCTAGGAGTGGGGTCCACT GATGAAAAGAGGTGTTT
110.11012	233.54346	218.27261	AHCTF1	ELYS; TMBS62; MSTP108; MST108; DKFZp434N093	NM_015446	Homo sapiens AT hook containing transcription factor 1 (AHCTF1), mRNA.	TGCAACCAGCTTATGAG GGCAATGGGGGCACCTA AACTCTTGATGAAAGA	ILMN_1656399	GGACTCGGTCTAGCAAGGCCATCTTGTTGCCGG ACCTTTCTGAACCAAAC
80.48529	203.1726	193.96011	CCDC5	FLJ40084; HEI-C; FLJ21094; HsT1461	NM_138443	Homo sapiens coiled-coil domain containing 5 (spindle associated) (CCDC5), mRNA.			TAGTAAAGTGGCGGGAGCCGCAGCTATGGAGCC GCAGGAGGAGAGAGAAA
533.70593	1004.2726	951.4435	CERK	KIAA1646; dA59H18.3; hCERK; dA59H18.2; FLJ23239; MGC131878; LK4; FLJ21430; DKFZp434E0211	NM_022766	Homo sapiens ceramide kinase (CERK), transcript variant 1, mRNA.	TGCATTTGTTTATGTAAT TTCAGGAGGAATACTGAA CATCTGAGTCCTGG	ILMN_1791466	GCTCTGATTTCCGGGGCAGCCTTTCAGATGCGG CAGACATACAACACCTG
1463.1393	1679.0435	1677.656	PRPF31	PRP31; RP11; DKFZp566J153; NY-BR-99	NM_015629	Homo sapiens PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae) (PRPF31), mRNA.	CTGGAACCAACTCTGCC CTACCTCCCTGCACTAAC CAGCTTTGAGGATGG	ILMN_1680591	GCATGGCTGAGTTCCTCAAGGTCAAGGGCGAGA AGAGTGGCCTTATGTCC
45.671036	205.44762	177.8393	GCUD2	RP11-312O7.1; MGC57827; GCUD2	NM_207418	Homo sapiens gastric cancer up-regulated-2 (GCUD2), mRNA.			GCATTCAGAGCTACAAAGGAATAGGAAAGTAGG GTAGTGTTGGATTCTGG
32.657547	142.01428	123.718445	MCM8	C20orf154; dJ967N21.5; MGC119522; MGC4816; MGC12866; REC; MGC119523	NM_032485	Homo sapiens minichromosome maintenance complex component 8 (MCM8), transcript variant 1, mRNA.			ACCAGCTTCAAACTATGTAAAAGGACTTCACCAA GTTAGGGCCTCCTGGG
2647.281	5440.789	5132.5977	TUBB2C	TUBB2	NM_006088	Homo sapiens tubulin, beta 2C (TUBB2C), mRNA.			CTCGGGGGCTAAAAATGTCCGCCACCTTCATTG GCAACAGCACGGCCATC
173.42262	1037.156	882.8059	PBK	Nori-3; SPK; FLJ14385; TOPK	NM_018492	Homo sapiens PDZ binding kinase (PBK), mRNA.			GACTCTGGTTACAGATTGTCTTGATCTCTTGGAT CTCCTCAGATCTTTGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
335.93097	638.3101	604.33093	BXDC5	DKFZp761M0215; RPF1; RP11-118B23.1; DKFZp761G0415; FLJ12475	NM_025065	Homo sapiens brix domain containing 5 (BXDC5), mRNA.	AGATCCTGGCTTTCCAG GGTGGGCAAGGGCAAG GAGCAGGCTTGGAGCCA	ILMN_1664723	GGAGAGTATGAATGGGTCCATAAGCCCCGGGAA ATGGATACAAGTAGAAG
71.35876	107.89358	101.93515	TTRAP	EAP2; AD022; MGC111021; MGC9099; dJ30M3.3; RP1-30M3.3	NM_016614	Homo sapiens TRAF and TNF receptor associated protein (TTRAP), mRNA.	AGGAGGTGATGCTGGTC CCTGGCCACCTCTACAG CCCTGAACTCTTGAGA	ILMN_1735735	GGCAAAGTTAAGCTTGATGATGGTTAAAATCGGT TTGATAGCACCATGGG
104.66432	220.28094	206.79346	TRIOBP	TARA; FLJ39315; KIAA1662; dJ37E16.4; HRIHFB2122; DFNB28	NM_138632	Homo sapiens TRIO and F-actin binding protein (TRIOBP), transcript variant 2, mRNA.	CTCAGGTATGGGAAACT AGGCCGCCCAGTCGCGC GCCTCTCCAAAACGTT	ILMN_1699565	ACAGGGGAGCCTCCAGTAGCCCTCAGAGAATGC ACCGTCCGCCTAGGACA
132.77261	183.9018	179.16428	SLC25A11	SLC20A4; OGC	NM_003562	Homo sapiens solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11 (SLC25A11), nuclear gene encoding mitochondrial protein, mRNA.			GGAAACCAAGGCAGAGCTGAGGGGACAGGGAG GAGCAGAAGCCATCAAGA
66.09779	509.8393	421.01843	C11ORF82	FLJ38838; FLJ13936; FLJ25416	NM_145018	Homo sapiens chromosome 11 open reading frame 82 (C11orf82), mRNA.			GGCCCACCTTCAGTGTGTGAAACTCGAAGTGCT TGGTCACCTGAATTGTT
1513.5643	2691.8394	2570.2393	HNRNPAB	ABBP1; FLJ40338	NM_004499	Homo sapiens heterogeneous nuclear ribonucleoprotein A/B (HNRNPAB), transcript variant 2, mRNA.	GCATGAGGACTTAATGAA TCCAAACCTGTGTCATGC CTGTGTGCATACCC	ILMN_1811592	GCGGCAGCAGGAGCGACCAACTGATCGCACACA TGCTTTGTTTGGATATG
1104.106	3893.0476	3498.181	UBE2C	UBCH10; dJ447F3.2	NM_181803	Homo sapiens ubiquitin-conjugating enzyme E2C (UBE2C), transcript variant 6, mRNA.			CCCTCATGAACCCAACATTGATAGTCCCTTGAAC ACACATGCTGCCGAGC
940.48096	1841.3392	1748.2059	TTC4	MGC5097	NM_004623	Homo sapiens tetratricopeptide repeat domain 4 (TTC4), mRNA.	CCCCCTGACATGGAAGA CGATTACGAACCTGAGC TGCTGTTAATGCCATC	ILMN_1661674	TGGAGGACTGTGACAGACTTTGGACAGTGGCCT CTTGAGTTCCTCTGCAG
56.023453	81.14087	77.63129	SCAF1	SR-A1; SRA1; FLJ00034	NM_021228	Homo sapiens SR-related CTD-associated factor 1 (SCAF1), mRNA.	GGGGCCCATGTTCACAC TGGCTCTCAGTCTAGTCA GGTGCAATGTTCTTG	ILMN_1813938	CCCTCACCTCTTTGAAACTCTGGACGTATTTATG GCTCCACCTCCCCACC
233.91429	1013.7476	906.5143	NEK2	NLK1; NEK2A; HsPK 21; HsPK21	NM_002497	Homo sapiens NIMA (never in mitosis gene a)-related kinase 2 (NEK2), mRNA.			CTGTTTAACAGAATATGAGCTGTCTGTCATTTAC CTACTTCTTTCCCACT
21.907574	132.75595	114.33511	MFHAS1	MASL1; FLJ23354	NM_004225	Homo sapiens malignant fibrous histiocytoma amplified sequence 1 (MFHAS1), mRNA.			GGAATGGCCTGGACTGCACTACACCGTGCACAT TCTCTGTTCTAAGTGCC
560.20593	1188.0476	1144.506	DUSP5	HVH3; DUSP	NM_004419	Homo sapiens dual specificity phosphatase 5 (DUSP5), mRNA.			CTCCCTGCCCCTGGAGGTTGTCTTCAAGCTGTG GACTTCTGGGATTTGCA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
234.09344	586.4393	541.34344	TIMELESS	TIM; FLJ12640; TIM1; FLJ20714; hTIM	NM_003920	Homo sapiens timeless homolog (Drosophila) (TIMELESS), mRNA.	CCACTGGTATTCCTGAG CCTCTCCCAGCTCCACTT CTAATGCTAGAGAAT	ILMN_1684401	TGGTCTGTTCCTTTGGCTTTCTCTTGGAGGTGG GTCGCAGCACCAGATGG
475.78094	1371.5143	1272.7476	USP16	UBP-M	NM_006447	Homo sapiens ubiquitin specific peptidase 16 (USP16), transcript variant 1, mRNA.			GAACACAGTGGTACTATGAGGTCGGGGCATTAC ACTGCCTATGCCAAGGC
541.2101	1060.9309	1005.88513	RRP15	KIAA0507; CGI-115; MGC22291	NM_016052	Homo sapiens ribosomal RNA processing 15 homolog (S. cerevisiae) (RRP15), mRNA.	GCTAATAGCCTAACTGCA GAGGAACTGAGTGGATG GGGTAGCTGCTGTAT	ILMN_1790008	CTGCTTGACCAGCGAGATGTGCATTTTGCCAGG ATCATATTGGTCATGTC
84.40606	640.20593	560.2268	SSBP3	CSDP; FLJ10355; SSDP1; SSDP	NM_018070	Homo sapiens single stranded DNA binding protein 3 (SSBP3), transcript variant 2, mRNA.	TGGGACTCTTCGAAGAC ACCAATCTGTGCGCTATT CACGCTAAACGCGTC	ILMN_1712184	ATAAGTGGCATTAGCAATCCTCCAGGCACCCCTC GAGATGACGGCGAGCT
1436.9309	1946.3226	1901.406	CNIH	CNIH1; CNIL; TGAM77; MGC117156	NM_001009551	Homo sapiens cornichon homolog (Drosophila) (CNIH), transcript variant 2, mRNA.			ATCTGACTAGTGGGAAACTTCATGGGTTTCCTCA TCTGTCATGTCGATGA
63.72792	157.73929	148.22263	C1ORF124	DKFZP547N043; PRO4323; DDDL1880; dJ876B10.3; RP5-876B10.3	NM_001010984	Homo sapiens chromosome 1 open reading frame 124 (C1orf124), transcript variant 2, mRNA.	TACCAGACTCCGACACA ATGGGCCACCACCAGTG TGACAGCAGGACATCC	ILMN_1804419	GGGTGCTACATTCACTCTTGCCTTAGGTATACTG TAACCCAGGTTCTGCC
824.2726	1602.881	1524.1143	STK39	DCHT; PASK; SPAK; DKFZp686K05124	NM_013233	Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA.	GCCCAAGGGAGGTTAAA GTGGTGGCCAAAGGATT TTGTAGTGCCAATGGG	ILMN_1812463	CAAGGAGGTGGGCTCCCAGGATGGTACCATTGC TCTTTCCTAGCTAACCC
231.84763	921.56433	824.6601	POLA2	FLJ37250; FLJ21662	NM_002689	Homo sapiens polymerase (DNA directed), alpha 2 (70kD subunit) (POLA2), mRNA.			TCCAGAAGTAAGCCAGCTGTGGATCCCGCCCAC TCAGAAAAGGCGAGAAG
97.08522	449.45593	403.53094	PLCXD1	LL0XNC01-136G2.1; FLJ11323	NM_018390	Homo sapiens phosphatidylinositol-specific phospholipase C, X domain containing 1 (PLCXD1), mRNA.			GTACCCGGTTGCTACGGTGAAATGAAGGTGCCC CGCATCCAGAAAGACGC
425.65594	2938.7725	2542.1892	CCNA2	CCN1; CCNA	NM_001237	Homo sapiens cyclin A2 (CCNA2), mRNA.			CCTTGTCTCATGGACCTTCACCAGACCTACCTCA AAGCACCACAGCATGC
1387.4226	3433.0142	3224.0393	POLE3	YBL1; p17; CHARAC17; CHRAC17	NM_017443	Homo sapiens polymerase (DNA directed), epsilon 3 (p17 subunit) (POLE3), mRNA.			CTGTTGGCCTTTCTTAGCCTTTTTCTGTTTCCATT CAGTGCTCCAAGCGC
1099.8726	1408.9727	1392.9226	EIF4E2	EIF4EL3; 4E-LP; 4EHP; IF4e	NM_004846	Homo sapiens eukaryotic translation initiation factor 4E family member 2 (EIF4E2), mRNA.			CCGGGACACACTTCGGCGAGTGCTTAACCTACC TCCCAACACCATTATGG
108.09762	202.44345	193.83511	RAPGEF6	RA-GEF-2; DKFZp686I15116; DKFZp667N084; PDZGEF2; PDZ-GEF2; KIA001LB	NM_016340	Homo sapiens Rap guanine nucleotide exchange factor (GEF) 6 (RAPGEF6), mRNA.	CTCTCGCTTGCTCTCTCT CACCATGTGACACACTG GCTCCCCTTCACCTT	ILMN_1718309	TTCTGCAGCATGCCTCCCCCACATCTCATAGCAC CAGGTTGTGTCTGACC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
485.8226	1109.6477	1040.1393	NOP5/NOP58	HSPC120	NM_015934	Homo sapiens nucleolar protein NOP5/NOP58 (NOP5/NOP58), mRNA.			ATCACCCGGACACACATCATGCTTAAGATTCAAC TGGGAGCATACCAGGG
46.02639	67.066345	64.4395	CPSF6	HPBRII-4; HPBRII-7; CFIM; CFIM68	NM_007007	Homo sapiens cleavage and polyadenylation specific factor 6, 68kDa (CPSF6), mRNA.			GCACCTGACTAGCATGTGTTCTTGATTGCAAAAT TGGCAGAGGCAGGGTG
91.26848	131.16428	128.30594	ANTXR1	ATR; FLJ21776; FLJ11298; TEM8; FLJ10601	NM_053034	Homo sapiens anthrax toxin receptor 1 (ANTXR1), transcript variant 2, mRNA.	GAGTGGAGAGGTTTCTC TAGAGGTGTAGGGGACT GGAAACCACATCCAGG	ILMN_1794353	GAAGTTGGCATGAAAGCTGCACTCCAGGTCAGC ATGAACGATGGCCTCTC
139.63928	247.73929	237.26012	SRRD	HC/HCC; SRR1L	NM_001013694	Homo sapiens SRR1 domain containing (SRRD), mRNA.	GGAGGCTGGCAGGGACA AATTCCCTAAAAGAGGGA CCAAGCGTCAGCTCC	ILMN_1682444	AGAAGCTGCCACCAGAGACTAAAGGGAAGGCTG CTATGGAGGAACTACAG
720.58093	978.506	958.0559	COPS6	MOV34-34KD; CSN6	NM_006833	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis) (COPS6), mRNA.	GGAGTGTGGAGGGGTC GATGACTTGTGCAGGGT CATATGGTACCTAAGGG	ILMN_1813768	CCCTGCTGGTGGCTCTGTCCTCTGTTAGGCACC ACACTGGTTGGTCAACT
42.396423	114.61012	105.19762	DLEU1	XTP6; MGC22430; DLB1; LEU1; BCMS	NR_002605	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1) on chromosome 13.	AGTGAGCTGATGTGCCC ACCACCGTGTCATGAGA GAATGGGTTTACTCTC	ILMN_1759232	CCTAGGAGGCTAGAAGAGCCAACCAACAGAGAA GGGAAAGCAGTCTGTTC
2046.706	2748.7227	2696.0308	TMEM85	PIG17; MGC24415; FLJ90746	NM_016454	Homo sapiens transmembrane protein 85 (TMEM85), mRNA.	TCCTTGAAGCAAAAGAGT AAACACGGCCCAGCGGT GGAACCAGCCATTCC	ILMN_1667016	GCCTTCATTGAGCCCCCTGAGAGAATGGAGTTC AGTGGTGGAGGACTGCT
300.44763	531.756	514.2351	DHX9	NDH II; LKP; DDX9; RHA; NDHII	NM_001357	Homo sapiens DEAH (Asp-Glu Ala-His) box polypeptide 9 (DHX9), mRNA.	CCCTCTTCCTCACTGACT TCCCCTTGCACAGGGGC TTCTGTTTTATCCCA	ILMN_1695135	CTCCTTTGGGACGAATCCTGGCTAAACTCCCCAT TGAGCCTCGTTTTGGC
184.88095	244.12262	237.01428	CBR1	CBR; hCBR1	NM_001757	Homo sapiens carbonyl reductase 1 (CBR1), mRNA.	GAGCAGAATCTCCGGGA AATGACTTAGTCTGGCCA CATGCATAGCCCATC	ILMN_1769720	GAACTGACATGGCGGGACCCAAGGCCACCAAGA GCCCAGAAGAAGGTGCA
42.928158	85.26502	80.189476	PPIL3	CYPJ	NM_130906	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 3 (PPIL3), transcript variant PPIL3b, mRNA.	AAGGGGAGTTTACAGAC GCTCCCTCACATCGGGG ACGCGGCTCCTTTAAG	ILMN_1662934	GGAAGAGGAGGCAACAGTATTTGGGGCAAGAAG TTTGAGGATGAATACAG
183.43929	306.50595	297.05594	TMEM199	MGC45714; C17orf32	NM_152464	Homo sapiens transmembrane protein 199 (TMEM199), mRNA.	CCGCCTCATTTGCGCCT TGCAGCACTGCTGGACC AGGTTACAAGATGTTC	ILMN_1723398	GAGAAAGATGGGTTGCTAGAGGATGGTAGAACT GGAAGCAAGGCAGCTAC
470.18927	845.82263	810.86426	CERK	KIAA1646; dA59H18.3; hCERK; dA59H18.2; FLJ23239; MGC131878; LK4; FLJ21430; DKFZp434E0211	NM_182661	Homo sapiens ceramide kinase (CERK), transcript variant 2, mRNA.	GGTGATTACCCTGTGTAT AAGAGTATGTGTCTCACT GCACCTTCAATGGC	ILMN_1766176	GGGAAAGTCTGAGTGAAAGGATGGCCTCATTCT CTTTCTAATCTTGCTGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
80.866684	148.47263	145.20595	C20ORF55	bA371L19.3; MGC4675; F10; MGC2450	NM_031424	Homo sapiens chromosome 20 open reading frame 55 (C20orf55), transcript variant 1, mRNA.			CCTTTGCTGACTTCCTCTTCCTTACCCAGCAGAA CTCACCCTGGGGTCGG
866.7476	1267.7142	1227.7144	CNOT7	CAF1; hCAF-1	NM_013354	Homo sapiens CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA.	TGTGGTGAATGTAACAAT ATATGTTCTTCATATTTA GCCAATATATTAAT	ILMN_1652376	GAACGGATAGGACCACAACATCAGGCAGGATCT GATTCATTGCTCACAGG
1092.3392	1926.3226	1893.5892	SMARCA2	Sth1p; SNF2L2; SWI2; FLJ36757; SNF2; BAF190; MGC74511; BRM; hBRM; SNF2LA; hSNF2a	NM_003070	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (SMARCA2), transcript variant 1, mRNA.			CTTTGCTTTCTTTGCACAATGTCTTTGGTTGCAA GTCATAAGCCTGAGGC
98.13929	1494.8977	1370.0643	PTBP2	PTBLP; nPTB; nPTB7; PTB; nPTB8; nPTB6; FLJ34897; MIBP; nPTB5; brPTB	NM_021190	Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), mRNA.	GCTGTGGATTACATCTTG TGTGTGTCAGAGAAACT GCAGAGAACCTGGAG	ILMN_1712360	GTGGCAGTTTTCTAAAACTGACAACCAGGTGGG ACCAAAGTTTATGTGCC
30635.855	45105.215	44286.258	TUBA1B	K-ALPHA-1	NM_006082	Homo sapiens tubulin, alpha 1b (TUBA1B), mRNA.	GGACAATGCTGGCCACT GCCATTCTGTGTTCAGAA AGACTATGAGACCTG	ILMN_1703273	GGAGAGGAATACTAATTATCCATTCCTTTTGGCC CTGCAGCATGTCATGC
233.58095	596.81433	576.7643	UBFD1	UBPH; FLJ42145; FLJ38870	NM_019116	Homo sapiens ubiquitin family domain containing 1 (UBFD1), mRNA.	TTATCCAGGCTTTTTGAC CACGCTATGCTCCAAGC CCATCGCGCGCACCA	ILMN_1693617	TGGCCCAGGAGACTGACCCAAAGTGAAGGACAT TGCCGGGAGAGGCCTGC
11.266656	101.42207	87.65945	XDH	XOR; XO	NM_000379	Homo sapiens xanthine dehydrogenase (XDH), mRNA.			GAATAGGGTCGGGAAGGGTTTGTGCTATTCCCC ACTTACTGGACAGCCTG
3413.0728	4105.9644	4090.4976	SNRPB2	MGC45309; MGC24807	NM_198220	Homo sapiens small nuclear ribonucleoprotein polypeptide B" (SNRPB2), transcript variant 2, mRNA.	AAGATTGAGAAGAACGG GAAGGTCAGCGGGACCA AGAAGGAGAACTGCCC	ILMN_1726043	GGAGCTGCCAGGGATGCTTTACAGGGATTTAAG ATCACACCGTCCCATGC
33.57508	187.11845	173.23096	ZWILCH	FLJ10036; FLJ16343; KNTC1AP; MGC111034; hZwilch	NM_017975	Homo sapiens Zwilch, kinetochore associated, homolog (Drosophila) (ZWILCH), transcript variant 1, mRNA.	CACTACTGCTATCATAAG GGGTCAGGGACATTCCG GGGAGAAGTGACCAC	ILMN_1769032	TCTCTACTGGCGAAAATGTTGGACCACTTGCTTT ACCAGTTGGGAAGGCA
269.0893	814.8143	772.8059	CKAP2	TMAP; FLJ10749; LB1; se20-10	NM_018204	Homo sapiens cytoskeleton associated protein 2 (CKAP2), mRNA.	ATTCAGTGGAGACTCAG GAGGAGCCACACCGTGG GAACAGGGCTGATGCT	ILMN_1716546	TTATTGACTTCTCATGTTCTAGAGAGTAGGACTT TTATTCCGTGTACCTG
228.61844	905.0226	848.89343	RFC4	A1; RFC37; MGC27291	NM_181573	Homo sapiens replication factor C (activator 1) 4, 37kDa (RFC4), transcript variant 2, mRNA.			AGATGAGGGTCATGCAGCAACTCAGCTCGTCAA TCAACTCCATGATGTGG
62.354637	98.17263	98.60626	TTLL5	KIAA0998; STAMP; MGC117189	NM_015072	Homo sapiens tubulin tyrosine ligase-like family, member 5 (TTLL5), mRNA.	TGGGCCACATCCCCTCC ATCTACACAGACACCTGA AGGAGCCCCCACATG	ILMN_1736101	ACCTTCCCTTTGCCCCATGCCCCCAAACTGCTTA GGTCTTCTCTGTCCCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
45.426586	78.1189	76.198074	PSD3	DKFZp761K1423; EFA6R; HCA67	NM_206909	Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3), transcript variant 2, mRNA.	CGAAAGCTGCTCTTCAAT GAGGAAGCCATGGGGAA GGTAGATGCTTCACC	ILMN_1772780	TTGGGAGCTGAAGAATACTGGACGGGGCTTCGG AGAGGAAGGATGGTCCA
337.58093	539.60596	528.34766	MRPS2	MRP-S2; CGI-91	NM_016034	Homo sapiens mitochondrial ribosomal protein S2 (MRPS2), nuclear gene encoding mitochondrial protein, mRNA.			AGAAGATGCTGCTGTCCCTGTGATCCCAGCAGC CCTCCCTTCACCGTGAC
8.065878	87.49576	78.70299	MATR3	DKFZp686K23100; DKFZp686K0542; KIAA0723; MGC9105	NM_018834	Homo sapiens matrin 3 (MATR3), transcript variant 2, mRNA.			ATTGTGGGAGTCTCCGCGTCCCGCTCGCTGGGA GAGAGGTACCTCTCCTT
110.555954	237.12677	228.32262	UBIAD1	RP4-796F18.1; TERE1	NM_013319	Homo sapiens UbiA prenyltransferase domain containing 1 (UBIAD1), mRNA.	AAGCTGGGTTGTGTACTT TCTGGTGACACTCCTGG GCTCCTCCCCATCCC	ILMN_1793033	GGAATGTGATTTGGCAGTCAGGGTACTAAGCAT GGGTGGGAACTCCTGCC
319.7226	388.7143	386.43512	C19ORF52		NM_138358	Homo sapiens chromosome 19 open reading frame 52 (C19orf52), mRNA.	CTCAGCTTCCAGCCAAAA TGGCGGAGAACAGCGAG AGTCTGGGCACCGTC	ILMN_1679687	AGCCACCTGGGTCCGGGAGTTGGGGACAGCAG AACGACTTGACACATGTT
248.97263	658.35596	637.3393	HMG1L1	HMG1L7; dJ579F20.1	NM_001008735	Homo sapiens high-mobility group (nonhistone chromosomal) protein 1-like 1 (HMG1L1), mRNA.			ACTGGGAGAGATGTGGAATAACACTGCTGCAGA TGACAAGCAGCCTGGTG
134.78928	213.25177	208.60596	PAK1IP1	hPIP1; RP11-421M1.5; PIP1; MAK11; FLJ20624; bA421M1.5; WDR84	NM_017906	Homo sapiens PAK1 interacting protein 1 (PAK1IP1), mRNA.	GCCGCAGTGCCCCCCAA CCCAGGCCTCTATTGTTC CATGTTGTAAATACC	ILMN_1659823	GAGCCTGGTGACACAGTGCACAAAGAAGAAAAG CGGTCAAAACCTAACAC
294.1768	963.69763	917.1101	CDCA4	MGC19517; FLJ20764; HEPP	NM_145701	Homo sapiens cell division cycle associated 4 (CDCA4), transcript variant 14, mRNA.			TTCCACTCCTGCCCCGCCTCACCCCACATGCTC CCTGTTTCTCATGCTTT
484.37262	849.19763	831.78094	UBQLN1	DA41; XDRP1; DSK2; FLJ90054; PLIC-1	NM_053067	Homo sapiens ubiquilin 1 (UBQLN1), transcript variant 2, mRNA.			GCAGCTATTGAAAGGTTACTGGGCTCCCAGCCA TCATAGCAGCATTTCTG
140.35596	231.39761	229.91428	NDST2	HSST2; NCST2; NST2; MGC129697; MGC129705	NM_003635	Homo sapiens N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 (NDST2), mRNA.	GGCTTCACATTCACTCCC ATCACCATGACCTTCCCC TTCCGTGGATCCCG	ILMN_1793151	CTTTAGCCAGGCAGTGGGATCTACCTGTGGCCC GGCCTCCCTAATGTCAT
312.60178	1263.6726	1203.281	TRIP13	16E1BP	NM_004237	Homo sapiens thyroid hormone receptor interactor 13 (TRIP13), mRNA.	AGAACAGCCCCATCTCTT TCGCCTGCACACTTGGA ACTCAGCAAGAAGGG	ILMN_1718783	CGGTATGGGCGCCCCTGCATTGCTGGGATGTTT CTGCCCACGGTTTTGTT
203.43095	427.3643	415.4226	NME1	NDPKA; NM23-H1; NDPK-A; NM23; AWD; GAAD	NM_000269	Homo sapiens non-metastatic cells 1, protein (NM23A) expressed in (NME1), transcript variant 2, mRNA.	CTTCGGCAGTATCACAA GAAGATTAAAGTGGCAG ACACCCCTTCCAGCGG	ILMN_1702604	AAAATGCTTCCTCCCAGCATAGGATTCATTGAGT TGGTTACTTCATATTG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
695.57263	926.59766	912.46423	FN3KRP	FLJ12171	NM_024619	Homo sapiens fructosamine-3-kinase-related protein (FN3KRP), mRNA.	GTAATCTGAACATTTGGG AGGCTGAGGCAGGAAGA TCGCTTGAGGTCCAG	ILMN_1811221	GGTACATCCAGGAGTCTTCATTGCTTCTGTTATT ACCCCGTCTCCTCTGC
4094.1895	7717.1807	7593.0645	SNRPG	MGC117317; SMG	NM_003096	Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA.	ACCCCCGCGCTCCACCT GCAGTGTTTCTGCCCTG TAAATAGGACCAGTCT	ILMN_1659599	GGCTGTTCAGCAGAGAAACCCATGTCCTCTCTC CATAGGGCCTGTTTTAC
3172.3228	4313.8057	4289.2476	MYH10	NMMHCB; MGC134914; MGC134913	NM_005964	Homo sapiens myosin, heavy chain 10, non-muscle (MYH10), mRNA.	CTGACAACTGTGAAGCC ACCCTGGGCTACAGAAA CCACAGTCTTCCCAGC	ILMN_1713496	TTCCCCCTTTATGAACTGTACTGGCTGTTGACCA CCAGACACCTGACCGC
278.45178	453.2351	442.5268	C7ORF36	GK003	NM_020192	Homo sapiens chromosome 7 open reading frame 36 (C7orf36), mRNA.	CGCAGTCATGGATCTGG GTAGTCCGGAAAACAAA AGGAGGGAAGACAGCC	ILMN_1656826	GTTGTAGAACACAGGAGCATGCACATTCAGAAAA CCCAAGCCCCACATGG
42.223907	93.26013	93.41088	E2F5	E2F-5	NM_001951	Homo sapiens E2F transcription factor 5, p130-binding (E2F5), transcript variant 1, mRNA.	GTCACAGAGCAGCACCT ACCCCCTCCTCCTTTCCA CACCTGCAAACTCTT	ILMN_1701748	CTTCTGACGTGTTTCCTCTCTTAAGGCTTTCTCC TACCCCGGCAGATGAC
133.11429	269.9226	273.88928	HNRNPA3	2610510D13Rik; MGC142030; D10S102; MGC138232; FBRNP	NM_194247	Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRNPA3), mRNA.	CATGTCGCATCTGTTTTA ACTCCAGGCGTGGGGGC TCCTGGGGAAACGAC	ILMN_1791596	CGGAGGGAACTTTGGAGGTGGTGGAGGTAATTT TGGCCGTGGTGGAAACT
1270.9644	3463.3477	3396.0977	ATP2A2	DAR; ATP2B; MGC45367; DD; SERCA2	NM_170665	Homo sapiens ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 (ATP2A2), transcript variant 1, mRNA.			GCTGAACGTGACCCAGTGGCTGATGGTGCTGAA AATCTCCTTGCCCGTGA
229.33095	312.3643	306.6101	SCN3A	Nav1.3; KIAA1356; NAC3	NM_006922	Homo sapiens sodium channel, voltage-gated, type III, alpha subunit (SCN3A), transcript variant 1, mRNA.			ACCAGCTGACACTGCTGAGGAGAAACCCAATGG CTACCTAGACTATAGGG
804.31433	879.45593	875.8059	C3ORF10	MDS027; HSPC300; hHBrk1	NM_018462	Homo sapiens chromosome 3 open reading frame 10 (C3orf10), mRNA.			GCCTAGGTGGCTTACCAGCCCAAGTCCCCATGT TTGGACTTTCAGCTGAC
191.83096	706.30597	660.23096	GABPB2	NRF2B2; GABPB; E4TF1-47; E4TF1; NRF2B1; E4TF1B; E4TF1-53; BABPB2; GABPB1	NM_016655	Homo sapiens GA binding protein transcription factor, beta subunit 2 (GABPB2), transcript variant gamma-2, mRNA.	GCCACTAGCACAGGAAG CTCAGGACGAAGGCAGC GTTAGGAGAATAGTTG	ILMN_1775357	CTGTGGATGGTGCCATTCAGCAAGTAGTTAGTTC AGGGGGTCAGCAAGTC
61.719265	214.43929	202.09763	DONSON	B17; C21orf60; DKFZP434M035	NM_017613	Homo sapiens downstream neighbor of SON (DONSON), mRNA.	GGACTTCGAGATCGCAG CCAAGTACGTGTGTCGG ACCCTGGAGACACAGC	ILMN_1677955	TCCTGTTCCGAGCAGCAGGATTAGCTGGAAGTG ACTTAATCACAGCTCTC
49.792515	95.551834	91.747665	TM9SF1	HMP70; MP70	NM_001014842	Homo sapiens transmembrane 9 superfamily member 1 (TM9SF1), transcript variant 2, mRNA.			GGTTCCTCCTATCCCCAAGCAGGACTGAGCTTG AATGATATGAGAGTGTC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
109.79465	365.9601	341.88513	EXO1	HEX1; hExoI	NM_006027	Homo sapiens exonuclease 1 (EXO1), transcript variant 1, mRNA.	GAGTAACGGCTCTGCTG CCAGGGTTTCTCTGGGC TCATTCTTCCACTGAC	ILMN_1756669	GAAACCCCTGTCCCCAGTCAGAGATAACATCCAA CTAACTCCAGAAGCGG
201.79346	297.8476	295.34763	AP4B1	BETA-4	NM_006594	Homo sapiens adaptor-related protein complex 4, beta 1 subunit (AP4B1), mRNA.	GCCAAGAAGAGGCATTT CCATGAGCTCTGGACAG TGGCAGAGAGGCAGAG	ILMN_1702812	CGCAATGAGTAGGGCTGGGTCTCGGCCATGGAA AGCATACCTCAGTGCTC
559.0643	1454.031	1403.006	C19ORF48	MGC13170	NM_199250	Homo sapiens chromosome 19 open reading frame 48 (C19orf48), mRNA.	CACTCCATACAGTATTAG GTGAGGATGGATGCGGG CGCTGTCCTTGCCGG	ILMN_1651832	GCAGGCCAAGCAGGGCAACCCCACACCCTTGAC ATAAAAGCATCTTGAAG
184.02284	860.85596	788.65594	MCM10	PRO2249; CNA43; MGC126776	NM_018518	Homo sapiens minichromosome maintenance complex component 10 (MCM10), transcript variant 2, mRNA.			AGTTGTATAATATGCTTGTAAAGGCTGAGGGTGA GCTGTATCTGGATGCC
49.31388	113.19762	108.805954	ZNF681	FLJ31526	NM_138286	Homo sapiens zinc finger protein 681 (ZNF681), mRNA.			ACCCTACCAATGTGAAAAATGTGGCAAAGCTTTT AACCAGTCCTCAAACC
2301.456	3142.2227	3081.6309	NRD1	hNRD2; hNRD1	NM_002525	Homo sapiens nardilysin (N-arginine dibasic convertase) (NRD1), mRNA.			CAGCAGTACCTCTTTGACCGCCTTGCCCACGAG ATTGAAGCACTGAAGTC
668.006	1371.6477	1321.0143	EMG1	Grcc2f; C2F; NEP1	NM_006331	Homo sapiens EMG1 nucleolar protein homolog (S. cerevisiae) (EMG1), mRNA.	ACAAAAGAGGTCGCTCC AGCCCTACCACAGGTCT GACTGGCACTGCCTTT	ILMN_1732519	GGTGTCCATCAGTAACTACCCCCTTTCTGCTGCC CTCACCTGTGCAAAAC
163.11429	613.5143	584.7726	NETO2	FLJ14724; FLJ10430; NEOT2; FLJ90456	NM_018092	Homo sapiens neuropilin (NRP) and tolloid (TLL)-like 2 (NETO2), mRNA.	GGCAATACCTGATGTCA GTCACAGGCATCCAACT CATGACAAGAGATACC	ILMN_1811050	GTTCACATCAGTGGCTTTGTATGCAAATATGCTG TGTTGGACCTGGACGC
27.742947	75.85229	71.96585	CYORF15B		NM_032576	Homo sapiens chromosome Y open reading frame 15B (CYorf15B), mRNA.			CTCTAAAAGAGCCCCAGGAGTCCATCTGGAGGC TGACCCCAAAGGAATGA
57.9048	225.26428	208.50179	NUP35	MP44; NP44	NM_138285	Homo sapiens nucleoporin 35kDa (NUP35), mRNA.			GCCTTTACACCACCAATCAAAACTCTAGGTACAC CAACACAACCTGGAAG
497.82263	1120.3726	1068.8142	RECQL	RecQ1; RECQL1	NM_032941	Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 2, mRNA.			TTGGATGGGAAAGGGTGCAGCAAAACTGAGAGT AGCAGGTGTTGTGGCTC
76.20703	263.97263	245.56845	SLTM	Met; DKFZp762G052; FLJ13213; FLJ10005	NM_024755	Homo sapiens SAFB-like, transcription modulator (SLTM), transcript variant 1, mRNA.			ATAGCAGGTTCTGGTGATGGTACACAAGAAGTAT CTAAACCTCTTCCTTC
48.621887	107.44346	101.96846	C10ORF2	FLJ21832; C10orf2; TWINL; PEOA3; SANDO; PEO1; PEO	NM_021830	Homo sapiens chromosome 10 open reading frame 2 (C10orf2), mRNA.			GGGTACCAAGCTCCTCTGCTCCCCACTTTGTAG AGCCTAGCATGAGGTGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
8.405419	152.00595	128.38095	SPI1	SPI-A; OF; SFPI1; PU.1; SPI-1	NM_001080547	Homo sapiens spleen focus forming virus (SFFV) proviral integration oncogene spi1 (SPI1), transcript variant 1, mRNA.			GAGTCTCAAGTCCGTATGTAAATCAGATCTCCCC TCTCACCCCTCCCACC
1199.3394	2379.6309	2280.6392	EWSR1	EWS	NM_005243	Homo sapiens Ewing sarcoma breakpoint region 1 (EWSR1), transcript variant EWS, mRNA.			CCTGGAAAAATGGATAAAGGCGAGCACCGTCAG GAGCGCAGAGATCGGCC
410.4226	845.7476	812.22266	ANAPC10	DKFZP564L0562; APC10; DOC1	NM_014885	Homo sapiens anaphase promoting complex subunit 10 (ANAPC10), mRNA.	GCTGGTCTGGGTGTAGC TCTTAGAGGAAGGAGAT AGGGAAAAGGGGCTCC	ILMN_1658027	CGGCAACTTGAGTTGGTGGAACCAAGTGGCTGG ATTCATGTTCCCTTAAC
22.003632	58.809013	55.621006	EIF1AD		NM_032325	Homo sapiens eukaryotic translation initiation factor 1A domain containing (EIF1AD), mRNA.	GAATGACATACTGACTGT TGTTGCTTCTTTCTAGCA GTGCAGGGTGAAAC	ILMN_1680150	GCGTGCTGTAGAATCTCCCATCTCTGAAACAGG CGTGAAAACCTGTACTG
40.988365	98.38512	98.49486	TMEM34	FLJ10846	NM_018241	Homo sapiens transmembrane protein 34 (TMEM34), mRNA.	GTAGAACAGGCTCTGGC CCACCCATATCTGGAGC AGTATTACGACCCGAG	ILMN_1767320	ACCTAGGATGGGGTTTCTCTAATTGCTAATCACA ACCCCACTGGGTCATG
52.667854	152.75595	150.18512	C14ORF80	MGC16771	NM_173608	Homo sapiens chromosome 14 open reading frame 80 (C14orf80), mRNA.			CTAGCAGCACTGGGGACAGGAATGACTGGTCCC TTGAGGAGGTCGTGACA
125.51845	858.9226	840.9309	IPO7	RANBP7; FLJ14581; MGC138673	NM_006391	Homo sapiens importin 7 (IPO7), mRNA.	CATCATAAAAGCAAAGTC AGCCAGCTGATATTTTGG TTCTCAAAAACTGC	ILMN_1718001	GTGCTCCAGTTGTGCCAAGTTCTTTCAATTTTGG AGGCCCAGCACCAGGG
162.62679	374.98096	374.51013	SALL3	ZNF796	NM_171999	Homo sapiens sal-like 3 (Drosophila) (SALL3), mRNA.			GTGGTCTGTAGCCCAATAACTGGGGAACGAGTT ACAGACAAACATCACCG
2310.1895	3527.2893	3523.856	CNBP	ZCCHC22; CNBP1; RNF163; PROMM; ZNF9; DM2	NM_003418	Homo sapiens CCHC-type zinc finger, nucleic acid binding protein (CNBP), mRNA.			CAAGTAACATCTGTATCAGGCCCTACATAGAACA TACAGTTGAGTGGGAG
160.81429	704.59344	700.04346	RAD51AP1	PIR51	NM_006479	Homo sapiens RAD51 associated protein 1 (RAD51AP1), mRNA.	CTGGCTCCCGAGAACTT AAAAGAAGGGAGAAACC TCAACAAAGTCCAGCC	ILMN_1684439	CCCTTTTTCTTGATACCACTCATCCACGTGTTCC TGATTGTCCACATTTC
12.790279	104.77272	101.930954	DUSP10	MKP-5; MKP5	NM_007207	Homo sapiens dual specificity phosphatase 10 (DUSP10), transcript variant 1, mRNA.	TGAGAATACTTGTCCCTG GAGGATTATCACACCCC AAATGCATAATCTCG	ILMN_1757689	TGCCCTCCCAGCCACTTCACATAGTCCTCGAGTC CCTGAAGAGAGAAGGC
302.98096	995.9684	981.77673	PRSS3	TRY3; MTG; TRY4; PRSS4	NM_002771	Homo sapiens protease, serine, 3 (mesotrypsin) (PRSS3), mRNA.	AGCAGAGGGCAGCTGAG AGGCTGGGTGGCTGGG CCTGGGAGACACACAGA	ILMN_1660907	TGAGCTTTGGTGCTGACTACCCAGACGAGCTGA AGTGCCTGGATGCTCCG
107.53928	156.78928	156.68512	TYW3	C1orf171; FLJ40918	NM_138467	Homo sapiens tRNA-yW synthesizing protein 3 homolog (S. cerevisiae) (TYW3), mRNA.	AGGACGGTGAGGATGAG CCCACGCTGGTGCAGAA GGAGCCTGTAGAAGCA	ILMN_1725705	AGGAAATTTGGGCAGGAAAGGGAACTCACAGTG TCGGAATGCCTGGAGCA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
72.45313	79.997856	80.09802	AP2B1	DKFZp781K0743; AP105B; CLAPB1; ADTB2; AP2-BETA	NM_001282	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), transcript variant 2, mRNA.	GGCTCCAGCATCACTCC TCTGCCACCTTGGGGTG TGGGGCTGGATTAAAA	ILMN_1792521	GCAAAACCTGTTGCCTCCACCACGGCTTCCCTCT TGGCTCATTCCAAGCT
32122.414	45105.215	45011.883	UBA52	CEP52; HUBCEP52; MGC126881; MGC57125; RPL40; MGC126879	NM_001033930	Homo sapiens ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), transcript variant 1, mRNA.			GATGATCTGCCGCAAGTGCTATGCTCGCCTTCA CCCTCGTGCTGTCAACT
122.02549	448.93097	446.08093	FANCI	KIAA1794; FLJ10719	NM_018193	Homo sapiens Fanconi anemia, complementation group I (FANCI), transcript variant 2, mRNA.			TTGGTTAGGATGCCACCTCAAGAACTGTAACTGA GAGCTCAGAAGTGAGC
40.95214	182.5893	178.50177	XRCC3		NM_001100118	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 3 (XRCC3), transcript variant 3, mRNA.			CCTTACATCTGGCTGGAAAGCAGAGCCTCCTGG GAACACATCTGGCTGCA
12.538416	580.6726	576.1309	MDM2	hdm2; HDMX; MGC71221	NM_002392	Homo sapiens Mdm2 p53 binding protein homolog (mouse) (MDM2), transcript variant MDM2, mRNA.	TCCTGTCCTAGTAAAATG GGCAAGTCCCTCTACCC CCCACCCTCACCTGG	ILMN_1688439	CCCCCCTTCCATCACATTGCAACAGATGTTGGGC CCTTCGTGAGAATTGG
35.39872	140.40594	139.12679	EZH2	EZH1; ENX-1; MGC9169; KMT6	NM_152998	Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), transcript variant 2, mRNA.	GTCCTGGAGGTGTAGTG GAGAGCAGTGGAAATGC ACCAAGGAGATGAGGG	ILMN_1703172	CGGCATCGAAAGAGAAATGGAAATCCCTTGACAT CTGCTACCTCCTCCCC
181.74345	309.32263	308.95593	NKRF	ITBA4; NRF	NM_017544	Homo sapiens NFKB repressing factor (NKRF), mRNA.			GACTCACAGCAACTCTCCATTATAGCTTTCACAC GGTTTGGATGTGCAGC
472.3351	663.2976	662.5851	PGM3	AGM1; PAGM; DKFZp434B187	NM_015599	Homo sapiens phosphoglucomutase 3 (PGM3), mRNA.			GCTTGGCAGTATTTCAGCTGGCTGGAGGAATTG GAGAAAGGCCCCAACCA
193.15594	1886.5476	1927.6809	FXR2	FMR1L2	NM_004860	Homo sapiens fragile X mental retardation, autosomal homolog 2 (FXR2), mRNA.	AGCCAGCCTGGATCATT TGTTGGCAGTACATATTG GCTGAAGTCAGTTTT	ILMN_1696051	TGCTATCCCTCCTCCCATCCTGTACCCCCCATTT CTGGGGCCTCATCACT
108.42679	236.09763	235.98929	TRIM46	TRIFIC; GENEY; FLJ23229	NM_025058	Homo sapiens tripartite motif-containing 46 (TRIM46), mRNA.	CCCTTCAGGGACCAGCG TCACCCTCCACCATGCAA GATCTCAACACCATG	ILMN_1703864	CATGCTTTACCTGTCCCACACCCATGCCAATGTG CCAAGTCTCCCTTGGG
1515.8809	2342.356	2342.7476	AMD1	ADOMETDC; AMD; DKFZp313L1234; FLJ26964	NM_001033059	Homo sapiens adenosylmethionine decarboxylase 1 (AMD1), transcript variant 2, mRNA.	AGAGCCAGTCCTGTCGG CTGGGCCCTTGGACGGC TGTCAGTTTTGCACAT	ILMN_1784352	GGAGCTCTGTTTTGAGGACCAATGCTTAAGGTG GACTTTGTTCGTAAACA
12.764698	70.61104	66.103584	TNRC6A	MGC75384; GW182; TNRC6; FLJ22043; CAGH26; KIAA1460; DKFZp666E117; GW1	NM_014494	Homo sapiens trinucleotide repeat containing 6A (TNRC6A), mRNA.			ACCTCCACGATTTCGCCACCAGGAACACAAACA GCTTCTAAAGAGGGGTC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
840.48096	2027.4642	2006.231	HNRPDL	JKTBP2; JKTBP; laAUF1; HNRNP	NR_003249	Homo sapiens heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), transcript variant 3, transcribed RNA.	CACCAAAGAGGTTCCCA AGACAACTCGGAAGGGA AAAGGGACCCATCGAG	ILMN_1741604	CGCACGTTGCGGGCAGAGCGCAAGGCATACAC CAGAAAACGCTGTCCTGT
441.38513	1677.906	1687.5101	CDC2	DKFZp686L20222; CDK1; MGC111195; CDC28A	NM_001786	Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 1, mRNA.			GGGCACTCCCAATAATGAAGTGTGGCCAGAAGT GGAATCTTTACAGGACT
11.244767	407.4018	426.39758	HOXC4	cp19; HOX3E; HOX3	NM_014620	Homo sapiens homeobox C4 (HOXC4), transcript variant 1, mRNA.	CCAGTGGGCTCTGGCGC CTATGGCTCTGTGTGTG CTGCTTTTGACACAAA	ILMN_1788002	TATTGCAAGGTGTGATGGTCTGGCTTGGGTGAA TTTCAGGGGAAATGAGG
74.116936	117.96011	118.001785	METTL6	MGC24132	NM_152396	Homo sapiens methyltransferase like 6 (METTL6), mRNA.	TGATGGATCCTAGGGTT CTTCATCACATGGGTGG TATGGCAGGACTTCAG	ILMN_1753862	CAGACACTGGACCACCAGAGAGTTTGAGGAGCT AAGATCATGTAGAGAGT
56.55319	84.63132	84.2727	KLF10	TIEG; EGRA; TIEG1	NM_005655	Homo sapiens Kruppel-like factor 10 (KLF10), transcript variant 1, mRNA.			ACCTCCAACCCCTGCTCCCACACAGTGACAGAC CGGAAAGTGAAGAGTCA
128.36012	172.5476	172.32262	ALG14	MGC19780	NM_144988	Homo sapiens asparagine-linked glycosylation 14 homolog (S. cerevisiae) (ALG14), mRNA.	GGGGGTGGGGGCAGGG AATTAAGTTGGTGGGCT CGAAAATCCCATTCATA	ILMN_1680998	ACTACATTCACCGAATTCCAAGAAGCCGGGAGG TTCAGCAGTCCTGGCCC
226.25179	1373.3394	1408.856	FOXN2	HTLF	NM_002158	Homo sapiens forkhead box N2 (FOXN2), mRNA.	GACACTGGTCAGTATTTC TTTTTTGGGGGGAACTA GGAGAGCAGGAGTAG	ILMN_1781870	ACTGCCAGTAGATGACCAGTCACAAGTGAACCA CTTCTCAGTTGCCAATC
732.5476	886.2226	892.74347	MRPS28	FLJ22853; MRP-S35; MRP-S28; HSPC007; MRPS35	NM_014018	Homo sapiens mitochondrial ribosomal protein S28 (MRPS28), nuclear gene encoding mitochondrial protein, mRNA.			CCAGAAGTGGATGGAGAGAAATACCAGAAAGGA ACCAGGGTCCGGTTGCG
62.034218	100.08929	100.81013	MGC3207		NM_001031727	Homo sapiens hypothetical protein MGC3207 (MGC3207), transcript variant 1, mRNA.	GAGCTCTGAAGCTTTGA ATCATTCAGTGGTGGAG ATGGCCTTCTGGTAAC	ILMN_1780141	CCAGGCTGCCCAGATTCAAATCCTGACTCCGCC ACTTTTCCCACTGTATG
28.266582	83.68672	82.88114	C6ORF48	G8; D6S57	NM_001040437	Homo sapiens chromosome 6 open reading frame 48 (C6orf48), transcript variant 1, mRNA.			TGCCATGTTGTCCAGGCTGGTCTCTACTCCTGG GCTCAAGCAGTCCTCCT
123.72264	479.43927	487.8476	C15ORF23	FLJ14502; MGC141729; MGC141728; TRAF4AF1; HSD11	NM_033286	Homo sapiens chromosome 15 open reading frame 23 (C15orf23), mRNA.	CCAAAGAGGGAAGGGCC AAAGCTTTTTCTACCTGT GCATCCCACTTTTTG	ILMN_1790988	GCGGTGAGACCCTGGCATCACGACAAGAATCCA CTACTGATCACATGGAC
306.19763	412.28513	406.48096	HSPA4	hsp70; HS24/P52; RY; MGC131852; APG-2; hsp70RY	NM_002154	Homo sapiens heat shock 70kDa protein 4 (HSPA4), mRNA.	ATGCTGACACTGCCAAC CTCCAGTATCCTCACCCT CGCAGACGATATCTC	ILMN_1708619	GCCCTATAATTTCAAAGCCCAAACCCAAAGTGGA ACCTCCAAAAGAGGAA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
20.616997	122.33928	124.43512	MCM10	PRO2249; CNA43; MGC126776	NM_018518	Homo sapiens minichromosome maintenance complex component 10 (MCM10), transcript variant 2, mRNA.			ACCACAGCAAAGGTTTCATTCAGGAGATTCTTCC ATCTGGGCAACCTGGT
76.33147	94.85596	95.18513	ARHGAP11A	GAP (1-12); KIAA0013; MGC70740	NM_199357	Homo sapiens Rho GTPase activating protein 11A (ARHGAP11A), transcript variant 2, mRNA.			TTTTCTATCAACAATTGGGAAATGCTTATACATGT AAATATGAAAATGTT
441.6768	879.9351	886.3476	RQCD1	RCD1; CNOT9; RCD1+	NM_005444	Homo sapiens RCD1 required for cell differentiation1 homolog (S. pombe) (RQCD1), mRNA.			CTTGGGTAAGATGGTCCTGCAGCTATCCAAAGA GCCTTCTGCCCGTCTGC
99.4518	170.81845	163.95596	LIN7C	LIN-7C; MALS-3; FLJ11215; VELI3; LIN-7-C	NM_018362	Homo sapiens lin-7 homolog C (C. elegans) (LIN7C), mRNA.			TGCTAGTAGTGTTTCTTCAAAGGTTATTCCAGGT ATGGTTAAGTAGTGAG
1738.856	2057.906	2062.0977	CALR	FLJ26680; cC1qR; RO; SSA	NM_004343	Homo sapiens calreticulin (CALR), mRNA.			CCCTCCAACCTGGGGGGCAGTGGTGTGGAGAA GCCACAGGCCTGAGATTT
16.963947	136.51012	138.08928	LOC653604		XM_497711	PREDICTED: Homo sapiens similar to H3 histone, family 2 isoform 2 (LOC653604), mRNA.	CCAGGAGCCCGAGAAGA AATCCCAGATGCCCAAC ACCACTGAGAAGCTGC	ILMN_1688877	ATGGCCCGTACTAAGCAGACTGCCCGCAAGTCG ACCGGCGGCAAGGCCCC
847.6476	1748.281	1721.4559	C18ORF55	HSPC154	NM_014177	Homo sapiens chromosome 18 open reading frame 55 (C18orf55), mRNA.	GCCTTTGCCTCGCCGAG GGAGGTCTTGCTGGAGC GGCCGTGCTGGCTGGA	ILMN_1717780	GGCGTGGACTCGCTACTCCGTTCTTCACAGCTG CCTTCCAGAATGTGTTC
56.54869	132.51012	128.14345	CCT6AP1	DKFZp779B0634	NR_003110	Homo sapiens chaperonin containing TCP1, subunit 6A (zeta 1) pseudogene 1 (CCT6AP1) on chromosome 7.	CCGAGGAAGCTGGGCG GTACCTGGAGACCTACA AGGCCTATGAGCAGAAA	ILMN_1726562	GTCCTAATCATTGGAGAGCTGCTGAAACAGGCA GATCTCTACATTTCTGA
71.97715	179.47263	174.62262	LNPEP	P-LAP; PLAP; IRAP; CAP	NM_175920	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), transcript variant 2, mRNA.	GGACATGCCAACTCGGA GAAAGCTCCCCTGCGGA AAACTTCAGAGGCTGC	ILMN_1659378	TTCTACCCTAAGAGCCGCCATCACTTCAGGCCG CTGGTTTGTCAGCCATC
7.0834045	110.33098	101.03097	CPEB1	MGC34136; CEBP; CPE-BP1; MGC60106; CPEB; FLJ13203	NM_001079534	Homo sapiens cytoplasmic polyadenylation element binding protein 1 (CPEB1), transcript variant 4, mRNA.	TCGGGGACCTCCAAAGA CTAAACTGACAAGCCTTC AAGGAGCCCAGGGGT	ILMN_1677532	GCCCCTCCTAGGGAAGCTGTGTGCCAAAGAACC AGTGTCATAACCCCTCC
203.72678	235.29346	230.28928	ASCC3	RNAH; ASC1p200; dJ121G13.4; HELIC1; DJ467N11.1; MGC26074	NM_006828	Homo sapiens activating signal cointegrator 1 complex subunit 3 (ASCC3), transcript variant 1, mRNA.			CTAACTCTGCCGCATAAACTATAAATCTGTAAGG TGGTACACAGCGTGTC
2167.7642	3435.281	3388.8975	RARS	ArgRS; DALRD1; MGC8641	NM_002887	Homo sapiens arginyl-tRNA synthetase (RARS), mRNA.	CTCACCCGCCATTTTGTA GGTCTGAGGGTGCTTGG ACATACTCTTCGAGC	ILMN_1657440	TGTGGCGTATGCTGCTATGTGAAGCAGTAGCTG CTGTCATGGCCAAGGGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
8.083271	149.43094	137.69762	MYB	c-myb_CDS; Cmyb; c-myb; efg	NM_005375	Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA.	AGCAACATGCTTGGTAAT TTGGCATCTGTTAAGGTA GGAGAGTGGTGAAC	ILMN_1788778	GTGTTTGCAACTGGGGAGACAGAAACTGTGGTT GATAGCCAGTCACTGCC
129.96011	446.98926	436.03094	QKI	DKFZp586I0923; Hqk; QK3; QK	NM_006775	Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 1, mRNA.	GGAAGGGCAGGATGTAC CCCTGAAACCGGATGCT GAGTACCCTGAATGGC	ILMN_1658486	GTTCGAAGGCACGATATGCGTGTCCATCCTTAC CAAAGGATTGTGACCGC
1999.3477	2354.4893	2349.7227	SF3A2	SF3a66; SAP62; PRPF11; PRP11	NM_007165	Homo sapiens splicing factor 3a, subunit 2, 66kDa (SF3A2), mRNA.			TTTTGTACTGCCCCCCGCTCATTAAACAGCCTCC CCCAGCCCTGAGTGCA
178.42679	511.58093	497.9018	C19ORF48	MGC13170	NM_199250	Homo sapiens chromosome 19 open reading frame 48 (C19orf48), mRNA.			CCACACACCCAGGAGAAGGTGGATAAGTGGGCT ACCAAGGGCTTCCTGCA
69.454895	135.61429	132.41846	HOXD13	SPD; BDE; HOX4I; BDSD	NM_000523	Homo sapiens homeobox D13 (HOXD13), mRNA.	GTGCGACCTCGATCTGT CCCAAGCATTCATGTTCC CTCACCAGCTGTAGT	ILMN_1757336	CCAGGTTGGCCACAGACAGCTTAGAAGCCATTC GGTTGTCTCCAAAAGGC
19.312956	129.08928	120.33511	FAM134B	FLJ22155; FLJ20152; FLJ22179	NM_001034850	Homo sapiens family with sequence similarity 134, member B (FAM134B), transcript variant 1, mRNA.	TTGGCAAAGGTCAGGCA GGGGCTGGGAAAGCATT AGGTGGACCAGGCATG	ILMN_1754132	GCCTCATGACTGTGTTTGATGTCCTTTATTGATA CAAAGTGAGCCTGTGC
16.30287	96.785126	91.89351	ATP11C	ATPIQ; ATPIG	NM_173694	Homo sapiens ATPase, class VI, type 11C (ATP11C), transcript variant 1, mRNA.	GCTGTGCCCTGCGTGTC GCCCAGGCAGGTGTTTG TTTTTGAGCGCAGATT	ILMN_1684192	ATCTGAGCTGTAGAAGGGCATCTGACTCATTATC CGCCAGACCTTCAGTC
161.82689	806.4143	784.256	TTK	PYT; MPS1L1; FLJ38280; ESK	NM_003318	Homo sapiens TTK protein kinase (TTK), mRNA.			CTGGGCCAACTTGTTGGTCTGAATTCTCCTAACT CCATTTTGAAAGCTGC
1693.3893	6151.7144	6040.7812	PURB	MGC126786; MGC126784; PURBETA	NM_033224	Homo sapiens purine-rich element binding protein B (PURB), mRNA.			GCAGAGTCCAGACGGGCTGTTGATCTCACTGCC TGTAGGTTGAAGCTCAG
79.35768	162.73096	160.38928	KIAA0586	Talpid3	NM_014749	Homo sapiens KIAA0586 (KIAA0586), mRNA.	CGCAGGGAGACAGTTCA GTCACTGCAATCTTCATG CCCATCAGTTTCTTG	ILMN_1659452	GAGTCTCAGCACAATGCAGGAGGACATGGAGTC TTCGGGGGCAGATACCT
1226.231	1403.0143	1393.7268	MKI67IP	NIFK; Nopp34	NM_032390	Homo sapiens MKI67 (FHA domain) interacting nucleolar phosphoprotein (MKI67IP), mRNA.	GGAGTGGTGTGTACCCC TAAATCCTCCCACCCCAG CACTGCCCATCTGTA	ILMN_1736936	GTCCATCTACATGGTTTGTCGGGGACATTTAACT CATGGAGGTGCTTTAG
2181.9226	3025.9143	3039.3892	ARS2	ASR2; MGC126427	NM_015908	Homo sapiens arsenate resistance protein 2 (ARS2), transcript variant 1, mRNA.	CAGAGGAAACAGAAGAT AACGCTCAAGTGGCTGA ACAAATGGCCAGTGGA	ILMN_1753658	TCCCCCGTTCCTCAGTCCTGTATCATCCATACTT GTACTACCTTGTCCTA
151.73096	293.97263	288.75595	ARID4B	BCAA; RBP1L1; MGC163290; BRCAA1; SAP180; RBBP1L1; DKFZp313M2420	NM_016374	Homo sapiens AT rich interactive domain 4B (RBP1-like) (ARID4B), transcript variant 1, mRNA.			GAGTGCTATCCACCAGGCATGAAAGTCCAAGTG CGGTATGGACGAGGGAA
856.08093	1023.3476	1015.5518	ETV5	ERM	NM_004454	Homo sapiens ets variant gene 5 (ets-related molecule) (ETV5), mRNA.	TGCCTTCCTTGACCATCT ACCTTGAACTAACCCACT CCCAGCTCCCAGCC	ILMN_1794213	GGGCATAGGACAGCGGCATCACGGTTGCATTCC CATTGGACTCATGCACC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1250.0226	3548.356	3498.4058	PRC1	MGC1671; ASE1; MGC3669	NM_199413	Homo sapiens protein regulator of cytokinesis 1 (PRC1), transcript variant 2, mRNA.	GCAGCATAGTTGGGAGC TTCTGGATTCCATCTGCA CCTGTGAGCCCCATG	ILMN_1698463	CATGTCACTACTGGGGAGGTGTTCCTGCTCTAG CTTCCACGATGAGGCGC
23.841621	100.60186	99.15615	CDC25C	CDC25	NM_001790	Homo sapiens cell division cycle 25 homolog C (S. pombe) (CDC25C), transcript variant 1, mRNA.			GCCGCTGTCTGCGTGAAGAGGACAGGTCTCTGA ACCAGTATCCTGCATTG
323.2101	1128.1476	1109.4226	NUP107	NUP84	NM_020401	Homo sapiens nucleoporin 107kDa (NUP107), mRNA.			GCTCAGAGAGTCCTCTCTAATGCTCCTAGACCAG GGACTTGACCCATTAG
998.3726	7531.0977	7367.3975	BRPF1	BR140	NM_004634	Homo sapiens bromodomain and PHD finger containing, 1 (BRPF1), transcript variant 2, mRNA.	TTTCGTACCTTCCCACTG GCCTCAAGTGAGCCAAG AAACACTGCCTGCCC	ILMN_1727458	TATTCTCATTTGTAACTGCGTTTCCGGGTCGCGC CAGAGTCATTTGGTAC
112.73512	467.56012	462.85596	TMPO	MGC61508; PRO0868; CMD1T; TP; LAP2	NM_003276	Homo sapiens thymopoietin (TMPO), transcript variant 1, mRNA.			CCATGGGAAATGCCACTGTAGGTCGTCGATACC TCTGGCTGAAGGATTGC
1147.0227	1608.281	1601.781	STIP1	HOP; STI1L; IEF-SSP-3521; P60	NM_006819	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA.			GAAGACACAGAGACTCGTACCTGCGCTGTTTGT GCCGCCGCTGCCTCTGG
1743.7976	2611.331	2611.931	SCFD1	KIAA0917; C14orf163; SLY1; RA410; STXBP1L2	NM_016106	Homo sapiens sec1 family domain containing 1 (SCFD1), transcript variant 1, mRNA.	AATGTGTAGGAAAAGCCT TCTGGCCACCCAGAGAG CCGGAGCCCTGCTTG	ILMN_1812080	CCATTCCAAGAGGCCATTGTTTTTGTGGTGGGA GGAGGCAACTACATTGA
261.34763	1780.4309	1733.2686	NUP153	HNUP153; N153	NM_005124	Homo sapiens nucleoporin 153kDa (NUP153), mRNA.	CTTGAGTGTCTTGCTGA GGGTTACTGTATCTAGCA GGTGATGGAGCTTGG	ILMN_1750412	CACTGATTTGACATAGTCTGGCTGTACCCAGGAA TGGAGCCTGCACGGTG
177.69763	1035.9476	993.8143	HMMR	RHAMM; MGC119495; IHABP; MGC119494; CD168	NM_012484	Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR), transcript variant 1, mRNA.			TTTCTTCAGAGTTTGTCATATACTGCTTGTCATCT GCATGTCTACTCAGC
24.850307	195.65594	186.78513	BLM	MGC126616; RECQL2; BS; RECQ2; MGC131620; RECQL3; MGC131618	NM_000057	Homo sapiens Bloom syndrome (BLM), mRNA.	CCCTCAATATCACCTCCC TTCAGATGCACTCCCTGA GACTCCTGAGCCAG	ILMN_1743219	TGCCAGCCTCCCAAAGGTCTAAGAGGAGAAAAA CTGCTTCCAGTGGTTCC
248.83928	379.18927	378.13095	SAP130	FLJ12761	NM_024545	Homo sapiens Sin3A-associated protein, 130kDa (SAP130), mRNA.			CCACCCCATTCGGTTCTTCTGCCTGACCTTCAAA TGCCCATGTTGGCCTT
160.64345	490.5518	480.81012	CSNK1A1	HLCDGP1; PRO2975; CK1	NM_001892	Homo sapiens casein kinase 1, alpha 1 (CSNK1A1), transcript variant 2, mRNA.	AGAAGGAATGGCTGGTC CAGAGGCTTTTGTCCACT CCCTCTCACTGGAAG	ILMN_1654612	GCAGGCCCAAACCCCCACAGGCAAGCAAACTGA CAAAACCAAGAGTAACA
70.993546	244.42262	237.16013	C1ORF135	FLJ14264; MGC2603	NM_024037	Homo sapiens chromosome 1 open reading frame 135 (C1orf135), mRNA.	AGCCTTAGTCCAGGGGT GTGGCTCTGTCCGGGTG CAGTATGCAGTCATGT	ILMN_1783448	TCTGGATGTGACTCTGTTACCCTTTTCCCACAAG ATAGGAGGGAATCCCC
91.381386	422.91846	411.98096	ESPL1	SEPARIN; ESP1; KIAA0165; FLJ46492	NM_012291	Homo sapiens extra spindle pole bodies homolog 1 (S. cerevisiae) (ESPL1), mRNA.			GCTGGCATCGTGCTCAAGTACATCATGGCTGGT TGCCCCTTGTTTCTGGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
167.52261	455.8476	443.16846	PPAT	ATASE; GPAT; PRAT	NM_002703	Homo sapiens phosphoribosyl pyrophosphate amidotransferase (PPAT), mRNA.	AATTGCCTTGGGTCCTG CCGCACAGAGCGGCCTG TCTTTATCAGAGGTCC	ILMN_1702706	GGCAGCATGGAGGAGGCAAGACCTGTGGGTCA ATTTTGAACTGGCCTTAC
85.30209	114.43512	109.29346	ANKRD27	PP12899; FLJ00040; VARP; DKFZP434L0718	NM_032139	Homo sapiens ankyrin repeat domain 27 (VPS9 domain) (ANKRD27), mRNA.	CCCATTCCAGAGAGGGT CCTGCCCCATACCCAGA AGGAAAGAATGCTGCT	ILMN_1712936	GAGGCCAGGCTGAAATGTCATATCTGAAGGAAG AAAGCAGCAGCTGGACA
39.615562	75.048676	68.04352	SART3	RP11-13G14; P100; TIP110; KIAA0156; p110(nrb); DSAP1; MGC138188	NM_014706	Homo sapiens squamous cell carcinoma antigen recognized by T cells 3 (SART3), mRNA.			CCTCTTGTGGGGGTGGGTCTGAGGGAAGTCAGC TATAAAACATTTGCTGG
525.9226	697.71423	673.08093	SLC30A5	ZnT-5; MGC5499; ZTL1; FLJ12496; ZNTL1; FLJ12756; ZNT5	NM_022902	Homo sapiens solute carrier family 30 (zinc transporter), member 5 (SLC30A5), transcript variant 1, mRNA.	GGCAGCACTTATGCTCT GTGACAGTATTGTGTGTC ATAGTTGAGCAGTAG	ILMN_1673478	CATGCAGTTGCTGGGTGTATTATTTCACTCTTGT GGTTTTTTGGCCTCAC
123.21847	191.62679	180.03928	MLX	MXD7; MAD7; TCFL4	NM_198204	Homo sapiens MAX-like protein X (MLX), transcript variant 2, mRNA.			TGAAGGGTGAAAGGGCACCTTGTGCCTAGACTA GGGCTGCCTGGTCAGTC
47.54752	76.73982	70.03239	CEP290	FLJ21979; FLJ13615; KIAA0373; 3H11Ag; 3H11	NM_025114	Homo sapiens centrosomal protein 290kDa (CEP290), mRNA.	GCTTTCTGGGTCGGGTG TGGTGGTTCTTGCCTATA GTCCCAGTGCTTTGG	ILMN_1688281	GCTAACAAGGACCAAAGTGGAGCTGAAAGCACC ATACCTGATGCTGATCA
161.24762	802.0476	651.1726	LRP8	HSZ75190; APOER2; MCI1	NM_017522	Homo sapiens low density lipoprotein receptor-related protein 8, apolipoprotein e receptor (LRP8), transcript variant 3, mRNA.	GGTGGGCCTGTGGTGAT GGTTTGCATCCTTCCTCC CTTGTCCCAATAAAG	ILMN_1743747	GAGACGTTTCCAGATCAGCCCAAGTTTACTATAG AGACTGGCCCAGGCAC
71.06278	129.74345	123.28929	NMNAT2	C1orf15; PNAT2; KIAA0479; PNAT-2; MGC2756	NM_015039	Homo sapiens nicotinamide nucleotide adenylyltransferase 2 (NMNAT2), transcript variant 1, mRNA.			GGATCCACATGGTCTTGAGGGTTGGCATGAGGA GGGGGAAGCTTTTTTGA
579.96423	1030.0726	964.881	RAN	TC4; Gsp1; ARA24	NM_006325	Homo sapiens RAN, member RAS oncogene family (RAN), mRNA.			GCTCCACCTTCATATTGGCTAGGTAGGGTCACCT AGGGAAGCACTTGCTC
46.14446	75.77009	71.13081	PKNOX1	PREP1; pkonx1c	NM_004571	Homo sapiens PBX/knotted 1 homeobox 1 (PKNOX1), mRNA.	AGGGGGCGGGCCTGAG GGCGGCGGTTTCCCGAA CGGAGCGGGGCCTGCT G	ILMN_1651436	TGTCCAGAGGGGGTTCTGCCCCTTGTGAAGGCC CATTCCTGGCACTTAGA
196.69762	231.86429	227.64761	QKI	DKFZp586I0923; Hqk; QK3; QK	NM_006775	Homo sapiens quaking homolog, KH domain RNA binding (mouse) (QKI), transcript variant 1, mRNA.			TGAACCTAGTGGTGTATTAGGTGCGGTGGCTAC TAAAGTTCGAAGGCACG
322.3601	1652.281	1387.606	CLCF1	CISS2; NNT1; CLC; BSF3; NR6	NM_013246	Homo sapiens cardiotrophin-like cytokine factor 1 (CLCF1), mRNA.	GGCCAAGGTAAGAACTG AGAAGGGAGGCATGAGG CGTGAGGCTGGAAGAT	ILMN_1813307	CCAGTATTACGGTGCCTCTTCTCTGCCCCCTTTC CCAGGGTATCTGTGGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
150.27678	374.76846	334.32263	DIAPH3	FLJ34705; DRF3; DKFZP434C0931; diap3; DKFZp686A13178	NM_001042517	Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), transcript variant 1, mRNA.			GACACTCATACGTCTACTGGGAGGATCAAGGCA GCTGAGAAGAAGGAAGC
113.89345	275.18097	253.24762	ABHD10	FLJ11342	NM_018394	Homo sapiens abhydrolase domain containing 10 (ABHD10), mRNA.	TCTGACTTCATATCTGTG GGATCCACACAATGGGG AGGTACTGGCCTTGG	ILMN_1696318	CCAGGCAGAGACTACCTTTGTGACCAGCTCCCA GTAAAAACCCCAGGCAC
216.73929	301.65594	292.0476	THOC2	CXorf3; dJ506G2.1; THO2	NM_020449	Homo sapiens THO complex 2 (THOC2), transcript variant 2, mRNA.	TGACCTTTCTCTGGCCC CCAGCTCTAGTGTTTGA GTAAAGGAGACTGAGG	ILMN_1688479	GAGAAGATGGATAAAATCTCCTCCGGTGGCAAA AAGGAGTCCAGGCATGA
40.681957	377.0476	294.6101	RNF44	KIAA1100	NM_014901	Homo sapiens ring finger protein 44 (RNF44), mRNA.			CCCAGCCCTGGCTGGGCCCAGCGCCTGTGTTCT GTGTTAGAAAGGTTTTA
67.59301	124.67262	112.96011	ZC3HAV1	FLJ13288; ZC3HDC2; MGC48898; DKFZp686F2052; FLB6421; ZC3H2; ZAP; DKFZp686H1869; DKFZp686O19171	NM_020119	Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, mRNA.	GGCGGCCCCGTCTCTGT TTTCATTCCCTGAGATGT GGTGCTTTCTCTCCT	ILMN_1780406	CCAACATTTGTGCCTCAGTGGTATGTGCAGCAG ATGAAGAGAGGGCCAGA
58.873806	465.8976	355.44763	POLQ	DKFZp781A0112; PRO0327; POLH	NM_199420	Homo sapiens polymerase (DNA directed), theta (POLQ), mRNA.	CTGAAGAAACAACGCAG TGTCACGCAAGCCACTC AGACAAGCCCAGGGGT	ILMN_1737705	CAGTCCCTTAGTGCCTCTTTCTGTTTGTGGCATG GTGAGAAAACCCATGC
9621.147	11266.139	11040.273	COX7A2	COX7AL1; MGC118950; MGC118952; MGC126877; COX7AL; MGC118951; MGC126875; COXVIIa-L MGC18000; CAP-H2; MGC8640; MGC5305; hCAP-H2; MGC2455; 384D8-2; MGC15858; 384D8_6; MGC4133	NM_001865	Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), mRNA.	GGAGGCCAGTGTAACGT TACATGACTCGTTGAGAA AGTTGAGGAATTTCC	ILMN_1746664	CGGAATCTGCTGGCTCTTCGTCAGATTGGGCAG AGGACGATAAGCACTGC
32.577946	91.414314	79.532104	NCAPH2		NM_152299	Homo sapiens non-SMC condensin II complex, subunit H2 (NCAPH2), transcript variant 2, mRNA.	CAGGATCGGCGGAGTTC GAAAACGAACTTCCCAC GTTTGCTATGTTGCCC	ILMN_1723230	AGGAGCAGCCAATGGAAGTTTCCGTGTGCAGGA GCCCTGTCCCAGCACTC
83.173096	394.44763	322.41428	SMC2	SMC2L1; hCAP-E; FLJ10093; CAPE; CAP-E	NM_001042550	Homo sapiens structural maintenance of chromosomes 2 (SMC2), transcript variant 1, mRNA.			GCAGCCTTGGATCTTTCTCATACCCAAAACATTG GACAGATGCTGCGTAC
79.006966	105.65186	101.706085	NR3C1	GCCR; GRL; GCR; GR	NM_001020825	Homo sapiens nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) (NR3C1), transcript variant 6, mRNA.	CATGACCACTGGGATCC AGCCAGCGGGGGATTTC TTTTCCTGATGGACTG	ILMN_1759504	CCTGGTCCACCCAGGATTAGTGACCAGGTTTTC AGGAAAGGATTTGCTTC
372.73096	626.68933	581.15594	H1FX	MGC8350; H1X; MGC15959	NM_006026	Homo sapiens H1 histone family, member X (H1FX), mRNA.	CCTGGGCTACTGCTGCC CTCTGGCCCAGCCCTGC TATCTCCCTCCGTCCT	ILMN_1710762	TGCTTTAGGTTTTTGAAACAGCCCCGGCGACGC CTCTATTGGCTCTCGGC
191.88095	244.94345	243.31012	EIF2B5	EIF-2B; EIF2Bepsilon; CACH; LVWM; CLE	NM_003907	Homo sapiens eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa (EIF2B5), mRNA.	ATGAAAGAGGACGCGAA AGGGAAGAGCGAGGAG GAGCTGGCCGAGTGCTT	ILMN_1693428	GAGGAGCTAAGCAGGCCCGGCAGTTGGAGGAA GGCCAGAGGAACAGCTTT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
196.98096	251.31012	242.53928	USP7	HAUSP; TEF1	NM_003470	Homo sapiens ubiquitin specific peptidase 7 (herpes virus-associated) (USP7), mRNA.			AGGTTAGTGGATCGGGGGTCCCTGGCTCAAGGT CTCTGGGCTGTCCCTAG
184.78928	332.7851	306.0476	CRLF3	CREME9; FRWS; CYTOR4; MGC20661	NM_015986	Homo sapiens cytokine receptor-like factor 3 (CRLF3), mRNA.			GCACGTGTGTATCCAATCTGCCTGTGACATGCAT TTTACTCTTTGCAGAG
90.59766	107.547615	107.33931	C19ORF29	cactin; NY-REN-24	NM_001080543	Homo sapiens chromosome 19 open reading frame 29 (C19orf29), transcript variant 1, mRNA.	CTCCTGGGACTCTCCAA CCAGGCTGAACATCAAA ACCTCCTCTTTGTGCT	ILMN_1663913	CCGACGGGAACATCTCCAACAGAAGCAAAACGG AAAGTGCCTCCCGGACC
131.81012	302.80594	275.93927	MMD	PAQR11; MMA	NM_012329	Homo sapiens monocyte to macrophage differentiation-associated (MMD), mRNA.			GGCTTGCCTTTAGATCGGGTGCTGATATTGCCT GTTTCCTAGTAATGGGC
69.019844	275.3393	223.28513	PHF19	MGC131698; PCL3; MGC23929; MGC149713; MGC149712	NM_001009936	Homo sapiens PHD finger protein 19 (PHF19), transcript variant 2, mRNA.	GCGCTGCTGTGGCTAAC ACCACTGTGTATGTTTCA TCATTGCTCTGAAGG	ILMN_1784083	AGTCCCTGCCTCTCCTGCCTCCTCCAGTGGGGC AGACCAGAGACTCCCAT
669.82263	1292.0476	1192.5725	TCF12	HEB; HsT17266; HTF4	NM_207037	Homo sapiens transcription factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12), transcript variant 2, mRNA.			CAGAAGTTGTTGCTTATGATGTGTGAGTGAACAT ATGCCACTGCCTGGCC
40.781334	276.7393	214.5893	C13ORF3	MGC4832; RAMA1	NM_145061	Homo sapiens chromosome 13 open reading frame 3 (C13orf3), mRNA.	CTGGGGAGACAAAAATA ACTGATCCGTTGGGTGT ATACCATGTGCCAAGC	ILMN_1659495	CCAAGGACCAAATCCTGGAGTTCTCCCAACTTTA GAGGATGGAAAGGGGC
79.977234	188.11844	165.91428	DARS2	FLJ10514; ASPRS; RP3-383J4.2; ASPRS. LBSL	NM_018122	Homo sapiens aspartyl-tRNA synthetase 2, mitochondrial (DARS2), nuclear gene encoding mitochondrial protein, mRNA.			ACATACTTGCCCTGGCTACCTCACCGGGCTGTT ATTGCTGGAATCAGAGG
142.40594	176.88928	171.15594	ZNF614	FLJ21941; MGC120638	NM_025040	Homo sapiens zinc finger protein 614 (ZNF614), mRNA.			GCTTACACTCCATCCAAACCTAACTCTGCCAACC ACTTTTCTCCTATCAG
537.1101	706.98096	682.1309	RBM25	S164; MGC105088; RNPC7; MGC117168; RED120	NM_021239	Homo sapiens RNA binding motif protein 25 (RBM25), mRNA.			ACACACCTGGAGAGGACATTTGAAAACACTGTTC TTACCCTCGAACCCTG
620.24756	1115.4309	1026.9976	NUP54	MGC13407	NM_017426	Homo sapiens nucleoporin 54kDa (NUP54), mRNA.			CTGTGTTTAATGATTATTGTCCATTGAGCCTGTA CTCTGCTTTCCATACC
1503.3142	2104.3726	2017.106	PSMC3	MGC8487; TBP1	NM_002804	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 3 (PSMC3), mRNA.	AGGCCATTTAATAAAAAG GGCACAAAGCCTGTCAG AGTTTTCAACGGTGC	ILMN_1785821	GAAAGCCAACCTACAATACTACGCCTAGGGCAC ACAGGCCAGCCCCAGTC
454.72678	1582.4559	1331.8851	ZWILCH	FLJ10036; FLJ16343; KNTC1AP; MGC111034; hZwilch	NR_003105	Homo sapiens Zwilch, kinetochore associated, homolog (Drosophila) (ZWILCH), transcript variant 2, transcribed RNA.	GAGTCCAGGAGTTTGAG ATGCGCCTGGGCAACAT AGAAACCTGTGTCTAC	ILMN_1668713	AGGCACTGGACATCCTCACGTGGAGTTCACAGG CTCATCAGTGAATTCTG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
106.33928	173.05179	161.53513	PAXIP1	TNRC2; PACIP1; CAGF29; PAXIP1L; CAGF28; PTIP; FLJ41049	NM_007349	Homo sapiens PAX interacting (with transcription-activation domain) protein 1 (PAXIP1), mRNA.	ACAGTCAGTGATGGTGG AGATGGAAGCAGCAGTG AGGAAATTAGGATTCC	ILMN_1699317	CCTTCACATGCTCTTGTTTTCCAGCTGCTTTCCT GGGGGATCAGACTGTG
105.026794	129.58511	126.42678	ZMAT5		NM_019103	Homo sapiens zinc finger, matrin type 5 (ZMAT5), transcript variant 1, mRNA.			ATGCTCCTGAGCTCCCCGAGGGCCATCTGGAGG ACTGGCTGGAGAAGAGA
656.0393	3382.8809	2864.7976	FEN1	RAD2; FEN-1; MF1	NM_004111	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA.			GAGAAGATGGGCAGAAAGCTGGAGCCCCTGGA GTTGGCTGTGTCTGTGTT
519.20593	791.2101	757.381	EXOSC6	hMtr3p; MTR3; p11; EAP4; Mtr3p	NM_058219	Homo sapiens exosome component 6 (EXOSC6), mRNA.	AACTGGGGGTGGTTCTA GGGGAACAGGGGGCGG GGGAGCTGTTTCTATTT	ILMN_1670508	TGTGTGTTTTCTGCGGCCCTGGATAATGCTGTAG CATTCAGGGTCGATTG
272.22263	727.42676	654.5768	RRS1	KIAA0112	NM_015169	Homo sapiens RRS1 ribosome biogenesis regulator homolog (S. cerevisiae) (RRS1), mRNA.	CAGAGCCTGAGATGGAC GTAAGGAAGAGAACTGG AGTGGCAGGGTCCCAG	ILMN_1664243	CCTGGCCGCTGCCTTCATTGAGTTTAAAGGGAC AGGATTGCCCTTCCGTC
83.48111	98.13928	96.48096	OR3A4	OR17-24; OR17-13; OLFRA06; OLFRA05; OR24; OR17-16; OR25; OR3A4P; OR3A5P; OR17-25	NM_001005334	Homo sapiens olfactory receptor, family 3, subfamily A, member 4 (OR3A4), mRNA.	TGTCGCTGAGCCGGACG ACTGCCACCATCGCGCC CATTCTTAGCGTGCCA	ILMN_1737435	CTTCGGACAAGGACAAGGGCATTGGCATCCTCA ACACTGTCATCAGCCCC
5152.1973	6490.298	6348.8726	S100A16	DT1P1A7; MGC17528; S100F; AAG13	NM_080388	Homo sapiens S100 calcium binding protein A16 (S100A16), mRNA.			GCTGTCTGGGGACCCTAAGAGTTTTCTCACCTGT TCAGTCTCATCTAACC
146.23096	550.32263	485.54346	KIF2C	KNSL6; MCAK	NM_006845	Homo sapiens kinesin family member 2C (KIF2C), mRNA.	TCCGTGAATCCCTTAGA GGTCTGTGAATTGTAGG TTAAGAACCCCTGCCC	ILMN_1762003	CTGGGGTTGTCCTGGCTCTGGGGAGAGAGACG GAGCCTTTAGTACAGCTA
133.14359	493.7726	429.7226	SPC24	SPBC24; FLJ90806	NM_182513	Homo sapiens SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae) (SPC24), mRNA.	CGCTGGTTTTGTCACATT CAGCATTATCCAGGCATC AGGCAACATCTGTC	ILMN_1725105	TAGAAGGCAGAGGCCGGCAGATCACTTGAGCCC AGGAGTTGGAGACCAGA
65.33041	287.8393	245.38928	ZWILCH	FLJ10036; FLJ16343; KNTC1AP; MGC111034; hZwilch	NM_017975	Homo sapiens Zwilch, kinetochore associated, homolog (Drosophila) (ZWILCH), transcript variant 1, mRNA.			GCATGTGACTTAGCAAGGGCTCTGAAATGACAAA GAGAACGAGCACCACA
430.88928	483.81427	478.3518	MYCBP2	FLJ21597; PAM; FLJ13826; FLJ10106; FLJ21646; DKFZp686M08244; KIAA0916	NM_015057	Homo sapiens MYC binding protein 2 (MYCBP2), mRNA.	GGACATGCATGGGGCTC TGGGAAGACTCCTAGAT AAACACTTTAAGAGGC	ILMN_1757546	GAGGTGTTTGCATGTGGCCATTACCGTCATTGG CCTGTGAAGCATTGGAC
252.13928	317.76013	311.75595	APTX	AOA; FLJ20157; AXA1; EAOH; MGC1072; EOAHA; AOA1; FHA HIT	NM_175071	Homo sapiens aprataxin (APTX), transcript variant 5, mRNA.			GATGGTGTGGGGGGTTGGAGTTTTCTTCTAATA CCGAGGGTTCCTGGCTG
165.94762	329.40594	313.8476	TTF2	HuF2	NM_003594	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA.	AGGGATCTCTCCCATAG AGATGGAAGGCACAGAA AGGTGCGACTGGAAAC	ILMN_1787013	CAGCCATCTCTGCAGTTCTCTCAGTGCAGGCAG TTCTTCCTCTCAGGCTG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
23.652443	79.79823	72.15463	USH1G	ANKS4A; SANS; FLJ33924	NM_173477	Homo sapiens Usher syndrome 1G (autosomal recessive) (USH1G), mRNA.	TGGATAGTTTTTTGCCCT ATTGAATCATTCAGTTGG TGTACAAACATGCC	ILMN_1799843	TGCCTGCCACCGCCATCTGGAGCCCACCACAGC TCTTCTCCCTGTTCTCT
158.17679	463.80597	411.76013	LRWD1	DKFZp434K1815	NM_152892	Homo sapiens leucine-rich repeats and WD repeat domain containing 1 (LRWD1), mRNA.	CTGGCAGCTTCCTGCTG CTCCCTGTCAGAGTCAAA GCACAAATCCTCAGG	ILMN_1698491	CCAATGCCTCCTTCACCTACCTCACCGCCCTGAC GGACTCCAACATCGTA
48.126793	63.12057	60.252254	ERCC8	CSA; CKN1	NM_001007234	Homo sapiens excision repair cross-complementing rodent repair deficiency, complementation group 8 (ERCC8), transcript variant 3, mRNA.			CTTTGTGCTGGTTGTTGAGACTCAGCAGGGAAAT AAAGATCCTTCTGTGC
116.98929	141.62262	138.01428	GPR89A	SH120; GPR89	NM_016334	Homo sapiens G protein-coupled receptor 89A (GPR89A), mRNA.	GCTGTCCCTCCACTACA GAAACCTCACAGAACACA GCAAAGGATAAGTGC	ILMN_1717234	GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTC CTGATCGACTCCAGCA
85.4478	175.89761	162.61012	ZDHHC18	DKFZp667O2416	NM_032283	Homo sapiens zinc finger, DHHC-type containing 18 (ZDHHC18), mRNA.	TCTGGGGTGAGTGGCTT TCAAAGCCTTTTAGCTTT TCCAGCACCTCAGCC	ILMN_1698516	TAGATATTGTTCCACCATCCCCCTCCTTGGCCCT TCAAGTGGGCTGAAGC
158.5893	457.08093	398.61844	HJURP	URLC9; FAKTS; hFLEG1; DKFZp762E1312	NM_018410	Homo sapiens Holliday junction recognition protein (HJURP), mRNA.			ATGGGGTGGACAACACCGTCAGACCGGGAGAC CAGGGCAGCTCTTCACAG
703.6393	1153.2727	1093.6434	GTF3C2	KIAA0011; TFIIIC-BETA; TFIIIC110	NM_001521	Homo sapiens general transcription factor IIIC, polypeptide 2, beta 110kDa (GTF3C2), transcript variant 1, mRNA.	CATTCCCTACTCTCTAAG GCCAAAATATCCTGAGCA AGGCTGGCAACCCC	ILMN_1739374	CCACAGACACCCTACCGATAGAACAGTGGCTCA GATCTTACTTGCTCCTG
234.96428	374.76428	355.78094	ANKRD54		NM_138797	Homo sapiens ankyrin repeat domain 54 (ANKRD54), mRNA.			AACAGAAGAGCAGGTGACGGGAGAGGAGGTTG GAGGTGTAGCGATGGAGC
89.585144	152.36429	149.66846	PDZD8	FLJ25412; PDZK8; bA129M16.2; FLJ34427	NM_173791	Homo sapiens PDZ domain containing 8 (PDZD8), mRNA.			CCTCGTATGCACTCTGGCCTGCTTCTCCAGTTAC TTGCTTGTGTAAGAAC
766.0893	1633.5809	1459.5227	G3BP1	HDH-VIII; G3BP; MGC111040	NM_005754	Homo sapiens GTPase activating protein (SH3 domain) binding protein 1 (G3BP1), transcript variant 1, mRNA.	CAGTGGAAGGCCAACCC GGAGACGGACCCTGAGG CCTTGTTCCAGAAGGA	ILMN_1701477	GCCCGTAAGAAGGAATGTTACTTTAATATTGGAC TTTGCTCATGTGCTCG
14.460508	77.59388	60.594433	RBL1	p107; PRB1; MGC40006; CP107	NM_002895	Homo sapiens retinoblastoma-like 1 (p107) (RBL1), transcript variant 1, mRNA.			GTACCACCGCCATTCAGAGTTGTCTCACCCCTTC TCGTGCCTTTTCTCTC
449.8351	877.7018	797.3684	PRMT5	SKB1; HRMT1L5; IBP72; SKB1Hs; JBP1	NM_001039619	Homo sapiens protein arginine methyltransferase 5 (PRMT5), transcript variant 2, mRNA.			GGTGCAGTACATCTATGGGCTGTGATTCCCCTT GCCCATCAGAGAGGAGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
128.95596	319.4893	279.57263	REXO1	REX1; EloA-BP1; TCEB3BP1; ELOABP1; KIAA1138	NM_020695	Homo sapiens REX1, RNA exonuclease 1 homolog (S. cerevisiae) (REXO1), mRNA.	ATACCGTGTTGGTGGTG AATGACTATTGATGACTG TGTTAAGTGCATCTG	ILMN_1748755	TCTCCGGACCCCCTTCCCCCTCACCTCCAGGCA GGGACAGAATAAATGTT
47.488747	118.40178	102.45595	DCLRE1A	SNM1; KIAA0086; PSO2	NM_014881	Homo sapiens DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae) (DCLRE1A), mRNA.			GTCCCCTGCCCTCCATGGGCAGTTATATTCTGCA TCAAGCCTTAGAAGAG
193.73096	464.76428	408.43927	AHCTF1	ELYS; TMBS62; MSTP108; MST108; DKFZp434N093	NM_015446	Homo sapiens AT hook containing transcription factor 1 (AHCTF1), mRNA.	TTTCGAAGGCCGCCGTG ACCTCTTCAAGGGCGTG GAGACGGGAAGGAAAA	ILMN_1720703	GACAGTGTGAAAGCAGTGCGAGTGCGGCCTTTT AGTCAGGTTAGTGATGG
94.28131	847.6851	609.6226	DUSP6	MKP3; PYST1	NM_022652	Homo sapiens dual specificity phosphatase 6 (DUSP6), transcript variant 2, mRNA.			GTTGTCGCAAAGGGGATAATCTGGGAAAGACAC CAAATCATGGGCTCACT
74.82347	168.59763	148.03094	ZMYND8	RACK7; PRO2893; PRKCBP1; ZMYND8; MGC31836	NM_183047	Homo sapiens zinc finger, MYND-type containing 8 (ZMYND8), transcript variant 1, mRNA.	GGGAGCTCAAGGGGTTA GCATGAGTGAGAACATC TTCCCTGAACTCTCGT	ILMN_1746831	CGGGAGTTTCGGCACAGACTATCCCATCAAGCC GTTGGCTCCTTTCAGCT
87.46965	118.73095	112.422615	GK	GKD; GK1	NM_203391	Homo sapiens glycerol kinase (GK), transcript variant 1, mRNA.			CGTATGGAGTCTCGAACCCGAGGATTTGTCTGC CGTCACGATGGAGCGGT
127.32507	192.70595	180.59763	INA	NF-66; NEF5; MGC12702; TXBP-1	NM_032727	Homo sapiens internexin neuronal intermediate filament protein, alpha (INA), mRNA.	CGCTTCGTACCCAGCCA GCACTATGTGTACATGTT CCTGGTGAAATGGCA	ILMN_1697309	GGACAGTCAGCTCTTCATCTGCCCAACTGTGTA GCATCTGCATTGCCCAG
44.175137	59.55816	57.331932	FLJ10357	SOLO	NM_018071	Homo sapiens hypothetical protein FLJ10357 (FLJ10357), mRNA.	GACATTGGCTGCTGAAT GGTCCTATCTGCTGGCT CTCCCCTGAGATCTGG	ILMN_1716105	CTCTGAAGCTCCTTCTCCCACACTGCACCTACTC CTTGAGGCTGAACTGG
24.49707	99.9268	84.75903	CCDC138	FLJ32745	NM_144978	Homo sapiens coiled-coil domain containing 138 (CCDC138), mRNA.	CTGCAGACACATACACAA CCCGTTTGCTGCAGAGC CGGACCCAGTGGCTA	ILMN_1813386	CGTACTTGCTCTGTGCTGCTTCGAGCCCCTAAG CTTGATCTTCAAATACT
1364.8018	2517.6143	2296.6892	SMS	SpS; SPMSY; MRSR; SRS	NM_004595	Homo sapiens spermine synthase (SMS), mRNA.	GGCTCTTTTACTGCATTG AGTCTTAAAAGGGGGGT TGAATTCCGAAGGGA	ILMN_1686477	CTGACAGAAGCACTGTCGCTCTATGAAGAACAG CTGGGGCGCCTGTATTG
279.88095	475.48096	439.01428	C9ORF114	RP11-545E17.7; HSPC109; MGC29492; DKFZP566D143	NM_016390	Homo sapiens chromosome 9 open reading frame 114 (C9orf114), mRNA.			CTGCCTGGCTCCTCCTTGAGGCTGGAACTCTCT CCAGGGTGGTTAACTCT
70.03271	160.08096	139.75595	PLAA	FLJ11281; PLA2P; PLAP; FLJ12699	NM_001031689	Homo sapiens phospholipase A2-activating protein (PLAA), transcript variant 1, mRNA.			ATGCTGTAGATTTATCCTAAATTTGCTGTAGCAG TGGGGAAGAGGGACGG
6355.2725	8885.373	8461.331	SAE1	SUA1; AOS1; HSPC140; FLJ3091	NM_005500	Homo sapiens SUMO1 activating enzyme subunit 1 (SAE1), mRNA.	GCACTTCCTCCCATGAC CTTACAGTAACCATACTG ATTGAATCCCCAGGG	ILMN_1728258	TGCGGCTCAAGTCACTCAGAGGCTGTTGCATTT CAGGGCTATGTTGGTCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
45.399323	65.647835	61.888664	CASP6	MCH2	NM_001226	Homo sapiens caspase 6, apoptosis-related cysteine peptidase (CASP6), transcript variant alpha, mRNA.			GCACCTGCGCAGATAGAGACAATCTTACCCGCA GGTTTTCAGATCTAGGA
39.764137	100.32924	93.993225	GFRA2	NTNRA; RETL2; TRNR2; NRTNR-ALPHA; GDNFRB	NM_001495	Homo sapiens GDNF family receptor alpha 2 (GFRA2), mRNA.			CTCTGGTGGGGGCTCCTGATCCGCATCCAAGCT TAACCAAGGCTCCAATA
31.449047	67.48719	59.891647	HTATIP	ESA1; HTATIP1; KAT5; TIP60; TIP; PLIP; cPLA2	NM_182709	Homo sapiens HIV-1 Tat interacting protein, 60kDa (HTATIP), transcript variant 3, mRNA.			GCGGGGAGAGGCCACAGATCACCATCAATGAGA TTAGTGAAATCACCAGC
891.6184	1051.1143	1043.406	SF3A3	SAP61; PRPF9; SF3a60; PRP9	NM_006802	Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA.			ACAGGATCCCCCAGAGACCCCATTTGCCTCTCA ACACTCAGACCTTCAAC
138.93512	238.75595	219.25595	MAFF	U-MAF	NM_012323	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) (MAFF), transcript variant 1, mRNA.			ACCTGCGGCTCAGAGCGGAGGGGAGACTGACC GGAGCGCGGATCGGGACA
100.68758	370.26428	299.65594	GINS3	FLJ13912; PSF3	NM_022770	Homo sapiens GINS complex subunit 3 (Psf3 homolog) (GINS3), mRNA.			GGCCCATTAGACTGTTTGCAGGGCATCACTGCT TCCCCCTGACACCTCAC
169.84763	215.32262	208.07262	CEP164	KIAA1052	NM_014956	Homo sapiens centrosomal protein 164kDa (CEP164), mRNA.			CAGCAAGGGGTCTTTGTGCAGTTGGAGATGCTG CCGTTGTGGCAGAGCGT
38.320362	108.85595	93.71022	NY-SAR-48	MGC20533	NM_033417	Homo sapiens sarcoma antigen NY-SAR-48 (NY-SAR-48), transcript variant 1, mRNA.			CGCAGAGGCAAGCAAAGAGGCAGCCTTGGCAAA CCAGGAAGTCTGGGAAG
237.62262	1429.9309	1080.2059	MPHOSPH1	DKFZp434P0810; DKFZp434B0435; MPP-1; KRMP1; MPP1	NM_016195	Homo sapiens M-phase phosphoprotein 1 (MPHOSPH1), mRNA.	AGGACAGGGCAAGGGAG GAAAGATAGGTACAGGA GTCCACAGGAGGCCAG	ILMN_1775688	CCAGCCACTGGTAACCATTCTTCTACTCTGTATG CCCATGAGGTCAATTG
173.1518	253.70595	238.02261	PPAN	SSF1; MGC14226; SSF2; BXDC3; SSF; MGC45852	NM_020230	Homo sapiens peter pan homolog (Drosophila) (PPAN), mRNA.			TGAGGACCTGTTCCCCGAGGCCAAGCAGAAACG GCTTGCCAAGTCTCCAG
1774.9143	2312.5476	2216.6812	STRAP	MAWD; PT-WD; UNRIP	NM_007178	Homo sapiens serine/threonine kinase receptor associated protein (STRAP), mRNA.	GAAGCTGGAGGCAGCAT AAAGGACTCAAGGACCA CAGCCTCTGCCCACCA	ILMN_1760288	CAAGTGTCAGATGAAGGGAGGTGGAGTTATCCT CTTATAGTACAGTGGCC
54.063	107.78512	96.00595	ZNF232	ZSCAN11	NM_014519	Homo sapiens zinc finger protein 232 (ZNF232), mRNA.	GCCAAGCCCAGGTCACA GATCTTCCCCCGACCAT GCTGGGAATCCAGAAA	ILMN_1753112	CTCAGAGCTCATTAGACATCGGAGAGTTCATGCC AGAAAAGAGCCTTCCC
57.62902	98.393456	90.772705	SCAPER	KIAA1454; Zfp291; FLJ31533; ZNF291; MSTP063; FLJ31953	NM_020843	Homo sapiens S phase cyclin A-associated protein in the ER (SCAPER), mRNA.			CCAAGACTATCTTGAGCTGGCTAACAGATTTCCT CAGCAGGCCTGGGAAG
337.18097	438.8643	420.2726	KIF2A	HK2; KIF2	NM_004520	Homo sapiens kinesin heavy chain member 2A (KIF2A), mRNA.			CCTTGCCCACTCCTAGAGACAGCTGTGCTCACTT TTCCTGCTTTGTGCCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
356.97263	453.83093	436.59763	ZNF274	ZKSCAN19; DKFZp686K08243; FLJ37843; HFB101; ZF2	NM_016324	Homo sapiens zinc finger protein 274 (ZNF274), transcript variant ZNF274b, mRNA.			CCTTGCCTTTTCAGCTTGACCCTGCAATATAACA TGCACAGGCCTGCTTG
394.43927	632.42676	586.57263	FAM136A	FLJ14668	NM_032822	Homo sapiens family with sequence similarity 136, member A (FAM136A), mRNA.	TCCAGCTGCTGGAATCC TACCATCCCAGGAGGCA GGCACAGCCAGGGAGA	ILMN_1715760	GGCTTGTGCAGCTGGCAGTGTTCCTGCCCCAGC ATGGCACCTTATTGTTT
187.26012	984.6809	764.9143	NRIP3	NY-SAR-105; C11orf14	NM_020645	Homo sapiens nuclear receptor interacting protein 3 (NRIP3), mRNA.			GCCAAGACTCCCATGCTGCCTCATTTGTATTCAA GCCTTTAACAGGAGGG
3107.4644	3894.3394	3749.2393	TCEB1	SIII	NM_005648	Homo sapiens transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C) (TCEB1), mRNA.			GGCACGATAAAAGCCATGTTGAGTGGCCCAGGT CAGTTTGCTGAGAACGA
80.70403	287.33093	231.11429	TYRO3	Sky; BYK; RSE; Brt; Tif; Dtk	NM_006293	Homo sapiens TYRO3 protein tyrosine kinase (TYRO3), mRNA.			CGGTGACCTTTAGTGCCAACTTCCCCTCTAACTG GACAGCCTCTTCTGTC
294.4018	403.63513	378.81012	ATP11C	ATPIQ; ATPIG	NM_173694	Homo sapiens ATPase, class VI, type 11C (ATP11C), transcript variant 1, mRNA.			GTCTTTGTAATTTTCACAACCGCTGTCCATTGTTT GAGGATGTTACCTAC
1012.0643	1669.906	1522.9976	SERTAD1	TRIP-Br1; SEI1	NM_013376	Homo sapiens SERTA domain containing 1 (SERTAD1), mRNA.			GAATCTAGTCCTGGGCAACTTCACATCCGTCCTC CTGTCTCAGGGCTGGC
534.7018	860.83923	791.22266	ODF2	ODF84; MGC9034; MGC111096; ODF2/2; ODF2/1; FLJ44866	NM_002540	Homo sapiens outer dense fiber of sperm tails 2 (ODF2), transcript variant 1, mRNA.			CCCAAGGCTCCCTTCCCAAGCTCAGTGCAAACC TCTCACTCCCAAGTTTC
79.286385	155.20178	145.16847	ZNF175	OTK18	NM_007147	Homo sapiens zinc finger protein 175 (ZNF175), mRNA.			ACACCAGGAGTCAACAAACTGTGGCCATTGGCC AAATATGGCCTCCCAAC
789.1892	4866.514	3465.9226	MT1X	MT1; MT-1I	NM_005952	Homo sapiens metallothionein 1X (MT1X), mRNA.	TCCCTCTGTGGCTATGG CTATGGATGCGGCTCTG GCTCTGGCTACTATTA	ILMN_1771218	CTGTCCCGCTGCGTGTTTTCCTCTTGATCGGGA ACTCCTGCTTCTCCTTG
63.040115	101.89763	92.52264	CLDND2	MGC33839	NM_152353	Homo sapiens claudin domain containing 2 (CLDND2), mRNA.			ATCAGTGGATTCCCCGTGTGTCTGTGACTGCAG CCTGCCTGGGGCAGAAT
106.814285	375.06012	296.94345	SMC2	SMC2L1; hCAP-E; FLJ10093; CAPE; CAP-E	NM_001042550	Homo sapiens structural maintenance of chromosomes 2 (SMC2), transcript variant 1, mRNA.	AAGTTTTCTACCTGGGCT GACGTTGCCTTGTCCGG AGGGGCTTGCAGGGT	ILMN_1787844	AGGAAACTTGCTCAGGGTGATAATACAGTTAGGA GTGTCAGGGCCCATGG
2343.106	3072.5977	2919.2893	ITGB1BP1	ICAP1B; ICAP-1alpha; ICAP1A; ICAP1; ICAP-1B; DKFZp686K08158; ICAP-1A	NM_004763	Homo sapiens integrin beta 1 binding protein 1 (ITGB1BP1), transcript variant 1, mRNA.			CTGGCTCTGAAGACCACAGATGCAAGCAATGAG GAATACAGCCTGTGGGT
49.875755	132.00595	108.66012	PGBD1	dJ874C20.4; SCAND4; HUCEP-4	NM_032507	Homo sapiens piggyBac transposable element derived 1 (PGBD1), mRNA.			CACAGAGCCTGTAACCCAGGTGCTTCTCTAGAC CCCTTGGATTTTCGGAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
92.17047	289.93097	237.63512	CENPA	CENP-A	NM_001042426	Homo sapiens centromere protein A (CENPA), transcript variant 2, mRNA.	AGAATGCTGGTTCTACAT CCCGAGGAGTGTCTGAG GTGCGCCCCACTCTG	ILMN_1725014	TGCAGGCCGAGTTACTCTCTTCCCAAAGGATGT GCAACTGGCCCGGAGGA
135.71011	269.43927	238.83095	PANX2	hPANX2; MGC119432	NM_052839	Homo sapiens pannexin 2 (PANX2), mRNA.			CCTCAGCCATGGAGACCATGTCATGCAGAATTAA CAAGGTAGCACCGAGC
183.96428	226.16013	218.39345	GTPBP8	HSPC135	NM_014170	Homo sapiens GTP-binding protein 8 (putative) (GTPBP8), transcript variant 1, mRNA.			ATGGGCTAGGTAAAAGGGGGCTGCTTTTCTGTT AAGCATCGATAGGTAAG
1063.6226	2120.3977	1893.3726	HSPH1	HSP105B; DKFZp686M05240; HSP105; HSP105A; NY-CO-25; KIAA0201	NM_006644	Homo sapiens heat shock 105kDa/110kDa protein 1 (HSPH1), mRNA.	AAGAGATGCCTGGGCGT CACCATGCCACAGCTAC CCACTTGTTGCCACCA	ILMN_1654156	CCTGCCAAGGTAGTTTTCTTGCATTTTGCTCTCC ATTCAGCATGTGTGTG
33.491653	51.75229	48.307663	CCDC32	MGC20481; FLJ25915	NM_001080791	Homo sapiens coiled-coil domain containing 32 (CCDC32), transcript variant 3, mRNA.	GGCAAAGAAAACCACTA GGACCACCAGGAGCACA CAACCCCAGACCCACG	ILMN_1663723	TGGGGCTGGCATGTGTGACTGTCTCGGATGAAG TGACTGACCCAGTGCAC
523.42676	1059.4559	931.98926	CDK2	p33(CDK2)	NM_001798	Homo sapiens cyclin-dependent kinase 2 (CDK2), transcript variant 1, mRNA.	GCCATTTGGAAGCTTTG GTTATGAAACATGTGGA GTGTATTAAGTGCAGC	ILMN_1749575	GGATCCCTGATCCCATTTTCCTCTGACGTCCACC TCCTACCCCATAGGAG
508.13928	650.9309	624.5226	TSR2	RP1-112K5.2; DT1P1A10; MGC20451	NM_058163	Homo sapiens TSR2, 20S rRNA accumulation, homolog (S. cerevisiae) (TSR2), mRNA.	AGGTCAGGGGTCAGAAG GAACAGGGCTGCAGCGT CAGGGTCCGAGAGGTT	ILMN_1672157	GGAATTCGAAGACCTTGGCTAGGTGGTGAGCTT GGAAGAGCTGGGCTTTG
130.13928	295.12262	254.40594	HNRNPA1	MGC102835; HNRNPA1	NM_031157	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRNPA1), transcript variant 2, mRNA.			TTATGGAGGAGGCGGCCCTGGTTACTCTGGAGG AAGCAGAGGCTATGGAA
1729.5559	1984.3893	1935.4017	TOMM20	TOM20; MOM19; KIAA0016; MGC117367; MAS20	NM_014765	Homo sapiens translocase of outer mitochondrial membrane 20 homolog (yeast) (TOMM20), nuclear gene encoding mitochondrial protein, mRNA.			GTAATCAGCTTGTTGTAGTGATGCTGGCCAAATG GTGCTCAGCAGGTGAG
32.685837	115.29762	92.11445	ZNF703		XM_001129663	PREDICTED: Homo sapiens zinc finger protein 703 (ZNF703), mRNA.			ATAATGTTAGCTTACAAGCTGGGAATATAAGTGC ATTAACGGCCCACATG
162.57678	247.53094	233.17262	DDX46	MGC9936; KIAA0801; FLJ25329	NM_014829	Homo sapiens DEAD (Asp-Glu Ala-Asp) box polypeptide 46 (DDX46), mRNA.	GACTGCAGACTTCCTGA GGGCACAGCCCACCCCT CATGCTTTGAGTTTCT	ILMN_1701881	TGGCAGTCCCACATCGATGATAATTGGTGCTCC CTTCATCCAACTGGATC
77.540054	114.77678	131.20178	HNRNPF	OK/SW-cl.23; HNRNPF; mcs94-1; MGC110997	NM_001098204	Homo sapiens heterogeneous nuclear ribonucleoprotein F (HNRNPF), transcript variant 2, mRNA.			AGCAGCACACATTCTGGGAAGCATCAAATAGACA CACGGCCCCAGCCACC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
315.91428	415.55594	457.2143	ZMYND19	MIZIP; RP11-48C7.4	NM_138462	Homo sapiens zinc finger, MYND-type containing 19 (ZMYND19), mRNA.	ACCAAGTGAGGAAGACC CAACCTTTGAAGACAACC CTGAAGTGCCTCCGC	ILMN_1739683	CAGGCAGTCTGTGTGGTTACAGCGCCCCTCAGT GTTCATCTCCAGCAGAG
114.89345	141.96428	151.82678	ZBTB24	ZNF450; BIF1; PATZ2	NM_014797	Homo sapiens zinc finger and BTB domain containing 24 (ZBTB24), mRNA.	TTATTGGGCAGGGGGAG GGGGAGGGCACAGGCA AGAAGAGATTCACAGTG	ILMN_1693975	TGGGGCTCCTGAAACACCTCGTTTTGAAGGTGA ATCTTTGGTTTTCTCCC
489.23096	807.7893	937.8976	CCNH	CAK; p34; p37	NM_001239	Homo sapiens cyclin H (CCNH), mRNA.			CCAAACATGAGGAGGAAGAATGGACTGATGACG ACCTGGTAGAATCTCTC
542.2976	765.64343	860.7143	SNRPA	U1A	NM_004596	Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA.			GCCTTCGTGGAGTTTGACAATGAGGTACAGGCA GGGGCAGCTCGCGATGC
1423.0559	1628.9727	1700.6893	TUFM	COXPD4; EF-TuMT; EFTU	NM_003321	Homo sapiens Tu translation elongation factor, mitochondrial (TUFM), nuclear gene encoding mitochondrial protein, mRNA.	CGAGGGATCTGACCTAC CAGGTGGTGTTGGGTGA GTACAACCTTGCTGTG	ILMN_1677559	CAGCGTTTCACCCTGCGAGATGGCAACCGGACT ATTGGCACCGGTCTAGT
72.91463	422.34763	709.9768	ITGA6	VLA-6; ITGA6B; CD49f	NM_000210	Homo sapiens integrin, alpha 6 (ITGA6), transcript variant 2, mRNA.	GGAGAGTGCAGGGATAT AAGAGGAAATGGGCAGC TGGGGTAAGGAAGGGG	ILMN_1800000	GTCCTGAAAAGGGTGTTGGGAGGGTGGTTCAAC AAAGAAACAAAGATGTT
127.83095	165.78513	178.46011	RBM18	MGC2734; RP11-498E2.2	NM_033117	Homo sapiens RNA binding motif protein 18 (RBM18), mRNA.			GAACCCTGGGATGCTCTAATTGGCTGGTTGGTT TGGATTTGTAACTCCAG
1112.5809	1668.631	1884.0726	BXDC1	FLJ21087; RPF2; bA397G5.4	NM_032194	Homo sapiens brix domain containing 1 (BXDC1), mRNA.	CCTCAGGCCACAGACTT GTAGTAATCATTTGAAGG CCTCACCTAGTGTCC	ILMN_1795336	TGGGACCCTCATTGGATCTGGTTCTGAGGAGGA CACACCTGGCATCGGAT
149.98929	286.85178	348.32678	FGA	MGC119425; MGC119423; Fib2; MGC119422	NM_021871	Homo sapiens fibrinogen alpha chain (FGA), transcript variant alpha, mRNA.			TCCTTGGGGGCAGGGCCTTTGTCTGTCTCATCT CTGTATTCCCAAATGCC
5620.8228	6905.4062	7376.1978	PSMA6	MGC22756; IOTA; MGC2333; p27K; PROS27; MGC23846	NM_002791	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA.	CAGAGAAACTCACCACA GTGTTTTTCCTTGGATCC CATGATGCCCAGATG	ILMN_1660541	CATTGTCGTTAGTTTACCAGATCCGTGATGCCAC TTACCTGTGTGTTTGG
413.03094	890.70593	1134.7893	GEMIN4	HC56; p97; DKFZP434B131; DKFZP434D174; HHRF-1; HCAP1	NM_015721	Homo sapiens gem (nuclear organelle) associated protein 4 (GEMIN4), mRNA.			GCTTCTTACCTGTGCGGGAGCGAAAAAGCTGGG CTTCAACATGGCAGGTC
56.344387	60.35604	63.147316	ZCCHC3	MGC104290; C20orf99	NM_033089	Homo sapiens zinc finger, CCHC domain containing 3 (ZCCHC3), mRNA.	GCCACGAGAACATCGAC CTCAGAAGGACTGGAGG AAGGTGAAGTGGAGGG	ILMN_1801907	GGTCCTTTGGAGGCCCTACCCCTTCCCCATTCAT TGCCACCAGTGAGAAA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2229.181	3685.406	4334.481	TAF15	TAFII68; TAF2N; RBP56; hTAFII68; Npl3	NM_139215	Homo sapiens TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa (TAF15), transcript variant 1, mRNA.	GCTTTGTTTTCCCACACA TATTCAAATCAGCAAGCT TGTAGCTGGACTGC	ILMN_1803748	TTGCCAGAGTTTTGCCTGCTGCTTTCCTCGTGGC CTCTTCTTGGGTAGTG
801.46844	1042.2476	1135.9143	TNPO1	TRN; IPO2; KPNB2; MIP; MIP1	NM_153188	Homo sapiens transportin 1 (TNPO1), transcript variant 2, mRNA.	TGCTGTCTGGAGCAGCA GGATCCCGGGACAGGAT GGGGGGCTTTGGGGAA	ILMN_1672653	CAGTCTTGGAGACTATAAGGGAGCCTCTGCACC CAGGGAAAATGTTACCC
118.31845	201.09763	237.58511	CCT4	MGC126164; Cctd; MGC126165; SRB	NM_006430	Homo sapiens chaperonin containing TCP1, subunit 4 (delta) (CCT4), mRNA.	ATGGCCCCAGTCCATGC TTCTAGCCTTGGTTCCTT CTGCCCCTCTGTTTG	ILMN_1728858	TAATGATCCAAGTGGCACCTCTCTGAACCTACTT TGGCTTGGGAGGCTGC
13.055626	122.243454	259.38095	DDIT4L	Rtp801L; REDD2	NM_145244	Homo sapiens DNA-damage-inducible transcript 4-like (DDIT4L), mRNA.	CGGACCCAGAACATTCT CCAGTAGTGCATTCAGTT CAACACAGCAAGTGC	ILMN_1673369	AGCTCCAAAGGTTCACTGTGTTTCTGCCGCTGTC CTGGAGTTGTCACCAC
183.63095	297.66846	374.09763	PSRC1	RP11-297O4.2; MGC1780; FP3214; DDA3	NM_001032290	Homo sapiens proline/serine-rich coiled-coil 1 (PSRC1), transcript variant 4, mRNA.			CCTGAATCGCATTCTCTACTGGACTCTGGCCTGC TTGGAGAGGTGGCAGC
24.109648	189.13095	381.7976	TP53BP2	p53BP2; ASPP2; 53BP2; PPP1R13A; BBP	NM_005426	Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), transcript variant 2, mRNA.	CTCCTGGATAGTTCCAAA CATCTTCCTTGTGGCAG GTTTCCTGGCTGAGC	ILMN_1724487	CATCATGTTGGCCAGGATGGTCTCGATCTCCTG ACCTTGTGATCCGCCTG
222.53094	613.7018	840.6726	C21ORF51		NM_001042401	Homo sapiens chromosome 21 open reading frame 51 (C21orf51), transcript variant 2, mRNA.	CAGTGTGTCAGGCAATC TGGACTTTGCCCTCAAAA GAGCAGTGGTTCCTG	ILMN_1696031	CACAGTCTACCATGAATTGGAAGGTTCTTGAGCA CGTGCCCCTGCTGCTG
158.25179	272.88095	330.24347	CEP192		NM_032142	Homo sapiens centrosomal protein 192kDa (CEP192), mRNA.			CCCAGCATTACATCAACATGCCCGTGCAGTTCAA ACCGAAGTCCGCAGGC
137.51428	278.1351	340.3976	CLK3	FLJ22858	NM_003992	Homo sapiens CDC-like kinase 3 (CLK3), transcript variant phclk3, mRNA.	CACTGCTGGCTGCCCAT TGCTGTGGATGGGGTAG AGCTGGAGTCACACAT	ILMN_1676247	AAGATGACAAGGAGGGTCACCTGGTGTGCCGGA TCGGCGATTGGCTCCAA
1531.8477	4589.1226	6351.1226	LOC100008589		NR_003287	Homo sapiens 28S ribosomal RNA (LOC100008589).			GCGGGCCGCCGGTGAAATACCACTACTCTGATC GTTTTTTCACTGACCCG
1487.006	2118.5476	2363.9312	CRLS1	C20orf155; GCD10; CLS1; dJ967N21.6	NM_019095	Homo sapiens cardiolipin synthase 1 (CRLS1), mRNA.	CTTGGTGCTGATGGCCT GAAGGGGCCTGAGCTGT GGGCAGATGCAGTTTT	ILMN_1757552	GTGAATACAGCAGTCCAGTTAATCTTGGTGGCA GCTTCTTTGGCAGCTCC
232.45596	283.2976	294.44345	LY96	MD-2	NM_015364	Homo sapiens lymphocyte antigen 96 (LY96), mRNA.	CCTCATAGTGAGCCAGA AGCAGCCTCATAACCCT GAATGTGGGGCTCTGG	ILMN_1815628	TGGGAGCCCAGAAGAAATGCTCTTTTGCTTGGA GTTTGTCATCCTACACC
24.084644	61.679188	81.160286	FUBP1	FBP; FUBP	NM_003902	Homo sapiens far upstream element (FUSE) binding protein 1 (FUBP1), mRNA.			CACTGGCATGTTTTTCCCCCCTTGCAGTATAGTG GTAGATTGGAGGATCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
795.0476	1597.8059	2005.1685	HSD17B4	MFE-2	NM_000414	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA.	TCTGGAAAGTCCTGGGG AACTCGCAGGGCACGGG CCGCTGTCGCGGTTGG	ILMN_1741592	GGCATTCTTTAGTGGCAGGCTGAAGGCCAGAGG GAACATCATGCTGAGCC
81.61041	111.52261	122.56845	ELP4	dJ68P15A.1; PAXNEB; C11orf19; PAX6NEB; FLJ20498	NM_019040	Homo sapiens elongation protein 4 homolog (S. cerevisiae) (ELP4), mRNA.	GAGGTCCTCTGTGTTTG AGACAATCCTGTGTGTG CCAGGAGGCTCCGTGT	ILMN_1789405	AAAATGGATCTGGCAGAATCCGCCAAGCGGCTG GGCCCAGGCTGTGGCAT
199.18927	284.6018	317.05176	ZRANB2	DKFZp686J1831; DKFZp686N09117; ZIS2; ZIS1; FLJ41119; ZIS; ZNF265	NM_005455	Homo sapiens zinc finger, RAN-binding domain containing 2 (ZRANB2), transcript variant 2, mRNA.			AAACAACCCTGAGCCCAGGGCCAACCCCTACGG AACACCACTACTTTACC
69.16031	107.62262	129.23097	FEZ1		NM_022549	Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 2, mRNA.	GCCTCCTGAGCAAGGTA CCATGGCTGCCAGACTT CAGGTGAACTCAAAGG	ILMN_1687835	GGTGGGGGATATGTTTTAAGACCCCCAGTTAAT GCCTGAAACCGCTGCTA
20.682758	82.376976	124.81012	PLS1	I-PLASTIN	NM_002670	Homo sapiens plastin 1 (I isoform) (PLS1), mRNA.			CTTTCTCCATCTTCCACTGTTAGTGCCAGTGAGC AATACTGTTGTGCAAC
410.73926	777.70593	932.58923	PIAS4	MGC35296; ZMIZ6; Piasg; FLJ12419; PIASY	NM_015897	Homo sapiens protein inhibitor of activated STAT, 4 (PIAS4), mRNA.	CAAAGGCACAGTTTAGA GGATTGGGGGAAGGGA GAACGAACCCAGGGAGC	ILMN_1738622	TTTCCACCCTTTTGCCTGGCTCCTGGCACCTGTA CCTCTGGACTCTCCTA
80.70643	107.23104	113.96846	EID1	C15orf3; PNAS-22; PTD014; MGC138883; IRO45620; EID-1; CRI1; RBP21; MGC138884; EID1	NM_014335	Homo sapiens EP300 interacting inhibitor of differentiation 1 (EID1), mRNA.			GCTGGTCTGGGAAAACCTGCCCTATCAATGAGT ATGTTGCCGTGGTTACC
262.91428	281.93097	290.23096	HADHA	LCHAD; MGC1728; HADH; TP-ALPHA; MTPA; GBP	NM_000182	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3 ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), nuclear gene encoding mitochondrial protein, mRNA.	CTTCCCTGGCCTTGAGT AGAAAAGTCGGGGATCG GGGCAAGAGAGGCTGA	ILMN_1809931	GCAGATGCTTTGCCCAGGCTTCTCACCACGGTG TACCGGGATATTAAACC
70.83869	122.65595	148.39761	LETM1		NM_012318	Homo sapiens leucine zipper-EF-hand containing transmembrane protein 1 (LETM1), nuclear gene encoding mitochondrial protein, mRNA.	GATCCCTTCCGGGCTCT GGTCTATCTTGTCTCCTT AGCTGGGGGCCTACA	ILMN_1803743	TAAGGTCAGGTTGGTTCCTGGCAAAAATGTACCT CCAGGGGCCTCCAAGC
48.69568	91.16849	113.97262	GPC6	MGC126288	NM_005708	Homo sapiens glypican 6 (GPC6), mRNA.	GAGAGAGACCCGTTTCC TTTCAGGGATGTGGACA GGGTAAGGGCAGCAAG	ILMN_1787922	ACCGGGTGCCAGACTGAACTGCTTCCTCTTTCCT TCAGCTATCTGTGGGG
898.08093	1111.0227	1192.031	TFB2M	FLJ22661; Hkp1; FLJ23182	NM_022366	Homo sapiens transcription factor B2, mitochondrial (TFB2M), nuclear gene encoding mitochondrial protein, mRNA.	TTGCAGGGGCCCGAGAC CCCACCATTGCACTCCA GTCCGGGAAACAAGAA	ILMN_1771320	GTCTTGCACAAGCCAGGCAGATCATTTCTCCTAA GCTGATATCATTGGCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
246.20595	411.60178	488.94763	PDPK1	MGC20087; MGC35290; PDK1; PRO0461; PkB-like; PkB-like 1	NM_002613	Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDPK1), transcript variant 1, mRNA.	AATGGAGCAGGATATTG CTGAAGTCTCCTGGCAT ATGTTACCGAATCAAA	ILMN_1672783	GTGTCTGCTTTAGAGTACTTGCACGGCAAGGGC ATCATTCACAGGGACCT
20.604572	90.649994	145.26012	CLYBL	bA134O15.1; CLB	NM_206808	Homo sapiens citrate lyase beta like (CLYBL), mRNA.	GAAGACAAAAGGTCTGC AAGGAACCACTGCACTTT CCAGACAAGCAGGCC	ILMN_1701077	TCGACATGCCATTACTGAAGCAGGCCCAGAACA CTGTTACGCTTGCCACC
67.74475	87.82377	94.56439	ZNF816A	MGC125619	NM_001031665	Homo sapiens zinc finger protein 816A (ZNF816A), mRNA.			GTAAGGGTGGCAAGGTCTTCACTCTGTGGTCAT TCCATGCAGAACATCAG
6773.4062	7431.1562	7710.7646	DYNLL1	PIN; DLC1; MGC126137; DLC8; DNCL1; MGC126138; LC8a; hdlc1; LC8; DNCLC1	NM_001037494	Homo sapiens dynein, light chain, LC8-type 1 (DYNLL1), transcript variant 1, mRNA.	CAGCGTGCATGATGGGT GTGACCTTCTGTGCCAAT AACCTTGTCAACCAC	ILMN_1720694	TCCCACCTGGCATTGCATCGTGGGGAGGAACTT CGGTAGTTATGTGACAC
666.5476	769.8268	807.11426	LASS2	SP260; CerS2; MGC987; TMSG1; L3; FLJ10243	NM_181746	Homo sapiens LAG1 homolog, ceramide synthase 2 (LASS2), transcript variant 1, mRNA.			CTACCTCTGCCAAAAAGTGGGGGCTGTACTGGG GACTGCTCGGATGATCT
58.268852	156.97678	225.90594	EDARADD	ED3; EDA3	NM_145861	Homo sapiens EDAR-associated death domain (EDARADD), transcript variant A, mRNA.			GCAACATTTGTAGGGGCCGCTGCTAGTTAGCTA CCCTTGCCCACCGCCGT
159.5476	200.0476	210.22678	HSPBP1		NM_012267	Homo sapiens hsp70-interacting protein (HSPBP1), mRNA.			GGAGCTGCTGGCCGACCTGTGTGAGAACATGGA CAATGCCGCAGACTTCT
119.805954	141.53928	150.88095	PIGC	GPI2; MGC2049	NM_153747	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class C (PIGC), transcript variant 1, mRNA.			TGGTGACATTTGCCATTCAGATTTTTGCCCTGTG GCCCATGTTGCAGAAG
31.961887	73.58183	98.45178	CBX3	HP1-GAMMA; HP1Hs-gamma; HECH	NM_007276	Homo sapiens chromobox homolog 3 (HP1 gamma homolog, Drosophila) (CBX3), transcript variant 1, mRNA.	CAGGCAGACACTAACGT CCAGACCCCTGCACCTG CTGCCAGTTCTGTGCC	ILMN_1659982	GCTGAGGAGACTCCGGTCACTGTCCTCGCCCCG CCTCCCCCTTCCCTCCC
4125.656	5043.2227	5418.9478	PSMB7	Z	NM_002799	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7), mRNA.			GCTGGATTTTCTCCGCCCATACACAGTGCCCAAC AAGAAGGGGACCAGGC
45.691605	96.46429	126.243454	INPP5F	SAC2; hSAC2; FLJ13081; MGC59773; MSTPO47; MSTP007; KIAA0966; MGC131851	NR_003252	Homo sapiens inositol polyphosphate-5-phosphatase F (INPP5F), transcript variant 2, transcribed RNA.			GGGGGGAGGGTTGACATTTTCCGACTGCCTGTT ACGTGCCAAGTGCTTTT
7.711319	105.24346	267.53928	HOXC6	CP25; HOX3C; HHO.C8; HOX3	NM_004503	Homo sapiens homeobox C6 (HOXC6), transcript variant 1, mRNA.	CTGAGTTCAGTCGGCCC TTCCTGGTGATGACTTTC CACACGGAAACAGGA	ILMN_1743046	AATTCCTACTTCACTAACCCTTCCTTATCCTGCCA CCTCGCCGGGGGCCA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1702.3226	2206.6143	2421.5476	PPT1	CLN1; INCL; PPT	NM_000310	Homo sapiens palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) (PPT1), mRNA.			TTGGAGAAATGATGAGCTACGCCTTGATGAAAGA ACCGTGTTGGTGCTGC
206.00179	312.7976	349.1143	CGI-96		XM_001125724	PREDICTED: Homo sapiens CGI-96 protein (CGI-96), mRNA.			CAGGAGAAGCCGGACCTGGCTGAGAGCCCAAA GGAGTCAAGGTCGAAGTT
86.19772	150.2143	185.10596	TOM1L2	FLJ32746	NM_001082968	Homo sapiens target of myb1-like 2 (chicken) (TOM1L2), transcript variant 3, mRNA.	AGGGACCGCTTGGAGCA GTTAGAAAGGAAGCGGG AGCGGGAGCGCAAGAT	ILMN_1711078	TGGCACGCTGCTGAGACGACACTACCAATAAAC CAAACTGCCACGCACAC
213.68512	450.03094	590.0393	HYLS1	FLJ32915; HLS	NM_145014	Homo sapiens hydrolethalus syndrome 1 (HYLS1), mRNA.	TGGTTCCCACAGCCCCA CGTGCCATGGAGGGACA TGGAAGGAAAGACGAT	ILMN_1688101	CCGTTGGGGTGTTCGTTGTGACCTTGCAAATGG TGTCATACCCAGGAAGC
2267.4976	2870.8809	3155.4727	STOML2	HSPC108; SLP-2	NM_013442	Homo sapiens stomatin (EPB72)-like 2 (STOML2), mRNA.			TGATCGAGTCAAGATGAGTTAGTGGAGCTGGGC TTGGCCAGGGAGTCTGG
42.61539	158.51845	298.18097	E2F2	E2F-2	NM_004091	Homo sapiens E2F transcription factor 2 (E2F2), mRNA.			CCGGCCTGGTTTCGCCTGGTCGTGTCTTTATGA GCACCATGTAAGCCTCC
44.949226	121.15178	174.01428	CSGALNACT2	FLJ43310; MGC40204; CSGalNAcT-2; GALNACT-2; GALNACT2; DKFZp686H13226; PRO0082	NM_018590	Homo sapiens chondroitin sulfate N-acetylgalactosaminyltransferase 2 (CSGALNACT2), mRNA.	TGTTAGTGGGATGGCAA ACACTGTGAACATTGCTG TTTCTAGTGGGCCAG	ILMN_1656436	TGGACGAGGACTAAATGTGGGTGCCCGAGCTTG GGACAAGGGAGAGGTCT
836.2518	1080.7227	1208.631	NT5C3	MGC27337; UMPH1; MGC87828; UMPH; MGC87109; PN-I; PSN1; cN-III; P5'N-1	NM_001002010	Homo sapiens 5'-nucleotidase, cytosolic III (NT5C3), transcript variant 1, mRNA.	GAAGCTCATCAAGCTGA AATAGCACAGCTGGCCA ATGAAAAGCAGAAGTG	ILMN_1799999	CTCCAAGAAGACCTCTCTCCTGTGGGTGCAATT GAACTGTTCATCCGTTC
50.35241	113.88512	152.2976	TIMM8A	DFN1; DDP; MTS; DDP1; MGC12262	NM_004085	Homo sapiens translocase of inner mitochondrial membrane 8 homolog A (yeast) (TIMM8A), nuclear gene encoding mitochondrial protein, mRNA.	GACAGGATGGGGTTCCC CTGTGCTTTTACCAGTAG CATGACCCCTTCTGA	ILMN_1720511	GATTTAGGCCAATCAGAAGCTAACAGCAGTTTCA GGTAGAGGTGCATGCC
4710.7393	11570.639	16113.105	CRYAB	CTPP2; HSPB5; CRYA2	NM_001885	Homo sapiens crystallin, alpha B (CRYAB), mRNA.	TGCTGCCAGGATGCCGA AGGATACCCCACTAGCA CCCCTGAGGGGGTCAT	ILMN_1686259	GTCCTCACTGTGAATGGACCAAGGAAACAGGTC TCTGGCCCTGAGCGCAC
2114.356	2237.4395	2303.6978	NRP1	DKFZp781F1414; VEGF165R; NRP; DKFZp686A03134; CD304	NM_003873	Homo sapiens neuropilin 1 (NRP1), transcript variant 1, mRNA.	CTAGGAGACTGGGACAA GCAAAAGGCTGCAAACA ACCCAGAAGCCCATCC	ILMN_1760718	CCTTCCCACATTGCTAGACGTCTCACTCAAAGAC ATTTGTTGGGAGTCAC
552.68097	1038.9642	1357.8477	TMEM106C	MGC5576; MGC111210	NM_024056	Homo sapiens transmembrane protein 106C (TMEM106C), mRNA.			ATGTGGGGCTTGATTCACCCTTCATCCATTGGCT GGAACATGGATTGGGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
334.50595	930.28094	1417.0977	CDKN3	CDI1; KAP; MGC70625; FLJ25787; CIP2; KAP1	NM_005192	Homo sapiens cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase) (CDKN3), mRNA.	GGAATGGGGCAATGGAT GCATTTCCCAAAACGTGT GAAAGCACTAACAGC	ILMN_1711542	CGCAGATGGAGGGACTCCTGACATAGCCAGCTG CTGTGAAATAATGGAAG
895.1226	1029.2643	1080.9727	TIPRL	RP1-69E11.1; MGC3794; dJ69E11.3; TIP; TIP41	NM_152902	Homo sapiens TIP41, TOR signaling pathway regulator-like (S. cerevisiae) (TIPRL), transcript variant 1, mRNA.	GCTTTTGCTCAGTAACTG TGTCATGAATTGCAAGAG TTTCCACAAACACT	ILMN_1680192	AGTGGCCTGTGCTGAAGAGTGGCAAGAAAGCAG GACGGAGGGTGAACACT
178.36429	208.59344	217.08096	LYPLA3	DKFZp564A0122; ACS; LPLA2; LLPL	NM_012320	Homo sapiens lysophospholipase 3 (lysosomal phospholipase A2) (LYPLA3), mRNA.			GGCAGTAGGCTCTAAGTGGGTGACTGGCCACAG GCCGAGAAAAGGGTACA
100.11013	153.40594	176.12262	LIAS	HUSSY-01; MGC23245; LIP1; LAS	NM_006859	Homo sapiens lipoic acid synthetase (LIAS), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.			GGAAATGAACTTGGATTTCATTATACTGCAAGTG GCCCTTTGGTGCGTTC
173.07262	265.44345	313.2726	MCFD2	DKFZp686G21263; LMAN1IP; F5F8D; SDNSF	NM_139279	Homo sapiens multiple coagulation factor deficiency 2 (MCFD2), mRNA.	GTGCCTGCACCACCCCA CTGCCTTCCTTCAGCAC CTTTAGCTGCATTTGT	ILMN_1741003	GAGAAGAAGCAGCAGATTGTAATTTGGTTTATTG GATGTGATGGACGTTC
2489.8394	3161.9395	3480.6643	U2AF2	U2AF65	NM_007279	Homo sapiens U2 small nuclear RNA auxiliary factor 2 (U2AF2), transcript variant 1, mRNA.	CGGCTGTAGCAGCAAGC AATCCCCAACCTCTGACT GCAATGACCTTTCTG	ILMN_1691264	CCCGTGGCCCCTGCCCCTCTCCTACTCTCTGTG GCAGTTTCATATTTGCT
31.474556	151.37262	266.07263	TMEM118	FLJ14627	NM_032814	Homo sapiens transmembrane protein 118 (TMEM118), mRNA.	CCTGAGCCAGAAGTGGG GTGCTTATACTCCCAAAC CTTGAGTGTCCAGCC	ILMN_1714433	AGCCATCTCCAGGGTGACGGAACCCAGTGTATT ACCTGCTGGAACCAAGG
68.129364	298.9643	553.1226	MMP3	STR1; STMY; MGC126102; STMY1; SL-1; MGC126103; MGC126104; MMP-3	NM_002422	Homo sapiens matrix metallopeptidase 3 (stromelysin 1, progelatinase) (MMP3), mRNA.	GGCATTAGCTGACAGGC TGGTAACAGTCCACACAA GATGGTATAGGCCTG	ILMN_1762993	CCTTGTCACATAGAGTGATCTTTCCCAAGAGAAG GGGAAGCACTCGTGTG
64.502495	83.617676	90.23161	ZBTB25	KUP; ZNF46	NM_006977	Homo sapiens zinc finger and BTB domain containing 25 (ZBTB25), mRNA.	AGAGCTGGCCGCCCAGG GGGAGTCGCAGAGTTTG GAAGATCTCTCTAACA	ILMN_1756826	AGCCATACTGTGACAGCTGGTCTGATGTCTCCCT GAAAAGTTCTCGCTTG
185.04346	299.3393	339.70593	BCL2L1	bcl-xL; BCLX; DKFZp781P2092; BCL-XL/S; Bcl-X; bcl-xS; BCL2L	NM_138578	Homo sapiens BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.			GTGGAAAGCGTAGACAAGGAGATGCAGGTATTG GTGAGTCGGATCGCAGC
3228.831	4719.748	5509.681	HEXB	ENC-1AS	NM_000521	Homo sapiens hexosaminidase B (beta polypeptide) (HEXB), mRNA.			CACTCCAAGATTATGGCCTCGGGCAAGTGCTGT TGGTGAGAGACTCTGGA
1554.7893	2479.8643	3014.2476	PARP1	pADPRT-1; PARP-1; ADPRT1; PARP; ADPRT; PPOL	NM_001618	Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA.	GGCTGTTGTCTTCGGCT TGGGTGAAATGACAGTT CCTCTTCATTCTAAAG	ILMN_1785292	ACCAAAGCTTCGTTAGAATGTCTGCCTTACTGGT TTCCCCAGGGAAGGAA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
121.76012	221.7143	282.08096	RPL23AP13	DKFZp547I014	NR_002229	Homo sapiens ribosomal protein L23a pseudogene 13 (RPL23AP13) on chromosome 2.			ATCCTCGGAAGACCACCCCCAGGAGAAACAAGC TTGACCACTATGCTATC
3837.7476	5455.7144	6306.0894	HMGN2	HMG17; MGC5629; MGC88718	NM_005517	Homo sapiens high-mobility group nucleosomal binding domain 2 (HMGN2), mRNA.			CTTTCAGCATAGACTTAACTCCCTTAAGCCCAGA CATCTGTTGAGACCTG
655.40173	827.7893	914.0893	CASP4	TX; Mih1/TX; ICH-2; ICE(rel)II; ICEREL-II	NM_001225	Homo sapiens caspase 4, apoptosis-related cysteine peptidase (CASP4), transcript variant alpha, mRNA.	CTAAGGAGTTTCCTGTAG TCCTGTAATGAGTTGGC CCTCAGTCATCCCCG	ILMN_1670093	ACTCCAAGGGCCAAAGCTCAAATGCCCACCATA GAACGACTGTCCATGAC
405.2351	833.57263	1108.2144	DYNLL2	MGC17810; DNCL1B; Dlc2	NM_080677	Homo sapiens dynein, light chain, LC8-type 2 (DYNLL2), mRNA.	GTTGGCGAGTCTGAGAG CAAGCCCAAATGTGTTCT TCAAAGGACAATGGG	ILMN_1726552	TCCTCCTCTTCAAGTCAGGCTAGGTGGCCATGG TGAAGGTGTCAGTGGCG
46.255108	63.44696	72.73763	CCDC101	FLJ32446	NM_138414	Homo sapiens coiled-coil domain containing 101 (CCDC101), mRNA.	CTTCTCATCCCGGGGCA AAGCAGGCATCAAAACC AGAATAGGCCAATCTC	ILMN_1734542	CAAGAAAAAGTGATGCCGCCTGGCAGACTCGCC ATCCCCCAACGACACAG
61.344444	84.19464	95.38106	AKAP1	D-AKAP1; AKAP149; MGC1807; AKAP121; SAKAP84; PRKA1; AKAP; AKAP84	NM_003488	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), nuclear gene encoding mitochondrial protein, mRNA.	GCAGAGCGTGCACCAAT GAGACCACGATGGGAAA GGGCCTATTTAACTCC	ILMN_1712545	TCAGGGAGCAAGACATGAACTGACTAATTGGTAT CCACTACTTGTACAGC
603.44763	668.58093	699.3393	IK	RED; MGC59741; IK protein; CSA2	NM_006083	Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA.	TGCACTATGCGCCACAC CAGATGAAGGATGTGCC CCTGATTAGCCTGGCC	ILMN_1660810	GGGGCCCTTAGGCCGTTGGGACTTTGATACCCA GGAAGAATACAGCGAGT
461.0976	802.40594	1006.2893	ACN9	DC11	NM_020186	Homo sapiens ACN9 homolog (S. cerevisiae) (ACN9), mRNA.	CAGAGGCTGTGGAGCGA GGGTAGTAGGAGCTTTT CCCAGAGTGCTGTGAC	ILMN_1798288	CTCTTCTCCCTGCATCACTGTTCATTCACAATGA AAGGTTAGGAAGAAGC
1392.106	1733.3893	1903.0393	MRPS33	FLJ21123; CGI-139; PTD003; MRP-S33	NM_016071	Homo sapiens mitochondrial ribosomal protein S33 (MRPS33), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.			CACACTTACGCTGAACTCATGCAGACGCTCCGAT TTCTTGGACTCTACAG
1512.9976	3258.281	4502.506	RPS24	DKFZp686N1586; DBA3	NM_001026	Homo sapiens ribosomal protein S24 (RPS24), transcript variant 2, mRNA.	CTTGAAGGCCTACTGTC ATCCACAAAGCTCCTTTT TTACGGGCATCCCAT	ILMN_1813455	GCCGGCGAATCGTGGTTCTCTTTTCCTCCTTGG CTGTCTGAAGATAGATC
269.43094	361.29346	402.8976	PFDN6	HKE2; PFD6; H2-KE2; KE-2; MGC70744	NM_014260	Homo sapiens prefoldin subunit 6 (PFDN6), mRNA.			TTAAACTTCTGGGTCCGGTGCTAGTCAAACAGGA GCTGGGGGAGGCTCGG
127.13928	263.83093	363.34763	PXN	FLJ16691	NM_002859	Homo sapiens paxillin (PXN), mRNA.	AGCGAGGCACCCTTACT GGCTTACCTCCTCATGG CAGCCTACTCTCCTTG	ILMN_1725560	ATGACCAGAAAGGGGCCACCGGGGTCTAATGGT GACAGTCCAAACCACTC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
472.33093	564.5393	611.381	CCT3	CCTG; TRIC5; TCP-1-gamma; PIG48; CCT-gamma	NM_001008800	Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), transcript variant 3, mRNA.			GCCAGGAACACTGTGGACGTCTTTGTTCAGAAG GGATCAGGTTGGGGGGC
489.1601	504.2601	511.05176	PRKAG1	MGC8666; AMPKG	NM_212461	Homo sapiens protein kinase, AMP-activated, gamma 1 non-catalytic subunit (PRKAG1), transcript variant 2, mRNA.	AAGGGAGAGGAGTAACA GCCAGACCCCCCATCAG TGGACAAGGGGAGAGT	ILMN_1802923	CAACTCACTGCCTGCTGGAAGCTCTGTGGGAAT CAGATGAAACTTGAGGG
222.87262	416.87677	547.8059	LOC57228	MGC149454; MGC149453	NM_001031628	Homo sapiens small trans-membrane and glycosylated protein (LOC57228), transcript variant 1, mRNA.	GAGGTTGGGGAAGTGGG TTGGGGTACAGACGAAA CAGGAGTAGGTGTGAG	ILMN_1793049	AACCTACAGAAGGTGAGCCCAGTGCCATCGTCC AGATGGAGAGTGACTTG
77.8527	207.0476	324.3018	CORO2B	KIAA0925; CLIPINC	NM_006091	Homo sapiens coronin, actin binding protein, 2B (CORO2B), mRNA.			CATGGCCGCCCTACGGAAAATCCCATCCACAGA GGCCAGGGCTACCCAAG
2746.581	3657.231	4099.8145	AXL	UFO	NM_021913	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA.	ACATTCAAAGCACTGATG TAGGAGATACACGGTAC TTGGAGCAGTCAGCC	ILMN_1788931	GGGATGGACGATCTCCCACCTTTCGGGCCATGT TGCCCCCGTGAGCCAAT
486.32263	636.80176	721.631	POLR1C	RPAC1; RPA5; RPA39; RP3-337H4.4; RPA40	NM_203290	Homo sapiens polymerase (RNA) I polypeptide C, 30kDa (POLR1C), transcript variant 1, mRNA.			GGTTCTGACTGACCCACCCTACAGGACTGCTGA ACAGAGAGCCCAGTGTG
1390.4392	1508.531	1533.0892	GOT1	GIG18	NM_002079	Homo sapiens glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) (GOT1), mRNA.			GATCAAGTTGTCTGAAGGAGCCAAAGTGTGAAT GTGGGTGTCGGCTGCGG
269.06427	359.95593	380.02264	NCOA5	CIA; bA465L10.6	NM_020967	Homo sapiens nuclear receptor coactivator 5 (NCOA5), mRNA.	TCACTGGGGACCACGAT GGGCATTCAGCCTGGTG TGTGGAATAATAGTGC	ILMN_1755769	AGAAGGAGGGTTTCTGGCTGTGGTTCTAAATGG AGCCCCAGGAAGCTGCC
505.9643	864.48096	955.08093	PSMC4	MIP224; MGC23214; TBP7; MGC13687; S6; MGC8570	NM_006503	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4), transcript variant 1, mRNA.			GCAGCAAGAGCTGGAGTTCCTGGAGGTGCAGGA GGAATACATCAAAGATG
92.135735	376.57263	496.21844	RGS20	ZGAP1; RGSZ1	NM_170587	Homo sapiens regulator of G-protein signaling 20 (RGS20), transcript variant 1, mRNA.	TAGTGCCCTGACTAGGG GGAGGATTTGGATGTGC TGCATTTCAAGCCGTG	ILMN_1682694	CCAGCAAGCTCGGTTTGAATACGTCACTTACCAG TGCCATTGCAGGACCC
2072.5977	3161.0059	3450.331	IMP3	BRMS2; MRPS4; C15orf12; FLJ10968; DKFZp586L0118	NM_018285	Homo sapiens IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast) (IMP3), mRNA.	GTCAGAATCACAAAGACA GAGTGGTGGTTGGCAGG GGCTGCAGGAAGGGG	ILMN_1717064	CTGGAAATCCCCACGCCCTGTTTCCCTTTATCGT CTTGTGGTTGGACTGG
192.82262	258.7101	272.4226	RNF4	RES4-26; SNURF	NM_002938	Homo sapiens ring finger protein 4 (RNF4), mRNA.			CCGCAGCTCTCATCATTGTGATGTGTAGCATGTC TGCCCTCTGACTGGAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
546.2143	716.2893	754.45593	PIGC	GPI2; MGC2049	NM_153747	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class C (PIGC), transcript variant 1, mRNA.	TTTCTCCTCCACCCATCG AAACCAGCCACCCCTTC CCTGTGCCACCAAGA	ILMN_1769721	GTGGGAGCCGTACTCTTTGCCCTTCTGCTGATG TCTATCTCATGTCTGTG
7.894367	59.186882	85.63135	DUSP13	DUSP13A; TMDP; SKRP4; BEDP; MDSP; FLJ32450; DUSP13B	NM_016364	Homo sapiens dual specificity phosphatase 13 (DUSP13), transcript variant 6, mRNA.			AGAGTCCTGCCCCTGCACCCACTCCCCCATTCC CGGCCCCAGGCCATGCC
9.466388	56.75773	86.15837	TEX11	TGC1; TSGA3	NM_001003811	Homo sapiens testis expressed 11 (TEX11), transcript variant 1, mRNA.			GATCTCGGCTCACTGCAACCTCCGCCTCCTGTG TTCAAGCGATTCTTCTG
12712.639	26651.996	31077.914	HINT1	PRKCNH1; HINT; PKCI-1	NM_005340	Homo sapiens histidine triad nucleotide binding protein 1 (HINT1), mRNA.	CTGCGTGAGCAGACACC TTCACAGCTTCCTCGCTG CTGTCACCTGCACTA	ILMN_1812976	GGATGACCGGTGCCTTGCTTTCCATGACATTTCC CCTCAAGCACCAACAC
156.89345	614.5143	823.3059	THOC3	TEX1; MGC5469	NM_032361	Homo sapiens THO complex 3 (THOC3), mRNA.	GGAAACCTTCCTTAGAGT CCTGTTGCTCAGTGTGG TCCATCAGACGGTAG	ILMN_1737312	CGTGGCACCCCAAAAGGCCTCTGCTGGCATTTG CCTGTGATGACAAAGAC
50.309315	369.07678	555.96844	MEIS2	MGC2820; MRG1; HsT18361	NM_172315	Homo sapiens Meis homeobox 2 (MEIS2), transcript variant g, mRNA.			TCGAACTCCAGCTTCAAGAATGTGTTTTCATGCC CGGCCTTTGTTCCTCC
194.93929	298.32263	325.14343	RDBP	RDP; NELF-E; D6S45; RD	NM_002904	Homo sapiens RD RNA binding protein (RDBP), mRNA.			ACATGGCCAGTGCCTGTTCCCCACTCCCTTGCC CCAAAAGGATCTGGAAC
632.43933	1600.8226	1954.6892	ABCF2	DKFZp586K1823; ABC28; M-ABC1; HUSSY-18; EST133090	NM_005692	Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.	GCAGTGATTTTTATCCAA TCTTGTTTCCAAAAACCA TGTCTCCCAGGGCC	ILMN_1756942	CCTGGAGACATCCTGGCTTACAAGGAGCACCTC AAGTCCAAGCTGGTGGA
79.105606	177.00595	213.50179	SHMT1	MGC15229; MGC24556; SHMT; CSHMT	NM_004169	Homo sapiens serine hydroxymethyltransferase 1 (soluble) (SHMT1), transcript variant 1, mRNA.			CCAGGCTTTCCTGCTCCACCTGAGATAACCAACT CCCTCCCGTAATCAGG
578.04346	952.7726	1057.781	CANT1	SCAN-1; SHAPY	NM_138793	Homo sapiens calcium activated nucleotidase 1 (CANT1), mRNA.	TACGTGTTGAGCGTGGC CTACGTGAGCCAACAAG AAGCAGGGGCCTCTGA	ILMN_1756573	TGCCTGGCTGTCTCCTTGACCCGCCTCCTAGAT CATTGTCCTTGATGTCC
596.4768	1081.3601	1203.581	ALG8	MGC2840	NM_001007027	Homo sapiens asparagine-linked glycosylation 8 homolog (S. cerevisiae, alpha-1,3-glucosyltransferase) (ALG8), transcript variant 2, mRNA.	TTTGGAAAGCAGGGTTC CTCTGCCTGCTAACAAG CCCACGTGGACCAGTC	ILMN_1715426	CAATTCTCCCAATGAGCCTTTTGTCTGTGGGAAA AGCAGGAGACGCTTCG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
5861.831	7272.006	7666.9395	PTBP1	HNRNPI; PTB-T; PTB3; PTB-1; MGC8461; HNRPI; HNRNP-I; PTB2; MGC10830; PTB; PTB4; pPTB	NM_002819	Homo sapiens polypyrimidine tract binding protein 1 (PTBP1), transcript variant 1, mRNA.	TGAGACCAAGGCCAGCA TCAATTCCAGACATCTTC ATGTTCCTAATAGGC	ILMN_1738346	GAAACTCCTCCCTTGTCTAGCCCTGTGTTCGCTG TGGACGCTGTAGAGGC
76.77359	115.35179	123.280945	C17ORF71	FLJ10587	NM_018149	Homo sapiens chromosome 17 open reading frame 71 (C17orf71), mRNA.	CGAGAGCTGGAGAGAAG AAGGTTTCCCAGTGGGC TTGAAGCTTGCTGTGC	ILMN_1785444	CCCCCCTAAGGAAAATGTGCAGTTAATGAGCTAC AAGGTGCTCCGTGGGG
10.132967	63.725624	92.73096	TMEM164	RP13-360B22.2; bB360B22.3; FLJ22679; FLJ20173	NM_032227	Homo sapiens transmembrane protein 164 (TMEM164), mRNA.			GACCATGACCCACGGGAAGCTGGTCATCCTGTT CTCATACATGGCTGGGC
1744.6643	3012.4644	3409.1143	SS18L2	KIAA-iso	NM_016305	Homo sapiens synovial sarcoma translocation gene on chromosome 18-like 2 (SS18L2), mRNA.			ACTGTGTGCTCCTTCCTATCAGTTTGTAAATGTG GTCCCCCTGACTGCTG
100.69855	271.86844	354.24347	CDCA4	MGC19517; FLJ20764; HEPP	NM_017955	Homo sapiens cell division cycle associated 4 (CDCA4), transcript variant 13, mRNA.	CCTTGGCCTAAAGCCTT GGTTCTCAAACTGGGTT CCTTGGGACCTCCGGG	ILMN_1806937	TCTTTGTGTCCCCCACTGTAGAGGACGGTGAGC CGCAGCTGCATCAACCT
1692.456	2121.6892	2237.7476	EIF4A3	eIF4AIII; MGC10862; hNMP265; NUK-34; KIAA0111; DDX48	NM_014740	Homo sapiens eukaryotic translation initiation factor 4A, isoform 3 (EIF4A3), mRNA.			CAGCAGATCAGTGGGATGAGGGAGACTGTTCAC CTGCTGTGTACTCCTGT
440.8976	1191.1018	1492.4559	CSTF3	MGC75122; MGC43001; MGC117398; CSTF-77	NM_001033505	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa (CSTF3), transcript variant 2, mRNA.	GCATCCCATTGCCAGCC TTGCTGTCAGATTCAAAA TTGCTTTTTCTAGAG	ILMN_1765620	AGCACGGAAGACTTATGAACGCCTTGTTGCCCA GTTCCCCAGTTCTGGCA
279.85178	408.35596	447.06012	DUS3L	FLJ13896; DUS3	NM_020175	Homo sapiens dihydrouridine synthase 3-like (S. cerevisiae) (DUS3L), mRNA.	AGAACATAAATGGCCTCC TGCCAGCTCCGGCGTCT CTCTGTGGTCTGCCT	ILMN_1760335	GAGAAGACCCGGCGCTTTCTGCTCGAGTGGCTG TCCTTCCTGTGCCGGTA
59.621773	117.45595	136.48096	ZNF30	KOX28; FLJ20562; DKFZp686N19164	NM_001099437	Homo sapiens zinc finger protein 30 (ZNF30), transcript variant 2, mRNA.			ATGAGTGTTATACCCTAAGAGTCTGAGGAGTGTG GGAAGTGCTTCGTGTG
1876.8394	5780.539	7408.589	LOC51035	2B28	NM_015853	Homo sapiens SAPK substrate protein 1 (LOC51035), mRNA.	GGCATGCTTTATCGTGT GGCTTTCCCCTCTTCAAA TATTAATGGCCAGGT	ILMN_1761963	CAGGACTCGTGCCTTCTGCTGTTCTCATTGTGG CCAAGAAATGTCCCAGC
93.12271	162.4643	184.81429	FASTKD2	KIAA0971	NM_014929	Homo sapiens FAST kinase domains 2 (FASTKD2), mRNA.	TGTCCCACTTCCTCTATG TCCCTTTCCTTGGTGTCT GTGTCTGTGGGGCC	ILMN_1748090	CCAGAAGGGTTATTTTTCCAACCACACCTATTCC CTCTAGTGCCCAGATA
186.51428	282.13928	300.7726	TMEM55A	DKFZp762O076	NM_018710	Homo sapiens transmembrane protein 55A (TMEM55A), mRNA.			GGAATCAGCTCTCGCACTGCCCATCTTTGCAGTT TTGAAAAAGAAATTGC
120.82678	483.78094	631.4143	USP21	MGC3394; USP16; USP23	NM_012475	Homo sapiens ubiquitin specific peptidase 21 (USP21), transcript variant 1, mRNA.			AGGTGGCATCCAGCGAGGGCTACGTGCTGTTCT ACCAACTGATGCAGGAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
175.22678	211.59761	219.64761	TIMM17B	TIM17B; JM3; DXS9822	NM_005834	Homo sapiens translocase of inner mitochondrial membrane 17 homolog B (yeast) (TIMM17B), nuclear gene encoding mitochondrial protein, mRNA.	AGAGTGCCAGAGAACCG TTGCTTTTCCGAGTTGCT CTTCTTCCAGGCTCC	ILMN_1655011	GTCCCCTTTTTCTCTCTCAGGGCACCCCAGCCC CACACTCACATGTACGA
1656.0476	3360.1392	3843.431	CD44	LHR; CDW44; ECMR-III; MGC10468; MDU2; CSPG8; Pgp1; IN; MUTCH-I; MIC4; MDU3; MC56; HCELL	NM_001001392	Homo sapiens CD44 molecule (Indian blood group) (CD44), transcript variant 5, mRNA.	CCTCGTCAGCCCCCGCT CAGGCCACGTTCATCAG CCCAAGCGAAGATTTT	ILMN_1768020	GCCACTCCAGGACAAGGTTCAAAATGGTTACAAC AGCCTCTACCTGTCGC
31.311932	134.10603	159.70595	PIAS2	SIZ2; MIZ1; miz; ZMIZ4; PIASX-ALPHA; MGC102682; PIASX-BETA	NM_004671	Homo sapiens protein inhibitor of activated STAT, 2 (PIAS2), transcript variant beta, mRNA.			GCCTGGCTATGCACCACCGCCTAAAAATGGGAT TGAACAGAAGCGCCCTG
349.53513	659.881	745.61426	POP5	HSPC004; RPP20; RPP2	NM_198202	Homo sapiens processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae) (POP5), transcript variant 3, mRNA.	CTCCTGCTGTGAGAACA AGTGGATGTCCCTCTCC CCGCCCTCCTGCTGAA	ILMN_1802872	GCAGAAGCAATGGAGTGAACCTCTGCTCCCCAC ACAGCTGGCTACACTGC
184.2976	294.47678	323.28928	LOC441743	rjd10; c367G8.3; RPL2B; RPL23AL	NM_001045548	Homo sapiens similar to C367G8.3 (novel protein similar to RPL23A (60S ribosomal protein L23A)) (LOC441743), mRNA.			CACAAGATGGCGCTGAAAGCAAAGAAGGAAGCT CCTGCCTCTCCTGAAGC
1668.3059	2884.0225	3275.1895	LSM2	G7b; snRNP; C6orf28; YBL026W	NM_021177	Homo sapiens LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae) (LSM2), mRNA.			CCAGGGCAGCATGTGATTCATTTGGGGATGGAA GGAATCTGTCCCGCATC
16.089306	96.69799	131.63928	EXOC7	Exo70p; 2-5-3p; DKFZp686J04253; FLJ40965; EXO70; YJL085W; FLJ46415; EXOC1; EX070	NM_001013839	Homo sapiens exocyst complex component 7 (EXOC7), transcript variant 1, mRNA.			CCCAGCATGGTCTAGATGGGAAAAAGGGGGGCT CTAACCTCATTCCTCTG
28.94812	127.26845	181.77261	NRGN	RC3; hng	NM_006176	Homo sapiens neurogranin (protein kinase C substrate, RC3) (NRGN), mRNA.			GATCCGGGGCGAGATGAAGGGAAGAGGGTTGT TTTGGTTTCGGACGACCC
9.176077	44.750954	59.422947	KRTAP10-2	KRTAP18-2; KAP10.2; KAP18-2; KRTAP10.2; KRTAP18.2; KAP18.2	NM_198693	Homo sapiens keratin associated protein 10-2 (KRTAP10-2), mRNA.			CCTCTGTGTCCCTCCTCTGCCGCCCCGTGTGCT CCCGCCCAGCCTCCTGC
97.12001	131.84344	141.86845	CCM2	MGC74868; MGC4067; MGC4607; C7orf22; PP10187	NM_031443	Homo sapiens cerebral cavernous malformation 2 (CCM2), transcript variant 2, mRNA.	AGCGCCTCAAGGGGGCC TCGGAGAACGAGGAAGA GGACGACGACTACAAT	ILMN_1680904	GGCCGCGGGAGCCGCACGCGGCGATATGGAAG AGGAGGGCAAGAAGGGCA
69.25007	190.79346	227.14761	RSBN1L	FLJ45813; FLJ42526; MGC71764	NM_198467	Homo sapiens round spermatid basic protein 1-like (RSBN1L), mRNA.	GGCGAAGCCCAGGAGAC CACCGAGGAGTTTAATC GAGAGATGTTCTGGAG	ILMN_1658743	GTGCCTGTCCATAACTGTGAAGTATTAAGCACTT AGGGCCAGATGCACTG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
975.8142	1063.1143	1075.6226	PNRC2	MGC99541; FLJ20312	NM_017761	Homo sapiens proline-rich nuclear receptor coactivator 2 (PNRC2), mRNA.			GTTTGGTCAAGGGGTAGGTGCAACCCAATGGAC CACTTATGCAAAAGATG
716.98926	2313.3892	2875.356	CAPRIN1	M11S1; p137GPI; GPIP137; GPIAP1; caprin-1	NM_005898	Homo sapiens cell cycle associated protein 1 (CAPRIN1), transcript variant 1, mRNA.	ACATGCCCCGAGTGCGG AAGAGGATTTACAAGGA GCTATGTGAGTGCCGG	ILMN_1675501	CGGGGCCCTGCCAATGGATTCAGAGGAGGATAT GATGGTTACCGCCCTTC
1257.1685	3625.4143	4412.081	ZNF207	DKFZp761N202	NM_001032293	Homo sapiens zinc finger protein 207 (ZNF207), transcript variant 2, mRNA.	GCACCACTGCGTCAATT CCCCAGGCTCCTATTTCT GTCACTGCCAAGTTG	ILMN_1737503	CCCAGCTGTGGACCACTGCCTGAAAGGTTTGTA CAGATGCATGCCACAGT
2512.0642	8593.535	10802.214	ETFA	GA2; MADD; EMA	NM_000126	Homo sapiens electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II) (ETFA), nuclear gene encoding mitochondrial protein, mRNA.	GGGAACCCCTTGTGAGC ATGCTCAGTATCATTGTG GAGAACCAAGAGGGC	ILMN_1727041	TGGTGCTTCCCGTGCTGCTGTTGATGCTGGCTT TGTTCCCAATGACATGC
341.7351	482.9726	522.15594	VPS26B	Pep8b; MGC10485	NM_052875	Homo sapiens vacuolar protein sorting 26 homolog B (S. pombe) (VPS26B), mRNA.			AGCAGCAGGAAGTGGTGTTGTGGCGGAAGGGT GACATCGTACGGAAGAGC
1039.1226	1771.2476	1943.9392	CGI-96	MGC150422; BK126B4.3; MGC150423	NM_015703	Homo sapiens CGI-96 protein (CGI-96), mRNA.			TCTTGCCTCCACACCCTCCTCTCCAGGACCCTG GATGAATCCGTTCTGTG
291.9226	460.37677	514.40594	LCMT2	TYW4; PPM2; MGC9534; KIAA0547	NM_014793	Homo sapiens leucine carboxyl methyltransferase 2 (LCMT2), mRNA.	CCTGCTAGCCAGCCCCA GCCCTTTTCAGCCCAAG GAGACATGGAAGAAAA	ILMN_1687782	GCTGAAGACAGTGGCCATGCAGTCCGAGAGGAG TAGTGGTCTGCCTCTAA
3641.4727	4454.8975	4713.3643	NOL7	RARG-1; dJ223E5.2; MGC71933; C6orf90	NM_016167	Homo sapiens nucleolar protein 7, 27kDa (NOL7), mRNA.	ACTGTTGAGCAGGCCTC TCTGCCTGTGGCCTTCC GGCCGGTTTCCAGACG	ILMN_1808066	GTTCCTGTCTCTTGCCAACAAGAGGTTACCAGTG AAAAGAGCTGCTGTCC
428.97263	469.6601	483.7226	CEP63	MGC78416; FLJ13386	NM_025180	Homo sapiens centrosomal protein 63kDa (CEP63), transcript variant 1, mRNA.			GGAAGAGGAGGAACTGAGGTCTCATCACATTCT AGAGCGCTTGGATGCCC
39.25047	237.97263	334.4268	FLJ35409		XR_017838	PREDICTED: Homo sapiens FLJ35409 protein (FLJ35409), misc RNA.	AGACGGGCAGCGGCACC ATCCTCACACCTCTGCAT TCTGATAGAAGTCTG	ILMN_1672908	GTCACCACTAGTCAATGACTGCTTTTGCCCTGTC ACTGTCCATAGCCATG
307.5351	642.23096	781.16016	FAM64A	FLJ10491; FLJ10156	NM_019013	Homo sapiens family with sequence similarity 64, member A (FAM64A), mRNA.			AGTCACTCACCCACTGTGTTTCTGGTGCCAAGG CTCTTGAGGGCCCCACT
442.99762	1175.356	1469.1393	PITX1	POTX; PTX1; BFT	NM_002653	Homo sapiens paired-like homeodomain transcription factor 1 (PITX1), mRNA.			GGCCCGCGCCCCTGTTTACAGCGTCCCTGTGTA TGTTGGACTGACTGTAA
265.31012	324.69763	340.44763	TEX264	FLJ13935; SIG11; ZSIG11; DKFZp451H0417	NM_015926	Homo sapiens testis expressed 264 (TEX264), mRNA.	TATTGCTGATTGTACTGG TTGTTGCTTGTTGACTGT ACTATTCAGATGGC	ILMN_1684563	CTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGG CTCCCAGGGCCAGAGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
970.4143	2483.306	3106.2227	PSMC4	MIP224; MGC23214; TBP7; MGC13687; S6; MGC8570	NM_006503	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4), transcript variant 1, mRNA.			CACAGAGGCCGGCTTGGTCACTATGGAGGAGAT AGGCATCTTGGTGGAGA
2378.5977	3701.0728	4118.606	SDHB	SDHIP; SDH; SDH1; PGL4; IP	NM_003000	Homo sapiens succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (SDHB), mRNA.	CCTGCCCCTCTGTTTCC GATGAGGTGTACGGATG AGTGACCTGCACTAAG	ILMN_1728626	CCTGGCCAAGCTGCAGGACCCATTCTCTCTATAC CGCTGCCACACCATCA
1167.956	1455.9644	1538.5227	CIRH1A	FLJ14728; TEX292; KIAA1988; NAIC; CIRHIN	NM_032830	Homo sapiens cirrhosis, autosomal recessive 1A (cirhin) (CIRH1A), mRNA.			ACACTCGTGGCAGTAGAACGGCCTCTGGATGAC ATCATTGCTCAGCTCCC
957.07263	1494.9392	1727.8643	TK1	TK2	NM_003258	Homo sapiens thymidine kinase 1, soluble (TK1), mRNA.	TACTGAAGTCCCTTTGTG CCAGTGGATCCTGGAGG GCCTGGGGCTGGGCA	ILMN_1807249	TGACATCAGCCTGCTTCTTCCCCTCTGCGGCTTT CACTGCTGAGTTTCTG
995.3893	1845.756	2129.8809	PDCD2	RP8; MGC12347; ZMYND7	NM_002598	Homo sapiens programmed cell death 2 (PDCD2), transcript variant 1, mRNA.	CCAGGGACGCCTTGGAA GAGTCACTCAAGCTGAA AAACTGGAGTTGCAGC	ILMN_1684570	GCAAGAGCATTGACTGGGGCATCCTGGCTGTCT TCACCTGTGCTGAGAGC
934.8893	1027.2767	1062.4476	GPS1	COPS1; CSN1; MGC71287	NM_004127	Homo sapiens G protein pathway suppressor 1 (GPS1), transcript variant 2, mRNA.			GTTCCCGCCTCAGTCAGGTGCAGACAAGTGGGC GGTGTCCATTAAAGAGC
89.19764	148.06429	161.96011	GALE		NM_000403	Homo sapiens UDP-galactose-4-epimerase (GALE), transcript variant 1, mRNA.	ACCATGATGCTGGATGG AAGCTACAGTGAGTCTG AGGCCAACAGCCTGGC	ILMN_1676870	GGCCAAGGGCTCCACTGACCAGGAGGCCGAGG TCTCTAACTCTTATCTTC
53.229553	191.06845	252.47263	CAMTA2	KIAA0909	NM_015099	Homo sapiens calmodulin binding transcription activator 2 (CAMTA2), mRNA.	GACTCGGCCAGCCCCCT CTTCCCCGTGTGTGTCAT AGTTGTGCCATTCTT	ILMN_1812062	ACCCGACTCCGCATGTTTGCGTCTGTTTCCTCCC TCTCTGGCCCTGTCTT
259.71844	286.81427	298.54346	TRMT12	FLJ20772; TRM12; TYW2	NM_017956	Homo sapiens tRNA methyltransferase 12 homolog (S. cerevisiae) (TRMT12), mRNA.			GAAGGAGGGCCAAGATGGAAACAGAGAGACCAG TGAGGAGGCTTCTGTGG
187.31429	476.84763	593.8976	USP21	MGC3394; USP16; USP23	NM_012475	Homo sapiens ubiquitin specific peptidase 21 (USP21), transcript variant 1, mRNA.	ACATGTCCTGGGTGACA TGGGATGTGACTTTCGG GTGTCGGGGCAGCATG	ILMN_1717702	CGGAGAATGCCCCAGTGTGTGACCGATGTCGGC AGAAAACTCGAAGTACC
1490.9768	2150.2852	2332.2144	PSMA3	MGC32631; HC8; PSC3; MGC12306	NM_152132	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3), transcript variant 2, mRNA.			TGCAGACAGAGTGGCCATGTATGTGCATGCATA TACACTCTACAGTGCTG
1827.8976	3785.4893	4519.889	CCT3	CCTG; TRIC5; TCP-1-gamma; PIG48; CCT-gamma	NM_005998	Homo sapiens chaperonin containing TCP1, subunit 3 (gamma) (CCT3), transcript variant 1, mRNA.	GCTGAGATGGCTGTGCC CCAACTCCCATTCACCCA CCATGGACCCAATAA	ILMN_1727723	ACCATCCGTCTACTTACCTCCCTTCGGGCCAAGC ACACCCAGGAGAACTG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
416.06427	770.131	891.2226	EXOSC3	RP11-3J10.8; RRP40; MGC723; hRrp40p; MGC15120; p10; Rrp40p; bA3J10.7; CGI-102	NM_016042	Homo sapiens exosome component 3 (EXOSC3), transcript variant 1, mRNA.			GAATGGGTGTCATTGGACAGGATGGTCTGCTTT TTAAAGTGACTCTGGGC
1211.5768	2899.7727	3621.2559	AKR1A1	ALR; ALDR1; MGC1380; MGC12529	NM_006066	Homo sapiens aldo-keto reductase family 1, member A1 (aldehyde reductase) (AKR1A1), transcript variant 1, mRNA.			ATCTTGCTCAGGTGGCAGGTCCAGCGGAAAGTG ATCTGCATCCCCAAAAG
542.3726	753.84766	807.8726	MRPS7	RP-S7; RPMS7; MRP-S; MRP-S7	NM_015971	Homo sapiens mitochondrial ribosomal protein S7 (MRPS7), nuclear gene encoding mitochondrial protein, mRNA.			GCCCTCTGCCGCAAGAAACAGTGTGAGCTACTG CCACGCTGAAAACTACC
741.2726	1041.781	1135.9727	MRPL13	L13mt; L13; RPML13; RPL13	NM_014078	Homo sapiens mitochondrial ribosomal protein L13 (MRPL13), nuclear gene encoding mitochondrial protein, mRNA.	TGGCATCGTCCCTGAAA CGTGGATTGATGGCCCC AAAGACACATCAGTGG	ILMN_1695576	CTGCTACAGTTCAGCACCTGTTTTATGTGCCGAA TCACTGTGGGGAAAGG
290.03094	306.7143	310.89343	TATDN2	MGC126819; KIAA0218; MGC126825	NM_014760	Homo sapiens TatD DNase domain containing 2 (TATDN2), mRNA.	TGACTGCTTCTAGAGCT GGGAGGATCTGCAGACT TTCACGGATTCATGGA	ILMN_1682553	CTGCAGGTGAAACCAACCAGCCCTGTGTTAGAG GAGGAAAAGCGGAGATG
2342.2644	3571.7476	3968.5645	CENPB		NM_001810	Homo sapiens centromere protein B, 80kDa (CENPB), mRNA.	CATCTGGAGTTCTCAAAG ACCTGGGGCTGCTGTGA AGCTGGAACTGCGGG	ILMN_1671316	GGGCCCAGAGTCCAGCCGTCCAGCTGCTCCTTT CCCAGTTTGATTTCAAT
2929.731	7191.539	9034.797	BCL2L1	bcl-xL; BCLX; DKFZp781P2092; BCL-XL/S; Bcl-X; bcl-xS; BCL2L	NM_138578	Homo sapiens BCL2-like 1 (BCL2L1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GCAGTGTGAGAACTGAA GTATTTCTGATCACTCTC AGACTGTCCTCCGTG	ILMN_1792472	AGCGTGTCTGTATTTATGTGTGAGGAGCTGCTG GCTTGCAGTGCGCGTGC
512.9143	552.23926	560.9518	COMMD5	FLJ13008; HT002; HCARG; MGC72046	NM_014066	Homo sapiens COMM domain containing 5 (COMMD5), transcript variant 1, mRNA.	GCAAGCAGTAATAAAGTC TCCCTTAAAATGCACCCT CCTTCCACCTGGCC	ILMN_1765146	ATTCAGATCCGGCTTGGACAGGCACCTGAGATG GTGCCAAAGTGCAGCTG
998.9226	2565.8809	3237.7808	TRAPPC3	BET3	NM_014408	Homo sapiens trafficking protein particle complex 3 (TRAPPC3), mRNA.	TGCCCAGGGGAGGGAGT GTGGACAGTATCTGGAA GTTCTGGGATTCAGGT	ILMN_1706609	TGGGAAGCCACCCAGGTCTCATTCCTCCCTGCT GTTGGAGGCAACATCTC
879.9393	1397.3767	1565.5184	ARPC1B	p41-ARC; ARC41; p40-ARC	NM_005720	Homo sapiens actin related protein 2/3 complex, subunit 1B, 41kDa (ARPC1B), mRNA.	AGTGAGGCTGGAGGTGG CAGCTTCACAGAACTGG AGAACCAGGCCAAGTC	ILMN_1777261	GAGCCCATCAGCTGCCACGCCTGGAACAAGGAC CGCACCCAGATTGCCAT
133.95178	300.37677	367.74347	FAM49B	L1; DKFZp686B04128; BM-009	NM_016623	Homo sapiens family with sequence similarity 49, member B (FAM49B), mRNA.			CTCCTGCATGGCAAAACTGCCTATTCTGCTATTT AAAAACCCTCAATGAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
1698.2476	2644.5645	2982.7642	PRICKLE4	OEBT; MGC120398; OBTP; C6orf49	NM_013397	Homo sapiens prickle homolog 4 (Drosophila) (PRICKLE4), mRNA.			GGCACCTCAGCCAGGGGTGTAGCCAAGTAGACA AATGGAATCCTGTGCTG
1811.381	9582.072	15217.964	HMGA1	MGC12816; MGC4854; HMG-R; MGC4242; HMGIY	NM_145899	Homo sapiens high mobility group AT-hook 1 (HMGA1), transcript variant 1, mRNA.	CGCAGTAATTCTCATGTC CCCATAAGCAGAGCTGT CACAGTGTGCACTAC	ILMN_1708147	CCCCCCAAGGTTCTGGTTCCATTTTTCCTCTGTT CACAAACTACCTCTGG
5528.731	6396.8477	6640.664	TIMM23	PRO1197; TIMM23B; MGC22767; TIM23	NM_006327	Homo sapiens translocase of inner mitochondrial membrane 23 homolog (yeast) (TIMM23), nuclear gene encoding mitochondrial protein, mRNA.	CCTGTGTGAGGGCACAA CCAGGCCACGGGACCTT CTATCCTCTGTATTTG	ILMN_1683462	TCCTCCCCCATGAACTAGAAAACCACTTACTCCC AGAATTCAGGTCGTGC
1866.0059	2078.7559	2134.5393	LAMP2	LAMPB; CD107b; LAMP-2C	NM_013995	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2B, mRNA.			ACCTTGATGGTAACGCTCTATCTGGTTTTGGGTG TTTTTCATGTTTTAGC
355.7726	584.4393	669.40594	CMIP	KIAA1694	NM_030629	Homo sapiens c-Maf-inducing protein (CMIP), transcript variant Tc-mip, mRNA.	AGTTGCCTCCTTCAAAGA AGCATGCATGGTCCTTG CAGGTCACTGTGCCC	ILMN_1788764	TCTTTCCCCCCTCCGGTCCCATACTTCACAGCAC TCTGGTGCGGGAAGAA
1017.0226	1381.4768	1497.106	C14ORF112	HSPC203	NM_016468	Homo sapiens chromosome 14 open reading frame 112 (C14orf112), mRNA.			CTGGAAGAATATTCGAGGACCCAGGCCTTGGGA AGATCCTGACCTCCTCC
1708.2059	5548.764	7530.789	TAF10	TAF2H; TAF2A; TAFII30	NM_006284	Homo sapiens TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa (TAF10), mRNA.			GGACTTGACCCCTGCCCTCAGCGAGTATGGCAT CAATGTGAAGAAGCCGC
35.913116	63.528175	71.57934	DEPDC7	dJ85M6.4	NM_001077242	Homo sapiens DEP domain containing 7 (DEPDC7), transcript variant 1, mRNA.			GCAAGAGGCTGTACCTAAAATTCCTCAACCTAAG AGGCAGTCCACCATGG
3695.531	4974.5645	5419.0645	PSMD6	p44S10; KIAA0107; S10; SGA-113M	NM_014814	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 (PSMD6), mRNA.	AAGTTGTTCCCTGGCCG GGAGCGTTTGCTTTCGC CTGTAATCCCAACACT	ILMN_1653180	GGTGTGGAATTCATTGATCAGGAACTGTCCAGG TTTATTGCTGCCGGGAG
149.53094	184.55594	197.64346	ABCF2	DKFZp586K1823; ABC28; HUSSY-18; EST133090; M-ABC1	NM_007189	Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 2 (ABCF2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	CTGCAGGTGAAACCAAC CAGCCCTGTGTTAGAGG AGGAAAAGCGGAGATG	ILMN_1734138	CACCTGTAATCCGACTGTAAGCTCATCACCTTGG GAGGCCACTGTAGGAG
63.66634	114.57262	135.08095	ANP32A	C15orf1; PP32; PHAPI; MGC150373; PHAP1; I1PP2A; LANP; MAPM; MGC119787	NM_006305	Homo sapiens acidic (leucine-rich) nuclear phosphoprotein 32 family, member A (ANP32A), mRNA.			GGGGTCAGAAGCGAAAACGAGAACCTGAAGATG AGGGAGAAGATGATGAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
147.68095	168.86429	178.55594	DET1	FLJ10103; MGC126157; MGC126156	NM_017996	Homo sapiens de-etiolated homolog 1 (Arabidopsis) (DET1), mRNA.	TGGAGTTCCAGTGATCC CGGAGTCTGAACCGGCA GTGAGAGTGGGGAAAG	ILMN_1681724	GCTCTGTTAGTTCCAGCCTGCTATACCTCAGATG GGAGAGAGCCAGAGAG
28.060312	76.87431	110.8413	MLF1IP	CENPU; KLIP1; FLJ23468; CENP-50; CENP50; PBIP1; CENP-U(50); CENP-U	NM_024629	Homo sapiens MLF1 interacting protein (MLF1IP), mRNA.	TTGCTCTTCCGTTGCCCC GTGGCTTCAGCTCATCTT TGGCAGGAAGGCGA	ILMN_1720764	CAGTTCTGTGCACATACTTTTCAATACTCCCCGA CGGAAGAGCAAGGGTG
3022.8142	4676.356	5290.5645	BOLA3		NM_212552	Homo sapiens bolA homolog 3 (E. coli) (BOLA3), transcript variant 1, mRNA.	CCTCAACAGGCCCAGGG AGGGAAGTGTGAGCGCC TTGGTATGACTTAAAA	ILMN_1708375	CATGGATTGCGGATATTTACCTCTGTCCCCAAAC GCTGACCACGCCCTGG
4024.7227	4793.0557	5058.8975	KHDRBS1	Sam68; FLJ34027; p62	NM_006559	Homo sapiens KH domain containing, RNA binding, signal transduction associated 1 (KHDRBS1), mRNA.			TCCATTTGAGATTCTGCACTCCATGAAAAGTTCA CTTGGACGCTGGGGCC
127.41104	554.1309	853.3185	MT1G	MT1; MT1K; MGC12386	NM_005950	Homo sapiens metallothionein 1G (MT1G), mRNA.			CGCCTGATGTCGGGACAGCCCTGCTCCCAAGTA CAAATAGAGTGACCCGT
119.63095	254.85596	313.9768	BCCIP	TOK-1	NM_016567	Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant A, mRNA.			GGTTCACGGGGGCAAGTGACAGCCCTGGTTTCT CTGAAGGCTGGACTAAT
4153.7725	5038.9395	5354.7144	BANF1	D14S1460; BCRP1; BAF; MGC111161	NM_003860	Homo sapiens barrier to autointegration factor 1 (BANF1), mRNA.	AGAAAGGCACAGGACTC GCTAAGTGTTCGCTACG CGGGGCTACCGGATCG	ILMN_1766762	GCTTCGGATGCCTTCGAGAGTGGTGCGACGCCT TCTTGTGATGCTCTCTG
41.88808	85.87268	104.83512	ZFP91	PZF; FKSG11; ZNF757	NM_053023	Homo sapiens zinc finger protein 91 homolog (mouse) (ZFP91), mRNA.	CATGTATCGGAACTTAGA ACTGGTGGGCGCGGTG GCTCTTGCCTGTAATC	ILMN_1661519	GAAGAAGGACAGCGTAGTGGCACACAAGGCAAA AAGCCACCCTGAGGTGC
30.141129	54.211746	66.565834	GPER	LyGPR; DRY12; GPCR-Br; LERGU; MGC99678; GPR30; CEPR; CMKRL2; FEG-1; LERGU2	NM_001039966	Homo sapiens G protein-coupled estrogen receptor 1 (GPER), transcript variant 3, mRNA.	CTCAGCCCGACATCCAA CAGGCGCCAAACTCACA GAGCCCTTGTGCAGAT	ILMN_1763207	GAGGCTGGTGACGTTCAGCCTTTGTCAATAAAC CTGTCATGTGCGGATCC
449.00595	508.8518	527.14343	SEPHS1	MGC4980; SELD; SPS; SPS1	NM_012247	Homo sapiens selenophosphate synthetase 1 (SEPHS1), mRNA.			TCAGCAGCTGTTTGGCCTAATTCTTAGCATTATT TTGTCCTTTGCGCCAG
82.160805	130.31012	141.89761	CXORF39		NM_207318	Homo sapiens chromosome X open reading frame 39 (CXorf39), mRNA.	CTTTATGCAAAATGGCTC CTGTGAGGGCTGCAAGC TGGAGGGTGGTGCAG	ILMN_1784780	GTGGATAGCATTTTGAAGGTGACCGTGATTCTGT AGGAAGAGCTGTAATC
11.189314	51.7182	76.05653	HIST1H3C	H3/c; H3FC; H3.1	NM_003531	Homo sapiens histone cluster 1, H3c (HIST1H3C), mRNA.	GTCCAGATGAGAGCAGA GATACAGTGAGAAATTAT GTGATCTGTGTGTTG	ILMN_1742324	TGGGACTCTTCGAAGACACCAATCTGTGCGCTAT TCACGCTAAACGCGTC
70.712296	106.30179	109.28928	SCML1		NM_001037540	Homo sapiens sex comb on midleg-like 1 (Drosophila) (SCML1), transcript variant 1, mRNA.	GCACGAAGTCCCTCTGC CCTACTCCCTATTCAAGG ATATTACTCACTGCA	ILMN_1751569	ACCCGATCCTCAGCCGCACTCCGAGTCCAGTGC ATCCCTCAGATTTCTCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
48.944515	98.38512	102.126785	C1ORF74	FLJ25078	NM_152485	Homo sapiens chromosome 1 open reading frame 74 (C1orf74), mRNA.	CACTCTATGGGAAACTCT TCAGCACCTACCTGCGC CCCCCACACACCTCT	ILMN_1674759	TATACCTGCTCTATGTGGGTGCTGCATGCTAGGA AAGTAGGGCTGGGGGC
210.33928	644.66016	676.57263	CDC42	CDC42Hs; G25K	NM_001039802	Homo sapiens cell division cycle 42 (GTP binding protein, 25kDa) (CDC42), transcript variant 3, mRNA.			AGCCGAGGAGACCCCGCGCAGTGCTGCCAACG CCCCGGTGGAGAAGCTGA
146.50595	164.78511	167.24762	C12ORF49	FLJ21415	NM_024738	Homo sapiens chromosome 12 open reading frame 49 (C12orf49), mRNA.			TGCAGCAGGACTACATCGAACTCTGATGTGCCG GATTGTGGCATGTCTGC
23.136848	93.47684	100.16429	MKI67	KIA; Ki-67	NM_002417	Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67), mRNA.	CTTGCCCGGAGACCAAG AAGGCGCGCGATGCGTG TATCATCGAGAAAGGA	ILMN_1770885	CCTTAGGCAGGCACCTCCAACCACCACACACTC CCTGCTGTTTTCCCTGC
33.740974	649.4226	768.68097	SALL2	FLJ10414; KIAA0360; HSAL2; ZNF795; p150(Sal2)	NM_005407	Homo sapiens sal-like 2 (Drosophila) (SALL2), mRNA.	ATCTCTCTTTGTCTTGAG GGGGCTGTTGAGTGGTC GCGGACCTGGGCTCT	ILMN_1663234	CAGCTCCAGGTGGCGTCCTCCCTGCCTCTCCGT CTTGTAATGAGTTGTAG
229.61012	5597.581	6559.8477	TSC22D1	TSC22; TGFB1I4; RP11-269C23.2; DKFZp686O19206; MGC17597	NM_006022	Homo sapiens TSC22 domain family, member 1 (TSC22D1), transcript variant 2, mRNA.	GGAAAGGGTTAAAGTGA GGAAGGTGTACGTGAAG GGTCTGGGGTTGCTGG	ILMN_1797801	TCCCAATGGTGTAGACCAGTGGCGATGGATCTA GGAGTTTACCAACTGAG
1232.4393	2136.8977	2228.5642	NUP37	MGC5585; p37; FLJ22618	NM_024057	Homo sapiens nucleoporin 37kDa (NUP37), mRNA.	GACCCGGAGTAGGGGG GCTCGGGACCATGAGGA TGACCAGCAAAATTCAA	ILMN_1790741	GACTGTCCTGGCATCGAACTCTCCCTCTGTGTGT AATTGGAGGAGACCAC
118.530945	208.69762	213.66428	MRPL35		NM_016622	Homo sapiens mitochondrial ribosomal protein L35 (MRPL35), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.			CAGCATGTCAGGCCAGGATTATTAGGGAGATTC CTCGAAACTAGTGTGTG
107.87272	134.40594	136.58928	OSGIN2	C8orf1; hT41	NM_004337	Homo sapiens oxidative stress induced growth inhibitor family member 2 (OSGIN2), mRNA.	CTGGTGGGATGGGTATG GGACCAGGTGGCCCAGG AATGATTACTATCCCA	ILMN_1725199	CTCTCAGGCCCCACAACTTACTTCCTGCATTTTA ACAAGATCCCCAAGGG
1428.6309	2147.3643	2198.7517	DBN1	DKFZp434D064; D0S117E	NM_004395	Homo sapiens drebrin 1 (DBN1), transcript variant 1, mRNA.	GCGCTCCAATATCGTGG ACCTGCTGTTTGTCAAAG ACTTGGCCTTCGTGG	ILMN_1663975	AAAACATGGCAATAAATGGCTCGTGGGCTCTGG CTCCCTGGGACCCCCTC
567.3143	1870.4893	1958.0977	PRPF3	HPRP3P; HPRP3; Prp3p; RP18; PRP3	NM_004698	Homo sapiens PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae) (PRPF3), mRNA.	TTCATGCTCACACAGGCT ATGGGGATGGTGGGCTC CAGGTCAGCTCTGCA	ILMN_1715705	GCATGGGGCTGAACACTACTGGGACCTTGCGCT GAGTGAATCTGTGTTAG
178.45178	331.76013	340.76013	FBXW8	FBX29; FBXO29; FBW6; MGC33534; FBW8	NM_012174	Homo sapiens F-box and WD repeat domain containing 8 (FBXW8), transcript variant 2, mRNA.	ATGGCCCAGACTGACTC CATCCCCTGACTTTCCCT TTGACTTCACCCTGT	ILMN_1703701	GGGGAGCTGGATGGTGAAACACCTGAAGATCTC ATATCGCCTCTCAAAAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
112.01012	427.2726	448.43097	TRIM3	BERP; HAC1; RNF22; RNF97; FLJ16135	NM_006458	Homo sapiens tripartite motif-containing 3 (TRIM3), transcript variant 1, mRNA.			ACAGGAGTCCCTCTAGTTGTCTCCCTACCACCCT ATACACACTGACAGAG
1009.3893	1681.731	1705.4976	CEBPZ	NOC1; CBF2; HSP-CBF	NM_005760	Homo sapiens CCAAT/enhancer binding protein zeta (CEBPZ), mRNA.			CAGCTTAGATGGGAGGCTGAACGTGATGACTGG CTACACAACAGAGATGC
267.06845	967.98926	1024.0892	KIF11	KNSL1; EG5; HKSP; TRIP5	NM_004523	Homo sapiens kinesin family member 11 (KIF11), mRNA.			CCCTTAGGACTCTGGTATTTTTGATCTGGCAACC ATATTTCTGGAAGTTG
1857.3142	2786.906	2849.2642	NUP62	p62; SNDI; FLJ43869; IBSN; DKFZp547L134; FLJ20822; MGC841	NM_016553	Homo sapiens nucleoporin 62kDa (NUP62), transcript variant 2, mRNA.			CAGCTTCCAGTGGTGGCCGTAGACTTGGCTCGG AACTTAGTGGCACCAGA
75.89065	90.831	93.34393	SRPK2	FLJ36101; SFRSK2	NM_182692	Homo sapiens SFRS protein kinase 2 (SRPK2), transcript variant 1, mRNA.			GCAGTGGGCAGAATACTTCTCACAGCTCAAAGAT AACAGTGATCACATTC
354.3976	1968.3225	2073.4475	TNPO3	TRN-SR; TRN-SR2; TRNSR; MTR10A; IPO12	NM_012470	Homo sapiens transportin 3 (TNPO3), mRNA.	CACAGTCCAGGCCAAAA AGACAGGGGCAAAGCCC TCACAAGCCAGGAAGG	ILMN_1663179	ACTGTGTCCCACAATCAGAAACCTCCGTTGTGGC AGAGGGGCCTTCACCG
192.56012	600.04346	624.76013	TACC3	MGC133242; ERIC1; MGC117382	NM_006342	Homo sapiens transforming, acidic coiled-coil containing protein 3 (TACC3), mRNA.	AACAGCCCCACACACAG CAGGGGCCTGAGAAGTT AGCGGGAAACGCCGTC	ILMN_1783673	GGAGCAGAAGACTAAAGAGAACGAGGAGCTGAC CAGGATCTGCGACGACC
693.23926	777.30597	778.7893	C14ORF32	MGC23138; MISS; c14_5346	NM_144578	Homo sapiens chromosome 14 open reading frame 32 (C14orf32), mRNA.			ACCCCTGGATAAAGGCACTTTCACTGCCTGTCAC TGATCAGCAGATACTG
13.068526	240.40594	263.88928	HMGA2	HMGI-C; HMGIC; LIPO; BABL; STQTL9	NM_003483	Homo sapiens high mobility group AT-hook 2 (HMGA2), transcript variant 1, mRNA.	CTTGTGTAACCACTTGTC GCCTTAGGGCCAGATTC CCCTCTCTAGTCCCC	ILMN_1765829	CCCAGGGGAAGACCCAAAGGCAGCAAAAACAAG AGTCCCTCTAAAGCAGC
338.0893	1330.5059	1407.3809	KIFC1	HSET; MKLP2; RAB6-KIFL; KNSL2; MGC1202; MGC149736; MGC149737	NM_002263	Homo sapiens kinesin family member C1 (KIFC1), mRNA.			GAACGTCTCCGAGTCCCTCAACTCTCTACGCTTT GCCTCCAAGGTGAACC
219.6518	384.55176	387.81012	G3BP1	HDH-VIII; G3BP; MGC111040	NM_198395	Homo sapiens GTPase activating protein (SH3 domain) binding protein 1 (G3BP1), transcript variant 2, mRNA.			AAGAAGACTCGAGCTGCCAGGGAAGGCGACCGA CGAGATAATCGCCTTCG
35.27672	86.82265	89.897705	C10ORF119	FLJ36756; FLJ13081; MCMBP; MCM-BP	NM_024834	Homo sapiens chromosome 10 open reading frame 119 (C10orf119), mRNA.			CAGCGTTAATCCTGTATGGCCAGGAAACTGAGTA GACTCCTGTGTAACCC
193.01846	267.00177	270.74762	MRPL47	CGI-204; MGC45403; NCM1	NM_177988	Homo sapiens mitochondrial ribosomal protein L47 (MRPL47), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.			CACCTGCTACCTTAGAGTGTGAAGGTGATGGTA ACTGCCACAGCAAAGGC
1139.0726	3410.1394	3595.4475	PTTG3	rcPTTG1	NR_002734	Homo sapiens pituitary tumor-transforming 3 (PTTG3) on chromosome 8.	GGTCCCAGACCAGCCCT CTTCTCCCTGAATGTGTT GAGTTGGTGGCAGGA	ILMN_1670572	GCTTCGAGAGTTTTGACCTGCCTGAAGAGCACC AGATTGCACATCTCCCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
294.78094	1111.935	1178.1309	SEH1L	Seh1; SEH1A; SEC13L; SEH1B	NM_001013437	Homo sapiens SEH1-like (S. cerevisiae) (SEH1L), transcript variant 1, mRNA.	CCTACTCATCCAAGACCC AGCTTCATTGTCTCCATC TCTGGGAAGCCTGC	ILMN_1717195	ATGCTGACACTGCCAACCTCCAGTATCCTCACCC TCGCAGACGATATCTC
49.57187	98.82262	100.61429	DDX11	CHL1; KRG2; MGC9335; CHLR1; MGC133249	NM_030653	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11), transcript variant 1, mRNA.			GGGCCGTTAGGCTCTCAACATGACTATAGAGAC CCCGTGTCATCACGGAG
9.840411	134.94345	140.86429	CMIP	KIAA1694	NM_198390	Homo sapiens c-Maf-inducing protein (CMIP), transcript variant C-mip, mRNA.			GGCGACATTCAGGTCTGTGTCATCCGGCACCCG CGGACCTTTCTCAGCAA
1221.5809	2071.7227	2095.281	CCT6A	HTR3; TCPZ; Cctz; MGC126214; MGC126215; TCP-1-zeta; TCP20; MoDP-2; TTCP20; CCT-zeta-1; CCT-zeta; CCT6	NM_001009186	Homo sapiens chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), transcript variant 2, mRNA.			ACAGGCAGAGGTAAAAAGATGATGGAAGGTGTG GTGACTAAGGGCCACGG
1268.0809	4787.389	4966.9976	YY1	UCRBP; YIN-YANG-1; DELTA; NF-E1	NM_003403	Homo sapiens YY1 transcription factor (YY1), mRNA.	ATGCTCTTTTAGAACGGG AAACGGCTCAGATCCTG CTGTGGCACGGGGCC	ILMN_1658800	TGCCTGTTCAGTTACAGAAAGTGGTGCTCAGTTG TAGAATGTATTGTACC
157.60596	249.41846	251.95595	CLP1	HEAB; hClp1	NM_006831	Homo sapiens CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae) (CLP1), mRNA.	GAGAAGAAGGTGAAATC TTGTGCTGAGTGGGTGT CTCTCTCAAAGGCCAG	ILMN_1794912	CCTAGAGGCAGATGGGCTGAGATAAAAGACTGT TGGGGCCACCTGACCAG
78.25325	562.4393	587.91846	PSMD11	S9; p44.5; MGC3844	NM_002815	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA.	GAAGCCGGTGGGGCCTT CGGAAAGAGAGAGCAGG CTGAAGAGGAACGATA	ILMN_1727332	GGGATTTTGGACCAGGGGGAGGGTGTCCTGATT ATTTTCGATGAACCCCC
130.30594	198.03928	209.11844	STOML1	hUNC-24; FLJ36370; SLP-1; STORP	NM_004809	Homo sapiens stomatin (EPB72)-like 1 (STOML1), mRNA.	GGTCTTCCAGTATCGCA GTTCTTCGAATGAAAGCC AAGGAGCACACCGCC	ILMN_1724540	AGGGCCTGCTGCTTCCCTGGCGCTGCTCCCAAA GATTTCTGACTCATCTG
125.526566	284.47678	313.79764	CXCL6	GCP2; GCP-2; CKA-3; SCYB6	NM_002993	Homo sapiens chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2) (CXCL6), mRNA.	TGAACATCCTGCTTTTCG ATTGGCCAGCGATGGGT GTCTGCGCGCCTTGG	ILMN_1729963	TCCTGTGTGTCATGTTGGTTTTTGGTACTTGTAT TGTCATTTGGAGAAAC
142.86429	299.2143	304.97263	LOC440145	MGC150539; FLJ21869	NM_001071775	Homo sapiens similar to RIKEN cDNA 2410129H14 (LOC440145), mRNA.			CCAGAAGCTTTATCATCGGTTATTAAGGAGCTTC GCAAGGCTACTGAAGC
182.68094	457.98096	468.56012	HSPA14	HSP70-4; HSP70L1; MGC131990	NM_016299	Homo sapiens heat shock 70kDa protein 14 (HSPA14), transcript variant 1, mRNA.			GGACTCCTTTGCCAGCTCGAAGACAACACACATT GCAAGCCCCTGGAAGC
55.95943	96.48512	97.847626	C1ORF124	DKFZP547N043; PRO4323; DDDL1880; dJ876B10.3; RP5-876B10.3	NM_032018	Homo sapiens chromosome 1 open reading frame 124 (C1orf124), transcript variant 1, mRNA.			GCCATCCCAGGATGTGAGTGGGTCTGAAGATAC ATTCCCAAATAAACGAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
120.20178	213.32262	221.06012	SNORD36A	RNU36A; U36a	NR_002448	Homo sapiens small nucleolar RNA, C/D box 36A (SNORD36A) on chromosome 9.			CACTGAATTCAACCTTGAAGTGCGAATCCATGAG CTTTTTAACCCTGAGC
85.935165	131.38512	133.49344	ADORA3	AD026; RP11-552M11.7; A3AR; bA552M11.5	NM_000677	Homo sapiens adenosine A3 receptor (ADORA3), transcript variant 2, mRNA.	GCAGCGAGAGCTCACGG AATTCCTCTCGTGCCAAA AGGAAACCCAGTTGG	ILMN_1795139	CCTTCAGATTCCCCATCAACAAACACTTGAGGGC CTGTATGCCTGGGCCA
5437.798	9738.855	9947.848	PPA1	PP1; IOPPP; MGC111556; PP; SID6-8061	NM_021129	Homo sapiens pyrophosphatase (inorganic) 1 (PPA1), mRNA.	GCCTTTATGGGTGATCC AGGGAAGATTGGTTTTG CTGATCAGATTCCACC	ILMN_1745529	GAGAGCCCCTTCAAGTGTGATCCTGATGCTGCC AGAGCCATTGTGGATGC
567.63513	870.59766	880.19763	SKIV2L2	MGC142069; Dob1; KIAA0052; Mtr4	NM_015360	Homo sapiens superkiller viralicidic activity 2-like 2 (S. cerevisiae) (SKIV2L2), mRNA.	CTGCTCAAATTCTGCGAT TGCTGCACATAGAGGAG CTCAGAGAGCTACAG	ILMN_1696708	GAAGGCAGCATAATTCGTTGTATGAGGCGCCTG GAAGAATTGCTTCGACA
63.04388	251.50595	267.49344	MCM7	MCM2; CDC47; P1.1-MCM3; P1CDC47; CDABP0042; P85MCM; PNAS-146	NM_005916	Homo sapiens minichromosome maintenance complex component 7 (MCM7), transcript variant 1, mRNA.			AGATTCTCAGCTTCCCCAGGAGCAAGACCTCTG AGCCCGCCAAGCGCGGC
100.36924	179.62262	182.95595	RRP1B	RRP1; KIAA0179; Nnp1	NM_015056	Homo sapiens ribosomal RNA processing 1 homolog B (S. cerevisiae) (RRP1B), mRNA.			GTCCTATAAATGCACCTCCTGTCAAAACCATGCC TGAGAGGTCCCGGCTG
48.680367	1090.3142	1207.7059	EZH2	EZH1; ENX-1; MGC9169; KMT6	NM_152998	Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), transcript variant 2, mRNA.	AGCACCCCTCAGTTCCT GTGCCTCAGCCCACAGG CCACTGTGATAATGGT	ILMN_1720998	AGTGTGACCCTGACCTCTGTCTTACTTGTGGAGC CGCTGACCATTGGGAC
1132.3392	1816.0726	1832.031	TXNDC14	DKFZp781O2021; TMX2; CGI-31; MGC111151; PIG26	NM_015959	Homo sapiens thioredoxin domain containing 14 (TXNDC14), mRNA.	CTTTCCCTGGAGAATGG GATGTGAAGCAGTAGAC CGCAGCCACGCCGATG	ILMN_1697440	CCCCCAAGGACTCTTGCTTCCTCAAGCCCTTCTG GCTTCGTTTATGGTCT
217.96011	470.3018	481.2976	KIAA0182	GSE1	NM_014615	Homo sapiens KIAA0182 (KIAA0182), mRNA.	GCTCAAGGAAAGATAAA GCTGGGCGGAAGGAGG TGTGCGTGGCTTCTGGG	ILMN_1700681	CCGGTGCCTCGGTCACTCTGGGGGCAGTTTAGA TGCTGTGAAATTAAACC
78.95362	253.95595	259.16428	ATRIP	MGC20625; ATRIP; DKFZp762J2115; DRN3; FLJ12343; MGC21482; DKFZp434J0310; MGC26740; AGS1	NM_032166	Homo sapiens ATR interacting protein (ATRIP), transcript variant 2, mRNA.	GCTGGCGTGCCCATGTT GCAGATATTTTCCCGAGT TCCCCAGAATGGATG	ILMN_1653292	GAAACCGATGTGGAAGACCCCGAGGTGGAGTGT GGCTGAGGCCCTGAGTG
894.0893	4321.798	4493.3975	UPF2	smg-3; KIAA1408; MGC138835; HUPF2; DKFZP434D222; RENT2; MGC138834	NM_080599	Homo sapiens UPF2 regulator of nonsense transcripts homolog (yeast) (UPF2), transcript variant 1, mRNA.	CCCCAGCAGAGTTGAGT AGTTGTAGCAGACACCA CATGCCCTTGAGCCTA	ILMN_1808765	TGCTGCCCAATCTTCACCAGCTTCAGAAATCTGA CCTTTGCCGATGCTGC
915.15594	1379.1809	1389.4309	VARS	G7A; VARS2	NM_006295	Homo sapiens valyl-tRNA synthetase (VARS), mRNA.	CTGTGGAGGATGCAGGA TTACCTTCTTATGAACAG GCAGTGGCGCTGACC	ILMN_1661809	AGCTCCAACAGACAGAAGCAGAGCTCAGGAAGG TGGATGAGGCCATCGCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
93.41439	620.2768	656.36426	ARL6IP2	FLJ23293; ARL3IP2; atlastin2; ATL2	NM_022374	Homo sapiens ADP-ribosylation factor-like 6 interacting protein 2 (ARL6IP2), mRNA.	CCTGAATACCATTTGTGT CTGAAGGGCTGAAGATG TGGACAGGCTCTAGC	ILMN_1657603	GCAGGCCTGACTGACCAGGTGTCTCATCATGCC AGATTAAAGACAGACTG
837.256	6743.214	7131.7227	NUP88	MGC8530	NM_002532	Homo sapiens nucleoporin 88kDa (NUP88), mRNA.			ACCCACCATTATTCTCAGTGCCTACCAGCGAAAG TGCATTCAGTCCATCC
223.60178	2991.606	3160.0894	PIAS2	SIZ2; MIZ1; miz; ZMIZ4; PIASX-ALPHA; MGC102682; PIASX-BETA	NM_004671	Homo sapiens protein inhibitor of activated STAT, 2 (PIAS2), transcript variant beta, mRNA.	TCACCAGCCCTGAGATT GAGGCCCCATACACCAG TGAAGAGGAGCAGGAG	ILMN_1696151	CAGCCATCTTCTGTAAGGGTGCCCAGTGTGACT TCGGTTGATCCTGCTGC
472.5268	1606.2976	1639.231	FOSL1	fra-1; FRA1	NM_005438	Homo sapiens FOS-like antigen 1 (FOSL1), mRNA.	CTCCTACAACGACTTCCT CCGGGCATTCCTCCAGT AGACACCCCTGCTGT	ILMN_1669465	CACTGCCACACTCTCCATCACCCTCTTCCTGTGA TCCACCCAACCCTATC
34.76181	177.58095	183.65594	NUPL1	PRO2463; KIAA0410	NM_014089	Homo sapiens nucleoporin like 1 (NUPL1), transcript variant 1, mRNA.	ATTACTGTACATAGAGAG ACAGGTGGGCATTTTTG GGCTACCTGGTTCGT	ILMN_1735930	GTTACTACTGGACCCACTCCTTTCAGCACCATGC CAAACGCAGCAGCCGT
42.81552	93.3937	97.13196	MAP2K7	MKK7; Jnkk2; PRKMK7; MAPKK7	NM_145185	Homo sapiens mitogen-activated protein kinase kinase 7 (MAP2K7), mRNA.	CATTGGCGTCAAGTACT CGGAGAAGCAGGAGCG GAATTTCGACGATGCCA	ILMN_1708486	TTTTATGAGTGTGTGTCCGCCCACCCCCACCCC CTTCAGTGTTAAGTGGG
529.11426	3493.1309	3912.9893	SNX2	TRG-9; MGC5204	NM_003100	Homo sapiens sorting nexin 2 (SNX2), mRNA.			CAAGCTGCATGTCCTGACCCTCTTTGAATTAAGT GGACTGTGGCATGACA
234.11844	377.87262	388.31012	DHX36	MLEL1; DDX36; KIAA1488	NM_020865	Homo sapiens DEAH (Asp-Glu Ala-His) box polypeptide 36 (DHX36), mRNA.			GCCATTCTTCATCATTGTTTAAATTTTGGCTGGAT GCCAAACCCTGGGAC
191.00595	239.23929	242.87677	ZNF586	FLJ20070	NM_017652	Homo sapiens zinc finger protein 586 (ZNF586), mRNA.	CGCAATGAGTAGGGCTG GGTCTCGGCCATGGAAA GCATACCTCAGTGCTC	ILMN_1669377	TTCCAGCCTGCCAGTCATGAATCTCAGACAGCCT GCCACCTATTGCCCTG
39.06421	79.81967	82.77318	ZNF823	HSZFP36	NM_001080493	Homo sapiens zinc finger protein 823 (ZNF823), mRNA.			ATTGCAGGGGATTGGTTCCAGCACCCTCTAAATC CACAGATGCCAAGTCC
349.9268	829.26013	875.84766	NUP155	N155; KIAA0791	NM_153485	Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 1, mRNA.			CTCTGCCTGGATGCTGTTTGTGGTTACCTTGTTG AGCTCCAGTCTATGAG
1311.756	1648.0642	1680.6976	CCDC59	FLJ10294; HSPC128	NM_014167	Homo sapiens coiled-coil domain containing 59 (CCDC59), mRNA.	GTCCGCCCTGCTGCGTC TGTTCGTCAGCTGAGTTC CTTGTGAATCTCTGT	ILMN_1695792	ATCTGCTGCCTATTAGGTTCTTCTGTGACATGTG CCTCCCAGCAGTGAAC
577.30597	1287.0559	1349.5269	FAM111A	KIAA1895; FLJ22794; DKFZp686A06175	NM_022074	Homo sapiens family with sequence similarity 111, member A (FAM111A), transcript variant 1, mRNA.			GTGCCGGTAGTACAGATAACCCCTCATAAAGATG CTTATCTAACCTCCCC
187.45595	375.13928	390.2226	C5ORF32	ORF1-FL49	NM_032412	Homo sapiens chromosome 5 open reading frame 32 (C5orf32), mRNA.	GCCTGGAGGTCTTCAAG GAGTCCCTAATGCTACA GTGCGGCCACTCCTAC	ILMN_1667416	GCCACCTCTGACAGGTGTGCCTGCCCCCATCTC TTCTGATTGCTGTTAAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
987.28094	3387.906	3652.931	SERTAD2	Sei-2; TRIP-Br2; MGC126688; MGC126690	NM_014755	Homo sapiens SERTA domain containing 2 (SERTAD2), mRNA.	GGAATGTACTTCAGGGT CTAAAGAGATGGCTTCT GGAGATAGCTCAACCG	ILMN_1665873	GGAGGTATAACCTTTCCCCCACAGACCTGAGAG CTGTGCCTTTTCTATGC
51.295555	453.38095	516.2476	TMEM48	FLJ12556; NDC1; NET3; FLJ34120; FLJ10407; RP4-654H19.1	NM_018087	Homo sapiens transmembrane protein 48 (TMEM48), mRNA.			CCTCATGCTTCCAGTAAACCACCCCGGATTTCAG GAAGCCTTGTGGACAC
16.709297	786.7643	1026.9143	HOXC6	CP25; HOX3C; HHO.C8; HOX3	NM_004503	Homo sapiens homeobox C6 (HOXC6), transcript variant 1, mRNA.	GGGTTTGGCTGTCAGTG GACATGGGGAGCTGGAT GGAAATGCCTCTCACT	ILMN_1716907	TCCCTTCGTGTTACCCTCCTGTATAAATCCAACC TCTGGGTCCGTTCTCG
104.825165	800.60596	930.3476	RRM2	RR2M; R2	NM_001034	Homo sapiens ribonucleotide reductase M2 polypeptide (RRM2), mRNA.	CCCGGGAGGGCAGAGC CAGAAGAAGGCTCATTA GACCTGGGGGACCCAAA	ILMN_1711491	GTGTCCTGGGATTCTCTGCCCCCTCTGAGTAGA GTGTTGTGGGATAAAGG
20.801231	108.09762	122.40595	UBE2MP1		NR_002837	Homo sapiens ubiquitin-conjugating enzyme E2M pseudogene 1 (UBE2MP1) on chromosome 16.	ATTATACGCTGGCAACAC AGAGGCAGCCCGCACAC CTGCGAGTGGCAAAC	ILMN_1741673	CGGCAGCGGTAGGATGATCAAGCTGTTCTCGCT GAAGCAGCAGAAGAAGG
1259.8976	1850.6892	1894.731	SRRM1	POP101; SRM160; MGC39488; 160-KD	NM_005839	Homo sapiens serine/arginine repetitive matrix 1 (SRRM1), mRNA.	AGAGTCGAGCAAAAGCC TTCTCCACCTGCTCCCC CCAGCTCATTGTCATC	ILMN_1705745	CAACTTTCAGAGCCTCTTGTATTTGGAAGGCTGG AAGGGCCCAGACTTTG
17962.023	43682.43	46068.223	UBB	FLJ25987; MGC8385	NM_018955	Homo sapiens ubiquitin B (UBB), mRNA.	CTGCCTAGTGTATTCAAC AGAAGGACTGTGGTCAT GTAACAGGTAACCAC	ILMN_1668778	CCCTGCACCTGGTCCTGCGCCTGAGGGGTGGC TGTTAATTCTTCAGTCAT
7.6144457	215.80594	255.22678	ICA1	ICAp69; ICA69	NM_004968	Homo sapiens islet cell autoantigen 1, 69kDa (ICA1), transcript variant 2, mRNA.			AGACCTGACTGCCTGGTTCAGCCTCTTCGCTGA CCTCGACCCACTCTCAA
898.2476	2028.6809	2172.3142	TUSC3	D8S1992; N33; OST3A; MGC13453	NM_006765	Homo sapiens tumor suppressor candidate 3 (TUSC3), transcript variant 1, mRNA.			AAGAACCCACACAATGGACAAGTGAGCTACATTC ATGGGAGCAGCCAGGC
7551.456	11201.215	11606.256	KPNB1	IPOB; NTF97; MGC2157; Impnb; MGC2155; IMB1; MGC2156	NM_002265	Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA.	GGCTCGAAAGGCAAGAG CCCAGCATCGGTTTTCA GAACACCTACATCTGG	ILMN_1805998	TCAGAATTGGCAGCACAAAGAAAACGCCCTCTCC TGACTTGTATTGTGGC
248.23096	552.6726	581.0393	INTS4	MGC16733; INT4; MST093	NM_033547	Homo sapiens integrator complex subunit 4 (INTS4), mRNA.	GAGGCACTCCCGGAGCA AAGTCTATGAAGGATCTT CTGCAAGAGGCTGCC	ILMN_1789361	CACAGGTGGAAACCAGCATCGAGGGCACCATTC CCTTCAGCAAGCCTGTA
149.97678	418.44763	449.33096	DIAPH3	FLJ34705; DRF3; DKFZP434C0931; diap3; DKFZp686A13178	NM_001042517	Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), transcript variant 1, mRNA.			GTCCGGGGCTGCCTTCCGCGACAGAAGAAAAAG GACACCGATGCCAAAAG
