SUPPLEMENTAL METHODS

Flow cytometry analysis
Phycoerythrin (PE)-conjugated monoclonal antibodies (mAb) to CD3 (clone UCHT1), CD10 (clone ALB1), CD19 (clone J4.119), CD34 (clone 581), CD45 (clone J33), CD54 (clone 84H10), CD86 (clone HA5.2B7), HLA-DR (clone Immu-357), CD105 (clone 1G2), and CD120a (clone H398); Fluorescein IsoThioCyanate (FITC)-conjugated mAb to CD19 (clone J4.119), CD20 (clone B9E9), and CD44 (clone J-173); and Phycocyanin (PC)7- and PC5-conjugated mAb to CD14 (clone RMO52), CD19 (clone J4.119), and CD20 (clone B9E9) were provided by Beckman Coulter (Villepinte, France). PE-conjugated mAb to CD73 (clone AD2), CD90 (clone 5E10), LTβR (clone hTNF-RP-M12), and CD120b (clone hTNFR-M1) were provided by Becton Dickinson (Le Pont de Claix, France) whereas PE-conjugated mAb anti-CD106 (clone 1.G11B1) was from Chemicon (Temecula, CA).

Proliferation assay was performed using the allophycocyanin (APC)-BrdU Flow kit and apoptosis evaluation using PE-conjugated active caspase-3 apoptosis kit (Becton Dickinson). Isotype-matched mAb were used as negative control and, unless otherwise specified, all analyses were performed on TOPRO-3<sup>neg</sup> viable cells (Invitrogen) using a FACSCalibur (Becton Dickinson) or a Gallios (Beckman Coulter) flow cytometer. Cell-sorting was performed on DAPI<sup>neg</sup> viable cells (Sigma, St Louis, MO) using a FACSArray cell sorter (Becton Dickinson).

Microarray and bioinformatics analysis
Scanned Affymetrix raw data were uploaded at https://webpub.chu-rennes.fr/extranetdim/echantadn/acces/editer.php Expression signal values and P-values were obtained for each probeset (PS) using the Partek Genomics Suite software (Partek, St Louis, MO) by the Robust Multichip Averaging algorithm using GC content of probes in normalization (GC-RMA).

Background noise was decreased by eliminating PS with a low standard deviation to mean ratio and unsupervised classification was performed with hierarchical clustering using Cluster and Treeview softwares (http://rana.lbl.gov/EisenSoftware.htm). To compare HD-MSC and FL-MSC and generate the FL-MSC signature, supervised analyses were carried out by combining: i) Significance Analysis of Microarray (SAM) software using 1000 permutations (http://www-stat.stanford.edu/~tibs/SAM/) resulting
in the selection of PS with a $|\text{FC}| > 2$ and a false discovery rate (FDR) < 5%, and ii) unpaired Mann-Whitney non parametric $U$-test carried out with Partek Genomics Suite software allowing the selection of PS with a $|\text{FC}| > 2$ and a $P$-value less than .05.

To define the TNF/LT signature, data from paired HD-MSC treated or not with TNF/LT were compared using the same approach was used except that we crossed a SAM analysis retaining PS with a $|\text{FC}| > 2$ and a FDR < .1% with a paired Student t-test selecting PS with a $|\text{FC}| > 2$ and a $P$-value less than .005. The FL-MSC and TNF/LT signatures corresponded each time to overlapping PS.

Generated PS lists were analyzed by Ingenuity Pathway Analysis (Ingenuity® Systems, http://www.ingenuity.com) and classified by Gene Ontology subcellular localization. Gene Set Enrichment Analysis (GSEA)¹ software was used to assess the overexpression of the TNF/LT signature in the FL-MSC versus HD-MSC microarray data. Non redundant datasets were generated and the signal-to-noise ratio (SNR) statistic was used to rank the genes. A $P$-value was calculated for a weighted enrichment score (ES) by using a sample-based permutation test procedure including 1000 permutations.

**CCL2 depletion**

CCL2 was specifically depleted in MSC supernatants using magnetic beads. Briefly, $2 \times 10^7$ Dynabeads pan mouse IgG (Invitrogen) were conjugated to 10 μg anti-CCL2 antibody (R&D systems) before a 2-hour incubation with MSC supernatants. Supernatants were thereafter seeded inside a magnetic field to allow CCL2 retention. We checked by ELISA (R&D Systems) that CCL2 was undetectable in depleted MSC supernatants whereas the level of IL-8, another highly expressed chemokine, was not affected. Conversely, the use of an isotype-matched control mAb instead of specific anti-CCL2 antibody did not modify the concentration of CCL2 in MSC supernatants.
REFERENCES

Table S1. FL patient characteristics

<table>
<thead>
<tr>
<th>Bioclinical characteristics (n=10)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Tumor grade</strong>*</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3a</td>
</tr>
<tr>
<td>3b</td>
</tr>
<tr>
<td><strong>FLIPI risk group</strong>*</td>
</tr>
<tr>
<td>Low</td>
</tr>
<tr>
<td>Intermediate</td>
</tr>
<tr>
<td>High</td>
</tr>
<tr>
<td><strong>IgH-BCL2 gene fusion</strong>*</td>
</tr>
<tr>
<td>Negative</td>
</tr>
<tr>
<td>Positive</td>
</tr>
<tr>
<td><strong>Bone marrow infiltration†</strong></td>
</tr>
<tr>
<td>Negative</td>
</tr>
<tr>
<td>Positive</td>
</tr>
</tbody>
</table>

* FL patients were classified into grades 1, 2, 3a, or 3b according to the WHO diagnosis criteria.
** Follicular Lymphoma International Prognostic Index (FLIPI) values were classified as low (0-1), intermediate (2), or high (3 to 5).
*** BCL2 rearrangements were determined by PCR according to Biomed2 recommendations† or by FISH analysis.
† Bone marrow infiltration was determined by classical histopathological analysis on bone marrow biopsies and by evaluation of the κ/λ light chain ratio among CD10<sup>POS</sup> B cells on bone marrow aspirates.

Reference:
Table S2. Taqman Gene Expression Assays used for RQ-PCR experiments

<table>
<thead>
<tr>
<th>Gene Symbol</th>
<th>Gene Name</th>
<th>Unigene ID</th>
<th>Assay ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>CCL2</td>
<td>chemokine (C-C motif) ligand 2</td>
<td>Hs.303649</td>
<td>Hs.00234140_m1</td>
</tr>
<tr>
<td>CCL5</td>
<td>chemokine (C-C motif) ligand 5</td>
<td>Hs.514821</td>
<td>Hs.00174575_m1</td>
</tr>
<tr>
<td>CHST2</td>
<td>carbohydrate (N-acetylglycosamine-6-O) sulfotransferase 2</td>
<td>Hs.8786</td>
<td>Hs.01921028_s1</td>
</tr>
<tr>
<td>CLU</td>
<td>clusterin</td>
<td>Hs.436657</td>
<td>Hs.00156548_m1</td>
</tr>
<tr>
<td>DUSP6</td>
<td>dual specificity phosphatase 6</td>
<td>Hs.298654</td>
<td>Hs.00737962_m1</td>
</tr>
<tr>
<td>GAPDH</td>
<td>glyceraldehyde-3-phosphate dehydrogenase</td>
<td>Hs.598320</td>
<td>Hs.99999905_m1</td>
</tr>
<tr>
<td>HBEGF</td>
<td>Heparin-binding EGF-like growth factor</td>
<td>Hs.799</td>
<td>Hs.00961131_m1</td>
</tr>
<tr>
<td>IL10</td>
<td>interleukin 10</td>
<td>Hs.193717</td>
<td>Hs.99999035_m1</td>
</tr>
<tr>
<td>IL12A</td>
<td>Natural killer cell stimulatory factor1, p35</td>
<td>Hs.673</td>
<td>Hs.00168405_m1</td>
</tr>
<tr>
<td>IL15</td>
<td>interleukin 15</td>
<td>Hs.654378</td>
<td>Hs.00174106_m1</td>
</tr>
<tr>
<td>IL6</td>
<td>interleukin 6</td>
<td>Hs.654458</td>
<td>Hs.00174131_m1</td>
</tr>
<tr>
<td>IL8</td>
<td>interleukin 8</td>
<td>Hs.624</td>
<td>Hs.00174103_m1</td>
</tr>
<tr>
<td>PGF</td>
<td>placental growth factor</td>
<td>Hs.252820</td>
<td>Hs.00182176_m1</td>
</tr>
<tr>
<td>TNFRSF10A</td>
<td>tumor necrosis factor receptor superfamily, member 10A</td>
<td>Hs.591834</td>
<td>Hs.00269492_m1</td>
</tr>
<tr>
<td>TNFSF2</td>
<td>tumor necrosis factor (ligand) superfamily, member 2</td>
<td>Hs.241570</td>
<td>Hs.00174128_m1</td>
</tr>
<tr>
<td>TNFSF4</td>
<td>tumor necrosis factor (ligand) superfamily, member 4</td>
<td>Hs.181097</td>
<td>Hs.00182411_m1</td>
</tr>
<tr>
<td>VEGFA</td>
<td>vascular endothelial growth factor A</td>
<td>Hs.73793</td>
<td>Hs.00173626_m1</td>
</tr>
</tbody>
</table>
### Table S3. Genes differentially expressed in FL-MSC compared with HD-MSC

Red line indicates genes overexpressed in FL-MSC, and green line indicates genes overexpressed in HD-MSC. Fold change indicates the ratio of median in FL-MSC/median in HD-MSC, when >2, or -1/(ratio of median in FL-MSC/median in HD-MSC) when <.5

<table>
<thead>
<tr>
<th>Location</th>
<th>Fold Change</th>
<th>ProbeSet ID</th>
<th>UniGene ID</th>
<th>Gene Symbol</th>
<th>Gene Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>Extracellular Space</td>
<td>3.7</td>
<td>209277_at</td>
<td>Hs.439231</td>
<td>TFPI2</td>
<td>tissue factor pathway inhibitor 2</td>
</tr>
<tr>
<td></td>
<td>3.6</td>
<td>228885_at</td>
<td>Hs.547172</td>
<td>HAMOC2</td>
<td>membrane domain containing 2</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>208791_at</td>
<td>Hs.436657</td>
<td>CLU</td>
<td>clustatin</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>205174_s_at</td>
<td>Hs.79033</td>
<td>OCT (includes EG:25797)</td>
<td>glutaminyl-peptide cyclotransferase</td>
</tr>
<tr>
<td></td>
<td>2.8</td>
<td>1552457_at</td>
<td>Hs.522019</td>
<td>ADAMTS11</td>
<td>ADAMTS-11</td>
</tr>
<tr>
<td></td>
<td>2.7</td>
<td>2149313</td>
<td>Hs.590919</td>
<td>ADAMTS13</td>
<td>ADAM metallopeptidase with thrombospondin type 1 motif, 3</td>
</tr>
<tr>
<td></td>
<td>2.6</td>
<td>218454_at</td>
<td>Hs.131933</td>
<td>PLBD1</td>
<td>phospholipase B domain containing 1</td>
</tr>
<tr>
<td></td>
<td>2.6</td>
<td>201348_at</td>
<td>Hs.386793</td>
<td>GPX3</td>
<td>glutathione peroxidase 3 (plasma)</td>
</tr>
<tr>
<td></td>
<td>2.6</td>
<td>209278_s_at</td>
<td>Hs.438231</td>
<td>TFPI2</td>
<td>tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)</td>
</tr>
<tr>
<td></td>
<td>2.5</td>
<td>228885_at</td>
<td>Hs.547172</td>
<td>MAMDC2</td>
<td>MAM domain containing 2</td>
</tr>
<tr>
<td></td>
<td>2.4</td>
<td>205174_s_at</td>
<td>Hs.79033</td>
<td>QPCT (includes EG:25797)</td>
<td>glutaminyl-peptide cyclotransferase</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>208791_at</td>
<td>Hs.436657</td>
<td>CLU</td>
<td>clustatin</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>205174_s_at</td>
<td>Hs.79033</td>
<td>OCT (includes EG:25797)</td>
<td>glutaminyl-peptide cyclotransferase</td>
</tr>
<tr>
<td></td>
<td>2.2</td>
<td>211596_s_at</td>
<td>Hs.518059</td>
<td>LRIG1</td>
<td>leucine-rich repeats and immunoglobulin-like domains 1</td>
</tr>
<tr>
<td></td>
<td>2.2</td>
<td>209278_s_at</td>
<td>Hs.438231</td>
<td>TFPI2</td>
<td>tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)</td>
</tr>
<tr>
<td></td>
<td>2.1</td>
<td>229461_s_at</td>
<td>Hs.146542</td>
<td>NEGR1</td>
<td>neuronal growth regulator 1</td>
</tr>
<tr>
<td>Plasma Membrane</td>
<td>4.6</td>
<td>218309_at</td>
<td>Hs.197922</td>
<td>CAMK2N1</td>
<td>calcium/calmodulin-dependent protein kinase II inhibitor 1</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>1554902_at</td>
<td>Hs.179675</td>
<td>XG</td>
<td>Xg blood group</td>
</tr>
<tr>
<td></td>
<td>3.8</td>
<td>229151_at</td>
<td>Hs.101307</td>
<td>SLC4A4</td>
<td>solute carrier family 4, sodium bicarbonate cotransporter, member 7</td>
</tr>
<tr>
<td></td>
<td>3.8</td>
<td>205856_at</td>
<td>Hs.101307</td>
<td>SLC4A4</td>
<td>solute carrier family 4, sodium bicarbonate cotransporter, member 7</td>
</tr>
<tr>
<td></td>
<td>3.6</td>
<td>231775_at</td>
<td>Hs.591834</td>
<td>TNFRSF10A (includes EG:8797)</td>
<td>tumor necrosis factor receptor superfamily, member 10a</td>
</tr>
<tr>
<td></td>
<td>3.6</td>
<td>210386_s_at</td>
<td>Hs.250072</td>
<td>SLC4A1</td>
<td>solute carrier family 4, sodium bicarbonate cotransporter, member 7</td>
</tr>
<tr>
<td></td>
<td>3.4</td>
<td>202920_at</td>
<td>Hs.620557</td>
<td>ANK2</td>
<td>ankym 2, neuronal</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>230311_s_at</td>
<td>Hs.531987</td>
<td>KRIT1</td>
<td>KRIT1, ankym repeat containing</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>1554957</td>
<td>Hs.824592</td>
<td>ATP2A1B</td>
<td>ATPase, class VI, type 1B</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>224923_at</td>
<td>Hs.594243</td>
<td>SGM62</td>
<td>sphingomyelin synthase 2</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>220254_at</td>
<td>Hs.654804</td>
<td>LRP12</td>
<td>low density lipoprotein-related protein 12</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>224341_s_at</td>
<td>Hs.174312</td>
<td>TLR4</td>
<td>toll-like receptor 4</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>232068_s_at</td>
<td>Hs.174312</td>
<td>TLR4</td>
<td>toll-like receptor 4</td>
</tr>
<tr>
<td></td>
<td>2.9</td>
<td>210139_at</td>
<td>Hs.480411</td>
<td>CLP2F1M1</td>
<td>cleft lip and palate associated transmembrane protein 1</td>
</tr>
<tr>
<td></td>
<td>2.9</td>
<td>200736_at</td>
<td>Hs.156727</td>
<td>ANKH</td>
<td>anklylosis, progressive homolog (mouse)</td>
</tr>
<tr>
<td></td>
<td>2.8</td>
<td>211343_at</td>
<td>Hs.69534</td>
<td>COL13A1</td>
<td>collagen, type XIII, alpha 1</td>
</tr>
<tr>
<td></td>
<td>2.8</td>
<td>222088_s_at</td>
<td>Hs.419240</td>
<td>SLC2A3</td>
<td>solute carrier family 2, facilitated glucose transporter, member 3</td>
</tr>
<tr>
<td></td>
<td>2.8</td>
<td>218451_at</td>
<td>Hs.470693</td>
<td>CDCP1</td>
<td>CUB domain containing protein 1</td>
</tr>
<tr>
<td></td>
<td>2.6</td>
<td>203508_at</td>
<td>Hs.256278</td>
<td>TNFRSF18</td>
<td>tumor necrosis factor receptor superfamily, member 1B</td>
</tr>
<tr>
<td></td>
<td>2.6</td>
<td>213413_s_at</td>
<td>Hs.156727</td>
<td>ANKH</td>
<td>anklylosis, progressive homolog (mouse)</td>
</tr>
<tr>
<td></td>
<td>2.5</td>
<td>229176_at</td>
<td>Hs.156727</td>
<td>ANKH</td>
<td>anklylosis, progressive homolog (mouse)</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>226383_at</td>
<td>Hs.532698</td>
<td>APN18</td>
<td>anterior photic system 1 homolog B (C. elegans)</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>214374_at</td>
<td>Hs.172445</td>
<td>PPF1BP1</td>
<td>PTPRF interacting protein, binding protein 1 (spermin beta 1)</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>205579_at</td>
<td>Hs.1570</td>
<td>HRH1</td>
<td>histamine receptor H1</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>228239_at</td>
<td>Hs.65195</td>
<td>FAM165B</td>
<td>family with sequence similarity 165, member B</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>203496_at</td>
<td>Hs.524265</td>
<td>GRK5</td>
<td>G protein-coupled receptor kinase 5</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>242317_at</td>
<td>Hs.7917</td>
<td>HGD1A</td>
<td>HDG1 domain family, member 1A</td>
</tr>
<tr>
<td></td>
<td>2.3</td>
<td>225571_s_at</td>
<td>Hs.133421</td>
<td>LIFR</td>
<td>leukemia inhibitory factor receptor alpha</td>
</tr>
<tr>
<td></td>
<td>2.2</td>
<td>202053_s_at</td>
<td>Hs.654804</td>
<td>LRP12</td>
<td>low density lipoprotein-related protein 12</td>
</tr>
<tr>
<td></td>
<td>2.2</td>
<td>200503_at</td>
<td>Hs.654652</td>
<td>DOC4K</td>
<td>dedicator of cytokinesis 4</td>
</tr>
<tr>
<td></td>
<td>2.1</td>
<td>235901_s_at</td>
<td>Hs.439200</td>
<td>KIAA0090</td>
<td>KIAA0090</td>
</tr>
<tr>
<td></td>
<td>2.1</td>
<td>201635_at</td>
<td>Hs.133397</td>
<td>ITGA6</td>
<td>integrin, alpha 6</td>
</tr>
<tr>
<td>Gene Symbol</td>
<td>Classification</td>
<td>Description</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>-------------</td>
<td>----------------</td>
<td>-------------</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAGI2</td>
<td>Membrane associated guanylate kinase, W and PDZ domain containing 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GNG2</td>
<td>Guanine nucleotide binding protein (G protein), gamma 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAGI2</td>
<td>Membrane associated guanylate kinase, WW and PDZ domain containing 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EPB41L2</td>
<td>Erythrocyte membrane protein band 4.1-like 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAGI2</td>
<td>Membrane associated guanylate kinase, WW and PDZ domain containing 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIGLEC15</td>
<td>Sialic acid binding Ig-like lectin 15</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAGI2</td>
<td>Membrane associated guanylate kinase, WW and PDZ domain containing 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DOCK9</td>
<td>Dedicator of cytokinesis 9</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FAR2</td>
<td>Fatty acyl-CoA reductase 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GNG2</td>
<td>Guanine nucleotide binding protein (G protein), gamma 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARSB</td>
<td>Arylsulfatase B</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>UST</td>
<td>Uronyl-2-sulfotransferase</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CLN8</td>
<td>Ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SEC62</td>
<td>SEC62 homolog (S. cerevisiae)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PDLIM5</td>
<td>PDZ and LIM domain 5</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GALNT4</td>
<td>UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ATG4B</td>
<td>Autophagy-related 4B</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NAAA</td>
<td>N-acetylenolamide acid amidase</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SGPP1</td>
<td>Sphingosine-1-phosphate phosphatase 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RAB10</td>
<td>RAB10, member RAS oncogene family</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PI3K</td>
<td>Phosphoinositide 3-kinase</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IL17RD</td>
<td>Interleukin 17 receptor D</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GAPRAPL1</td>
<td>GABA(A) receptor-associated protein like 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gene ID 1</td>
<td>Gene ID 2</td>
<td>Gene ID 3</td>
<td>Gene ID 4</td>
<td>Gene ID 5</td>
<td>Description</td>
</tr>
<tr>
<td>----------</td>
<td>-----------</td>
<td>-----------</td>
<td>-----------</td>
<td>-----------</td>
<td>-------------</td>
</tr>
<tr>
<td>2.3</td>
<td>218748_s_at</td>
<td>Hs.655158</td>
<td>EXOC5</td>
<td>exocyst complex component 5</td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>333212_s_at</td>
<td>Hs.523178</td>
<td>SFN</td>
<td>striatin</td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>203285_s_at</td>
<td>Hs.48823</td>
<td>HS2ST1</td>
<td>heparan sulfate 2-O-sulfotransferase 1</td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>214260_at</td>
<td>Hs.531713</td>
<td>COP5B</td>
<td>COP9 constitutive photomorphogenic homolog subunit B (Arabidopsis)</td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>214855_s_at</td>
<td>Hs.113150</td>
<td>GARNL1</td>
<td>GTPase activating Rap/RanGAP domain-like 1</td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>226602_s_at</td>
<td>Hs.218888</td>
<td>BCR</td>
<td>breakpoint cluster region</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>229331_at</td>
<td>Hs.527090</td>
<td>SPATA18</td>
<td>spermato genesis associated 18 homolog (rat)</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>220038_at</td>
<td>Hs.656798</td>
<td>SGK3</td>
<td>ser um/glucocorticoid regulated kinase family, member 3</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>205083_at</td>
<td>Hs.406238</td>
<td>AOX1</td>
<td>aldehyde oxidase 1</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>235103_at</td>
<td>Hs.432822</td>
<td>MAN2A1</td>
<td>man nosidase alpha, class A, member 1</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>212221_x_at</td>
<td>Hs.469060</td>
<td>IDS</td>
<td>idur anate 2-sulfatase</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>203910_at</td>
<td>Hs.483238</td>
<td>ARHGAP29</td>
<td>Rho GTPase activating protein 29</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>40148_at</td>
<td>Hs.479602</td>
<td>APB2</td>
<td>amyl oid beta (A4) precursor protein-binding, family B, member 2</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>210602_s_at</td>
<td>Hs.114193</td>
<td>ZCCHC2</td>
<td>zinc finger, CCHC domain containing 2</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>213750_at</td>
<td>Hs.401842</td>
<td>RSL1D1</td>
<td>ribosomal L1 domain containing 1</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>213552_at</td>
<td>Hs.183006</td>
<td>GLCE</td>
<td>glucuronic acid epimerase</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>230174_at</td>
<td>Hs.657617</td>
<td>LYLAL1</td>
<td>lysophospholipase-like 1</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>229331_at</td>
<td>Hs.372801</td>
<td>ARL6</td>
<td>ADP-ribosylation factor-like 6</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>221589_s_at</td>
<td>Hs.293970</td>
<td>ALDH6A1</td>
<td>al dehyde dehydrogenase 6 family, member A1</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>202660_at</td>
<td>Hs.512235</td>
<td>ITPR2</td>
<td>inositol 1,4,5-triphosphate receptor, type 2</td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>206113_s_at</td>
<td>Hs.8786</td>
<td>CHST2</td>
<td>carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>222637_s_at</td>
<td>Hs.591162</td>
<td>FGFR10P2</td>
<td>FGF1 oncogene partner 2</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>226335_at</td>
<td>Hs.445387</td>
<td>RPS6KA3</td>
<td>ribosomal protein S6 kinase, 90kDa, polypeptide 3</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>203921_at</td>
<td>Hs.8786</td>
<td>CHST2</td>
<td>carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>214700_s_at</td>
<td>Hs.115325</td>
<td>RAB7L1</td>
<td>RAB7, member RAS oncogene family-like 1</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>243438_at</td>
<td>Hs.652367</td>
<td>PDE7B</td>
<td>phosphodiesterase 7B</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>234988_at</td>
<td>Hs.632066</td>
<td>VCP-P1</td>
<td>villin containing protein (p97)polycomplex interacting protein 1</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>155405_at</td>
<td>Hs.90458</td>
<td>SPTL1C</td>
<td>serine palmitoyltransferase, long chain base subunit 1</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>218313_s_at</td>
<td>Hs.548088</td>
<td>GALNT7</td>
<td>UDP-N-acetyl-alpha-D-galactosaminepolyeppeptide N-acetylglactosaminyltransferase 7 (GalNAC-T7)</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>36920_at</td>
<td>Hs.655056</td>
<td>MMT1</td>
<td>myotubulin 1</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>224858_at</td>
<td>Hs.497873</td>
<td>WDR26</td>
<td>WD repeat domain 26</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>212414_s_at</td>
<td>Hs.387255</td>
<td>SEPT6</td>
<td>septin 6</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>52285_f_at</td>
<td>Hs.236940</td>
<td>CEPT6</td>
<td>centrosomal protein 76kDa</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>235635_at</td>
<td>Hs.592313</td>
<td>ARHGAP5</td>
<td>Rho GTPase activating protein 5</td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>229478_at</td>
<td>Hs.378414</td>
<td>MPHAS1</td>
<td>malignant fibrous histiocytoma amplified sequence 1</td>
<td></td>
</tr>
</tbody>
</table>

**Nucleus**

<table>
<thead>
<tr>
<th>Gene ID 1</th>
<th>Gene ID 2</th>
<th>Gene ID 3</th>
<th>Gene ID 4</th>
<th>Gene ID 5</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>5.3</td>
<td>230438_at</td>
<td>Hs.146196</td>
<td>TBX15</td>
<td>T-box 15</td>
<td></td>
</tr>
<tr>
<td>4.7</td>
<td>236313_at</td>
<td>Hs.72901</td>
<td>CDKN2B</td>
<td>cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)</td>
<td></td>
</tr>
<tr>
<td>4.3</td>
<td>231071_s_at</td>
<td>Hs.484500</td>
<td>HIST1H2AC</td>
<td>histone cluster 1, H2ac</td>
<td></td>
</tr>
<tr>
<td>3.5</td>
<td>23148_at</td>
<td>Hs.654412</td>
<td>PBRM1</td>
<td>pre-B-cell leukemia homebox 1</td>
<td></td>
</tr>
<tr>
<td>3.5</td>
<td>231929_at</td>
<td>Hs.604950</td>
<td>IKZF2</td>
<td>IKAROS family zinc finger 2 (Helios)</td>
<td></td>
</tr>
<tr>
<td>3.1</td>
<td>233819_s_at</td>
<td>Hs.288773</td>
<td>RNF160</td>
<td>ring finger protein 160</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>211090_r_at</td>
<td>Hs.159014</td>
<td>PRPF4B</td>
<td>pre-mRNA processing factor 4 homolog B (yeast)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>231862_s_at</td>
<td>Hs.643464</td>
<td>DDX2</td>
<td>DHX52 dimeric control homolog (S. cerevisiae)</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>206115_at</td>
<td>Hs.534313</td>
<td>EGR3</td>
<td>early growth response 3</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>230063_at</td>
<td>Hs.516364</td>
<td>ZNF264</td>
<td>zinc finger protein 264</td>
<td></td>
</tr>
<tr>
<td>2.9</td>
<td>230291_at</td>
<td>Hs.644095</td>
<td>NFIIB</td>
<td>nuclear factor I/B</td>
<td></td>
</tr>
<tr>
<td>2.8</td>
<td>225061_at</td>
<td>Hs.51053</td>
<td>DHAJ1A4</td>
<td>DhaJ (Hsp40) homolog, subfamily A, member 4</td>
<td></td>
</tr>
<tr>
<td>2.7</td>
<td>157324_s_at</td>
<td>Hs.285197</td>
<td>SFRP2</td>
<td>SFRP protein kinase 2</td>
<td></td>
</tr>
<tr>
<td>2.6</td>
<td>231975_s_at</td>
<td>Hs.657594</td>
<td>MIER3</td>
<td>mesoderm induction early response 1, family member 3</td>
<td></td>
</tr>
<tr>
<td>2.5</td>
<td>209290_s_at</td>
<td>Hs.644095</td>
<td>NFIIB</td>
<td>nuclear factor I/B</td>
<td></td>
</tr>
<tr>
<td>2.5</td>
<td>221911_at</td>
<td>Hs.22634</td>
<td>ETV1</td>
<td>ets variant 1</td>
<td></td>
</tr>
<tr>
<td>2.5</td>
<td>203347_s_at</td>
<td>Hs.31016</td>
<td>MTF2</td>
<td>metal response element binding transcription factor 2</td>
<td></td>
</tr>
<tr>
<td>2.5</td>
<td>206511_s_at</td>
<td>Hs.101937</td>
<td>SIX2</td>
<td>SIX homeobox 2</td>
<td></td>
</tr>
<tr>
<td>2.4</td>
<td>222762_s_at</td>
<td>Hs.193370</td>
<td>LIMD1</td>
<td>LIM domains containing 1</td>
<td></td>
</tr>
<tr>
<td>Log2 Fold Change</td>
<td>Probe ID</td>
<td>Description</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>-----------------</td>
<td>----------</td>
<td>-------------</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.4</td>
<td>204622_s_at</td>
<td>Hs.563344 NR4A2 nuclear receptor subfamily 4, group A, member 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.4</td>
<td>212731_at</td>
<td>Hs.530199 ANKRD46 ankyrin repeat domain 46</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.4</td>
<td>205372_at</td>
<td>Hs.14968 PLAG1 pleiomorphic adenoma gene 1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.4</td>
<td>202221_s_at</td>
<td>Hs.517517 EP300 E1A binding protein p300</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>231188_at</td>
<td>Hs.594023 ZSCAN2 zinc finger and SCAN domain containing 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>242704_at</td>
<td>Hs.586165 HMG1 mastermind-like 1 (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>155790_at</td>
<td>Hs.655964 SDC4CAG1 serologically defined colon cancer antigen 1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>206310_at</td>
<td>Hs.101937 SIX2 SIX homeobox 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>209289_at</td>
<td>Hs.644095 NFB nuclear factor I/B</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>212594_at</td>
<td>Hs.711490 PDCD4 programmed cell death 4 (neoplastic transformation inhibitor)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>232103_at</td>
<td>Hs.406134 BPIST1 3'UTR, 5'-phosphatase nucleotidase 1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>211352_s_at</td>
<td>Hs.592142 NCOA3 nuclear receptor coactivator 3</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.3</td>
<td>213147_at</td>
<td>Hs.592166 HOX10 homeobox A10</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>212593_s_at</td>
<td>Hs.711490 PDCD4 programmed cell death 4 (neoplastic transformation inhibitor)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>207108_s_at</td>
<td>Hs.481927 NIPBL Nipped-B homolog (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>216248_s_at</td>
<td>Hs.563344 NR4A2 nuclear receptor subfamily 4, group A, member 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>214684_at</td>
<td>Hs.268675 MEF2A (includes EG:4205) myocyte enhancer factor 2A</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>203845_at</td>
<td>Hs.533055 KAT2B K(lysine) acetyltransferase 2B</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>227020_at</td>
<td>Hs.463613 YPEL2 yippee-like 2 (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>229317_at</td>
<td>Hs.182971 KPNA5 karyopherin alpha 5 (importin alpha 6)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>201086_s_at</td>
<td>Hs.481927 HIPBL Hippel-Lindau homolog (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.2</td>
<td>216248_at</td>
<td>Hs.563344 NR4A2 nuclear receptor subfamily 4, group A, member 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>227020_at</td>
<td>Hs.463613 YPEL2 yippee-like 2 (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>229317_at</td>
<td>Hs.182971 KPNA5 karyopherin alpha 5 (importin alpha 6)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>217934_at</td>
<td>Hs.182971 KPNA5 karyopherin alpha 5 (importin alpha 6)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>216248_at</td>
<td>Hs.563344 NR4A2 nuclear receptor subfamily 4, group A, member 2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>212593_s_at</td>
<td>Hs.711490 PDCD4 programmed cell death 4 (neoplastic transformation inhibitor)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>227934_at</td>
<td>Hs.182971 KPNA5 karyopherin alpha 5 (importin alpha 6)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>224847_at</td>
<td>Hs.119882 CDK6 cyclin-dependent kinase 6</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>224848_at</td>
<td>Hs.119882 CDK6 cyclin-dependent kinase 6</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>217427_s_at</td>
<td>Hs.474206 HIRA HIR histone cell cycle regulation defective homolog A (S. cerevisiae)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>226069_at</td>
<td>Hs.524348 PRKCIK1l prickle homolog 1 (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>217427_s_at</td>
<td>Hs.474206 HIRA HIR histone cell cycle regulation defective homolog A (S. cerevisiae)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>226069_at</td>
<td>Hs.524348 PRKCIK1l prickle homolog 1 (Drosophila)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>226736_at</td>
<td>Hs.434075 MED28 mediator complex subunit 28</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Unknown**

<table>
<thead>
<tr>
<th>Log2 Fold Change</th>
<th>Probe ID</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.6</td>
<td>226598_at</td>
<td>LOC653071 similar to CG22820-PA, isoform A</td>
</tr>
<tr>
<td>4.4</td>
<td>244640_at</td>
<td>Hs.406307 LOC342892 zinc finger protein 850 pseudogene</td>
</tr>
<tr>
<td>4.2</td>
<td>226490_at</td>
<td>Hs.652741 NHSL1 NHS-like 1</td>
</tr>
<tr>
<td>4.2</td>
<td>204160_s_at</td>
<td>Hs.643497 ENPP4 ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)</td>
</tr>
<tr>
<td>3.4</td>
<td>224588_s_at</td>
<td>Hs.642877 MALAT1 metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)</td>
</tr>
<tr>
<td>3</td>
<td>232080_at</td>
<td>Hs.654742 HECT2 HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2</td>
</tr>
<tr>
<td>3</td>
<td>155140_at</td>
<td>Hs.49421 WDR78 WD repeat domain 78</td>
</tr>
<tr>
<td>2.9</td>
<td>228152_s_at</td>
<td>Hs.535011 DDX60L DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like</td>
</tr>
<tr>
<td>2.9</td>
<td>1553106_at</td>
<td>Hs.406549 CSF2R24 chromosome 3 open reading frame 24</td>
</tr>
<tr>
<td>2.8</td>
<td>221727_at</td>
<td>Hs.69800 CDK18 chromosome 3 open reading frame 18</td>
</tr>
<tr>
<td>2.8</td>
<td>218967_s_at</td>
<td>Hs.714420 PTK phosphotyrosinase related</td>
</tr>
<tr>
<td>2.8</td>
<td>219094_at</td>
<td>Hs.266826 ARMC8 armadillo repeat containing 8</td>
</tr>
<tr>
<td>2.7</td>
<td>1569129_at</td>
<td>Hs.518099 CD3RF38 chromosome 3 open reading frame 38</td>
</tr>
<tr>
<td>2.7</td>
<td>243982_at</td>
<td>Hs.653206 KLHL24 kelch-like 28 (Drosophila)</td>
</tr>
<tr>
<td>2.7</td>
<td>209343_at</td>
<td>Hs.516769 EFHD1 EF-hand domain family, member D1</td>
</tr>
<tr>
<td>2.7</td>
<td>232112_at</td>
<td>Hs.709811 RALGPS2 Ral GEF with PH domain and SH3 binding motif 2</td>
</tr>
<tr>
<td>2.6</td>
<td>228608_at</td>
<td>Hs.525146</td>
</tr>
<tr>
<td>2.6</td>
<td>225166_at</td>
<td>Hs.484858</td>
</tr>
<tr>
<td>2.6</td>
<td>1558943_x_at</td>
<td>Hs.710250</td>
</tr>
<tr>
<td>2.6</td>
<td>235061_at</td>
<td>Hs.291000</td>
</tr>
<tr>
<td>2.6</td>
<td>225922_at</td>
<td>Hs.709500</td>
</tr>
<tr>
<td>2.6</td>
<td>225487_at</td>
<td>Hs.43899</td>
</tr>
<tr>
<td>2.6</td>
<td>226533_at</td>
<td>Hs.72325</td>
</tr>
<tr>
<td>2.5</td>
<td>229748_x_at</td>
<td>Hs.487562</td>
</tr>
<tr>
<td>2.5</td>
<td>225957_at</td>
<td>Hs.484195</td>
</tr>
<tr>
<td>2.5</td>
<td>225989_at</td>
<td>Hs.51891</td>
</tr>
<tr>
<td>2.5</td>
<td>227268_at</td>
<td>Hs.531701</td>
</tr>
<tr>
<td>2.4</td>
<td>214791_at</td>
<td>Hs.662198</td>
</tr>
<tr>
<td>2.4</td>
<td>220329_s_at</td>
<td>Hs.492121</td>
</tr>
<tr>
<td>2.4</td>
<td>227514_at</td>
<td>Hs.529341</td>
</tr>
<tr>
<td>2.4</td>
<td>220172_at</td>
<td>Hs.659439</td>
</tr>
<tr>
<td>2.4</td>
<td>237862_at</td>
<td>Hs.479954</td>
</tr>
<tr>
<td>2.4</td>
<td>223142_x_at</td>
<td>Hs.487562</td>
</tr>
<tr>
<td>2.1</td>
<td>220172_at</td>
<td>Hs.659439</td>
</tr>
<tr>
<td>2.1</td>
<td>223142_x_at</td>
<td>Hs.487562</td>
</tr>
<tr>
<td>2.1</td>
<td>225561_at</td>
<td>Hs.369052</td>
</tr>
<tr>
<td>2.1</td>
<td>229256_at</td>
<td>Hs.26612</td>
</tr>
<tr>
<td>2.1</td>
<td>241933_at</td>
<td>Hs.406917</td>
</tr>
<tr>
<td>No.</td>
<td>Gene ID</td>
<td>Description</td>
</tr>
<tr>
<td>-----</td>
<td>-----------</td>
<td>--------------------------------------</td>
</tr>
<tr>
<td>2.1</td>
<td>234491_s_at</td>
<td>Hs.642842 SAV1 salavador homolog 1 (Drosophila)</td>
</tr>
<tr>
<td>2</td>
<td>226436_at</td>
<td>Hs.522895 RASSF4 Ras association (RagD/5/AF-6) domain member 4</td>
</tr>
<tr>
<td>2</td>
<td>220241_at</td>
<td>Hs.317593 TMCO3 transmembrane and coiled-coil domains 3</td>
</tr>
<tr>
<td>2</td>
<td>218610_s_at</td>
<td>Hs.460002 FLJ11151 hypothetical protein Flj 11151</td>
</tr>
<tr>
<td>2</td>
<td>228749_at</td>
<td>Hs.110489 ZDBF2 zinc finger, DBF-type containing 2</td>
</tr>
<tr>
<td>2</td>
<td>225956_at</td>
<td>Hs.481915 CSORF41 chromosome 5 open reading frame 41</td>
</tr>
<tr>
<td>2</td>
<td>235484_at</td>
<td>Hs.714854 PTAR1 protein prenyltransferase alpha subunit repeat containing 1</td>
</tr>
<tr>
<td>2</td>
<td>223167_s_at</td>
<td>Hs.473370 USP25 ubiquitin specific peptidase 25</td>
</tr>
<tr>
<td>2.9</td>
<td>236089_at</td>
<td>Hs.632121</td>
</tr>
<tr>
<td>5.1</td>
<td>1558605_at</td>
<td>Hs.597446</td>
</tr>
<tr>
<td>4.9</td>
<td>224444_at</td>
<td>Hs.632997</td>
</tr>
<tr>
<td>3.8</td>
<td>235427_at</td>
<td>Hs.611075</td>
</tr>
<tr>
<td>3.8</td>
<td>1558236_at</td>
<td>---</td>
</tr>
<tr>
<td>3.7</td>
<td>235230_at</td>
<td>Hs.655022</td>
</tr>
<tr>
<td>3.6</td>
<td>239566_at</td>
<td>Hs.656072</td>
</tr>
<tr>
<td>3.5</td>
<td>221590_s_at</td>
<td>Hs.663176 // Hs.708053</td>
</tr>
<tr>
<td>3.4</td>
<td>227051_at</td>
<td>Hs.43047</td>
</tr>
<tr>
<td>3.3</td>
<td>226192_at</td>
<td>Hs.76704</td>
</tr>
<tr>
<td>3.2</td>
<td>217540_at</td>
<td>Hs.598134</td>
</tr>
<tr>
<td>3.2</td>
<td>242245_at</td>
<td>Hs.533853</td>
</tr>
<tr>
<td>3.1</td>
<td>1558105_at</td>
<td>Hs.91389</td>
</tr>
<tr>
<td>3.1</td>
<td>228740_at</td>
<td>Hs.26766</td>
</tr>
<tr>
<td>3.1</td>
<td>215287_at</td>
<td>Hs.128434</td>
</tr>
<tr>
<td>2.9</td>
<td>230161_at</td>
<td>Hs.495605</td>
</tr>
<tr>
<td>2.8</td>
<td>238178_at</td>
<td>Hs.559668</td>
</tr>
<tr>
<td>2.6</td>
<td>243299_at</td>
<td>Hs.666703</td>
</tr>
<tr>
<td>2.6</td>
<td>227368_at</td>
<td>Hs.662821</td>
</tr>
<tr>
<td>2.5</td>
<td>235046_at</td>
<td>Hs.176376</td>
</tr>
<tr>
<td>2.5</td>
<td>242289_at</td>
<td>---</td>
</tr>
<tr>
<td>2.5</td>
<td>234986_at</td>
<td>Hs.596052</td>
</tr>
<tr>
<td>2.4</td>
<td>226197_at</td>
<td>Hs.76704</td>
</tr>
<tr>
<td>2.4</td>
<td>228333_at</td>
<td>Hs.621487</td>
</tr>
<tr>
<td>2.4</td>
<td>225035_at</td>
<td>Hs.655146</td>
</tr>
<tr>
<td>2.3</td>
<td>244663_at</td>
<td>Hs.156256</td>
</tr>
<tr>
<td>2.3</td>
<td>1556346_at</td>
<td>Hs.660628</td>
</tr>
<tr>
<td>2.3</td>
<td>234987_at</td>
<td>Hs.660221</td>
</tr>
<tr>
<td>2.3</td>
<td>222111_at</td>
<td>Hs.595286</td>
</tr>
<tr>
<td>2.3</td>
<td>235782_at</td>
<td>Hs.527515</td>
</tr>
<tr>
<td>2.3</td>
<td>238658_at</td>
<td>Hs.444083</td>
</tr>
<tr>
<td>2.3</td>
<td>228812_at</td>
<td>Hs.632900</td>
</tr>
<tr>
<td>2.3</td>
<td>229885_at</td>
<td>Hs.572073</td>
</tr>
<tr>
<td>2.2</td>
<td>AFFX-r2-Bs-phe-5_at</td>
<td>---</td>
</tr>
<tr>
<td>2.2</td>
<td>235010_at</td>
<td>Hs.706957</td>
</tr>
<tr>
<td>2.2</td>
<td>229130_at</td>
<td>Hs.409256</td>
</tr>
<tr>
<td>2.1</td>
<td>235505_s_at</td>
<td>Hs.40966</td>
</tr>
<tr>
<td>2.1</td>
<td>226520_at</td>
<td>Hs.658311</td>
</tr>
<tr>
<td>2.1</td>
<td>230300_at</td>
<td>Hs.586550</td>
</tr>
<tr>
<td>2.1</td>
<td>213138_at</td>
<td>Hs.592414</td>
</tr>
<tr>
<td>2.1</td>
<td>234259_at</td>
<td>Hs.594784</td>
</tr>
<tr>
<td>2</td>
<td>239866_at</td>
<td>Hs.110940</td>
</tr>
<tr>
<td>2</td>
<td>1558401_at</td>
<td>Hs.408497</td>
</tr>
<tr>
<td>Gene</td>
<td>Description</td>
<td>Expression</td>
</tr>
<tr>
<td>------</td>
<td>-------------</td>
<td>------------</td>
</tr>
<tr>
<td><strong>Extracellular Space</strong></td>
<td>1556316_s_at</td>
<td>Hs.707281</td>
</tr>
<tr>
<td>-3.9</td>
<td>228332_s_at</td>
<td>Hs.25391</td>
</tr>
<tr>
<td><strong>Plasma Membrane</strong></td>
<td>1567213_at</td>
<td>Hs.409965</td>
</tr>
<tr>
<td>-5.2</td>
<td>224321_s_at</td>
<td>Hs.146513</td>
</tr>
<tr>
<td>-5.8</td>
<td>1555826_at</td>
<td>Hs.713220</td>
</tr>
<tr>
<td>-3.3</td>
<td>209972_s_at</td>
<td>Hs.301613</td>
</tr>
<tr>
<td><strong>Cytoplasm</strong></td>
<td>1567213_at</td>
<td>Hs.409965</td>
</tr>
<tr>
<td>-2.3</td>
<td>220538_s_at</td>
<td>Hs.271954</td>
</tr>
<tr>
<td>-2.8</td>
<td>205000_s_at</td>
<td>Hs.432395</td>
</tr>
<tr>
<td>-2.5</td>
<td>205072_at</td>
<td>Hs.709876</td>
</tr>
<tr>
<td>Change</td>
<td>Description</td>
<td>Gene Accession</td>
</tr>
<tr>
<td>--------</td>
<td>-------------</td>
<td>----------------</td>
</tr>
<tr>
<td>-7.8</td>
<td>226014_at</td>
<td>LOC100133577</td>
</tr>
<tr>
<td>-5</td>
<td>229420_at</td>
<td>Hs.632573</td>
</tr>
<tr>
<td>-4.5</td>
<td>229538_s_at</td>
<td>Hs.591495</td>
</tr>
<tr>
<td>-4.1</td>
<td>225423_s_at</td>
<td>Hs.708096</td>
</tr>
<tr>
<td>-3.9</td>
<td>213297_at</td>
<td>Hs.519044</td>
</tr>
<tr>
<td>-3.6</td>
<td>222487_s_at</td>
<td>Hs.108957</td>
</tr>
<tr>
<td>-3.1</td>
<td>229594_s_at</td>
<td>Hs.182698</td>
</tr>
<tr>
<td>-3.1</td>
<td>221936_s_at</td>
<td>Hs.708096</td>
</tr>
<tr>
<td>-2.8</td>
<td>221997_s_at</td>
<td>Hs.355935</td>
</tr>
<tr>
<td>-2.5</td>
<td>211531_s_at</td>
<td>Hs.631176</td>
</tr>
<tr>
<td>-2.2</td>
<td>224271_s_at</td>
<td>Hs.652967</td>
</tr>
<tr>
<td>-2.2</td>
<td>1564257_at</td>
<td>Hs.713960</td>
</tr>
<tr>
<td>-1.9</td>
<td>222968_at</td>
<td></td>
</tr>
<tr>
<td>-1.9</td>
<td>231387_at</td>
<td>Hs.712966</td>
</tr>
<tr>
<td>-1.4</td>
<td>216054_s_at</td>
<td></td>
</tr>
<tr>
<td>-1.4</td>
<td>234225_at</td>
<td></td>
</tr>
<tr>
<td>-1.3</td>
<td>221995_s_at</td>
<td></td>
</tr>
<tr>
<td>-1.3</td>
<td>210098_s_at</td>
<td></td>
</tr>
<tr>
<td>-1.3</td>
<td>1563431_s_at</td>
<td>Hs.713288</td>
</tr>
<tr>
<td>-1</td>
<td>212952_at</td>
<td>Hs.593218</td>
</tr>
<tr>
<td>-0.9</td>
<td>1567913_at</td>
<td>Hs.621508</td>
</tr>
<tr>
<td>-0.8</td>
<td>216246_at</td>
<td></td>
</tr>
<tr>
<td>-0.7</td>
<td>230350_at</td>
<td>Hs.594199</td>
</tr>
<tr>
<td>-0.7</td>
<td>213048_s_at</td>
<td></td>
</tr>
<tr>
<td>-0.6</td>
<td>214395_s_at</td>
<td>Hs.707453</td>
</tr>
<tr>
<td>-0.4</td>
<td>213813_s_at</td>
<td></td>
</tr>
<tr>
<td>-0.4</td>
<td>211464_s_at</td>
<td></td>
</tr>
<tr>
<td>-0.3</td>
<td>233810_s_at</td>
<td></td>
</tr>
<tr>
<td>-0.2</td>
<td>229798_s_at</td>
<td></td>
</tr>
<tr>
<td>-0.2</td>
<td>221419_s_at</td>
<td></td>
</tr>
<tr>
<td>-0.1</td>
<td>1567105_at</td>
<td></td>
</tr>
<tr>
<td>-0.1</td>
<td>224375_at</td>
<td></td>
</tr>
</tbody>
</table>
Table S4. Genes differentially expressed in HD-MSC +TNF/LT compared with HD-MSC

Red line indicates genes overexpressed in HD-MSC stimulated by TNF+LT for 3 days compared to unstimulated HD-MSC and green line indicates genes overexpressed in resting HD-MSC Fold change indicates the ratio of mean expression in HD-MSC treated by TNF+LT/mean expression in resting HD-MSC when FC>2;
-1/(ratio of mean expression in HD-MSC treated by TNF+LT/mean expression in resting HD-MSC) when FC<.5.