479.2893	1386.7893	1501.8893	NUSAP1	LNP; FLJ13421; SAPL; BM037; PRO0310p1; Q0310; ANKT	NM_018454	Homo sapiens nucleolar and spindle associated protein 1 (NUSAP1), transcript variant 2, mRNA.	GGAGTATGTCACCTTCCT GGGGGCCTTGGCTTTGA TCTACAATGAAGCCC	ILMN_1713636	CTAGGCTTTGCTTAGTATCATGTCCATGTTTCCT TCACCTCAGTGGAGCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
131.57295	472.89764	522.35596	FGF5	HBGF-5; Smag-82	NM_004464	Homo sapiens fibroblast growth factor 5 (FGF5), transcript variant 1, mRNA.	CCCTCCACGTTGGTTTG GCTATGATAGGGAAGGA AACCCTGTTACAGAGC	ILMN_1791253	GCTGTGTCTCAGGGGATTGTAGGAATACGAGGA GTTTTCAGCAACAAATT
95.51432	138.53513	142.09763	THAP7	MGC10963	NM_030573	Homo sapiens THAP domain containing 7 (THAP7), transcript variant 1, mRNA.			GCCTTACTCTGGAAGCGGCGAGCCGAGGCAGC CCTTGATGCCCTTGACAA
256.12262	446.43927	464.6518	GART	PRGS; PAIS; GARS; AIRS; PGFT; GARTF; MGC47764	NM_175085	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART), transcript variant 2, mRNA.			CAGTCACAGCCATCCGGGAAAATCTCATATCAGC CCTTGAGGAAGCCAAG
16.64628	163.63095	189.49345	C6ORF106	FP852; FLJ32402; MGC4614; dJ391O22.4; RP3-391O22.4; FLJ22195	NM_024294	Homo sapiens chromosome 6 open reading frame 106 (C6orf106), transcript variant 1, mRNA.	ATTTGCCCGCATCCTCCT ACTGACCTAGTGGCATT CAACCTCCAGGATCC	ILMN_1684623	AGCCCCAAGAGATTGCAGATGTCAGCGTCCAGA TGTGCAGCCCCAGCAGA
120.10595	144.36844	146.72263	SUPV3L1	SUV3	NM_003171	Homo sapiens suppressor of var1, 3-like 1 (S. cerevisiae) (SUPV3L1), mRNA.			CCAGCCCCGATGCAGGAGAGCTGTCCCTTGCTT CCAGATTGGTGCAGCAA
409.16846	1014.6809	1091.781	SRXN1	Npn3; SRX1; C20orf139; YKL086W; dJ850E9.2	NM_080725	Homo sapiens sulfiredoxin 1 homolog (S. cerevisiae) (SRXN1), mRNA.	GGCCAAAGGAGCAGCTG TGGAAGTGAACCTAAACA CAATGACAAGTGTGG	ILMN_1721926	GGCAGGCCTTGTTCTCACTGCCCTCTAAGGGAA CTTGGTCACTCGGCACT
2406.7893	2986.6392	3030.056	C14ORF166	CGI-99; LCRP369; CLE7; CGI99; CLE	NM_016039	Homo sapiens chromosome 14 open reading frame 166 (C14orf166), mRNA.			CTGCTCAAATTCTGCGATTGCTGCACATAGAGGA GCTCAGAGAGCTACAG
123.40178	190.28928	195.89761	C13ORF1	CLLD6	NM_020456	Homo sapiens chromosome 13 open reading frame 1 (C13orf1), mRNA.	TCCCAGATTTACCTCCTG GGGGAGGGCTGGACTG CAAGGCCACTGTCATT	ILMN_1803357	GACACTCTCAGAACCCACACCAGACCCACCAAAT CAGTTTGAGAACTGCC
6977.6973	11413.522	11833.23	HNRNPAB	ABBP1; FLJ40338	NM_004499	Homo sapiens heterogeneous nuclear ribonucleoprotein A/B (HNRNPAB), transcript variant 2, mRNA.			CCAGAGCTCTAGGTGTTTAGGCAGCGTGTGGTG TCTGAGAGGCCATAGCG
97.751785	254.51428	271.75177	NME1	NDPKA; NM23-H1; NDPK-A; NM23; AWD; GAAD	NM_198175	Homo sapiens non-metastatic cells 1, protein (NM23A) expressed in (NME1), transcript variant 1, mRNA.	CTGACTCCTGCAGGCAC TGGGGAGCTCTGCTGGA ATTGGGGGTTTAAAAC	ILMN_1652865	GGGCCAAGAGATGGTGCTACTGTCTACTTTAGG GATCGTCTTTCAAGGCG
340.91428	453.3643	462.51843	LOC283951	MGC104723; gs103	NM_001010878	Homo sapiens hypothetical protein LOC283951 (LOC283951), mRNA.			GCACTGAAGGACTTGGCTGGTGGATGGGGCACT TGGCTATGCTGATTCGC
59.4769	284.19763	320.04346	MND1	GAJ	NM_032117	Homo sapiens meiotic nuclear divisions 1 homolog (S. cerevisiae) (MND1), mRNA.	AGGCTTTAGCCCTGGAC CCAGCAGGTGAGGCTCG GCTTGGATTATTCTGC	ILMN_1709623	CAAAAGCAGGATGATAACCATATCCCCCCAGTGC TCATCAAAGTAGGACA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
93.736435	257.13928	283.1726	LIG1	MGC130025; MGC117397	NM_000234	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA.	CAACCACTACTACCCATT CAGAAGAGCAGAAAGCA TCTGCTGTGTGAGCG	ILMN_1673535	CTTCCCTCGGTTTATTCGAGTCCGTGAAGACAAG CAGCCGGAGCAGGCCA
9.651041	55.656067	68.971115	AFMID	KF; DKFZp686F03259	NM_001010982	Homo sapiens arylformamidase (AFMID), mRNA.	TCCCCACTCTAAGCACTG CCTCCCCTACTCCCCGC ATCTTTGGGGAATCG	ILMN_1739605	GGCGTGAGCCACTGCGCCCGGCCAGAATGGCA TTATATTTAAATAGTTCA
7.4541283	50.58486	57.21771	NUP155	N155; KIAA0791	NM_153485	Homo sapiens nucleoporin 155kDa (NUP155), transcript variant 1, mRNA.	CCGTGGGCTTCCGGCTC TCTGTGGATGGCAGGTC ATGTGAAGACATCAAT	ILMN_1722713	AGTTGCAAGAGGACCGCATGTACCCGGACCTTT CCGAGCTGCTTATGGTG
245.96844	482.19763	511.6018	RNMTL1	FLJ10581; HC90	NM_018146	Homo sapiens RNA methyltransferase like 1 (RNMTL1), mRNA.	GATCGGCCCTGAACCCA CAAAGGACTCCTCGCTC CTTCAAGCCTCCACCA	ILMN_1729402	TCGCCAAGCACCAGCTATAGGTCACAGCCACAT CACTCACAGCTGATCAC
88.07495	289.88095	329.1476	SLC29A1	MGC3778; MGC1465; ENT1	NM_001078174	Homo sapiens solute carrier family 29 (nucleoside transporters), member 1 (SLC29A1), nuclear gene encoding mitochondrial protein, transcript variant 4, mRNA.			ACTGATCCCTGCTTGTGCAGGCCAGTGGAGGCT CTTGGGCTTGGAGAACA
52.675934	134.08928	152.05179	RPS6KA3	pp90RSK2; MAPKAPK1B; CLS; RSK2; RSK; S6K-alpha3; p90-RSK2; ISPK-1; MRX19; HU-3	NM_004586	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 3 (RPS6KA3), mRNA.	ACCCACCAGGAGACCAG GTGTCTGAAGTGGACTG TGTGAGCCTGGGCATT	ILMN_1741491	GATTCACCTGGCATTCCACCTAGTGCTAATGCAC ATCAGCTTTTTCGGGG
604.73926	1096.881	1164.2726	XAB1	MBDIN; ATPBD1A; NTPBP	NM_007266	Homo sapiens XPA binding protein 1, GTPase (XAB1), mRNA.	GCGGTGTCAGCCTTTTC TTCAGAGCATTTGTTTGA CTGACTTCCAAAGCA	ILMN_1682910	GCCTCTACTCCCCCAGCTTCTTGCTCTTGACCCT GCACTGTAAGTTGCCC
1898.981	9793.772	11573.923	EWSR1	EWS	NM_005243	Homo sapiens Ewing sarcoma breakpoint region 1 (EWSR1), transcript variant EWS, mRNA.	GCAGCCCCAACCCTACC TCATCTGTGCTGAAAGAC GCTGAAACTGCCTGG	ILMN_1762498	GGGAACCCCTTGTGAGCATGCTCAGTATCATTGT GGAGAACCAAGAGGGC
142.1726	256.6726	265.96844	TSEN2	MGC4440; MGC2776; SEN2; SEN2L	NM_025265	Homo sapiens tRNA splicing endonuclease 2 homolog (S. cerevisiae) (TSEN2), mRNA.			GCACTTTCATACGCAGGCATCTCTTGTTACCTAC ATCTAAGCTGTTCCCG
837.1476	1399.685	1470.6226	ATL3	ATL3; DKFZp564J0863	NM_015459	Homo sapiens atlastin 3 (ATL3), mRNA.	AGAACACAACAAGCCCC TACTGATTTCTGGGTTTC TGCCACGGCCACAGG	ILMN_1751086	AGAACACAACAAGCCCCTACTGATTTCTGGGTTT CTGCCACGGCCACAGG
1448.8477	3326.581	3601.4395	ACTR1A	ARP1	NM_005736	Homo sapiens ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) (ACTR1A), mRNA.			GCACAGCCTCGCACAAACCACATTGCCTGGTGG GGCCCAGTGTACTGAAA
146.90178	199.99762	206.26845	BTBD14A	BTBD14; MGC23427	NM_144653	Homo sapiens BTB (POZ) domain containing 14A (BTBD14A), mRNA.	GATCCATCACAAAGCGA AGTCATGGGAGAGCCAC ACTTGATGGTGGAATA	ILMN_1693287	GGTGGCTGCGCGAGGGACCGAGTACTAGAGCT GCTTGCATGCGTTACTAA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
9985.873	27013.773	29913.398	PCBP2	MGC110998; HNRPE2; hnRNP-E2	NM_005016	Homo sapiens poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA.			CCACCCATGATCCATCTGTGTAGTTTCTGAACAG TCAGCGATTCCAGGTT
208.6726	437.1143	469.36847	FAM111A	KIAA1895; FLJ22794; DKFZp686A06175	NM_022074	Homo sapiens family with sequence similarity 111, member A (FAM111A), transcript variant 1, mRNA.	ATAAAATTGTTTATCCTC CACAACTGCCTGGAGAA CCTCGGAGACCAGCA	ILMN_1663220	CAAGCACCCTCCCTCTAGGTCCAGGGACTATCA CAGAAGAAGCAGGCATG
94.81317	421.45593	495.66846	CDC2	DKFZp686L20222; CDK1; MGC111195; CDC28A	NM_001786	Homo sapiens cell division cycle 2, G1 to S and G2 to M (CDC2), transcript variant 1, mRNA.	ACCCTGCAGAGCTATGG TGAGGTGTGGATAAGGC TTAGGTGCCAGGCTGT	ILMN_1681591	GACAAAGGAACAATTAAACTGGCTGATTTTGGCC TTGCCAGAGCTTTTGG
132.47261	227.32678	237.89345	SLC30A1	ZNT1; ZRC1	NM_021194	Homo sapiens solute carrier family 30 (zinc transporter), member 1 (SLC30A1), mRNA.			GAAGCCCAGGAGGACTAAAGCTGAAAACATCCC TGCTGTTGTGATAGAGA
252.15596	502.88513	533.98926	POP7	0610037N12Rik; RPP20; RPP2	NM_005837	Homo sapiens processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae) (POP7), mRNA.	CACAGGGAGCCAGTGAG GTCCCAGTAGTCTAAAAC AGTTCATGTGTTCAC	ILMN_1765480	CCAATACCTCCACCGTGGAGCTTGTTGATGAGC TGGAGCCAGAGACCGAC
398.16013	719.631	769.4976	TRIP4	HsT17391	NM_016213	Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), mRNA.	CCTTCACCCATAGTAATC CTCCTGGGGCAGAAACA TAACACCCCAAAGGC	ILMN_1790645	CGTCAGGTTGTCTTCTGGGCTGTGTGGACCTAA TTGACTGCTTGTCCCAG
40.647335	285.57263	330.38095	PKIA	PRKACN1	NM_006823	Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), transcript variant 6, mRNA.			CTCCTTGCAATCATGTGGACACCAATCACAAAAG TAAAGCCCTGGTGTTG
16421.506	36480.812	39688.508	MT2A	MT2	NM_005953	Homo sapiens metallothionein 2A (MT2A), mRNA.	GCCAGCGGTGATTGCTA CTTGAGGTAGTTTTTTAC AACTACCATTTCCCC	ILMN_1797372	GAACCCGCGTGCAACCTGTCCCGACTCTAGCCG CCTCTTCAGCACGCCAT
532.12256	593.756	600.0143	ARMCX6	FLJ20811	NM_019007	Homo sapiens armadillo repeat containing, X-linked 6 (ARMCX6), transcript variant 1, mRNA.	GTGAGTGGTCTCTGTCG GGAAAGATGTAGGGATT GGTTCTCCAGGATCTT	ILMN_1800654	CCAGGCAGGGGCTCCCACAGAGCTTTGAGTAAC TTCTTGGTTGTGCAGTC
958.0976	8540.373	10471.031	KIAA0101	L5; p15(PAF); OEATC1; OEATC-1; NS5ATP9	NM_014736	Homo sapiens KIAA0101 (KIAA0101), transcript variant 1, mRNA.	GCTGCCAGGGCAACCTG AGATAACAAACGCCCTCA TCGCAAGTTAGGAGC	ILMN_1742179	AGGAGGGAACCCCGTTTGCGTGCGCCCAACTCC CAAGTGGCAAAAAGGAA
37.473682	121.33095	135.51012	SMTN	FLJ38597; FLJ35365	NM_134269	Homo sapiens smoothelin (SMTN), transcript variant 2, mRNA.			AAGACCTCAGCCTCCCAGGCGCGCAAGGCCATG ATTGAGAAGCTGGAGAA
2150.4392	8893.723	10224.697	DNAJA2	RDJ2; DNAJ; DJA2; DNJ3; HIRIP4; PRO3015; CPR3	NM_005880	Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 2 (DNAJA2), mRNA.			AAAAAATGGGCTTTGCACACAATGGGTTTGGAGC TGACTGGGAACAATGG
644.8059	802.11426	815.23096	SMYD3	bA74P14.1; ZMYND1; ZNFN3A1; FLJ21080; MGC104324	NM_022743	Homo sapiens SET and MYND domain containing 3 (SMYD3), mRNA.	ATCTGCTGTGCGGCCGT GAACTGCTCCAACCGGC AGGGAAAGGGCGAGAA	ILMN_1677530	GAAGAATGCGACGCCAACATCAGAGCATCCTAA GGGAACGCAGTCAGAGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
10242.464	17927.297	18862.014	EIF4G2	AAG1; NAT1; p97; FLJ41344; DAP5	NM_001418	Homo sapiens eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2), transcript variant 1, mRNA.			ATGGGCTTTATGTGCTAGATTTTAATATCCTTGA GCCTGGGCAAGTGCAC
143.31934	522.09766	616.73096	C9ORF140		NM_178448	Homo sapiens chromosome 9 open reading frame 140 (C9orf140), mRNA.	GTGTGTGCCCTCTGCCA GTCTTCGCTCTGTCCCC GTTCAATCAACCCCAT	ILMN_1745623	AGCGTCCCTGGGCTCTATCCGCGAGGTGCCAGT AGCGTGTGCAGGTACAT
15.717052	520.7101	726.1226	VPS53	MGC39512; hVps53L; HCCS1; pp13624; FLJ10979	NM_018289	Homo sapiens vacuolar protein sorting 53 homolog (S. cerevisiae) (VPS53), mRNA.			CTGCACATCAAGCAGAACGTCCCCATCATCCGT GACAACCTGGCTTCCAC
150.82678	593.35596	669.7976	DIAPH3	FLJ34705; DRF3; DKFZP434C0931; diap3; DKFZp686A13178	NM_030932	Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), transcript variant 2, mRNA.			GATGAGACAGGAGTGATGGATAATCTGCTGGAG GCCTTGCAGTCCGGGGC
638.0476	743.3726	755.2893	CCDC44		NM_016360	Homo sapiens coiled-coil domain containing 44 (CCDC44), mRNA.			GACTCTGATGTTGGGTAGCTGGCCTCTGTGGGG ATTGTAAGTGCCCTGAG
4291.506	14515.355	16241.322	PRDX4	PRX-4; AOE37-2	NM_006406	Homo sapiens peroxiredoxin 4 (PRDX4), mRNA.			CTGCCCTGCTGGCTGGAAACCTGGTAGTGAAAC AATAATCCCAGATCCAG
142.87262	230.03094	240.28928	MGC39900		NM_194324	Homo sapiens hypothetical protein MGC39900 (MGC39900), mRNA.	CTGTATTTAAGGGTAAGC CCCACAGCGGGCAGCAC AAACAGCCTGGGAGC	ILMN_1748366	CCTGGGTCTCAGCCCCGCGTACGGCCTTTCACG AGTCTTCAAGCCTTCAG
230.53094	320.81845	331.38095	TFIP11	FLJ22086; TIP39; bK445C9.6	NM_012143	Homo sapiens tuftelin interacting protein 11 (TFIP11), transcript variant 2, mRNA.	GCCCCAGGATTAAGATG GATGCCTTAAGCGATGG CCCAGGGGTGCTTGGT	ILMN_1746682	GGCATTGGCGTGGCCGCTAGCTCTGTGCCCATG AACTTTAAGGACCTCAT
135.32262	261.88095	278.5518	IDH3A		NM_005530	Homo sapiens isocitrate dehydrogenase 3 (NAD+) alpha (IDH3A), nuclear gene encoding mitochondrial protein, mRNA.	TTCTTCCCCTTCATTTAC AAACTGTCTGTTAACAGA TTGGCAACCAAGAC	ILMN_1677061	GAGCTTGGGCTTAGGCTTGGGCTCAGCTTTTGA CCCTCAGGCATCTCCTT
665.8976	1327.6685	1401.8226	PSMD12	MGC75406; p55	NM_002816 XM_946055 XM_946058	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA.	ATGCTGTTCTTCACAGAT TTCATGGGCCAGATTGT GTACCGCGGGGATCC	ILMN_1654165	GGATGGCACAGCTTCTGGATCTATCTGTTGATGA GTCCGAAGCCTTTCTC
426.94763	1782.8643	2022.106	MTMR3	KIAA0371; FLJ32333; FYVE-DSP1; ZFYVE10	NM_021090	Homo sapiens myotubularin related protein 3 (MTMR3), transcript variant 3, mRNA.	GACACACCTAAACATGTG GAATCCCAATGCCGGTG GGCCCCCTCATCCTG	ILMN_1795944	CCTAGTGACAGGTGCCAAGAGGTTATGATACGG GTTTCTTGGGTCTGATG
6.8824196	342.9726	468.9226	HIST1H2AB	H2A/m; H2AFM	NM_003513	Homo sapiens histone cluster 1, H2ab (HIST1H2AB), mRNA.			GGCGTGTGACCATCGCGCAGGGTGGCGTTTTGC CTAATATTCAGGCGGTG
44.41431	76.09089	81.747665	CRSP9	CRSP33; MGC12284; MED7	NM_004270	Homo sapiens cofactor required for Sp1 transcriptional activation, subunit 9, 33kDa (CRSP9), mRNA.	CAGGGTTTGAACCGGAA GCGGGAGTAGGTAGCTG CGTGGCTAACGGAGAA	ILMN_1713630	GGCAGTAATTTCGCTGTATAACAAGCATAGACAA ATGAGTGTCCCTGCAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
7.985589	362.76428	511.08093	SIGLEC12	Siglec-XII; FLJ38600; Siglec-12; S2V; SIGLECL1; SLG; Siglec-L1	NM_033329	Homo sapiens sialic acid binding Ig-like lectin 12 (SIGLEC12), transcript variant 2, mRNA.	CCCACTTGCCTGGGATG GCCCCACACTGTCACTC AGCTGTTCTTTGATCA	ILMN_1659523	ATGCTGCTGCCCCTGCTATGGGCAAATGAAGAG AGGGACAGTGGGGGCTG
84.40608	163.46844	167.50595	LIN52	C14orf46; c14_5549	NM_001024674	Homo sapiens lin-52 homolog (C. elegans) (LIN52), mRNA.			GGGGAGTCTCACCACGGCTAATTTGATGGAGAA GGTTCGAGGCCTACAGA
14.2168865	88.09766	103.430954	CENPP	RP11-19J3.3; FLJ33928; CENP-P	NM_001012267	Homo sapiens centromere protein P (CENPP), mRNA.			GTCCCACAGCGAGCCCTGGAGCTGGACAAGAAC AGAGCCATAGAAACTGC
857.83093	1573.5393	1642.7227	MSH6	HSAP; HNPCC5; GTBP	NM_000179	Homo sapiens mutS homolog 6 (E. coli) (MSH6), mRNA.	CCCTGGCACAAGAAATT CCAGTCATGTGAAGCAA ACTGCCCTTTGTCCTC	ILMN_1753554	TCGGGAAGTTTGCCTGGCTAGTGAAAGGTCAAC TGTAGATGCTGAAGCTG
235.08096	950.0476	1073.2976	TBC1D19	FLJ11082	NM_018317	Homo sapiens TBC1 domain family, member 19 (TBC1D19), mRNA.	ATGCACTTGGCAGTTAAT GGATCTGCTGTTGCTGG AGTGTGAGCGTGGAC	ILMN_1801822	GCCGTGTTTGCTTTCCGAGCAGTGAACCTGATG GAGGTGACATCACTGGC
34.590996	296.59344	363.56427	ZC3H14	UKp68; FLJ11806; MGC26892; NY-REN-37	NM_024824	Homo sapiens zinc finger CCCH-type containing 14 (ZC3H14), transcript variant 1, mRNA.	GTAGCAGAAGAGGAGGA GTGGCTACACAAACAAG CTGAGGCACGAAGAGC	ILMN_1812523	GATGGTGTCCCCAGCCCCCCAGGATACATGTCA GATCAAGAGGAGGACAT
16.468401	80.09903	98.07051	RCC1	RCC1-l; CHC1	NM_001269	Homo sapiens regulator of chromosome condensation 1 (RCC1), transcript variant 3, mRNA.			AGCGCCGGAGTTCCTTGTGGCCGACGTGCACCA AGGACAGGAAGATGTCA
674.506	994.9643	1055.381	ICMT	MST098; PCMT; PCCMT; PPMT; HSTE14; MSTP098; MGC39955	NM_012405	Homo sapiens isoprenylcysteine carboxyl methyltransferase (ICMT), mRNA.	GTAGGAGAGAGGAGAAA TGCTGGAAAGGTCGACA GTGTGGGGAGTTGGAG	ILMN_1659543	CCTCGGCCTCTCTGTCATGCTGGGAAGTGCCTA CTCTCTGGGCCACTGCT
108.66822	267.53928	338.85596	CADM1	sgIGSF; Necl-2; IGSF4; MGC149785; DKFZp686F1789; TSLC1; synCAM1; RA175; SYNCAM; IGSF4A; sTSLC-1; BL2; MGC51880; ST17; NECL2	NM_014333	Homo sapiens cell adhesion molecule 1 (CADM1), transcript variant 1, mRNA.	TTGCCATGGGGACTGCC ATCTGCTGTGTGGATAC CCATCGGAGGGGCCCA	ILMN_1675375	CTGCAGCTCTATTCCGAGCCCTTAGCACCCATTC CGACCATAGTATAATC
235.38928	404.05597	441.24762	EBP	CDPX2; CPXD; CHO2; CPX	NM_006579	Homo sapiens emopamil binding protein (sterol isomerase) (EBP), mRNA.			TGCATGGAAACCATCACAGCTTGCCTGTGGGGA CCACTCAGCCTGTGGGT
619.6476	761.84766	787.4101	C1ORF77	pp7704; MGC86949; RP1-178F15.2; MGC131924; DKFZP547E1010	NM_015607	Homo sapiens chromosome 1 open reading frame 77 (C1orf77), mRNA.	ACATCAACGAGCTGACTA TGAAGCTGAGCGTGGAG GACGTGCTGACCCGC	ILMN_1756542	ATGGCGCAGACAGATCCCGAAACCAATGATTGA AGCCTGCCCATCCTCCC
565.5393	951.5893	1029.2059	SLBP	HBP	NM_006527	Homo sapiens stem-loop binding protein (SLBP), mRNA.			GCACTAGTTAGACTCTTTAGAATACTCCAAGAGT TAGGGCAGCAGAGTGG
619.2476	923.3393	984.58093	FXR1		NM_005087	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), transcript variant 1, mRNA.			GACATCAGCGTGACAGCAGGAGACGCCCAGGA GGAAGAGGCAGAAGTGTT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
350.78928	511.0476	541.6184	MFSD5	MGC11308	NM_032889	Homo sapiens major facilitator superfamily domain containing 5 (MFSD5), mRNA.			TGAGGAGCCCTATGCCCCTGAGCTGTAACCCCA CTCCAGGACAAGATAGC
42.5214	118.030945	148.51428	C16ORF59	FLJ13909	NM_025108	Homo sapiens chromosome 16 open reading frame 59 (C16orf59), mRNA.	GAGTGTTGCTGCTGAAG CACATCCTTGCAATGTG GGAGTGCACAGGAGTC	ILMN_1713380	AGGTGGCCTCACTGGCTCTTCTCAGGACAACTA AGCCTGCTGGTCAGGGC
81.918564	138.20595	146.72263	OGFRL1	dJ331H24.1; FLJ21079; MGC102783	NM_024576	Homo sapiens opioid growth factor receptor-like 1 (OGFRL1), mRNA.			GGGCTGTTAACTGGCAGGAAAGATTTCAGCATC TGAATGAGTCCCAGCAC
1456.5809	2403.906	2593.8894	CDC25B		NM_004358	Homo sapiens cell division cycle 25 homolog B (S. pombe) (CDC25B), transcript variant 2, mRNA.	GGGCTTTTCCAAAAGCAA ACAAAGATAGGTTCCTCA GGTGACCAAAACTG	ILMN_1672947	GCGCAGTGCCTTGCATACCCAAACCAGGTGGGA GCGTTTTGTTGAGCATG
50.199356	54.988075	59.103683	RAD51	HsT16930; BRCC5; HRAD51; RECA; HsRad51; RAD51A	NM_133487	Homo sapiens RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae) (RAD51), transcript variant 2, mRNA.	AAAAATGTAAGCAAAATT ACAGTATGTAAAACACAC ATTGCTAATGGAGA	ILMN_1651456	GTGCCAAACCTACTAGGCCATTAGCCCTTCACCA TCTACCTGCTTGGTCT
209.07262	261.62677	271.32263	LOC93622		XR_017952	PREDICTED: Homo sapiens hypothetical protein BC006130 (LOC93622), misc RNA.	TGATGGCTTCATGATCCA GCACAGTGCCTCACACA AAGAACTATTGGGTG	ILMN_1774800	CAAGCTGGCCATGGGGGTCCCAAACAGTCATTC CAGGCTTAGATGATGAC
387.69763	1604.6726	1975.231	AMD1	ADOMETDC; AMD; DKFZp313L1234; FLJ26964	NM_001634	Homo sapiens adenosylmethionine decarboxylase 1 (AMD1), transcript variant 1, mRNA.			ACCACCCTCTTGCTGAAAGCACTGGTTCCCCTGT TGAAGCTTGCTAGGGA
155.23096	318.8601	354.5518	ZBTB9	MGC23166	NM_152735	Homo sapiens zinc finger and BTB domain containing 9 (ZBTB9), mRNA.	TTGCGTAATTCTTGCCGC TCCCCCCAGCCCATCGT TCCCTGGTTCTGTGA	ILMN_1657148	CCTTGGTCAGAGGGACTCAGGTTTGGGACAGCA CAAGCTGAAGGCTGGAG
401.06427	497.35596	514.64764	AGK	MULK; FLJ10842	NM_018238	Homo sapiens acylglycerol kinase (AGK), mRNA.			CTGCCCTTCCCAGGTGATTCTGTAAGTTGTCCCT CAACTGTACTTGGAGA
206.03094	819.78094	1007.14764	MAPK1	p40; PRKM2; MAPK2; PRKM1; p38; p41; ERK; ERT1; P42MAPK; p41mapk; ERK2	NM_138957	Homo sapiens mitogen-activated protein kinase 1 (MAPK1), transcript variant 2, mRNA.			GTAGAACAGGCTCTGGCCCACCCATATCTGGAG CAGTATTACGACCCGAG
1280.3309	3190.3892	3651.7144	UBL5	HUB1; MGC131795; FLJ46917	NM_001048241	Homo sapiens ubiquitin-like 5 (UBL5), transcript variant 2, mRNA.			CCACGTGTCTCTGGGGGACTATGAAATCCACGA TGGGATGAACCTGGAGC
144.59763	253.23094	274.1476	PNO1	KHRBP1	NM_020143	Homo sapiens partner of NOB1 homolog (S. cerevisiae) (PNO1), mRNA.	GCAGATGGGGGCAGAGA TGTGAAACAGCTGCAGA GCGGGACAAGGGTGCT	ILMN_1665356	GCTTAGCCTACCTTAAAAGGGCTCCGAACACTAC ATTAGCCTACAGTTGG
307.9143	429.6101	450.3393	DEF8	MGC104349; FLJ20186	NM_017702	Homo sapiens differentially expressed in FDCP 8 homolog (mouse) (DEF8), transcript variant 2, mRNA.	AGATACGAACACAACAGA AATTTCAGCAACTAGTGG ACTAGTTCCTGGAG	ILMN_1675092	CCAGGAGCTGAAGGACCCCAATGAGGATGAGCC AAACATCCGAGTGCTCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
54.97604	217.83095	278.32678	PKMYT1	MYT1; DKFZp547K1610; FLJ20093	NM_182687	Homo sapiens protein kinase, membrane associated tyrosine/threonine 1 (PKMYT1), transcript variant 2, mRNA.			GTTTGCTCCTGGACAGCAGCCTCTCCAGCAACT GGGATGACGACAGCCTA
75.85225	442.2893	546.8684	PKIA	PRKACN1	NM_181839	Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), transcript variant 7, mRNA.	GCTATGGCGGAGGATGG GTTGCTTTTCAAATGTCT AGCTCAAATCAATTC	ILMN_1711451	ACTGTGTTTGATGGCCTCTGCTGTGTTTTAACAT CGTGCTTCTTATATGG
2137.956	3198.7227	3379.4143	PTGES3	TEBP; P23	NM_006601	Homo sapiens prostaglandin E synthase 3 (cytosolic) (PTGES3), mRNA.			GATGACTTGTCAGTGTTCCAGGTGTATCTTAGCT AAAACTAGAGAATGCC
11368.031	26813.564	30259.54	S100A6	2A9; PRA; CABP; 5B10; CACY	NM_014624	Homo sapiens S100 calcium binding protein A6 (S100A6), mRNA.			GGAGTATGTCACCTTCCTGGGGGCCTTGGCTTT GATCTACAATGAAGCCC
915.24756	2998.3809	3608.6558	IDH3G	H-IDHG	NM_174869	Homo sapiens isocitrate dehydrogenase 3 (NAD+) gamma (IDH3G), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.	ACTACACCTTATTTGGTC GCAGCTACTGAGGGATG AACGAAAGCCCCCTC	ILMN_1783695	GATGCTGGACCACCTCAAGCTGCACTCCTATGC CACCTCCATCCGTAAGG
66.99746	124.501785	138.60596	ATG4A	APG4A; AUTL2	NM_178270	Homo sapiens ATG4 autophagy related 4 homolog A (S. cerevisiae) (ATG4A), transcript variant 2, mRNA.			GCAGGCCATGCGGCCTCTGTCACATCTACTCAA CTCTGCTGTTGACATGC
123.69762	149.90594	154.57262	ENOSF1	RTS beta; TYMSAS; RTS alpha; HSRTSBETA; RTS	NM_017512	Homo sapiens enolase superfamily member 1 (ENOSF1), mRNA.	GCCCAGGCTTTTCCTGC TCTGGCTCACTGCTGCT CACAGATATGCAAAAC	ILMN_1731223	CCTACCGATCAAGATGAGTTCAGCTAGAAGTCAT ACCACCCTCAGGAATC
15.035133	49.04393	65.24001	C1ORF165	FLJ11588	NM_024603	Homo sapiens chromosome 1 open reading frame 165 (C1orf165), mRNA.			CCGAGCCGGAGTTACGGAGCACTTTCAGTGAGG AAGCAAATACGTCGTCC
13507.34	17170.13	17881.822	ANXA1	LPC1; ANX1	NM_000700	Homo sapiens annexin A1 (ANXA1), mRNA.			CCTGGTGGCTCTTTGTGGAGGAAACTAAACATTC CCTTGATGGTCTCAAG
52.75612	97.87054	103.03929	PPP2R3B	PR48; NY-REN-8; PPP2R3LY; PPP2R3L	NM_013239	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B", beta (PPP2R3B), transcript variant 1, mRNA.	ACCCACTTATTGCCTAAT TAGTCATAGTTTGACAAT TGCCCTTGTATTCC	ILMN_1661188	CTACGTCATCTACTGCAAGTTCTGGGAGCTGGA CACGGACCACGACCTGC
692.0559	790.32263	810.0393	ZNF598	FLJ00086; DKFZp762F135	NM_178167	Homo sapiens zinc finger protein 598 (ZNF598), mRNA.			GAGCTGAAAGCTGCGGCGCCACTGGTGCCAGA GTCAGATGTCACAGATGT
94.71979	226.95596	264.33093	TMEM194	KIAA0286; DKFZp686N1768	NM_015257	Homo sapiens transmembrane protein 194 (TMEM194), mRNA.			GCCAACACCAACTCGTAGCTTTAGTGGCAGATG GGAGTGGTCACAGACTC
96.67679	157.73096	172.63928	RPL41		NM_001035267	Homo sapiens ribosomal protein L41 (RPL41), transcript variant 2, mRNA.			ACCCGGCGCTCCATTAAATAGCCGTAGACGGAA CTTCGCCTTTCTCTCGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
508.1976	645.07263	677.7976	ATP2C1	SPCA1; PMR1; HHD; hSPCA1; ATP2C1A; KIAA1347; BCPM	NM_001001486	Homo sapiens ATPase, Ca++ transporting, type 2C, member 1 (ATP2C1), transcript variant 4, mRNA.	ACATCTCCCTGACAACAC AAAACTAGAGCCAGGGG CCTCCGTGAACTCCC	ILMN_1667018	AGGCTGCAGACATTGGAGTTGCGATGGGCCAGA CTGGTACAGATGTTTGC
160.67679	349.89343	398.81845	MAX	MGC11225; MGC10775; MGC34679; MGC36767; orf1; MGC18164	NM_002382	Homo sapiens MYC associated factor X (MAX), transcript variant 1, mRNA.	GGAGGCCCTTCCCAAGG TGTGGTGACTGTGCCTT ACTGTACATGCTCGGA	ILMN_1719661	CGAAAACGTAGGGACCACATCAAAGACAGCTTTC ACAGTTTGCGGGACTC
750.3893	1242.4434	1339.0017	CKLF	UCK-1; CKLF1; CKLF4; CKLF2; CKLF3; C32; HSPC224	NM_001040139	Homo sapiens chemokine-like factor (CKLF), transcript variant 6, mRNA.			CAGCCGAAAATAAAACATCGCCCCTTCTGCTTCA GTGTGAAAGGCCACGT
37.936943	95.99776	109.368454	NHLRC2	FLJ20147; FLJ33312; MGC45492; FLJ25621; DKFZp779F115	NM_198514	Homo sapiens NHL repeat containing 2 (NHLRC2), mRNA.	CTCCCTAGGAGGCTTTT GCCCTCAGCTTGAATACA GTTCCTGGTGCATCA	ILMN_1728742	GCTAGCAACCCATTGCCACCACCTACTGTCTCCC ATCCTGACTATCACTG
386.91428	550.4143	574.20593	FARS2	dJ520B18.2; FARS1; HSPC320; PheRS	NM_006567	Homo sapiens phenylalanyl-tRNA synthetase 2, mitochondrial (FARS2), nuclear gene encoding mitochondrial protein, mRNA.			ACATCCAAAGACGCACAAGACCAGCCACTGCTA CCGCATCACGTACCGCC
579.65594	2180.8225	2545.3892	FAM53C	C5orf6	NM_016605	Homo sapiens family with sequence similarity 53, member C (FAM53C), mRNA.			GCCCTTCACTCCCACCTGCTGCCAAAGTCCCTG TGCTAATGGGATTACAA
1712.0476	3678.0728	4010.7476	PSMD14	rpn11; PAD1; POH1	NM_005805	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 14 (PSMD14), mRNA.	GGGAAGACGACGGAACT TGCCACAGCGACAGACT TCTCCCAAACAGGAAA	ILMN_1674580	GACACCTGAACAGCTGGCAATAAAGAATGTTGG CAAGCAGGACCCCAAAC
85.660355	154.18095	163.14761	MOCS1	MOCS1B; MIG11; MOCS1A; KIAA0381; MOCOD	NM_001075098	Homo sapiens molybdenum cofactor synthesis 1 (MOCS1), transcript variant 4, mRNA.	CCTGCGCCGGCAACCAC CTAGTGGCCCAGGGAAG GCCGATAATTTAAACA	ILMN_1666392	CTCTCTGTATAGCCCCGCTATGGGAAAATAAAGT GGAGTAGGGGGCATAG
130.38095	1541.7976	2045.5476	MTHFD1	MTHFC; MTHFD	NM_005956	Homo sapiens methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (MTHFD1), mRNA.			CTTAGTAGGAACGATGAGCACAATGCCTGGACT CCCCACCCGGCCCTGTT
16.31407	94.81847	118.01428	PCDHGB6	PCDH-GAMMA-B6	NM_018926	Homo sapiens protocadherin gamma subfamily B, 6 (PCDHGB6), transcript variant 1, mRNA.			GACTGGCGTTTCTCTCAGGCCCAGAGACCCGGC ACCAGCGGCTCCCAAAA
136.06429	181.5476	188.88095	C14ORF169	FLJ21802	NM_024644	Homo sapiens chromosome 14 open reading frame 169 (C14orf169), mRNA.	CTCGTGCACATGTGAAG TGCCCTCTGAGTTTAAG GTTTGGTTAATACTGG	ILMN_1719343	TGGATCTTTCATCTGAGTTCTTTTTCATGGGCGG GTCGGGGTCAGTATCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
38.03733	275.7143	344.60596	HNRNPA3P1	HNRPA3; D10S102; FBRNP	NR_002726	Homo sapiens heterogeneous nuclear ribonucleoprotein A3 pseudogene 1 (HNRNPA3P1) on chromosome 10. XR_000879 XR_001292 XR_001293 XR_001294 XR_001295 XR_001296 XR_001297	AGAAGGAGGGTTTCTGG CTGTGGTTCTAAATGGA GCCCCAGGAAGCTGCC	ILMN_1770035	CACAGAGGGGTCGTGGAGGTGGATCTGGCAATT GTATGGGTCACAGAGGA
117.91428	165.06429	172.33511	MAD2L1BP	RP1-261G23.6; CMT2; MGC11282; KIAA0110	NM_014628	Homo sapiens MAD2L1 binding protein (MAD2L1BP), transcript variant 2, mRNA.	GAGACTTGATAAATCGG CCTGAGAAAATAAGTAAT GCTCCAGACTAGCTC	ILMN_1797554	TCGTGATGGCGGCGCCGGAGGCGGAGGTTCTG TCCTCAGCCGCAGTCCCT
56.971184	217.01846	249.64761	RANBP9	RANBPM	NM_005493	Homo sapiens RAN binding protein 9 (RANBP9), mRNA.	TGGAAGGAGGGTTCTAC AGGAACTGGCAGAGCTG AGACTGGGACGCAACC	ILMN_1737663	GAGGGGAAGGAAATGGAACAAGTTGTGTTTGTG TTAGCATGTGGGTGATG
434.23096	560.83093	584.41846	CHCHD3	FLJ20420	NM_017812	Homo sapiens coiled-coil-helix-coiled-coil-helix domain containing 3 (CHCHD3), mRNA.			TGGAGTGGGGCGAGGAGAGAGCCAGAAAACATA GATCCGAGGGCAGCAGT
143.36429	398.68927	446.32678	ARMC8	MGC10058; MGC4880; HSPC056; S863-2	NM_015396	Homo sapiens armadillo repeat containing 8 (ARMC8), transcript variant 2, mRNA.	TACCCGCCACAGGCACT CGGCCCTGATGCCCTCG TGTCCACTTGTGTCCA	ILMN_1770203	CTCCGCCAGGCTGCATTCAAGCTCTATGCCTCT CTTGGAGCAAATGATGA
87.76892	199.01012	217.24762	P2RX7	MGC20089; P2X7	NM_002562	Homo sapiens purinergic receptor P2X, ligand-gated ion channel, 7 (P2RX7), mRNA.			CCCCAAGACCTAAGGGTTTTATCTCCTCCCCTTG AATATGGGTGGCTCTG
646.53094	1030.0393	1089.2434	MRPL39	RPML5; PRED66; MGC3400; L39mt; C21orf92; FLJ20451; MGC104174; PRED22; MSTP003; MRP-L5	NM_017446	Homo sapiens mitochondrial ribosomal protein L39 (MRPL39), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	CGTCAGCAGGTTCGCTA TCAGAAGTCAGCATCAG CAGCTAGAACAGGCCC	ILMN_1680320	GGCATATTGGCGTTCCTGTGCTATGATGATGGG CTGTGTGATAGAGAGGG
1131.8893	4095.1475	4844.8057	APRT	MGC125857; AMP; MGC125856; DKFZp686D13177; MGC129961	NM_000485	Homo sapiens adenine phosphoribosyltransferase (APRT), transcript variant 1, mRNA.	AGGTGTGTGGGAACCCC AAAAGCAGGGAGGTGCA GAGAGCCATGAAGCTC	ILMN_1782596	TGAGGTCCTGGAGTGCGTGAGCCTGGTGGAGCT GACCTCGCTTAAGGGCA
79.03133	123.44762	133.2976	PRPF38B	MGC163218; RP11-293A10.1; MGC41809; FLJ10330	NM_018061	Homo sapiens PRP38 pre-mRNA processing factor 38 (yeast) domain containing B (PRPF38B), mRNA.			GAAACGTCAGTAGAGTCACACTTTGTGTACAGG GATGTCTTAGTGCCCAG
6136.8477	10230.447	10951.897	EEF1B2	EEF1B; EF1B; EEF1B1	NM_001959	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2), transcript variant 1, mRNA.			GTGTCCAGCCCACCGCCTGCCGACTTGTGTCAT GCCCTACGTTGGTATAA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
921.23926	1067.1976	1089.9976	NDUFB6	MGC13675; B17; CI	NM_002493	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa (NDUFB6), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	CAACAGCGATTCAGGAC CCAAGTGTGAACAACACT CAGCCCGCCCTCTGG	ILMN_1719064	CTCGGGAGCCGGTGCTGCCCCCACAGAAGATG GGGCCTATGGAGAAATTC
243.00595	266.75595	272.25595	ZNF746	FLJ31413	NM_152557	Homo sapiens zinc finger protein 746 (ZNF746), mRNA.			TTGTTGAAGCAGCCACTGGTCCTCTTGTTTCCCC TGCAGACGGAGGGACC
658.3476	886.08093	919.32263	TPM3	TM30; MGC3261; TRK; NEM1; TM30nm; FLJ41118; OK/SW-cl.5; TM-5; TPMsk3; hscp30; MGC14582; TM3; MGC72094	NM_152263	Homo sapiens tropomyosin 3 (TPM3), transcript variant 1, mRNA.	GCTGCATTTAGATCACC GTGTGCTCAGGCCAGGT GTGAATCCTGAGGTCC	ILMN_1799951	CGTGCTCAGGAGCGCCTGGCCACTGCCCTGCAA AAGCTGGAAGAAGCTGA
105.180954	437.8393	515.3185	PSMD10	p28; dJ889N15.2	NM_002814	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 10 (PSMD10), transcript variant 1, mRNA.	TGCTTGGACTGTCTTTGA ACTCTGCACCTCCTTCCA GGCCATCTTGTGAG	ILMN_1722089	GTACTACAAAGCATCCACAAACATCCAAGACACT GAGGGTAACACTCCTC
644.11426	1080.7393	1147.7393	SAAL1	FLJ41463	NM_138421	Homo sapiens serum amyloid A-like 1 (SAAL1), mRNA.	GCTTCTCTCAGTCTCTGT CTTTGAATATCTGAATGT TCTGGCCCTTCAAC	ILMN_1673503	CAAAGGAGACGGTGGCTCAGGGAGTAAAGGAAG GCCAGTTGAGCAAACAG
3173.081	3362.206	3387.6895	PSMB4	HsN3; PROS26; HN3	NM_002796	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 4 (PSMB4), mRNA.			TGGAGAAGCAGCCAGTGCTAAGCCAGACCGAGG CCCGCGACTTAGTAGAA
436.66428	1643.3225	1892.3477	FBXO33	c14_5247; Fbx33	NM_203301	Homo sapiens F-box protein 33 (FBXO33), mRNA.			CCTTTTGACAGGTGTGCACTGTTTTGTCTCCAGT GAGCACATACCATGCG
883.9143	984.881	997.0976	SLC39A3	ZIP3	NM_144564	Homo sapiens solute carrier family 39 (zinc transporter), member 3 (SLC39A3), transcript variant 1, mRNA.			AGGCTGTGCCCCCGATCCTACACCCTGAGCCTC AGAGCACTGCTACTTTT
249.62262	366.20596	382.32263	GRB2	MST084; ASH; EGFRBP-GRB2; MSTP084; Grb3-3	NM_002086	Homo sapiens growth factor receptor-bound protein 2 (GRB2), transcript variant 1, mRNA.			AGCAAACAGCGGCACGATGGGGCCTTTCTTATC CGAGAGAGTGAGAGCGC
279.06427	356.41428	365.0893	C6ORF130	MGC19570; dJ34B21.3	NM_145063	Homo sapiens chromosome 6 open reading frame 130 (C6orf130), mRNA.	CCCAGGGCAGGTTTGCT TGACCTCTGCCTCAGTTC TCGACTCTAAAGGAC	ILMN_1807873	CCTTTTTCTCCAGTATGCTACCTGATTTGTTTGG CTGGCCACTAGGTGGC
3156.031	4608.7812	4809.0894	HDAC2	YAF1; RPD3	NM_001527	Homo sapiens histone deacetylase 2 (HDAC2), mRNA.	GATGCCTTCTGGATCTTA AGCCAGTTGTCAGTGGA GGTCCTCAGGGCTGC	ILMN_1739496	AGGAACCAAATCAGAACAGCTCAGCAACCCCTG AATTTGACAGTCTCACC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
71.69888	201.23929	224.89346	PARP2	ADPRTL3; PARP-2; ADPRTL2; ADPRT2; pADPRT-2	NM_001042618	Homo sapiens poly (ADP-ribose) polymerase family, member 2 (PARP2), transcript variant 2, mRNA.	GGAGCCTCTCTCCCTAC TGCTGCTACACAAGACC CTGAGACTGACCTGCA	ILMN_1651958	CAAGGTAAACATAGCACCAAGGGGCTGGGCAAG ATGGCTCCCAGTTCTGC
489.0476	1291.1809	1439.8601	MEA1	MEA; HYS	NM_014623	Homo sapiens male-enhanced antigen 1 (MEA1), mRNA.			AGTGGGAAGATGTGGTACAGAAAGCCCTCCAAG CCCGGCAGGCATCCCCT
117.22262	175.89761	186.7143	RTN2	NSP2; NSPL1	NM_005619	Homo sapiens reticulon 2 (RTN2), transcript variant 1, mRNA.			CCAATTTTGGAATTGTCCCCACCTCTGTGGACAG CCATTGGCTGGGTCCA
317.3393	553.5143	585.53516	ENSA	MGC4319; MGC78563; MGC8394	NM_207168	Homo sapiens endosulfine alpha (ENSA), transcript variant 8, mRNA.	AAGCACCGGAATGCCAA TTAACTAGAGACCCTCCA GCCCCCAAGGGGAGG	ILMN_1670272	GCCTAGGACAAAAGCCTGGAGGCTCCGACTTCC TCATGAAGAGACTCCAG
787.98926	1567.1393	1681.4226	PPP2R2A	MGC52248; FLJ26613; PR55A; B55A; PR52A	NM_002717	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha isoform (PPP2R2A), mRNA.			TACAGCTCATTCTTACTGTGGCTTGTAGCATTCC TCCTCTTCTGGCCTCC
446.63513	1094.56	1235.2769	LYAR	ZLYAR; FLJ20425	NM_017816	Homo sapiens Ly1 antibody reactive homolog (mouse) (LYAR), mRNA.	GGGCCCCTTGATCTGTA AAGGTGTCTTCCACGCT ATAGTCTCTGGAGGTC	ILMN_1710734	ACACAGTGACAGATGAGCATCACAGATCCGAAG AGGAACTCCTGGTCATC
289.23096	362.4643	373.37262	FBXO28	FLJ10766; KIAA0483; Fbx28	NM_015176	Homo sapiens F-box protein 28 (FBXO28), mRNA.	GTCATCTCCGTAGCCCT CCCAGTTGTGCCTCCTG CACATTGATGAGTGCC	ILMN_1805930	CCGTCCACCGTGACATGGTTATGCATCCTTTAGA TTAACCTCACCAAATG
120.564285	307.08096	347.26428	RFC2	A1; RFC40; MGC3665	NM_181471	Homo sapiens replication factor C (activator 1) 2, 40kDa (RFC2), transcript variant 1, mRNA.	TAAGCCAGGACAAGAAG TGCAAATGCCTCTTTGAA GCAATTCAGGCTAGG	ILMN_1807357	AAGTCACTCTTCCCAAAGGCCGACATAAGATCAT CATTCTGGATGAAGCA
1222.7144	2909.481	3226.6309	RSPRY1	KIAA1972	NM_133368	Homo sapiens ring finger and SPRY domain containing 1 (RSPRY1), mRNA.	CACCGGGTTCACTGTCC TTGTGGGGCTGGAGAGA TGGGCATAAGTCAGGA	ILMN_1772233	GACCTGTGCATGGATTGTGCCTTGCAGCTGGAG ACCTGCCCATTGTGTCG
1014.61426	1637.406	1739.1726	MRPS17	RPMS17; HSPC011; MRP-S17	NM_015969	Homo sapiens mitochondrial ribosomal protein S17 (MRPS17), nuclear gene encoding mitochondrial protein, mRNA.	CTCAACATGTGCTTCCCA CCTGACCGCAGTCACCA TTTTCTATGGGACAC	ILMN_1720756	CCTGGAGAGTCCGTTGAGTTCGGAAACCACCCA GCTAAGCAAAAATCTGG
1078.2227	1788.7686	1935.1477	FBL	RNU3IP1; FLRN; FIB	NM_001436	Homo sapiens fibrillarin (FBL), mRNA.			CGTGGTCGTGGGAGTGTACAGGCCACCCCCCAA GGTGAAGAACTGAAGTT
8.1390505	65.53415	67.01494	PIGA	GPI3; PIG-A	NM_002641	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria) (PIGA), transcript variant 1, mRNA.	CTCTAGGTAAGACACTTG GTAGATGAGAGACGGAA GGCATTGTCAAGAAC	ILMN_1713752	TGGCCCATGATGCTCTCTTCCACGCCAAGACAAT GGGGCTTCAGACAGTC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
403.44345	962.0393	1094.1726	ITPA	HLC14-06-P; dJ794I6.3; ITPase; C20orf37	NM_033453	Homo sapiens inosine triphosphatase (nucleoside triphosphate pyrophosphatase) (ITPA), transcript variant 1, mRNA.			AGAGGCTGCCAGGACTTTGGCTGGGACCCCTGC TTTCAGCCTGATGGATA
87.15669	163.84763	179.78928	NUDT6	ASFGF2; gfg-1; FGF-AS; bFGF; FGF2AS; FGF-2; gfg	NM_007083	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 6 (NUDT6), transcript variant 1, mRNA.			GACTCTGTGGCTGAGAGAAGGGCCCAGCAGATT ACCAGGATATGCTTCAC
135.09344	184.4018	193.46011	HEATR3	FLJ20718	NM_182922	Homo sapiens HEAT repeat containing 3 (HEATR3), mRNA.	GCATTTCCGCATCCATG CAAACGAGTCACATATG GTGGGACTGGAGCCAT	ILMN_1665572	CCACCAAAGATCCTTCCCTTGTGGTAGCAGGAG AAGCTTTGGATGCCCTC
216.25595	458.63928	507.38095	ASPH	BAH; junctin; CASQ2BP1; JCTN; HAAH	NM_004318	Homo sapiens aspartate beta-hydroxylase (ASPH), transcript variant 1, mRNA.			TAGGAATCTATGATGCTGATGGTGATGGAGATTT TGATGTGGATGATGCC
42.49556	108.70178	124.77261	OSGEPL1		NM_022353	Homo sapiens O-sialoglycoprotein endopeptidase-like 1 (OSGEPL1), mRNA.	TGTACTGTGCTAGTGACT GGAGGCCCTGCTACTGC AAATATAAAACCTAA	ILMN_1666904	CGTGCTGGCTTGGGCATTTTACATGACATAGAAG GCATCCGCTATGAACC
395.05597	588.7018	618.97266	MTIF2		NM_001005369	Homo sapiens mitochondrial translational initiation factor 2 (MTIF2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	AACCAGGGAGGGCGTGG AAGCTCTGCATCCCTTCT CCCATACCTTGCTCT	ILMN_1653120	GCTGTGGAAGAGCACCCAGTAGGTGAGGCATCT ATACTAGCTACCTTCTC
456.31427	632.256	661.20593	E2F4	E2F-4	NM_001950	Homo sapiens E2F transcription factor 4, p107/p130-binding (E2F4), mRNA.	TCTGTACATTCTGTAAAA ACTTCAAAACCTGGCCA GGCATGGTGGCTCAC	ILMN_1666082	AGCCCTGATGATTGGCCCCACCTCCTGCTGCCC CATAACCCTCTCTTCAT
295.45178	936.66846	1115.5977	MCM5	MGC5315; CDC46; P1-CDC46	NM_006739	Homo sapiens minichromosome maintenance complex component 5 (MCM5), mRNA.	GGGCAACTGGTGTGTTT ATATGCCTGACATTATTT GGGTTTTCCCCCCTC	ILMN_1667120	GGACTTCACCAAGCAGAAATACCCGGAGCACGC CATCCACAAGGTGCTGC
134.50179	1430.731	1968.81	PPM1A	PP2CA; PP2C-ALPHA; MGC9201	NM_177952	Homo sapiens protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), transcript variant 3, mRNA.			CGTGGTCATTCTTTGCTGTGTATGATGGGCATGC TGGTTCTCAGGTTGCC
56.989162	125.49762	140.01428	C14ORF130	FLJ10483; MGC9518	NM_001100417	Homo sapiens chromosome 14 open reading frame 130 (C14orf130), transcript variant 3, mRNA.	TCCTGTGCTTGGGACCT GTTTTACTGCTGAGGCTT CATTCAGTCCTGCCC	ILMN_1787288	AGGGAAGATTGCCCAGGCCACTGACAGGAGCGA TCCCCTAATGGATACCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
7.3495235	59.093536	81.198135	ANXA8	bA301J7.3; ANX8	NM_001040084	Homo sapiens annexin A8 (ANXA8), mRNA. XM_931361 XM_931369 XM_931374 XM_931375 XM_931378 XM_931383 XM_931388 XM_931391 XM_931399 XM_931404 XM_931411	GGCCATCCCAAAGCTATT CTGGGGGCAACAGAGGT GAAACTACTGGGCCA	ILMN_1744914	GGCCCTTATGTACCCGCCATACAGATACGAAGC CAAGGAGCTGCATGACG
128.06429	163.01845	169.71428	ZNF330	NOA36; HSA6591	NM_014487	Homo sapiens zinc finger protein 330 (ZNF330), mRNA.	GGAGCTGCTTCAGTCCA TCTCCCAGAGGCATTTG GTCTGTATCTTTGCTC	ILMN_1770936	CTTCTCTTTCTTCACAATGTATGTCCTCAGTGGT ACCTATTATTGATGCC
1930.4727	3445.7227	3751.2227	CSE1L	CAS; MGC117283; XPO2; MGC130036; MGC130037; CSE1	NM_001316	Homo sapiens CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA.	CCTGGTGATAGGCCTCG TCCTCCTGGGTAGAATC CTCTCGGAATCACTCC	ILMN_1652490	GGTTCCATCAATGGTGAGCACCAGCCTGAATGC AGAAGCGCTCCAGTATC
87.94475	123.86012	131.42262	DDX31	helicain B; helicain C; FLJ13633; FLJ14578; helicain A; FLJ23349	NM_022779	Homo sapiens DEAD (Asp-Glu Ala-Asp) box polypeptide 31 (DDX31), transcript variant 1, mRNA.	AGAGTTCTGACCAGCAC CAGATAAGCTTCAGTGCT CTCCTTTCTTTGGCC	ILMN_1673191	TGCGCGTCAGCCTGGAACGGGCTTGATTGCTGC CCTTAACTGTGTTCTGA
591.5685	2112.3477	2567.5728	AP3S1	CLAPS3; Sigma3A	NM_001002924	Homo sapiens adaptor-related protein complex 3, sigma 1 subunit (AP3S1), transcript variant 2, mRNA.	GGCAACACACCAAACTG TCCATCCAGCTCCTCAAC TAACGATTTTCAGGC	ILMN_1795275	AATCTGAGGCTGGCTTAGCAGGAGCTCCAGCCC GTGCTGTATCAGCTGTA
136.56409	514.88513	649.1268	CDCA7	MGC34109; JPO1; FLJ14736; FLJ14722	NM_031942	Homo sapiens cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA.	CTGTGGGGAGAGAATGA CGCATTCATGGAGGTTG AGATGGCTGAAGTCAC	ILMN_1719498	CTCTGCCAGTCTAGTTTCTGGGCAGGTTTCCTGT GTCAGTATTCCCCCTC
1594.6309	6830.9727	8530.181	SLC25A4	PEO2; ANT1; PEO3; T1; ANT	NM_001151	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 (SLC25A4), nuclear gene encoding mitochondrial protein, mRNA.			GTGCCTGGTCCAATGTGCTGAGAGGCATGGGCG GTGCTTTTGTATTGGTG
139.78928	157.06429	162.48096	RBM12	KIAA0765; HRIHFB2091; SWAN	NM_006047	Homo sapiens RNA binding motif protein 12 (RBM12), transcript variant 1, mRNA.	AGGCAGGACGGCAGGG GTGAGCAGCTTTGGGAG AGACACCTGGCCTTTTT	ILMN_1654032	ATGGCCACAACATTGCCAGCAAATACTGCCTTGG CATCACTCAGCAGAGG
1637.4559	1763.0476	2040.4309	SRM	SRML1; SPDSY; PAPT; SPS1	NM_003132	Homo sapiens spermidine synthase (SRM), mRNA.			GACCTCCTGCTGGCTCTCGCCCACCAACCAAGT GTTACAAGCCCCAGAAT
119.23096	172.18512	312.50595	RPL36A	RPL44; MGC72020; MIG6; L44L	NM_021029	Homo sapiens ribosomal protein L36a (RPL36A), mRNA.	GCGCATCTACAAGCACC CGTTCTACAATCTCTACA CGCTCGACTACGACG	ILMN_1770387	GAGGAAGTGCGATCGGGAACCTCCTATATACTT CCGTTTGCCTCGCGGTT
23.30068	33.729633	66.06581	LOC168474		NR_002789	Homo sapiens selenophosphate synthetase pseudogene (LOC168474) on chromosome 7.			AACCCCTGGATTGTCCTGGGAAGAGTCACTACC ACTGTCTGTCAGCCCAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
539.5143	559.0226	580.5476	UBE4A	UFD2; KIAA0126; UBOX2; MGC133315; E4	NM_004788	Homo sapiens ubiquitination factor E4A (UFD2 homolog, yeast) (UBE4A), mRNA.			GGTGCAAGTGAAGGTGCCAGTTGCTATTTGATAT CACACTCTACAAAAGC
1082.2893	1199.2976	1450.5642	OBFC2A	MGC111163; FLJ13624; FLJ22833; DKFZp667M1322	NM_001031716	Homo sapiens oligonucleotide/oligosaccharide-binding fold containing 2A (OBFC2A), mRNA.			CAGCCTGGAGTGAAAATCCTGGGTACTGACTTT GAGAGGAGTGAGTGTGC
37.738613	44.43756	59.434685	FXN	FA; X25; FRDA; FARR; MGC57199; CyaY	NM_181425	Homo sapiens frataxin (FXN), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.	GTGTAGACTCTCAAGAG GACTAAAGGTCATATGAA GAATGATGAGAGAAC	ILMN_1759922	AGCACTTCTGAGCTCTTTAGCATTGAAGTGTCGA AAGCAACTCACACGGG
309.2393	389.12262	539.8893	NAP1L5	DRLM	NM_153757	Homo sapiens nucleosome assembly protein 1-like 5 (NAP1L5), mRNA.	GGAAATTCAGCTTCTCCT GAGGGAAAGGCCAGCCG GTTTGAGAAGACCTC	ILMN_1666781	ACTTGAAGAACCAATCCAAGTGTGTGCCCCTACC CCCAGCTCAGAAGTAG
158.39345	177.58095	215.2976	PPARD	PPARB; NUCI; FAAR; PPAR-beta; NUC1; NUCII; MGC3931; NR1C2	NM_006238	Homo sapiens peroxisome proliferative activated receptor, delta (PPARD), transcript variant 1, mRNA.	CAGCTCCGTGTGTGAGA TGTGCAGGTTTTTTCTAG GGGGTAGGGGGAGAC	ILMN_1777783	ACCTACCCAGCTGATGGGGGTTGGGGTGCTTCC TTTCAGGCCAAGGCTAT
181.68097	216.00595	352.95593	TNFAIP3	A20; MGC138687; OTUD7C; TNFA1P2; MGC104522; MGC138688	NM_006290	Homo sapiens tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA.			CCCCAGAGATAAAGGCTGCCATTTTGGGGGTCT GTACTTATGGCCTGAAA
295.44763	346.61847	449.34344	UBL7	TCBA1; MGC14421; BMSC-UbP	NM_201265	Homo sapiens ubiquitin-like 7 (bone marrow stromal cell-derived) (UBL7), transcript variant 2, mRNA.	GAACCAGGAGACACGTG TGGCGGGCAGTGGGAC CCATAGATCTTCTGAAA	ILMN_1775182	AGCTCATCTTTGCTGGAGGAGCCCCATGAACTC CCTGCTTCCCCTGAACC
512.73926	555.1893	636.3101	SPAG9	FLJ34602; MGC14967; MGC117291; FLJ26141; JLP; HLC4; FLJ13450; PHET; MGC74461; HSS; PIG6; FLJ14006; KIAA0516	NM_003971	Homo sapiens sperm associated antigen 9 (SPAG9), mRNA.	CTGAGGATAGCCAGACC CCCCAAACAAGGCTTGA ATAACTCTCCACCCGT	ILMN_1762631	GCCACAGTCTAATGTCATTCACTTCATTTGATGG GGTCACTTGTTAGCTG
3410.9312	3833.1729	4694.7144	GLTP		NM_016433	Homo sapiens glycolipid transfer protein (GLTP), mRNA.	GTTCTTGAAGTAGTGAAG ATTCAGGGACTTTATTCT CCCAAGTGTCATGA	ILMN_1677633	CGCCTCACTGCCTTAACCTTAACTGTTCTTCCTG GCGCTAAAAAGAGCTG
1912.0476	2120.856	2539.106	BZW2	MST017; MSTP017; HSPC028	NM_014038	Homo sapiens basic leucine zipper and W2 domains 2 (BZW2), mRNA.	AGTGAGGCTGAGATGAC AGAGGTGGTCATGGCTG GCACAGGGCTCAGGTA	ILMN_1700994	AAATGGAGCCCTGAGGCATCAGCTATTATACTTG GGACTCTACCTCTCAC
242.26013	273.24762	335.43512	SGTA	hSGT; SGT	NM_003021	Homo sapiens small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha (SGTA), mRNA.	ATTCCCACTCCCTTGGTT TTCGCCTGCCCAGCGTT GCTGTTTGCGTGGAG	ILMN_1747460	CACCTTGGCCCTAAAACAGCCACCAGGAAAGCA GCCGGAGAGCCGGACAG
685.0559	760.67676	921.69763	AK2	ADK2	NM_001625	Homo sapiens adenylate kinase 2 (AK2), transcript variant AK2A, mRNA.	CGTGGGCTCCAAGTGCC TGTGGACATACGAGATC CAGTTCTCTCAGGACG	ILMN_1703041	CCATCCCTGTGAGGCAATGGGTGGGAATGATAG GACAGGCAAAGAGAAGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
113.29345	127.32262	155.91013	ANKRD34A	ANKRD34; DKFZp761F202	NM_001039888	Homo sapiens ankyrin repeat domain 34A (ANKRD34A), mRNA.			GTCTCATTTTCCCAGGGGGTGGGTCATGGGCTC TAAGCTGCTCTTCTGTC
1267.4727	1353.5684	1523.3225	MGC10997		NR_001565	Homo sapiens pseudogene MGC10997 (MGC10997) on chromosome 15.	ACCCCTGCTCTGTGGGA GAGTGGGGGCTAAGGAA CAGAAGGATTACCTGC	ILMN_1724709	CTTCTGCCATGATTGTGAGGCCTCCCCAGCCAT GTGGAACTGTGAATCCA
120.66012	137.53094	167.19762	MUTYH	MGC4416; MYH	NM_001048172	Homo sapiens mutY homolog (E. coli) (MUTYH), transcript variant gamma2, mRNA.			TGGGTTCCAAAAGGTCCCAGGTGTCCTCTCCGT GCAGTCGGAAAAAGCCC
515.28094	899.60596	2851.6558	IL8	GCP-1; MDNCF; NAP1; CXCL8; AMCF-I; TSG-1; LYNAP; NAP-1; MONAP; GCP1; SCYB8; LUCT; K60; LECT; 3-10C; b-ENAP; NAF	NM_000584	Homo sapiens interleukin 8 (IL8), mRNA.	TGACCAGGGGACAGCTC CAGCACCTTGGCACAAG AGGGAGCAACACTTCC	ILMN_1652872	CCCAGTCTTGTCATTGCCAGCTGTGTTGGTAGT GCTGTGTTGAATTACGG
713.8684	798.4768	959.0143	TSPYL1	TSPYL	NM_003309	Homo sapiens TSPY-like 1 (TSPYL1), mRNA.	ACTCCCAAGGAGACTTAA GAATGGCAGATGGAGTG GCCAATGTTGAGCAC	ILMN_1769734	GAGGCATGGGCCAGGTAAAAATTGGGCCTAGAG TGAAGACTGTGCTGTCG
49.850822	62.93331	86.781525	NOL6	MGC20838; NRAP; MGC14921; bA311H10.1; MGC14896; UTP22; FLJ21959	NM_022917	Homo sapiens nucleolar protein family 6 (RNA-associated) (NOL6), transcript variant alpha, mRNA.	AAGGCCACTGCAAACCT TGGACAGACTGCTGCTG GAGGTGCCGCCGTCGA	ILMN_1743100	CCCTTGGACATTTACGACGTGCTGATTCGCCTGT CTCCTCGCCATATCCC
554.37256	593.90594	648.1309	HTR2A	5-HT2A; HTR2	NM_000621	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 2A (HTR2A), mRNA.	GGAGGAAGGCTGCTGG GCTGAAGAAGAGGAGCA GGTCTGGCTATAAGAAG	ILMN_1795739	GAGCCAAGTTCACACCACTGCCATTTCCTCCTGG GCAACAGAGTGAGACC
635.55597	848.4768	1302.7935	THOC4	ALY; BEF	NM_005782	Homo sapiens THO complex 4 (THOC4), mRNA.	GTACAAGGCTTCAAAGTA CCTGTGTGTGTCCCTCAT GGAGCCACCTGCAG	ILMN_1726415	TGGACATGTCTCTGGACGACATCATTAAACTGAA CCGGAGCCAGCGAGGC
100.03512	112.06012	132.00179	ST7	DKFZp762O2113; RAY1; TSG7; ETS7q; FAM4A1; SEN4; HELG	NM_018412	Homo sapiens suppression of tumorigenicity 7 (ST7), transcript variant a, mRNA.	TCTGTGAATCTTGGCTG GGACTTCCTCTGAGTGA TGCCTGAGGGTCAGCT	ILMN_1709750	GTCTGTGGCACCAGCTAACACGGATCTGAGAGA AGCCCTGTCCTCCACTC
315.4643	342.0851	392.76428	MRPL45	MGC11321	NM_032351	Homo sapiens mitochondrial ribosomal protein L45 (MRPL45), nuclear gene encoding mitochondrial protein, mRNA.	GCCTTATGCCCTTAGGT GCTGAGTTTCATTAAGTA CTGTCACGTTTTCTC	ILMN_1655446	CAGACCATGACCGACTTCATACCTTGGTAACTGA ACACTGTTTTCCAGAC
736.94763	845.7143	1043.8977	GPR177	FLJ23091; C1orf139; WLS; EVI; MGC131760; MRP; MGC14878	NM_024911	Homo sapiens G protein-coupled receptor 177 (GPR177), transcript variant 1, mRNA.			CCTTTGCGGTCCCAGTCCAAGGTAGGCTGGTGT CATAGTCTTCTCACTCC
171.43927	226.30594	353.00177	SLC37A4	G6PT3; GSD1b; TRG19; PRO0685; G6PT2; GSD1d; GSD1c; MGC15729; G6PT1	NM_001467	Homo sapiens solute carrier family 37 (glucose-6-phosphate transporter), member 4 (SLC37A4), mRNA.	GCATTAGCCTGCATGTTT CTAGGTCTTCTGCCAAGT GCTTTTCTCAGTTG	ILMN_1805645	GACTGCTGTTGCCAATACCTCAGACTCCAGGGA AAGAGAGGAGGCCATCA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
92.87685	125.69762	198.26845	MGC4172	FLJ39232; ARPG836	NM_024308	Homo sapiens short-chain dehydrogenase/reductase (MGC4172), mRNA.			TCCCCTCCTGGGGTCATCCCTCCACTCTGACTCT GACTATGGCAGCAGAA
1412.8643	1522.0977	1708.2102	SF3B14	Ht006; SF3B14a; SAP14; CGI-110; HSPC175; P14	NM_016047	Homo sapiens splicing factor 3B, 14 kDa subunit (SF3B14), mRNA.	CTGAGAACCAAGGACGC CTGGCTTACAGTGCGCA GCCAGAAGGAGATGTG	ILMN_1798914	GGGGAACACACCTGAAACTAGAGGAACAGCTTA TGTGGTCTATGAGGACA
35.784462	55.86602	96.18932	PSTK	PSTK; C10orf89; MGC35392	NM_153336	Homo sapiens phosphoseryl-tRNA kinase (PSTK), mRNA.	TGTCGTTGGTGGAGAGC GGACAGGCGCCAAAGGC CTCTTCCCGGACTTTG	ILMN_1740494	GGCTGGTTGCAGTGTTGCAGAATCGAGAAGAGG CCATTGAGCACGGGGTG
400.63928	567.1226	944.1476	IER5L	MGC70833; bA247A12.2	NM_203434	Homo sapiens immediate early response 5-like (IER5L), mRNA.			AACTTGATCTCCATCTTTGGCTCCGGCTTCTCGG GGCTGGTGAGCCGACA
1066.9727	1182.5559	1354.3726	RSL1D1	MGC142259; CSIG; L12; PBK1; DKFZP564M182; MGC138433	NM_015659	Homo sapiens ribosomal L1 domain containing 1 (RSL1D1), mRNA.			CCTCAATGCTGCCTCCAGAGCTTTTTGGAAATAC TCAGATCCTGGCCGCC
1670.6643	1720.5476	1779.4893	HSPA4	hsp70; HS24/P52; RY; MGC131852; APG-2; hsp70RY	NM_198431	Homo sapiens heat shock 70kDa protein 4 (HSPA4), transcript variant 2, mRNA.	ACAGTACCTGTACCTGCA CGGTCACCCGCTCCGTG TGTCGCCCTATATTG	ILMN_1724480	CACAGCTGTGCCTTCGGATTCAGACAAGAAGCTT CCTGAAATGGACATTG
544.35596	755.35596	1207.8477	ITPR3	FLJ36205; IP3R; IP3R3	NM_002224	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3), mRNA.			AGGGCTGAGCTGCGCTTGCGTGGCTGTTTCATG ACCGCTTGTTTTTCTCC
1507.3977	1648.2976	1852.281	TIMM23	PRO1197; TIMM23B; MGC22767; TIM23	NM_006327	Homo sapiens translocase of inner mitochondrial membrane 23 homolog (yeast) (TIMM23), nuclear gene encoding mitochondrial protein, mRNA.	AGGTTTTATGGGAGGCT GTGCATTGCTCAAAAGCT GTTGGGAACGCCTTC	ILMN_1713759	CTGTGATGAAAATCCTGGATGGCTGACCAAGACT GGCACTTGTTCCAGCC
166.03928	282.70593	562.1268	CDKN2C	INK4C; p18; p18-INK4C	NM_078626	Homo sapiens cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (CDKN2C), transcript variant 2, mRNA.			CCAGTCCTTCTGTCAGTCTCCGATGCCATCATGC AGCCTGGTTAGGAGCA
363.8393	411.36847	483.0518	MNAT1	MAT1; RNF66	NM_002431	Homo sapiens menage a trois homolog 1, cyclin H assembly factor (Xenopus laevis) (MNAT1), mRNA.	GCTGGGAAATCACCATG TGGAAACCAAGCAAACG TGTTGTGCATCAGCCG	ILMN_1685854	GCCCAGTTAACCATTTATAAGATTTGGACCTTGG AGCTGAACCAGGGAGC
132.18512	149.06429	173.93929	C15ORF40	MGC29937	NM_144597	Homo sapiens chromosome 15 open reading frame 40 (C15orf40), mRNA.			CTGTTGGGGGGCCTTTGATTTCCTATATCCAGAA GTTGAGAGACTTACTC
43.350636	75.71889	146.85596	HSD17B8	FABGL; FABG; dJ1033B10.9; RING2; H2-KE6; KE6; D6S2245E; HKE6	NM_014234	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 8 (HSD17B8), mRNA.	GATGCTCACGTACCTGT GCTGCATCCTCATGCTTC TCACCCCCATCATGG	ILMN_1744834	CCGATGGGACACTTGGGGGACCCTGAGGATGT GGCAGATGTGGTCGCATT
1123.8976	1198.4476	1307.4976	SAMM50	OMP85; TOB55; YNL026W; CGI-51; SAM50; TRG-3	NM_015380	Homo sapiens sorting and assembly machinery component 50 homolog (S. cerevisiae) (SAMM50), mRNA.	CAGATGTGACCCTACTT GAGGCCGCCTTGGCTTT TGGGTCACCCTGTCTC	ILMN_1806500	GTGATGGCGTCCAGTTTGGAGCTGGGATAAGGT TCCTGTAGCCGACACCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
576.6226	666.9976	829.19763	U2AF1	RN; DKFZp313J1712; U2AFBP; U2AF35; RNU2AF1; FP793	NM_001025203	Homo sapiens U2 small nuclear RNA auxiliary factor 1 (U2AF1), transcript variant b, mRNA.			GCGGGAGCTGTATGGCCGCCGTCGCAAGAAGC ATAGATCAAGATCCCGAT
1018.7976	1243.1476	1658.7393	LTB4DH	MGC34943	NM_012212	Homo sapiens leukotriene B4 12-hydroxydehydrogenase (LTB4DH), mRNA.			CGTCTACCGCTGGCAAGGAGATGCCCGCCAAAA AGCTCTGAAGGACTTGC
1776.9226	1916.381	2123.281	CAB39	FLJ22682; CGI-66; MO25	NM_016289	Homo sapiens calcium binding protein 39 (CAB39), mRNA.	GTTTGGGATCTTCTCTCC CACCCACACTTATCTCCC CCAGGGCCACTCCA	ILMN_1699852	GCAGTGAGGTCGTAGCCTTTTAGGTGGAAGAAG TGAGGGTGCAGCGTGTC
865.2643	983.77264	1169.5476	NSL1	MIS14; C1orf48; DKFZP566O1646; DC8	NM_001042549	Homo sapiens NSL1, MIND kinetochore complex component, homolog (S. cerevisiae) (NSL1), transcript variant 2, mRNA.	CAGGGCCTCCTGGAAAA TCATCATCCCTCATCACC CACAGTCGCCCGATT	ILMN_1723709	CTGTCCTTAAGTGCCATCAACTCTCAGCTCCCTT GTAGCTTTTGTGGGAT
15.0491295	33.810135	99.881546	RIMS2	RAB3IP3; DKFZp781A0653; RIM2; KIAA0751; OBOE	NM_014677	Homo sapiens regulating synaptic membrane exocytosis 2 (RIMS2), transcript variant 2, mRNA.	CCTCAAGCTCCGGGGAA AGGACATTGGAAAGCCC ATCGAGAAGGGGCCTA	ILMN_1696544	AGAAGTGGTCAGGAACAATCATCAGCCCTCCTCT GGGCGGGAATCAGAGC
166.59344	181.94762	196.7351	PUS1	MLASA; MGC11268	NM_001002019	Homo sapiens pseudouridylate synthase 1 (PUS1), transcript variant 2, mRNA.			AAGTACAACCAGCGCTTTGGCAACGATGGGCTG CATGAGCCGCTGGACTG
590.95593	734.381	945.51013	DDX47	FLJ30012; E4-DBP; DKFZp564O176; MSTP162; HQ0256	NM_016355	Homo sapiens DEAD (Asp-Glu Ala-Asp) box polypeptide 47 (DDX47), transcript variant 1, mRNA.	CCCCCAGAAGCCTTAGT GACCCAGATCTCAACCA GAGACTCAAGATAGCC	ILMN_1789999	ACAGCTTTGCTACTGCGAAATCTTGGCTTCACTG CCATCCCCCTCCATGG
71.775536	72.94891	80.102356	CCDC4	MGC157807; FLJ35632; MGC157808; FLJ43965	NM_207406	Homo sapiens coiled-coil domain containing 4 (CCDC4), mRNA.			AAGGAAAAGGTCAGTGCAGTCAGGAGAGACAGG TCCCGAAAGACGCCCTC
567.91016	586.58093	598.1809	NUDT3	DIPP1; DIPP	NM_006703	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 3 (NUDT3), mRNA.	CTAGGAAGACTACGATTC CCATCCAGCCCCACGAG TCTCGGGCAAGTAGT	ILMN_1672538	TCTGAAGAGAGGCCAACAGCCTTCCCCTGCCTT GGATTCTGAAGTGTTCC
41.978256	50.885155	66.31154	C5	CPAMD4; FLJ17816; MGC142298; FLJ17822	NM_001735	Homo sapiens complement component 5 (C5), mRNA.	TACCCCGCAGCAATACG CACTCTTGGGACCTCGC TGATCTAGGATGGGGA	ILMN_1692148	GGAACACCTCCTCAAACCTACCACTCAGGAATGT TTGCTGGGGCCGAAAG
593.9518	697.4309	850.83093	CBX3	HP1-GAMMA; HP1Hs-gamma; HECH	NM_016587	Homo sapiens chromobox homolog 3 (HP1 gamma homolog, Drosophila) (CBX3), transcript variant 2, mRNA.	GTGAATTCTTCTAGAGGC TTGTGTACACTACTGGTT GTTTTAGTTGGGCC	ILMN_1703572	TCCCCCTTCGGATGTGGCTTGAGCTGTAGGCGC GGAGGGCCGGAGACGCT
370.48096	420.93927	491.74347	POLR3B	RPC2; FLJ10388	NM_018082	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide B (POLR3B), mRNA.			GGTCAGCCTGGCTTTTGTCGTGGTGGCTGGCTC GGATAAATTTTCCCAAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
216.02261	302.3393	457.9726	MET	AUTS9; RCCP2; HGFR	NM_000245	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA.	CTTTTCCTTTCTTCAGCC TAACCCGCGGTGGCCCT CGCGGAGTCCGGTCA	ILMN_1765451	GTCTCTACCAGGGTCAAGAGCATGAACGCATCA ATAGAAAGAACTCGGGG
102.82678	122.81845	144.03513	CPT1A	CPT1; CPT1-L; L-CPT1	NM_001031847	Homo sapiens carnitine palmitoyltransferase 1A (liver) (CPT1A), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.	GGAGCACAGTGGATGGC CTTGTGTCCCTCGGGCA TGACAGGCAGAAACGA	ILMN_1691487	GGTTGCTGATGACGGCTATGGTGTGTCGTACAT CCTTGTGGGAGAGAACC
616.9976	714.1226	827.0643	FHOD1	FHOS	NM_013241	Homo sapiens formin homology 2 domain containing 1 (FHOD1), mRNA.			GCCTGGAGGTGTGAAGGTGCTGTATCCCGGAAA TCTATCTGGACCCTGGA
35.22553	51.316242	64.13252	TAC3	PRO1155; NKB; ZNEUROK1; NKNB	NM_001006667	Homo sapiens tachykinin 3 (neuromedin K, neurokinin beta) (TAC3), transcript variant 1, mRNA.	CTATGAGGGGAGGAGGA ATGGGAGAGGGGGCTCA GGGGCCAATAAACTCT	ILMN_1655039	TCCTCGGCCCCTTCATCCCAATCAGCTTGGATCC ACAGGAAAGTCTTCCC
1645.5559	2152.306	2787.6643	ATP5G1	ATP5G; ATP5A	NM_001002027	Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9) (ATP5G1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA.			CTCCATGGGGGGTCACCGGCCTGTTGCTACTGC AACTCCACACCATTCTT
173.56429	196.72263	222.9851	PET112L	PET112; HSPC199	NM_004564	Homo sapiens PET112-like (yeast) (PET112L), mRNA.	TTCCTGGAGCAGAACAAT TTTTCCCCGAATACAAGA ACGCAGAAAGCACG	ILMN_1707328	TTCATCCACATCAGGAGGGTCCGGTGAGGCTGC AGCAGTGGTTAAGGAGT
18901.94	23054.006	27857.047	JUND		NM_005354	Homo sapiens jun D proto-oncogene (JUND), mRNA.	GATCACATTGCACGCCT CCCCCCTCACTTGTCCT CCTGATCCTGACACAT	ILMN_1697519	GCTACGAGTCCACATTCCTGTTTGTAATCCTTGG TTCGCCCGGTTTTCTG
175.39761	206.3601	241.89761	UCRC	HSPC151; HSPC051; HSPC119	NM_013387	Homo sapiens ubiquinol-cytochrome c reductase complex (7.2 kD) (UCRC), transcript variant 1, mRNA.			CCTAGGGTATAGTTCAGGGGTATCCAATCCTTTG GCTTCCCTGGGCCATG
17568.94	19765.197	22155.14	RPL24		NM_000986	Homo sapiens ribosomal protein L24 (RPL24), mRNA.			GTCTTTCCGTGGAGCTGTCGCCATGAAGGTCGA GCTGTGCAGTTTTAGCG
982.19763	1481.3893	2209.1392	BUB3	BUB3L; hBUB3	NM_001007793	Homo sapiens BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), transcript variant 2, mRNA.			CGCCAAGTGACAGATGCAGAAACAAAACCCAAG TCCACCTAATCATCCTG
81.63524	105.86429	139.09761	DDX28	MDDX28; FLJ11282	NM_018380	Homo sapiens DEAD (Asp-Glu Ala-Asp) box polypeptide 28 (DDX28), nuclear gene encoding mitochondrial protein, mRNA.			CCTTGAGGGCGGGATGAACTGCTTTGTGACTTG GAAAGGTACGCTGCTGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
99.24762	128.94762	165.18094	THG1L	FLJ20546; ICF45; FLJ11601	NM_017872	Homo sapiens tRNA-histidine guanylyltransferase 1-like (S. cerevisiae) (THG1L), mRNA.	TGCAGAGTGCCATCTGG AGGATGCTCACAGGGAG GCGGTCACTGGCTTGA	ILMN_1798534	GGTGGCTGTAGCATCCCTACCACCCAGGACACT GGTGCGAATGACACAAC
147.74762	154.56429	157.93094	RBBP5	RBQ3; SWD1	NM_005057	Homo sapiens retinoblastoma binding protein 5 (RBBP5), mRNA.			TGCAGACATTATATCCATTCCAGTCCTCTGCACT GTACACTGCAGCAGTG
165.69345	232.59761	308.19345	MCRS1	ICP22BP; P78; MSP58; MCRS2	NM_006337	Homo sapiens microspherule protein 1 (MCRS1), transcript variant 1, mRNA.			TCACCTGGTCAGAATCCTTGGATGAGCCTGTGG GACCGTTCCTCCTAGCC
1126.6226	1602.0642	2307.706	EFHD2	MGC4342; RP3-467K16.3	NM_024329	Homo sapiens EF-hand domain family, member D2 (EFHD2), mRNA.	AAGAGTCCTCCTCAGAG ACCAGGATGGTGGTGAC ATTCCTCGTGTCTGCC	ILMN_1680501	CAGCGCAGCAGCCTCGGACCCGGATTGCGTTTG CCTTAGCGGATATGTTT
153.83511	187.93094	225.72263	FLJ20628	DKFZp564I2178	NM_017910	Homo sapiens hypothetical protein FLJ20628 (FLJ20628), mRNA.	CGAGGAAGAAGATGTGG AGATGAGTGAGGACGCC TACACGGTGCTGACCC	ILMN_1708808	AGTACACTGGCAACCTGGTCATACAGCTTTTCTT GTCAAGTTGAGGAAGG
262.94345	338.5268	419.80597	NUP62	p62; SNDI; FLJ43869; IBSN; DKFZp547L134; FLJ20822; MGC841	NM_153719	Homo sapiens nucleoporin 62kDa (NUP62), transcript variant 1, mRNA.	GAGAATTTCAACCAGAAA GAACAGCCAGTGCAAAG GCCCAGAGACAGGAA	ILMN_1703667	GCTAACCACCAAGGCAAAGCAGCACAGTGTGAA TAGAACAGAGCGGGATC
99.607666	184.90594	350.13095	APOBEC3B	FLJ21201; APOBEC1L; ARCD3; DJ742C19.2; PHRBNL; ARP4; bK150C2.2	NM_004900	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B (APOBEC3B), mRNA.			ACCCTTTGGTCCTTCGACGGCGCCAGACCTACT TGTGCTATGAGGTGGAG
25.261665	49.28775	114.94768	EZH2	EZH1; ENX-1; MGC9169; KMT6	NM_004456	Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), transcript variant 1, mRNA.	CGCTGGGCCTTCTTTTC CCTCCTGCAACAGAGGC TGCTATGTCCCACAGA	ILMN_1722282	TGCAGTTGCTTCAGTACCCATAATGTATTCTTGG TCTCCCCTACAGCAGA
174.03513	219.95595	269.91846	ABCC4	MOATB; EST170205; MRP4; MOAT-B	NM_005845	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4), mRNA.			CACACAGCTAACTGCCAAAATACATTGACCGTAG TAGCTGTTCAACTCCT
344.83093	360.13095	384.87677	SAFB	DKFZp779C1727; SAFB1; HET; HAP	NM_002967	Homo sapiens scaffold attachment factor B (SAFB), mRNA.			GCAGGCCCAGCGATGCCCGCTTCACTCGCCGCT ACTGAGTACTTGGAATC
10223.314	12736.689	16504.613	RPS26	MGC104292	NM_001029	Homo sapiens ribosomal protein S26 (RPS26), mRNA.			AATGGTCGTGCCAAAAAGGGCCGCGGCCACGTG CAGCCTATTCGCTGCAC
1289.2059	1422.0559	1585.9476	CLNS1A	CLNS1B; CLCI; ICln	NM_001293	Homo sapiens chloride channel, nucleotide-sensitive, 1A (CLNS1A), mRNA.	GCCCTGAGCAGCATTTC CACGGGTGTTTCTTCAG AGGACAGTGAGTTCCC	ILMN_1713867	CTGTGTCTGGGTACCCTCTGAGTAGGCCTATAAT TCCTACCTTGACTGTG
1494.2059	1535.7142	1572.4976	CAPN1	CANPL1; CANP; muCL; muCANP	NM_005186	Homo sapiens calpain 1, (mu/I) large subunit (CAPN1), mRNA.			AAAGGGGACTCTTCAGGGACTTGTGTACTGGTT ATGGGGGTGCCAGAGGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
345.99762	482.79346	689.64343	SPA17	SP17; SP17-1	NM_017425	Homo sapiens sperm autoantigenic protein 17 (SPA17), mRNA.	CCAGGTCAGAAACCATT GTTCAGAAGACCTCCCT GTGAGAGAGTTGCTCC	ILMN_1787552	CTGTCAAAATCCAAGCTGCCTTCCGGGGACACA TAGCCAGAGAGGAGGCA
578.58923	624.83093	673.98096	ATPBD1B	FLJ10349	NM_018066	Homo sapiens ATP binding domain 1 family, member B (ATPBD1B), mRNA.			GGCCCTGCCACCAGAAAGTCGAGCACTGGTCCT AGTCAGGCTGTGATGAA
279.3476	316.51428	360.69763	C12ORF32	MGC13204; HKMT1188	NM_031465	Homo sapiens chromosome 12 open reading frame 32 (C12orf32), mRNA.			CTCTGTGACTCTATGGTTGACTGCCACCTCTGCA ACCTTGACTCATCTGC
390.39764	389.5518	396.41428	SLC9A6	KIAA0267; NHE6	NM_001042537	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), member 6 (SLC9A6), transcript variant 1, mRNA.	CACCCCGCCACTGCTCA AACTCTCTTGCTCTGATA CCCACTTCAATGGCA	ILMN_1780952	GGGGAACCAAGCCTGCTGTGCTTACATCAGCAT CTGGAAGACTTTCCTCT
77.86545	113.50595	170.58928	MMACHC	RP11-291L19.3; FLJ25671; DKFZp564I122	NM_015506	Homo sapiens methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria (MMACHC), mRNA.			CCTGTGGCGTCAGTCGCAGTGCTCTGGCCAACA CTATAGCAGGGCTTATT
102.218445	112.48929	124.09761	MAX	MGC11225; MGC10775; MGC34679; MGC36767; orf1; MGC18164	NM_145114	Homo sapiens MYC associated factor X (MAX), transcript variant 4, mRNA.	CATCTTGAAAGTGAGTG GTGTCCTTTGGAGGCAT GGTGGATGAAAGGCGC	ILMN_1794349	TGGGTCTGTGCTGACTCTGGCCTTACAACCTTCC AGCCTCCTTTGCTGGC
139.76428	188.3601	270.5476	MAP2K3	MEK3; MKK3; MAPKK3; PRKMK3	NM_002756	Homo sapiens mitogen-activated protein kinase kinase 3 (MAP2K3), transcript variant A, mRNA.			CCCCCGGAACCTGGACTCCCGGACCTTCATCAC CATTGGAGACAGAAACT
11.887703	27.598335	71.617485	LOC641522		NM_001039083	Homo sapiens ADP-ribosylation factor-like protein (LOC641522), mRNA.	CCTTAGGCAGGCACCTC CAACCACCACACACTCC CTGCTGTTTTCCCTGC	ILMN_1734827	TCTGGGATTATAGGCGTGAGCCACCGTGTCCGG CCTGCGTTATTACTTTT
324.6101	388.01428	468.51428	TADA3L	FLJ21329; hADA3; ADA3; FLJ20221	NM_133480	Homo sapiens transcriptional adaptor 3 (NGG1 homolog, yeast)-like (TADA3L), transcript variant 2, mRNA.	ATGGTGGTCTAGCAGCC AGGTATCAATCAGCTCTG TTACCACACAAAGGG	ILMN_1679542	GCATACTAAGTCCCTGGAGAGCCGCATCAAGGA GGAGCTAATTGCCCAGG
72.31564	97.305954	134.5476	PINX1	LPTS; MGC8850; FLJ20565; LPTL	NM_017884	Homo sapiens PIN2-interacting protein 1 (PINX1), mRNA.	GTTCTGCGCGGCGGGG GCCGTACCCGCGGCGGA GCGAGGAGGCGAGAATG	ILMN_1707099	TTCCAAATGAATCCTTCCCAGCCGGGGCCTTCC GACCACTCAGCTGTCAG
42.44354	80.54361	167.60596	RGMB	FLJ90406; MGC86970; DRAGON	NM_173670	Homo sapiens RGM domain family, member B (RGMB), transcript variant 2, mRNA.			AGGTGACTGCCAACAGCCAGCCCAATGTCGAAT CCAGAAATGCACCACGG
410.36426	460.26428	527.79346	FAM133B	MGC40405	NM_152789	Homo sapiens family with sequence similarity 133, member B (FAM133B), transcript variant 1, mRNA.	CTGTTGGATGTTCATGTG TTTGAACTTTTGCGCACC GGATAGACCCCTTG	ILMN_1679747	ATCATCTGAGTCCTTGTCAGAATCAGAGTATATT GAGGAGGTGCGAGCAA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
55.85033	61.69506	71.64295	NLGN1	KIAA1070; MGC45115	NM_014932	Homo sapiens neuroligin 1 (NLGN1), mRNA.	GAGCCCCTGGAACTCAT GGTCTCAGCCTCACACG CCAAGGATTACACAGT	ILMN_1651404	GATGGAACCAACTTTGTACATCTTGGCCATGTCA CTGGTCATTGTGTGAA
105.33929	121.46011	137.11845	SF3A1	SF3A120; SAP114; PRPF21; PRP21	NM_001005409	Homo sapiens splicing factor 3a, subunit 1, 120kDa (SF3A1), transcript variant 2, mRNA.	TGCCAGCCTCCCAAAGG TCTAAGAGGAGAAAAACT GCTTCCAGTGGTTCC	ILMN_1709484	AGTGCTCCTGTTGCAGGACTGCTGGGAAAACAG GTGGTGTGGGACTTAAG
579.14764	863.95593	1217.4976	ZFP36L2	ERF2; ERF-2; TIS11D; RNF162C; BRF2	NM_006887	Homo sapiens zinc finger protein 36, C3H type-like 2 (ZFP36L2), mRNA.			GGACTTCAGGAAAAATCAACCCAGCACCAGCAG CTACCAACCACCATTCC
6.0669327	27.049189	94.91589	RPRM	FLJ90327; REPRIMO	NM_019845	Homo sapiens reprimo, TP53 dependent G2 arrest mediator candidate (RPRM), mRNA.			GCTCGTGACTGCACGGTTTACGCCACAAAAGTG CTCTTGACATCCGTGAC
1139.656	1167.156	1196.8059	GRSF1	FLJ13125	NM_001098477	Homo sapiens G-rich RNA sequence binding factor 1 (GRSF1), transcript variant 2, mRNA.	CCCTCAAAGTGTCACAAT GCTCCTCCTGATGACTC CTCCCCAGAAAACCA	ILMN_1723035	GTATGCTTTCTTTGCCTTGTTCCTGTTCTCAGGG TGACGACTGCCACCAG
1287.581	1500.6934	1722.231	MRPS22	MRP-S22; RPMS22; GIBT; GK002; COXPD5; C3orf5	NM_020191	Homo sapiens mitochondrial ribosomal protein S22 (MRPS22), nuclear gene encoding mitochondrial protein, mRNA.			AGATGGCCAGTCGGCTCAAGGGGCCAAGGATCA GGCTGCTGAGGGAATAA
62.246246	71.12819	81.06526	CHMP7	MGC29816	NM_152272	Homo sapiens CHMP family, member 7 (CHMP7), mRNA.			CTGAGCCAGGATGTGCAATAGAAGCAGGGGTTG TCCCCTCTGCCAGATCT
50.648537	97.8643	186.53928	C18ORF56		NM_001012716	Homo sapiens chromosome 18 open reading frame 56 (C18orf56), mRNA.			CGTCACAGCTTTCCTGGGTTGTTGAGCCTCTAAG ATGGTCTTTTCCTCTG
62.22528	84.099304	112.88609	GBP3	DKFZp686L15228; DKFZp686E0974; FLJ10961	NM_018284	Homo sapiens guanylate binding protein 3 (GBP3), mRNA.	CGTCCTGCGTCTTTTTG GGGAATCCTCGACAGGT GCTGGAAAATTGTGTT	ILMN_1667443	CCTGATTCTTAAAGGTCATACTTGAAATCCTGCC AATTTTCCCCAAAGGG
26.742214	47.455154	69.00805	DDX31	helicain B; helicain C; FLJ13633; FLJ14578; helicain A; FLJ23349	NM_138620	Homo sapiens DEAD (Asp-Glu Ala-Asp) box polypeptide 31 (DDX31), transcript variant 2, mRNA.	GGAGACTGAGCCTGTGG GCGTGGCTTGCTCCCAG AGAACCTTATGGAAGA	ILMN_1785933	GGTTCCCAGCAAACTGAGGCTTGTCTGCCTAGC GGCCTTCATCCTTCAGA
219.61844	347.22263	519.66016	VPS37D	WBSCR24; MGC35352	NM_001077621	Homo sapiens vacuolar protein sorting 37 homolog D (S. cerevisiae) (VPS37D), mRNA.	GCATAGAACAACACTACC CTCCTCTCTTCCCAGATG TGACCACTGAGGGC	ILMN_1680569	GCTTTTTGAGGGCAGGTCCTTGTCTTTGTACGTT CTGTCCCCAGCCCCGC
251.49762	391.0268	577.98926	TOB1	MGC104792; TROB; APRO6; TROB1; PIG49; TOB; MGC34446	NM_005749	Homo sapiens transducer of ERBB2, 1 (TOB1), mRNA.	AACGTGGTGAACGTGGC TGGAGGCTTCAGCCTGC ATCAAGACCCCACACG	ILMN_1759732	CCAATGGAATGTTCCCAGGTGACAGCCCCCTTA ACCTCAGTCCTCTCCAG
71.17618	94.39435	117.189316	RBED1	ELMOD3; FLJ35601; MGC111036; RBM29; FLJ21977	NM_032213	Homo sapiens RNA binding motif and ELMO/CED-12 domain 1 (RBED1), mRNA.	CCTTGCCCACTCCTAGA GACAGCTGTGCTCACTTT TCCTGCTTTGTGCCT	ILMN_1734476	GGCCATTCACTTACCCACTCTCTTCTCCCCCTGA CCCCCGCTCCATTGTT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
44.576775	62.62991	84.70191	LOC124512		NM_001080510	Homo sapiens hypothetical protein LOC124512 (LOC124512), mRNA.			CCTGGCCCAGTACCTTTGGTTTCACAGAAGATCT CTGCCAGGCAAGGCCA
1096.0143	1291.6809	1531.4893	ADCY3	AC3; KIAA0511	NM_004036	Homo sapiens adenylate cyclase 3 (ADCY3), mRNA.	CGGAGGTGACCAGAAAG ATCTCCATCGGTTGCCC AAGGCTGTAAGTAGTG	ILMN_1788347	CTTGCCTTTTGAGCTCTTGCTACAGTCGCCTTTG CTACTGCTTTAAGAGA
83.16478	103.20595	135.49345	MXD3	MAD3; MGC2383	NM_031300	Homo sapiens MAX dimerization protein 3 (MXD3), mRNA.			GCCTTCAGGGCTGCTCGGAGTCACCTGTTGGAA TGGACTAAAAGGACCCT
385.39764	487.63928	596.7018	XRCC5	Ku86; KARP1; FLJ39089; KARP-1; NFIV; KU80; KUB2	NM_021141	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining; Ku autoantigen, 80kDa) (XRCC5), mRNA.			CCAACAAGCAGCTGGGTTAGGAAAACCATGGGT AAGGACGGACTCACTTC
125.00595	162.74762	195.2768	C12ORF45	MGC40397	NM_152318	Homo sapiens chromosome 12 open reading frame 45 (C12orf45), mRNA.	TTGGGCTTCTTCCTCCTC CATCACCTGAAACACTG GACCTGGGGGTAGCC	ILMN_1812262	GCCGCGGAGGTATATGGGACAGGTTGCTCATCA ACTCCCAACCTAAGTCC
32.914406	84.31038	186.65594	SLC25A10	DIC	NM_012140	Homo sapiens solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 (SLC25A10), nuclear gene encoding mitochondrial protein, mRNA.	CAGATGTGAAGCCTGGA GCTTTCCTGATGATGCTG GCCCTACAGTACCCC	ILMN_1682514	CCACCTGGGAAGGGCAGTGTGCTCTGTGGGGG CTGCAATCAATAAATGCC
3764.5476	4209.5225	4638.2393	CCDC72	HSPC016	NM_015933	Homo sapiens coiled-coil domain containing 72 (CCDC72), mRNA.	CTTGAAGCTGAGAAGGC ACAGGGCAAGGAGCCAA GGACCACAGAGCCTCA	ILMN_1729767	CGCCATGTCCGGCCGCGAAGGTGGCAAGAAGA AGCCACTGAAACAGCCCA
401.94345	537.55597	681.34766	RG9MTD1	FLJ20432	NM_017819	Homo sapiens RNA (guanine-9-) methyltransferase domain containing 1 (RG9MTD1), mRNA.	GTGCCATTGTCTCTCCCT AGACTGTTGGCTTCCTG AGGGCAGGCACTTTG	ILMN_1748891	GCAAGAGGCTCTGCAATTCGTTCCCAAGAGAAA ACATACTGGTTTTCTGG
189.89761	331.55594	517.45593	ZNF219	ZFP219	NM_016423	Homo sapiens zinc finger protein 219 (ZNF219), mRNA.			GTCACAGTGCCTTAGAAGTGGCAGAGGTGAGGG TCAAAGAACGGGGTCCC
626.881	705.9726	762.7143	RAP1GDS1	MGC118861; MGC118859; GDS1	NM_021159	Homo sapiens RAP1, GTP-GDP dissociation stimulator 1 (RAP1GDS1), mRNA.			GCATGTGATGTTCTAATACCAATTGAAGAACCGC TGTAGGTACCTCCCTA
318.2143	363.66428	396.99347	SIP1	GEMIN2; SIP1-delta	NM_001009182	Homo sapiens survival of motor neuron protein interacting protein 1 (SIP1), transcript variant beta, mRNA.			GGCTCATTCACTGATTCGGCAGCTTGCAAGAAG GTGCTCTGAAGTGAGGC
59.48646	77.56108	95.3154	SULF2	KIAA1247; HSULF-2; MGC126411; FLJ90554; DKFZp313E091	NM_018837	Homo sapiens sulfatase 2 (SULF2), transcript variant 1, mRNA.			ATCCCTCGCAGTTGTGGACATTTCTGTTCCTGTC CAGATACCATTTCTCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
4322.4062	4878.5894	5299.9644	TINP1	NSA2; HCL-G1; YR-29; CDK105	NM_014886	Homo sapiens TGF beta-inducible nuclear protein 1 (TINP1), mRNA.			GCCACCTTTTGCCTACCAATACTTGGTGTAAAGA AGAATCCCTCATCCCC
131.43929	153.18929	168.43929	PMVK	PMK; PMKASE; PMKA; HUMPMKI	NM_006556	Homo sapiens phosphomevalonate kinase (PMVK), mRNA.			CTGAGGGGGTTGGTGGATATTGGGCAAGGCAG GAAACCTCTGGAGACCTC
93.13097	209.77261	360.63928	RGMB	FLJ90406; MGC86970; DRAGON	NM_173670	Homo sapiens RGM domain family, member B (RGMB), transcript variant 2, mRNA.			GTGTCCCGACTAACCACCTCCTTCCGTGTCTTTT CCAACCACAAAACCAC
32921.37	35538.15	37443.07	RPL3	MGC104284; TARBP-B	NM_001033853	Homo sapiens ribosomal protein L3 (RPL3), transcript variant 2, mRNA.	GAACGTGCCATCTGTAAA GCACTCAGAAGGCAGCC ATCCCTAGATGTTGG	ILMN_1727045	GGAAGAAGGAGCTTAATGCCAGGAACAGATTTT GCAGTTGGTGGGGTCTC
190.97263	222.97263	251.49762	PLCL2	PLCE2; KIAA1092; FLJ13484	NM_015184	Homo sapiens phospholipase C-like 2 (PLCL2), mRNA.	TGCCCACGCATGTGGAA GCTAGGTGGGACTCATT CCTAATTCTGCCGTTG	ILMN_1697218	GGACTGAAGCTCCCTGGCTGAAGATACATGCCG AGTCAGCACATGGGTAG
129.7768	168.14761	200.33928	SLC2A4RG	GEF; Si-1-2; Si-1-2-19; HDBP1	NM_020062	Homo sapiens SLC2A4 regulator (SLC2A4RG), mRNA.	GTAGCAGCAGAGTTGAG CAGTTGTGACAGGAGAC CATGTGGCCTGCAGAG	ILMN_1766544	CACAGAGAGGCAGGACGGCAGAGCCATGATTTC CCACCGAGCGATTACGA
385.13095	487.83093	572.6393	MRPS23	HSPC329; MRP-S23; CGI-138	NM_016070	Homo sapiens mitochondrial ribosomal protein S23 (MRPS23), nuclear gene encoding mitochondrial protein, mRNA.	AGCATCTTTCATATGGTA GGAACCAACAAGGAAAC TTTCCTTTAACTCCC	ILMN_1729019	GAAGTTCCACAGGACCAGCATTTGGAGGCACCT GCAGACCAGTCGAAAGG
60.730915	89.49367	123.7769	ACPT		NM_033068	Homo sapiens acid phosphatase, testicular (ACPT), mRNA.	TGAAGCTCAACACCAAG GTCAGGTAGCCAGGCGG TGAGGAGTCCAGCACA	ILMN_1765954	AATGTCACCGTCTCCCTCTTCTACCGCAATGACT CCGCCCACCTGCCCCT
302.51428	548.18097	806.56433	RAD51C	MGC104277; RAD51L2	NM_002876	Homo sapiens RAD51 homolog C (S. cerevisiae) (RAD51C), transcript variant 2, mRNA.			CAGCACTGGAACTTCTTGAGCAGGAGCATACCC AGGGCTTCATAATCACC
519.6893	869.1726	1210.7643	TSPAN5	TSPAN-5; TM4SF9; NET-4	NM_005723	Homo sapiens tetraspanin 5 (TSPAN5), mRNA.	CCCCATGTGCTGCTGAG TGGCCAAGATGATGCCA GGCTGCCCTATACACT	ILMN_1769787	GGCTGTGTGCCCCAGTTTGAGAAGTGGTTGCAG GACAATTTAACCATCGT
105.18929	120.09762	131.31012	HSF2	MGC117376; MGC75048; MGC156196	NM_004506	Homo sapiens heat shock transcription factor 2 (HSF2), mRNA.			CCACACACTCTTGCAGAGCTTTCAGGTGTTACTC AGCTGCATAGTTACGC
3153.2725	3864.481	4434.5557	SUMO3	SMT3H1; SMT3A; SUMO-3	NM_006936	Homo sapiens SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae) (SUMO3), mRNA.	-		CATAGTTCTGCCTATTGTCCTTCCCTGAGGCTCC ATTGCTGCTTGGTGGC
389.70596	432.59763	465.97678	RSRC1	BM-011; MGC12197	NM_016625	Homo sapiens arginine/serine-rich coiled-coil 1 (RSRC1), mRNA.			GCATCCCTACTGCTATCAAGTACCAAGATGACAA TTCCCTGGCCCATCCA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
875.9309	1107.8601	1320.5059	STARD7	GTT1	NM_139267	Homo sapiens START domain containing 7 (STARD7), transcript variant 2, mRNA.			CACTGTTCAGATAAGGTCACAATCTGATGCTGTC AGTTTGACCGAGCTGG
6340.664	7155.039	7819.965	UQCRH	MGC111572; QCR6	NM_006004	Homo sapiens ubiquinol-cytochrome c reductase hinge protein (UQCRH), mRNA.			CTGAACTGGGTTAGGTGCCGCTGTTGCTGCTCG TGTTGAATCTAGAACCG
525.40594	683.04346	846.98926	MRPL22	HSPC158; DKFZp781F1071; RPML25; MRP-L25	NM_014180	Homo sapiens mitochondrial ribosomal protein L22 (MRPL22), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GATCAGCATCATTGGAAC ATGGGGACGAGTGACGG CAGGAGGACCACGAG	ILMN_1770338	ATAAAATTGTTTATCCTCCACAACTGCCTGGAGA ACCTCGGAGACCAGCA
766.0893	948.8768	1120.9392	CPSF3	CPSF; CPSF73; CPSF-73	NM_016207	Homo sapiens cleavage and polyadenylation specific factor 3, 73kDa (CPSF3), mRNA.			AGCGTCACAGTGGACGGGAAAACTGCCAACCTT AACTTGGAGACACGGAC
234.03513	296.4601	356.2393	NUDCD2	DKFZp686E10109	NM_145266	Homo sapiens NudC domain containing 2 (NUDCD2), mRNA.	TCACACAAACCCAGTGA CAGACCCAACGGTGAGG CAAAGACCGAGCTCTG	ILMN_1716680	GACTTCAGTGGAGCAGAAATCTCAGGAAACTACA CTAAAGGTGGACCAGA
68.43742	99.185135	132.44762	C21ORF51		NM_001042401	Homo sapiens chromosome 21 open reading frame 51 (C21orf51), transcript variant 2, mRNA.			TGTAGTTTTCCCCGGCAGGACGGTAGAAGTCGT GGTTTGTGCGCGGCCAG
367.4268	407.33093	441.76428	GTPBP8	HSPC135	NM_014170	Homo sapiens GTP-binding protein 8 (putative) (GTPBP8), transcript variant 1, mRNA.			GGCTTTATTTTCACTGGCCCCTGAGGTTGAAGTC AGAGTCTCCAAAAAAC
205.26012	312.5976	429.28094	C3ORF68	DKFZp779D0833; MGC61571	NM_182523	Homo sapiens chromosome 3 open reading frame 68 (C3orf68), mRNA.			GATGGCGCTCGACCCCGCAGACCAGCATCTCAG ACATGTCGAAAAAGATG
62.607315	74.41977	79.09792	METT5D1	FLJ33979	NM_152636	Homo sapiens methyltransferase 5 domain containing 1 (METT5D1), mRNA.	GTGTGGGGTAGGGCAG GGTCCACACTCCTTCCC ATCCATTTTAGAGGAGG	ILMN_1686381	GAGACACAGGGGAGAATGCCACATGAAGCTGGA GGCAGAGATTGGAGTGA
1044.2684	1314.1226	1548.6726	DRG1	NEDD3; DKFZp434N1827	NM_004147	Homo sapiens developmentally regulated GTP binding protein 1 (DRG1), mRNA.			GCCAGTTACCAGATTACACATCCCCAGTGGTGCT TCCTTACTCCAGGACC
116.289276	147.4643	175.61429	TBC1D10B	FP2461; DKFZP434P1750	NM_015527	Homo sapiens TBC1 domain family, member 10B (TBC1D10B), mRNA.	GGTTGCACACCGGAGAG AAACCCTACAAATGTGGA GAATGTGGCAAAGCC	ILMN_1802053	GGGACATGCACTGGAATAGGAAATGTCCCCCAT CTCCCTTCCTGCACCCT
1210.4226	1625.8977	2010.1809	PTPLAD1	B-IND1; HSPC121; FLJ90376	NM_016395	Homo sapiens protein tyrosine phosphatase-like A domain containing 1 (PTPLAD1), mRNA.			ATGCAGCAATTGGAGTCACTACGTCACCGGTGC TGCCTTCTCTGATCCAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
9.127583	41.544678	68.42629	MAX	MGC34679; MGC36767; MGC11225; MGC10775; orf1; MGC18164	NM_145113	Homo sapiens MYC associated factor X (MAX), transcript variant 3, mRNA.			CTTTGTTCCTGGGGAATTCACTTCTCTTCCTCCC TCATGGAAGATGCAAG
71.44855	97.7227	120.52261	RPS6KA3	pp90RSK2; MAPKAPK1B; CLS; RSK2; RSK; S6K-alpha3; p90-RSK2; ISPK-1; MRX19; HU-3	NM_004586	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 3 (RPS6KA3), mRNA.	CTGCAGAAGGAGTCGGC GTATGGAGTCTCGAACC CGAGGATTTGTCTGCC	ILMN_1725471	GTACTTATTTTGCATTTTTGGTCATGGGTGGGAA TGGGGTGGGTGCCTAC
26.263805	99.731186	265.7143	CDCP1	SIMA135; TRASK; CD318	NM_178181	Homo sapiens CUB domain containing protein 1 (CDCP1), transcript variant 2, mRNA.			GCGGGGAACTTCAACCTCTCTCTGCAAGGCTGT GACCAAGATGCCCAAAG
1840.1477	2150.4934	2388.331	DDX47	DKFZp564O176; FLJ30012; E4-DBP; MSTP162; HQ0256	NM_201224	Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 (DDX47), transcript variant 2, mRNA.	CCTCATAGGGACTTTGC CTCCTGACAGCAGTTTAT GGGTGTTCATTGTGG	ILMN_1724789	GCCTTTTTTAGCTGCAAGTCAAGGACTAGGTTGA TGATGCCCATGACCTG
922.0143	1785.2559	2437.2893	TMEM5	HP10481	NM_014254	Homo sapiens transmembrane protein 5 (TMEM5), mRNA.			GAGGCTTGCTCCTATGGCTCCATTCCTGTGGTG GAAGACGTGATGACAGC
45.807354	84.72783	116.49763	MAP3K14	FTDCR1B; HSNIK; HS; NIK	NM_003954	Homo sapiens mitogen-activated protein kinase kinase kinase 14 (MAP3K14), mRNA.	GCAGCGACAACCCGTCC TCTCCCGAGTTTTTCATA ACTGAGCCCACTCGC	ILMN_1719543	AAGAATAGCACCCCCTTCCCCATTGCCCCAGCTT AGCCTCTTCTCCCAGG
203.72263	222.41846	230.66013	EIF2S1	EIF2A; EIF-2A; EIF2; EIF-2; EIF-2alpha	NM_004094	Homo sapiens eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa (EIF2S1), mRNA.	CAGGGGAATCCACACAG CCCGCTCCCAGGAGCTA ATGGTAGAGCGTCCTT	ILMN_1728724	CTGTTGATTAAGGGGAGGTCCAAGCATTTGTACT TGGCAGGAATGCTGGC
83.33174	160.34763	197.57262	SCAMP2		NM_005697	Homo sapiens secretory carrier membrane protein 2 (SCAMP2), mRNA.	GACGTTTCCATCAGGTTC CATCCCGAAAATCTCTCG GTTCCACGTCCCCC	ILMN_1804922	AGCTTCCAGCAGGCCCAGGAGGAGTTTTCCCAG GGCATCTTCAGCAGCAG
142.58511	182.2768	198.81012	TSFM	EF-TS; COXPD3; EF-Tsmt	NM_005726	Homo sapiens Ts translation elongation factor, mitochondrial (TSFM), mRNA.	CCCTTTGTACCAGATGTT GAGTGACCAGCTCTGTG GCCCTGTGTCGTCAG	ILMN_1689989	TCCCTGGACGATGAGCCTGGGGGAGAGGCAGA GACTAAGATGCTGTCCCA
14.431595	39.072433	60.51908	PPIL5	MGC20689; 4-1BBLRR; LRR-1	NM_152329	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 5 (PPIL5), transcript variant 1, mRNA.			GCTGCAAGCACCATTAACTTTATTGGAATCTTCT GCACGAACCATATTAC
549.57263	789.5143	941.11426	CRYZL1	QOH-1; 4P11	NM_145858	Homo sapiens crystallin, zeta (quinone reductase)-like 1 (CRYZL1), mRNA.	GCAGCCTTGGATCTTTCT CATACCCAAAACATTGGA CAGATGCTGCGTAC	ILMN_1748923	TTGGATCCTCCAGATAGCCACTGCCTTTTCCTCA AGGGAGCAACGTTAGC
249.2768	318.9643	360.78094	USP10	MGC2621; UBPO; KIAA0190	NM_005153	Homo sapiens ubiquitin specific peptidase 10 (USP10), mRNA.	TGATAGGCCCAGAAGCC CATGTTAGTTAGGGGAA GGGAGCAGGAAGAGGG	ILMN_1725969	GATCAACCAGTACCAGGTGGTGAAACCAACTGC TGAACGCACAGCCTACC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
59.501015	175.70595	297.94345	NFS1	IscS; NIFS; HUSSY-08	NM_021100	Homo sapiens NFS1 nitrogen fixation 1 homolog (S. cerevisiae) (NFS1), nuclear gene encoding mitochondrial protein, mRNA.	GCTGCTGAAGTAGTGTTT AGGATCCTCCATGGCAG TTAGTGAATGTAAGA	ILMN_1694491	ATGGCTGGGAGAGTGAGGCAGCCATGGAACGT GCTCGTCAGCAAGTAGCA
1107.5559	1609.0143	1907.4226	EIF2B2	EIF-2Bbeta; EIF2B	NM_014239	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa (EIF2B2), mRNA.			GAGTGTTGCTGCTGAAGCACATCCTTGCAATGT GGGAGTGCACAGGAGTC
1018.48096	1200.0559	1297.3643	FAM152B	DJ347H13.4; D15Wsu75e; MGC138384	NM_015704	Homo sapiens family with sequence similarity 152, member B (FAM152B), mRNA.	CCATGGGAAACAGGTGG AGATGGGGAAGCCGTCT CTTCTGCATGGTTTAT	ILMN_1799104	GGCACAGTTCCTGACTGGGCGGAAGATTCCTTC TTACATCACAGACCTGC
29.577679	53.728767	68.31653	THNSL1	FLJ22002; TSH1	NM_024838	Homo sapiens threonine synthase-like 1 (S. cerevisiae) (THNSL1), mRNA.	GGGCAGGATCCCTGGAC ACTTACGTACAATGCTTC GTGCTGCCTGATGAC	ILMN_1750785	TCAGCAGGATTTTGTAGCTGACTGGTGCTCTGA GGGAGAGTGCCTAGCAG
105.97262	123.030945	132.17262	USP14	TGT	NM_001037334	Homo sapiens ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase) (USP14), transcript variant 2, mRNA.	GCTGCTCCGGGACCGCT TGGTATTGGGCAAGGCC TACTCATACTCTGCTA	ILMN_1726880	TCCTGAATGTGCCTTATATGCTGTGCCACTCACA CCGAGGCCATCATCTC
4553.3394	5298.048	5703.706	EIF3B	EIF3-P116; MGC131875; EIF3-P110; EIF3S9; PRT1; MGC104664; EIF3-ETA; eIF3b	NM_001037283	Homo sapiens eukaryotic translation initiation factor 3, subunit B (EIF3B), transcript variant 2, mRNA.	TTTTTTGAGACAGAGTCT CACTCCAGCCTGGGTGA CAGAGCAAGACTCCG	ILMN_1814204	CCCACCGTGCAGGTTGTGGCCGGTTTTCTCCGC AGGTTGAACATGGAAAT
1442.5143	1877.3226	2110.5142	ATP6V1A	VA68; Vma1; HO68; ATP6V1A1; VPP2; ATP6A1	NM_001690	Homo sapiens ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A (ATP6V1A), mRNA.	CTGGCCAGCTTGGTGCT CACAGCTGCTGGGTAAG CTCTTGCCTAAGGAGC	ILMN_1789455	GATGATGCAGTTCTGTATTTATTGTGCTGTGTCT GGTCCTAAGTGGAGCC
77.63964	83.456055	89.22834	DIP2A	DIP2; C21orf106	NM_015151	Homo sapiens DIP2 disco-interacting protein 2 homolog A (Drosophila) (DIP2A), transcript variant 1, mRNA.	ATACTAAATCCAGAGGG GGATGTCAACTCTGCCA AAGTCTGTGCCCACAT	ILMN_1701229	GAGGTGTGCTGCTTGTCAGCATGTATTGTCACG GACACTCAATAAGTGCC
763.2643	914.6226	991.97266	PSME3	PA28-gamma; Ki; PA28G; REG-GAMMA	NM_005789	Homo sapiens proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) (PSME3), transcript variant 1, mRNA.			TGAACTGGTTCAAGGCGCGTCCTACCCAGTCAT TTTCTTTACCTTATACT
1586.5227	1702.5894	1764.131	HDGF	DKFZp686J1764; HMG1L2	NM_004494	Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA.	CGTCTGATTTATGAAGCT CCCCATCCACCTATCTGA GTACCTGACTTCTC	ILMN_1674984	GTGCTCTCCATTCTGCTCCTTCCCCATCGTTGCC CCCATTTCTGAGGTGC
472.7101	535.9226	570.03094	KLC1	KLC1; KLC; KNS2; KNS2A; MGC15245	NM_005552	Homo sapiens kinesin light chain 1 (KLC1), transcript variant 1, mRNA.	GCATGCGTGTGCAGGAC TGGCTGTGTGCTTGGAC TCGGCTCCAGGTGGAA	ILMN_1783753	GCTCGGACTCCGGGTCTCCCTAGGATATGCCCC AGTAGCATTTGCTGTGT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
976.6809	1291.606	1491.381	RUVBL2	TIP49B; TIP48; TIH2; RVB2; CGI-46; ECP51	NM_006666	Homo sapiens RuvB-like 2 (E. coli) (RUVBL2), mRNA.	GCAGACATCCCTCCCAA TCTTGCCCACACACTGA GAAGTAACTCGGAGCT	ILMN_1673544	GAGGAGGGCAAGGCGGAGATCATCCCTGGAGT GCTGTTCATCGACGAGGT
1800.3977	3486.5562	4846.831	BAX	Bax zeta	NM_138765	Homo sapiens BCL2-associated X protein (BAX), transcript variant sigma, mRNA.	TCCCTGCCCAGCAAGAA GCAGTATCGACTCAGCA TGGAACGCCTGCAACG	ILMN_1684919	TCAGAACCATCATGGGCTGGACATTGGACTTCCT CCGGGAGCGGCTGTTG
354.32263	671.25183	916.61426	UCHL5	UCH37; CGI-70	NM_015984	Homo sapiens ubiquitin carboxyl-terminal hydrolase L5 (UCHL5), mRNA.			GCAACATCCTAATTGGCTCAGTGCACGTTTGGCA ATAGTGCCAGCCTGTC
896.94763	1556.7559	2043.3228	TCTEX1D2	MGC33212	NM_152773	Homo sapiens Tctex1 domain containing 2 (TCTEX1D2), mRNA.			AGAGGTGAAGGAGTATTCATGGCTTCTCGCTGTT TCTGGGATGCTGACAC
71.213806	83.78555	91.38513	SLC30A5	ZnT-5; MGC5499; ZTL1; FLJ12496; ZNTL1; FLJ12756; ZNT5	NM_022902	Homo sapiens solute carrier family 30 (zinc transporter), member 5 (SLC30A5), transcript variant 1, mRNA.			GTACAGAAACAGAGTTCCCTACTACTGGATCAAG GAATCTTTCTTGAAGG
98.21846	149.82678	177.98929	C15ORF41	FLJ22851; MGC11326; HH114	NM_032499	Homo sapiens chromosome 15 open reading frame 41 (C15orf41), mRNA.	CTTTGCTCTTCCTGTTTT TGGTGCCTGTTCCAGGT CATGGAGGAATCATA	ILMN_1684308	GCCTGCTGCTTTTCCTTTTGAAGGACACAAACCT GGTCCCAACATGTGTG
35.061398	80.86612	118.680954	DMD	DXS272; DXS269; DXS230; DXS268; DXS270; DXS239; DXS142; DXS206; CMD3B; DXS164; BMD	NM_004010	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD), transcript variant Dp427p2, mRNA.	CAAATCTTTCCTGGCGAA GGGGAGGGAAGGGGTG TTCTGGTGGAGTGGGA	ILMN_1786361	CCATTCAGAAGAATGATAAATGCCACAAGCATTT GGAAACAGGCTTCCCT
21.830338	51.64456	78.34192	C1ORF103	RIF1; FLJ11269; RP11-96K19.1	NM_018372	Homo sapiens chromosome 1 open reading frame 103 (C1orf103), transcript variant 1, mRNA.			CCCAGCTTGCTTCCATGGCCAATCTAAGGGCAG AGAAGAATAAAGTGGAG
158.11429	202.05179	230.10596	DHX30	KIAA0890; FLJ11214; Ret-CoR; DDX30	NM_014966	Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 30 (DHX30), transcript variant 2, mRNA.			AGCTGGCTGCACTTCCCCCCAGCGTACAGGAGG AGCACGGGCAGCTGCTT
173.40594	221.56012	256.3851	C8ORF41	FLJ23263	NM_025115	Homo sapiens chromosome 8 open reading frame 41 (C8orf41), mRNA.	CCCTGTGCAAATCAGAG TATGTGAGTGGAAGAAG GGGTGAGTCCTAACTG	ILMN_1691693	GACCGCCGTTCTCAAGGACGGGTAAAGGGTCTC CTGGCCAAAATTCCCCA
706.7143	1131.3893	1462.6809	XTP3TPA	RS21C6; CDA03; MGC5627	NM_024096	Homo sapiens XTP3-transactivated protein A (XTP3TPA), mRNA.			AGGGGTGCCTCTGAGACCCATTCTCGTGTTTCC CTGTTGTACCTTTTGCC
11.402901	72.201614	229.13097	LGMN	AEP; LGMN1; PRSC1	NM_001008530	Homo sapiens legumain (LGMN), transcript variant 2, mRNA.	CCCAGCAGGGCCAGGTC GGAAGGTGATTGAATAC AAAAGCACCAGGGACC	ILMN_1804444	TGGCACAATCTTGGCTCACTGCAACCTCTGCCTC CCGGGTTCAAGCAATT
100.95239	139.13928	165.78513	C21ORF7	TAKL-2; TAK1L; TAKL-1; HC21ORF7; TAKL	NM_020152	Homo sapiens chromosome 21 open reading frame 7 (C21orf7), mRNA.			GTGACCTCACAGTAAACATCTCTGCCTTTGCCTG TGTGTGTTCTGGGGGA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
484.38095	706.5643	851.9976	SRPK1	SFRSK1	NM_003137	Homo sapiens SFRS protein kinase 1 (SRPK1), mRNA.	GCTAAAGAATAAGACCTT GCTTGAGAAGGCTGACC TGGACCCCTCCCTGG	ILMN_1659985	GGCAGCTGTAGATCTTGATCTTCCAGGTACCCC ATGTACCTTTATTGAGC
428.2976	591.48096	695.9976	CSTF3	MGC75122; MGC43001; MGC117398; CSTF-77	NM_001326	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa (CSTF3), transcript variant 1, mRNA.	CCACAGTGTGTGGCGCT GATGGAGATGTCAGAAC CGAGAACACTTAACCT	ILMN_1658149	GTGGCAGAACCACATTTTGTTCCCTCTTCAAGGG TGTCTTGTATGTGCCG
81.127106	113.42678	136.53928	GATC	MGC129938; FLJ37000; 15E1.2	NM_176818	Homo sapiens glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial) (GATC), mRNA.			GAATTACTACAAAACTCCCATCGCGTCGTGGAG GAGTACTTTGTGGCCCC
1195.1809	1545.0476	1746.5393	NAT5	dJ1002M8.1; NAT3	NM_181528	Homo sapiens N-acetyltransferase 5 (NAT5), transcript variant 3, mRNA.	CTCACTGTACTGGCCCC CAATGGCTTCTACATGC GAGCCGACCAAAGTGG	ILMN_1689635	GTCACAGCTCTGTCTGTTGCCCCAGAATTTCGAC GCCTTGGTTTGGCTGC
350.56012	394.4851	418.32678	PIAS1	MGC141879; MGC141878; GU/RH-II; GBP; ZMIZ3; DDXBP1	NM_016166	Homo sapiens protein inhibitor of activated STAT, 1 (PIAS1), mRNA.	TGGGCCAGGACTGCTCT GAGATTTGAGGGAAACA TGGACCCTTTTGGCCC	ILMN_1804652	CTGCCAACCACCAATGGAAGCAGTAGTGGCAGT AACAGCAGCCTGGTTTC
3481.7642	3877.056	4115.556	PSMB3	HC10-II; MGC4147	NM_002795	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 3 (PSMB3), mRNA.	GCATTATTGTGACAGCCA CGAACCCATTGCCCACA ACCCCTCCACCCTCG	ILMN_1769665	GCTGAATGCTGTGGACCGGGATGCAGTGTCAGG CATGGGAGTCATTGTCC
258.15594	381.31012	482.16428	SHPK	CARKL; FLJ32478; SHK	NM_013276	Homo sapiens sedoheptulokinase (SHPK), mRNA.	GCCTGGTGTGCTGCGCC TATCCGCCGGGAGCCTT TGTGTCCGTGTCCCGA	ILMN_1769822	CACGGTGTCACTTTCCATGGGTTCAGTTATCTGC GGTCAACCACGGTCTG
124.42678	145.66428	159.68927	HPS3	SUTAL; DKFZp686F0413; FLJ22704	NM_032383	Homo sapiens Hermansky-Pudlak syndrome 3 (HPS3), mRNA.			GCCGGCCTCAGTGTCCATGTTCTGTGTCGTACA CGCTTGAAAGAGTATGA
275.38928	418.2726	552.40594	BDNF	MGC34632	NM_001709	Homo sapiens brain-derived neurotrophic factor (BDNF), transcript variant 4, mRNA.			CTTGCTGTGGTCTCTTTGTGGCAGAAGTGTTTCA TGCATGGCAGCAGGCC
3719.6812	4091.8018	4318.756	ATIC	PURH; IMPCHASE; AICARFT; AICAR	NM_004044	Homo sapiens 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase (ATIC), mRNA.	CTCGCTATGACAGTGGA CAGGACCTAGATGAGGA GGGCATGAATATGGGT	ILMN_1663616	CGTAGACAGAGCTAAAAGGAGTGGTGTGGCGTA CATTGCGGCTCCCTCCG
6640.664	7340.506	7809.5557	SNHG5	MGC16362; U50HG; bA33E24.2; C6orf160	NR_003038	Homo sapiens small nucleolar RNA host gene (non-protein coding) 5 (SNHG5) on chromosome 6.	CCTGCTTACAAATGTCTA AGGTCCCCACTGCCTGC TGGAGAGAAAACACA	ILMN_1691803	GTCTGGGCGGGTGGTAGGAACAATGGCGCTGT CTTCAGTGGCACAGTGGA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
853.60596	1265.4309	1657.0476	TNFRSF21	MGC31965; BM-018; DR6	NM_014452	Homo sapiens tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), mRNA.	TGTACATACGGCCCACAT CTGATCGCTCCCCTATG CAGGACAAGCTGGTG	ILMN_1699872	ATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTG GTGGGATTCCTTCACC
439.62262	522.9143	579.40594	ALKBH3	MGC118790; DEPC-1; MGC118792; MGC118793; PCA1; ABH3; DEPC1	NM_139178	Homo sapiens alkB, alkylation repair homolog 3 (E. coli) (ALKBH3), mRNA.	CTTTCAGCTCAAGAGCCA GAAGCGCTATCACGAAG ATATCTTTGGTGCTG	ILMN_1747882	AGAGAACCGAGAGTGAACCTGACCTTTCGGACA GTCTATCCAGACCCTCG
1677.4727	1904.4559	2082.2642	MRPL21	MGC62013	NM_181515	Homo sapiens mitochondrial ribosomal protein L21 (MRPL21), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GCTGTCCTGTTCTCCATC TCCATTTCTTCCCATGCT GTAACCCCAGGCTC	ILMN_1680782	GACCTTGCGTGTGGAGAGAGAATTCGACTGGAG AAGGTCCTGCTGGTTGG
751.44763	930.2726	1037.6685	PSME3	PA28-gamma; Ki; PA28G; REG-GAMMA	NM_005789	Homo sapiens proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki) (PSME3), transcript variant 1, mRNA.			TCCTTCCCGAGTGATACCCATGAACTGCCAGTAG AGGCTGCTATCGTTCC
9695.331	13327.147	16151.356	YWHAQ	HS1; 14-3-3; 1C5	NM_006826	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide (YWHAQ), mRNA.	GAAACTGAGCTGGGACT GGAAAGGACAGCCCTTG ACCTGGGTTCTGGGTA	ILMN_1707342	CATGCAGATTTGTGCACATGTGAGAGGGTGTCC AGTTTGTCTAGTGATTG
49.40931	56.330696	62.008263	FLJ21865	DKFZp434P174	NM_022759	Homo sapiens endo-beta-N-acetylglucosaminidase (FLJ21865), mRNA.			TTGTGGGGGGCGCAGCATCCACGCCTTGCTGCC CTTCTTTCATGAAGTCT
802.10596	898.2851	958.83093	BRD7	CELTIX1; NAG4; BP75	NM_013263	Homo sapiens bromodomain containing 7 (BRD7), mRNA.			GTTCCAGAGGTTGGACTTGTATTAGGTAATAAAG CTGGACCTGGGACTCG
50.42256	118.52679	194.92679	GSR	MGC78522	NM_000637	Homo sapiens glutathione reductase (GSR), mRNA.			CATGGGGTTTCTCCATGTTGGTCAGGCTGGTCT CAAACTCCCACCTTCAG
328.0476	398.93512	457.01428	EXOSC4	Rrp41p; p12A; FLJ20591; hRrp41p; Ski6p; RRP41A; SKI6; RRP41	NM_019037	Homo sapiens exosome component 4 (EXOSC4), mRNA.			GCAGGTGCTACAGGCAGATGGTGGGACCTATGC AGCTTGTGTGAATGCAG
41.459953	114.1893	203.28513	EVI1	EVI-1; PRDM3; MGC163392; MDS1-EVI1; AML1-EVI-1	NM_005241	Homo sapiens ecotropic viral integration site 1 (EVI1), mRNA.	GGGACACTACCACAAGC CCCTTCTGGAAAGGATG CAGAAAAGACCCCAGC	ILMN_1745021	CCAGGGCTGCGGCGGAATCCAGTGCTATCCAGT CCATAAGCCACGTATGA
1475.6643	1705.1643	1860.7227	CNIH	CNIH1; CNIL; TGAM77; MGC117156	NM_005776	Homo sapiens cornichon homolog (Drosophila) (CNIH), mRNA.			CTTTGTGCAGCAGAGTGGCTTACACTGGGTCTC AATATGCCCCTCTTGGC
523.28516	673.0476	780.4393	RPS6KA4	RSK-B; MSK2	NM_001006944	Homo sapiens ribosomal protein S6 kinase, 90kDa, polypeptide 4 (RPS6KA4), transcript variant 2, mRNA.	ATGTGTGCTGGCAATCA GGGCCGCAGTGTGTTCT GCGCCTGCCCAGAGCT	ILMN_1771651	GGCCCTGGGGGACCCTCTGAAGCATTTCTGCCT CACTTTATGTCATCTGC
41.199665	65.63173	86.96097	EGFLAM	AGRINL; AGRNL; FLJ39155	NM_182801	Homo sapiens EGF-like, fibronectin type III and laminin G domains (EGFLAM), transcript variant 4, mRNA.	GAGGACATGCCTCCCAC CAAATGTCCCCTGCTCCA GTCCCACTCCTGTCA	ILMN_1669382	GGCCCTTGGATTGTTCGGATTAACCCCTTCCACT CCTCACTGGCTGGTTC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
106.53929	151.86845	185.98929	CKAP5	KIAA0097; TOG; TOGp; FLJ35359; ch-TOG	NM_001008938	Homo sapiens cytoskeleton associated protein 5 (CKAP5), transcript variant 1, mRNA.	CCCAACATGGAGCTGTG CAGGGACATCCCGCAGT TGAAGCTGGTGAACGA	ILMN_1706832	CGATGAGGTCCTGAGACAGGAAGACAAAGCTGA AGCCATGTCCGGCCATA
1124.2643	1624.1809	1985.7476	H2AFY	H2A.y; H2A/y; H2AF12M; MACROH2A1.1; mH2A1; macroH2A1.2; H2AFJ	NM_138609	Homo sapiens H2A histone family, member Y (H2AFY), transcript variant 1, mRNA.			GACAGTGATGCTGTCGTTCACCCGACAAACACT GACTTCTACATCGGTGG
132.27261	169.2143	193.9643	ARMC6	R30923_1; MGC19595	NM_033415	Homo sapiens armadillo repeat containing 6 (ARMC6), mRNA.	TAGACAGGGGCTTGCTA TAGTGTCCAGGCTGGTC TGAAACCCTTGAGCTC	ILMN_1704163	GCACGGATGTTACTGTCCTGCTCCTTCCCCCAG CCCCACGCCCTACCAGA
83.714355	82.581055	85.651855	CTBP2		NM_001329	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA.			TTTCGCCGTGGACGCCGACCGTCCGGGACGAG GGTTTCATCACCTTAAAT
512.74347	590.23096	636.79346	MCM3AP	FLJ44336; MAP80; FLJ45306; KIAA0572; GANP	NM_003906	Homo sapiens minichromosome maintenance complex component 3 associated protein (MCM3AP), mRNA.			TGCTAGACATGGTGGACATTTGAGCAGCCTGAC CTGTGGGGAGGGGGTCT
54.723366	99.51428	137.15594	LRRC20	FLJ10751; FLJ10844	NM_018239	Homo sapiens leucine rich repeat containing 20 (LRRC20), transcript variant 2, mRNA.	CACCTGGGAGAAAAGTG ACCCAGTTTAGGAGCTG GAGGGGGGTCTTTGTC	ILMN_1683905	TCTGCTTGGAGAGTTTGCCCTTGTCTGTCTTGGA AAGTGTGGGCAGCCAC
46.426277	74.59414	96.368454	FTSJ3	FLJ20062; EPCS3	NM_017647	Homo sapiens FtsJ homolog 3 (E. coli) (FTSJ3), mRNA.			TCCCAGGAGAGCATGGGGACTAGGAGGAAGGG TGTGGCATGGCTCAGTCT
228.07262	274.68094	304.98096	PSIP1	MGC74712; PAIP; LEDGF; p75; PSIP2; p52; DFS70	NM_033222	Homo sapiens PC4 and SFRS1 interacting protein 1 (PSIP1), transcript variant 2, mRNA.	GAACACCTGCCTTCTACC CTCTGGTTGGGAGATGC AGCCACCACATCCCT	ILMN_1764228	TGAATATTAGGGTCATTTGGCACTTCTCAGCAAG TAGGATACTTCTCATG
3550.6226	4031.106	4290.9644	GLO1	GLYI; GLOD1	NM_006708	Homo sapiens glyoxalase I (GLO1), mRNA.	GCACCGATGCACACACC GCACCCCACCACTGTAC TCTGAAATTGGCGAGT	ILMN_1691843	GTGCTCTTGGCTCTTGGGCTGGAGTACCGTGGT GAGGGAGTAAACACTAG
119.15595	167.28094	198.92262	AZI1	AZ1; Cep131	NM_014984	Homo sapiens 5-azacytidine induced 1 (AZI1), transcript variant 1, mRNA.			ACAGAGGCTGGTGGTTGAGATGCCCACGGCTAA GCACCTGTGGCTGCATT
723.85596	836.20593	911.6268	GRWD1	RRB1; KIAA1942; WDR28; GRWD	NM_031485	Homo sapiens glutamate-rich WD repeat containing 1 (GRWD1), mRNA.	CTCAAACCCCCTTCACCC AGGCCCCAGAACAGCTT ACTCCACGGCATACA	ILMN_1781031	GGAGGTGTGGGTTCCTCCAACACAATTTGCTTCT GCCCGTTGTCTTCCTG
20.042871	54.71792	88.37347	TJP2	MGC26306; X104; ZO-2; ZO2	NM_004817	Homo sapiens tight junction protein 2 (zona occludens 2) (TJP2), transcript variant 1, mRNA.	TTCTAGGAACTTGACGTG ATGGGGCTTCCTGAGGA GCGGGTCCGGAGCGG	ILMN_1697510	GCAAAACCTACCTTTGGGCGGTCTATACTGAAGC CCTCCACTCCCATCCC
994.0476	1247.9727	1433.5977	CSNK1D	HCKID	NM_139062	Homo sapiens casein kinase 1, delta (CSNK1D), transcript variant 2, mRNA.	TGGCTAAGCATGAGTTAA GCAGCAAAACGCTCCTC CATGTCTGGATGGGG	ILMN_1714828	ATAGCATTCCTTTCGAACACCACGGCAAGTAGCT GCTCGTCTCCCATCGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
345.56427	447.9643	518.08093	CSRP2BP	CRP2BP; PRO1194; MGC15388; dJ717M23.1	NM_020536	Homo sapiens CSRP2 binding protein (CSRP2BP), transcript variant 1, mRNA.			CCCTCAACAGTGATGAAGGAGACGTGTCTTGGA TGGAGGAGCAGCTGTCC
31810.18	34256.547	35732.973	RPS17	MGC72007; RPS17L1; RPS17L2	NM_001021	Homo sapiens ribosomal protein S17 (RPS17), mRNA.	ATCCTCAGGTTGTGGGG TATTTGTTTCTACTCCAG CCTGGCAGGCAAGGC	ILMN_1727603	GCGAATTCAGAGAGGCCCAGTAAGAGGTATCTC CATCAAGCTGCAGGAGG
41.71138	57.59533	70.47686	SLC30A3	ZNT3	NM_003459	Homo sapiens solute carrier family 30 (zinc transporter), member 3 (SLC30A3), mRNA.	CCATGGGGGCTGGAGG GGGGCAGCTGGGACTCT GGAATCTTCTTTATAAT	ILMN_1675222	CTGTTTGGGGGTCTATCTCTCCATCCCTCTGTTG GTGCTGTGCCCTTGGC
379.51428	978.15594	783.7476	ELOVL6	FAE; MGC5487; FLJ23378; LCE	NM_024090	Homo sapiens ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast) (ELOVL6), mRNA.	GCAGGGCCACTCTTGGC AGAGACTTTGGGTTTGTA GGGGTCCTCAAGTGC	ILMN_1749213	CTGTCAGAGATGGCAAGGGCTTTTTCAGCATCTC GTTTATGTGTGGAATT
79.481705	242.98929	189.52261	DPH3	MGC20197; DPH3A; DELGIP1; ZCSL2; DELGIP; KTI11; DESR1	NM_001047434	Homo sapiens DPH3, KTI11 homolog (S. cerevisiae) (DPH3), transcript variant 2, mRNA.	GCTCGCATGGCAGCCGC TTCGGCGCCCGGCCCCG CGGCCAGCTAGGGGCG	ILMN_1662010	TTCCGGCGAAGTTAAACCCTCGGAGCTGGCCTC GGACTGCTGGGGCGTTA
87.48932	193.38095	160.58095	LPCAT1	FLJ12443; PFAAP3; lpcat; LPCAT1; AYTL2	NM_024830	Homo sapiens lysophosphatidylcholine acyltransferase 1 (LPCAT1), mRNA.			TGCTGGGGTGTGAGGGCAGAGGGAGGGTTGCC ATGAAGGAACTTGGGATT
700.70593	1353.2393	1158.4642	EXOSC8	CIP3; Rrp43p; EAP2; bA421P11.3; RRP43; OIP2; RP11-421P11.3; p9	NM_181503	Homo sapiens exosome component 8 (EXOSC8), mRNA.			GGCAAACTCTGTTGTCTTCACAAACCAGGTGGAA GTGGGCTAACTGGAGC
116.73512	759.0059	494.1601	SATB2	FLJ21474; MGC119474; FLJ32076; MGC119477; KIAA1034	NM_015265	Homo sapiens SATB homeobox 2 (SATB2), mRNA.	CTCCCAGCCATCTCCTCT TCCCTAAGGCCTCTGTCT CCATAGCTCTGGTT	ILMN_1804993	GCAGTGGTTCTAAGTGAATCTGTGGGCATTTTAG CCTGTGGTCTTGCCAG
1028.9644	1799.281	1572.7935	Mar-04	MARCH-IV; RNF174; MGC104908	NM_020814	Homo sapiens membrane-associated ring finger (C3HC4) 4 (MARCH4), mRNA.			CCTGCCAGGGAAGGCCACTGGGTGTTCACCTGC AAAGTTTCTGGTTGTCA
112.42262	254.42679	209.56012	MTF2	dJ976O13.2; PCL2; M96; RP5-976O13.1	NM_007358	Homo sapiens metal response element binding transcription factor 2 (MTF2), mRNA.	CGTGGGATCTGCACACG TCTTTGTCAGTTGTGGTC ATGATCTTAGTCACC	ILMN_1664016	GCACTCTGATTTTCTGTAGGTACAGTTCAAAGCC CTAAAGGGAGTCTGGC
85.481	133.4643	119.47261	FASTKD1	KIAA1800; FLJ21901	NM_024622	Homo sapiens FAST kinase domains 1 (FASTKD1), mRNA.	CTGGGCACAGAGCCAAT GTTCGTCATTGCAGCTCT CAGCAAACTGGGTCA	ILMN_1738237	CGAAATAGTTGGATCAAGGCTGCCACCAGGGGC TGAAAGGATTGCTTTGG
84.53935	110.501785	103.493454	AIFM1	MGC111425; PDCD8; AIF	NM_004208	Homo sapiens apoptosis-inducing factor, mitochondrion-associated, 1 (AIFM1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GCTGCTCCCGGAAATGC AAATGAGACTCCTGGAAA CTGGGTGGGAATTGG	ILMN_1769158	GGCTAGCTCTGGTGCATCAGGGGGCAAAATCGA TAATTCTGTGTTAGTCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
154.9226	219.33928	202.85596	ZNF35	Zfp105; HF.10; HF10	NM_003420	Homo sapiens zinc finger protein 35 (ZNF35), mRNA.			CTAGTCTCCATGGCCAAGCACTCAAGGATTGATG GACACCACACACCAGC
162.88928	251.75179	227.22678	PUS3	FKSG32; FLJ23638; 2610020J05Rik	NM_031307	Homo sapiens pseudouridylate synthase 3 (PUS3), mRNA.			CCATAGACAATTTGCCAGGATCTAGGAACCACCT AATGGTAGGTGGACAG
147.03928	180.1518	170.95595	ZNF280D	ZNF634; MGC61687; MGC21637; SUHW4	NM_001002843	Homo sapiens zinc finger protein 280D (ZNF280D), transcript variant 2, mRNA.	CGGGATTGAGGAAGGTC CGCACAGCCTGTCTCTG CTCAGTTGCAATAAAC	ILMN_1756920	ACAAGTCAACACTACACGAATCCAACATCAAATC CAGTGCCTGCCTCACC
41.826195	170.65178	120.64762	AKT3	PRKBG; PKBG; DKFZP434N0250; RAC-gamma; RAC-PK-gamma; STK-2	NM_181690	Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma) (AKT3), transcript variant 2, mRNA.	GGGGATTGGTTCCAGAC CCCCTAAGCATACCTAAA TCCACAGATGCTGTG	ILMN_1663754	GGGCTCTTGATAAAGGATCCAAATAAACGCCTTG GTGGAGGACCAGATGA
97.897705	188.71011	161.43512	SSH2	KIAA1725; MGC78588; SSH-2	NM_033389	Homo sapiens slingshot homolog 2 (Drosophila) (SSH2), mRNA.	CCACTTGGAGAGCAAGA GGGCTTGTGGACTTGGG GGAGCGGTTGTGAGAA	ILMN_1794156	GTCCAGAAGACTCTCCTCTGACTGTTACCTTTGC CCCAAGCCACCCCAAA
15.098658	61.392067	43.381256	NEDD1	TUBGCP7; FLJ35902; GCP-WD	NM_152905	Homo sapiens neural precursor cell expressed, developmentally down-regulated 1 (NEDD1), mRNA.			GGATGACTTTAGAGAAGCATGCCATAGGGACATT GTGAATTTGCAAGTGG
1415.4559	2785.056	2346.2144	DKC1	NAP57; NOLA4; XAP101; dyskerin; DKC	NM_001363	Homo sapiens dyskeratosis congenita 1, dyskerin (DKC1), mRNA.	GGGGAGGAAGACACCTC ATATCAGCCCTCAAAGG CTCCCCTCACTGTCTC	ILMN_1686587	GTACAGTGCTCACCTAAATCCATCTGACTACTTG TTCCTGTGCCCTCTTG
180.93095	413.0268	330.43512	ZNF365	MGC87345; KIAA0844; MGC41821; UAN; ZNF365D; Su48	NM_014951	Homo sapiens zinc finger protein 365 (ZNF365), transcript variant A, mRNA.			CTTTGTCCACATGGGCCGTTGACCTTAGAGTTAA GGCGGTTGCTTTTTTG
317.0893	711.34766	585.39764	CP110	KIAA0419; DKFZp781G1416	NM_014711	Homo sapiens CP110 protein (CP110), mRNA.			CACATTCTTTTTTGGTGTTCATAGCTTCTTCTCAT ACAGGTGCCAGACAC
47.102837	140.5476	113.47699	ZNF654	FLJ10997; FLJ21142	NM_018293	Homo sapiens zinc finger protein 654 (ZNF654), mRNA.	ATGGGCTGAGCTGCACC AGACCCTCACACACCAC AGCACTGCAAGCTGAT	ILMN_1759889	AGATGTGGCAAATGCCTGACCACCTACTGTAATG CAGAAGCACTTGAGGC
2363.0725	3810.781	3395.3228	COX17	MGC117386; MGC104397	NM_005694	Homo sapiens COX17 cytochrome c oxidase assembly homolog (S. cerevisiae) (COX17), nuclear gene encoding mitochondrial protein, mRNA.			GAGGCTGGCATAGATTTGGCTGTCTCCGCTCAT AGCTGCTTTTGGCGCGA
28440.006	39688.508	36654.75	VIM	FLJ36605	NM_003380	Homo sapiens vimentin (VIM), mRNA.			CCAAACTTTTCCTCCCTGAACCTGAGGGAAACTA ATCTGGATTCACTCCC
118.03512	197.74344	174.48929	TMEM170	FLJ37611	NM_145254	Homo sapiens transmembrane protein 170 (TMEM170), mRNA.	GGGCCTCTCCTCAAGGA GAGATGGAGGGATACAA TTCTTGGTTCAGTGGG	ILMN_1678862	GCCAAGTCAACAGTGTCTCTGGGGTGGCATCCT TTGCACTGAAATTTACA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
5486.298	7623.1396	7028.6978	SRP9	ALURBP; MGC110981	NM_003133	Homo sapiens signal recognition particle 9kDa (SRP9), mRNA.			TGACACCCCTGCCCATTTTCTGTCTTTAATTAAC CAAGGTGTTAGGTGTG
14.524389	108.62262	65.61335	VEPH1	MGC126709; FLJ12604; KIAA1692; MGC142115; MGC111426	NM_024621	Homo sapiens ventricular zone expressed PH domain homolog 1 (zebrafish) (VEPH1), mRNA.			AGTACAGAGTGTGAAGGCTGTGGCCAAGAAACG CAGGGACCGCTCTCTCC
25.04816	126.97262	85.306	MESDC1	MGC99595	NM_022566	Homo sapiens mesoderm development candidate 1 (MESDC1), mRNA.			GGTTGTGTTATCACTCCCACCCCCTACCCCAGC CCGTCTTCCGGAATTTC
441.83926	638.0893	578.2643	GFM1	hEFG1; FLJ12662; EFG1; EFG; EGF1; FLJ13632; GFM; FLJ20773; EFGM; COXPD1	NM_024996	Homo sapiens G elongation factor, mitochondrial 1 (GFM1), nuclear gene encoding mitochondrial protein, mRNA.	GATGCCGGGGACTCGGA CCCCGCACCCTGAGAGT CTTTGTTAATGGATGT	ILMN_1686854	GTTTCCAGAAAAAGTTGGGCTTTCCCAAGCAGTT CTATTACCCGGTTCAG
40.57228	137.48096	104.75186	SP4	MGC130009; SPR-1; HF1B; MGC130008	NM_003112	Homo sapiens Sp4 transcription factor (SP4), mRNA.	AATGCACCTCATTCTTCC CTGGCCTCTTTCCCACC CACAGCCCCCAGAGG	ILMN_1732323	ATGCATGTCACTAAGTTGTCATCCCACATAAATT GATGTGCAGCATAGGG
179.84763	286.62262	260.80597	KIAA1712	PS1TP3	NM_001040157	Homo sapiens KIAA1712 (KIAA1712), mRNA.			GTCAGTTGCTTGTGCTGCCCTGTCTATGTTATGC TCTGAATAGGTCTCGG
284.30594	485.92676	429.69345	MRPL48	CGI-118; MGC13323	NM_016055	Homo sapiens mitochondrial ribosomal protein L48 (MRPL48), nuclear gene encoding mitochondrial protein, mRNA.			GGAGTCAGACTGTCAGTGAAGGAGCACACTGAA GAAGACTTCAAGGGACG
57.59127	285.93094	193.49762	CENPQ	FLJ10545; C6orf139; CENP-Q	NM_018132	Homo sapiens centromere protein Q (CENPQ), mRNA.	CAAGTCTCAAGAGACACT TAATTCAGATGACTTGGA TGCCACTGACAAAC	ILMN_1720955	GCCAATGGCTTACAGTTTCTGTCTGGTCATCTGG AACTTGAAAAATCCTC
33132.957	43157.133	40647.273	TMSB10	MIG12; TB10	NM_021103	Homo sapiens thymosin beta 10 (TMSB10), mRNA.			AAGAACACCCTGCCGACCAAAGAGACCATTGAG CAGGAGAAGCGGAGTGA
36.41363	79.64813	66.65614	CCBL1	GTK; MGC29624; KATI	NM_004059	Homo sapiens cysteine conjugate-beta lyase, cytoplasmic (CCBL1), transcript variant 1, mRNA.	CCCATTCGTCTGTCCCA GAGCTTATTGGCCACTG GGTCTCACTCCTGAGT	ILMN_1697559	CCTTCCCTGGCTCATCTTGGCCTTGGGGAGTTG CCTTTAGGCTTGAGTCC
1290.2476	1853.4976	1714.781	ZMIZ1	MIZ; Zimp10; FLJ13541; hZIMP10; KIAA1224; RAI17	NM_020338	Homo sapiens zinc finger, MIZ-type containing 1 (ZMIZ1), mRNA.	TGCTTTGTGGCCCAGAA TATGGGCTATCTTGGTAT GAGTTACATGTTCAC	ILMN_1738124	CGTACACACATAAACACACCCACCAGTGCAGCCT GAAGTAACTCCCACAG
16.033009	2107.0393	704.32263	ESM1	endocan	NM_007036	Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA.	TTGGGGGTCAGGCAGCC AGTGAGATGAGGGATGG GCCTGGCATTCTTGTA	ILMN_1815522	CTGCTGATGTAGTTCCCGGGTTACCTGTATCTGA AGGACGGTTCTGGGGC
8600.764	19942.09	16475.582	CCND1	PRAD1; D11S287E; BCL1; U21B31	NM_053056	Homo sapiens cyclin D1 (CCND1), mRNA.	TCAGAAGCACATAGCTAT TGCCATTCATCCTCCGCA GCCGGCTGGGCAGT	ILMN_1678974	CGGCGCTTCCCAGCACCAACATGTAACCGGCAT GTTTCCAGCAGAAGACA
115.88095	181.66846	164.44762	COBRA1	RP13-122B23.3; DKFZP586B0519; NELF-B; NELFB	NM_015456	Homo sapiens cofactor of BRCA1 (COBRA1), mRNA.			TGACGCGGATGGTGGGGAAGAACGTGAAGCTGT ACGACATGGTGCTGCAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
120.95178	161.75177	150.66846	GLRB		NM_000824	Homo sapiens glycine receptor, beta (GLRB), mRNA.			GCCTCCCCCTGCGAAACCTGTTATTCCAACAGCA GCAAAGCGAATTGATC
310.4768	675.97266	569.45593	RECQL	RecQ1; RECQL1	NM_002907	Homo sapiens RecQ protein-like (DNA helicase Q1-like) (RECQL), transcript variant 1, mRNA.			ATCAAGGGATGTCCAATCTTTTGGCTTCCCTGAG CCAGCGAATTGTGCAC
97.55867	191.01428	166.51845	GNB1L	FKSG1; GY2; DGCRK3; WDR14; KIAA1645; WDVCF	NM_053004	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1-like (GNB1L), mRNA.			TTTCCTTTTGTGGAGTGCCTCATCACAGGACGGT GACTCTGGGGGCCAGC
10.28856	267.38928	140.40182	SLC35F3		XM_001132419	PREDICTED: Homo sapiens solute carrier family 35, member F3 (SLC35F3), mRNA.			ATGGTGCATTCTGTAACCATGGAGTCTTCTGTTT CCTGGGGGAAAGGGGC
344.85596	471.82263	441.62262	STARD3NL	MGC3251; MENTHO	NM_032016	Homo sapiens STARD3 N-terminal like (STARD3NL), mRNA.	GATGCACAGAGGACACA GAAGGACTTGGCAGCAG GGTGATGACCTGATCA	ILMN_1684943	GAGTCTCCCTGTCGACAGTAAAGTTGAAATGGT GACGTCCACTGCTGGCT
15.44992	85.425766	55.37774	CSNK1G3		NM_004384	Homo sapiens casein kinase 1, gamma 3 (CSNK1G3), transcript variant 1, mRNA.	GCCTCGCCCCAACACTG TCCTTCCCTGCCACTTCA ACCCCCAGCTAATAA	ILMN_1763749	GGACTCCCAGCAGGCAAATCCCCACCATTTGAG AGCTCACCTTGCAGCAG
993.98096	1341.0894	1257.6477	API5	AAC-11; AAC11; API5L1	NM_006595	Homo sapiens apoptosis inhibitor 5 (API5), mRNA.	TGCCACCAGACCAACAC CCCCAGACTTCCCCACC TTCAGCCACCATCAGA	ILMN_1784477	GACCAGCTAATCTGGACCTCAGAGATAGATCAG CCAGTGGCCCAAAGCCA
173.95178	231.68927	217.56427	PRDM4	MGC45046; PFM1	NM_012406	Homo sapiens PR domain containing 4 (PRDM4), mRNA.			TGCTCAAGGCACAACCTCTGGGCTGGAGTAGAG GACTCTGGTGGGAAGGT
990.80176	1176.9976	1134.9226	MRFAP1L1	PP784; MGC9651	NM_203462	Homo sapiens Morf4 family associated protein 1-like 1 (MRFAP1L1), transcript variant 2, mRNA.			TCAGGGCCTGGAAAGTCTCTTCCAGTTCATCAG GGTAGTAGACCTGTCAG
5.8615985	86.02163	47.72538	DACH1	DACH; FLJ10138	NM_080760	Homo sapiens dachshund homolog 1 (Drosophila) (DACH1), transcript variant 2, mRNA.	CAGTGACCACACAGCTC CTCCATGCCTGACCAAC AGGCCCAGCTTTCCCT	ILMN_1694950	GGTAGCCTAGTTATTTGAGCCTGGTTTCAATGTG AGAACCACGTTTACTG
116.47678	302.63095	248.1101	RNF219	DKFZp686N15250; DKFZp686O03173; DKFZp686A01276; FLJ13449; FLJ25774	NM_024546	Homo sapiens ring finger protein 219 (RNF219), mRNA.	TGCCCCAAGCTCCAGCG GTATTCTATCAGCCCATC CTCCTGGAAAGCCTG	ILMN_1796950	GGTTTGAAAGAGCTCATCGCCAAGTTCTTGATCC ACTTGCATTCCAGGGG
238.72263	278.53094	270.3643	ZDHHC5	DKFZP586K0524; ZNF375; KIAA1748	NM_015457	Homo sapiens zinc finger, DHHC-type containing 5 (ZDHHC5), mRNA.			CAGCCCACCTCACTATGGTGCTGGGTAGAGGGG ATACCTGGGTTCTAACC
32.233047	90.307846	74.51542	M160	CD163B	NM_174941	Homo sapiens scavenger receptor cysteine-rich type 1 protein M160 (M160), mRNA.			GATGCTAGCGACACATCGCTGTTGGGAGTTCTT CCTGCCTCTGAAGCCAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
153.40594	190.4851	182.12262	LSP1	WP34; pp52	NM_001013255	Homo sapiens lymphocyte-specific protein 1 (LSP1), transcript variant 4, mRNA.	CCCATTTCAGACAGCAAC ATGTAGAAGATGTTCAGC GTGCAGGGCTTGCT	ILMN_1773388	TCCTGCAAGGATATTGTGGCTGGAGACATGAGC AAGAAAAGCCTCTGGGA
29.96322	82.90193	69.49157	SLC25A19	TPC; MCPHA; DNC; MUP1	NM_021734	Homo sapiens solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19 (SLC25A19), nuclear gene encoding mitochondrial protein, mRNA.			ACACTCCTGGTCTGGATGGGGCTGCTGCTTGAG TGCAGAGGGCTGCGGTA
6.5091376	66.356186	49.971592	RSAD2	vig1; cig33; 2510004L01Rik; cig5	NM_080657	Homo sapiens radical S-adenosyl methionine domain containing 2 (RSAD2), mRNA.			CGCTGGAACCTTGGGCAAGGAAGAATGTGAGCA AGAGTAGAGAGAGTGCC
143.5893	396.08093	317.9268	HDHD1A	DXF68S1E; GS1; FAM16AX	NM_012080	Homo sapiens haloacid dehalogenase-like hydrolase domain containing 1A (HDHD1A), mRNA.	GGGTCTTGGGAGCTTCT GTCCCTTGCCCTCTCTTG TCCAGGTCAGCATCT	ILMN_1670453	GCTCAGCCCTTCCTAGGGGCCTCTGCCCTTTGA TGTCCTTGAGCTACTCT
14.668591	175.89345	107.243546	SEMA7A	MGC126692; MGC126696; H-SEMA-K1; JMH; H-Sema-L; CD108; CDw108; SEMAK1; H-Sema K1; SEMAL	NM_003612	Homo sapiens semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group) (SEMA7A), mRNA.			CCTGGGTCCCACAGGACAGCCGCCTTGCATGTT TATTGAAGGATGTTTGC
910.0643	1386.106	1269.2059	KPNA3	IPOA4; SRP4; hSRP1; SRP1gamma	NM_002267	Homo sapiens karyopherin alpha 3 (importin alpha 4) (KPNA3), mRNA.			CCCTTAAAAGTCCAAATCTTCTTGATATTGTGAAC CGTACCCCTTCCAGT
46.393356	91.756096	79.3021	TUBA3E		NM_207312	Homo sapiens tubulin, alpha 3e (TUBA3E), mRNA.			GGTCCCCAAAGACGTCAATGCGGCCATCGCCAC CATCAAGACCAAGCGCA
246.66011	372.00177	342.20593	EEF2K	MGC45041; HSU93850; eEF-2K	NM_013302	Homo sapiens eukaryotic elongation factor-2 kinase (EEF2K), mRNA.	AGCTGGAGAGCTACAAC CTCAGGGCACAGTGGGA AAGGATGAGCAGGCCC	ILMN_1670975	GGCTTTGCAGGCCATATAGCCTCTGCTGCAAAT GCTCAGCCCTGCTGTTG
93.69795	231.24762	192.03928	POLR3F	MGC13517; RPC6; RPC39	NM_006466	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa (POLR3F), mRNA.	CCTTTGTCAGACCATAAG AGTTTCTCCAAAAGTGGT CAGTTTGGCTGGGC	ILMN_1807554	GCCATGTGAAAGGGAGAAGACAAACATCCACGA ACCAGGAAGTGGGTCCT
337.0893	487.28094	451.56845	RBMS2	SCR3	NM_002898	Homo sapiens RNA binding motif, single stranded interacting protein 2 (RBMS2), mRNA.			CAGAAAGGTGTGGTGCTGGAACATCGATGAAGG AGCCCTACTTACTGAGC
109.42679	150.0893	141.96011	C2ORF43	FLJ21820	NM_021925	Homo sapiens chromosome 2 open reading frame 43 (C2orf43), mRNA.	TTCACCGTCTCACATTAG ACAGGCCAATGCATCCC TTAGGAGCTGCCCCA	ILMN_1654632	GGGAAAAGCCAAGCTCCAGACAAGGAGTGCTGT TAGCCCAAGGGGAAGAG
306.97263	786.57263	652.2101	CHEK1	CHK1	NM_001274	Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA.			GATCGGACCATCGGCTCTGGGGAATCCTGGTGA ATATAGTGCTGCTATGT
54.894432	131.88928	112.2518	PGGT1B	BGGI; GGTI	NM_005023	Homo sapiens protein geranylgeranyltransferase type I, beta subunit (PGGT1B), mRNA.			GTAGGGGGATTTGCCAAGTGGCCAGACAGTCAT CCAGATGCTTTGCATGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
471.8643	617.56433	589.9226	RAP2A	KREV; RAP2; RbBP-30; K-REV	NM_021033	Homo sapiens RAP2A, member of RAS oncogene family (RAP2A), mRNA.			TATCAGCAGTCTTGTGTTAGCACTGGGTAAGCTT TAATTGTCCCTTAGCC
347.93094	412.13513	403.28094	CDK5RAP1	HSPC167; CDK5RAP1.3; C20orf34; CGI-05; CDK5RAP1.4; C42	NM_016408	Homo sapiens CDK5 regulatory subunit associated protein 1 (CDK5RAP1), transcript variant 1, mRNA.			GGACCACTCTGAGGGACTCTTCTGCATATTGCT GACCTGAGAGGATGGCC
97.09683	317.51843	250.49344	OSBPL6	ORP6; MGC59642; FLJ36583	NM_032523	Homo sapiens oxysterol binding protein-like 6 (OSBPL6), transcript variant 1, mRNA.	CTGTGAACTTCATGGCA GAAACATACCTGCTGTTA TTGAACAACCCCTGG	ILMN_1668795	CCACACGATTGTTCCACTGTCTGGAAGCACCATC CCCTATCGCAGGACTC
289.5893	434.2976	401.78094	TMEM138	HSPC196	NM_016464	Homo sapiens transmembrane protein 138 (TMEM138), mRNA.	GGGCTCACACAAAACAT AACGAAGAGACTGGAGA CAATGTGGGCCCTCTG	ILMN_1761781	GGACAGAAGGACCTCCCAGCCCCCAAAGGATCT CCCAGTGACCAAAGGAT
1053.0892	1227.2976	1196.606	CCM2	MGC74868; MGC4067; MGC4607; C7orf22; PP10187	NM_001029835	Homo sapiens cerebral cavernous malformation 2 (CCM2), transcript variant 1, mRNA.			AGAGCCAGTCCTGTCGGCTGGGCCCTTGGACG GCTGTCAGTTTTGCACAT
44.263145	59.016945	55.715096	MOSPD2	MGC26706	NM_152581	Homo sapiens motile sperm domain containing 2 (MOSPD2), mRNA.			GTACCCACCCGGTATTCCTAAAATCCTAAAAAGA TACACCTTGCAGTAGC
468.0476	620.3809	589.4976	CS		NM_004077	Homo sapiens citrate synthase (CS), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	GGCTGTTCAGCAGAGAA ACCCATGTCCTCTCTCCA TAGGGCCTGTTTTAC	ILMN_1683562	CCTCAGGCAGAGGATGTTCTGGACCTCCCCCTC TTGGTCCCTACTAGAGA
339.63928	504.99762	467.48096	PIGK	MGC22559; GPI8	NM_005482	Homo sapiens phosphatidylinositol glycan anchor biosynthesis, class K (PIGK), mRNA.			GCTGAAAGACTGGCATCCTCCTGGGGGCTTTAT TCTGGGATTATGGGCAC
59.74224	119.22433	91.96892	TCP1	TCP-1-alpha; CCT1; D6S230E; CCTa; CCT-alpha	NM_030752	Homo sapiens t-complex 1 (TCP1), transcript variant 1, mRNA.			GCCCAAGGCTATAGCCCCTCCTTCAATATTGACC TAACGGGGGAGAAAAG
213.33095	573.9851	480.01013	C5ORF30	FLJ25291	NM_033211	Homo sapiens chromosome 5 open reading frame 30 (C5orf30), mRNA.	CGGAGCACGGAAGCACA CACAAGCTCTTTATGAAT TCTGCTCTCCATCAG	ILMN_1810593	AGGAAACACAACTGGTTACCTATGAGACCTGTTC TGTCCGTGTGCCTACG
761.8726	1867.8477	1582.4226	RBMS1	MGC3331; MSSP-1; MSSP; YC1; SCR2; MSSP-3; MGC15146; MSSP-2	NM_002897	Homo sapiens RNA binding motif, single stranded interacting protein 1 (RBMS1), transcript variant 3, mRNA.			TAGTCCGACTTCACCCATGGTGTTCTGTGCTTGC AGTGCGAGTGTTGCTG
555.83093	695.68933	657.5268	LARP7	MGC104360; DKFZP564K112; HDCMA18P	NM_015454	Homo sapiens La ribonucleoprotein domain family, member 7 (LARP7), transcript variant 2, mRNA.			GCACAGAGCCTCTACCTGGCAGGAAACAAGTCC GGGATACTTTGGCAGCA
45.755493	104.51428	86.25282	ALG13	YGL047W; GLT28D1; MDS031	NM_018466	Homo sapiens asparagine-linked glycosylation 13 homolog (S. cerevisiae) (ALG13), mRNA.			AGGACTTACTATTGTTTTTTAAGGATCTCCTCTCA CAGTGGTAATGAAAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
270.4893	984.07263	693.7643	CCDC99	FLJ20364	NM_017785	Homo sapiens coiled-coil domain containing 99 (CCDC99), mRNA.	CCAGCCCTCGACTCTTA GTAAATTTGAGAGTTTAT ATGGAACACAAACCC	ILMN_1769099	GCTTGACTCTAACCTGGAGAGCTTCTTAAGTGAT GCCCCTTCATGGAGCT
952.28094	1644.1393	1439.1519	C20ORF20	MRG15BP; MRGBP; FLJ10914; Eaf7	NM_018270	Homo sapiens chromosome 20 open reading frame 20 (C20orf20), mRNA.	GTCCTCAGTTCCCGTCC ACCCTTCAACCAGTGGC TCCTGGGAGACTTTTC	ILMN_1679646	GGCCGCCCCAGTGCTGATGGAGATGCCACTTTC GTGTGACTGCGAACATT
254.10596	288.93097	279.15594	PAPD1	mtPAP; RP11-305E6.3; FLJ10486	NM_018109	Homo sapiens PAP associated domain containing 1 (PAPD1), mRNA.			CTCATTGGCCCCCTTAACCTGGTCTGAAGTTCTG GGATGTTTTCAGTTTG
965.58093	1133.6643	1090.3351	KDELC2	MGC33424	NM_153705	Homo sapiens KDEL (Lys-Asp-Glu-Leu) containing 2 (KDELC2), mRNA.			CAGCAGCCTTAATCTACATAATTCTTCATCTCGC CAATTCAGCCGCAGCC
672.7476	1111.356	971.08093	TBRG4	FASTKD4; CPR2; KIAA0948	NM_199122	Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 3, mRNA.	GCTTATGCAAGTGACGG TGCTGCTCTTGTTCCACC CCCACCCAGATGGTC	ILMN_1683316	CTACCTCAAGGACAAGATGCGCAAAGCGGTGGC TGAGGAGCTGGCCAAGT
454.5226	740.58093	653.48096	TMEM167	MGC23909; DKFZp686I1152; FLJ30508	NM_174909	Homo sapiens transmembrane protein 167 (TMEM167), mRNA.			TGCCAGAATGTAGTTGCCATCAGATTTGATTGTG AACAAGGACTGACTGC
45.112694	106.09761	85.70657	ZNF200	MGC45293	NM_198088	Homo sapiens zinc finger protein 200 (ZNF200), transcript variant 3, mRNA.	GCAGGGGTGTCTCGGTT TGCATTTCTGTTGGAATG ATCCGAACTGGACTC	ILMN_1736619	GGCCAGCGGTGCCTTTACGGACTGATCGTGTGG TGCGATTTAGGGATTCT
497.13513	868.0393	748.63513	VKORC1L1	DKFZp762H0113	NM_173517	Homo sapiens vitamin K epoxide reductase complex, subunit 1-like 1 (VKORC1L1), mRNA.			TGTAGCCCTAGCCCCCTGCCCTCAATTGTAAAGT GAGCAACCATTGCTAG
154.14345	218.06845	199.94762	ARHGAP30	FLJ00267; RP11-544M22.6; FLJ44128	NM_001025598	Homo sapiens Rho GTPase activating protein 30 (ARHGAP30), transcript variant 1, mRNA.			CAGCTCCCCACCCTCTGCCTCCAGTCACCATGT GCAAGAGAGGTCCTGTA
40.46819	83.69798	71.10375	HS2ST1	FLJ11317; MGC131986; dJ604K5.2; KIAA0448	NM_012262	Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), mRNA.			ACTTGCAGTGGCTGAACAAAGAGCATGGCTTGA GAATCAAAGGGATCTGC
3017.3975	4302.481	3910.281	MATR3	DKFZp686K23100; DKFZp686K0542; KIAA0723; MGC9105	NM_199189	Homo sapiens matrin 3 (MATR3), transcript variant 1, mRNA.	GCAACTTACACTGAGGG CATGTATCCTAGCATCTG TGTGGAAGCCACAGA	ILMN_1792383	GGCCATAATCCTAGATGCACGCTTCTAATTCATG TACCTGCACATGTGAC
121.44762	154.91428	144.69762	ZNF193	ZSCAN9; PRD51	NM_006299	Homo sapiens zinc finger protein 193 (ZNF193), mRNA.			ACTGCAACCTCATTCGCCATCAGAAGATCCACAC AGTGGCTGAGCTGGTC
185.98929	298.1601	262.03094	RNF126	MGC14317; MGC1022; FLJ20552	NM_194460	Homo sapiens ring finger protein 126 (RNF126), mRNA.	CATGGAGCTCAAGATGT CTTGTGTCTGTGTGGCT AGATGGCCTCTGCTTG	ILMN_1739876	CAACTCGTGAGCCCACGTCGGCCGTCGGGAAAG CACGGGGCCTTTCCCAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
71.19125	125.86012	106.67262	TSPAN6	T245; TSPAN-6; TM4SF6	NM_003270	Homo sapiens tetraspanin 6 (TSPAN6), mRNA.	TGTGGTGGTGCCATGCA ATCCCCTTTTGGTAGAAT TGCCACAAACAAGGC	ILMN_1793549	CTGCTGGAATGGTTGTTGTTTTCCACTGAGAAAG CTAAGCCCTACATTTC
69.435295	84.74206	79.401505	HSD3B7	PFIC4	NM_025193	Homo sapiens hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7 (HSD3B7), mRNA.	GTGACTTCACTTTTCTAA GACCCCTCAGCGTTCAG CAGCCCACAGCTCTG	ILMN_1767649	TCCTCTGTCCTCTCATCCCAGTCCTGATGGCCG CTTGGTGAGTGTCTGGT
240.73096	342.93927	311.48096	RBM45	MGC42237; FLJ44612; DRB1	NM_152945	Homo sapiens RNA binding motif protein 45 (RBM45), mRNA.	AAGATGCTGAGTGTCTG CACTGCTCCACTTGTCC CCCCGCTCTCTCCTCA	ILMN_1697800	CCTGATAGTCTGTGTACAGCATTGTTTTGTCTGG GAAGCAGGGATTGCTG
350.00595	445.98096	417.4726	UBE2G1	UBE2G; UBC7; E217K	NM_003342	Homo sapiens ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast) (UBE2G1), mRNA.	GATGTATGGTATCTCCCT TTGCCAAGCCATCCTGG ATGAAACCAAAGGAG	ILMN_1681783	TTGATATGCCCACTCACCCTCGACGAATCTGCCC GCTTTGGGCTGTGGTG
41.58118	93.91014	76.44257	FBXO11	FLJ12673; PRMT9; UG063H01; MGC44383; FBX11; VIT1	NM_018693	Homo sapiens F-box protein 11 (FBXO11), transcript variant 2, mRNA.	TCCCCCCAGTCATATCTC ATGATTTCCACAGTTGTT GTATTGGTGTGGAG	ILMN_1808636	CAATACTTTTCCTTTTGTAGCCACTTTGAGTCTG CAGTTGTCAGTAAGCC
647.68933	881.8893	810.01843	DPH2	DPH2L2	NM_001384	Homo sapiens DPH2 homolog (S. cerevisiae) (DPH2), transcript variant 1, mRNA.			CAAGTGTTCAGACAGCCACATGAGGGGACAGTG CAGCTACAGGATATGCC
37.06746	1408.2059	489.7976	PLEK2		NM_016445	Homo sapiens pleckstrin 2 (PLEK2), mRNA.	CAGCTGGGCAGATTTGG CCTGCAGGGTATAGTTG GCTGACCTCAATCTAG	ILMN_1726930	CATTCAGGCCAGCAGCAAGGCTGAGCGAGCCGA GTGGATTGAAGCTATCA
117.32262	185.55594	162.64761	SMYD4	KIAA1936; ZMYND21	NM_052928	Homo sapiens SET and MYND domain containing 4 (SMYD4), mRNA.	AAAAAATCAGCAAAGAAG AAAAGACTCCTGGCTGT GTGAAAATTAAAAAA	ILMN_1652104	GCCTGCTTACCTCCAGAGACACACCGTTCCACTT ACAGTATCTAGCTTCC
38.335567	223.62262	135.40594	WWC1	KIBRA; FLJ23369; FLJ10865; KIAA0869	NM_015238	Homo sapiens WW and C2 domain containing 1 (WWC1), mRNA.	CTAATAAAGTGGGCGCG AGAGGAGGCTGCTGTGT GTTTCCTGCCCCAGCC	ILMN_1685037	CTTCTTGAGCTGTGACGTGTTTTTATGTGGCTGC CCAACGTGGAGCGGGC
86.901825	151.98929	129.13095	METTL4	MGC117235; FLJ23017; HsT661	NM_022840	Homo sapiens methyltransferase like 4 (METTL4), mRNA.	GGCCTTTCGTCATGCCA CAAGCCTCATATATCATG ACCGAACTCATGCTG	ILMN_1780146	CTTTTGCAGTCAATCCCCTGCTCCTATCCTTGGC CCCTGGCAAACACTGG
134.15178	270.0851	219.89761	ZMYM1	MYM; RP11-181E22.4; FLJ23151; FLJ43753	NM_024772	Homo sapiens zinc finger, MYM-type 1 (ZMYM1), mRNA.			GCCATCTATAAGGATTGTGCCAGTTTACAGTCCC ACCCACAATGCATGAG
221.30594	338.0351	301.9268	DPP8	FLJ20283; MSTP141; MGC26191; FLJ14920; DPRP1; DP8	NM_130434	Homo sapiens dipeptidyl-peptidase 8 (DPP8), transcript variant 1, mRNA.	GGACACCGACTTGGGAG GACAGGTCCTGAATGTC CTTTCTCCAGTGTAAC	ILMN_1759252	TGGGTCACCCTGACCAGAATGAACAGGGCTATT ACTTAGGATCTGTGGCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
118.35178	188.68929	164.88512	C14ORF172	TRM61; FLJ40452; GCD14; Gcd14p	NM_152307	Homo sapiens chromosome 14 open reading frame 172 (C14orf172), mRNA.	ACTCCAGCCCGCAGCAC ATTTCCGCTGTCCGTCA GTAATTGTGTCCTCTC	ILMN_1722056	TCTGACAGCCTCAAGGAAGGAGCAGTGCCTGTG TCAGCCATGGGGCCCTT
1416.2893	2033.2517	1844.6643	NUDT5	hYSAH1; YSA1H	NM_014142	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 5 (NUDT5), mRNA.	GATATGGTGCCCTGTGT ATCCCAGAGATGCTAGA AAACTGTTCTTTGCTC	ILMN_1676448	GCCGAAAACGCAAGGCCGAAGCCAAAGCCAGG GGATGGAGAGTTTGTGGA
44.34806	82.63162	68.80901	XKR6	XRG6; C8orf7; C8orf21	NM_173683	Homo sapiens XK, Kell blood group complex subunit-related family, member 6 (XKR6), transcript variant 2, mRNA.			CTGTGTCGCCTCTCCGTGTGGATCTGGCAGTCG GTCATCCACCTGCTGCA
97.51536	179.03513	144.40594	XRCC1	RCC	NM_006297	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1), mRNA.	GGAGGCTCTGGCTCAAA CAGCAATAGGGTCTTCC TCACTGACCTTGGAGG	ILMN_1790317	ATCCCAGCTTTGAGGAGGCCCTGATGGACAACC CCTCCCTGGCATTCGTT
1692.406	1942.8394	1862.7976	CCDC56	HSPC009	NM_001040431	Homo sapiens coiled-coil domain containing 56 (CCDC56), mRNA.	TGTGCTAGGTAGGTGAA CCAGAAACCACCCTCGC CACCAAGACTCGCTCC	ILMN_1732187	CCCCTTCACCTTCCAGGGACGCAGTTGTTACGA GGTTAGACGTGGCAGCT
142.12262	268.1726	221.7768	HIRIP3		NM_003609	Homo sapiens HIRA interacting protein 3 (HIRIP3), mRNA.			GCAGCTCCCAAGGACACAAGCTGTTGGGATGCT ACTTCTCAGCTTCACGC
1364.006	2881.1726	2254.156	SDF2L1		NM_022044	Homo sapiens stromal cell-derived factor 2-like 1 (SDF2L1), mRNA.	GGAGAACCAGCCCAGTA ACATTGTGTCTCTTCAAA CTGAGCCATCAAGGC	ILMN_1749218	GCAGGGCCACTCTTGGCAGAGACTTTGGGTTTG TAGGGGTCCTCAAGTGC
19.714184	378.05597	150.90594	CEP170	FAM68A; KAB; KIAA0470	NM_001042404	Homo sapiens centrosomal protein 170kDa (CEP170), transcript variant beta, mRNA.	GCCAGACACAGAAGGAA AAATACCAGATGATCCCA CTTATATGAGGTACC	ILMN_1771494	GGACTGCTCATCGAGAAGAGATAGCCAGGATCA GCCAAGATCTTGCTCTC
388.98096	486.93927	454.24762	ARL5A	ARFLP5; ARL5	NM_001037174	Homo sapiens ADP-ribosylation factor-like 5A (ARL5A), transcript variant 3, mRNA.	ACGCTCGTGAGCGTGAG AAGCCATAAGAGAGAGA CCGAATTCTGTGGCTC	ILMN_1666076	TTAACACGATATCAGCACATTCCCTTGTCATCAT CAAGGTGTTGGCTCAG
450.90594	703.90594	624.5226	H3F3B	H3F3A; H3.3B	NM_005324	Homo sapiens H3 histone, family 3B (H3.3B) (H3F3B), mRNA.	CTTCCTCGGGCTGGGCC TTATCATCCATCACAGGA GTCAGAAAGGGCTCC	ILMN_1661266	GAGCACTCAACCCAGAAGGCGAAGATAGCTTTT GGTTGTAGGCGGCTTCC
176.53094	179.91013	181.71844	SRPX2	SRPUL; RESDX	NM_014467	Homo sapiens sushi-repeat-containing protein, X-linked 2 (SRPX2), mRNA.	CCGCGTATAGCTTCTGG CCTGGGCTTGGCCTGGA TTGTTGGACGAGTTCT	ILMN_1751956	CCAGCGTCGGGAGCAAAGGGACATATGCGAGTG AACTTGAGCCAGGGCAT
780.3518	1177.9976	1046.0559	EXOSC10	PMSCL2; PM-Scl; PM/Scl-100; PMSCL; RRP6; p4; Rrp6p; p2; p3	NM_001001998	Homo sapiens exosome component 10 (EXOSC10), transcript variant 1, mRNA.	AGGAGAGAGGTTTGAGT TCTGGGTATCCTCCCTTT CTGTAACAGCCTCAA	ILMN_1685472	GACAGAGGCTTCAGGTACAACTGGCCACAGAGA TAGTCCTGGAAGACACG
50.594986	121.82262	92.48931	TRMT6	GCD10; MGC5029; Gcd10p; CGI-09	NM_015939	Homo sapiens tRNA methyltransferase 6 homolog (S. cerevisiae) (TRMT6), mRNA.			CAACGTAACTAAAACATGGCGGGTACCGAAAGG AGGGCAATTCATGGAAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
537.4351	1787.8643	1237.5393	KIAA1754	bA127L20.2; RP11-127L20.4; DANGER; bA127L20	NM_033397	Homo sapiens KIAA1754 (KIAA1754), mRNA.	GGGAGAGATCAGAGGTC ATACTGTGAAGCACCTTT GGATAAACGGCAGGG	ILMN_1771012	GCCTCCAGAAGCCAAAACCATGCCTGGATCTCC CATAGCTTCTCCTTTGC
23.469658	68.873795	49.915268	HMG2L1	HMGBCG; THC211630	NM_014250	Homo sapiens high-mobility group protein 2-like 1 (HMG2L1), transcript variant 2, mRNA.	GGCGTCAAGTACATCGT CCAAATCCCTGTCTCTTC AGCTTCTCTGATGCT	ILMN_1686516	GGGGGGTGAAGCTGTCAATGCCACCAGTTGGAC CTCCATACATTCTGAGC
504.3601	644.6809	592.94763	GCN1L1	GCN1; GCN1L; KIAA0219	NM_006836	Homo sapiens GCN1 general control of amino-acid synthesis 1-like 1 (yeast) (GCN1L1), mRNA.			CCCTGTCAGATGAAAATGATTCACAGCTCTGGCA GTTCCCAAGTCTGGGG
156.00595	270.13095	227.76012	APOO	MGC4825; My025; FAM121B	NM_024122	Homo sapiens apolipoprotein O (APOO), mRNA.	TGCCTGTGTTTGTGTTG GTGGGGGTAAGGGGCA GTGGTGTGAAGGGACCA	ILMN_1680264	CCCTCTATTATCCACAACAAGCCATCGTGTTTGC CCAGGTCAGTGGGGAG
620.83093	1338.9644	1058.406	RAD21	KIAA0078; hHR21; NXP1; FLJ40596; HRAD21; FLJ25655; SCC1; HR21; MCD1	NM_006265	Homo sapiens RAD21 homolog (S. pombe) (RAD21), mRNA.	TTGCAGTGGTGGATTGA GAAGTCCAGTTTGATTTC ATTGGGACAGACTGC	ILMN_1700202	GCAGCTTTATATTCAATATGATGTGCCTGTAAAC CAAGGAGTTTTCCCCG
1657.0393	1833.5559	1773.5977	DPM1	MPDS; CDGIE	NM_003859	Homo sapiens dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1), mRNA.	CTTTAGGACTGAAAGCTA GGCGTCCTCTCCCACAA AAAAGTCCTGCCCTC	ILMN_1763144	CTAAAGGCTACGTCTTCCAGATGGAGATGATTGT TCGGGCAAGACAGTTG
163.45595	351.30176	280.7393	NUDT15	FLJ10956; RP11-90M2.1; MGC104352; MTH2	NM_018283	Homo sapiens nudix (nucleoside diphosphate linked moiety X)-type motif 15 (NUDT15), mRNA.	GGATCCACTAGGGTGAT ATGGCTTCAGCAACCAG GAGGGATTGACTGAGA	ILMN_1665775	AGGCTGAATGCAAAAGCAGATACAAGATTCCAGC TTTCGTCTGTCATCAG
193.20595	353.8976	279.59344	OTUD6B	CGI-77	NM_016023	Homo sapiens OTU domain containing 6B (OTUD6B), mRNA.			GGCCAATGTGGTTATGAACAAGATTTGTATGGTC AGCTTCTGTTCTTTCC
548.8976	694.7226	634.7101	AOF2	LSD1; KDM1; KIAA0601; BHC110; RP1-184J9.1	NM_015013	Homo sapiens amine oxidase (flavin containing) domain 2 (AOF2), transcript variant 2, mRNA.	TCATCGGGAGGATCGTC ATTGGCCAGTACTCTTCA GGCCCCTCTGAGACC	ILMN_1657760	GGAGCTTGCCTCCTTTGAATGACCTAGAGCACA GGGAGGAACTTGTCCAT
665.48926	1023.98926	874.3976	EXOSC10	PMSCL2; PM-Scl; PM/Scl-100; PMSCL; RRP6; p4; Rrp6p; p2; p3	NM_002685	Homo sapiens exosome component 10 (EXOSC10), transcript variant 2, mRNA.			CAGTTTGATCCAAATAAACAGACCCCGTCTGGCA AGAAATGCATTGCAGC
121.860115	879.07263	412.32263	PMAIP1	APR; NOXA	NM_021127	Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA.	GGGTACTTGTAGGAATA CAATGAGGAGCTTGAAT GCCACCTTCTGACATG	ILMN_1696079	CAGCCTAGAGGCAGCTATTTTACCATCTGGTATT TATGGTCTAATTTGTA
276.01428	792.90594	541.16846	PTPRF	LAR	NM_130440	Homo sapiens protein tyrosine phosphatase, receptor type, F (PTPRF), transcript variant 2, mRNA.			ATCAGTCCTTATTATCCCAGCTTGCTGAGGGGCA GGGAGAGCGCCTCTTC
93.568535	127.922615	112.83511	RCE1	FACE2; RCE1B; RCE1A	NM_001032279	Homo sapiens RCE1 homolog, prenyl protein peptidase (S. cerevisiae) (RCE1), transcript variant 2, mRNA.	TCGTCCATGCCAAAGTG TGCGGCCCTTCCTGACA TCACCACAGTCTGAGC	ILMN_1786843	ATTACATGGGTTTCCCAGCTGTTTGCGCGGCCTT GGAGCACCCACAGAGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
85.46019	116.75595	103.40178	C18ORF19	HsT2329; MGC24180	NM_152352	Homo sapiens chromosome 18 open reading frame 19 (C18orf19), mRNA.			TTCATTCAGGAGGGTTTTTTCATCCAGTGCCACA GCTCAGGGAACTCCGG
16.499748	120.60178	56.10531	SLC6A15	FLJ10316; DKFZp761I0921; NTT73; hv7-3; MGC87066; V7-3	NM_182767	Homo sapiens solute carrier family 6, member 15 (SLC6A15), transcript variant 1, mRNA.	TGCTGCTCTCGGGAAGG ACGAAAGTGACCTGCAA GGAGAGAAATGCAACC	ILMN_1719143	CAGTGTGAAGTAAGTTCTCATCCAACATTTCTCC TGGCCATCCATTCTCC
173.81429	192.27261	190.23929	PHF20L1	CGI-72; MGC64923	NM_198513	Homo sapiens PHD finger protein 20-like 1 (PHF20L1), transcript variant 3, mRNA.	TGATGTGGCTGTTGGGA AGATGGTGGGGTTTGTT TGCCAGCTTGGAGTCC	ILMN_1703105	ATGCACATTAAAGCCATGCCCGAGGATGCTAAG GGGCAGGATTGGATAGC
738.6893	1103.9143	942.0226	ZDHHC6	ZNF376; FLJ21952	NM_022494	Homo sapiens zinc finger, DHHC-type containing 6 (ZDHHC6), mRNA.			GCCTACTCTGGTTAAGATGTTCTTTTCCTCAAAG GTGCCCTAGTGCCATG
17.460238	84.81557	48.62852	TSPAN13	FLJ22934; NET-6; TM4SF13	NM_014399	Homo sapiens tetraspanin 13 (TSPAN13), mRNA.			TACCTTCAGCCTCCATCAGAATGGAACGAGTTTT GAGTAATCAGGAAGTA
6.671953	86.99765	35.163696	LRRC4C	KIAA1580; NGL1; NGL-1	NM_020929	Homo sapiens leucine rich repeat containing 4C (LRRC4C), mRNA.			TTACGGGAGACACACCCATGGAAAGCCACCTGC CCATGCCTGCTATCGAG
327.0893	588.98096	464.68097	SLK	KIAA0204; MGC133067; bA16H23.1; STK2; se20-9	NM_014720	Homo sapiens STE20-like kinase (yeast) (SLK), mRNA.	GCACACGTGCAGCCTAT ATGGGAAAACCTTCCCTC TGTACCTGCCTCAAA	ILMN_1718633	AGCATAATTTACTTGGACAACTTCGTAGGTAGCC TTAACTTCTGGCCAAG
106.15178	236.34763	171.78094	Sep-10	FLJ11619	NM_144710	Homo sapiens septin 10 (SEPT10), transcript variant 1, mRNA.	CGCCTGGCCTATTGAAG GTTTTTAATCTTCAGAGT TTCGACTTTATCAAC	ILMN_1658713	GCACTGACTTGACCCCACAAGTGGAAAATTCCC CACCCGACACCTTTGCT
59.718147	145.43512	97.835144	EFNB3	EPLG8; EFL6; LERK8	NM_001406	Homo sapiens ephrin-B3 (EFNB3), mRNA.			GGTTGGCCACCTCAATCACCAGCCAAGATGGTT GCTTTGTCCACCAGAGG
232.24344	325.3018	285.96844	RCE1	FACE2; RCE1B; RCE1A	NM_001032279	Homo sapiens RCE1 homolog, prenyl protein peptidase (S. cerevisiae) (RCE1), transcript variant 2, mRNA.			CAGGTCCCAGGAGCCACACACTCCCTTCCTCAC TTTGGACTGCTGCTTCT
682.65594	709.8518	700.2143	PPP1R7	SDS22	NM_002712	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 7 (PPP1R7), mRNA.	ACTTGCTTTGGAATTTTC AAGTCAAAGTCCCAACC CTTTGCCTCTCCCCC	ILMN_1766652	GAGTTCTGGATGAACGACAATCTCCTTGAGAGCT GGAGCGACCTCGACGA
35.882004	90.96088	62.20516	PAIP1	MGC12360	NM_182789	Homo sapiens poly(A) binding protein interacting protein 1 (PAIP1), transcript variant 2, mRNA.	CCTTAGTGGCCAGAGAC TGACTTCAAGGTTTTATT CCAGAGACTCCAGAG	ILMN_1808157	GGGGGGAAAAACCCAACTTGGTGAACTCCCAGC TAAACAACCAAGACTTC
198.60178	397.93512	298.51428	MDC1	NFBD1; DKFZp781A0122; KIAA0170	NM_014641	Homo sapiens mediator of DNA damage checkpoint 1 (MDC1), mRNA.	GGTATGTGAAGCAAAAG GGGCAGGTGCACACACC TCCACAGTGACCTCTG	ILMN_1655720	TGGGGTCAGGAACTTGAAGGGATGCTTGGAGTG AGTAGATTTGAGGGTCC
80.50197	135.68095	109.73095	NVL		NM_206840	Homo sapiens nuclear VCP-like (NVL), transcript variant 2, mRNA.	GCTGGGCACTATGCTAA GCACTTTGGGAGCAAGA ACCTCCTACCTTCCAG	ILMN_1690887	CCATCAAGCCGGCAGAGAATCCCCCACACGCTC TGAAGGACCCACTTTCA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
60.22267	163.00179	107.30179	FAM91A1	DKFZp666B104; FLJ23790	NM_144963	Homo sapiens family with sequence similarity 91, member A1 (FAM91A1), mRNA.	ACTCTAACAGCTGTCCAG TGTTGGTGATTCCAGTG GACTGTATCTCTGTG	ILMN_1707858	TCAGAATGGAGTGGACGGTCACCTTCCTCACTT CTTATTGCTAATCTCCA
424.76013	499.5476	467.71844	LGALS8	Gal-8; PCTA-1; Po66-CBP; PCTA1	NM_201545	Homo sapiens lectin, galactoside-binding, soluble, 8 (galectin 8) (LGALS8), transcript variant 4, mRNA.			GAAAGTGTACGCCAACTAAGGGACCCACAAAGC AGGCAGAGGTAATGCAG
234.19345	388.03094	314.5976	AUP1		NM_181575	Homo sapiens ancient ubiquitous protein 1 (AUP1), mRNA.	TCCCCCGGCGGAGCCAA CCCTCACTGATGGGAGC CCTGGGGTCATCTGTG	ILMN_1658427	TACGCAAGAAGGAGATTCACAGAGAGACGAGCC CAGGAGGCTGACTGAGC
60.339027	73.44124	68.83369	NDUFS1	PRO1304; MGC26839; CI-75Kd	NM_005006	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (NDUFS1), nuclear gene encoding mitochondrial protein, mRNA.			GCTTGCCCAAGGCCACACAGCAAAAGTCACCAA CTCAAACCTACTTCTTA
511.37262	1017.006	749.70593	GMPPB	KIAA1851	NM_021971	Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 2, mRNA.	CCCCCATCCCTTCCTCC CTTACCCAGCTATGATTC AGTTGTCTCTGCCCT	ILMN_1670076	CCTGGGACCTGGCGTGGTGGTCGAAGATGGTGT GTGTATCCGGCGGTGCA
164.5893	327.6726	246.74762	LARP2	MGC75174; DKFZp686L13217; MGC117277	NM_032239	Homo sapiens La ribonucleoprotein domain family, member 2 (LARP2), transcript variant 3, mRNA.	GGAAAGGCTGCTCTTGC TCTCCCTCCCAGGGCTT GAGGCTCCCTATACTT	ILMN_1697081	TTCTCTGCAGGGTAGGTAAGATAGGTCAGTCAA GTTGGTAATGCCTGTCC
421.5851	437.4726	431.2226	SMEK2	PSY2; FLFL2; FLJ31474; smk1; KIAA1387	NM_020463	Homo sapiens SMEK homolog 2, suppressor of mek1 (Dictyostelium) (SMEK2), mRNA.	GTCGAGCATCTCCCCGC AGCCAACGGCAAGGGCG GCGAGGCTCCGGCCAA	ILMN_1662140	TCCTTAGATCACCCTTGTAATGTGTTACGGGTCC ATTTTTCCTGGAATCG
643.7143	809.57263	732.90173	NMD3	CGI-07; FLJ21053	NM_015938	Homo sapiens NMD3 homolog (S. cerevisiae) (NMD3), mRNA.	GCTAGCATTTTTCCAACG AGGGAACTTATTCCGCA CGGGCCTACTGTAGG	ILMN_1750158	TTGCCAGTTTAGGGCAGTAGCTGCTTTTGTCATA AATATCTTCCTACCAC
273.35596	637.45593	452.7851	KATNAL1	MGC2599	NM_001014380	Homo sapiens katanin p60 subunit A-like 1 (KATNAL1), transcript variant 2, mRNA.	AACGCCCCGGGCAAAGG GTCTTTTGCAGCTTTTGC AGACGGGCAAGAAGC	ILMN_1753550	TCATATGATGGTACGGCAGCAGGGAGTGGCCCC CAGTTAACATGGCTGTG
1498.0143	2427.2393	1995.406	PELO	PRO1770; CGI-17	NM_015946	Homo sapiens pelota homolog (Drosophila) (PELO), mRNA.			CCGCTTCCCTGTTCCCGAACTTTCTGACCAAGAG GGTGATTCCAGTTCTG
135.41428	490.40594	295.85596	JMJD1C	TRIP8; DKFZp761F0118; KIAA1380; FLJ14374; RP11-10C13.2	NM_032776	Homo sapiens jumonji domain containing 1C (JMJD1C), transcript variant 1, mRNA.	CTCTTTTTTGGACATGTG TCTCTCCACTGCCACAAC ACCCAAGATGATCA	ILMN_1722496	GTTCCTTGGTGATGCTATTGTTTTGCCAGCGGGA GCACTTCATCAGGTTC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
50.314907	80.52324	66.92281	DHX34	KIAA0134; HRH1; DDX34	NM_014681	Homo sapiens DEAH (Asp-Glu Ala-His) box polypeptide 34 (DHX34), mRNA.	CGGCTCTGTTGTTTGAAT AAACGTGAACGTGAACC CAGGCGGAAGGGACC	ILMN_1663927	CCCCTTGAAGTAGGGGGACCCTGAATTTGCCCA TCCACCTGGGTCACTTT
157.51012	204.67679	184.51428	PSMD3	RPN3; P58; S3	NM_002809	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3), mRNA.			GCCCAGGGCACTGTCCCCATTTTCCCACACACA GCTCATATGCTGCATTC
41.03135	106.53512	72.34765	ASL	ASAL	NM_001024943	Homo sapiens argininosuccinate lyase (ASL), transcript variant 1, mRNA.			TTTGGAAGGGCAAGGTGCGAGGATGCTTGAGGC CAGGAGTTTGACACAGC
290.20593	3843.0308	1301.0143	LPXN	LDPL	NM_004811	Homo sapiens leupaxin (LPXN), mRNA.	TCATGATGTTAAGCTGCC TCTTTCTTCTGAAGGCAC TTCTTGCTCTTGGG	ILMN_1673537	CACGTTTTCCCATTTGCCCTGTGGCTCACTGTCT TACAATCACTGCTGTG
1214.8059	1815.1477	1524.5393	PSME4	FLJ21864; MGC142228; MGC138374; PA200; KIAA0077	NM_014614	Homo sapiens proteasome (prosome, macropain) activator subunit 4 (PSME4), mRNA.			AAAGAGGGCAAGTCCTGAACCTAACCAATGACCT GATGGATTGCTCGACC
875.90594	1971.3394	1404.06	DOCK10	Nbla10300; DKFZp781A1532; DRIP2; ZIZ3	NM_014689	Homo sapiens dedicator of cytokinesis 10 (DOCK10), mRNA.	TGGGCTGGCTTCCAGTT TTATGTTTCCCAAATGGT GATTCAGCTGTTCCA	ILMN_1691228	CCCTAAGTTTGCTGTCAGTTATTGTATGGTCAGT ACCCCAGTCCTAGTAC
246.58511	485.35596	362.12262	SERPINB8	CAP2; PI8	NM_002640	Homo sapiens serpin peptidase inhibitor, clade B (ovalbumin), member 8 (SERPINB8), transcript variant 1, mRNA.	GCTGCTGCCCACACCGC GTCGACGCCTTCACTGC CATCCCCGCTGTCCTT	ILMN_1738473	AGGAGCTGAGCATGGTCATTCTGCTTCCCGATG ACAACACGGACCTCGCC
93.27301	99.9893	95.626785	RAPSN	MGC3597; RNF205; CMS1E; CMS1D	NM_005055	Homo sapiens receptor-associated protein of the synapse (RAPSN), transcript variant 1, mRNA.	CTCGTCTGGCCCATCTA CCTGCTGACAGAGCATG ACAAAGATGACGCTCA	ILMN_1707551	TCCTCGCCACTCCTGCTCTTTCTCCACTGCACGC CAGAGGCCCATTTACT
12.910944	432.0476	102.84102	FLRT3		NM_198391	Homo sapiens fibronectin leucine rich transmembrane protein 3 (FLRT3), transcript variant 2, mRNA.			AGTGCATTGTACGCCCTTTGGCCAGTCTTGTATG TGCCTTGATCCAACGC
1017.8809	1229.7393	1130.356	ARMCX6	FLJ20811	NM_019007	Homo sapiens armadillo repeat containing, X-linked 6 (ARMCX6), transcript variant 1, mRNA.	GAGATATGGGTGCCCTT TTGTACGTCTAGGCCTA GGTAACCAGTGGAGTG	ILMN_1763196	GGCCTGTAGGTTTCGGCACAAGTTTCAGCGAGA GAAGGAGAAAACTGCCT
127.45178	310.4101	218.01428	POPDC3	MGC22671; bA355M14.1; POP3	NM_022361	Homo sapiens popeye domain containing 3 (POPDC3), mRNA.	TCTTAACCAGCTGAGGG AGCTTGTACAACACCTTA TGTATGCTGGTTGGG	ILMN_1805148	CAGCCTGAGGGTGGGTTGCTACTGTCCACATAG GCATTTCCGGAATTCAC
387.25177	780.5393	573.6643	HMGCR		NM_000859	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA.	GTTCCCTCAAAACTGATG TGGGCACTTGGCCCAGA AGTTGTTTGCTAATG	ILMN_1782881	CTTGGATGGACCCACGAACGCTCTTAGCTTTCTC AGGGGGTCAGCAGAGT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
230.30595	244.9851	235.95595	TNRC6B	KIAA1093	NM_015088	Homo sapiens trinucleotide repeat containing 6B (TNRC6B), transcript variant 1, mRNA.			CTAGGCACTTTAGAGGTGCACTTGCATGGCAGG CTGGGCCCCCTTTTCTA
290.3351	495.43097	388.2768	KTI12	TOT4; SBBI81; MGC20419; RP11-91A18.3	NM_138417	Homo sapiens KTI12 homolog, chromatin associated (S. cerevisiae) (KTI12), mRNA.	CTGGCGGAGATGCTTCT AAGGCATGGTCGGGGGA GAGGGCCAACAACTGT	ILMN_1668850	TGGGCTATCACAGAGCATTGACCATTGGCTTCC CTCATCTGAGGCGTGGG
1487.3226	2584.6392	2014.4727	CTPS		NM_001905	Homo sapiens CTP synthase (CTPS), mRNA.			TCCCCATGCCTGTGCGTGCGCTTCCTATTTCTAG GGCTGGGAAACACTCC
686.5226	827.9976	760.5393	ARMC1	FLJ10511; Arcp	NM_018120	Homo sapiens armadillo repeat containing 1 (ARMC1), mRNA.			CTAACATTGTCACCTTCTGGAGAGAGAGTTAATG GGGGGCATTGAGGATG
164.94345	366.78928	256.31427	LOC90379	MGC99481	NM_138353	Homo sapiens hypothetical protein BC002926 (LOC90379), mRNA.			AGGGCAGCCTCTGTTGGCCTGAGGGTCTGGAC GCTTTTTATTTATGCCTA
1102.6643	1206.281	1177.7476	SMARCA4	SNF2L4; BRG1; SWI2; SNF2; hSNF2b; BAF190; FLJ39786; SNF2-BETA; SNF2LB	NM_003072	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA.	GGAGAGTGTTACATGGT GTTGGGGGAAGAAAACC TACGCTTCAGGCTCAG	ILMN_1685259	CCGTCCACTCCTCCTACTGTATTTTATTGGACAG GTCAGACTCGCCGGGG
86.368546	94.75597	91.164345	ZNF45	KOX5; ZNF13	NM_003425	Homo sapiens zinc finger protein 45 (ZNF45), mRNA.			GAGGGCAGGGACTTTGTTGACTGCCAAATCTAC TCTGCCTTTTCAGTGCC
58.08082	96.18097	76.31546	HEL308	MGC20604	NM_133636	Homo sapiens DNA helicase HEL308 (HEL308), mRNA.	AGAGAGAAGTCACCCAA GTTCCGCTTCCCCAGGG TGTCCCTAAGCCCCAA	ILMN_1786648	CTGTGAGGAGCTTGAGGAGTTTTGGGTTTACAG AGCCCTTTTGGTAGAAC
44.8308	58.485714	52.343422	USP26	MGC120066; MGC120068; MGC120067	NM_031907	Homo sapiens ubiquitin specific peptidase 26 (USP26), mRNA.			GAAGAGAATGCCCAGCTTAATAGCAAGGAGGTA GAGGAGACCCTTCAGAA
2065.4392	2823.2144	2446.7144	ACOT7	hBACH; LACH; LACH1; RP1-120G22.10; BACH; ACH1; MGC1126; ACT; CTE-II	NM_181864	Homo sapiens acyl-CoA thioesterase 7 (ACOT7), transcript variant hBACHb, mRNA.			CCGAGCACGCTGTAGGGTATGGGAAGAACCCAG CACCACTAATAAAGCTG
5.6919904	62.14904	22.580227	OVOL1	HOVO1	NM_004561	Homo sapiens ovo-like 1(Drosophila) (OVOL1), mRNA.			GCCAAACCCCACCTGAAGCAGAACCACTTTGGC CTCCCCTGCCCAAAATG
2506.0142	3428.8977	3079.7144	ZMPSTE24	FLJ14968; STE24; FACE-1; Ste24p; FACE1	NM_005857	Homo sapiens zinc metallopeptidase (STE24 homolog, S. cerevisiae) (ZMPSTE24), mRNA.			GGGATCAACTGTACGCCTTTGGTATCTGACCATA AAGTCTTTTGCTCCGC
95.53514	272.41846	190.7976	HMGB3	MGC90319; HMG4; HMG2A	NM_005342	Homo sapiens high-mobility group box 3 (HMGB3), mRNA.	GATGAACGAGTCTTGTTT CTCTCCCCTGCAAGGAA GGTCCAAGCAGGCCC	ILMN_1756424	GTTGAGGCCACTTGGTCCATTAGCTGGGGCAGC AAGATCACTACTCAACG
1660.6976	2824.7642	2361.5059	CCND3		NM_001760	Homo sapiens cyclin D3 (CCND3), mRNA.	GGCTCGCTCCAGGACCT TCTTCACAAGATGACTTG CTCGCTGTTACCTGC	ILMN_1698019	GCCCTGTTGACACAGGTCTTTCCTAAGGCTGCA AGGTTTAGGCTGGTGGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
760.83923	1516.3893	1199.5143	TXNDC1	TMX; DKFZP564E1962; TXNDC	NM_030755	Homo sapiens thioredoxin domain containing 1 (TXNDC1), mRNA.			CAATTTCTGTAATGTCCCCTTCTTTCTAGGCTCT GTTGCTGTGTGAATCC
150.26428	1099.731	562.4643	PLAUR	UPAR; URKR; CD87	NM_002659	Homo sapiens plasminogen activator, urokinase receptor (PLAUR), transcript variant 1, mRNA.			AGTGCCGCAGCCCTGAAGAACAGTGCCTGGATG TGGTGACCCACTGGATC
13961.072	26786.61	21429.812	CALM2	PHKD; CAMII; PHKD2	NM_001743	Homo sapiens calmodulin 2 (phosphorylase kinase, delta) (CALM2), mRNA.			GTTGTTGAAGTGTGGAGTTGTAACTCTGCGTGG ACTATGGACAGTCAACA
254.39761	289.3476	275.95593	SH3D19	MGC118913; EVE1; MGC118910; Kryn; SH3P19; MGC118911; MGC118912; MGC105136; EBP	NM_001009555	Homo sapiens SH3 domain containing 19 (SH3D19), mRNA.	GCAGGCCCAGCGATGCC CGCTTCACTCGCCGCTA CTGAGTACTTGGAATC	ILMN_1722059	CAAGTGGCCACACTTTTACGTGACTACAACCTGG AGTTCTGCAAAGAAGG
62.020805	109.46428	92.36513	APOOL	MGC129748; UNQ8193; FAM121A; CXorf33	NM_198450	Homo sapiens apolipoprotein O-like (APOOL), mRNA.			CAGGTGCAACCCAGTTTATGCCTGACCCCAAGC TCATGGATCACGGGCAG
1834.1184	2495.3394	2266.306	RBM10	MGC997; DXS8237E; KIAA0122; ZRANB5; GPATC9; GPATCH9; MGC1132	NM_152856	Homo sapiens RNA binding motif protein 10 (RBM10), transcript variant 2, mRNA.			GAGGTGGTGACTTTTGTTGGAAAATTGGGCTGG GATCACGTCCTGTTTTG
63.734966	114.05179	92.5643	DYRK3	DYRK5; hYAK3-2; RED; REDK	NM_003582	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3 (DYRK3), transcript variant 1, mRNA.	ATGAAGGACGAGGTAGC TCTACTGGCTGCTGTCA CCCTCCTGGGAGTCCT	ILMN_1668247	AAGTCTGTCCCCAGACCTCTCACCACCATAGACA AGGTGTCAGGGAAACG
674.4351	1369.106	1071.856	RIN2	RASSF4	NM_018993	Homo sapiens Ras and Rab interactor 2 (RIN2), mRNA.			CCAGTTTGCAGGTGCACAAACTATGAGGGTCTT GTATCCACGTAACACAG
68.03358	133.34763	103.930954	NKX3-1	NKX3A; BAPX2; NKX3; NKX3.1	NM_006167	Homo sapiens NK3 homeobox 1 (NKX3-1), mRNA.	CCCATCGTTGCTATCACC AGTACCTCTCAGCTTACT CTTCAGGGGATATG	ILMN_1698191	CCATCTTGCTTTCCCCATTGGAACTAGTCATTAA CCCATCTCTGAACTGG
200.39761	214.30594	208.89345	C1ORF109	FLJ20508	NM_017850	Homo sapiens chromosome 1 open reading frame 109 (C1orf109), mRNA.	CATGGGTCTCCAGGAAG TGACCTTGGATGGGGGT GGGAAGGGGCTGCTGG	ILMN_1764355	GCCAGCCCAGAGTCAGTCCATCGGGGTTACATT TCCAAGGTCTGCTGCCT
181.21428	207.28094	196.33095	PAK4		NM_001014832	Homo sapiens p21(CDKN1A)-activated kinase 4 (PAK4), transcript variant 3, mRNA.			TAACACTCTAGCCCCTGCCCTTATTGGGGGACA GATGGTCCCTGTCCTGC
53.191994	73.49957	66.87561	LIPT1	MGC13378; MGC12290	NM_015929	Homo sapiens lipoyltransferase 1 (LIPT1), transcript variant 1, mRNA.			GAGCCCTTACCAAGGGATCAGGAGCAATGCCAC TGCTAGCATACCTTCCT
169.93094	246.37679	217.87262	SLC36A4	FLJ38932; PAT4	NM_152313	Homo sapiens solute carrier family 36 (proton/amino acid symporter), member 4 (SLC36A4), mRNA.			AGCTCTCTCCAGATCATCCCTGTGAATGCCAAAG TAAACTTTATGTACAG
124.42679	293.48096	228.11429	PITPNC1	RDGBB; RDGB-BETA; RDGBB1	NM_181671	Homo sapiens phosphatidylinositol transfer protein, cytoplasmic 1 (PITPNC1), transcript variant 2, mRNA.			GCAATCAGCATTCCTCCCCTGTGGATGACATAGA GAGTCATGCCCAAACA