<table>
<thead>
<tr>
<th>Location</th>
<th>Fold Change</th>
<th>ProbeSet ID</th>
<th>UniGene ID</th>
<th>Gene Symbol</th>
<th>Gene Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>Extracellular Space</td>
<td>20.5</td>
<td>200465_s_at</td>
<td>Hs.514821</td>
<td>CCL5</td>
<td>chemokine (C-C motif) ligand 5</td>
</tr>
<tr>
<td></td>
<td>2036.6</td>
<td>202859_s_at</td>
<td>Hs.624</td>
<td>IL8</td>
<td>interleukin 8</td>
</tr>
<tr>
<td></td>
<td>1035.1</td>
<td>1405_s_at</td>
<td>Hs.514821</td>
<td>CCL5</td>
<td>chemokine (C-C motif) ligand 5</td>
</tr>
<tr>
<td></td>
<td>876.1</td>
<td>155575_s_at</td>
<td>Hs.514821</td>
<td>CCL5</td>
<td>chemokine (C-C motif) ligand 5</td>
</tr>
<tr>
<td></td>
<td>358.3</td>
<td>211506_s_at</td>
<td>Hs.624</td>
<td>IL8</td>
<td>interleukin 8</td>
</tr>
<tr>
<td></td>
<td>247</td>
<td>39402_at</td>
<td>Hs.126256</td>
<td>IL1B</td>
<td>interleukin 1, beta</td>
</tr>
<tr>
<td></td>
<td>138</td>
<td>202357_s_at</td>
<td>Hs.408903</td>
<td>C2</td>
<td>complement component 2</td>
</tr>
<tr>
<td></td>
<td>125.1</td>
<td>203828_s_at</td>
<td>Hs.943</td>
<td>IL3</td>
<td>interleukin 3</td>
</tr>
<tr>
<td></td>
<td>118.9</td>
<td>214974_s_at</td>
<td>Hs.89714</td>
<td>CXC15</td>
<td>chemokine (C-X-C motif) ligand 5</td>
</tr>
<tr>
<td></td>
<td>93.1</td>
<td>210118_s_at</td>
<td>Hs.1272</td>
<td>IL1A</td>
<td>interleukin 1, alpha</td>
</tr>
<tr>
<td></td>
<td>89.8</td>
<td>206363_at</td>
<td>Hs.164021</td>
<td>CXC16</td>
<td>chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)</td>
</tr>
<tr>
<td></td>
<td>81.1</td>
<td>207426_s_at</td>
<td>Hs.181097</td>
<td>TNFSF4</td>
<td>tumor necrosis factor (ligand) superfamily, member 4</td>
</tr>
<tr>
<td></td>
<td>66.6</td>
<td>209267_at</td>
<td>Hs.126256</td>
<td>IL1B</td>
<td>interleukin 1, beta</td>
</tr>
<tr>
<td></td>
<td>61.3</td>
<td>204585_s_at</td>
<td>Hs.592122</td>
<td>TYMP</td>
<td>thymidine phosphorylase</td>
</tr>
<tr>
<td></td>
<td>54.7</td>
<td>216598_s_at</td>
<td>Hs.303449</td>
<td>CCL2</td>
<td>chemokine (C-C motif) ligand 2</td>
</tr>
<tr>
<td></td>
<td>40.5</td>
<td>235717_at</td>
<td>Hs.389748</td>
<td>TSLP</td>
<td>thymic stromal lymphopoietin</td>
</tr>
<tr>
<td></td>
<td>25.2</td>
<td>209840_s_at</td>
<td>Hs.3781</td>
<td>LRRN3</td>
<td>leucine rich repeat neuronal 3</td>
</tr>
<tr>
<td></td>
<td>24.6</td>
<td>205483_s_at</td>
<td>Hs.458485</td>
<td>ISG15</td>
<td>(includes EG ISG15 ubiquitin-like modifier)</td>
</tr>
<tr>
<td></td>
<td>22.3</td>
<td>209603_s_at</td>
<td>Hs.288034</td>
<td>SLC29A8</td>
<td>solute carrier family 29 (zinc transporter), member 8</td>
</tr>
<tr>
<td></td>
<td>18.3</td>
<td>205992_s_at</td>
<td>Hs.654378</td>
<td>IL15</td>
<td>interleukin 15</td>
</tr>
<tr>
<td></td>
<td>16.7</td>
<td>206025_s_at</td>
<td>Hs.437722</td>
<td>TNFAIP6</td>
<td>tumor necrosis factor, alpha-induced protein 6</td>
</tr>
<tr>
<td></td>
<td>13.4</td>
<td>206026_s_at</td>
<td>Hs.437722</td>
<td>TNFAIP6</td>
<td>tumor necrosis factor, alpha-induced protein 6</td>
</tr>
<tr>
<td></td>
<td>13.4</td>
<td>209841_s_at</td>
<td>Hs.3781</td>
<td>LRRN3</td>
<td>leucine rich repeat neuronal 3</td>
</tr>
<tr>
<td></td>
<td>12.4</td>
<td>206254_s_at</td>
<td>Hs.419815</td>
<td>EGF</td>
<td>epidermal growth factor (beta-urogastrone)</td>
</tr>
<tr>
<td></td>
<td>11.7</td>
<td>209302_s_at</td>
<td>Hs.525607</td>
<td>TNFAIP2</td>
<td>tumor necrosis factor, alpha-induced protein 2</td>
</tr>
<tr>
<td></td>
<td>10.8</td>
<td>209277_s_at</td>
<td>Hs.438231</td>
<td>TFPI2</td>
<td>tissue factor pathway inhibitor 2</td>
</tr>
<tr>
<td></td>
<td>8.7</td>
<td>241986_at</td>
<td>Hs.60998</td>
<td>BMPER</td>
<td>BMP binding endothelial regulator</td>
</tr>
<tr>
<td></td>
<td>7.5</td>
<td>213817_at</td>
<td>Hs.54861</td>
<td>IRAK3</td>
<td>interleukin-1 receptor-associated kinase 3</td>
</tr>
<tr>
<td></td>
<td>6.7</td>
<td>208747_s_at</td>
<td>Hs.458355</td>
<td>C15</td>
<td>complement component 1, s subcomponent</td>
</tr>
<tr>
<td></td>
<td>6.4</td>
<td>205174_s_at</td>
<td>Hs.79033</td>
<td>QPCT</td>
<td>(includes EG glutaminyl-peptide cyclotransferase</td>
</tr>
<tr>
<td></td>
<td>6.1</td>
<td>213967_s_at</td>
<td>Hs.58055</td>
<td>LRH1</td>
<td>leucine-rich repeats and immunoglobulin-like domains 1</td>
</tr>
<tr>
<td></td>
<td>5.7</td>
<td>205207_s_at</td>
<td>Hs.654458</td>
<td>IL6</td>
<td>interleukin 6 (interferon, beta 2)</td>
</tr>
<tr>
<td></td>
<td>5.3</td>
<td>209788_s_at</td>
<td>Hs.436166</td>
<td>ERAP1</td>
<td>endoplasmic reticulum aminopeptidase 1</td>
</tr>
<tr>
<td></td>
<td>5.2</td>
<td>211896_s_at</td>
<td>Hs.706262</td>
<td>DCN</td>
<td>decorin</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>1552312_s_at</td>
<td>Hs.432818</td>
<td>MFAP3</td>
<td>microfibril-associated protein 3</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>203788_s_at</td>
<td>Hs.269109</td>
<td>SEMA3C</td>
<td>sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C</td>
</tr>
<tr>
<td></td>
<td>4.9</td>
<td>212067_s_at</td>
<td>Hs.534234</td>
<td>CIR</td>
<td>complement component 1, s subcomponent</td>
</tr>
<tr>
<td></td>
<td>4.9</td>
<td>209335_s_at</td>
<td>Hs.706262</td>
<td>DCN</td>
<td>decorin</td>
</tr>
<tr>
<td></td>
<td>4.8</td>
<td>206814_s_at</td>
<td>Hs.2561</td>
<td>NGF</td>
<td>nerve growth factor (beta polypeptide)</td>
</tr>
<tr>
<td></td>
<td>4.7</td>
<td>204614_s_at</td>
<td>Hs.594481</td>
<td>SERPINA2</td>
<td>serpin peptidase inhibitor, clade B (ovalbumin), member 2</td>
</tr>
<tr>
<td></td>
<td>4.7</td>
<td>209278_s_at</td>
<td>Hs.438231</td>
<td>TFPI2</td>
<td>tissue factor pathway inhibitor 2</td>
</tr>
<tr>
<td></td>
<td>4.5</td>
<td>203744_s_at</td>
<td>Hs.406475</td>
<td>LUM</td>
<td>lumican</td>
</tr>
<tr>
<td></td>
<td>4.5</td>
<td>220147_s_at</td>
<td>Hs.590154</td>
<td>FAM8A</td>
<td>(includes EG family with sequence similarity 60, member A</td>
</tr>
<tr>
<td></td>
<td>4.3</td>
<td>217738_s_at</td>
<td>Hs.48965</td>
<td>NAMPT</td>
<td>nicotinamide phosphoamoanptide transferase</td>
</tr>
<tr>
<td></td>
<td>4.2</td>
<td>38037_at</td>
<td>Hs.799</td>
<td>HBEFG</td>
<td>hepin-binding EGF-like growth factor</td>
</tr>
<tr>
<td></td>
<td>3.9</td>
<td>211739_s_at</td>
<td>Hs.49415</td>
<td>NAMPT</td>
<td>nicotinamide phosphoamoanptide transferase</td>
</tr>
<tr>
<td></td>
<td>3.8</td>
<td>214719_s_at</td>
<td>Hs.112167</td>
<td>SLC46A3</td>
<td>solute carrier family 46, member 3</td>
</tr>
<tr>
<td></td>
<td>3.8</td>
<td>219201_s_at</td>
<td>Hs.514685</td>
<td>TWSG1</td>
<td>twisted gastrulation homology 1 (Drosophila)</td>
</tr>
<tr>
<td></td>
<td>3.6</td>
<td>218907_s_at</td>
<td>Hs.232750</td>
<td>KTEL1</td>
<td>KTEL (lys-Tyr-Glu-Leu) containing 1</td>
</tr>
<tr>
<td></td>
<td>3.6</td>
<td>221577_s_at</td>
<td>Hs.619692</td>
<td>GDF15</td>
<td>growth differentiation factor 15</td>
</tr>
<tr>
<td></td>
<td>3.6</td>
<td>213800_s_at</td>
<td>Hs.363396</td>
<td>CFIH</td>
<td>complement factor H</td>
</tr>
<tr>
<td></td>
<td>3.5</td>
<td>203765_s_at</td>
<td>Hs.1114</td>
<td>BMP1</td>
<td>bone morphogenetic protein 1</td>
</tr>
<tr>
<td></td>
<td>3.5</td>
<td>201893_s_at</td>
<td>Hs.706262</td>
<td>DCN</td>
<td>decorin</td>
</tr>
<tr>
<td></td>
<td>3.4</td>
<td>203789_s_at</td>
<td>Hs.269109</td>
<td>SEMA3C</td>
<td>sema domain, immunoglobulin domain (lg), short basic domain, secreted, (semaphorin) 3C</td>
</tr>
<tr>
<td></td>
<td>3.3</td>
<td>218903_s_at</td>
<td>Hs.821730</td>
<td>CBL</td>
<td>complement component 1, s subcomponent-like</td>
</tr>
<tr>
<td></td>
<td>3.2</td>
<td>210385_s_at</td>
<td>Hs.436186</td>
<td>ERAP1</td>
<td>endoplasmic reticulum aminopeptidase 1</td>
</tr>
<tr>
<td>Gene Name</td>
<td>Description</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>-----------</td>
<td>-------------</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CLDN1</td>
<td>Claudin 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BMP1</td>
<td>Bone morphogenetic protein 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>POSTN</td>
<td>Peristin, osteoblast specific factor</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>KTEL1</td>
<td>KTEL (Lys-Tyr-Glu-Leu) containing 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TFGB1</td>
<td>Transforming growth factor, beta 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>HBG1</td>
<td>Heparin-binding EGF-like growth factor</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EDN1</td>
<td>Endothelin 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SERPINF1</td>
<td>Serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SPARC</td>
<td>Secreted protein, acidic, cysteine-rich (osteonectin)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FGFB</td>
<td>Fibroblast growth factor 2 (basic)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DCBLD1</td>
<td>Discoidin, CUB and ECLCL domain containing 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>EDN1</td>
<td>Endothelin 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PGCP</td>
<td>Plasma glutamate carboxypeptidase</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>COLIA3</td>
<td>Collagen, type III, alpha 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>COLIA1</td>
<td>Collagen, type I, alpha 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MFAP2</td>
<td>Microfibrillar-associated protein 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TWSG1</td>
<td>Twist caused gastrulation homolog 1 (Drosophila)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RNASE4</td>
<td>Ribonuclease, A family, 4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DKK3</td>
<td>Dickkopf homolog 3 (Xenopus laevis)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ICAM1</td>
<td>Intercellular adhesion molecule 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GPRC5B</td>
<td>G protein-coupled receptor, family C, group 5, member B</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TNFRSF9</td>
<td>Tumor necrosis factor receptor superfamily, member 9</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC38A1</td>
<td>Solute carrier family 38, member 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GPRC5B</td>
<td>G protein-coupled receptor, family C, group 5, member B</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CDB3</td>
<td>CDB3 molecule</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SYNGR2</td>
<td>Synaptogyrin 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ICAM2</td>
<td>Intercellular adhesion molecule 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC7A1</td>
<td>Solute carrier family 7, member 1 (cations, amino acid transporter, y+ system)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC22A3</td>
<td>Solute carrier family 22, member 3 (sodium-dependent vitamin B12 transporter)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IRAK2</td>
<td>Interleukin-1 receptor-associated kinase 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC7A1</td>
<td>Solute carrier family 7, member 1 (cations, amino acid transporter, y+ system)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NR2P2</td>
<td>Neurilin 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC7A5</td>
<td>Solute carrier family 7, member 5 (cations, amino acid transporter, y+ system)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>KCNJ15</td>
<td>Potassium inwardly-rectifying channel, subfamily J, member 15</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC22A6</td>
<td>Solute carrier family 22, member 6 (sodium-dependent pyrimidine transporter)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABCA1</td>
<td>ATP binding cassette, sub-family A (ABCG1), member 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC7A1</td>
<td>Solute carrier family 7, member 1 (cations, amino acid transporter, y+ system)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NR2P2</td>
<td>Neurilin 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CDS8</td>
<td>CDS8 molecule</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CDS8</td>
<td>CDS8 molecule</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GALNAc4S-6ST</td>
<td>B cell RAG-associated protein</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CLDN1</td>
<td>Claudin 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IFNAR2</td>
<td>Interferon (alpha, beta and omega) receptor 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DPP4</td>
<td>Dipeptidyl-peptidase 4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>JAM2</td>
<td>Junctional adhesion molecule 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IFNGR1</td>
<td>Interferon gamma receptor 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>UNC5B</td>
<td>Unc-5 homolog B (C. elegans)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TLR3</td>
<td>Toll-like receptor 3</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IFG2A2</td>
<td>Integrin, alpha 2 (C:D49B, alpha 2 subunit of VLA-2 receptor)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IFNGR1</td>
<td>Interferon gamma receptor 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PLCR1</td>
<td>Phospholipid scramblase 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NRP2</td>
<td>Neurilin 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLC19A2</td>
<td>Solute carrier family 19 (thiamine transporter), member 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BRR4A</td>
<td>Brain protein 4A</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ITGAV</td>
<td>Integrin, alpha L, beta 7</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ITGAV</td>
<td>Integrin, beta 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Plasma Membrane**

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>IL7R</td>
<td>Interleukin 7 receptor</td>
</tr>
<tr>
<td>PLSCR1</td>
<td>Prefoldin 1</td>
</tr>
<tr>
<td>ITGA2</td>
<td>Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)</td>
</tr>
<tr>
<td>UNC5B</td>
<td>Unc-5 homolog B (C. elegans)</td>
</tr>
<tr>
<td>DPP4</td>
<td>Dipeptidyl-peptidase 4</td>
</tr>
<tr>
<td>IFNAR2</td>
<td>Interferon (alpha, beta and omega) receptor 2</td>
</tr>
<tr>
<td>NRP2</td>
<td>Neurilin 2</td>
</tr>
<tr>
<td>SLC19A2</td>
<td>Solute carrier family 19 (thiamine transporter), member 2</td>
</tr>
<tr>
<td>BRR4A</td>
<td>Brain protein 4A</td>
</tr>
<tr>
<td>ITGAV</td>
<td>Integrin, alpha L, beta 7</td>
</tr>
</tbody>
</table>

**Other Proteins**

<table>
<thead>
<tr>
<th>Gene Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DPP4</td>
<td>Dipeptidyl-peptidase 4</td>
</tr>
<tr>
<td>IFNAR2</td>
<td>Interferon (alpha, beta and omega) receptor 2</td>
</tr>
<tr>
<td>NRP2</td>
<td>Neurilin 2</td>
</tr>
<tr>
<td>SLC19A2</td>
<td>Solute carrier family 19 (thiamine transporter), member 2</td>
</tr>
<tr>
<td>BRR4A</td>
<td>Brain protein 4A</td>
</tr>
<tr>
<td>ITGAV</td>
<td>Integrin, alpha L, beta 7</td>
</tr>
</tbody>
</table>