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
129.99345	160.33096	148.23096	CDC42BPA	DKFZp686P1738; KIAA0451; FLJ23347; DKFZp686L1738; PK428; MRCK; MRCKA	NM_003607	Homo sapiens CDC42 binding protein kinase alpha (DMPK-like) (CDC42BPA), transcript variant B, mRNA.	CCAAGTCAGCAGTCCTA GCCCCAAACCAGCCCAG AGCAGGGTCTCTCTAA	ILMN_1690170	CGACTGGCTTCCTCTCTCAGGTGCTGGATTGTG GGGTTAGTGGCATTTCC
50.945847	75.02017	66.25397	TICAM1	MGC35334; TRIF; TICAM-1; PRVTIRB	NM_182919	Homo sapiens toll-like receptor adaptor molecule 1 (TICAM1), transcript variant 2, mRNA.	CCCCACTGTGGCTGATT TGGAATTTTGTGCCCCCA TGTAAGCACCCCTTC	ILMN_1794386	GCTGCAACCCCTCATTATCCACCACGCACAGAT GGTACAGCTGGGGCTGA
11.707075	89.48955	46.772972	ABCC9	ABC37; FLJ36852; SUR2; CMD1O	NM_020298	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 9 (ABCC9), transcript variant SUR2A-delta-14, mRNA.	AGACGTTCGGGGCAGGG TGGGAGTGGGTATGGAG ATGCAATTTGGGACTG	ILMN_1664896	CCTGGAGGTCTAGATGCGGTTGTCACTGAAGGT GGGGAGAATTTTAGCGT
70.53033	204.23096	147.19762	GMPPB	KIAA1851	NM_021971	Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 2, mRNA.			GACCCTGGACTTGTCATTATTTGTCTGGGGGGC ACTGGGTGAAGCTGAAG
45.404335	92.56014	75.18869	MRPL3	MRL3; RPML3	NM_007208	Homo sapiens mitochondrial ribosomal protein L3 (MRPL3), nuclear gene encoding mitochondrial protein, mRNA.			GTGAAATAGTGGTTGTGGAACAGTAGAAAACCAT ATGGGGACTATAGTGC
196.4851	228.02678	217.91428	ZNRD1	hZR14; tctex-6; MGC13376; Rpa12; HTEX-6	NM_014596	Homo sapiens zinc ribbon domain containing 1 (ZNRD1), transcript variant b, mRNA.			AGTCGGACCTGGATTTCTGTTCAGATTGCGGCT CGGTCCTGCCTCTGCCC
1257.9559	1361.406	1329.2227	EIF2B4	EIF-2B; DKFZp586J0119; EIF2Bdelta; EIF2B	NM_015636	Homo sapiens eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa (EIF2B4), transcript variant 3, mRNA.	TATCAAAAAGGCCACGG TCATCGGGTGAACACAG ACCCCTCAGTCCTCCC	ILMN_1758790	GCGCTGGCTAACTGGCAGAACCACGCATCCCTA CGGTTGTTGAATCTAGT
29.255331	66.14261	52.73044	PDE8A	HsT19550; FLJ16150	NM_002605	Homo sapiens phosphodiesterase 8A (PDE8A), transcript variant 1, mRNA.			AGCCCCCGATCTGCATAGCCTGTGAAAGCCCAC GGGGACATCAGTAACCT
155.36845	342.91846	266.2101	GALNT6	GalNAcT6; GALNAC-T6	NM_007210	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) (GALNT6), mRNA.			AGCAACATAGTGAGGATCCCATCTCTACGCCCA CCCTCCCCCCGGCAAAA
170.0268	470.73096	340.55594	TMEM132A	DKFZp547E212; HSPA5BP1; FLJ20539; GBP; MGC138669	NM_178031	Homo sapiens transmembrane protein 132A (TMEM132A), transcript variant 2, mRNA.			TGGGTGTGTGAGGACATGGGGCTGAAGGACCCT GAGGAGCTTCGCAACTA
117.37262	301.45596	220.89345	STX3	STX3A	NM_004177	Homo sapiens syntaxin 3 (STX3), mRNA.			GGCCGGTCACAATCCAGCACTCAGACAGAGCCA AGGCAATATCCTCTTGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
312.87677	611.23096	490.18094	ISG15	UCRP; IFI15; G1P2	NM_005101	Homo sapiens ISG15 ubiquitin-like modifier (ISG15), mRNA.	GCATTTAGGCGGGGACC ACAACGAATCCGGGAGT TGGCCAGAAGGATCCA	ILMN_1803979	ACCTGAAGCAGCAAGTGAGCGGGCTGGAGGGT GTGCAGGACGACCTGTTC
808.3893	880.2268	853.1226	OGFOD1	KIAA1612; TPA1; FLJ10826	NM_018233	Homo sapiens 2-oxoglutarate and iron-dependent oxygenase domain containing 1 (OGFOD1), mRNA.	GATGAGCTTTGTCTACTT CAAAAGTTTGTTTGCTTA CCCCTTCAGCCTCC	ILMN_1769388	GACACAGTGAGTCATCACATTTCCTCCCACTGCC TGTGGCCTTGTTCCAC
42.835217	76.035995	64.70339	CCDC21	FLJ22000; FLJ13976; DKFZP434L0117; DKFZp434P232	NM_022778	Homo sapiens coiled-coil domain containing 21 (CCDC21), mRNA.	CCCTGGCGGGTAAATTA GGAATCTGCACTATTTTG GAGGACAAGTAGCAC	ILMN_1724984	TGCTTAAAGGCAGAGCCGCCTGGTTGGTCTCCA CCCTGTGCATTGGGAGC
35.23066	70.61986	56.22285	WDR4	TRM82	NM_033661	Homo sapiens WD repeat domain 4 (WDR4), transcript variant 2, mRNA.			CATGCCAAGAAGATGAGACCGGGGGAGGCGAC GCTAAGTTGCTGATCGTG
406.62677	676.4351	574.70593	BCAP29	DKFZp686M2086; BAP29	NM_018844	Homo sapiens B-cell receptor-associated protein 29 (BCAP29), transcript variant 2, mRNA.	CCGTGGCCTGGGACGTG GCTGGTAGTGTTTGTGT GGGAAGCAGCTCAAGA	ILMN_1697905	TACCATTGAGAAGAGCTCCACCAGCAGACCTGA TGCCTATGAACACACAC
21.131958	124.92678	73.60788	CASC5	KNL1; D40; AF15Q14; KIAA1570	NM_144508	Homo sapiens cancer susceptibility candidate 5 (CASC5), transcript variant 2, mRNA.	TCGAATTGGCTCTGACC CTTACCTGGGGCAGCGT CTGGACAGTGAGGCCT	ILMN_1691855	CAGGACTGCCATTTCTACCACTAGACCCTTGGAC CACCATTGGAACAACC
25.152565	109.23095	70.3501	C6ORF167	FLJ46180; dJ39B17.2; KIAA1900; DKFZp686C20164; DKFZp781C2113	NM_198468	Homo sapiens chromosome 6 open reading frame 167 (C6orf167), mRNA.	GCCTTGGCAGGGCACAA TGACCTTGTCGAAATCCA CCTGTCAGGACGCCT	ILMN_1800354	TCAGAGCAGAAATGGGGCCTTGGCAGGAATATA GCACAAAGGGAAGCCTA
35.82373	96.50598	72.8966	ZNF215	BAZ2	NM_013250	Homo sapiens zinc finger protein 215 (ZNF215), mRNA.	CCTTGGGCTGCAGATCC ATAAGGACTTCCTGTTCT TGGGTGCCAATGTCC	ILMN_1732538	GCAGACTTACTGTACCTTTGGGAATTTAGGCTGG AGAGACGTCCATAGCC
1810.9976	2217.8894	2059.0393	TMEM32		NM_173470	Homo sapiens transmembrane protein 32 (TMEM32), mRNA.			GCATTGTGGCTTCTCAGTGGCTTGACAGCATCTT CCTGGTTGTATGTGGC
122.38928	195.67262	165.40178	SNIP1	RP3-423B22.3; dJ423B22.2; FLJ12553	NM_024700	Homo sapiens Smad nuclear interacting protein 1 (SNIP1), mRNA.			CCCAAGGTTGGAAAGCAGGGGAATTTCCCAGTG TCCTAGTTTTCCACCAG
29.258165	58.965145	46.503334	TAOK1	TAO1; MAP3K16; KIAA1361; PSK2; MARKK; FLJ14314	NM_020791	Homo sapiens TAO kinase 1 (TAOK1), mRNA.			GCCACAGTGAACCAGGAGTCACTGAGCCAATGA CTTTACCAGCTGCTGAC
1270.1976	1513.781	1420.3394	PRELID1	CGI-106; MGC87972; PRELI; PX19	NM_013237	Homo sapiens PRELI domain containing 1 (PRELID1), mRNA.			TCATGTCTGAGCCAGGTCTGCTTATTCTCCCATT GGGCAGCTGAGGACCG
1685.0476	2777.6978	2321.6143	SSR2	HSD25; DKFZp686F19123; TRAPB; TLAP	NM_003145	Homo sapiens signal sequence receptor, beta (translocon-associated protein beta) (SSR2), mRNA.			GGGAGGAATCCTGGCTCAGCGGGAGTTTGACAG GCGATTCTCCCCTCATT
25.775208	88.84413	55.2799	LAMC2	BM600; EBR2; MGC141938; MGC138491; LAMB2T; LAMNB2; EBR2A; B2T	NM_005562	Homo sapiens laminin, gamma 2 (LAMC2), transcript variant 1, mRNA.			CGCTGGGGTTACAATCCAAGACACACTCAACACA TTAGACGGCCTCCTGC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
623.006	977.7143	829.4976	FADD	GIG3; MORT1; MGC8528	NM_003824	Homo sapiens Fas (TNFRSF6)-associated via death domain (FADD), mRNA.	CGGGACCTTGACAACAC CTGGCCCCACCCACACG TCCTGCAATATTCACT	ILMN_1717295	CTCTGAGACTGCTAAGTAGGGGCAGTGATGGTT GCCAGGACGAATTGAGA
166.16013	228.75595	207.98096	FURIN	PACE; FUR; SPC1; PCSK3	NM_002569	Homo sapiens furin (paired basic amino acid cleaving enzyme) (FURIN), mRNA.			ACTGTGCCCTGGTGGAGAAAGCACTGACCTGTC ATGCCCCCCTCAAACCT
46.664833	90.48932	69.267075	POLR2K	RPB12; RPABC4; RPB7.0; RPB10alpha; hRPB7.0; ABC10-alpha; hsRPB10a	NM_005034	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa (POLR2K), mRNA.			GACTACAGGTAACCAAAACCACAGAAAGGGAAA CTTTGGATGAGGGGGGC
12.405609	163.94762	62.987476	C14ORF145	C14orf61	NM_152446	Homo sapiens chromosome 14 open reading frame 145 (C14orf145), mRNA.	AAGCACATTCCTGCCTCA GGGCCTTTGTACCTGTT GTTCCCTCCACCTGG	ILMN_1778382	AGTGTCTAAGAACGTATTCCCTTTACACGCTGAT CTCCTAGTGGAGAAGG
50.690506	79.08385	65.074554	TAF5L	PAF65B	NM_014409	Homo sapiens TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa (TAF5L), transcript variant 1, mRNA.	TGCCTCACTCCCCTCAG CCCCTGCCGACCTTAGC TTATCTGGGAGAGAAA	ILMN_1682459	GAGGGCACCTTCTCTGCTTTTAATCTTTCAGGTT TGACTCCTGGCACTGG
36.069866	370.73096	155.53513	STEAP2	STMP; PCANAP1; STAMP1; IPCA1; IPCA-1	NM_152999	Homo sapiens six transmembrane epithelial antigen of the prostate 2 (STEAP2), mRNA.			GTGTTGGCCAGTGAGATGAAGTCTCCTCAAAGG AAGGCAGCATGTGTCCT
412.07263	493.6476	466.06012	RPUSD2	C15orf19; FLJ31409; C18B11	NM_152260	Homo sapiens RNA pseudouridylate synthase domain containing 2 (RPUSD2), mRNA.			GGACGGGCTTCTAAAGAGACCTGCTCATACTTG CTACCTCCTTCCAGTGG
2467.2227	3473.456	3067.6477	PCMT1		NM_005389	Homo sapiens protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA.	TGTATGCGCCAGGGCTC GTTCTCACTGCTTATGTT CTTCGGGATTCTGGG	ILMN_1774584	GTGTAAGCTGTGTCCTAGTTCTTGAACAGTTTAT GCAGTGCTGCTTTGCC
160.52261	221.23096	196.98929	KIAA1468	HsT885; HsT3308; FLJ33841	NM_020854	Homo sapiens KIAA1468 (KIAA1468), mRNA.	CTGTCCCAGTGTAGGAA CAGAGACCCGCCTTAAG AGACTGGATCGCACAC	ILMN_1727389	GCAGGAAAGAAGCCCCCAGTAAACACTAAGATG GACCTCAAGCCGACTGG
159.7976	309.36844	239.46844	ERO1L	ERO1-alpha	NM_014584	Homo sapiens ERO1-like (S. cerevisiae) (ERO1L), mRNA.			TCTTCTGTGTCCCTAAGGCCTGGTACAGTGCCAA GCACATACTTGGTATC
29.329708	78.22399	54.512367	STRN	MGC125642; SG2NA	NM_003162	Homo sapiens striatin, calmodulin binding protein (STRN), mRNA.			ATAGCCCAAAGAGTATGGTTAACTTCACGCAGCT GCTTTTGCAGAAGCAC
781.79346	856.70593	827.8601	CAST	MGC9402; BS-17	NM_001042445	Homo sapiens calpastatin (CAST), transcript variant 11, mRNA.			GCTGTCCCTCCACTACAGAAACCTCACAGAACAC AGCAAAGGATAAGTGC
143.48929	254.96428	206.68929	GTF2E1	TFIIE-A; FE	NM_005513	Homo sapiens general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD) (GTF2E1), mRNA.			GAGACTGGTCCTGGTTTTGTTCCCTTTGGTACAG ACCTCTTGTCAGTGCT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
62.819923	214.32262	135.33096	B3GALTL	beta3Glc-T; B3Glc-T; B3GTL; Gal-T	NM_194318	Homo sapiens beta 1,3-galactosyltransferase-like (B3GALTL), mRNA.			CCCTGGCTGCCTACACCAGTGGAAAAGAGTCTC CAGTTCTGCTCTGGCCT
188.62679	466.90594	332.88928	FRMD4A	FRMD4; KIAA1294; bA295P9.4; FLJ10210	NM_018027	Homo sapiens FERM domain containing 4A (FRMD4A), mRNA.	GGCAGGAACCACCTTCC TCCAAGATCCTCACTATG GCAACTGTGGACCCC	ILMN_1762170	CCCCATCCAGGTGCTATCAGATGACCAGTTACTG CTTAGTTAACTAGGTG
1366.2476	1761.2769	1598.6643	RUSC1	NESCA; DKFZp761A1822	NM_014328	Homo sapiens RUN and SH3 domain containing 1 (RUSC1), mRNA.	TCTGAGGGTAATATGCCT CTGCCCTTTAGTCAGACT CTGTGCAAATTGTG	ILMN_1684447	GGTGGGCCTGTGGTGATGGTTTGCATCCTTCCT CCCTTGTCCCAATAAAG
25.589949	60.99272	44.06006	MARK2	Par1b; MGC99619; EMK1; PAR-1	NM_001039468	Homo sapiens MAP/microtubule affinity-regulating kinase 2 (MARK2), transcript variant 3, mRNA.	AGCGCTGTTTGCAGCAT CAGGAAGTGAAGCCCTA CACCCTGGCGTTGGCT	ILMN_1772302	CCCTGGCCCTTCTCAGTTTTCTCCCACATTCACC CCTGCCCAGAGATTCC
364.69345	467.60596	426.4643	SLC11A2	FLJ37416; NRAMP2; DCT1; DMT1	NM_000617	Homo sapiens solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 (SLC11A2), mRNA.	CTTCCCGCACAAATTCCA CATAGAGGCCTTCCCAT CCAGCTCTACGTGAT	ILMN_1697919	GCTCTTGGCTCCCTTGAGGTTCTGCTAGTGGTG TTAGGAGTGGTTACAAC
417.98096	474.25595	452.00595	MAPK9	SAPK; JNK2B; JNK-55; JNK2; JNK2BETA; p54aSAPK; p54a; JNK2ALPHA; PRKM9; JNK2A	NM_002752	Homo sapiens mitogen-activated protein kinase 9 (MAPK9), transcript variant JNK2-a2, mRNA.	GCGGATGCTGGATGGGC CTGCAGAAACAACACTCA CCACACACACTTCCT	ILMN_1731287	GGAACTCTCACCTCCGTGGGCCTGAAATGCTTG GGAGTTGATGGAACCAA
116.95179	135.68929	126.08928	INVS	MGC133081; KIAA0573; INV; NPH2; NPHP2; MGC133080	NM_183245	Homo sapiens inversin (INVS), transcript variant 2, mRNA.	ACACACCTGCCAACTGC ACCTATCTTGACCTGCTG GGCACCTGGGTCTTC	ILMN_1792885	AGCCTCTTCTGTGCTGCGTCTCAACTCAGTGAG CAACCTACAGTGTATAC
208.2976	325.12677	272.5476	NEU1	NEU; SIAL1	NM_000434	Homo sapiens sialidase 1 (lysosomal sialidase) (NEU1), mRNA.	GAGCCCAAGAACACTGG TGGCCAAAGGATGGTGT CTTGTGAAAGGAGGGC	ILMN_1661076	CTTTAGGACTGAAAGCTAGGCGTCCTCTCCCACA AAAAAGTCCTGCCCTC
106.868454	126.53928	115.618454	AFG3L1	FLJ45200; AFG3	NM_001031805	Homo sapiens AFG3 ATPase family gene 3-like 1 (yeast) (AFG3L1), transcript variant 2, mRNA.	CCTGAATCGCATTCTCTA CTGGACTCTGGCCTGCT TGGAGAGGTGGCAGC	ILMN_1671843	CGGGGATGACTCTGATTGTCCTTCAGCAGGGAT GAGTCTGTTTTGCTCCG
181.51428	241.13928	208.36429	WDR74		XM_001125771	PREDICTED: Homo sapiens WD repeat domain 74 (WDR74), mRNA.	TCTCTAGAACACATCCAG GTGTCGGAGCTAAGGTG TTCAGCTCGGCTGTG	ILMN_1762407	CGGGAGGCAACTCAGTGATTGTGGGAAACACTC ATGGGCAGCTGGCAGAA
86.29766	133.59761	107.564285	C9ORF64	MGC10999; RP11-575L7.5	NM_032307	Homo sapiens chromosome 9 open reading frame 64 (C9orf64), mRNA.			GCCACAGTCACGCCACTGCATTCTATCCTGGGC AACAGATGGAGACCTTG
81.1565	277.7393	155.10594	HYI	MGC20767; HT036; RP11-506B15.5	NM_031207	Homo sapiens hydroxypyruvate isomerase homolog (E. coli) (HYI), mRNA.			TACTTCCTGGACACGCCCCAGCAGGCGGCAGCC ATCTTACAGAAGGTAGG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
50.83008	73.62764	61.11802	FBXO11	FLJ12673; PRMT9; UG063H01; MGC44383; FBX11; VIT1	NM_018693	Homo sapiens F-box protein 11 (FBXO11), transcript variant 2, mRNA.	CTGGCGGCATGGTGAGC AGAGTGCCCTATCCCAG TCCCACTTGTGTCAAA	ILMN_1659572	GCTGGAGTCTGGGTGACAACTGGCAGCACTCCA GTACTGAGAAGAAACCG
177.76428	257.2726	212.11429	AZIN1	ODC1L; OAZIN; OAZI; MGC3832; MGC691	NM_148174	Homo sapiens antizyme inhibitor 1 (AZIN1), transcript variant 2, mRNA.			TTGCCATATCTGCAGGAGAGCTGTTCTATAAGAA ATAGCTCAGAGTTGCA
3265.5476	3877.7476	3548.9644	FEZ2	MGC117372; HUM3CL	NM_005102	Homo sapiens fasciculation and elongation protein zeta 2 (zygin II) (FEZ2), transcript variant 1, mRNA.	AGACTTCCCTACTGAGC CACCTTCTCTGCCACGAA CCGGTCGGGCTAGGA	ILMN_1777663	AGTGTGTGTCCTCTGAGGTGCTTGAGAAAGTGT ACACTGCAGAACTGCCC
76.41078	128.2976	103.59079	CAPRIN2	MGC134848; MGC102894; MGC134847; FLJ11391; caprin-2; C1QDC1; EEG-1; FLJ22569; EEG1	NM_023925	Homo sapiens caprin family member 2 (CAPRIN2), transcript variant 2, mRNA.			GGACAAGGAGACTCCCGTAGCATGACCCCTGTG GATGTGCCAGTGACAAA
65.23072	90.26953	75.491394	PDS5B	AS3; PDS5B; FLJ23236; RP1-267P19.1; KIAA0979; APRIN; CG008	NM_015032	Homo sapiens PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae) (PDS5B), mRNA.	CACTGCAGAGAGCCAAT CAGACGTCGCAGAGCCC CGACGACACTATGCTT	ILMN_1767343	CTTGCTGCAGTGCAACAGGAGGCTTTTTCAGTG ATCTTCACTGTATATGT
133.3451	1190.356	259.39346	PCOLCE2	PCPE2	NM_013363	Homo sapiens procollagen C-endopeptidase enhancer 2 (PCOLCE2), mRNA.			CAGAGGAGCAGCTATCTGATTGGAAACCTGCCG ACTTAGTGCGGTGATAG
326.47263	417.87262	365.58093	COPS8	COP9; MGC43256; MGC1297; CSN8; SGN8	NM_006710	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis) (COPS8), transcript variant 1, mRNA.			CCCCCACCTCCTGAGAGCCACTAATGTAAGATAC AGAAACATAGCTGAGG
4313.0312	5972.9727	5009.164	ARHGDIA	GDIA1; RHOGDI-1; MGC117248; RHOGDI	NM_004309	Homo sapiens Rho GDP dissociation inhibitor (GDI) alpha (ARHGDIA), mRNA.	ACCCGACTCCGCATGTT TGCGTCTGTTTCCTCCCT CTCTGGCCCTGTCTT	ILMN_1798867	CAGGCCTTCCCTGACCCAGCCAGGAACAAACAA GGGACCAAGTGCACACA
349.34344	392.29346	366.28513	GNB2		NM_005273	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 2 (GNB2), mRNA.			GTTTGGTTCCTCCCGGGGCCCCCACTGTGGAGA TAAGAAGGGGATGGAAT
123.78928	221.89761	162.55594	C9ORF6	CG-8; FLJ20457	NM_017832	Homo sapiens chromosome 9 open reading frame 6 (C9orf6), mRNA.	TGCAAGGGACAGGGGGC CTGACTACCCAGTCTTTG ACTTGTATCCTCTCC	ILMN_1749006	CTTCTGTCCCCCTTATGCCAACAAGATGGCCTTC CCCTCTGAAACAAAGT
111.08511	217.31429	151.24345	SYNJ1	INPP5G	NM_203446	Homo sapiens synaptojanin 1 (SYNJ1), transcript variant 2, mRNA.			AAGTCAGTGGTACACAGACATTCTGTACATATCC TGTGAAACGTGCTGTC
959.94763	1160.781	1051.9309	QRICH1	FLJ20259; MGC131838	NM_017730	Homo sapiens glutamine-rich 1 (QRICH1), transcript variant 1, mRNA.			AATCTCCCCAGCCGACTTCCACTGGGCTGACAG ACTTTGCTGACCACAGG
884.95593	1847.8809	1258.581	TMEM166	FLJ13391	NM_032181	Homo sapiens transmembrane protein 166 (TMEM166), mRNA.	GTACTGCTTTCAGTGTGT TCCCCCTCAGCCCCTCC GGCGTGTCAGGCATA	ILMN_1652722	CTTGTGTTGCAAGGGCAACCTCGTCCATTTTAAC TGGCACCTCAGGGATT