**References**

- IL7R: Interleukin 7 receptor
- PLSCR1: Prefoldin 1
- ITGA2: Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)
- UNC5B: Unc-5 homolog B (C. elegans)
- DPP4: Dipeptidyl-peptidase 4
- IFNAR2: Interferon (alpha, beta and omega) receptor 2
- NRP2: Neurilin 2
- SLC19A2: Solute carrier family 19 (thiamine transporter), member 2
- BRR4A: Brain protein 4A
- ITGAV: Integrin, alpha L, beta 7
<table>
<thead>
<tr>
<th>Position</th>
<th>Gene</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>5.3</td>
<td>210405_x_at</td>
<td>HS.521456</td>
</tr>
<tr>
<td>5.2</td>
<td>210229_x_at</td>
<td>HS.511887</td>
</tr>
<tr>
<td>5.2</td>
<td>204715_at</td>
<td>HS.591976</td>
</tr>
<tr>
<td>5</td>
<td>205775_at</td>
<td>HS.714863</td>
</tr>
<tr>
<td>4.8</td>
<td>207310_at</td>
<td>HS.525572</td>
</tr>
<tr>
<td>4.8</td>
<td>200924_s_at</td>
<td>HS.502769</td>
</tr>
<tr>
<td>4.6</td>
<td>204717_s_at</td>
<td>HS.82002</td>
</tr>
<tr>
<td>4.6</td>
<td>204806_x_at</td>
<td>HS.519972</td>
</tr>
<tr>
<td>4.5</td>
<td>213909_at</td>
<td>HS.288467</td>
</tr>
<tr>
<td>4.5</td>
<td>213194_c_at</td>
<td>HS.13840</td>
</tr>
<tr>
<td>4.5</td>
<td>209295_s_at</td>
<td>HS.615388</td>
</tr>
<tr>
<td>4.3</td>
<td>223249_at</td>
<td>HS.258576</td>
</tr>
<tr>
<td>4.3</td>
<td>203441_s_at</td>
<td>HS.464892</td>
</tr>
<tr>
<td>4.3</td>
<td>230425_at</td>
<td>HS.116092</td>
</tr>
<tr>
<td>4.3</td>
<td>205327_s_at</td>
<td>HS.470174</td>
</tr>
<tr>
<td>4.2</td>
<td>203223_at</td>
<td>HS.513457</td>
</tr>
<tr>
<td>4.2</td>
<td>209131_s_at</td>
<td>HS.714865</td>
</tr>
<tr>
<td>4.2</td>
<td>200929_s_at</td>
<td>HS.521456</td>
</tr>
<tr>
<td>4.1</td>
<td>221875_s_at</td>
<td>HS.519972</td>
</tr>
<tr>
<td>4.1</td>
<td>209147_s_at</td>
<td>HS.696231</td>
</tr>
<tr>
<td>4.1</td>
<td>211799_x_at</td>
<td>HS.654404</td>
</tr>
<tr>
<td>4</td>
<td>203866_s_at</td>
<td>HS.109225</td>
</tr>
<tr>
<td>3.9</td>
<td>213110_at</td>
<td>HS.491232</td>
</tr>
<tr>
<td>3.8</td>
<td>223499_at</td>
<td>HS.632102</td>
</tr>
<tr>
<td>3.8</td>
<td>208729_x_at</td>
<td>HS.634404</td>
</tr>
<tr>
<td>3.7</td>
<td>224082_c_at</td>
<td>HS.524625</td>
</tr>
<tr>
<td>3.7</td>
<td>1554557_at</td>
<td>HS.478429</td>
</tr>
<tr>
<td>3.7</td>
<td>203125_s_at</td>
<td>HS.505545</td>
</tr>
<tr>
<td>3.7</td>
<td>211529_x_at</td>
<td>HS.512152</td>
</tr>
<tr>
<td>3.7</td>
<td>214544_s_at</td>
<td>HS.714865</td>
</tr>
<tr>
<td>3.6</td>
<td>209663_at</td>
<td>HS.81629</td>
</tr>
<tr>
<td>3.6</td>
<td>221872_at</td>
<td>HS.131269</td>
</tr>
<tr>
<td>3.6</td>
<td>20516_s_at</td>
<td>HS.506276</td>
</tr>
<tr>
<td>3.5</td>
<td>222060_at</td>
<td>HS.654891</td>
</tr>
<tr>
<td>3.4</td>
<td>207177_at</td>
<td>HS.654365</td>
</tr>
<tr>
<td>3.3</td>
<td>22042_at</td>
<td>HS.17458</td>
</tr>
<tr>
<td>3.3</td>
<td>218239_at</td>
<td>HS.656195</td>
</tr>
<tr>
<td>3.3</td>
<td>213191_s_at</td>
<td>HS.549053</td>
</tr>
<tr>
<td>3.3</td>
<td>227396_s_at</td>
<td>HS.31847</td>
</tr>
<tr>
<td>3.3</td>
<td>235198_at</td>
<td>HS.714371</td>
</tr>
<tr>
<td>3.2</td>
<td>209612_s_at</td>
<td>HS.654352</td>
</tr>
<tr>
<td>3.2</td>
<td>224341_s_at</td>
<td>HS.174312</td>
</tr>
<tr>
<td>3.2</td>
<td>211528_x_at</td>
<td>HS.512152</td>
</tr>
<tr>
<td>3.2</td>
<td>204932_at</td>
<td>HS.81791</td>
</tr>
<tr>
<td>3.2</td>
<td>201875_s_at</td>
<td>HS.493919</td>
</tr>
<tr>
<td>3.1</td>
<td>203971_at</td>
<td>HS.524213</td>
</tr>
<tr>
<td>3.1</td>
<td>203987_at</td>
<td>HS.521863</td>
</tr>
<tr>
<td>3.1</td>
<td>226825_s_at</td>
<td>HS.47966</td>
</tr>
<tr>
<td>3.1</td>
<td>209545_s_at</td>
<td>HS.10375</td>
</tr>
<tr>
<td>3.1</td>
<td>210094_s_at</td>
<td>HS.493919</td>
</tr>
<tr>
<td>3.1</td>
<td>210077_s_at</td>
<td>HS.493919</td>
</tr>
<tr>
<td>3.1</td>
<td>209295_at</td>
<td>HS.521456</td>
</tr>
<tr>
<td>3.1</td>
<td>226045_at</td>
<td>HS.503446</td>
</tr>
<tr>
<td>3.1</td>
<td>208456_s_at</td>
<td>HS.502004</td>
</tr>
<tr>
<td>3.1</td>
<td>219125_s_at</td>
<td>HS.292154</td>
</tr>
<tr>
<td>3.1</td>
<td>212831_s_at</td>
<td>HS.654352</td>
</tr>
<tr>
<td>3.1</td>
<td>230875_s_at</td>
<td>HS.29189</td>
</tr>
<tr>
<td>3.1</td>
<td>208925_at</td>
<td>HS.709386</td>
</tr>
<tr>
<td>3.1</td>
<td>218196_at</td>
<td>HS.226780</td>
</tr>
<tr>
<td>3.1</td>
<td>213353_at</td>
<td>HS.421474</td>
</tr>
<tr>
<td>3.1</td>
<td>218901_at</td>
<td>HS.477869</td>
</tr>
<tr>
<td>3.1</td>
<td>204785_s_at</td>
<td>HS.708185</td>
</tr>
<tr>
<td>3.1</td>
<td>210946_at</td>
<td>HS.696231</td>
</tr>
</tbody>
</table>
2.9 205618_at  a  Hs.190341  PRKG1  proline rich Gis (G-carboxyglutamic acid) 1
2.8 219314_at  a  Hs.132114  ELTD1  EGF, latrophilin and seven transmembrane domain containing 1
2.8 202234_s_at  a  Hs.75221  SLC16A1 solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
2.8 204191_at  a  Hs.59400  IFNAR1  interferon (alpha, beta and omega) receptor 1
2.7 1553780_s_at  a  Hs.694701  RHEB Ras homolog enriched in brain
2.7 1558115_at  a  Hs.714748  RECK  reversion-inducing-cysteine-rich protein with kazal motifs
2.7 218856_at  a  Hs.443577  TMF45F21 tumor necrosis factor receptor superfamily, member 21
2.7 201642_at  a  Hs.614632  IFNGR2  interferon gamma receptor 2 (interferon gamma transducer 1)
2.7 210514_s_at  a  Hs.512152  HLA-G major histocompatibility complex, class I, G
2.7 208783_s_at  a  Hs.510402  CD46  CD46 molecule, complement regulatory protein
2.7 201647_s_at  a  Hs.349656  SCARB2 scavenger receptor class B, member 2
2.6 220092_s_at  a  Hs.165859  ANTXR1  anthrax toxin receptor 1
2.6 220025_s_at  a  Hs.654804  LRPI2  low density lipoprotein-related protein 12
2.6 201374_at  a  Hs.49319  MPZL1 myelin protein zero-like 1
2.6 204204_at  a  Hs.24030  SLC31A2 solute carrier family 31 (copper transporters), member 2
2.6 212930_at  a  Hs.506276  ATP2B1 ATPase, Ca++ transporting, plasma membrane 1
2.6 204720_at  a  Hs.453836  CDH12 cadherin 12, N-cadherin (neutrophil)
2.6 225243_s_at  a  Hs.476432  SLMAP sarcolemna associated protein
2.6 226353_at  a  Hs.401537  SPP2LA signal peptide peptidase-like 2A
2.6 201334_at  a  Hs.714756  BAMB1 BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
2.5 215707_s_at  a  Hs.472010  PRNP prion protein
2.5 202514_at  a  Hs.292549  DLG1 discs, large homolog 1 (Drosophila)
2.5 225059_at  a  Hs.464438  AGTRAP angiotensin II receptor-associated protein
2.5 211530_s_at  a  Hs.512152  HLA-G major histocompatibility complex, class I, G
2.5 227059_at  a  Hs.443429  GPC6 glypican 6
2.5 219572_at  a  Hs.709214  CADPS2 Ca++-dependent secretion activator 2
2.5 218095_s_at  a  Hs.479766  TMEM165 transmembrane protein 165
2.5 211355_s_at  a  Hs.26487  FGFR1 fibroblast growth factor receptor 1
2.5 212398_at  a  Hs.592082  IL6ST interleukin 6 signal transducer (gp130, Oncostatin M receptor)
2.5 1555736_a_at  a  Hs.464438  AGTRAP angiotensin II receptor-associated protein
2.4 235068_at  a  Hs.649522  ZDHHC21 zinc finger, DHHC-type containing 21
2.4 201302_at  a  Hs.427986  ANXA4 annexin A4
2.4 243463_s_at  a  Hs.401334  RT1A Ras-like without CAAX 1
2.4 203440_at  a  Hs.44829  CD2 cadherin 2, type 1, N-cadherin (neuronal)
2.4 226651_at  a  Hs.591761  HOMER1 homer homolog 1 (Drosophila)
2.4 224709_s_at  a  Hs.508829  CDC42SE2 CDC42 small effector 2
2.4 209900_s_at  a  Hs.75231  SLC16A1 solute carrier family 16, member 1 (monocarboxylic acid transporter 1)
2.4 203124_s_at  a  Hs.505435  SLC11A2 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
2.4 200620_at  a  Hs.523262  TMEB59 (includes) transmembrane protein 59
2.4 209656_s_at  a  Hs.8769  TME47 transmembrane protein 47
2.3 1558116_s_at  a  Hs.714748  RECK reversion-inducing-cysteine-rich protein with kazal motifs
2.3 203042_at  a  Hs.496684  LAMP2 lysosomal-associated membrane protein 2
2.3 224793_s_at  a  Hs.496422  TGFBR1 transforming growth factor, beta receptor 1
2.3 225847_at  a  Hs.444099  AADACL1 arylacetamide deacetylase-like 1
2.3 212632_at  a  Hs.593148  STX7 syntaxin 7
2.3 213728_at  a  Hs.494419  LAMP1 lysosomal-associated membrane protein 1
2.2 209882_at  a  Hs.492324  RT1A Ras-like without CAAX 1
2.2 202351_at  a  Hs.436873  ITGA4 integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
2.2 203045_at  a  Hs.494557  NIN1  ninpin 1
2.2 212111_at  a  Hs.523835  STX12 syntaxin 12
2.2 202947_s_at  a  Hs.59138  GYP1C glycoprotein C (Gerbich blood group) 2
2.2 200821_at  a  Hs.496684  LAMP2 lysosomal-associated membrane protein 2
2.2 209492_at  a  Hs.335933  CHIC2 cytosine-rich hydrophobic domain 2
2.2 236217_at  a  Hs.532315  SLC31A1 solute carrier family 31 (copper transporters), member 1
2.2 203123_s_at  a  Hs.505443  SLC11A2 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
2.1 214459_s_at  a  Hs.654404  HLA-C major histocompatibility complex, class I, C
2.1 200973_s_at  a  Hs.50628 TSPAN3 tetraspanin 3
2.1 228181_at  a  Hs.519469  SLC30A1 solute carrier family 30 (zinc transporter), member 1
2.1 217456_s_at  a  Hs.468017  HLA-E major histocompatibility complex, class I, E
2.1 223090_x_at  a  Hs.24135 VEZT vezatin, adherens junctions transmembrane protein
2.1 211075_at  a  Hs.446414 CD49D CD49 molecule
2.0 221584_s_at  a  Hs.144705 KCNM1 potassium large conductance calcium-activated channel, subfamily M, alpha member 1
2.0 203041_s_at  a  Hs.496684  LYSZ lysosomal-associated membrane protein 2
297.9 210538_s_at Hs.127709 BIRC3 baculoviral IAP repeat-containing 3
240.1 204224_s_at Hs.80742 GCH1 GTP cyclohydrolase 1
166.5 204802_at Hs.1027 RADR Ras-related associated with diabetes
159.9 224477_s_at Hs.48046 SOD2 superoxide dismutase 2, mitochondrial
131.6 202411_at Hs.512634 IP27 interferon, alpha-inducible protein 27
129.6 220892_s_at Hs.494261 PSAT1 phosphoserine aminotransferase 1
119 204939_s_at Hs.11038 PLN phospholamban
89.2 202902_s_at Hs.181301 CTSS cathepsin S
77.7 215223_s_at Hs.48046 SOD2 superoxide dismutase 2, mitochondrial
70.5 204802_s_at Hs.1027 RADR Ras-related associated with diabetes
51.4 21641_s_at Hs.48046 SOD2 superoxide dismutase 2, mitochondrial
43.6 202901_s_at Hs.181301 CTSS cathepsin S
43.4 209928_s_at Hs.442619 MSC (includes EGF:1) mitogen-activated protein kinase 8
38.1 204285_s_at Hs.96 PMAP1 phorbol-12-myristate-13-acetate-induced protein 1
32 202295_s_at Hs.148441 CTSH cathepsin H
29.4 226181_at Hs.34851 TUBE1 tubulin, epsilon 1
29.2 202887_s_at Hs.521012 DDT4 DNA damage-inducible transcript 4
27 223062_s_at Hs.494261 PSAT1 phosphoserine aminotransferase 1
26.3 213256_at Hs.132441 MARCH3 membrane-associated ring finger (C 3HC4) 3
25.7 204415_at Hs.511371 IF6 interferon, alpha-inducible protein 6
24.1 204286_s_at Hs.96 PMAP1 phorbol-12-myristate-13-acetate-induced protein 1
23.6 202181_s_at Hs.533013 CBS (includes EGF:1) cystathionine-beta-synthase
21.8 202647_at Hs.76512 PKC2 phosphoinositol-4-phosphate 5-kinase 2 (mitochondrial)
20.1 204493_at Hs.591054 BID BH3 interacting domain death agonist
18.4 239629_at Hs.390736 CFLAR CASP8 and FADD-like apoptosis regulator
18.3 202626_s_at Hs.699154 LYN v-yes-1 Yamaguchi sarcoma viral oncogene homolog
17.3 232617_at Hs.181301 CTSS cathepsin S
15.6 217127_at Hs.19964 CTH cystathionase (cystathionine gamma-lyase)
15.2 201660_at Hs.516135 HTR2B inositol 1,4,5-trisphosphate receptor, type 2
14.1 238669_at Hs.201978 PTGS1 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
14.1 211862_s_at Hs.390736 CFLAR CASP8 and FADD-like apoptosis regulator
13.6 235489_at Hs.663194 RHOT ras homolog gene family, member J
13.2 201502_s_at Hs.81328 NFKB1A nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
13 240983_s_at Hs.274873 CAR5 cysteiny1-RNA synthetase
12.2 202625_at Hs.699154 LYN v-yes-1 Yamaguchi sarcoma viral oncogene homolog
11.9 1553972_s_at Hs.533013 CBS (includes EGF:1) cystathionine-beta-synthase
11.8 211087_f_at Hs.474377 APO3L3 (includes EGF:1) apolipoprotein L, 3
10.8 213132_s_at Hs.437277 SOSTM1 sequestosome 1
10.4 207076_s_at Hs.160786 ASS1 argininosuccinate synthetase 1
10.1 207076_s_at Hs.160786 ASS1 argininosuccinate synthetase 1
9.6 209193_at Hs.81170 PIM1 pim-1 oncogene
9.5 200625_s_at Hs.497599 WARS tryptophanyl-tRNA synthetase
9.3 218319_at Hs.7886 PELI1 pellino homolog 1 (Drosophila)
9.3 203879_at Hs.518451 PKC3D phosphoinositide-3-kinase, catalytic, delta polypeptide
9.2 200889_s_at Hs.524250 GABARAP1A gamma-aminobutyric acid A receptor-associated protein like 1
9 210564_s_at Hs.390736 CFLAR CASP8 and FADD-like apoptosis regulator
8.7 210564_s_at Hs.390736 CFLAR CASP8 and FADD-like apoptosis regulator
8.7 206085_s_at Hs.159044 CTH cystathionase (cystathionine gamma-lyase)
8.2 201761_at Hs.443093 MTHFD2 methylenetetrahydrofolate dehydrogenase (NADP + dependent), 2. methylenetetrahydrofolate cyclohydrolase
8.2 211865_s_at Hs.522357 CBRF8F1 chromosome 9 open reading frame 91
7.9 209933_x_at Hs.390736 CFLAR CASP8 and FADD-like apoptosis regulator
7.9 235252_s_at Hs.113354 KSR1 kinase suppressor of ras 1
7.8 232322_x_at Hs.188606 STARD10 STAR-related lipid transfer (START) domain containing 10
7.6 225668_at Hs.239360 TRIM47 tripartite motif-containing 47
7.5 204347_at Hs.10862 AK3L1 adenylate kinase 3-like 1
7.5 210630_at Hs.10862 AK3L1 adenylate kinase 3-like 1
7.2 215833_s_at Hs.201978 PTGS1 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
7.1 201754_at Hs.699154 LYN v-yes-1 Yamaguchi sarcoma viral oncogene homolog
7 201430_s_at Hs.519659 DPTSL3 dihydroorotidindase-like 3
6.9 202301_s_at Hs.352018 TAP1 transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
6.8 219024_at Hs.71366 PLEKH1A pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1
6.6 205128_x_at Hs.201978 PTGS1 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
6.5 226046_at Hs.138821 MAPK8 mitogen-activated protein kinase 8
6.5 223195_s_at Hs.469543 SESN2 sestrin 2
| 6.2 | 218170_s_at | Hs.483296 | ISG1 | isochromatase domain containing 1 |
| 6.0 | 242907_at | -- | GBP1 | guanylate binding protein 2, interferon-inducible |
| 6.1 | 223103_at | Hs.188606 | STARD10 | STAR-related lipid transfer (START) domain containing 10 |
| 6.0 | 201993_at | Hs.207459 | ST6GAL1 | ST6 beta-galactosamidase alpha 2-6-sialyltransferase 1 |
| 6.0 | 226624_at | Hs.739566 | PLEKH1A | pleckstrin homology domain-containing family A (phosphoinositide binding specific) member 1 |
| 5.9 | 223196_s_at | Hs.469543 | SESN2 | sestrin 2 |
| 5.9 | 205113_s_at | Hs.603730 | UST | uronyl-2-sulfotransferase |
| 5.8 | 211316_x_at | Hs.380736 | CFLAR | CASP8 and FADD-like apoptosis regulator |
| 5.8 | 203964_at | Hs.54483 | NMI | N-myc (and STAT) interactor |
| 5.8 | 210600_s_at | Hs.656274 | TNFAIP8 | tumor necrosis factor, alpha-induced protein 8 |
| 5.6 | 227143_s_at | Hs.591054 | BID | BH3 interacting domain death agonist |
| 5.5 | 201445_s_at | Hs.823166 | IFI44 | interferon-induced protein 44 |
| 5.5 | 203931_at | Hs.469529 | CNN1 | calponin 1, basic, smooth muscle |
| 5.5 | 225894_at | Hs.655519 | SYNO2 | synaptotagmin 2 |
| 5.4 | 221357_s_at | Hs.62661 | GBP1 | guanylate binding protein 1, interferon-inducible, 67kDa |
| 5.4 | 226051_at | Hs.55940 | SELM | Seltenoprotein M |
| 5.4 | 211725_s_at | Hs.591054 | BID | BH3 interacting domain death agonist |
| 5.3 | 229580_at | Hs.516632 | DNAJ C10 | DNAJ (Hsp40) homolog, subfamily C, member 10 |
| 5.3 | 211455_s_at | Hs.431893 | RBP1 | branched chain aminotransferase B, cytosolic |
| 5.3 | 200629_at | Hs.497599 | WARS | tryptophanyl-tRNA synthetase |
| 5.2 | 40148_at | Hs.478602 | APBA2 | amyloid beta (A4) precursor protein-binding, family B, member 2 |
| 5.1 | 202557_at | Hs.352341 | HSPA13 | heat shock protein 70kDa family, member 13 |
| 5 | 228872_at | Hs.42151 | HNMT | histamine-N-methyltransferase |
| 5 | 204070_at | Hs.17486 | RARAES3 | retinoic acid receptor responder (tazarotene induced) 3 |
| 4.9 | 201312_s_at | Hs.544830 | ST3GAL1 | ST3 beta-galactoside alpha-2,3-sialyltransferase 1 |
| 4.9 | 202270_at | Hs.62661 | GBP1 | guanylate binding protein 1, interferon-inducible, 67kDa |
| 4.8 | 204085_s_at | Hs.30213 | CLN5 | cereol-ipolysucinosis, neuronal 5 |
| 4.8 | 221789_at | Hs.516632 | DNAJ C10 | DNAJ (Hsp40) homolog, subfamily C, member 10 |
| 4.8 | 205501_at | Hs.348762 | PDE10A | phosphodiesterase 10A |
| 4.7 | 226004_s_at | Hs.334305 | DGAT1 | diacylglycerol O-acyltransferase homolog 2 (mouse) |
| 4.7 | 204112_s_at | Hs.42151 | HNMT | histamine-N-methyltransferase |
| 4.7 | 212231_at | Hs.499884 | SGPL1 | sphingosine-1-phosphate lyase 1 |
| 4.6 | 208296_s_at | Hs.656274 | TNFAIP8 | tumor necrosis factor, alpha-induced protein 8 |
| 4.5 | 219343_at | Hs.561954 | CDC37L1 | cell division cycle 37 homolog (S. cerevisiae) like 1 |
| 4.5 | 202703_at | Hs.332706 | OPTN | optineurin |
| 4.4 | 202269_s_at | Hs.62661 | GBP1 | guanylate binding protein 1, interferon-inducible, 67kDa |
| 4.4 | 209451_at | Hs.556406 | TANK | TRAF family member-associatd Nrf2 activator |
| 4.3 | 221781_at | Hs.516632 | DNAJ C10 | DNAJ (Hsp40) homolog, subfamily C, member 10 |
| 4.2 | 204345_s_at | Hs.10862 | AK31 | adenylate kinase 3-like 1 |
| 4.1 | 219773_at | Hs.371036 | MOX4 | NADPH oxidase A |
| 4.1 | 201272_at | Hs.522112 | AKR1B1 | aldo-keto reductase family 1, member B1 (aldose reductase) |
| 4.1 | 226799_at | Hs.506381 | FGDC6 | FYVE, RhoGEF and PH domain containing 6 |
| 4.1 | 201397_at | Hs.497296 | PHGDH | phosphoglyceraldehyde dehydrogenase |
| 4.1 | 204214_s_at | Hs.287714 | RAB32 | RAB32, member RAS oncogene family |
| 4.1 | 228967_at | Hs.15080 | EIF1 | eukaryotic translation initiation factor 1 |
| 4.0 | 235745_at | Hs.700027 | ER11 | endoplasmic reticulum to nucleus signaling 1 |
| 4.0 | 225604_at | Hs.493819 | GLP2R | GLI pathogenesis-related 2 |
| 3.9 | 223263_s_at | Hs.591162 | FGFR1PD2 | FGFR1 oncogene partner 2 |
| 3.9 | 155414_s_at | Hs.478031 | SLC33A1 | solute carrier family 33 (acetyl-CoA transporter), member 1 |
| 3.9 | 209185_s_at | Hs.442344 | IRS2 | insulin receptor substrate 2 |
| 3.9 | 238905_at | Hs.656339 | RH0J | ras homolog gene family, member J |
| 3.9 | 201718_s_at | Hs.9216 | CASP7 | caspase 7, apoptosis-related cysteine peptidase |
| 3.9 | 204279_at | Hs.654585 | PSMB9 | proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2) |
| 3.9 | 217867_s_at | Hs.529408 | BACE2 | beta-site APP-cleaving enzyme 2 |
| 3.8 | 220153_s_at | Hs.709660 | ENTPD1 | ectonucleoside triphosphate diphosphohydrolase 7 |
| 3.8 | 201431_s_at | Hs.519659 | DYSPL3 | dehydrogenase-like 3 |
| 3.8 | 222446_s_at | Hs.529408 | BACE2 | beta-site APP-cleaving enzyme 2 |
| 3.8 | 203165_s_at | Hs.708031 | SLC33A1 | solute carrier family 33 (acetyl-CoA transporter), member 1 |
| 3.7 | 216250_at | Hs.125474 | LPXN | leupaxin |
| 3.7 | 208829_at | Hs.714746 | TAPBP | TAP binding protein (tapasin) |
| 3.7 | 209566_at | Hs.7089 | INSG2 | insulin induced gene 2 |
| 3.6 | 222846_at | Hs.389733 | RAB8B | RAB8B, member RAS oncogene family |
2.8
23502_s_at  Hs.432822  MAN2A1  mannosidase, alpha, class 2A, member 1
2.8
213702_s_at  Hs.507243  ATP2C1  ATPase, Ca++ transporting, type 2C, member 1
2.8
204332_s_at  Hs.207776  ATP6AP2  ATPase, H+ transporting, lysosomal accessory protein 2
2.8
201631_s_at  Hs.591785  YARS  tyrosyl-tRNA synthetase
2.8
221471_s_at  Hs.632707  PLEKHA3  pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3
2.8
221471_s_at  Hs.632707  AZIN1  antizyme inhibitor 1
2.8
201737_s_at  Hs.524502  STAU2  protamine (prosome, macropain) subunit, subunit 1 (PA28 alpha)
2.8
204015_s_at  Hs.30213  CARS  cysteinyl-tRNA synthetase
2.8
223982_s_at  Hs.617340  PCMTD1  protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
2.8
212375_s_at  Hs.387096  PSME1  peptidylprolyl isomerase C (cyclophilin C)
2.8
223949_s_at  Hs.29491  SAT1  spermidine/spermine N1-acetyltransferase 1
2.8
209579_s_at  Hs.403346  DCI  decenyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
2.8
235612_s_at  Hs.23406  PAGT1B  peptidylglycine alpha methylation transferase (glycine N-acetyltransferase) type B
2.8
201962_s_at  Hs.514502  RNF41  ring finger protein 41
2.8
209666_s_at  Hs.188998  CHUK  Cdc2 4a/b kinase
2.8
20895_s_at  Hs.154023  ERP44  endoplasmic reticulum protein 44
2.8
214231_s_at  Hs.524910  FTHL1  ferritin, heavy polypeptide 1
2.8
223982_s_at  Hs.617340  PLEKHA3  pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3
2.8
221471_s_at  Hs.632707  YARS  tyrosyl-tRNA synthetase
2.8
221471_s_at  Hs.632707  AZIN1  antizyme inhibitor 1
2.8
201737_s_at  Hs.524502  STAU2  protamine (prosome, macropain) subunit, subunit 1 (PA28 alpha)
2.8
204015_s_at  Hs.30213  CARS  cysteinyl-tRNA synthetase
2.8
223982_s_at  Hs.617340  PCMTD1  protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
2.8
212375_s_at  Hs.387096  PSME1  peptidylprolyl isomerase C (cyclophilin C)
2.8
223949_s_at  Hs.29491  SAT1  spermidine/spermine N1-acetyltransferase 1
2.8
209579_s_at  Hs.403346  DCI  decenyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
2.4 22157_1_st Hs.510528 Traf3 Tnf receptor-associated factor 3
2.4 212184_5_st Hs.269775 MAPK7ip2 mitogen-activated protein kinase kinase kinase 7 interacting protein 2
2.4 219122_5_st Hs.353090 Thg1l trNA-histidine guanylyltransferase 1-like (S. cerevisiae)
2.4 213754_5_st Hs.567029 Pamp1 poly(A) binding protein interacting protein 1
2.4 214649_5_st Hs.181126 Mtrm2 myotubularin related protein 2
2.4 209898_6_st Hs.432652 Itsn2 intersectin 2
2.4 204188_6_st Hs.581125 Prp6 peptidyl-prolyl isomerase D
2.4 203380_6_st Hs.469537 Aldh1a3 aldehyde dehydrogenase 3 family, member A3
2.4 217168_6_st Hs.146393 Herpud1 homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
2.4 204910_6_st Hs.421194 Tp53tp1 tyrosine phosphatase, subunit 1
2.4 227904_6_at Hs.706616 Az1 S-arachidonate induced 2
2.4 156000_6_st Hs.523715 Vps37c vacuolar protein sorting 37 homolog C (S. cerevisiae)
2.4 218665_6_at Hs.119889 Raph2c RAP2C, member of RAS oncogene family
2.4 213372_5_at Hs.607312 Parg3 progerin and adipocyte receptor family member III
2.4 223309_6_at Hs.617340 Pnpl8a patatin-like phospholipase domain containing B
2.4 205995_6_at Hs.470907 Ak2 adenylyl kinase 2
2.4 204274_6_at Hs.491668 Ebag9 estrogen receptor binding site associated, antigen, 9
2.4 205571_6_at Hs.714759 Lipt1 lipoyltransferase 1
2.4 208315_6_at Hs.510528 Traf3 Tnf receptor-associated factor 3
2.4 213939_5_at Hs.571333 Fkp14 FK506 binding protein 14, 22 kDa
2.4 213902_6_at Hs.527412 Asah1 N-acetylphosphosine amidohydrolase (acid ceramidase) 1
2.4 210283_5_at Hs.567029 Parp1 poly(A) binding protein interacting factor 3
2.4 214096_6_at Hs.714300 Shmt2 serine hydroxymethyltransferase 2 (mitochondrial)
2.4 224787_6_at Hs.406799 Rab18 Rab18, member RAS oncogene family
2.4 216060_6_at Hs.634934 Dan1 dishevelled associated activator of morphogenesis 1
2.4 200969_6_at Hs.531826 Serp1 stress-associated endoplasmic reticulum protein 1
2.4 209040_5_at Hs.180062 Psm8 proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)
2.4 202006_6_at Hs.618182 Pfpm12 protein tyrosine phosphatase, non-receptor type 12
2.4 208666_5_at Hs.523662 Cschnk1a1 casein kinase 1, alpha 1
2.4 217819_6_at Hs.654773 Golk1a7 golgi autoantigen, golgin subfamily a, 7
2.4 225602_6_at Hs.493819 Glpfr2 GLI pathogenesis-related 2
2.4 218744_6_at Hs.605158 Eoxc5 exocyst complex component 5
2.4 204054_6_at Hs.500466 Pten phosphatase and tensin homolog
2.4 201425_6_at Hs.632733 Aldh9 Aldo dehydrogenase 9 family (2) (mitochondrial)
2.4 224025_6_at Hs.390127 Atg7 ATG7 autophagy related 7 homolog (S. cerevisiae)
2.4 200902_6_at Hs.362728 Sept15 septin 15 kDa selenoprotein
2.4 218617_6_at Hs.356554 Trf1 trNA isopenityltransferase 1
2.4 209285_6_at Hs.38909 Rcat1 branched chain aminotransferase 1, cytosolic
2.4 223370_6_at Hs.41068 Plect1 homolog domain containing, family A (phosphoinositide binding specific) member 3
2.4 220731_5_at Hs.437385 Necap2 necap endocytosis associated 2
2.4 200748_5_at Hs.524810 Fth1 ferritin, heavy polypeptide 1
2.4 201625_5_at Hs.520819 Ins1, insulin induced gene 1
2.4 210592_5_at Hs.28491 Sat1 spermidine/spermine N1-acetyltransferase 1
2.4 202929_5_at Hs.181907 Csehfr3 chromosome 5 open reading frame 3
2.4 221808_5_at Hs.495704 Rab9a Rab9a, member RAS oncogene family
2.4 210293_5_at Hs.36973 Sec23b Sec23 homolog B (S. cerevisiae)
2.4 222754_5_at Hs.567495 Trf11 RNA nucleolytic transference, CCA-adding, 1
2.4 207855_6_at Hs.658489 Cllc1 chloride channel CLIC-like 1
2.4 209799_5_at Hs.43322 Prkaa1 protein kinase, AMP-activated, alpha 1 catalytic subunit
2.4 224893_5_at Hs.59864 Erf23 mukacytic translation initiation factor 2a subunit 3 gamma, 53Da
2.4 207564_5_at Hs.405410 Ogt (includes EGFl2-linked N-acetylgalcosamine (GlcNAc) transferase (UDP-N-acetylgalcosamine:polypeptide-N-acetylgalcosaminylin transferase)
2.4 207274_5_at Hs.48732 Prkacb protein kinase, CAMP-dependent, catalytic, beta
2.4 225291_5_at Hs.38731 Pnh1 poly(ADP-ribose)polymerase 1
2.4 218034_5_at Hs.699155 Canx calnexin
2.4 202569_5_at Hs.35828 Mark3 Map/microtubule affinity-regulating kinase 3
2.4 223019_5_at Hs.469612 Trpm13 tripartite motif-containing 13
2.4 223209_5_at Hs.32148 Sel5 selenoprotein 5
2.4 201661_5_at Hs.655772 Acsl3 acyl-CoA synthetase long-chain family member 3
2.4 217826_5_at Hs.163776 Ubq2 ubiquitin-conjugating enzyme E2 J 1 (UBC6 homolog, yeast)
2.4 155248_5_at Hs.410388 Lct8 lactamase, beta
2.4 209072_5_at Hs.508148 Abil abI inhibitor 1
2.4 209082_5_at Hs.508148 Abil abI inhibitor 1
2.4 226317_5_at Hs.431092 Pps4r2 protein phosphatase 4, regulatory subunit 2
| 2.2 | 222014_s_at | Hs.591679 | NFKBIA | NFKBIA, member of NF-kappa B family |
| 2.2 | 223651_at | Hs.438993 | BIRC5 | BIRC5, member of IAP family |
| 2.2 | 218085_at | Hs.635133 | CHP85 | chromatin modifying protein 5 |
| 2.2 | 222023_s_at | Hs.120319 | RDN16 | retinol dehydrogenase 14 (all-trans/R/11-cis) |
| 2.2 | 209146_at | Hs.102649 | SC4DMO1 | steroid C4-methyl oxidase-like |
| 2.2 | 201765_s_at | Hs.604479 | HEXA | hexaminidase A (alpha polypeptide) |
| 2.1 | 222442_s_at | Hs.436274 | LARS | leucyl-RNA synthetase |
| 2.1 | 201097_s_at | Hs.465764 | TMEM44 | translocase of inner mitochondrial membrane 44 homolog (yeast) |
| 2.1 | 204549_s_at | Hs.321045 | IKKKE | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon |
| 2.1 | 209069_s_at | Hs.482018 | PAP1 | poly(A) binding protein interacting protein 1 |
| 2.1 | 208726_s_at | Hs.429180 | EIF2S2 | eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa |
| 2.1 | 223295_s_at | Hs.16803 | LUC7L | LUC7-like (s. cerevisiae) |
| 2.1 | 218666_at | Hs.119899 | RAP2C | RAP2C, member of RAS oncogene family |
| 2.1 | 223046_at | Hs.44450 | EGLN1 | egl nine homolog 1 (c. elegans) |
| 2.1 | 202631_at | Hs.654626 | LPPAT1 | lysophosphatidylglycerol acyltransferase 1 |
| 2.1 | 201736_at | Hs.315230 | EIF1B | eukaryotic translation initiation factor 1B |
| 2.1 | 204053_s_at | Hs.21160 | ME1 | malic enzyme 1, NADP(+)-dependent, cytosolic |
| 2.1 | 208985_s_at | Hs.404056 | EIF3J | eukaryotic translation initiation factor 3, subunit J |
| 2.1 | 203867_s_at | Hs.11590 | CTSP | cathespin P |