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
131.62679	262.1518	182.15594	TMTC3	DKFZp686M1969; FLJ90492; DKFZp686O2342; DKFZp686O22167; DKFZp686C0968; SMILE	NM_181783	Homo sapiens transmembrane and tetratricopeptide repeat containing 3 (TMTC3), mRNA.	TTCCATACTGCAAGGGC AACGTCATACCCCACAC CTACTGTGACCACATG	ILMN_1770442	CTGATACCAGTGGGAGTTGGTCTTGATCTAGGA GATTCTGTTAAGCATCC
227.68929	267.26843	245.73929	ZNF770	FLJ20582; PRO1914	NM_014106	Homo sapiens zinc finger protein 770 (ZNF770), mRNA.	GATGATGGCTGATGTGT GTGAGTGTGATGGCCCT GAAGGGCTGTAGGACG	ILMN_1676774	GGGGGACGGTCCAGGAACCAATACCCCATGGAT ACCAAGGGACAACTGTA
373.44345	462.93097	413.87262	FAM58A	MGC29729	NM_152274	Homo sapiens family with sequence similarity 58, member A (FAM58A), mRNA.	GGACCCAAGGCTCAGAA GGACCGAGTCATAAAGT GTGAATGGCATAGAGG	ILMN_1714739	GTGTGCAGCTGACCCAAGGCAGCCACATCTGCG TTTGTCCTTTGAGAGGA
71.61555	182.42262	113.04346	GNPNAT1	Gpnat1; GNPNAT; FLJ10607	NM_198066	Homo sapiens glucosamine-phosphate N-acetyltransferase 1 (GNPNAT1), mRNA.	CCACTAGCCCCTTACCC AGAGTGGCCCACAGGAA ACAGCCTGCACCATTT	ILMN_1699599	GGTGATCTTAGATTTGATGAAGCACAGTATGCAG GTAGGCCTAATGGGGG
59.11771	166.31012	94.493515	NRM	NRM29	NM_007243	Homo sapiens nurim (nuclear envelope membrane protein) (NRM), mRNA.	TATGAAGAGAAGCCCTCT GCTGTGTGTCCGTGGTG AGTTCTGGGGTGCGC	ILMN_1807206	GTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA GGCCCCAACCTTGCCT
3423.356	4084.5396	3712.7559	C15ORF24	C11orf3; HT022; ORF1-FL1	NM_020154	Homo sapiens chromosome 15 open reading frame 24 (C15orf24), mRNA.			CAGAGCTGGCATTTGCACAAACACGGCAACACT GGGTGGCATCCAAGTCT
2375.5642	2536.8809	2495.931	PRKAR1A	CAR; PPNAD1; MGC17251; TSE1; CNC; CNC1; PKR1; PRKAR1; DKFZp779L0468	NM_002734	Homo sapiens protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1) (PRKAR1A), transcript variant 1, mRNA.			CTGCTCTAGAAAGTATAGATGGCCAAAGGACCG TTTTGTATTGCTTCCTG
247.08095	402.9893	308.43097	ANKRD50	KIAA1223	NM_020337	Homo sapiens ankyrin repeat domain 50 (ANKRD50), mRNA.			TGTTTTCACCCCCACCCTCACTGGAATTCTCACC AAAAATAGTTTGATAC
326.0893	475.65594	388.37677	ADNP	ADNP1; KIAA0784	NM_181442	Homo sapiens activity-dependent neuroprotector homeobox (ADNP), transcript variant 2, mRNA.	CTGGCTGTCCTATGTCC AGGAAGAAGCCCATTTG TTGAGGCTGACCTTCC	ILMN_1743303	GCACATAACCTTGTACAATCTTGCAACAGAGGCC AGCCACGTAAGATATA
417.86847	867.0143	582.5143	BCAP29	BAP29; DKFZp686M2086	NM_001008405	Homo sapiens B-cell receptor-associated protein 29 (BCAP29), transcript variant 1, mRNA.			CCATTGAGAAGAGCTCCACCAGCAGACCTGATG CCTATGAACACACACAG
1766.6143	3042.081	2264.8477	DNAJB11	PRO1080; HEDJ; ABBP-2; UNQ537; hDj9; EDJ; ERdj3; ERj3; ABBP2	NM_016306	Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 11 (DNAJB11), mRNA.	TTGGGGCAGTCAGGCAT TTGTATCTTTGGTAGGGC AACAAGTAAAACATG	ILMN_1700257	ACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTG CCGCCTGAGTTTCAAG
789.5018	2990.6978	1580.9976	TMEM200A	TTMC	NM_052913	Homo sapiens transmembrane protein 200A (TMEM200A), mRNA.			TGCCTTGAAGTTTACCTTGTGCTGGAGAGCCTTA TGATAACTCCAAAGAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
178.23096	228.92262	200.6726	TXNDC5	UNQ364; ERP46; MGC3178; EndoPDI	NM_030810	Homo sapiens thioredoxin domain containing 5 (TXNDC5), transcript variant 1, mRNA.	CACCAGGTGGTCTCCTC TGACTTCAACAGCGACA CCCACTCCTCCACCTT	ILMN_2038778	GAGGACGGACAGGACCCGCACAGCAAGCACCT GTACACGGCCGACATGTT
162.59344	225.3601	195.0893	AKAP8	AKAP95; DKFZp586B1222	NM_005858	Homo sapiens A kinase (PRKA) anchor protein 8 (AKAP8), mRNA.			AATGGCCCTGCTGTGTCAGTTTCCCTGTGGCCT TTTGAACTGTACATCTC
20.54899	82.18157	42.857296	VEGFA	VPF; VEGF-A; MGC70609; VEGF	NM_001025367	Homo sapiens vascular endothelial growth factor A (VEGFA), transcript variant 3, mRNA.	GGAGAAAATCCAACCAG CTCTTCAGGAGAAGCAC GCCATGAAACAGGCCG	ILMN_1755536	ATTTAATTTTGCTAACACTCAGCTCTGCCCTCCC CGATCCCCTGGCTCCC
404.1726	555.2351	477.35596	FEM1C	FEM1A; EUROIMAGE686608; KIAA1785; EUROIMAGE783647	NM_020177	Homo sapiens fem-1 homolog c (C. elegans) (FEM1C), mRNA.	AGACCATTTCTGCAGTTT GCCCAAACCTCTACTGTT TGGGACAGTAAGCC	ILMN_1773643	GCCCTTATGTGTCACTAAACAACTAGTTTCTCTC CCTTTTGTCAGTTCCC
112.45178	133.71011	124.72679	NFX1	MGC20369; NFX2; DKFZp779G2416	NM_147133	Homo sapiens nuclear transcription factor, X-box binding 1 (NFX1), transcript variant 2, mRNA.	GATCCCAGAGGCTGAGG GTTGGGGGGAGGAAGC CATCATCTCATTACCTC	ILMN_1672081	CCCCCTGAATGTACCCAAACCTGCGCTAGAGTC CATGAGTGTGACCATCC
7813.531	11723.522	9620.764	SEC61G	SSS1	NM_001012456	Homo sapiens Sec61 gamma subunit (SEC61G), transcript variant 2, mRNA.			GCTACGTGTCCCTGGCATTTTAGGTGTCGGTTG GGCAGTCATGGATCAGG
297.98096	366.23926	333.9893	WDR74		XM_001125771	PREDICTED: Homo sapiens WD repeat domain 74 (WDR74), mRNA.			CCTGGGTCCACCAGCCCCTGACGCCCCTGTGCC CACTTTGTAAATAAACT
1086.8143	1516.6685	1292.0435	WSB2	SBA2; MGC10210	NM_018639	Homo sapiens WD repeat and SOCS box-containing 2 (WSB2), mRNA.			GGAGGCCAGTGTAACGTTACATGACTCGTTGAG AAAGTTGAGGAATTTCC
167.31012	252.61429	208.35596	ETNK1	EKI1; EKI; Nbla10396	NM_018638	Homo sapiens ethanolamine kinase 1 (ETNK1), transcript variant 1, mRNA.			GCACGATTCTGTGACTGTTTTTCTCTGTTTCACG TTCGTTGAGTGTAAGC
179.26428	508.6643	312.66013	PGM2	MSTP006; FLJ10983	NM_018290	Homo sapiens phosphoglucomutase 2 (PGM2), mRNA.	AGAGTCCTGGGGAGCTT CTGTCCACCTGTCCTGC AGAGGAGTCGTTTCCA	ILMN_1661589	GGTCTTACAGCCTTCCAAAATAACTCCAGTTGGG CACCCATGAGCTAGGA
822.2893	880.61426	850.83093	ANAPC11	HSPC214; MGC882; Apc11p; APC11	NM_001002246	Homo sapiens APC11 anaphase promoting complex subunit 11 homolog (yeast) (ANAPC11), transcript variant 4, mRNA.	CAGCCATCTTCTGTAAG GGTGCCCAGTGTGACTT CGGTTGATCCTGCTGC	ILMN_1694799	AATGGAAGTTCAAGGAGTGAGGCCCGACCTGGC TCTCGCTGGAGGGGCAT
75.286316	116.97678	93.6893	TARBP1	TRP-185; FLJ30482; TRP185; TRM3	NM_005646	Homo sapiens TAR (HIV-1) RNA binding protein 1 (TARBP1), mRNA.	TCATTCCTTGGCTGAGG GAGAGGCTGAGAACTGG GCAGACACCCCTGGAG	ILMN_1795845	GAAATTCCTCAACAGGGCATTATCCGCTCCCTGA ATGTCCATGTGAGTGG
230.33511	393.76013	299.93097	C1ORF55	FLJ35382; RP4-671D7.1; dJ671D7.1	NM_152608	Homo sapiens chromosome 1 open reading frame 55 (C1orf55), mRNA.			TAGCCACTGCAGCCTTCTTAAGCTTAGTGTTTGC ACAGTATACCTCTTTC
339.82263	620.02673	461.2268	LRP11	MANSC3; FLJ14735; bA350J20.3; MGC39092	NM_032832	Homo sapiens low density lipoprotein receptor-related protein 11 (LRP11), mRNA.	CTTCTCTTCAAGCTGCGC CCACCCCGACCACACCA AGGAAGCCGCCGAGG	ILMN_1813719	AGGCAAATCATTCCCACCATCACTTAACGCCGG GATTATACACATTCTAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
32.976276	68.41696	48.57859	ZNF200	MGC45293	NM_198088	Homo sapiens zinc finger protein 200 (ZNF200), transcript variant 3, mRNA.			ACTGTACCCGGCATGAGAAAACCCACTCAGCCT GTAAGACCCGAAAGCAG
899.23096	1138.3893	1010.80597	KTELC1	MDSRP; MDS010; C3orf9; MGC32995; hCLP46; CLP46; KDELCL1	NM_020231	Homo sapiens KTEL (Lys-Tyr-Glu-Leu) containing 1 (KTELC1), mRNA.			GGATTTCAGGTTCCCTTTTTGTGCCTTCATGCCC TACTTCTTAATGCCTC
197.60178	234.52261	215.20595	TARBP2	TRBP1; TRBP; TRBP2	NM_134324	Homo sapiens TAR (HIV-1) RNA binding protein 2 (TARBP2), transcript variant 2, mRNA.			CTGATGATGACCACTTCTCCATTGGTGTGGGCTC CCGCCTGGATGGTCTT
77.23142	211.53513	127.91428	C10ORF88	FLJ13490	NM_024942	Homo sapiens chromosome 10 open reading frame 88 (C10orf88), mRNA.	CCTCGAGGACTCTCTGC GTCTCTGGAGACAAGGG CACTACACGCACTTCA	ILMN_1676689	GAGGCTCTCCATGGAAGGATGAACACATATGAG TCAAGGGATTGCAATTC
48.435146	133.48096	83.31879	LOC401233		NM_001013680	Homo sapiens similar to HIV TAT specific factor 1; cofactor required for Tat activation of HIV-1 transcription (LOC401233), mRNA.			CTTTAGGACACAGCCTTGCATAAGAGCCGTGAA GAACTTGGGGCAGTTGC
47.609894	75.78342	59.948616	ABHD6		NM_020676	Homo sapiens abhydrolase domain containing 6 (ABHD6), mRNA.	GCCTTCGGTTGTAAGTA GCCAGATCCCTCTCCAG TGACATTGGAACATGC	ILMN_1687375	AGGTATGTTCTGAGTGAACCCACAGCAGTCGCA GAATGAGCACCTGGCAG
2172.3975	3349.0059	2703.7227	ATP6V0B	HATPL; ATP6F; VMA16	NM_004047	Homo sapiens ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b (ATP6V0B), transcript variant 1, mRNA.	CTCTGGAGGATTTGGGG TGCCCCTCTCGGCAGGG AACAGGAAGTAGGAAT	ILMN_1813374	GGCCCTCCCTGCACTCCCCTCTTGCTGCGTGTT GATTTGGAGGCACTGCA
525.0018	720.2643	619.57263	TMEM2		NM_013390	Homo sapiens transmembrane protein 2 (TMEM2), mRNA.	CTCCCTTGGGGTGGGAA TCTATGATGGAGGTTACT GGGGAAACAGCTCAG	ILMN_1705035	GGCTGATGGCCTCTACCTTTGTATCCAGGAGAA ACTGCAGAGCAGCCCTG
73.981735	127.314285	100.72284	TRAF6	MGC:3310; RNF85	NM_004620	Homo sapiens TNF receptor-associated factor 6 (TRAF6), transcript variant 2, mRNA.			TATTAGTGCGCTGTGAGGTCTCCACCCGCTTTGA CATGGGTAGCCTTCGG
311.9226	347.7226	325.81845	FAM18B	NPD008; YDR084C; FLJ46240; CGI-148	NM_016078	Homo sapiens family with sequence similarity 18, member B (FAM18B), mRNA.	GTAACCACGGGGTCCAT CTTTTACATCTGGTACAC ACAACAGACGCTCAG	ILMN_1732468	AGGTGCCAACCTGTATGGTTACATCAGGTGTAA GGTGCGCAGCAGAAAGC
269.72263	644.381	391.3601	ARID3A	E2FBP1; DRIL3; BRIGHT; DRIL1	NM_005224	Homo sapiens AT rich interactive domain 3A (BRIGHT-like) (ARID3A), mRNA.	GGCAGACCTGACTCTCT TAAGGAGGCTGAGAGCC CAAACTGCTGTCCCAA	ILMN_1768482	CCACACACTCACCACTCCCAGCTTCTCGTGTCCA GTGAAACCCCTGAACC
237.28929	501.38095	317.16428	PREB	SEC12; MGC3467	NM_013388	Homo sapiens prolactin regulatory element binding (PREB), mRNA.			TGGCATTTGCTGGGGAAGGGACTGGCCTGGTAC TTGCTGTTAGGGCAGGA
355.3393	1111.4185	563.21423	UBA6	MOP-4; UBE1L2; UBA6; FLJ10808; FLJ23367	NM_018227	Homo sapiens ubiquitin-like modifier activating enzyme 6 (UBA6), mRNA.	GATGGTGTGGGGGGTTG GAGTTTTCTTCTAATACC GAGGGTTCCTGGCTG	ILMN_1726752	GCCATGATTTCTTCTGTTTGGTTCTACTAAGCTA GAAAGCCAGGGTGAAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
64.37612	151.12679	94.044495	ERN1	MGC163279; IRE1; IRE1P; FLJ30999; MGC163277	NM_152461	Homo sapiens endoplasmic reticulum to nucleus signalling 1 (ERN1), transcript variant 2, mRNA.			ACTGACATGTGTGTGCCTGAGTGCCAGCCACCG TGTGAACTCTTTGGAGG
130.14761	178.64345	143.72261	SNW1	SKIIP; Prp45; SKIP; NCOA-62; Bx42; MGC119379; PRPF45	NM_012245	Homo sapiens SNW domain containing 1 (SNW1), mRNA.	AGGTTCAGGTGTAGCGT CCCTGGAGGTTGACTGT GCCAAAGAGGGCAATC	ILMN_1751164	TCTGGGTGCCAGATCCCAGCACTACTTTTTATTA CTGGAGAAATGGGGGG
177.37262	199.86429	192.48929	CENTD3	FLJ21065; ARAP3; DRAG1	NM_022481	Homo sapiens centaurin, delta 3 (CENTD3), mRNA.	CGACCGTTGCGAGACGT TGAGCTGCGGAAGATGA GTCCAAAGCCGAGAGC	ILMN_1651789	CATTCTGGGACTACCGTGAAGCCTGGAGTAGGG AGAGCGAGTTTGGGAGC
1923.5309	7437.856	3208.2976	RALA	MGC48949; RAL	NM_005402	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA.	CACCTGTAATCCGACTGT AAGCTCATCACCTTGGG AGGCCACTGTAGGAG	ILMN_1669201	GCTTTGAGACCTTTCCTCTCCTGGGTACTGAGGT GCTATGAAGCCAACTG
46.24128	57.777557	50.697205	UTRN	DRP; DRP1; DMDL; FLJ23678	NM_007124	Homo sapiens utrophin (UTRN), mRNA.			ACCGCACGACACCAGCACGGATCTCACGGAGGT CATGGAGCAGATTCACA
204.14761	288.45593	234.33511	TGDS	TDPGD	NM_014305	Homo sapiens TDP-glucose 4,6-dehydratase (TGDS), mRNA.	GTCCTCTCCATCATCCTC AGTGTGAGTCCTCAGAG CCTCCATCTGCCAAG	ILMN_1661695	CCTGATTCGGACAACCATGAGGGGTAGTGGTGC TAGGGAGAAGGCAACCT
2715.3726	4372.927	3372.281	FKBP1A	PKCI2; FKBP12C; PPIASE; PKC12; FKBP-12; FKBP1; FKBP12	NM_000801	Homo sapiens FK506 binding protein 1A, 12kDa (FKBP1A), transcript variant 12B, mRNA.			CTGTCCCTGGGCCAGCAGGGACCTCTGAAGCCT TCTTTGTGGCCTTTTTT
3417.9644	5128.006	4050.8228	RPRC1	PARCC1; FLJ10350	NM_018067	Homo sapiens arginine/proline rich coiled-coil 1 (RPRC1), mRNA.			GGTACCCATGCCCCCTGCCCTCGCCTGGAATCA GTGTTACTGCATCTGAT
95.23512	117.95595	105.20596	KIAA1279	DKFZP586B0923; KBP; TTC20	NM_015634	Homo sapiens KIAA1279 (KIAA1279), mRNA.	AAATACTGGTGATGCTCC CTAGAGCAGGAGGCCCG GAAGTGCTGACGCAG	ILMN_1758392	AGATTCCTTGTAAGAAAAAATGCTGGGTAATGTA CCTGGTAACAAGCCTG
933.9309	1139.56	1015.4851	ACADM	MCADH; ACAD1; MCAD	NM_000016	Homo sapiens acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRNA.			GACTGTTGGTCTCTAGGTAGCCTTTGGTCTATTG TACACAATCTCATTTC
371.78928	542.4143	434.6143	DPP8	FLJ20283; MGC26191; MSTP141; FLJ14920; DPRP1; DP8	NM_017743	Homo sapiens dipeptidyl-peptidase 8 (DPP8), transcript variant 2, mRNA.	CGGAACATATCCAGTACT CCTGGTTCCTAGGTGAG CAGGTGATGCCCCAG	ILMN_1675939	GGGTCACCCTGACCAGAATGAACAGGGCTATTA CTTAGGATCTGTGGCCA
195.21428	342.32678	250.28513	ROCK1	P160ROCK; MGC131603; MGC43611	NM_005406	Homo sapiens Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA.	TTAAACTTCTGGGTCCG GTGCTAGTCAAACAGGA GCTGGGGGAGGCTCGG	ILMN_1661490	GTGCACATAGGAATGAGCTTCAGATGCAGTTGG CCAGCAAAGAGAGTGAT
297.73096	393.12677	337.5476	TFIP11	FLJ22086; TIP39; bK445C9.6	NM_012143	Homo sapiens tuftelin interacting protein 11 (TFIP11), transcript variant 2, mRNA.	GTGTACTCTCACGACTG GCTAAGACTTGCTGGAC TGACACCTATGGCTGG	ILMN_1762810	GTCTTCATGCCCGTCATTGGGAAGCGACACGAA GGGAAGCAGCTCTACAC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
31.612083	271.9101	81.1853	HERC3	KIAA0032	NM_014606	Homo sapiens hect domain and RLD 3 (HERC3), mRNA.	GAATGGCAGGACCCTGA GTTGATGAGAGACGTGG AAGCAGCCACAGGGCA	ILMN_1729827	TCACCTTCCTCTGTACACTTGGAAATGCCTCTGG CTTGTTGCAGCCCTCC
1980.8394	3020.7017	2354.7976	CCDC50	C3orf6; DFNA44; YMER	NM_174908	Homo sapiens coiled-coil domain containing 50 (CCDC50), transcript variant 1, mRNA.			CTCCTGTGTTTGCATTCCTGGGATTTATCCTCAA GTGCATTTCTGACCAT
339.22678	421.76843	371.5851	MRPL43	MGC48892; bMRP36a; MGC17989	NM_032112	Homo sapiens mitochondrial ribosomal protein L43 (MRPL43), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA.	ACCCTCTAGCTCCCATTG GCTGAAGACACTGAAGT AGCCCACCCCTGCAG	ILMN_1659462	AATACCTTAACGGGGCTGTGCGCGAGGAGAGCA TCCACTGCAAGTCGGTC
1260.5977	2879.1643	1856.481	MSX1	HOX7; HYD1	NM_002448	Homo sapiens msh homeobox 1 (MSX1), mRNA.	GGAGCCAGGCCCCCGCT TCAGTCAAGACCTGCCTA GAAAAAGGAAGTGGA	ILMN_1699170	GGTCCCCAGCAGAATTGACAGTTGAACAGAGCT AGAGGCCATGTCTCCTG
114.276794	138.77261	122.68095	TMEM93	MGC2963	NM_001014764	Homo sapiens transmembrane protein 93 (TMEM93), transcript variant 1, mRNA.			ACCCTCAATCTCCTCGGCGTCTTTGGAAGATCC GAGGCCCAGGACTGGTG
22.742645	76.266525	37.63667	RANBP6		NM_012416	Homo sapiens RAN binding protein 6 (RANBP6), mRNA.			TTCTCCCTGCAAAGCAGCTCAACAAGAGAAAAAG CTCTAGTTATAGGGCT
107.59761	169.43929	133.7768	ALKBH1	alkB; hABH; ALKBH; ABH	NM_006020	Homo sapiens alkB, alkylation repair homolog 1 (E. coli) (ALKBH1), mRNA.			AGTCAGTCCAAGGAGGTATGTTCTTCCACAACAG CCTTCTCAGCCTCTGC
280.78094	324.95178	298.5518	PVR	Necl-5; HVED; NECL5; TAGE4; PVS; CD155	NM_006505	Homo sapiens poliovirus receptor (PVR), mRNA.	GGAGGAGGGGACCCATA GGACGCGTTAACATGGA CCTGGAAAACAAAGTG	ILMN_1679546	GAGCCGGGAACAGAGAAGTGTGGGGAAGAGAT AGGAACCAGCAGGATGGC
475.65594	1145.9644	699.8268	YRDC	RP11-109P14.4; FLJ23476; SUA5; DRIP3; IRIP; FLJ26165	NM_024640	Homo sapiens yrdC domain containing (E. coli) (YRDC), mRNA.	GTCTTCAGCTTCTTGGCC AACTTAGTTTGCCACAGA GATTGTTCTTTTGC	ILMN_1798636	GGTGTAATAGTGGGATGTCTGCTTAGTTGGCAG GGGTTCAGTCCAAATGG
140.33095	170.37262	152.71844	ELL	C19orf17; ELL_HUMAN; DKFZp434I1916; ELL1; Men	NM_006532	Homo sapiens elongation factor RNA polymerase II (ELL), mRNA.			CCTCTGCCCTGGGAACCAGTCCAAGGGGCTGTC AGTTGAATTTGCCTTTT
293.4226	439.37262	350.9226	CBL	C-CBL; CBL2; RNF55	NM_005188	Homo sapiens Cas-Br-M (murine) ecotropic retroviral transforming sequence (CBL), mRNA.	GCCTGGCGTCTGTCCTG GCCCCGCCTGTCAGAAG ATGAACATGTATAGTG	ILMN_1707748	GTCCTCCTTATTCAAGATTTTGAAATTCTTAGCCT GGGAGTGCTGGAGAG
530.7643	1025.9601	710.1476	MTMR6		NM_004685	Homo sapiens myotubularin related protein 6 (MTMR6), mRNA.			TGCTCACAGGTGGACTGAGAAATCAGTTACATCT TAAGTGACCTACAGGG
659.9518	935.47266	771.90173	C14ORF135	FLJ38170; FBP2; FLJ12799	NM_022495	Homo sapiens chromosome 14 open reading frame 135 (C14orf135), mRNA.	CCCCCCAGCCCCTGCCA GCTCCACACTATCTCTTA GCTGAGTTTTTGCAA	ILMN_1798885	TGGCCAATATTTGTGCCCTCTGGACTTTAGTAGG CTTTGGTAAATGTGAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
358.90594	691.92676	481.08093	FNDC3A	KIAA0970; bA203I16.5; FNDC3; RP11-203I16.5; bA203I16.1; FLJ31509	NM_001079673	Homo sapiens fibronectin type III domain containing 3A (FNDC3A), transcript variant 1, mRNA.	GGTGTGGGAGATGTGAG ACCATTCTGAGGTCAGC GATAGCCCAAAGGCTC	ILMN_1724410	GTGCCACATTTGGCAGTACAAATGAGTCTGAGT GTAATAGCCCAGAGATT
2390.5393	2671.681	2513.6726	LOC26010	DNAPTP6; DKFZp564A2416	NM_001100422	Homo sapiens viral DNA polymerase-transactivated protein 6 (LOC26010), transcript variant 2, mRNA.			CCCTGCCCGAGGTGCTGACCCAATTCGCTGCCA AAAGAGTGTCAATCAGA
327.18512	752.1476	472.37262	HDGFRP3	HDGF2; CGI-142	NM_016073	Homo sapiens hepatoma-derived growth factor, related protein 3 (HDGFRP3), mRNA.	AGGCAAACACAACTCTTG ACTGCCCTCCCACCCTC CTACCTGTTCAGTAC	ILMN_1764617	TAAAGCTGGAATCAGCAACAGCCCTATGGGAAA CCAGACAAAGCATTGAC
403.8393	505.46426	446.2143	SLC35E3	BLOV1	NM_018656	Homo sapiens solute carrier family 35, member E3 (SLC35E3), mRNA.			AGGAAGGACACACAGTAGCTCTCTGCTTGCTGA TAGATGGTTTCCCAGTG
1935.4727	2192.5142	2045.3643	CNIH4	HSPC163	NM_014184	Homo sapiens cornichon homolog 4 (Drosophila) (CNIH4), mRNA.	GCACCTTTGCTGCCTGT CATTGTTGCCTGAAGAA GGCTGGAGTTGCTCTG	ILMN_1750718	GCACAGTTGAGGAGCCAGAGACTTCTTAAATCAT CCTTAGAACCGTGACC
74.58643	146.61429	97.964294	SOAT1	SOAT; ACAT1; STAT; ACACT; ACAT; RP11-215I23.2	NM_003101	Homo sapiens sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1 (SOAT1), transcript variant 688113, mRNA.	CCACGCTCAGTTTGGAC CATTGGAGGAACTTAGT GTCACGCACAAATGGG	ILMN_1735199	GAGCATTGGAAGGGGTATCAGAGACCATGTAGT TCAACTTTCCACTCAAA
52.89282	84.82271	65.104935	TADA2L	KL04P; FLJ12705; ADA2; hADA2	NM_001488	Homo sapiens transcriptional adaptor 2 (ADA2 homolog, yeast)-like (TADA2L), transcript variant 1, mRNA.	CTTCCTCATTGCAGGGC TGGGGGAGTCACTTAAC CTGTCTGGGGCTCAGT	ILMN_1664351	GACTGGCGCAGGCAAGAGCACTCATCAAGATAG ATGTGAACAAAACCCGG
942.36426	1298.8059	1112.56	GPR172A	GPCR41; PAR1; D15Ertd747e; GPCR	NM_024531	Homo sapiens G protein-coupled receptor 172A (GPR172A), mRNA.			AGGCCCGCACACCGGTACACTCGTGGACACCTA CACACTCCATAGGAGAT
111.33095	160.8601	130.1518	TRIM11	RNF92; BIA1	NM_145214	Homo sapiens tripartite motif-containing 11 (TRIM11), mRNA.	CTGGGTTTTCAGTGTCCT AGCGGAATGCAAGTAGG CAGCCAGCCCGTCTG	ILMN_1694325	AGTCTCTCTACCCTGGGGAGGAACAGTGGCTTC TCAGAGCCTGGGGCATA
1473.506	1846.6393	1602.5559	UBP1	LBP-1B; LBP1A; LBP1B; LBP-1a; DKFZp686L1745	NM_014517	Homo sapiens upstream binding protein 1 (LBP-1a) (UBP1), mRNA.			CCTTTGCTTTCGTGTGACCACATGTTTTCTGTAC CAGTCACTGGGGAAAG
299.33093	437.2351	344.64764	HYOU1	DKFZp686N08236; ORP150	NM_006389	Homo sapiens hypoxia up-regulated 1 (HYOU1), mRNA.	GGATGTGGCTGGCTCGT GGGAAACAGCAAAACAC TAAGCCTGACCTCTCC	ILMN_1735055	AGGGTCAGGGCTGGCCTTCCTCTGTGCATCACT CTGCTAGGTTGGGGGCC
426.75595	515.8601	456.84344	GNPAT	DAP-AT; DAPAT; DHAPAT	NM_014236	Homo sapiens glyceronephosphate O-acyltransferase (GNPAT), mRNA.	CCAGAAACTGGCTTAGA GGAGCTCCAAATATGTG GAATTACCACACTCTG	ILMN_1776164	GCAGAAAAACGCCTTAGCAGCCTGTGTGAGGCT CGGAGTAGTGGAGAAGA
260.82263	317.2976	279.93512	PCGF1	RNF68; 2010002K04Rik; RNF3A-2; FLJ43754; MGC10882; NSPC1	NM_032673	Homo sapiens polycomb group ring finger 1 (PCGF1), mRNA.	ATGTGGAAAAGCCGTTAA TATCTGCTCACATCTTAC TCAGCATCAGAAAG	ILMN_1747824	GATCACATGACAATGAAGCAGATATGGCTCTCCC GCTGGTTCGGCAAGCC

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
286.82263	349.80597	315.0226	ZFYVE19	FLJ14840; MPFYVE	NM_001077268	Homo sapiens zinc finger, FYVE domain containing 19 (ZFYVE19), mRNA.			GATAGGCCCCTTCCTGAGCCTTGGTGTCCCTGG AATGAGGAAAGATTCTC
5084.048	9495.839	6432.231	GSTO1	P28; GSTTLp28; DKFZp686H13163	NM_004832	Homo sapiens glutathione S-transferase omega 1 (GSTO1), mRNA.	GGGACTTCCCTTGACTG GGTTGTGTTTCTTTTCCT GCCTCAGCCCAGCTC	ILMN_1796288	GACTGGCAAGGTTTCCTAGAGCTCTACTTACAGA ACAGCCCTGAGGCCTG
693.23096	931.11426	772.4976	ZZZ3	DKFZP564I052; FLJ10362; DKFZp313N0119	NM_015534	Homo sapiens zinc finger, ZZ-type containing 3 (ZZZ3), mRNA.			TTAGTCTGCACAGTGAGCAAGGGTTCACATGCAT TCTTTTATACTGCTGG
7601.7812	8121.856	7786.681	EPN1		NM_013333	Homo sapiens epsin 1 (EPN1), mRNA.	AAGCCAGAAAGTGGAGT TCTGTCCGCTGCGAGCC TGGAGATGGGGAACAG	ILMN_1667022	CCCTCACGCACCCGCTCACGCACCCTCGGTGAA TCCTTGGTGATGATTTT
842.95593	1355.5143	1014.90173	C3ORF17	DKFZP434F2021	NM_001025072	Homo sapiens chromosome 3 open reading frame 17 (C3orf17), transcript variant 2, mRNA.			CATATAAGCCCTGGGTCGGGGGGTAACTGTGGG GATCACTGCCTGAGACA
676.0893	731.6893	693.8185	DIP2B	KIAA1463; MGC104005	NM_173602	Homo sapiens DIP2 disco-interacting protein 2 homolog B (Drosophila) (DIP2B), mRNA.			TCTGGTTTAGGTGTATGTAGTTGGGCCATGTTAC TTGTCCAGAGGAAGAG
4705.131	7564.8896	5537.3394	TFRC	TFR; TFR1; CD71; TRFR	NM_003234	Homo sapiens transferrin receptor (p90, CD71) (TFRC), mRNA.	AGCTGTCTTCTTGCCCC GGTCAGTGCCAGCCGTA CTATTCACAACACTGC	ILMN_1685327	GCTCCTGGTCTTGAGATGTCTTCTCGTTAAGGAG TAGGGCCTTTTGGAGG
71.97383	149.24762	92.99792	RRN3	MGC104238; TIFIA; DKFZp566E104	NM_018427	Homo sapiens RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) (RRN3), mRNA.			CGAAATTCCCCAGAAATTAGTAGTAAGTGGGGTC TTTGTGGGTTGGGAAG
194.07262	265.2268	215.32262	C8ORF32	FLJ10204	NM_018024	Homo sapiens chromosome 8 open reading frame 32 (C8orf32), mRNA.	CGCTGATATCTGTCTGG GTGATAAGCAGTTTGGC GTTCTGTGATTCCAGC	ILMN_1763313	GCCAGTAATCGTTTTTGTTCAGATAGAGGTGTGG AGGTAGAGCCAGCCCC
97.80019	196.12679	117.776794	IL4R	IL4RA; CD124	NM_000418	Homo sapiens interleukin 4 receptor (IL4R), transcript variant 1, mRNA.			TGTGGGCCGGGCAATCCAGACAGCAGGCATAAG GCACCAGTTACCCTGCA
1279.4392	2050.7644	1507.4976	RALB		NM_002881	Homo sapiens v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein) (RALB), mRNA.			GAGAGAGATAAGCCATCGCCCCTTTGCCTCTGA GAATTGGCTGCTGTTTC
255.89761	298.7768	268.38928	CD164	endolyn; MGC-24; MUC-24	NM_006016	Homo sapiens CD164 molecule, sialomucin (CD164), mRNA.	GCCCCCGAGAGACATGA CTTCCAAGCCGCATTCC GACTGGATTCCCTACA	ILMN_1779579	GTTAGATTTTGCAAGTCTACAAATGAGCTCTTGC AACAGAACTCACAGCC
318.06427	330.3601	321.58093	ADAT1	HADAT1	NM_012091	Homo sapiens adenosine deaminase, tRNA-specific 1 (ADAT1), mRNA.			GGGACTGCCGGTGGCCATCTTTTCCTACTACCT AGAGAAAGCCAGCAAAG