**Nucleus**

| 8.2 | 212909_at | Hs.183173 | IFNL1 | interferon induced with helicase C domain 1 |
| 3.8 | 228617_at | Hs.441975 | XAF1 | XIAP associated factor 1 |
| 3.0 | 206133_at | Hs.441975 | XAF1 | XIAP associated factor 1 |
| 28 | 39549_at | Hs.156832 | NPS2 | neuronal PAS domain protein 2 |
| 27.2 | 223611_at | Hs.72901 | CDKN2B | cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) |
| 26.1 | 202643_s_at | Hs.211600 | TNFAP3 | tumor necrosis factor, alpha-induced protein 3 |
| 23 | 1554966_a_at | Hs.110472 | FLIP | FLIP, Fas-associated death domain |
| 19.6 | 203927_at | Hs.458276 | NFKBIE | nuclear factor of kappa light polypeptide gene enhancer in B-cells, inhibitor, epsilon |
| 19 | 204702_s_at | Hs.404741 | MEF2L | nuclear factor (erythroid-derived 2)-like 3 |
| 16.8 | 202724_at | Hs.370666 | FOXO1 | forkhead box D1 |
| 14.2 | 213462_at | Hs.156832 | NPS2 | neuronal PAS domain protein 2 |
| 12.7 | 218543_s_at | Hs.12646 | PARP12 | poly (ADP-ribose) polymerase family, member 12 |
| 11.7 | 204135_at | Hs.104672 | FLIP | FLIP, Fas-associated death domain |
| 11.6 | 202843_at | Hs.6790 | DNAJ B9 | DNAJ (Hsp40) homolog, subfamily B, member 9 |
| 9.7 | 230636_s_at | Hs.150507 | KLF9 | Kruppel-like factor 9 |
| 9.2 | 227020_at | Hs.16803 | YPPF2 | yippee-like 2 (Drosophila) |
| 9.1 | 202644_s_at | Hs.211600 | TNFAP3 | tumor necrosis factor, alpha-induced protein 3 |
| 8.7 | 210285_s_at | Hs.440691 | WAP | Wilm tumor 1 associated protein |
| 8.2 | 155248_t_at | Hs.459153 | BNC1 | brain nucleolin 1 |
| 8 | 209290_s_at | Hs.209523 | SIAH1 | seven in absentia homolog 1 (Drosophila) |
| 8 | 221530_s_at | Hs.177841 | BHLHE41 | basic helix-loop-helix family, member e41 |
| 7.9 | 209415_s_at | Hs.632258 | IFUS | interferon-induced protein 35 |
| 7.8 | 218145_at | Hs.516826 | TRIB3 | tribbles homolog 3 (Drosophila) |
| 7.7 | 224848_at | Hs.119828 | CDK6 | cyclin-dependent kinase 6 |
| 7.7 | 209230_s_at | Hs.513463 | NUPR1 | nuclear protein 1 |
| 7.5 | 1554462_at | Hs.6790 | DNAJ B9 | DNAJ (Hsp40) homolog, subfamily B, member 9 |
| 7.4 | 207190_s_at | Hs.543880 | TNFAP1 | transforming growth factor alpha-inducing protein 1 |
| 7.3 | 226658_at | Hs.494269 | ARNTL2 | aryl hydrocarbon receptor nuclear translocator-like 2 |
| 7.0 | 205258_s_at | Hs.368341 | RUNX1T1 | runt-related transcription factor 1; translocated to, 1 (cycin D-related) |
| 7 | 204203_at | Hs.429666 | CEBPB | CCAAT/enhancer binding protein C/EBP, gamma |
| 6.8 | 204341_at | Hs.123534 | TRIM16 | tripartite motif-containing 16 |
| 6.7 | 216125_s_at | Hs.709269 | RANBP9 | RAN binding protein 9 |
| 6.6 | 203137_at | Hs.449051 | WAP | Wilm tumor 1 associated protein |
| 6.1 | 228348_at | Hs.127186 | NCOA7 | nuclear receptor coactivator 7 |
| 6.1 | 205255_s_at | Hs.368341 | RUNX1T1 | runt-related transcription factor 1; translocated to, 1 (cycin D-related) |
| 5.8 | 207039_at | Hs.512599 | CDKN2A | cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) |
| 5.8 | 216471_at | Hs.404741 | MEF2L | nuclear factor (erythroid-derived 2)-like 3 |
| 5.7 | 39548_at | Hs.156832 | NPS2 | neuronal PAS domain protein 2 |
| 5.7 | 218486_at | Hs.12229 | KLF11 | Kruppel-like factor 11 |
| 5.6 | 224847_at | Hs.119882 | CDK6 | cyclin-dependent kinase 6 |
| 5.4 | 224204_x_at | Hs.434269 | ARNTL2 | aryl hydrocarbon receptor nuclear translocator-like 2 |
| 5.2 | 223650_s_at | Hs.494288 | MIRF2 | nuclear receptor binding factor 2 |
| 5 | 202842_s_at | Hs.6790 | DNAJ B9 | DNAJ (Hsp40) homolog, subfamily B, member 9 |
| 5 | 209706_at | Hs.55999 | NXK3-1 | NK 3 homeobox 1
Rod1 regulator of differentiation 1 (S. pombe)

ASCC1

GTPase activating protein (SH3 domain) binding protein 2

ZBTB5

GTPase activating protein (SH3 domain) binding protein 2

RRM2B

Growth arrest and DNA-damage-inducible, alpha

GADD45A

Cysteine and glycine-rich protein 2

CSRP2

Threonyl-tRNA synthetase

TARS

Mdm2 p53 binding protein homolog (mouse)

MDM2

MAX interactor 1

MXI1

Metal response element binding transcription factor 2

MTF2

Cellular repressor of E1A-stimulated genes 1

CREG1

Ribosomal L24 domain containing 1

RPL24D1

Hepatoma-derived growth factor, related protein 3

HDGFRP3

 Aryl hydrocarbon receptor nuclear translocator-like 2

NR3C1

Aryl hydrocarbon receptor

NR1D2

Signal transducer and activator of transcription 5A

NRBF2

Signal transducer and activator of differentiation 1 (S. pombe)

ROD1

Activating signal cointegrator 1 complex subunit 1

AHR

Activating signal cointegrator 1 complex subunit 2

NR2F2
<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>224387_at</td>
<td>C0RMD5</td>
</tr>
<tr>
<td>225419_at</td>
<td>NGFRI1</td>
</tr>
<tr>
<td>212636_at</td>
<td>GKI</td>
</tr>
<tr>
<td>155313_at</td>
<td>CDK8</td>
</tr>
<tr>
<td>209704_at</td>
<td>MTF2</td>
</tr>
<tr>
<td>210320_s_at</td>
<td>DDX52</td>
</tr>
<tr>
<td>229836_at</td>
<td>NUP22</td>
</tr>
<tr>
<td>218499_at</td>
<td>RP6-213H12.1</td>
</tr>
<tr>
<td>228736_at</td>
<td>HELO</td>
</tr>
<tr>
<td>218572_at</td>
<td>CHMP4A</td>
</tr>
<tr>
<td>209924_at</td>
<td>HOGF9P3</td>
</tr>
<tr>
<td>227766_at</td>
<td>LIG4</td>
</tr>
<tr>
<td>221200_at</td>
<td>XPO1</td>
</tr>
<tr>
<td>221512_at</td>
<td>TP51NP1</td>
</tr>
<tr>
<td>202840_s_at</td>
<td>DEDD</td>
</tr>
<tr>
<td>221586_s_at</td>
<td>E2F5</td>
</tr>
<tr>
<td>222623_s_at</td>
<td>ZNF639</td>
</tr>
<tr>
<td>200779_s_at</td>
<td>ATF4</td>
</tr>
<tr>
<td>48825_s_at</td>
<td>ING4</td>
</tr>
<tr>
<td>224617_at</td>
<td>ROD1</td>
</tr>
<tr>
<td>223085_at</td>
<td>RNF19A</td>
</tr>
<tr>
<td>223268_at</td>
<td>C10ORF54</td>
</tr>
<tr>
<td>201473_at</td>
<td>JUNB</td>
</tr>
<tr>
<td>209644_x_at</td>
<td>CDK2NA</td>
</tr>
<tr>
<td>204430_at</td>
<td>NUP1</td>
</tr>
<tr>
<td>202981_x_at</td>
<td>SIAH1</td>
</tr>
<tr>
<td>224642_at</td>
<td>FTYTD1</td>
</tr>
<tr>
<td>203919_at</td>
<td>TCEA2</td>
</tr>
<tr>
<td>205548_s_at</td>
<td>BTG3</td>
</tr>
<tr>
<td>203675_at</td>
<td>DAD1</td>
</tr>
<tr>
<td>209339_at</td>
<td>SIAH2</td>
</tr>
<tr>
<td>229630_s_at</td>
<td>WTAP</td>
</tr>
<tr>
<td>204236_at</td>
<td>FLI1</td>
</tr>
<tr>
<td>227798_at</td>
<td>SMAD1</td>
</tr>
<tr>
<td>206216_s_at</td>
<td>CCR4-NOT</td>
</tr>
<tr>
<td>208762_at</td>
<td>SUMO1</td>
</tr>
<tr>
<td>1538700_at</td>
<td>ZNF620</td>
</tr>
<tr>
<td>206216_s_at</td>
<td>CCR4-NOT</td>
</tr>
<tr>
<td>206245_s_at</td>
<td>IWS1ABP</td>
</tr>
<tr>
<td>209748_at</td>
<td>SPAST</td>
</tr>
<tr>
<td>211296_at</td>
<td>DCP2</td>
</tr>
<tr>
<td>204488_at</td>
<td>HTATIP2</td>
</tr>
<tr>
<td>212855_at</td>
<td>DCUN1D4</td>
</tr>
<tr>
<td>203331_s_at</td>
<td>TGF1</td>
</tr>
<tr>
<td>217741_s_at</td>
<td>ZFAND5</td>
</tr>
<tr>
<td>202582_s_at</td>
<td>RANBP9</td>
</tr>
<tr>
<td>205539_at</td>
<td>ZNF295</td>
</tr>
<tr>
<td>212200_at</td>
<td>ANKLE2</td>
</tr>
<tr>
<td>222815_at</td>
<td>RLMIM</td>
</tr>
<tr>
<td>219351_at</td>
<td>ZNF547</td>
</tr>
<tr>
<td>203746_at</td>
<td>TP53</td>
</tr>
<tr>
<td>204831_at</td>
<td>CDK8</td>
</tr>
<tr>
<td>2058254_s_at</td>
<td>SRPK2</td>
</tr>
<tr>
<td>209674_at</td>
<td>CRY1</td>
</tr>
<tr>
<td>219336_s_at</td>
<td>ASCC1</td>
</tr>
<tr>
<td>210996_s_at</td>
<td>SMAD1</td>
</tr>
<tr>
<td>209586_s_at</td>
<td>PRUN1</td>
</tr>
<tr>
<td>213134_s_at</td>
<td>BTG3</td>
</tr>
<tr>
<td>228992_s_at</td>
<td>MED28</td>
</tr>
<tr>
<td>214714_at</td>
<td>ZNF39</td>
</tr>
<tr>
<td>226032_at</td>
<td>ANKRD11</td>
</tr>
<tr>
<td>1554036_at</td>
<td>ZBTB24</td>
</tr>
<tr>
<td>213743_at</td>
<td>CCNT2</td>
</tr>
<tr>
<td>Gene/Protein</td>
<td>Accession</td>
</tr>
<tr>
<td>-------------</td>
<td>-----------</td>
</tr>
<tr>
<td>TP53RK (includes EPABPC4L)</td>
<td>Hs.310458</td>
</tr>
<tr>
<td>TMEM217 (includes LOC401097)</td>
<td>Hs.371067</td>
</tr>
<tr>
<td>229429_x_at</td>
<td>Hs.645966</td>
</tr>
<tr>
<td>219131_at</td>
<td>Hs.522933</td>
</tr>
<tr>
<td>212328_at</td>
<td>Hs.335163</td>
</tr>
<tr>
<td>219093_at</td>
<td>Hs.310458</td>
</tr>
<tr>
<td>219270_at</td>
<td>Hs.405028</td>
</tr>
<tr>
<td>226952_at</td>
<td>Hs.474479</td>
</tr>
<tr>
<td>203077_s_at</td>
<td>Hs.12253</td>
</tr>
<tr>
<td>205299_s_at</td>
<td>Hs.371107</td>
</tr>
<tr>
<td>207338_s_at</td>
<td>Hs.632222</td>
</tr>
<tr>
<td>221598_s_at</td>
<td>Hs.371107</td>
</tr>
<tr>
<td>226117_at</td>
<td>Hs.310640</td>
</tr>
<tr>
<td>225817_at</td>
<td>Hs.148997</td>
</tr>
<tr>
<td>227099_s_at</td>
<td>Hs.714890</td>
</tr>
<tr>
<td>227609_at</td>
<td>Hs.546467</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
<tr>
<td>227617_at</td>
<td>Hs.155569</td>
</tr>
<tr>
<td>227625_at</td>
<td>Hs.593171</td>
</tr>
<tr>
<td>227657_at</td>
<td>Hs.659104</td>
</tr>
</tbody>
</table>
6.5 1560916_a_at Hs.408623 DPF19L1 dpy-19-like 1 (C. elegans)
6.4 242418_at Hs.655680 CDRF27 chromosome 2 open reading frame 27
6.3 219602_s_at Hs.585839 FAM188B family with sequence similarity 38, member B
6.2 219023_at Hs.435992 C4ORF16 chromosome 4 open reading frame 16
6.1 223194_s_at Hs.713388 SLC22A23 solute carrier family 22, member 23
6.6 226188_at Hs.372208 HSPC159 galectin-related protein
5.5 242477_at Hs.593830 TTC39B tetrahydrofolate repeat domain 39B
5.4 226135_at Hs.700656 UHRF1P1 UHRF1 binding protein 1
5.3 225003_at Hs.8036 TME205 transmembrane protein 205
5.2 227572_s_at Hs.445386 TME206 transmembrane protein 206
5.1 222893_at Hs.294103 LMBD2 LMB 1 domain containing 2
5.2 232080_at Hs.654742 HECW2 HECT C2 and WW domain containing E3 ubiquitin protein ligase 2
5.1 222001_at Hs.649566 FAM191A2 family with sequence similarity 91, member A2
5.1 219133_s_at Hs.15692 LRC49 leucine rich repeat containing 49
5.1 1568592_at Hs.489254 TRIM69 tripartite motif-containing 69
5.1 232183_at Hs.154706 SERAC1 serine active site containing 1
5.1 242009_at Hs.159430 FNDC3B fibronectin type III domain containing 38
4.9 1555870_at Hs.515688 RNF207 ring finger protein 207
4.8 213555_at Hs.709886 RWDO2A RWD domain containing 2A
4.7 213166_at Hs.211761 C14ORF104 chromosome 14 open reading frame 104
4.7 221756_at Hs.26670 PIK3P1 phosphoinositide-3-kinase interacting protein 1
4.7 238647_at Hs.82098 C14ORF28 chromosome 14 open reading frame 28
4.6 220244_at Hs.591661 LOHC8C2A loss of heterozygosity, 13, chromosomal region 2, gene A
4.6 243042_at Hs.632419 FAM73A family with sequence similarity 73, member A
4.5 38241_at Hs.167741 BTKNA3 butyrophilin, subfamily 3, member A3
4.5 224312_s_at Hs.651206 KLHL28 kelch-like 28 (Drosophila)
4.5 226601_at Hs.272251 KLHL5 kelch-like 5 (Drosophila)
4.5 227334_at Hs.657355 USP54 ubiquitin specific peptidase 54
4.4 204821_at Hs.187741 BTKNA3 butyrophilin, subfamily 3, member A3
4.3 235181_at Hs.204619 CDRF60 chromosome 2 open reading frame 60
4.2 226259_at Hs.650567 EXOC6 exocyst complex component 6
4.2 205298_s_at Hs.373938 BN2A2a butyrophilin, subfamily 2, member A2
4.2 221256_c_at Hs.280511 CCGP1 cell cycle progression 1
4.1 32541_at Hs.650661 PPP3CC protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform
4.1 232002_at Hs.42972 ALDH1L2 aldehyde dehydrogenase 1 family, member L2
4.1 220987_s_at Hs.131180 NUAK2 NUAK family, SNF1-like kinase, 2
4.2 231899_at Hs.376289 ZC3H12C zinc finger CCHC-type containing 12C
4.2 228917_at Hs.210586 C13orf31 chromosome 13 open reading frame 31
4.1 229678_at Hs.380738 LOC728431 hypothetical LOC728431
4 228133_at Hs.148741 RNF144B ring finger protein 144B
4 222409_s_at Hs.451590 YPELS ype1-like S (Drosophila)
4 233733_at Hs.561708 LOC401320 hypothetical LOC401320
3.9 225063_s_at Hs.440643 CDBRF33 chromosome 8 open reading frame 83
3.9 1566129_s_at Hs.518099 C3ORF38 chromosome 3 open reading frame 38
3.9 1555872_s_at Hs.380240 MGC21881 hypothetically locus MGC21881
3.9 227272_at Hs.32433 C15ORF52 chromosome 15 open reading frame 52
3.9 226748_at Hs.655657 LOX, putative peptidylglycan-binding, domain containing 2
3.9 217436_x_at Hs.181244 C13orf31 chromosome 13 open reading frame 31
3.9 217436_x_at Hs.181244 C13orf31 chromosome 13 open reading frame 31
3.8 227427_at Hs.233495 PLEKH8A pleckstrin homology domain containing, family A (phosphoinositide binding specific) member B
3.8 220329_s_at Hs.486835 RMDN1 required for mitotic nuclear division 1 homolog (S. cerevisiae)
3.7 220329_s_at Hs.486835 RMDN1 required for mitotic nuclear division 1 homolog (S. cerevisiae)
3.7 224739_at Hs.530381 PUM3 pum-3 oncogene
3.7 225819_at Hs.346410 TBRG1 includes Transforming growth factor beta regulator 1
3.7 213392_at Hs.480217 I0C0K I0 motif containing K
3.7 228149_at Hs.489374 C7ORF60 chromosome 7 open reading frame 60
3.6 226925_at Hs.657897 ACPL2 acid phosphatase-like 2
3.6 227256_at Hs.183817 USP31 ubiquitin specific peptidase 31
3.6 228482_at Hs.164595 CDR4 T cell malignant region transcript 4
3.6 224735_at Hs.2246 CYBASC3 cytochrome b, ascorbate dependent 3
3.6 155748_s_at Hs.221482 SHB Src homology 2 domain containing adaptor protein B
3.6 221511_x_at Hs.285051 CCGP1 cell cycle progression 1
3.6 209020_at Hs.75798 C2ORF111 chromosome 20 open reading frame 111
3.5 224839_s_at Hs.460693 OPT2 glutamic pyruvate transaminase (alanine aminotransferase) 2
3.5 227856_at Hs.34349 C4ORF32 chromosome 4 open reading frame 32

Gene names:
- kelch-like 5 (Drosophila)
- 225819_at Hs.436410
- 3.8
- 220329_s_at Hs.486835
- 227247_at Hs.32433
- 3.9
- 226748_at Hs.655657
- 3.9
- 226001_at Hs.654742
- 233732_at Hs.561708
- PLEKHA8
- HLA-J
- C15ORF52
- C3ORF38
- C13ORF31
- C14ORF28
- ALDH1L2
- GPT2
- C7ORF60
- KLHL5
- KLHL28
- FAM73A
- USP54
- C13ORF31
<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ENY2</td>
<td>enhancer of yellow 2 homolog (Drosophila)</td>
</tr>
<tr>
<td>RNF114</td>
<td>ring finger protein 114</td>
</tr>
<tr>
<td>TIPRL</td>
<td>TIP41, TOR signaling pathway regulator-like (S. cerevisiae)</td>
</tr>
<tr>
<td>MBNL2</td>
<td>muscleblind-like 2 (Drosophila)</td>
</tr>
<tr>
<td>C5ORF28</td>
<td>chromosome 5 open reading frame 28</td>
</tr>
<tr>
<td>TIPRL</td>
<td>TIP41, TOR signaling pathway regulator-like (S. cerevisiae)</td>
</tr>
<tr>
<td>C5ORF26</td>
<td>chromosome 5 open reading frame 26</td>
</tr>
<tr>
<td>SFT2D2</td>
<td>SFT2 domain containing 2</td>
</tr>
<tr>
<td>FNDC3B</td>
<td>fibronectin type III domain containing 3B</td>
</tr>
<tr>
<td>DPY19L1</td>
<td>dpy-19-like 1 (C. elegans)</td>
</tr>
<tr>
<td>C20ORF199</td>
<td>chromosome 20 open reading frame 199</td>
</tr>
<tr>
<td>SMYD4</td>
<td>SET and MYND domain containing 4</td>
</tr>
<tr>
<td>AMMECR1</td>
<td>Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1</td>
</tr>
<tr>
<td>GTPBP2</td>
<td>GTP binding protein 2</td>
</tr>
<tr>
<td>BTN3A1</td>
<td>transmembrane protein 33</td>
</tr>
<tr>
<td>TMCO3</td>
<td>transmembrane and coiled-coil domains 3</td>
</tr>
<tr>
<td>DPY19L1</td>
<td>dpy-19-like 1 (C. elegans)</td>
</tr>
<tr>
<td>C5ORF24</td>
<td>chromosome 5 open reading frame 24</td>
</tr>
<tr>
<td>TIPRL</td>
<td>TIP41, TOR signaling pathway regulator-like (S. cerevisiae)</td>
</tr>
<tr>
<td>LOC283567</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>PPP3CC</td>
<td>protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform</td>
</tr>
<tr>
<td>TMEM173</td>
<td>transmembrane protein 173</td>
</tr>
<tr>
<td>COBLL1</td>
<td>COBL-like 1</td>
</tr>
<tr>
<td>C5ORF28</td>
<td>chromosome 5 open reading frame 28</td>
</tr>
<tr>
<td>PKG</td>
<td>protein kinase (cAMP-dependent, catalytic) inhibitor gamma</td>
</tr>
<tr>
<td>C5ORF26</td>
<td>chromosome 5 open reading frame 26</td>
</tr>
<tr>
<td>SFT2 domain containing 2</td>
<td></td>
</tr>
<tr>
<td>C2ORF56</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>BC036928</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>ALK14247</td>
<td>hypothetical protein</td>
</tr>
<tr>
<td>Gene ID</td>
<td>Accession</td>
</tr>
<tr>
<td>-----------</td>
<td>------------</td>
</tr>
<tr>
<td>223192</td>
<td>Hs.403790</td>
</tr>
<tr>
<td>218826</td>
<td>Hs.524014</td>
</tr>
<tr>
<td>224826</td>
<td>Hs.636359</td>
</tr>
<tr>
<td>228024</td>
<td>Hs.343873</td>
</tr>
<tr>
<td>222825</td>
<td>Hs.30532</td>
</tr>
<tr>
<td>200868</td>
<td>Hs.149449</td>
</tr>
<tr>
<td>204656</td>
<td>Hs.521482</td>
</tr>
<tr>
<td>220808</td>
<td>Hs.446325</td>
</tr>
<tr>
<td>221423</td>
<td>Hs.372050</td>
</tr>
<tr>
<td>222751</td>
<td>Hs.706966</td>
</tr>
<tr>
<td>226301</td>
<td>Hs.347144</td>
</tr>
<tr>
<td>219774</td>
<td>Hs.107845</td>
</tr>
<tr>
<td>226496</td>
<td>Hs.634700</td>
</tr>
<tr>
<td>209479</td>
<td>Hs.420139</td>
</tr>
<tr>
<td>220235</td>
<td>Hs.25245</td>
</tr>
<tr>
<td>223860</td>
<td>Hs.227457</td>
</tr>
<tr>
<td>222370</td>
<td>Hs.714832</td>
</tr>
<tr>
<td>225955</td>
<td>Hs.591142</td>
</tr>
<tr>
<td>203695</td>
<td>Hs.520708</td>
</tr>
<tr>
<td>228652</td>
<td>Hs.109540</td>
</tr>
<tr>
<td>224831</td>
<td>Hs.127126</td>
</tr>
<tr>
<td>218647</td>
<td>Hs.301564</td>
</tr>
<tr>
<td>224953</td>
<td>Hs.372050</td>
</tr>
<tr>
<td>218277</td>
<td>Hs.28403</td>
</tr>
<tr>
<td>225439</td>
<td>Hs.558577</td>
</tr>
<tr>
<td>210004</td>
<td>Hs.708038</td>
</tr>
<tr>
<td>213082</td>
<td>Hs.654897</td>
</tr>
<tr>
<td>223349</td>
<td>Hs.293753</td>
</tr>
<tr>
<td>Gene</td>
<td>Description</td>
</tr>
<tr>
<td>------</td>
<td>-------------</td>
</tr>
<tr>
<td>3.5</td>
<td>239012_at</td>
</tr>
<tr>
<td>3.4</td>
<td>235733_at</td>
</tr>
<tr>
<td>3.3</td>
<td>228603_at</td>
</tr>
<tr>
<td>3.2</td>
<td>217604_at</td>
</tr>
<tr>
<td>3</td>
<td>225422_at</td>
</tr>
<tr>
<td>3</td>
<td>223549_at</td>
</tr>
<tr>
<td>2.9</td>
<td>224735_at</td>
</tr>
<tr>
<td>2.9</td>
<td>227585_at</td>
</tr>
<tr>
<td>2.8</td>
<td>235733_at</td>
</tr>
<tr>
<td>2.8</td>
<td>228603_at</td>
</tr>
<tr>
<td>2.7</td>
<td>217604_at</td>
</tr>
<tr>
<td>2.7</td>
<td>225422_at</td>
</tr>
<tr>
<td>2.6</td>
<td>229997_x_at</td>
</tr>
<tr>
<td>2.6</td>
<td>1558236_at</td>
</tr>
<tr>
<td>2.5</td>
<td>226779_at</td>
</tr>
<tr>
<td>2.4</td>
<td>229537_at</td>
</tr>
<tr>
<td>2.4</td>
<td>217625_x_at</td>
</tr>
<tr>
<td>2.3</td>
<td>229355_at</td>
</tr>
<tr>
<td>2.3</td>
<td>209140_x_at</td>
</tr>
<tr>
<td>2.3</td>
<td>226756_at</td>
</tr>
<tr>
<td>2.2</td>
<td>242300_at</td>
</tr>
<tr>
<td>2.2</td>
<td>214078_at</td>
</tr>
<tr>
<td>2.2</td>
<td>238739_at</td>
</tr>
<tr>
<td>2.2</td>
<td>235801_at</td>
</tr>
<tr>
<td>2.1</td>
<td>228312_at</td>
</tr>
<tr>
<td>2.1</td>
<td>227458_at</td>
</tr>
<tr>
<td>2.1</td>
<td>226520_at</td>
</tr>
<tr>
<td>2.1</td>
<td>227585_at</td>
</tr>
<tr>
<td>2.1</td>
<td>225412_at</td>
</tr>
<tr>
<td>2.1</td>
<td>238739_at</td>
</tr>
<tr>
<td>2.1</td>
<td>228520_s_at</td>
</tr>
<tr>
<td>2.1</td>
<td>226756_at</td>
</tr>
<tr>
<td>2.1</td>
<td>226756_at</td>
</tr>
<tr>
<td>2</td>
<td>209652_s_at</td>
</tr>
<tr>
<td>2</td>
<td>221029_s_at</td>
</tr>
<tr>
<td>2</td>
<td>202912_at</td>
</tr>
<tr>
<td>2</td>
<td>228253_at</td>
</tr>
<tr>
<td>2</td>
<td>220794_at</td>
</tr>
<tr>
<td>2</td>
<td>201860_s_at</td>
</tr>
<tr>
<td>2</td>
<td>212573_at</td>
</tr>
<tr>
<td>2</td>
<td>201508_at</td>
</tr>
<tr>
<td>2</td>
<td>211026_s_at</td>
</tr>
<tr>
<td>2</td>
<td>218421_at</td>
</tr>
<tr>
<td>2</td>
<td>1554428_s_at</td>
</tr>
</tbody>
</table>

**Extracellular Space**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Description</th>
<th>Expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.6</td>
<td>226779_at</td>
<td>Hs.599179</td>
</tr>
<tr>
<td>2.5</td>
<td>1560792_at</td>
<td>Hs.662003</td>
</tr>
<tr>
<td>2.4</td>
<td>229537_at</td>
<td>Hs.635110</td>
</tr>
<tr>
<td>2.4</td>
<td>217625_x_at</td>
<td>Hs.529860</td>
</tr>
<tr>
<td>2.3</td>
<td>229355_at</td>
<td>Hs.595430</td>
</tr>
<tr>
<td>2.3</td>
<td>209140_x_at</td>
<td>Hs.549053</td>
</tr>
<tr>
<td>2.3</td>
<td>226756_at</td>
<td>Hs.714959</td>
</tr>
<tr>
<td>2.2</td>
<td>214078_at</td>
<td>Hs.655757</td>
</tr>
<tr>
<td>2.2</td>
<td>238739_at</td>
<td>Hs.30280</td>
</tr>
<tr>
<td>2.2</td>
<td>228312_at</td>
<td>Hs.25391</td>
</tr>
<tr>
<td>2.2</td>
<td>217625_x_at</td>
<td>Hs.529860</td>
</tr>
<tr>
<td>2.1</td>
<td>226756_at</td>
<td>Hs.668867</td>
</tr>
</tbody>
</table>

**Plasma Membrane**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Description</th>
<th>Expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.6</td>
<td>226779_at</td>
<td>Hs.599179</td>
</tr>
<tr>
<td>2.5</td>
<td>1560792_at</td>
<td>Hs.662003</td>
</tr>
<tr>
<td>2.4</td>
<td>229537_at</td>
<td>Hs.635110</td>
</tr>
<tr>
<td>2.4</td>
<td>217625_x_at</td>
<td>Hs.529860</td>
</tr>
<tr>
<td>2.3</td>
<td>229355_at</td>
<td>Hs.595430</td>
</tr>
<tr>
<td>2.3</td>
<td>209140_x_at</td>
<td>Hs.549053</td>
</tr>
<tr>
<td>2.3</td>
<td>226756_at</td>
<td>Hs.714959</td>
</tr>
<tr>
<td>2.2</td>
<td>214078_at</td>
<td>Hs.655757</td>
</tr>
<tr>
<td>2.2</td>
<td>238739_at</td>
<td>Hs.30280</td>
</tr>
<tr>
<td>2.2</td>
<td>228312_at</td>
<td>Hs.25391</td>
</tr>
<tr>
<td>2.2</td>
<td>217625_x_at</td>
<td>Hs.529860</td>
</tr>
<tr>
<td>2.1</td>
<td>226756_at</td>
<td>Hs.668867</td>
</tr>
<tr>
<td>2</td>
<td>209652_s_at</td>
<td>Hs.252820</td>
</tr>
<tr>
<td>2</td>
<td>221029_s_at</td>
<td>Hs.306051</td>
</tr>
<tr>
<td>2</td>
<td>202912_at</td>
<td>Hs.491582</td>
</tr>
<tr>
<td>2</td>
<td>228253_at</td>
<td>Hs.591563</td>
</tr>
<tr>
<td>2</td>
<td>220794_at</td>
<td>Hs.98206</td>
</tr>
<tr>
<td>2</td>
<td>201508_at</td>
<td>Hs.462998</td>
</tr>
<tr>
<td>2</td>
<td>212573_at</td>
<td>Hs.167115</td>
</tr>
<tr>
<td>2</td>
<td>201508_at</td>
<td>Hs.462998</td>
</tr>
<tr>
<td>2</td>
<td>212573_at</td>
<td>Hs.167115</td>
</tr>
<tr>
<td>2</td>
<td>201508_at</td>
<td>Hs.462998</td>
</tr>
<tr>
<td>2</td>
<td>212573_at</td>
<td>Hs.167115</td>
</tr>
<tr>
<td>2</td>
<td>201508_at</td>
<td>Hs.462998</td>
</tr>
<tr>
<td>2</td>
<td>212573_at</td>
<td>Hs.167115</td>
</tr>
<tr>
<td>2</td>
<td>201508_at</td>
<td>Hs.462998</td>
</tr>
<tr>
<td>2</td>
<td>212573_at</td>
<td>Hs.167115</td>
</tr>
</tbody>
</table>

**Insulin-like growth factor receptor**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Description</th>
<th>Expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.6</td>
<td>229442_at</td>
<td>Hs.208701</td>
</tr>
<tr>
<td>2.5</td>
<td>1556316_s_at</td>
<td>Hs.707281</td>
</tr>
<tr>
<td>2.5</td>
<td>1554428_s_at</td>
<td>Hs.68229</td>
</tr>
</tbody>
</table>

**Glycosylation Inhibiting Factor**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Description</th>
<th>Expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.6</td>
<td>229442_at</td>
<td>Hs.208701</td>
</tr>
<tr>
<td>2.5</td>
<td>1556316_s_at</td>
<td>Hs.707281</td>
</tr>
<tr>
<td>2.5</td>
<td>1554428_s_at</td>
<td>Hs.68229</td>
</tr>
</tbody>
</table>

**Plasminogen activator, tissue**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Description</th>
<th>Expression</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.6</td>
<td>229442_at</td>
<td>Hs.208701</td>
</tr>
<tr>
<td>2.5</td>
<td>1556316_s_at</td>
<td>Hs.707281</td>
</tr>
<tr>
<td>2.5</td>
<td>1554428_s_at</td>
<td>Hs.68229</td>
</tr>
<tr>
<td>Gene ID</td>
<td>Description</td>
<td></td>
</tr>
<tr>
<td>---------</td>
<td>--------------------------------------------------</td>
<td></td>
</tr>
<tr>
<td>227411</td>
<td>WTP</td>
<td></td>
</tr>
<tr>
<td>2026466</td>
<td>AXL receptor tyrosine kinase</td>
<td></td>
</tr>
<tr>
<td>210220</td>
<td>FZD2</td>
<td></td>
</tr>
<tr>
<td>203124</td>
<td>EMP1</td>
<td></td>
</tr>
<tr>
<td>207373</td>
<td>PPFBP1</td>
<td></td>
</tr>
<tr>
<td>396_f</td>
<td>EPOR</td>
<td></td>
</tr>
<tr>
<td>226545</td>
<td>CD109</td>
<td></td>
</tr>
<tr>
<td>228660</td>
<td>SEMA4F</td>
<td></td>
</tr>
<tr>
<td>215034</td>
<td>TM4SF1</td>
<td></td>
</tr>
<tr>
<td>203131</td>
<td>PDGFRα</td>
<td></td>
</tr>
<tr>
<td>215050</td>
<td>EPMP2</td>
<td></td>
</tr>
<tr>
<td>227897</td>
<td>RAP2B</td>
<td></td>
</tr>
<tr>
<td>203017</td>
<td>S5ZIP</td>
<td></td>
</tr>
<tr>
<td>219282</td>
<td>TRPV2</td>
<td></td>
</tr>
<tr>
<td>226625</td>
<td>TGFBR3</td>
<td></td>
</tr>
<tr>
<td>226728</td>
<td>SLCC2A1</td>
<td></td>
</tr>
<tr>
<td>204973</td>
<td>EMP2</td>
<td></td>
</tr>
<tr>
<td>201325</td>
<td>EMP1</td>
<td></td>
</tr>
<tr>
<td>202756</td>
<td>GPC1</td>
<td></td>
</tr>
<tr>
<td>201951</td>
<td>ALCAM</td>
<td></td>
</tr>
<tr>
<td>225079</td>
<td>EPMP2</td>
<td></td>
</tr>
<tr>
<td>200623</td>
<td>CALM3</td>
<td></td>
</tr>
<tr>
<td>215783</td>
<td>ALPL</td>
<td></td>
</tr>
<tr>
<td>201952</td>
<td>ALCAM</td>
<td></td>
</tr>
<tr>
<td>215300</td>
<td>PDGFRα</td>
<td></td>
</tr>
<tr>
<td>201137</td>
<td>HLA-DRB1</td>
<td></td>
</tr>
<tr>
<td>230372</td>
<td>HAS2</td>
<td></td>
</tr>
<tr>
<td>214709</td>
<td>SNX1</td>
<td></td>
</tr>
<tr>
<td>218902</td>
<td>MOTC1</td>
<td></td>
</tr>
<tr>
<td>210124</td>
<td>SEMA4F</td>
<td></td>
</tr>
<tr>
<td>203065</td>
<td>CAV1</td>
<td></td>
</tr>
<tr>
<td>225867</td>
<td>VASH</td>
<td></td>
</tr>
<tr>
<td>204451</td>
<td>FZD1</td>
<td></td>
</tr>
<tr>
<td>204462</td>
<td>SLCC1A1</td>
<td></td>
</tr>
<tr>
<td>235518</td>
<td>solute carrier family 8 (sodium/calcium exchanger)</td>
<td></td>
</tr>
<tr>
<td>213000</td>
<td>solute carrier family 8 (sodium/calcium exchanger)</td>
<td></td>
</tr>
<tr>
<td>239217</td>
<td>ABCB3</td>
<td></td>
</tr>
<tr>
<td>225093</td>
<td>UTN</td>
<td></td>
</tr>
<tr>
<td>211235</td>
<td>ATP2B</td>
<td></td>
</tr>
<tr>
<td>212494</td>
<td>TEC1</td>
<td></td>
</tr>
<tr>
<td>202031</td>
<td>SFRP1</td>
<td></td>
</tr>
<tr>
<td>226571</td>
<td>PTPRS</td>
<td></td>
</tr>
<tr>
<td>208749</td>
<td>FLOT1</td>
<td></td>
</tr>
<tr>
<td>210142</td>
<td>FLOT1</td>
<td></td>
</tr>
<tr>
<td>226189</td>
<td>ITGB8</td>
<td></td>
</tr>
<tr>
<td>211600</td>
<td>PTPRO</td>
<td></td>
</tr>
<tr>
<td>201809</td>
<td>ENG</td>
<td></td>
</tr>
<tr>
<td>205532</td>
<td>CDH6</td>
<td></td>
</tr>
<tr>
<td>386711</td>
<td>PLXN1</td>
<td></td>
</tr>
<tr>
<td>213895</td>
<td>EMP1</td>
<td></td>
</tr>
<tr>
<td>219250</td>
<td>FLR3</td>
<td></td>
</tr>
<tr>
<td>209972</td>
<td>JTV1</td>
<td></td>
</tr>
<tr>
<td>203908</td>
<td>SLC4A4</td>
<td></td>
</tr>
<tr>
<td>212298</td>
<td>NR1P1</td>
<td></td>
</tr>
<tr>
<td>209815</td>
<td>PTHC1</td>
<td></td>
</tr>
<tr>
<td>227481</td>
<td>CNKSR3</td>
<td></td>
</tr>
<tr>
<td>223092</td>
<td>ANKH</td>
<td></td>
</tr>
<tr>
<td>222853</td>
<td>FLMR3</td>
<td></td>
</tr>
<tr>
<td>238140</td>
<td>EPHN5</td>
<td></td>
</tr>
<tr>
<td>223093</td>
<td>ANKH</td>
<td></td>
</tr>
<tr>
<td>212990</td>
<td>LYPD1</td>
<td></td>
</tr>
<tr>
<td>211432</td>
<td>TYRO3</td>
<td></td>
</tr>
</tbody>
</table>