Raw XS	pOS + 6 GFs Raw	pOS + no GFs Raw	Common	Synonyms	Genbank	Description	Probe_Sequence	Probe_Id	Probe_Sequence_I
2645.2976	3642.8062	2951.6475	ACTR3	ARP3	NM_005721	Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA.	CTGTCCAGAGGGTTATT CAGGAGGCTGGTGGTGG CATGATGAGTGTGGAG	ILMN_1695193	GAAGAGTAAAGACAAGAGTGTTGGACCAGTATT GCAGTTCTGTAGTGTCA
237.41428	449.5393	296.58096	SESTD1	DKFZp434O0515; SOLO	NM_178123	Homo sapiens SEC14 and spectrin domains 1 (SESTD1), mRNA.			GCGCTGCACTTCTCGGTCATCTGGGGATACACT TCCTCGACTGAACAGAG
87.08992	88.03931	89.86612	MRPS36	MRP-S36; MGC22896; DC47	NM_033281	Homo sapiens mitochondrial ribosomal protein S36 (MRPS36), nuclear gene encoding mitochondrial protein, mRNA.			TGGGGCCCCTCCTGTGCCAAGGGTACGTATATT GTGAAGTAAAGCCTCAC
53.36512	68.62071	57.733624	ZMYM5	ZNF237; MYM; HSPC050; ZNF198L1	NM_001039649	Homo sapiens zinc finger, MYM-type 5 (ZMYM5), transcript variant 2, mRNA.			GGTCATCCAGCTTGTCCTTTAGTCAGTAGATCTA GGAACTCACCAGTGGA
58.290684	66.20669	60.96512	LONP2	LONP; MGC4840; LONPL	NM_031490	Homo sapiens lon peptidase 2, peroxisomal (LONP2), mRNA.			TAGTCCAGCTACTTGAGGCTGAGATGGGAGGAT GAGGGAGGTCGGGGCTG
727.0893	864.7726	763.2976	TM9SF3	SMBP; EP70-P-iso; RP11-34E5.1	NM_020123	Homo sapiens transmembrane 9 superfamily member 3 (TM9SF3), mRNA.	GGAGACTGATCCTGCCA TCACTGCTGCAAAGCAG AACACGAGACTCAAGG	ILMN_1685750	ATCTGTTCAGGTTGGTGTACCGTGTAAAGTGGG GATGGGGTAAAAGTGGT
532.20593	732.60596	582.0643	SACM1L	SAC1; KIAA0851; DKFZp686A0231	NM_014016	Homo sapiens SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA.	CTCCTATTCCTACATGGT TCGTGGGGGCCACTTTG CGGCCTTTGAGGAGC	ILMN_1701025	CTGAACTGCTAATGTGGCTGCTTTGTAGGGAATG GACTAATATCAGTGTG
220.06429	321.3393	250.1726	TWF1	MGC41876; MGC23788; A6; PTK9	NM_002822	Homo sapiens twinfilin, actin-binding protein, homolog 1 (Drosophila) (TWF1), mRNA.			GCAGACTTCCTTTATGAAGAAGTACATCCCAAGC AGCATGCACACAAGCA
58.259773	170.37262	83.435196	SENP5	MGC27076; FLJ42398	NM_152699	Homo sapiens SUMO1/sentrin specific peptidase 5 (SENP5), mRNA.	GGAGGGCTGGAATCTGT CTTCCCTGACTCGGCTC CTCAGGTCTTTAGCCT	ILMN_1711786	ACATGCCCCGAGTGCGGAAGAGGATTTACAAGG AGCTATGTGAGTGCCGG
49.395973	125.39345	67.78848	ZDHHC2	ZNF372	NM_016353	Homo sapiens zinc finger, DHHC-type containing 2 (ZDHHC2), mRNA.	TGTCAGGACGCGGAAAG CAGGGAGGCAAGGCCC GCGCTAAGGCCAAGTCG	ILMN_1747589	GGACAGGATTCGATTAAGTATTCCCTCTTGTCAA ACTGGAAGCTAGGGGA
343.8393	360.49762	351.01013	KCTD21		NM_001029859	Homo sapiens potassium channel tetramerisation domain containing 21 (KCTD21), mRNA.	CATGGATCATTGTCCTAT GAGAGTGTAAGCTCCTC AAGCACAGCTCGTGC	ILMN_1743329	CAGGCCAAGGGTACTTGGGAGAGCCCCTCATGG AGAACCTAGTTTAGACC
73.393654	94.78099	79.0437	NAT1		XM_001127234	PREDICTED: Homo sapiens N acetyltransferase 1 (arylamine N-acetyltransferase) (NAT1), mRNA.	GGTACTGAGTGTCCAGA GCTGCCTCCCCAGGAGG TTAAGGTGGGGGCAAA	ILMN_1679746	TTGGTTTTGAGACCACGATGTTGGGAGGGTATG TTTACAGCACTCCAGCC
10.315353	227.28928	29.578827	MMP10	SL-2; STMY2	NM_002425	Homo sapiens matrix metallopeptidase 10 (stromelysin 2) (MMP10), mRNA.	CAGAAGTATGGCCCAGA AGAGCCCTTGCCCCGCC TGTCTGCCCTTGGTGG	ILMN_1657505	CAGTGGATCATCACAGTTTGAGTTTGACCCCAAT GCCAGGATGGTGACAC

CLAIMS

1. An isolated mammalian cell having the developmental potency of an embryonic stem cell (ESC), the cell being characterised in that the cell does not form a teratoma when provided in an immune deficient animal.

2. The isolated mammalian cell of Claim 1, wherein the cell does not contain, or contains a relatively low amount of one or more of the mRNAs shown in Table 3.

3. The isolated mammalian cell of Claim 1, which does not contain, or contains a relatively low amount of one or more of DNMT3b, HDAC2, Nanog, Sox 2, Oct3/4, SET, ZFP42, HMGB1 or ARID38 mRNA.

4. The isolated mammalian cell of any one of the preceding claims wherein the cell contains one or more mRNAs shown in Table 1 or Table 2.

5. The isolated mammalian cell of any one of the preceding claims wherein the cell contains one or more of SP1, ANP32A, Myc, HMGA1, SMARCAD1, SMARCC1, PTMA, MCM6, PCNA, HDAC1, KLF5, KLF4, BTBD14B, HoxA5, FoxA1, Meis1 and EN1 mRNA.

6. The isolated mammalian cell of any one of the preceding claims wherein the cell has a profile of mRNA expression as shown in Table 4.

7. The isolated mammalian cell of any one of the preceding claims which expresses one or more proteins set forth in Table 6.

8. The isolated mammalian cell of Claim 7, wherein the one or more proteins are expressed by at least 20% of isolated mammalian cells and/or wherein mean fluorescence is greater than 5000 units, and/or greater than 18,000 units..

9. The isolated mammalian cell of Claim 1, which expresses one or more of Oct4, Sox2, NANOG, KLF4, MVH, KIT and Nestin.

10 The isolated mammalian cell of any one of the preceding claims wherein the cell is produced by a process including culturing one or more cells tissues in a medium comprising one or more of FGF9, FGF2, SCF and leukaemia inhibitory factor (LIF), thereby providing the cell.

11. The isolated mammalian cell of Claim 10, wherein the cell is produced by a process including culturing neurospheres or a neurosphere –like cellular mass in a medium comprising one or more of FGF2, FGF9, SCF and/or LIF, thereby providing the cell.

12. The isolated mammalian cell of Claim 10 or Claim 11, which is a human cell, wherein the the medium comprises one or more of FGF2, FGF9, SCF, LIF, TGF-β2 and/or BMP-4.

13. The isolated mammalian cell of Claim 10, 11 or 12, which is produced by a process including:

(a) forming a neurosphere or neurosphere –like cellular mass from a sample of tissue;

(b) obtaining the cell from the neurosphere or neurosphere –like cellular mass, thereby providing the cell.

14. The isolated mammalian cell of any one of Claims 10 to 13, wherein the one or more cells or tissues are of adult origin.

15. The isolated mammalian cell of any one of Claims 13-16, wherein the cell or tissue comprises bone marrow, central nervous system tissue, neural tissue, skin, gut, pancreas, muscle, brain, heart, adipose, olfactory mucosa or other mucosa or epithelia.

16. The isolated mammalian cell of any one of the preceding claims, which is a germline competent cell.

17. The isolated mammalian cell of any one of the preceding claims, which is a pluripotent stem cell.

18. The isolated mammalian cell of any preceding claim which is of human, mouse or rat origin.

19. An isolated mammalian cell selected from the group consisting of:

(i) an isolated human cell designated human XY pOS-17 deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121602;

(ii) an isolated mouse cell designated B6 Rosa26-EGFP XY Pos deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121601; and/or

(i) an isolated rat cell designated SD Rat XY pOS deposited at the European Collection of Cell Cultures (ECACC) on December 16 2009 with accession number 09121603.

20. The isolated mammalian cell of any one of the preceding claims, which is genetically modified.

21. The isolated mammalian cell of Claim 21, which is genetically modified to express a therapeutic agent.

22. The isolated mammalian cell of Claim 22, wherein the therapeutic agent is a protein or an RNA molecule.

23. A method for producing an isolated, pluripotent mammalian cell including culturing one or more cells or tissues obtained from a mammal in a medium containing one or more of FGF2, FGF9, SCF and LIF, thereby producing the isolated, pluripotent mammalian cell.