**Table Notes:**
- **Wnts tumor 1 interacting protein**: A protein involved in various signaling pathways.
- **AXL receptor tyrosine kinase**: A key component in the regulation of cell growth and survival.
- **FZD2**: A member of the frizzled family, involved in Wnt signaling.
- **EMP1**: Required for the development of the blood vessel system.
- **PPFBP1**: Involved in the regulation of cell proliferation and migration.
- **EPOR**: Essential for erythropoiesis, the production of red blood cells.
- **CD109**: Plays a role in cell adhesion and signaling.
- **SEMA4F**: Involved in the development of the nervous system.
- **TM4SF1**: Involved in the regulation of cell adhesion and migration.
- **PDGFRα**: A receptor for platelet-derived growth factor, involved in cell proliferation.
- **EPMP2**: Crucial for epithelial membrane functions.
- **RAP2B**: Involved in cell adhesion and signaling.
- **S5ZIP**: Involved in the regulation of cell adhesion and migration.
- **TRPV2**: A member of the transient receptor potential family, involved in ion channel function.
- **TGFBR3**: A key component in the transforming growth factor beta signaling pathway.
- **SLCC2A1**: Soluble carrier family member, involved in the transport of various solutes.
- **CAV1**: A component of caveolae, involved in cell membrane signaling.
- **ALPL**: Involved in the transport of calcium and phosphate.
- **ALCAM**: Activated leukocyte cell adhesion molecule.
- **PDGFRα**: Platelet-derived growth factor receptor, alpha.
- **HLA-DRB1**: Major histocompatibility complex, class II, B beta 1.
- **HAS2**: Hyaluronan synthase 2.
- **SNX1**: Syntaxin 1, involved in vesicle trafficking.
- **MOTC1**: Motif of the CUB domain containing 1.
- **SEMA4F**: Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F.
<table>
<thead>
<tr>
<th>Log2 Fold Change</th>
<th>Gene ID</th>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>-0.9</td>
<td>210662_s_at</td>
<td>Hs.12104</td>
<td>CDH6</td>
</tr>
<tr>
<td>-0.7</td>
<td>212230_at</td>
<td>Hs.70850</td>
<td>PPAP2B</td>
</tr>
<tr>
<td>-0.7</td>
<td>219025_at</td>
<td>Hs.145727</td>
<td>CD248</td>
</tr>
<tr>
<td>-0.6</td>
<td>210510_s_at</td>
<td>Hs.113107</td>
<td>MRP1</td>
</tr>
<tr>
<td>-0.6</td>
<td>205533_s_at</td>
<td>Hs.111704</td>
<td>CD6</td>
</tr>
<tr>
<td>-0.5</td>
<td>204401_at</td>
<td>Hs.10082</td>
<td>KCN4</td>
</tr>
<tr>
<td>-0.5</td>
<td>203835_at</td>
<td>Hs.151044</td>
<td>LRRC32</td>
</tr>
<tr>
<td>-0.5</td>
<td>212226_s_at</td>
<td>Hs.405136</td>
<td>PPAP2B</td>
</tr>
<tr>
<td>-0.4</td>
<td>208161_s_at</td>
<td>Hs.463421</td>
<td>ABC3</td>
</tr>
<tr>
<td>-0.4</td>
<td>230147_at</td>
<td>Hs.42502</td>
<td>FZL2</td>
</tr>
<tr>
<td>-0.4</td>
<td>203869_s_at</td>
<td>Hs.482502</td>
<td>F2R</td>
</tr>
<tr>
<td>-0.3</td>
<td>219789_at</td>
<td>Hs.237028</td>
<td>NPR3</td>
</tr>
<tr>
<td>-0.3</td>
<td>223094_s_at</td>
<td>Hs.156872</td>
<td>ANKH</td>
</tr>
<tr>
<td>-0.3</td>
<td>202478_s_at</td>
<td>Hs.467751</td>
<td>TRIB2</td>
</tr>
<tr>
<td>-0.3</td>
<td>219416_at</td>
<td>Hs.128856</td>
<td>SCARA3</td>
</tr>
<tr>
<td>-0.3</td>
<td>209355_s_at</td>
<td>Hs.405136</td>
<td>PPAP2B</td>
</tr>
<tr>
<td>-0.2</td>
<td>227812_at</td>
<td>Hs.149168</td>
<td>THFRSF19</td>
</tr>
<tr>
<td>-0.2</td>
<td>224762_at</td>
<td>Hs.479384</td>
<td>SERINC2</td>
</tr>
<tr>
<td>-0.2</td>
<td>219790_at</td>
<td>Hs.237028</td>
<td>NPR3</td>
</tr>
<tr>
<td>-0.2</td>
<td>224647_at</td>
<td>Hs.112923</td>
<td>SCUBE3</td>
</tr>
<tr>
<td>-0.2</td>
<td>201650_at</td>
<td>Hs.514174</td>
<td>JUP</td>
</tr>
<tr>
<td>-0.2</td>
<td>205056_s_at</td>
<td>Hs.527295</td>
<td>ENPP1</td>
</tr>
<tr>
<td>-0.2</td>
<td>206631_at</td>
<td>Hs.2096</td>
<td>PTGER2</td>
</tr>
<tr>
<td>-0.1</td>
<td>224321_at</td>
<td>Hs.144513</td>
<td>TMEM22</td>
</tr>
<tr>
<td>-0.1</td>
<td>212558_at</td>
<td>Hs.436944</td>
<td>SPRF1</td>
</tr>
<tr>
<td>-0.1</td>
<td>219937_at</td>
<td>Hs.199814</td>
<td>TRIOH</td>
</tr>
<tr>
<td>-0.1</td>
<td>230290_at</td>
<td>Hs.12923</td>
<td>SLC3A2</td>
</tr>
<tr>
<td>-0.1</td>
<td>202191_s_at</td>
<td>Hs.464422</td>
<td>COLEC12</td>
</tr>
<tr>
<td>-0.1</td>
<td>200836_at</td>
<td>Hs.151307</td>
<td>SLC1A4A</td>
</tr>
<tr>
<td>-0.1</td>
<td>206766_at</td>
<td>Hs.158237</td>
<td>ITGA10</td>
</tr>
<tr>
<td>-0.1</td>
<td>205000_s_at</td>
<td>Hs.60339</td>
<td>NMT2</td>
</tr>
<tr>
<td>-0.1</td>
<td>222547_at</td>
<td>Hs.631550</td>
<td>MAP4K4</td>
</tr>
<tr>
<td>-0.1</td>
<td>210680_s_at</td>
<td>Hs.180408</td>
<td>SLC2A5</td>
</tr>
<tr>
<td>-0.1</td>
<td>221660_at</td>
<td>Hs.247831</td>
<td>MYC2P1L</td>
</tr>
<tr>
<td>-0.1</td>
<td>2152619_s_at</td>
<td>Hs.62180</td>
<td>ANLN</td>
</tr>
<tr>
<td>-0.1</td>
<td>202035_s_at</td>
<td>Hs.499886</td>
<td>ALDH3A2</td>
</tr>
<tr>
<td>-0.1</td>
<td>222154_s_at</td>
<td>Hs.511743</td>
<td>TUBB3</td>
</tr>
<tr>
<td>-0.1</td>
<td>203386_at</td>
<td>Hs.210891</td>
<td>TRC4D1</td>
</tr>
<tr>
<td>-0.1</td>
<td>209190_s_at</td>
<td>Hs.529451</td>
<td>DIAPH1</td>
</tr>
<tr>
<td>-0.1</td>
<td>203756_s_at</td>
<td>Hs.531719</td>
<td>ARHGEF17</td>
</tr>
<tr>
<td>-0.1</td>
<td>228310_at</td>
<td>Hs.69793</td>
<td>ENAM</td>
</tr>
<tr>
<td>-0.1</td>
<td>225665_at</td>
<td>Hs.444451</td>
<td>ZAK</td>
</tr>
<tr>
<td>-0.1</td>
<td>203216_at</td>
<td>Hs.367992</td>
<td>MMP2</td>
</tr>
<tr>
<td>-0.1</td>
<td>202238_s_at</td>
<td>Hs.518450</td>
<td>HTH</td>
</tr>
<tr>
<td>-0.1</td>
<td>222077_s_at</td>
<td>Hs.505469</td>
<td>RACGAP1</td>
</tr>
<tr>
<td>-0.1</td>
<td>208050_s_at</td>
<td>Hs.369829</td>
<td>CASP2</td>
</tr>
<tr>
<td>-0.1</td>
<td>209286_at</td>
<td>Hs.369934</td>
<td>CDC42EP3</td>
</tr>
<tr>
<td>-0.1</td>
<td>218424_at</td>
<td>Hs.647822</td>
<td>STEAP</td>
</tr>
<tr>
<td>-0.1</td>
<td>222942_s_at</td>
<td>Hs.538627</td>
<td>TIA1M2</td>
</tr>
<tr>
<td>-0.1</td>
<td>205125_at</td>
<td>Hs.80776</td>
<td>PLCG1</td>
</tr>
<tr>
<td>-0.1</td>
<td>227847_at</td>
<td>Hs.20820</td>
<td>EPM2AP1</td>
</tr>
<tr>
<td>-0.1</td>
<td>205640_s_at</td>
<td>Hs.528641</td>
<td>ALDH3B1</td>
</tr>
<tr>
<td>-0.1</td>
<td>222068_s_at</td>
<td>Hs.62180</td>
<td>ANLN</td>
</tr>
<tr>
<td>-0.1</td>
<td>207876_s_at</td>
<td>Hs.58414</td>
<td>FLNC</td>
</tr>
<tr>
<td>-0.1</td>
<td>211992_at</td>
<td>Hs.356604</td>
<td>WNK1</td>
</tr>
<tr>
<td>-0.1</td>
<td>206298_at</td>
<td>Hs.655672</td>
<td>ARNAGAP2</td>
</tr>
<tr>
<td>-0.1</td>
<td>212242_at</td>
<td>Hs.75318</td>
<td>TUBA4A</td>
</tr>
<tr>
<td>-0.1</td>
<td>226070_at</td>
<td>Hs.435714</td>
<td>PAK1</td>
</tr>
<tr>
<td>-0.1</td>
<td>32094_at</td>
<td>Hs.118804</td>
<td>CHST3</td>
</tr>
<tr>
<td>-0.1</td>
<td>222463_s_at</td>
<td>Hs.504003</td>
<td>BACE1</td>
</tr>
<tr>
<td>-0.1</td>
<td>225590_at</td>
<td>Hs.301804</td>
<td>SH3RF1</td>
</tr>
<tr>
<td>-0.1</td>
<td>224496_s_at</td>
<td>Hs.369520</td>
<td>SYT12</td>
</tr>
<tr>
<td>-0.1</td>
<td>209834_s_at</td>
<td>Hs.158304</td>
<td>CHST3</td>
</tr>
<tr>
<td>Hs.507362</td>
<td>VISA</td>
<td>virus-induced signaling adapter</td>
<td></td>
</tr>
<tr>
<td>Hs.434866</td>
<td>CDC5</td>
<td>cell division cycle-associated 5</td>
<td></td>
</tr>
<tr>
<td>Hs.648612</td>
<td>PCSK7</td>
<td>proprotein convertase subtilis/in/vernin type 7</td>
<td></td>
</tr>
<tr>
<td>Hs.637017</td>
<td>MAP1B</td>
<td>microtubule-associated protein 1B</td>
<td></td>
</tr>
<tr>
<td>Hs.647024</td>
<td>STX1A</td>
<td>syntaxin 1A (brain)</td>
<td></td>
</tr>
<tr>
<td>Hs.24587</td>
<td>EFS</td>
<td>embryonal Fyn-associated substrate</td>
<td></td>
</tr>
<tr>
<td>Hs.699209</td>
<td>ZNF395</td>
<td>zinc finger protein 395</td>
<td></td>
</tr>
<tr>
<td>Hs.598144</td>
<td>EML4</td>
<td>evisceroderm microtubule-associated protein like 4</td>
<td></td>
</tr>
<tr>
<td>Hs.247460</td>
<td>NNL</td>
<td>neurolysin (metalloproteinase M3 family)</td>
<td></td>
</tr>
<tr>
<td>Hs.500711</td>
<td>DNMBP</td>
<td>dynamin binding protein</td>
<td></td>
</tr>
<tr>
<td>Hs.15154</td>
<td>SRPX</td>
<td>sushi-repeat-containing protein, X-linked</td>
<td></td>
</tr>
<tr>
<td>Hs.3104</td>
<td>KIF14</td>
<td>kinesin family member 14</td>
<td></td>
</tr>
<tr>
<td>Hs.443134</td>
<td>GB2A</td>
<td>glucosidase, beta (bile acid) 2</td>
<td></td>
</tr>
<tr>
<td>Hs.708922</td>
<td>ASMT</td>
<td>aminopeptidase (V3 oxidation state) methyltransferase</td>
<td></td>
</tr>
<tr>
<td>Hs.54216</td>
<td>CDC3</td>
<td>cell division cycle-associated 3</td>
<td></td>
</tr>
<tr>
<td>Hs.16355</td>
<td>MYH10</td>
<td>myosin, heavy chain 10, non-muscle</td>
<td></td>
</tr>
<tr>
<td>Hs.443636</td>
<td>PXN</td>
<td>paxillin</td>
<td></td>
</tr>
<tr>
<td>Hs.637017</td>
<td>MAP1B</td>
<td>microtubule-associated protein 1B</td>
<td></td>
</tr>
<tr>
<td>---</td>
<td>ND2</td>
<td>NADH dehydrogenase, subunit 2 (complex I)</td>
<td></td>
</tr>
<tr>
<td>Hs.529793</td>
<td>SDCS</td>
<td>suppressor of cytokine signaling 3</td>
<td></td>
</tr>
<tr>
<td>Hs.457114</td>
<td>PAK1</td>
<td>p21 protein-activated protein kinase 1</td>
<td></td>
</tr>
<tr>
<td>Hs.648394</td>
<td>EIF4B</td>
<td>eukaryotic translation initiation factor 4B</td>
<td></td>
</tr>
<tr>
<td>Hs.119954</td>
<td>CIT</td>
<td>citron (rho-interacting, serine/threonine kinase 21)</td>
<td></td>
</tr>
<tr>
<td>Hs.269560</td>
<td>CDKS5</td>
<td>cyclin-dependent kinase 5</td>
<td></td>
</tr>
<tr>
<td>Hs.371240</td>
<td>AKAP12</td>
<td>A kinase (PKA) anchor protein 12</td>
<td></td>
</tr>
<tr>
<td>Hs.75602</td>
<td>GSTM5</td>
<td>glutathione S-transferase mu 5</td>
<td></td>
</tr>
<tr>
<td>Hs.91002</td>
<td>UBE2C</td>
<td>ubiquitin-conjugating enzyme E2 C</td>
<td></td>
</tr>
<tr>
<td>Hs.471508</td>
<td>IRS1</td>
<td>insulin receptor substrate 1</td>
<td></td>
</tr>
<tr>
<td>Hs.533446</td>
<td>BAALC</td>
<td>brain and acute leukemia, cytoplasmic</td>
<td></td>
</tr>
<tr>
<td>Hs.512639</td>
<td>TK1</td>
<td>thymidine kinase 1, mitochondrial</td>
<td></td>
</tr>
<tr>
<td>Hs.580566</td>
<td>NUDT17</td>
<td>nucleoside diphosphate-linked moiety X-type motif 17</td>
<td></td>
</tr>
<tr>
<td>Hs.527971</td>
<td>NES</td>
<td>nestin</td>
<td></td>
</tr>
<tr>
<td>Hs.446522</td>
<td>RPL14</td>
<td>ribosomal protein L14</td>
<td></td>
</tr>
<tr>
<td>Hs.269560</td>
<td>CDKS5</td>
<td>cyclin-dependent kinase 5</td>
<td></td>
</tr>
<tr>
<td>Hs.503043</td>
<td>CPT1A</td>
<td>carnitine palmitoyltransferase 1A (liver)</td>
<td></td>
</tr>
<tr>
<td>Hs.43908</td>
<td>PKAR2B</td>
<td>protein kinase, CAMP-dependent, regulatory, type II, beta</td>
<td></td>
</tr>
<tr>
<td>Hs.40660</td>
<td>RPS10</td>
<td>ribosomal protein S10</td>
<td></td>
</tr>
<tr>
<td>Hs.515122</td>
<td>TK1</td>
<td>thymidine kinase 1, soluble</td>
<td></td>
</tr>
<tr>
<td>Hs.63560</td>
<td>PDE1C</td>
<td>phosphodiesterase 1C, calmodulin-dependent 70kDa</td>
<td></td>
</tr>
<tr>
<td>Hs.73025</td>
<td>KIF20A</td>
<td>kinesin family member 20A</td>
<td></td>
</tr>
<tr>
<td>Hs.51612</td>
<td>CALR</td>
<td>calreticulin</td>
<td></td>
</tr>
<tr>
<td>Hs.50823</td>
<td>PDCD6</td>
<td>programmed cell death 6</td>
<td></td>
</tr>
<tr>
<td>Hs.194301</td>
<td>MAP1A</td>
<td>microtubule-associated protein 1A</td>
<td></td>
</tr>
<tr>
<td>Hs.52416</td>
<td>CDC3</td>
<td>cell division cycle-associated 3</td>
<td></td>
</tr>
<tr>
<td>Hs.371240</td>
<td>AKAP12</td>
<td>A kinase (PKA) anchor protein 12</td>
<td></td>
</tr>
<tr>
<td>Hs.515122</td>
<td>TK1</td>
<td>thymidine kinase 1, soluble</td>
<td></td>
</tr>
<tr>
<td>Hs.1030</td>
<td>RIN1</td>
<td>Ras and Rab interactor 1</td>
<td></td>
</tr>
<tr>
<td>Hs.89945</td>
<td>PSMB4</td>
<td>proteasome (prosome, macropain) subunit, beta type 4</td>
<td></td>
</tr>
<tr>
<td>Hs.3104</td>
<td>KIF14</td>
<td>kinesin family member 14</td>
<td></td>
</tr>
<tr>
<td>Hs.405662</td>
<td>CRABP2</td>
<td>cellular retinoic acid binding protein 2</td>
<td></td>
</tr>
<tr>
<td>Hs.57871</td>
<td>CARD10</td>
<td>caspase recruitment domain family, member 10</td>
<td></td>
</tr>
<tr>
<td>Hs.368982</td>
<td>CASP2</td>
<td>caspase 2, apoptosis-related cysteine peptidase</td>
<td></td>
</tr>
<tr>
<td>Hs.699998</td>
<td>ZNF395</td>
<td>zinc finger protein 395</td>
<td></td>
</tr>
<tr>
<td>Hs.500711</td>
<td>DNMBP</td>
<td>dynamin binding protein</td>
<td></td>
</tr>
<tr>
<td>Hs.488188</td>
<td>ATP5GVE1</td>
<td>ATPase, H+ transporting, lysosomal 9kDa, V0 subunit 1</td>
<td></td>
</tr>
<tr>
<td>Hs.213470</td>
<td>PSMB7</td>
<td>proteasome (prosome, macropain) subunit, beta type 7</td>
<td></td>
</tr>
<tr>
<td>Hs.515122</td>
<td>CALR</td>
<td>calreticulin</td>
<td></td>
</tr>
<tr>
<td>Hs.522413</td>
<td>DNM1</td>
<td>dynamin 1</td>
<td></td>
</tr>
<tr>
<td>Hs.471508</td>
<td>IR51</td>
<td>insulin receptor substrate 1</td>
<td></td>
</tr>
<tr>
<td>Hs.534612</td>
<td>RAB7B</td>
<td>RAB7, member RAS oncogene family</td>
<td></td>
</tr>
<tr>
<td>Hs.600940</td>
<td>RDH5</td>
<td>retinal dehydrogenase 5 (11-cis/9-cis)</td>
<td></td>
</tr>
</tbody>
</table>
-2.4 204568_at  Hs.709252  RAD54L  RAD54-like (S. cerevisiae)
-2.4 203046_s_at  Hs.118631  TIMELESS  timeless homolog (Drosophila)
-2.4 201697_at  Hs.202672  DNMT1  DNA (cytosine-5-)methyltransferase 1
-2.4 212691_at  Hs.308340  NUP188  nucleoporin 188kDa
-2.4 38158_at  Hs.153479  ESPL1  extra spindle pole bodies homolog 1 (S. cerevisiae)
-2.4 213344_s_at  Hs.477879  H2AFX  H2A histone family, member X
-2.4 221545_s_at  Hs.363107  MEDI6  mediator complex subunit 16
-2.4 202355_s_at  Hs.654530  NUP214  nucleoporin 214kDa
-2.4 201368_at  Hs.503093  ZFP33L2  zinc finger protein 33, C3H type-like 2
-2.4 212784_at  Hs.380236  CIC  capicua homolog (Drosophila)
-2.5 223133_s_at  Hs.197011  MEK6  NIMA (never in mitosis gene a)-related kinase 6
-2.5 203764_at  Hs.77695  DLGAP5  discs, large (Drosophila) homolog-associated protein 5
-2.5 209642_at  Hs.46649  BUB1  budding uninhibited by benzimidazoles 1 homolog (yeast)
-2.5 209920_at  Hs.701977  NRZ2  nuclear receptor subfamily 2, group F, member 2
-2.5 208079_s_at  Hs.250822  AURKA  aurora kinase A
-2.5 204124_s_at  Hs.474217  CDC45L  CDC45 cell division cycle 45-like (S. cerevisiae)
-2.5 216952_s_at  Hs.513286  LMNB2  lamin B2
-2.5 232231_at  Hs.535845  RUNX2  runt-related transcription factor 2
-2.5 201830_s_at  Hs.25155  NET1  neurepithelial cell transforming 1
-2.5 222236_x_at  Hs.593485  ZNF43  zinc finger protein 43
-2.5 201224_s_at  Hs.18192  SRRM1  serine/arginine repetitive matrix 1
-2.5 35671_at  Hs.372178  GTF3C1  general transcription factor IIIC, polypeptide 1, alpha 220kDa
-2.5 209713_s_at  Hs.226390  RRM2  ribonucleoside reductase M2 polypeptide
-2.7 218039_at  Hs.615092  NUSAP1  nucleolar and spindle associated protein 1
-2.7 212126_at  Hs.349823  CBX5  chromobox homolog 5 (HP1 alpha homolog, Drosophila)
-2.7 205345_at  Hs.591642  BARDO1  BRCA1-associated RING domain 3
-2.7 226388_at  Hs.446354  TCEA3  transcription elongation factor A (SIII, 3)
-2.7 220744_s_at  Hs.855284  IPT122  intralflagellar transport 122 homolog (Chlamydomonas)
-2.7 209660_s_at  Hs.436912  KIFC1  kinesin family member C1
-2.8 208711_s_at  Hs.523852  CCND1  cyclin D1
-2.8 229638_at  Hs.714419  SIX1  SIX homeobox 1
-2.8 228208_x_at  Hs.709873  ZNF354C  zinc finger protein 354C
-2.8 224572_s_at  Hs.693837  IRF2BP2  interferon regulatory factor 2 binding protein 2
-2.8 203755_at  Hs.631697  BUB1B  budding uninhibited by benzimidazoles 1 homolog (yeast)
-2.8 218663_at  Hs.567576  NAPC (includes E) non-SMC condensin I complex, subunit G
-2.8 208149_x_at  Hs.449600  DDX11  DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae)
-2.8 204092_s_at  Hs.290822  AURKA  aurora kinase A
-2.8 201663_s_at  Hs.58992  SMC4  structural maintenance of chromosomes 4
-2.9 1555653_at  Hs.518539  MCM2  minichromosome maintenance component 2
-2.9 218565_at  Hs.224137  C9orf114  chromosome 9 open reading frame 114
-2.9 222036_at  Hs.460184  MCM4  minichromosome maintenance complex component 4
-2.9 201904_s_at  Hs.479663  CTD5P1L  CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
-2.9 203422_at  Hs.297493  POLD1  polymerase (DNA directed), delta 1, catalytic subunit 125kDa
-2.9 212949_at  Hs.308045  NAPC  non-SMC condensin I complex, subunit H
-3.0 201850_at  Hs.516155  CAPG  capping protein (actin filament), gelsolin-like
-3.0 205240_at  Hs.584901  GPM2  G-protein signaling modulator 2 (AGS3-like, C. elegans)
-3.0 202726_s_at  Hs.1770  LUG1  ligase I, DNA, ATP-dependent
-3.0 218662_s_at  Hs.567567  NAPC (includes E) non-SMC condensin I complex, subunit G
-3.0 206699_s_at  Hs.79064  HPAS1  neuronal PAS domain protein 3
-3.0 204159_at  Hs.523524  CDKN2C  cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
-3.0 209400_at  Hs.717465  KIF2C  kinesin family member 2C
-3.0 202322_at  Hs.371178  GTF3C1  general transcription factor IIIC, polypeptide 1, alpha 220kDa
-3.0 202183_s_at  Hs.613351  KIF22  kinesin family member 22
-3.0 204817_at  Hs.153479  ESPL1  extra spindle pole bodies homolog 1 (S. cerevisiae)
-3.0 202870_s_at  Hs.528471  CDC20  cell division cycle 20 homolog (S. cerevisiae)
-3.0 205333_at  Hs.169348  BLM  Bloom syndrome
-3.0 205167_s_at  Hs.656  CDC25C  cell division cycle 25 homolog C (S. pombe)
-3.0 204812_s_at  Hs.1973  CCNF  cyclin F
-3.0 203276_s_at  Hs.89407  LMNB1  lamin B1
-3.0 202107_s_at  Hs.474881  MCM2  minichromosome maintenance complex component 2
-3.0 209199_s_at  Hs.683994  MEJ2C  myocyte enhancer factor 2C
-3.0 212803_at  Hs.159223  NAB2  NGF-I A binding protein 2 (EGR1 binding protein 2)
<table>
<thead>
<tr>
<th>Gene ID</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>203462_at</td>
<td>nuclear receptor subfamily 2, group F, member 2 (Drosophila)</td>
</tr>
<tr>
<td>218315_at</td>
<td>ribosomal protein L27a</td>
</tr>
<tr>
<td>205436_s_at</td>
<td>H2AFX</td>
</tr>
<tr>
<td>218003_s_at</td>
<td>PRKCI</td>
</tr>
<tr>
<td>230909_at</td>
<td>PRKCB1</td>
</tr>
<tr>
<td>213844_at</td>
<td>HOX5A2</td>
</tr>
<tr>
<td>216377_s_at</td>
<td>MCM5</td>
</tr>
<tr>
<td>204131_s_at</td>
<td>breast cancer 1, early onset</td>
</tr>
<tr>
<td>230165_at</td>
<td>SGO1</td>
</tr>
<tr>
<td>229487_at</td>
<td>EF1</td>
</tr>
<tr>
<td>218300_at</td>
<td>F-box only homology 2 domain containing 1</td>
</tr>
<tr>
<td>227242_s_at</td>
<td>E2F3</td>
</tr>
<tr>
<td>204444_at</td>
<td>KRF1</td>
</tr>
<tr>
<td>226665_at</td>
<td>PRKCB1</td>
</tr>
<tr>
<td>211519_s_at</td>
<td>KIF2C</td>
</tr>
<tr>
<td>209200_at</td>
<td>MEF2C</td>
</tr>
<tr>
<td>226661_at</td>
<td>CDCA2</td>
</tr>
<tr>
<td>208025_s_at</td>
<td>HMGA2</td>
</tr>
<tr>
<td>212919_s_at</td>
<td>LDB2</td>
</tr>
<tr>
<td>201774_s_at</td>
<td>NCAPD2</td>
</tr>
<tr>
<td>206074_at</td>
<td>MCM5</td>
</tr>
<tr>
<td>201831_at</td>
<td>ZFP36</td>
</tr>
<tr>
<td>218355_at</td>
<td>KIF4A</td>
</tr>
<tr>
<td>235442_at</td>
<td>SGO1L2</td>
</tr>
<tr>
<td>207069_s_at</td>
<td>SMAD6</td>
</tr>
<tr>
<td>209119_s_at</td>
<td>NRRF2</td>
</tr>
<tr>
<td>213979_s_at</td>
<td>CTBP1</td>
</tr>
<tr>
<td>218950_at</td>
<td>ERCC6</td>
</tr>
<tr>
<td>218585_s_at</td>
<td>DTL</td>
</tr>
<tr>
<td>201292_at</td>
<td>TOP2A</td>
</tr>
<tr>
<td>225655_at</td>
<td>UHRF1</td>
</tr>
<tr>
<td>216979_s_at</td>
<td>NPA51</td>
</tr>
<tr>
<td>219306_at</td>
<td>KIF15</td>
</tr>
<tr>
<td>221922_at</td>
<td>GPM32</td>
</tr>
<tr>
<td>201755_s_at</td>
<td>MCM5</td>
</tr>
<tr>
<td>212919_s_at</td>
<td>LDB2</td>
</tr>
<tr>
<td>21792_s_at</td>
<td>CDK25C</td>
</tr>
<tr>
<td>209918_s_at</td>
<td>ASPM</td>
</tr>
<tr>
<td>219729_at</td>
<td>PRKX2</td>
</tr>
<tr>
<td>227243_s_at</td>
<td>EF8</td>
</tr>
<tr>
<td>207147_at</td>
<td>DLX2</td>
</tr>
<tr>
<td>202580_s_at</td>
<td>FOXM1</td>
</tr>
<tr>
<td>227478_at</td>
<td>SETBP1</td>
</tr>
<tr>
<td>221520_s_at</td>
<td>CDCA8</td>
</tr>
<tr>
<td>209172_s_at</td>
<td>CENPF</td>
</tr>
<tr>
<td>207828_s_at</td>
<td>CENPF</td>
</tr>
<tr>
<td>212033_at</td>
<td>MKI67</td>
</tr>
<tr>
<td>220085_at</td>
<td>HELLS</td>
</tr>
<tr>
<td>222027_at</td>
<td>NUCKS1</td>
</tr>
<tr>
<td>212044_s_at</td>
<td>RPL27A (includes E ribosomal protein L27a)</td>
</tr>
<tr>
<td>208323_at</td>
<td>CASC5</td>
</tr>
<tr>
<td>1553015_s_at</td>
<td>RCLO4</td>
</tr>
<tr>
<td>227404_s_at</td>
<td>EGR1</td>
</tr>
<tr>
<td>221911_at</td>
<td>ETV1</td>
</tr>
<tr>
<td>209122_s_at</td>
<td>NRRF2</td>
</tr>
<tr>
<td>227719_at</td>
<td>SMAD9</td>
</tr>
<tr>
<td>215073_s_at</td>
<td>NRRF2</td>
</tr>
<tr>
<td>201306_s_at</td>
<td>ZFP36L2</td>
</tr>
<tr>
<td>201694_s_at</td>
<td>EGR1</td>
</tr>
<tr>
<td>208937_s_at</td>
<td>ID1</td>
</tr>
<tr>
<td>206481_s_at</td>
<td>LIM domain binding 2</td>
</tr>
<tr>
<td>212021_s_at</td>
<td>MKI67</td>
</tr>
<tr>
<td>DSEL</td>
<td>-9.2</td>
</tr>
<tr>
<td>-11</td>
<td>229092_at</td>
</tr>
<tr>
<td>-11.1</td>
<td>234464_s_at</td>
</tr>
<tr>
<td>-20.6</td>
<td>228989_at</td>
</tr>
<tr>
<td>-1.9</td>
<td>218462_at</td>
</tr>
<tr>
<td>-2</td>
<td>221863_at</td>
</tr>
<tr>
<td>-2</td>
<td>228837_at</td>
</tr>
<tr>
<td>-2</td>
<td>212098_at</td>
</tr>
<tr>
<td>-2</td>
<td>227490_at</td>
</tr>
<tr>
<td>-2</td>
<td>223482_at</td>
</tr>
<tr>
<td>-2.1</td>
<td>36030_at</td>
</tr>
<tr>
<td>-2.1</td>
<td>63825_at</td>
</tr>
<tr>
<td>-2.1</td>
<td>221335_s_at</td>
</tr>
<tr>
<td>-2.1</td>
<td>227188_at</td>
</tr>
<tr>
<td>-2.1</td>
<td>219063_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>225202_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>212906_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>223276_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>202389_s_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>214273_s_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>205631_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>213234_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>213835_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>226416_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>226118_at</td>
</tr>
<tr>
<td>-2.2</td>
<td>223348_s_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>232235_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>230972_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>206180_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>223019_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>212830_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>228654_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>221290_s_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>231411_s_at</td>
</tr>
<tr>
<td>-2.3</td>
<td>226559_at</td>
</tr>
<tr>
<td>-2.4</td>
<td>217275_at</td>
</tr>
<tr>
<td>-2.4</td>
<td>214672_at</td>
</tr>
<tr>
<td>-2.4</td>
<td>202975_s_at</td>
</tr>
<tr>
<td>-2.4</td>
<td>36888_at</td>
</tr>
<tr>
<td>-2.4</td>
<td>202976_s_at</td>
</tr>
<tr>
<td>-2.4</td>
<td>226456_at</td>
</tr>
<tr>
<td>-2.5</td>
<td>232826_s_at</td>
</tr>
<tr>
<td>-2.5</td>
<td>218843_at</td>
</tr>
<tr>
<td>-2.5</td>
<td>235092_at</td>
</tr>
<tr>
<td>-2.5</td>
<td>224932_at</td>
</tr>
<tr>
<td>-2.5</td>
<td>226485_at</td>
</tr>
<tr>
<td>-2.6</td>
<td>218717_s_at</td>
</tr>
<tr>
<td>-2.6</td>
<td>234994_at</td>
</tr>
<tr>
<td>-2.6</td>
<td>213862_s_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>221965_s_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>213422_s_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>224880_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>220233_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>227444_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>221191_s_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>225337_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>224771_at</td>
</tr>
<tr>
<td>-2.7</td>
<td>225533_at</td>
</tr>
<tr>
<td>-2.8</td>
<td>204094_s_at</td>
</tr>
<tr>
<td>-2.8</td>
<td>228836_at</td>
</tr>
<tr>
<td>-2.8</td>
<td>214772_at</td>
</tr>
<tr>
<td>-2.8</td>
<td>201813_s_at</td>
</tr>
<tr>
<td>-2.9</td>
<td>225337_at</td>
</tr>
</tbody>
</table>
-2.9 22274_5_at  Hs.656025  KIAA1244  KIAA1244  
-3.0 202214_s_at  Hs.109214  CUL4B  culin 4B  
-3.0 203255_at  Hs.352677  FBXO11  F-box protein 11  
-3.0 201895_s_at  Hs.405929  PSRC1  protocadherin-rich coiled-coil 1  
-3.1 2160292_at  Hs.152944  VWA5A  von Willebrand factor A domain containing 5A  
-3.1 23875_6_at  Hs.20575  GAS2L3  growth arrest-specific 2 like 3  
-3.3 226287_at  Hs.144373  C20orf34  coiled-coil domain containing 34  
-3.3 212736_at  Hs.466005  C16orf45  chromosome 16 open reading frame 45  
-3.3 225687_at  Hs.427216  FAM83D  family with sequence similarity 83, member D  
-3.3 235709_at  Hs.20575  GAS2L3  growth arrest-specific 2 like 3  
-3.3 222039_at  Hs.139094  KIF18B (includes Ekinase family member 188  
-3.4 217734_s_at  Hs.654815  WDR6 (includes EG W repeat domain 6  
-3.4 236834_at  Hs.302287  SCD2  sech family domain containing 2  
-3.5 222728_at  Hs.516777  SHHBP4  S-H junction binding protein 4  
-3.5 226923_at  Hs.302287  SCD2  sech family domain containing 2  
-3.6 222173_s_at  Hs.371016  TBCD2  TBC domain family, member 2  
-3.6 213118_at  Hs.716024  ANKR3D5  ankyrin repeat domain 35  
-3.6 212069_s_at  Hs.495349  BAT2L  HLA-B associated transcript 2-like  
-3.8 230020_at  Hs.195403  DOCK5  dedicator of cytokinesis 5  
-3.8 216048_s_at  Hs.445030  RHOBTB3  Rho-related BTB domain containing 3  
-3.8 229058_at  Hs.98052  C9orf109  chromosome 9 open reading frame 109  
-3.8 233548_at  Hs.502266  C11orf41  chromosome 11 open reading frame 41  
-3.9 2431920_s_at  Hs.579108  ARH1T1A  ADP-ribosylation factor-like 17 pseudogene 1  
-3.9 213273_at  Hs.211308  ODZ4 (includes EG ozd, odd Ozten-m homolog 4 (Drosophila  
-4.1 213273_at  Hs.193133  SASH1  SAM and SH3 domain containing 1  
-4.1 227058_at  Hs.614612  C13orf33  chromosome 13 open reading frame 33  
-4.1 221815_at  Hs.122337  ABHD2  abhydrolase domain containing 2  
-4.2 228117_s_at  Hs.188781  PLEKHG4  pleckstrin homology domain containing, family G (with RhGef domain) member 4  
-4.6 218888_at  Hs.448406  NET2  neuropilin (NRP) and bcl-2 (TLL) like 2  
-4.7 156085_at  Hs.351856  C10orf136  chromosome 10 open reading frame 136  
-4.8 221603_at  Hs.405929  FBXO16  F-box protein 16  
-4.9 219921_s_at  Hs.195403  DOCK5  dedicator of cytokinesis 5  
-4.9 230263_at  Hs.195403  DOCK5  dedicator of cytokinesis 5  
-5.1 213007_at  Hs.511126  FANCi  Fanconi anemia, complementation group I  
-5.3 40472_at  Hs.358214  LPCAT4  lysophosphatidylcholine acyltransferase 4  
-5.3 155576_at  Hs.589057  KRTAP2-1  keratin associated protein 2-1  
-5.8 209789_at  Hs.551213  CORO2B  coro2, actin binding protein, 2B  
-6.0 229442_at  Hs.612573  HGC 16001  ribosomal protein L23a pseudogene 42  
-6.0 235332_at  Hs.534499  KRTAP2-5  keratin associated protein 1-5  
-6.1 213008_at  Hs.511126  FANCi  Fanconi anemia, complementation group I  
-6.1 225767_at  Hs.370699  LOC 284801  hypothetical protein LOC 284801  
-6.1 227744_at  Hs.444406  NET2  neuropilin (NRP) and bcl-2 (TLL) like 2  
-6.2 212793_at  Hs.712560  DAAM2  dishevelled-associated activator of morphogenesis 2  
-6.3 219278_s_at  Hs.154694  MAPK6  mitogen-activated protein kinase kinase 6  
-6.3 219054_at  Hs.13928  C5orf23  chromosome 5 open reading frame 23  
-6.7 205376_at  Hs.658245  INPP4B  inositol polyphosphate-4-phosphatase, type II, 105kDa  
-6.9 226652_at  Hs.529857  TRPS1  immediate early response 5-like  
-9.1 1557180_at  Hs.172982  C11orf87  chromosome 11 open reading frame 87  
-10.1 226014_at  Hs.518930  C6orf62  chromosome 6 open reading frame 62  
-10.3 213757_s_at  Hs.519930  LOC 100133577  hypothetical protein LOC 100133577  
-13.5 224346_at  Hs.529857  TRPS1  immediate early response 5-like  
-17.2 1557181_at  Hs.172982  C11orf87  chromosome 11 open reading frame 87  
-19.1 229938_s_at  Hs.591945  IGAP3  IG motif containing GTPase activating protein 3  
-27.6 23632_at  Hs.172982  C11orf87  chromosome 11 open reading frame 87  
-51.9 230799_at  Hs.100143459  similar to HCG198771B  
-7.2 245147_at  Hs.657250  
-2.1 225906_at  Hs.594823  
-2.1 227545_at  Hs.54809  
-2.1 229313_s_at  Hs.712089  
-2.2 156238_at  Hs.408461  
-2.2 221821_at  Hs.28832  
-2.2 235363_at  Hs.28360  
-2.2 229465_s_at  Hs.644834
<table>
<thead>
<tr>
<th></th>
<th>Gene ID</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2.2</td>
<td>236632_at</td>
<td>Hs.632595</td>
</tr>
<tr>
<td>-2.3</td>
<td>1567913_at</td>
<td>Hs.621508</td>
</tr>
<tr>
<td>-2.3</td>
<td>230655_at</td>
<td>Hs.15422</td>
</tr>
<tr>
<td>-2.3</td>
<td>230740_at</td>
<td>Hs.648929</td>
</tr>
<tr>
<td>-2.4</td>
<td>229544_at</td>
<td>Hs.167087 // Hs.621424</td>
</tr>
<tr>
<td>-2.4</td>
<td>228309_at</td>
<td>---</td>
</tr>
<tr>
<td>-2.4</td>
<td>235609_at</td>
<td>Hs.598759</td>
</tr>
<tr>
<td>-2.4</td>
<td>226107_at</td>
<td>Hs.239666 // Hs.601347</td>
</tr>
<tr>
<td>-2.4</td>
<td>231431_s_at</td>
<td>Hs.530791</td>
</tr>
<tr>
<td>-2.5</td>
<td>224284_x_at</td>
<td>---</td>
</tr>
<tr>
<td>-2.5</td>
<td>213705_at</td>
<td>Hs.592466</td>
</tr>
<tr>
<td>-2.5</td>
<td>227432_s_at</td>
<td>Hs.705877</td>
</tr>
<tr>
<td>-2.6</td>
<td>234225_at</td>
<td>---</td>
</tr>
<tr>
<td>-2.6</td>
<td>2358250_s_at</td>
<td>Hs.23554</td>
</tr>
<tr>
<td>-2.6</td>
<td>216246_at</td>
<td>---</td>
</tr>
<tr>
<td>-2.7</td>
<td>208120_x_at</td>
<td>---</td>
</tr>
<tr>
<td>-2.8</td>
<td>1563431_x_at</td>
<td>Hs.713288</td>
</tr>
<tr>
<td>-2.8</td>
<td>233088_at</td>
<td>Hs.666722</td>
</tr>
<tr>
<td>-2.9</td>
<td>213048_s_at</td>
<td>---</td>
</tr>
<tr>
<td>-2.9</td>
<td>228273_at</td>
<td>Hs.633096</td>
</tr>
<tr>
<td>-3</td>
<td>228120_at</td>
<td>Hs.656677</td>
</tr>
<tr>
<td>-3</td>
<td>223797_at</td>
<td>Hs.655270</td>
</tr>
<tr>
<td>-3.1</td>
<td>241617_x_at</td>
<td>---</td>
</tr>
<tr>
<td>-3.2</td>
<td>211454_x_at</td>
<td>---</td>
</tr>
<tr>
<td>-3.3</td>
<td>212957_at</td>
<td>Hs.593218</td>
</tr>
<tr>
<td>-3.4</td>
<td>239474_at</td>
<td>Hs.664818</td>
</tr>
<tr>
<td>-3.5</td>
<td>228159_at</td>
<td>Hs.40506</td>
</tr>
<tr>
<td>-3.5</td>
<td>214395_x_at</td>
<td>Hs.704553</td>
</tr>
<tr>
<td>-4.7</td>
<td>229490_s_at</td>
<td>Hs.133294</td>
</tr>
<tr>
<td>-4.8</td>
<td>221990_s_at</td>
<td>---</td>
</tr>
<tr>
<td>-5.5</td>
<td>216554_s_at</td>
<td>---</td>
</tr>
<tr>
<td>-5.8</td>
<td>213813_x_at</td>
<td>---</td>
</tr>
<tr>
<td>-6</td>
<td>230345_at</td>
<td>Hs.170843</td>
</tr>
<tr>
<td>-6.3</td>
<td>239202_at</td>
<td>Hs.702338</td>
</tr>
<tr>
<td>-6.8</td>
<td>222968_at</td>
<td>---</td>
</tr>
<tr>
<td>-6.9</td>
<td>231387_at</td>
<td>Hs.712966</td>
</tr>
<tr>
<td>-7.4</td>
<td>244013_at</td>
<td>Hs.124976</td>
</tr>
<tr>
<td>-8</td>
<td>242890_at</td>
<td>Hs.658935</td>
</tr>
<tr>
<td>-8.4</td>
<td>230546_at</td>
<td>Hs.176376</td>
</tr>
<tr>
<td>-13.2</td>
<td>230750_at</td>
<td>Hs.594199</td>
</tr>
<tr>
<td>-26.3</td>
<td>229004_at</td>
<td>Hs.534221</td>
</tr>
</tbody>
</table>
Table S5. Common genes of the FL-MSC and TNF/LT signatures