24. The method of Claim 23, wherein the isolated mammalian cell is a human cell, the medium comprises one or more of FGF2, FGF9, SCF, LIF, TGF-β2 and/or BMP-4.

25. The method of Claim 23 or Claim 24 wherein the cell or tissue comprises, or is obtainable from, bone marrow, central nervous system tissue, neural tissue, skin, gut, pancreas, muscle, brain, heart, adipose, olfactory mucosa or other mucosa or epithelia.

26. The method of Claim 25 wherein the cell or tissue is obtainable from olfactory mucosa.

27. The method of Claim 26, including culturing neurospheres or a neurosphere-like cellular mass obtainable from olfactory mucosa.

28. The method of Claim 27, including

(a) forming a neurosphere or neurosphere-like cellular mass;

(b) isolating the pluripotent cell from the neurosphere or neurosphere-like cellular mass,.

29. The method of any one of Claims 23 to 28 wherein the one or more cells or tissues are of adult origin.

30. A composition comprising the isolated mammalian cell of any one of Claims 1-22 and a carrier, diluent or excipient.

31. An isolated mammalian cell according to any one of Claims 1-22 for use in treating a disease or condition in a mammal.

32. An isolated mammalian cell for use according to Claim 31, wherein the disease or condition is selected from the group consisting of: nerve injury, spinal

injury, schizophrenia, Parkinson's disease, Alzheimer's disease, bipolar disorder, mitochondrial disorders, epilepsy, diabetes, kidney failure, neuro-degenerative diseases, plastic anemia, immune-deficiency diseases, autoimmune diseases, cancers including lymphomas and leukemias, sickle cell anemia and osteoporosis.

33. An isolated mammalian cell for use according to Claim 31 or Claim 32, wherein the mammal is a human.

34. A method of treatment of a disease or condition in a mammal, said method including the step of administering an isolated mammalian cell according to any one of Claims 1-22, or a cell differentiated therefrom, to said mammal to thereby treat said disease or condition.

35. The method of Claim 34, wherein the isolated mammalian cell is autologous to said mammal.

36. The method of Claim 34 or Claim 35, wherein the disease or condition is selected from the group consisting of: nerve injury, spinal injury, schizophrenia, Parkinson's disease, Alzheimer's disease, bipolar disorder, mitochondrial disorders, epilepsy, diabetes, kidney failure, neuro-degenerative diseases, plastic anemia, immune-deficiency diseases, autoimmune diseases, cancers including lymphomas and leukemias, sickle cell anemia and osteoporosis.

37. The method of any one of Claims 34-36, wherein the mammal is a human.

38. A method of producing a non-human mammal, said method including the steps of:

(i) delivering one or more isolated mammalian cells of the aforementioned aspects to a blastocyst of a non-human mammal; and

(ii) producing one or more progeny from said blastocyst.

39. The method of Claim 38, wherein the one or more progeny comprise one or more cells or tissues that have a genetic complement of the one or more isolated mammalian cells delivered at step (i).

40. The method of Claim 39, further including the step of implanting or otherwise transferring the blastocyst produced at step (i) to a female non-human mammal.

41. The method of any one of Claims 38-40, wherein the one or more isolated mammalian cells delivered at step (i) are genetically modified, whereby the progeny produced at step (ii) are genetically modified.

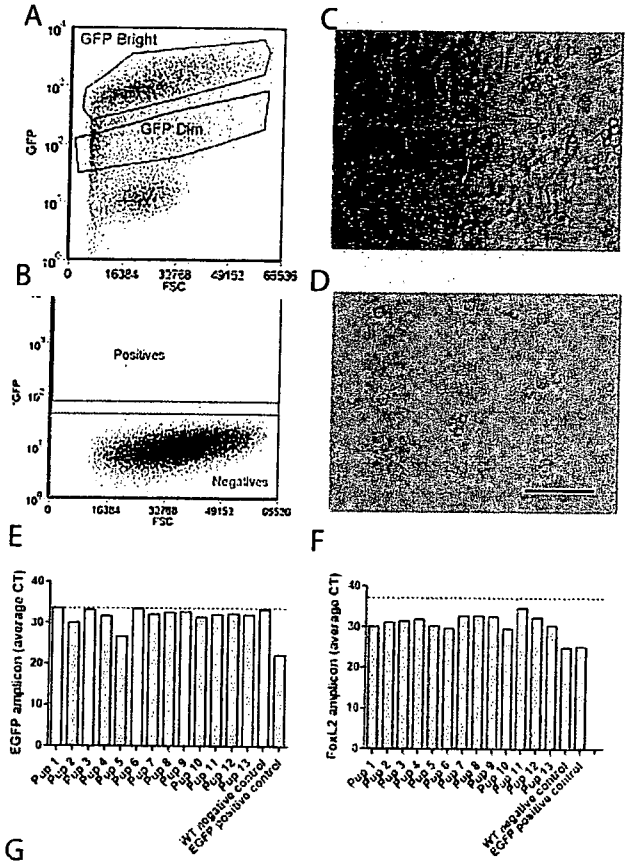
42. The method of any one of Claims 38-41, wherein the non-human mammal is a mouse or rat.

43. A method of identifying, designing, screening or otherwise producing a compound having a desired activity, said method including the step of contacting a candidate compound with an isolated mammalian cell of any one of Claims 1-22, or a cell differentiated therefrom, to thereby determine whether said compound has said activity.

44. A method of identifying, designing, screening or otherwise producing a compound having a desired activity, said method including the step of administering a candidate compound to a non-human mammal produced according to the method of any one of Claims 38-42, to thereby produce a compound having said activity.

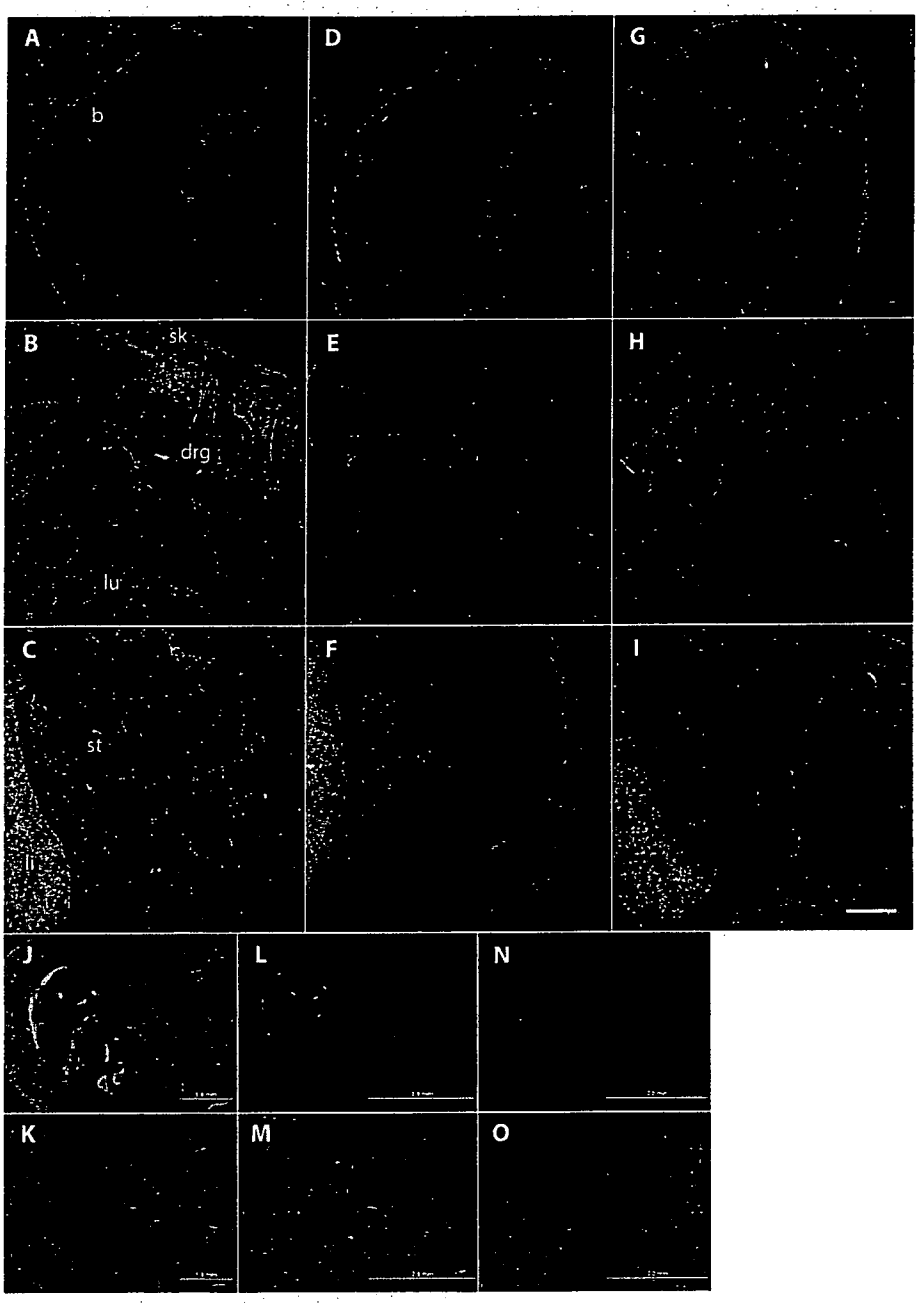
45. The method of Claim 43 or Claim 44, wherein the activity includes include cell growth and/or differentiation, anti-tumour activity, pro- or anti-apoptotic activity, neuropharmacological activity; regulation of metabolism; hormonal activity; gene regulatory activity; cell cycle regulation and immunoregulatory activity.

Figure 1



Experiment date	Blastocysts transplanted	Cell type	Cell state	Cells per blastocyst	Number offspring	Number chimeras	Mouse age
8/06/2007	28	EGFP-dim	Fresh	15-18	13	9	P14
7/11/2007	30	EGFP-dim	Thawed	20-25	5	0	P14
2/05/2008	14	EGFP-neg	Fresh	15-18	14	7	E16.5
7/05/2008	41	EGFP-neg	Thawed	15-18	15	9	E16.5
12/08/2008	20	EGFP-neg	Thawed	15-18	10	6	P14
3/10/2008	20	EGFP-neg	Thawed	1	15	15	E13.5
31/10/2008	14	EGFP-neg	Thawed	1	4	4	P14

Figure 2



b

Figure 3

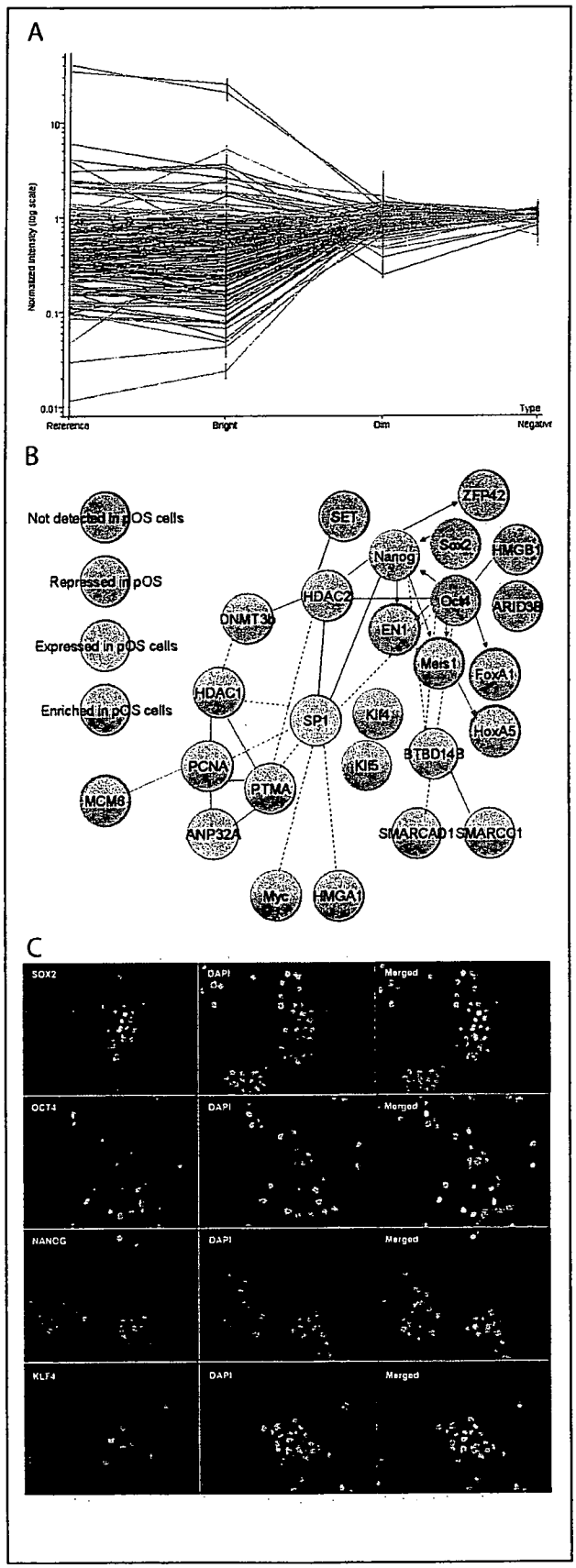

A
Normalized intensity (log scale)
10
1
0.1
0.01
Reference
Bright
Dim
Type
Negative
B
Not detected in pOS cells
Repressed in pOS
Expressed in pOS cells
Enriched in pOS cells
SET
ZFP42
Nanog
Sox2
HMGB1
HDAC2
OCH
ARID3B
DNMT3B
EN1
Meis1
FoxA1
HDAC1
SP1
KLF4
HoxA5
BTBD14B
KLF5
PCNA
PTMA
MCM6
ANP32A
SMARCAD1
SMARCC1
Myc
HMGA1
C
SOX2
DAPI
Merged
OCT4
DAPI
Merged
NANOG
DAPI
Merged
KLF4
DAPI
Merged

Figure 4

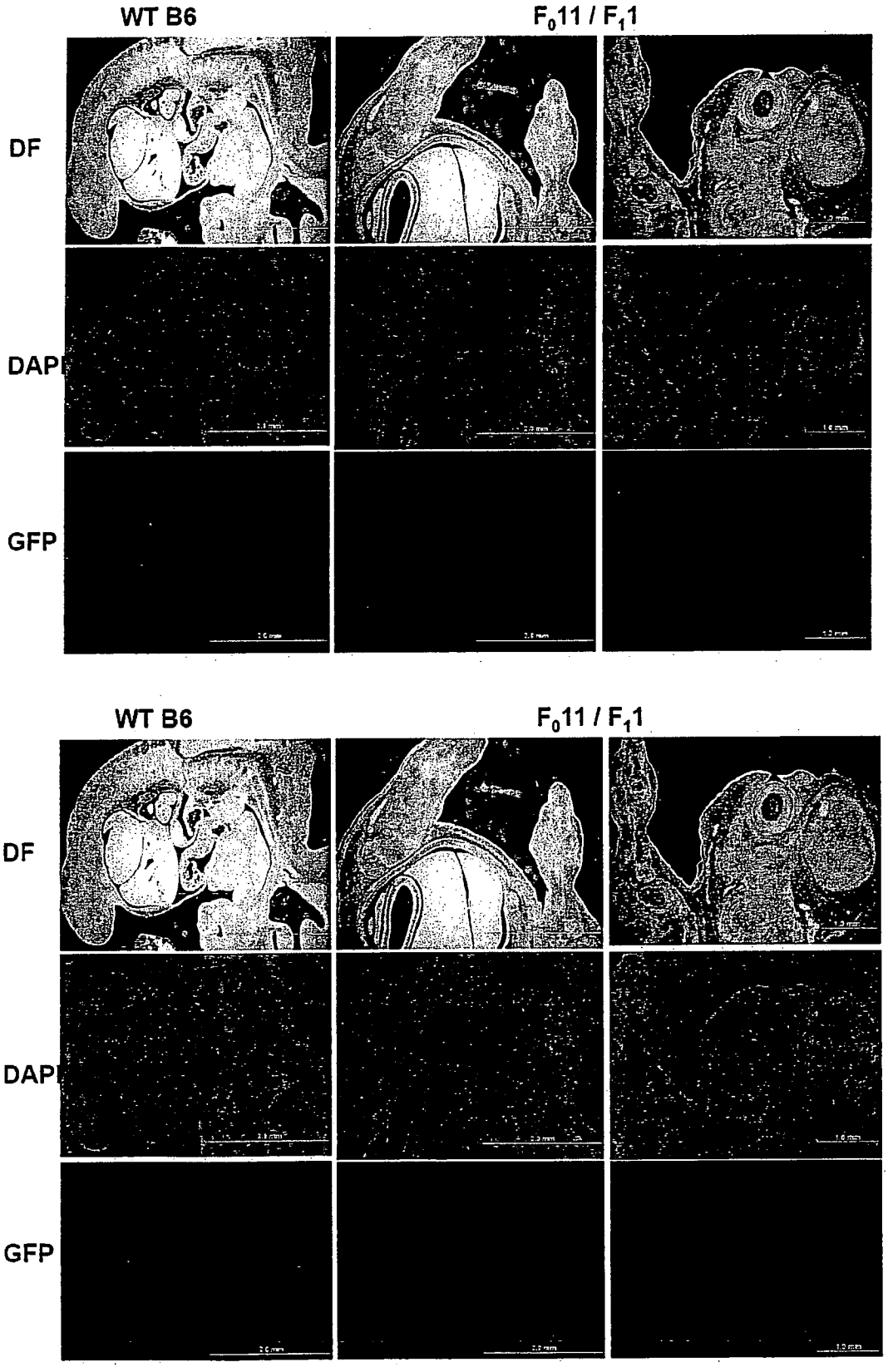


Figure 4/2

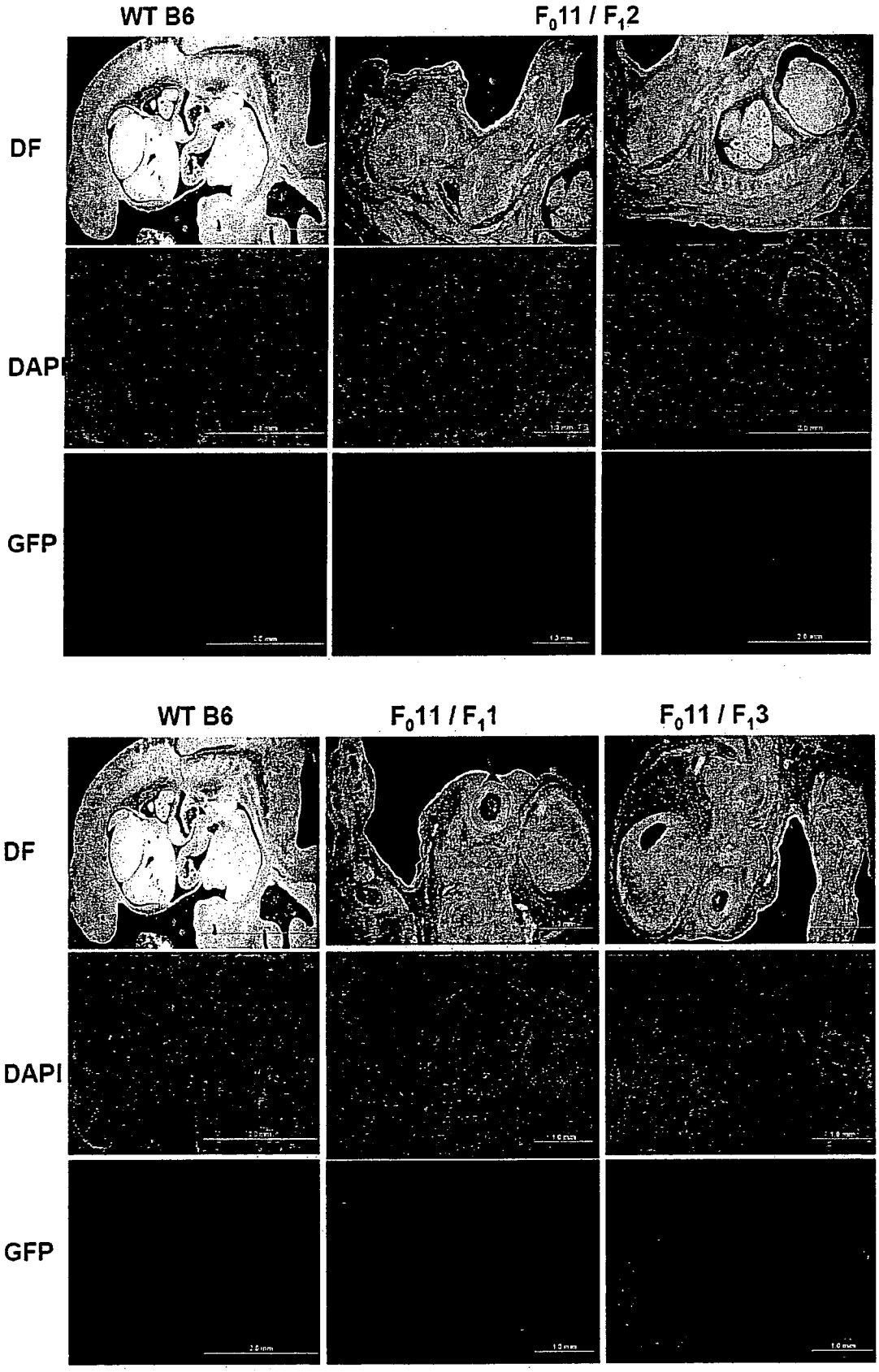


Figure 4/3

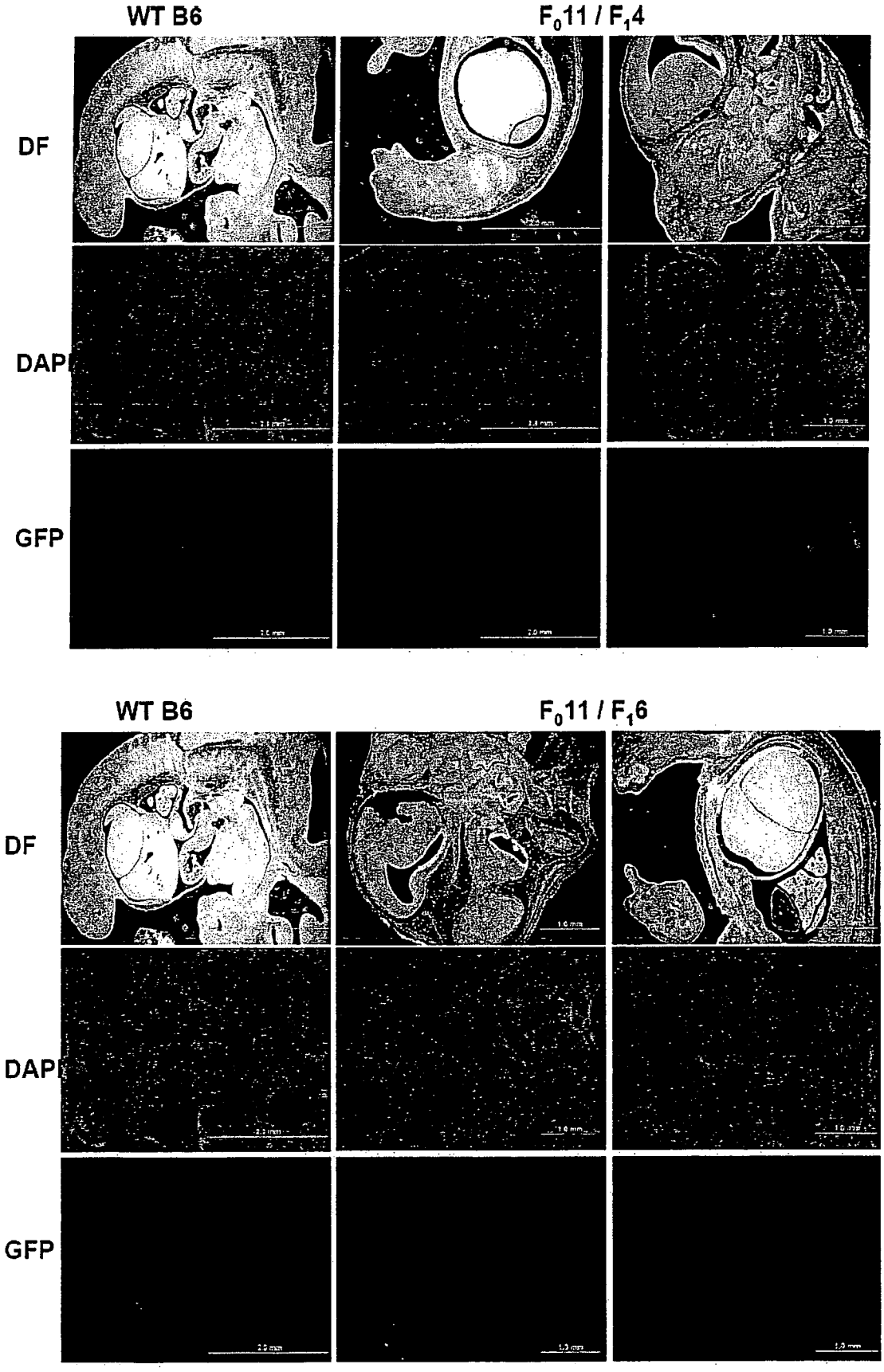


Figure 4/4

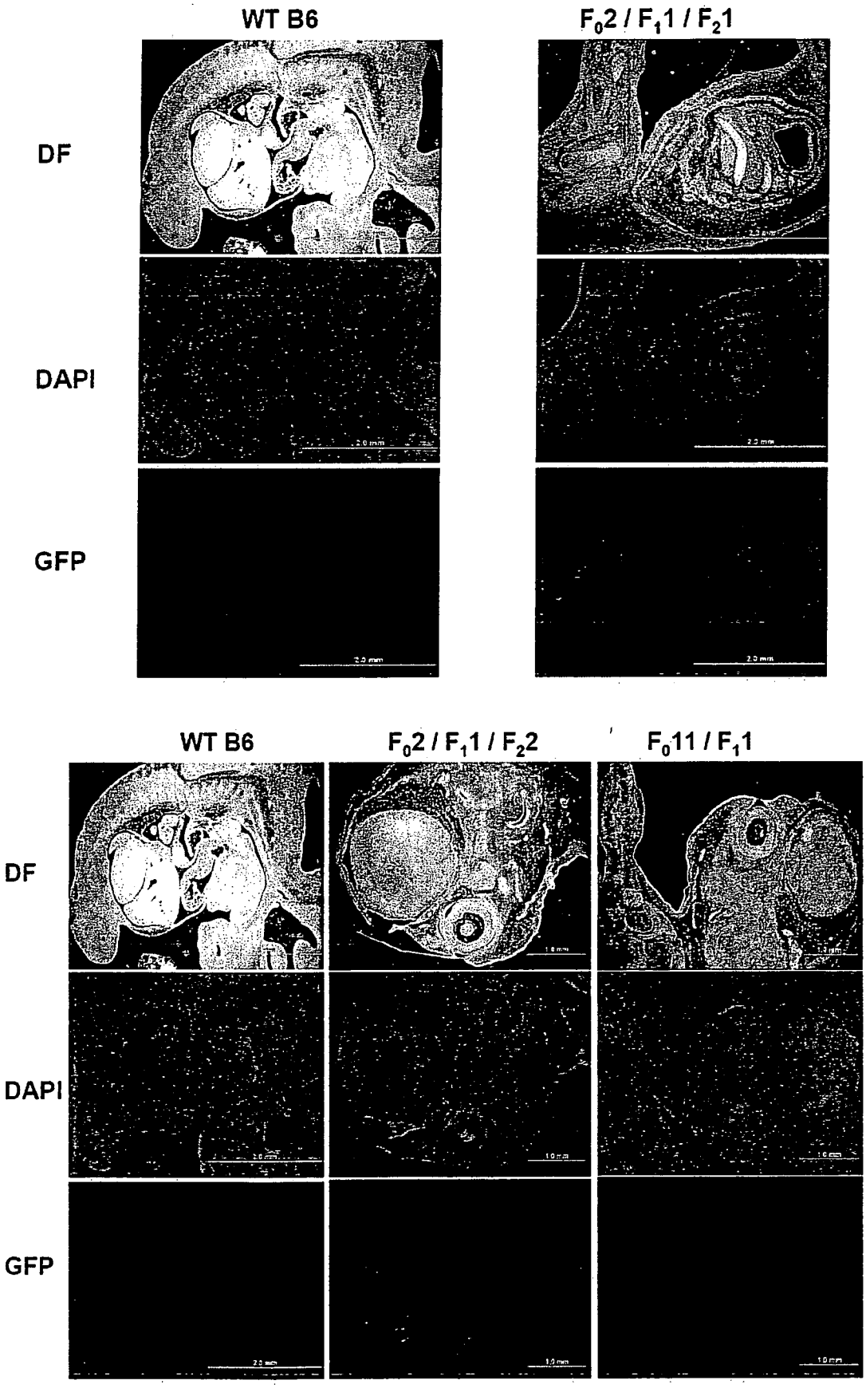

WT B6
F0 2 / F1 1 / F2 1
DF
DAPI
GFP
WT B6
F0 2 / F1 1 / F2 2
F0 11 / F1 1
DF
DAPI
GFP

Figure 4/5

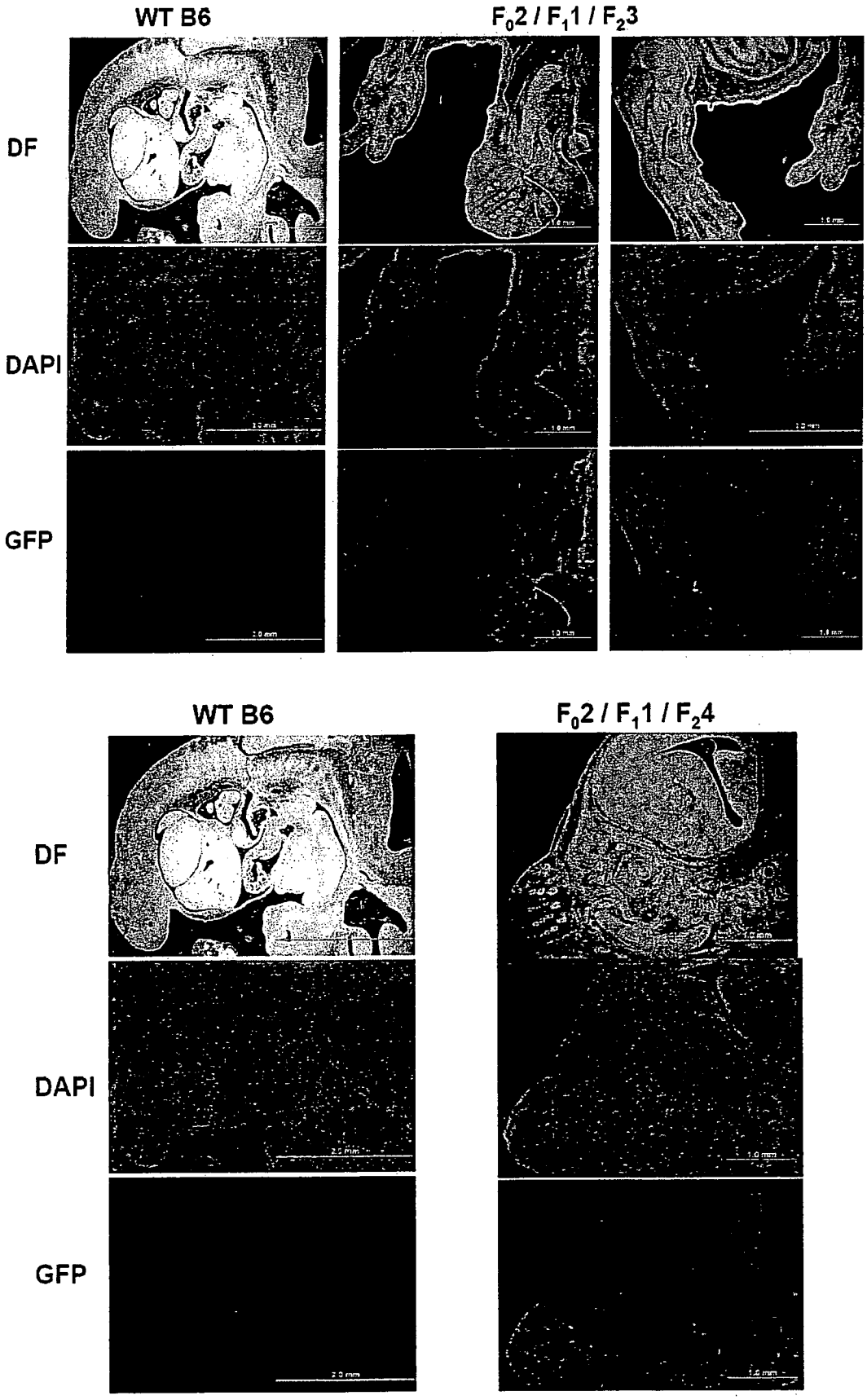


Figure 4/6

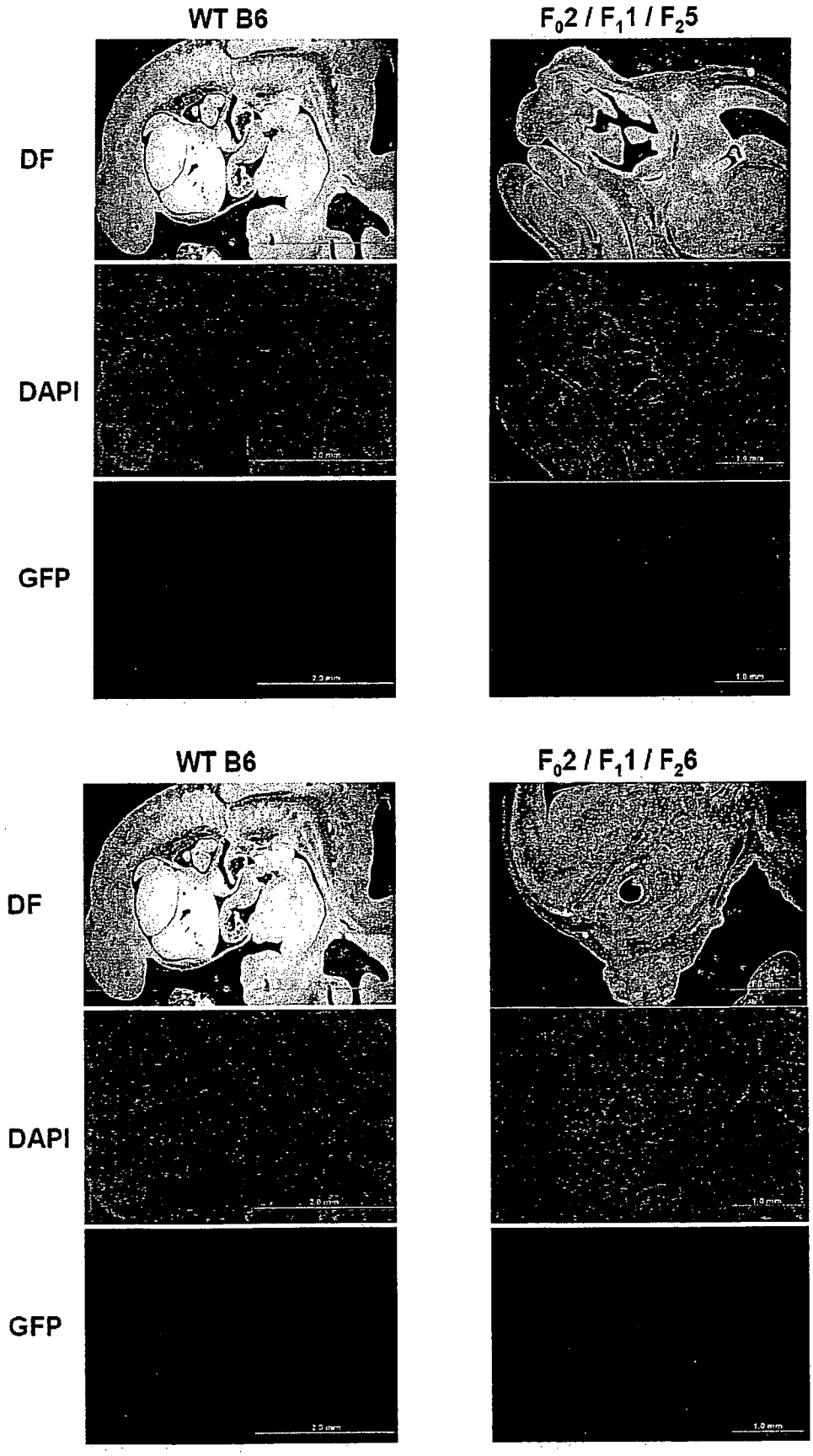
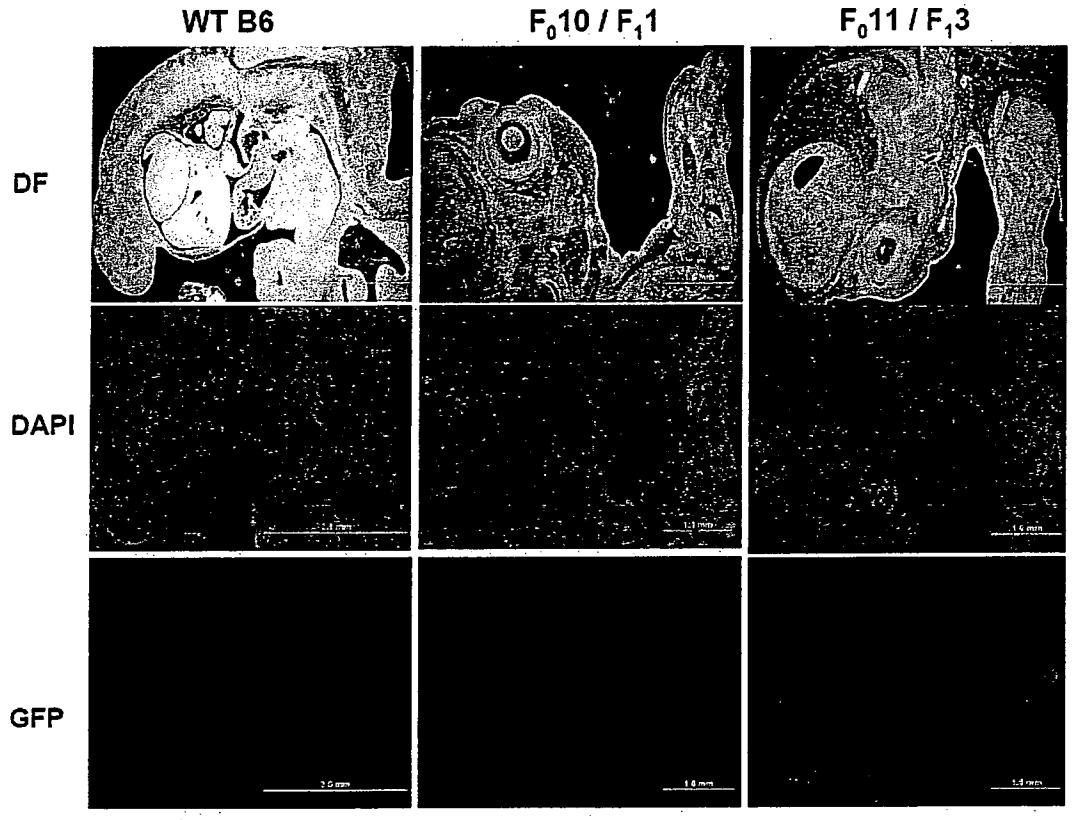


Figure 4/7


WT B6
F0 10 / F1 1
F0 11 / F1 3
DF
DAPI
GFP

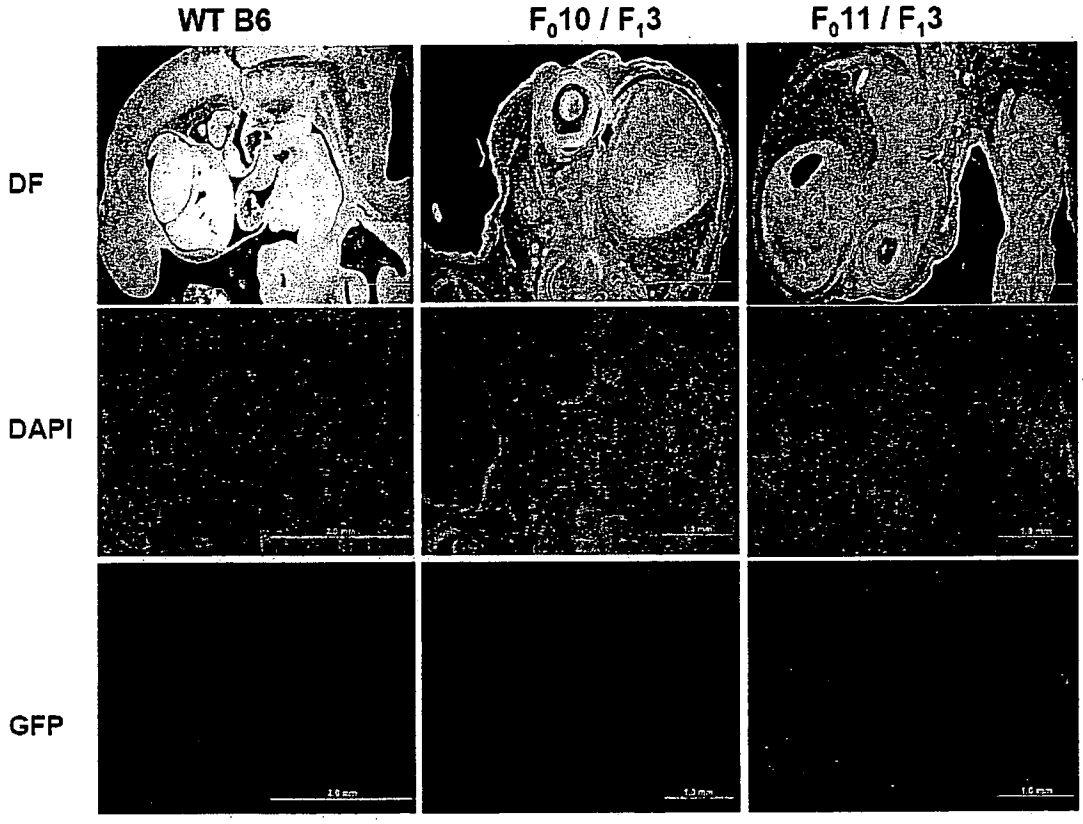

WT B6
F0 10 / F1 3
F0 11 / F1 3
DF
DAPI
GFP

Figure 4/8

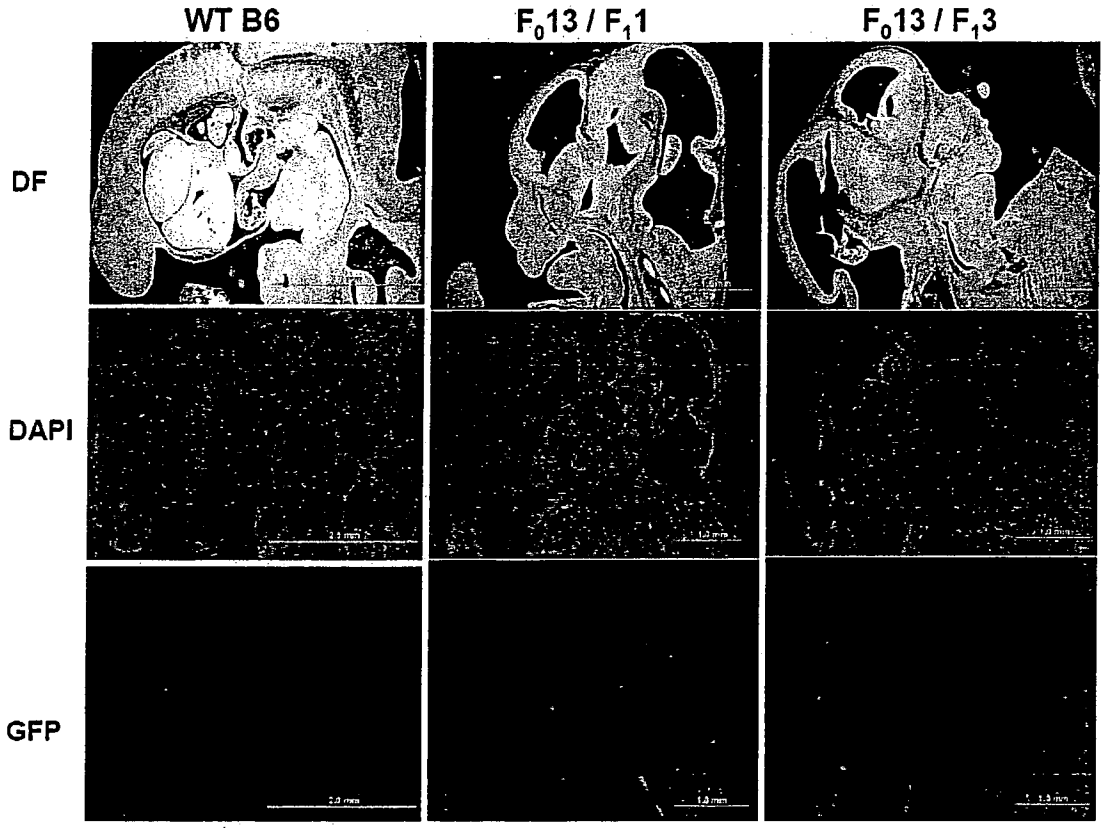


Figure 5

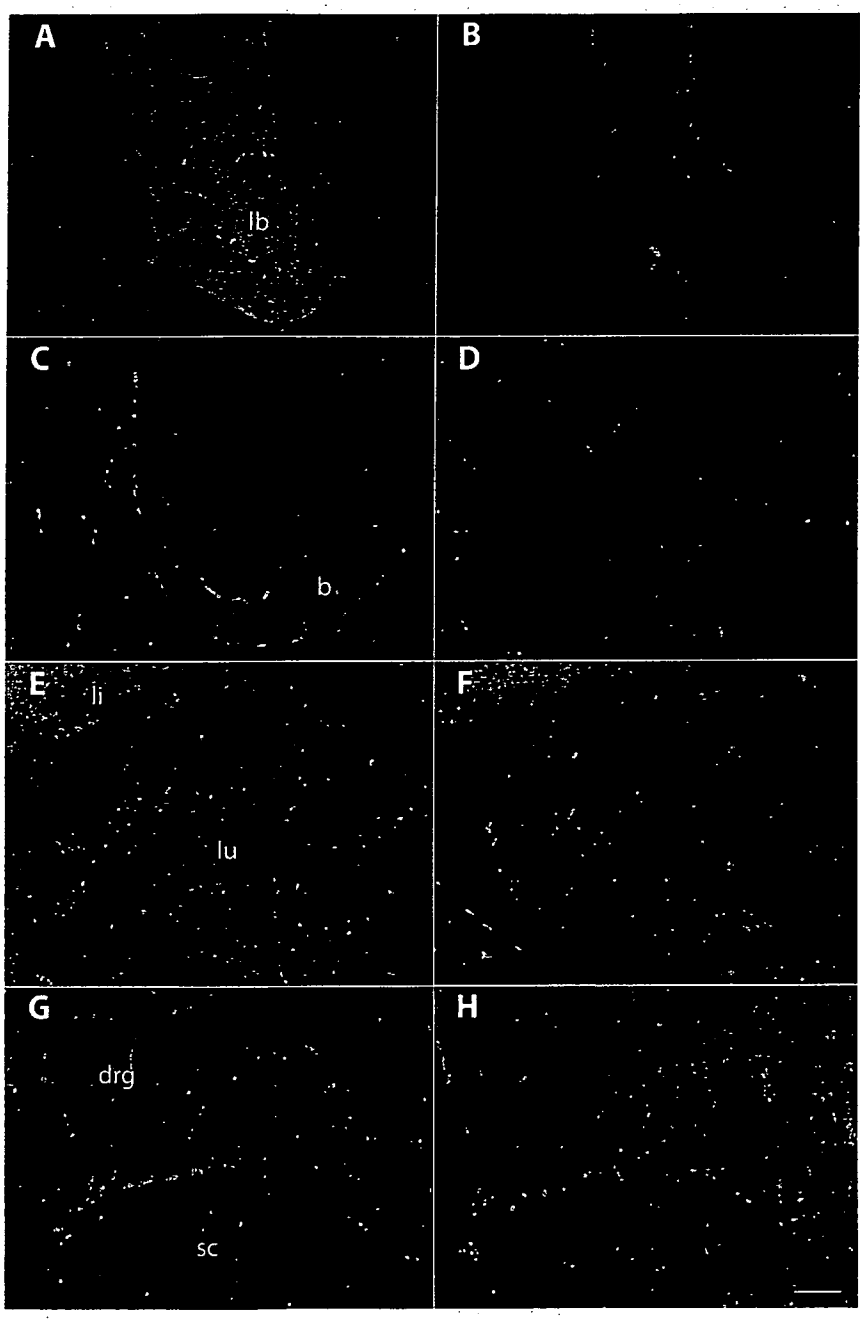
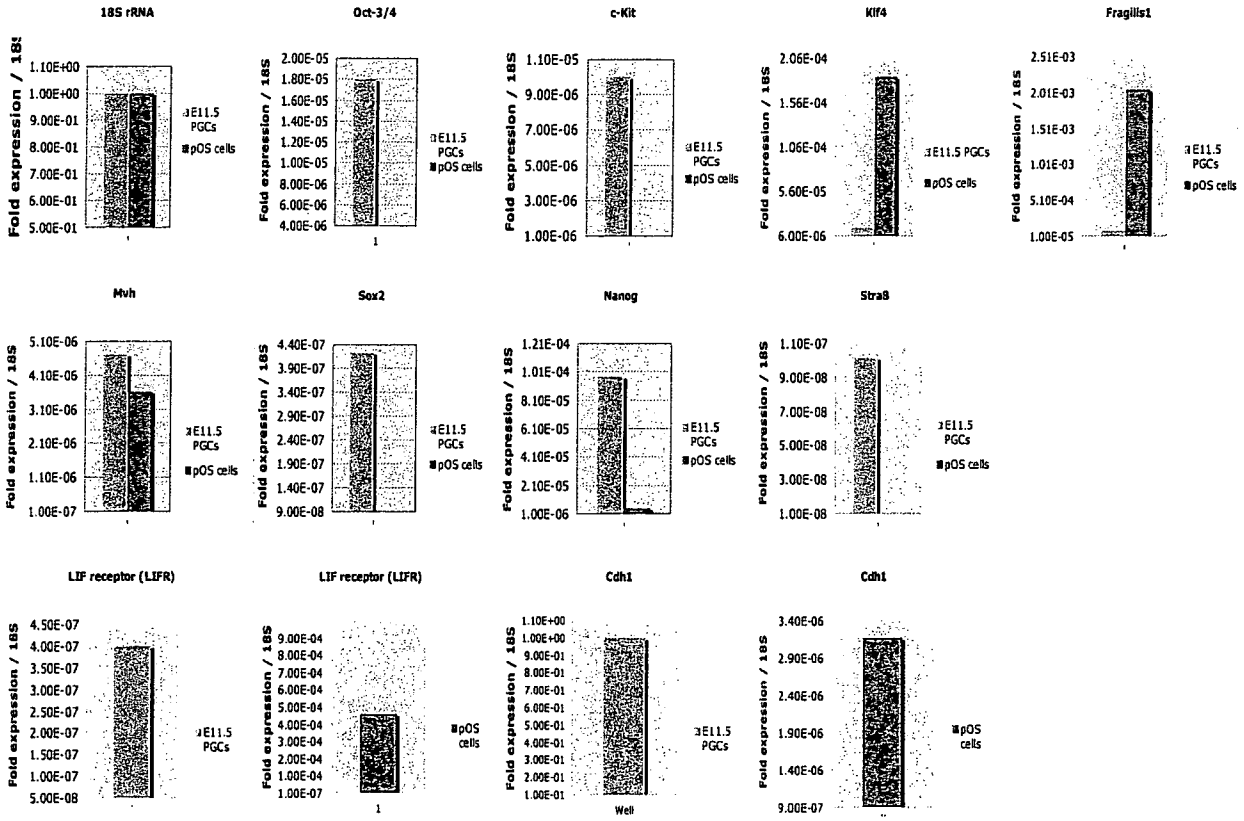


Figure 6


18S rRNA
Oct-3/4
c-Kit
Klf4
Fragilis1
Mvh
Sox2
Nanog
Stra8
LIF receptor (LIFR)
LIF receptor (LIFR)
Cdh1
Cdh1
Fold expression / 18S
E11.5 PGCs
pOS cells
Well

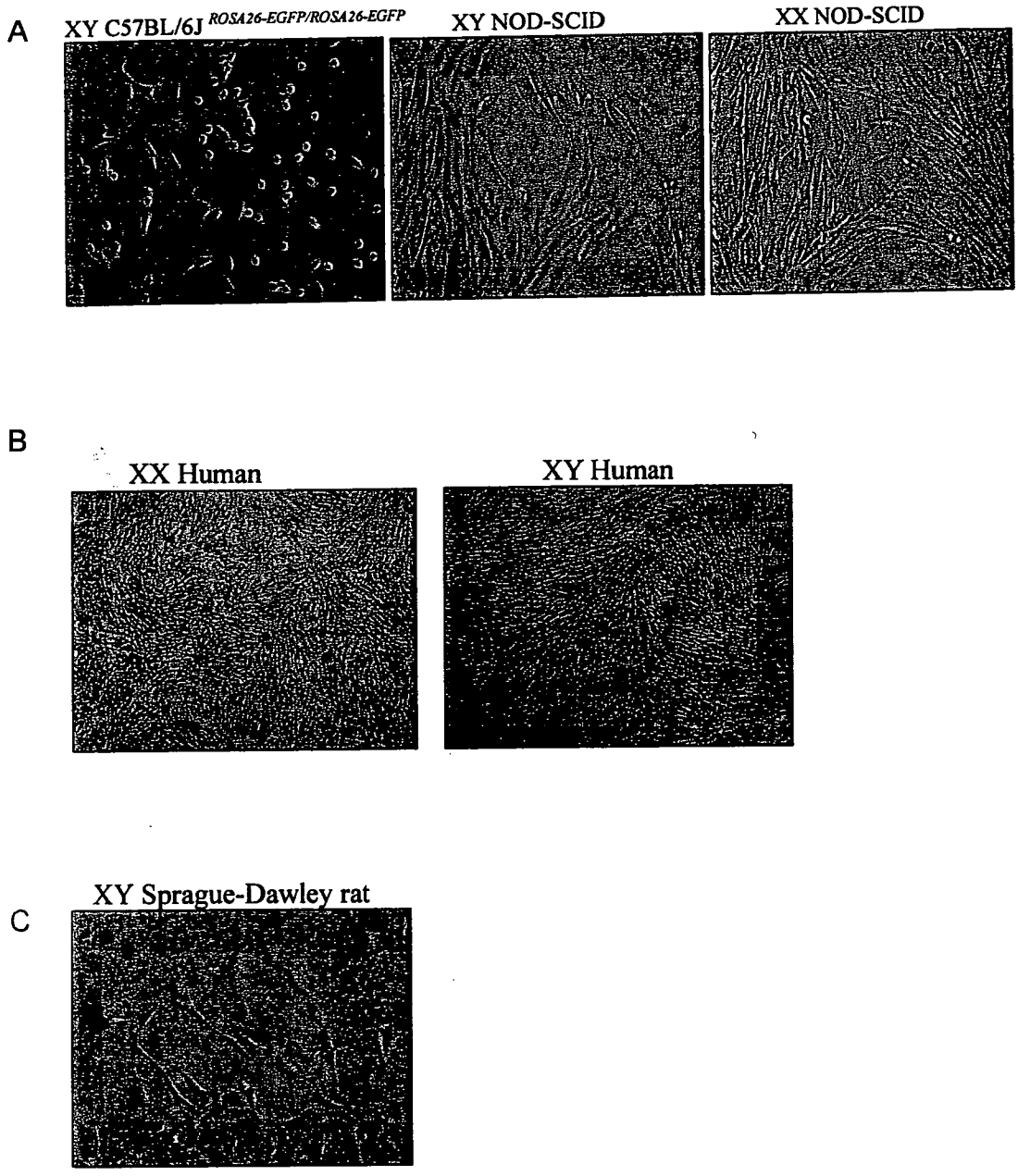

A
XY C57BL/6J ROSA26-EGFP/ROSA26-EGFP
XY NOD-SCID
XX NOD-SCID
B
XX Human
XY Human
C
XY Sprague-Dawley rat

Figure 7

1 XY pOS cell is sufficient to generate ♂ and ♀ chimaeric founders and transgenic F1 offspring

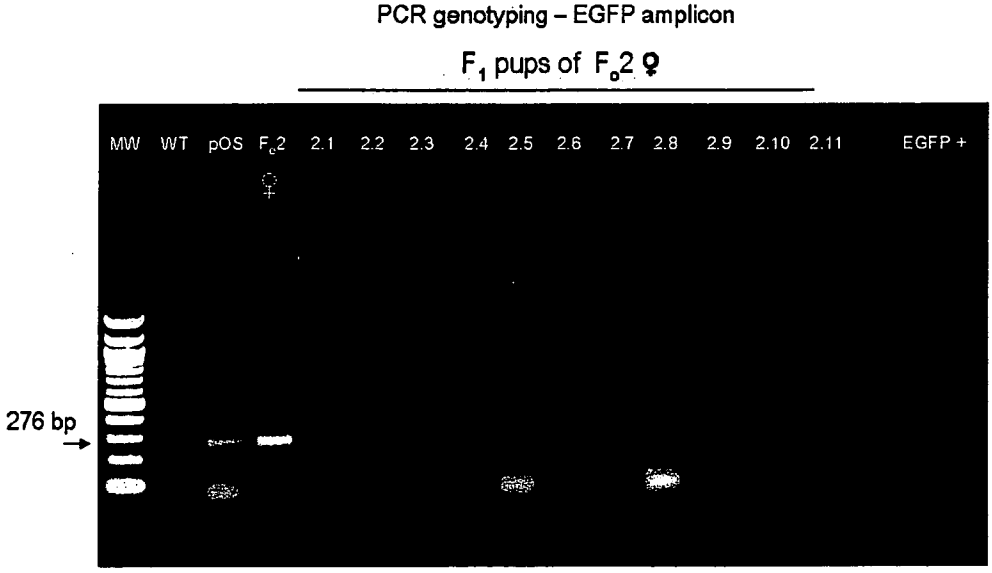


Figure 8

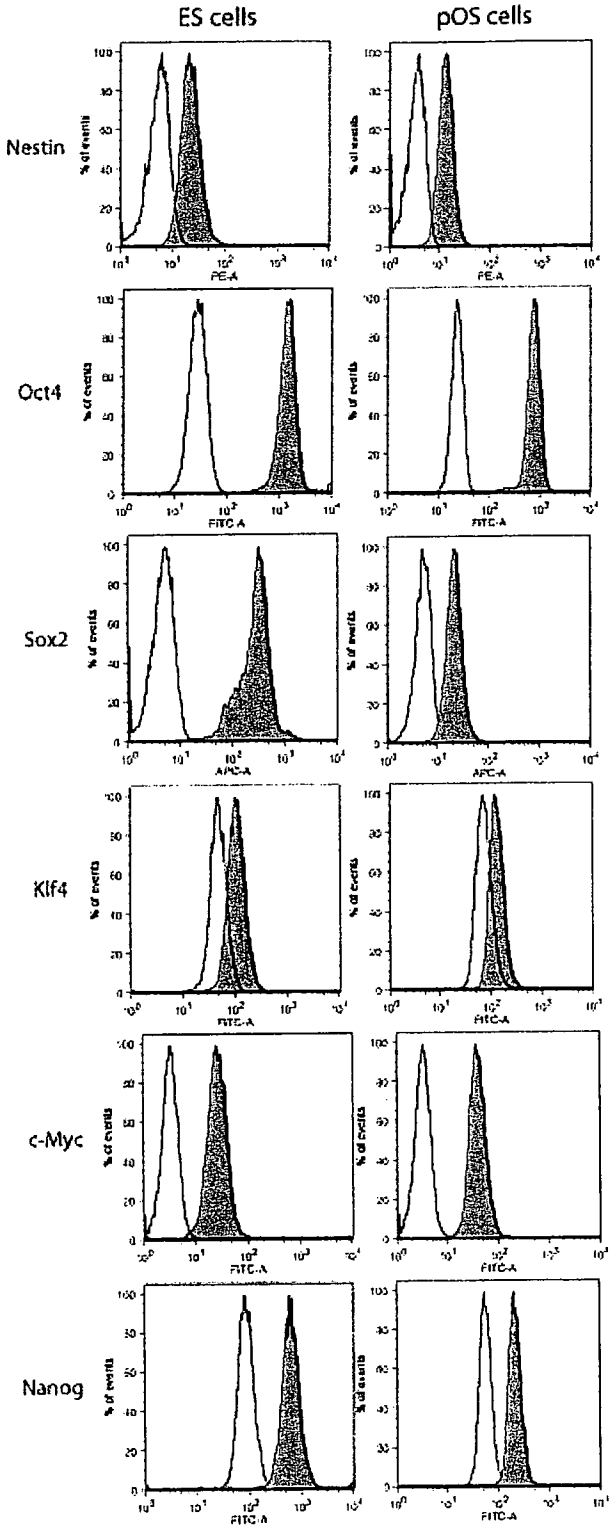
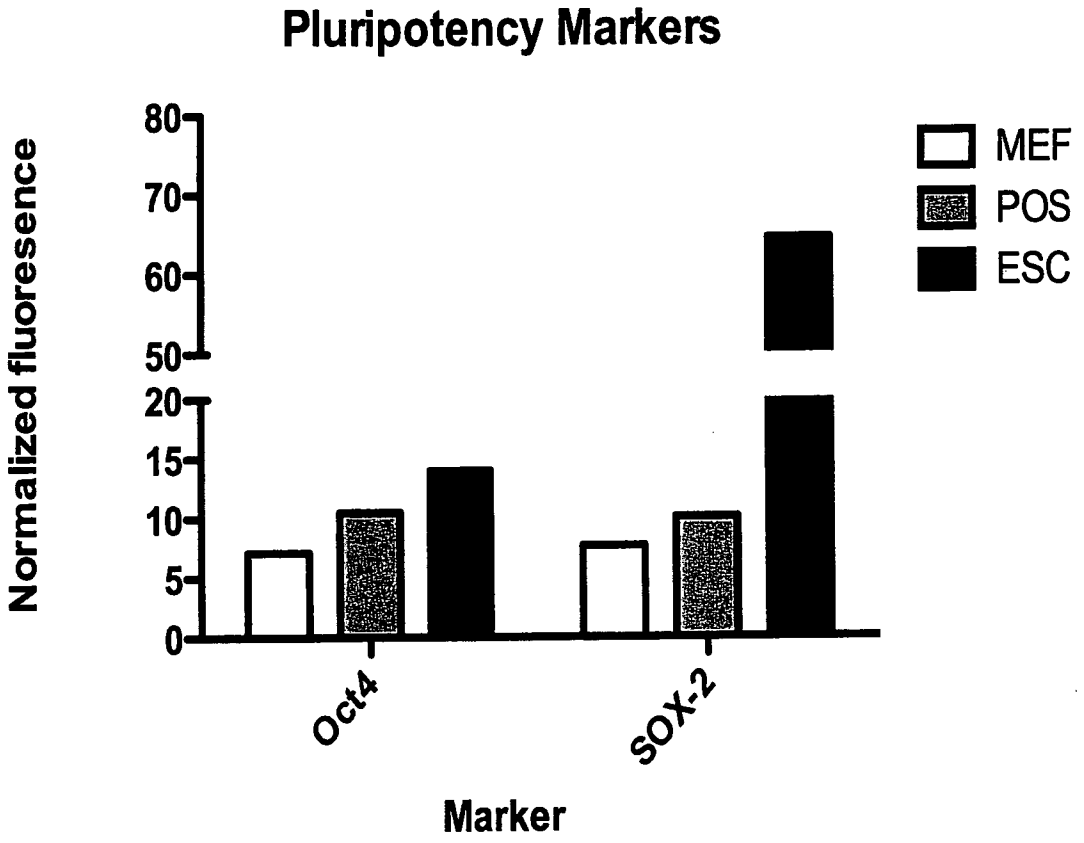

ES cells
pOS cells
Nestin
Oct4
Sox2
Klf4
c-Myc
Nanog
% of events
PE-A
FITC-A
APC-A

Figure 9

Figure 10


Pluripotency Markers
Normalized fluoresence
80
70
60
50
20
15
10
5
0
MEF
POS
ESC
Oct4
SOX-2
Marker

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2009/001665

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl.

C12N 5/074 (2010.01)

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPODOC, WPI, MEDLINE, HCA, BIOSIS (stem cell, pluripotent, multipotent, progenitor, adult, somatic, induced, iPS, teratoma, tumorigenic, olfactory, neurosphere, germline)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	TURNPENNY, L. et al. Evaluating Human Embryonic Germ Cells: Concord and Conflict as Pluripotent Stem Cells. Stem Cells. 2006, Vol. 24, No. 2, pages 212 – 220. See Abstract, pages 215 – 218.	1, 3, 9, 10, 12, 16 – 18, 30 – 37, 43 – 45
Y	As above.	20 – 22, 38 - 42
X	WO 2006/028723 A1 (MORAGA BIOTECH CORPORATION) 16 March 2006. See Abstract, [0035] – [0044].	1, 9, 16 – 18, 30 – 37, 43 – 45
Y	As above	20 – 22, 38 – 42

[X] Further documents are listed in the continuation of Box C [X] See patent family annex

* Special categories of cited documents:

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

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

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

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

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

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

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

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

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 April 2010	15 APR 2010

Name and mailing address of the ISA/AU

AUSTRALIAN PATENT OFFICE
PO BOX 200, WODEN ACT 2606, AUSTRALIA
E-mail address: pct@ipaustralia.gov.au
Facsimile No. +61 2 6283 7999

Authorized officer
JAMES ALDERMAN
AUSTRALIAN PATENT OFFICE
(ISO 9001 Quality Certified Service)
Telephone No : +61 3 9935 9613

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 2009/136283 A2 (CORETHERAPIX SLU) 12 November 2009. See Abstract; Claims; pg's 1 – 2; pg. 49 lines 1 – 16; pg. 19; Examples 12, 15, 19 and 26.	1, 4, 5, 7 – 10, 12, 14, 15, 17, 18, 30 – 33
Y	WO 2003/089631 A1 (GRIFFITH UNIVERSITY et al.) 30 October 2003. See Claims, pages 55 – 58.	20 – 22
Y	US 2008/0050350 A1 (YANG et al.) 28 February 2008. See Abstract, Claims, [0024] – [0036].	20 – 22, 38 – 43
A	MACKAY-SIM, A. & SILBURN, P. Stem cells and genetic disease. Cell Proliferation. 2008, Vol. 41, Suppl. 1 (February), pages 85 – 93. See whole document.	
A	MURRELL, W. et al. Olfactory Mucosa Is a Potential Source for Autologous Stem Cell Therapy for Parkinson's Disease. Stem Cells. 2008, Vol. 26, No. 8 (June), pages 2183 – 2192. See whole document.	
A	ALECKOVIC, M. & SIMON, C. Is teratoma in stem cell research a characterization tool or a window to developmental biology? Reproductive BioMedicine Online. 2008, Vol. 17, No. 2 (June), pages 274 – 284. See whole document.	
A	WERNIG, M. et al. c-Myc is Dispensable for Direct Reprogramming of Mouse Fibroblasts. Cell Stem Cell. 2008, Vol. 2, No. 1 (January), pages 10 – 12. See whole document.	
A	MURRELL, W. et al. Multipotent Stem Cells From Adult Olfactory Mucosa. Developmental Dynamics. 2005, Vol. 233, No. 2, pages 496 – 515. See whole document.	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2009/001665

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

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

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

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

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

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

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

See Supplemental Box.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claims 1 – 22, 30 – 45

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

Supplemental Box

Continuation of Box No III:

The Applicant has claimed more than one invention. Rule 13.1 of the PCT states the principle that an International Application should relate to only one invention or, if there is more than one invention, that the inclusion of those inventions in one International Application is only permitted if all inventions are so linked as to form a single general inventive concept.

Rule 13.2 of the PCT defines the method for determining whether the requirement of unity of invention is satisfied in respect of a group of inventions claimed in an International application. Unity of invention exists only when there is a technical relationship among the claimed inventions involving one or more of the same or corresponding "special technical features". The expression "special technical features" is defined in Rule 13.2 as meaning those technical features that define a contribution which each of the inventions, considered as a whole, makes over the prior art. The determination is made on the contents of the claims as interpreted in light of the description and drawings (if any).

The ISA has identified 7 inventions as follows:

1. Claims 1 – 22 and 30 – 45 relate to isolated mammalian cells (and methods of use), wherein said cells have the developmental potency of an embryonic stem cell and are characterised by not forming a teratoma when provided in an immune deficient animal.
2. Claims 23 – 29 (in part) relate to a method of producing an isolated pluripotent mammalian cell, said method comprising the culture of cells in a medium containing FGF2.
3. Claims 23 – 29 (in part) relate to a method of producing an isolated pluripotent mammalian cell, said method comprising the culture of cells in a medium containing FGF9.
4. Claims 23 – 29 (in part) relate to a method of producing an isolated pluripotent mammalian cell, said method comprising the culture of cells in a medium containing SCF.
5. Claims 23 – 29 (in part) relate to a method of producing an isolated pluripotent mammalian cell, said method comprising the culture of cells in a medium containing LIF.
6. Claims 23 – 29 (in part) relate to a method of producing an isolated pluripotent mammalian cell, said method comprising the culture of cells in a medium containing TGF-β2.
7. Claims 23 – 29 (in part) relate to a method of producing an isolated pluripotent mammalian cell, said method comprising the culture of cells in a medium containing BMP-4.

The feature common to the abovementioned groups is the isolation/production of adult stem cells. However, adult stem cells and methods for their isolation are know from the prior art. For example, the following documents disclose stem cells derived from adult olfactory mucosa:

- Mackay-Sim, A. & Silburn, P. Cell Proliferation. 2008, Vol. 41, Suppl. 1 (February), pages 85 – 93
- Murrell, W. *et al.* Stem Cells. 2008, Vol. 26, No. 8 (June), pages 2183 – 2192
- Murrell, W. *et al.* Developmental Dynamics. 2005, Vol. 233, No. 2, pages 496 – 515

Furthermore, the documents by Murrell *et al.* each disclose the culture of cells in growth factors such as FGF2 (bFGF). As such, the derivation of stem cells from adult tissue may not represent a special technical feature linking the abovementioned groups as a single invention. As there are no further common features, the claims are considered to lack unity *a posteriori*.

As no additional fees were paid, the International Search has been performed on the first invention (i.e. claims 1 – 22, 30 – 45).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU2009/001665

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member			
WO	2006/028723	EP	1789540	US	2009/0104158
WO	2009/136283	NONE			
WO	2003/089631	AU	2003218903		
US	2008/0050350	NONE			

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.

END OF ANNEX