Red lines indicates genes that are overexpressed in FL-MSC and HD-MSC + TNF/LT and green line indicates genes that are underexpressed in FL-MSC and HD-MSC + TNF/LT

The fold changes indicate either a ratio of mean expression (HD-MSC + TNF/LT versus HD-MSC) or a ratio of median expression (FL-MSC versus HD-MSC)

<table>
<thead>
<tr>
<th>ProbeSet ID</th>
<th>Gene Symbol</th>
<th>Gene Title</th>
<th>UniGene ID</th>
<th>Fold change HD-MSC+TNF/LT versus HD-MSC</th>
<th>Fold change FL-MSC versus HD-MSC</th>
</tr>
</thead>
<tbody>
<tr>
<td>216598_s_at</td>
<td>CCL2</td>
<td>chemokine (C-C motif) ligand 2</td>
<td>Hs.303649</td>
<td>54.7</td>
<td>2.2</td>
</tr>
<tr>
<td>226181_at</td>
<td>TUBE1</td>
<td>tubulin. epsilon 1</td>
<td>Hs.34851</td>
<td>29.4</td>
<td>2.7</td>
</tr>
<tr>
<td>236313_at</td>
<td>CDKN2B</td>
<td>cyclin-dependent kinase inhibitor 2B (p15. inhibits CDK4)</td>
<td>Hs.72901</td>
<td>27.2</td>
<td>4.7</td>
</tr>
<tr>
<td>204493_at</td>
<td>BID</td>
<td>BH3 interacting domain death agonist</td>
<td>Hs.791054</td>
<td>20.1</td>
<td>2.5</td>
</tr>
<tr>
<td>213142_x_at</td>
<td>PION</td>
<td>pigeon homolog (Drosophila)</td>
<td>Hs.186649</td>
<td>19.8</td>
<td>2.1</td>
</tr>
<tr>
<td>226533_at</td>
<td>HINT3</td>
<td>histidine triad nucleotide binding protein 3</td>
<td>Hs.72325</td>
<td>18.5</td>
<td>2.6</td>
</tr>
<tr>
<td>202660_at</td>
<td>ITPR2</td>
<td>inositol 1.4.5-triphosphate receptor. type 2</td>
<td>Hs.512235</td>
<td>15.2</td>
<td>2.1</td>
</tr>
<tr>
<td>209277_at</td>
<td>TFP12</td>
<td>tissue factor pathway inhibitor 2</td>
<td>Hs.438231</td>
<td>10.8</td>
<td>3.7</td>
</tr>
<tr>
<td>227020_at</td>
<td>YPEL2</td>
<td>yippee-like 2 (Drosophila)</td>
<td>Hs.463613</td>
<td>9.3</td>
<td>2.2</td>
</tr>
<tr>
<td>208868_s_at</td>
<td>GABARAPL1</td>
<td>GABA(A) receptor-associated protein like 1</td>
<td>Hs.524250</td>
<td>9.2</td>
<td>2.3</td>
</tr>
<tr>
<td>1553106_at</td>
<td>C5orf24</td>
<td>chromosome 5 open reading frame 24</td>
<td>Hs.406549</td>
<td>8.1</td>
<td>2.9</td>
</tr>
<tr>
<td>224848_at</td>
<td>CDK6</td>
<td>cyclin-dependent kinase 6</td>
<td>Hs.119882</td>
<td>7.7</td>
<td>2.0</td>
</tr>
<tr>
<td>205174_s_at</td>
<td>QPCT</td>
<td>glutaminyl-peptide cyclotransferase</td>
<td>Hs.79033</td>
<td>6.4</td>
<td>3.0</td>
</tr>
<tr>
<td>211596_s_at</td>
<td>LRIG1</td>
<td>leucine-rich repeats and immunoglobulin-like domains 1</td>
<td>Hs.518055</td>
<td>6.1</td>
<td>2.1</td>
</tr>
<tr>
<td>205139_s_at</td>
<td>UST</td>
<td>uronyl-2-sulfotransferase</td>
<td>Hs.657370</td>
<td>5.9</td>
<td>3.0</td>
</tr>
<tr>
<td>224847_at</td>
<td>CDK6</td>
<td>cyclin-dependent kinase 6</td>
<td>Hs.119882</td>
<td>5.7</td>
<td>2.1</td>
</tr>
<tr>
<td>40148_at</td>
<td>APBB2</td>
<td>amyloid beta (A4) precursor protein-binding. family B. member 2</td>
<td>Hs.479602</td>
<td>5.3</td>
<td>2.2</td>
</tr>
<tr>
<td>232080_at</td>
<td>HECW2</td>
<td>HECT. C2 and WW domain containing E3 ubiquitin protein ligase 2</td>
<td>Hs.654742</td>
<td>5.2</td>
<td>3.0</td>
</tr>
<tr>
<td>228772_at</td>
<td>HNMT</td>
<td>histamine N-methyltransferase</td>
<td>Hs.42151</td>
<td>5.0</td>
<td>3.1</td>
</tr>
<tr>
<td>222636_at</td>
<td>MED28</td>
<td>mediator complex subunit 28</td>
<td>Hs.430475</td>
<td>4.8</td>
<td>2.0</td>
</tr>
<tr>
<td>209278_s_at</td>
<td>TFP12</td>
<td>tissue factor pathway inhibitor 2</td>
<td>Hs.438231</td>
<td>4.7</td>
<td>2.6</td>
</tr>
<tr>
<td>243042_at</td>
<td>FAM73A</td>
<td>family with sequence similarity 73. member A</td>
<td>Hs.632419</td>
<td>4.6</td>
<td>2.5</td>
</tr>
<tr>
<td>231899_at</td>
<td>ZC3H12C</td>
<td>zinc finger CCCH-type containing 12C</td>
<td>Hs.376289</td>
<td>4.2</td>
<td>2.3</td>
</tr>
<tr>
<td>1569129_s_at</td>
<td>C3orf38</td>
<td>chromosome 3 open reading frame 38</td>
<td>Hs.518099</td>
<td>3.9</td>
<td>2.7</td>
</tr>
<tr>
<td>223263_s_at</td>
<td>FGFR1OP2</td>
<td>FGFR1 oncogene partner 2</td>
<td>Hs.591162</td>
<td>3.9</td>
<td>2.1</td>
</tr>
<tr>
<td>227247_at</td>
<td>PLEKHA8</td>
<td>pleckstrin homology domain containing. family A (phosphoinositide binding specif</td>
<td>Hs.233495</td>
<td>3.8</td>
<td>2.1</td>
</tr>
<tr>
<td>220329_s_at</td>
<td>RMND1</td>
<td>required for meiotic nuclear division 1 homolog (S. cerevisiae)</td>
<td>Hs.486835</td>
<td>3.8</td>
<td>2.3</td>
</tr>
<tr>
<td>204396_s_at</td>
<td>GRK5</td>
<td>G protein-coupled receptor kinase 5</td>
<td>Hs.524625</td>
<td>3.8</td>
<td>2.3</td>
</tr>
<tr>
<td>1554557_at</td>
<td>ATP11B</td>
<td>ATPase. class VI. type 11B</td>
<td>Hs.478429</td>
<td>3.7</td>
<td>3.3</td>
</tr>
<tr>
<td>216250_s_at</td>
<td>LPXN</td>
<td>leupaxin</td>
<td>Hs.125474</td>
<td>3.7</td>
<td>2.8</td>
</tr>
<tr>
<td>222846_at</td>
<td>RAB8B</td>
<td>RAB8B. member RAS oncogene family</td>
<td>Hs.389733</td>
<td>3.6</td>
<td>2.5</td>
</tr>
<tr>
<td>Gene ID</td>
<td>Description</td>
<td>Species ID</td>
<td>Ratio</td>
<td>Fold</td>
<td></td>
</tr>
<tr>
<td>---------</td>
<td>--------------------------------------------------</td>
<td>------------</td>
<td>-------</td>
<td>------</td>
<td>---</td>
</tr>
<tr>
<td>34408_at</td>
<td>RTN2 reticulon 2</td>
<td>Hs.47517</td>
<td>3.5</td>
<td>3.1</td>
<td></td>
</tr>
<tr>
<td>232060_at</td>
<td>ROR1 receptor tyrosine kinase-like orphan receptor 1</td>
<td>Hs.65491</td>
<td>3.5</td>
<td>2.4</td>
<td></td>
</tr>
<tr>
<td>216593_s_at</td>
<td>PIGC phosphatidylinositol glycan anchor biosynthesis. class C</td>
<td>Hs.188456</td>
<td>3.5</td>
<td>2.4</td>
<td></td>
</tr>
<tr>
<td>225922_at</td>
<td>FNIP2 folliculin interacting protein 2</td>
<td>Hs.709500</td>
<td>3.4</td>
<td>2.6</td>
<td></td>
</tr>
<tr>
<td>228239_at</td>
<td>FAM165B family with sequence similarity 165. member B</td>
<td>Hs.656195</td>
<td>3.3</td>
<td>2.3</td>
<td></td>
</tr>
<tr>
<td>229317_at</td>
<td>KPN A5 karyopherin alpha 5 (importin alpha 6)</td>
<td>Hs.182971</td>
<td>3.3</td>
<td>2.1</td>
<td></td>
</tr>
<tr>
<td>224341_x_at</td>
<td>TLR4 toll-like receptor 4</td>
<td>Hs.174312</td>
<td>3.2</td>
<td>3.1</td>
<td></td>
</tr>
<tr>
<td>33322_i_at</td>
<td>SFN stratifin</td>
<td>Hs.523718</td>
<td>3.2</td>
<td>2.3</td>
<td></td>
</tr>
<tr>
<td>203347_s_at</td>
<td>MTF2 metal response element binding transcription factor 2</td>
<td>Hs.31016</td>
<td>3</td>
<td>2.5</td>
<td></td>
</tr>
<tr>
<td>52285_f_at</td>
<td>CEP76 centrosomal protein 76kDa</td>
<td>Hs.236940</td>
<td>3</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>226520_at</td>
<td>--- ---</td>
<td>Hs.658311</td>
<td>2.9</td>
<td>2.1</td>
<td></td>
</tr>
<tr>
<td>235103_at</td>
<td>MAN2A1 mannosidase. alpha. class 2A. member 1</td>
<td>Hs.432822</td>
<td>2.8</td>
<td>2.2</td>
<td></td>
</tr>
<tr>
<td>213750_at</td>
<td>RSL1D1 ribosomal L1 domain containing 1</td>
<td>Hs.401842</td>
<td>2.8</td>
<td>2.2</td>
<td></td>
</tr>
<tr>
<td>220241_at</td>
<td>TMCO3 transmembrane and coiled-coil domains 3</td>
<td>Hs.317593</td>
<td>2.7</td>
<td>2.1</td>
<td></td>
</tr>
<tr>
<td>1558236_at</td>
<td>--- ---</td>
<td>Hs.369451</td>
<td>2.7</td>
<td>3.8</td>
<td></td>
</tr>
<tr>
<td>220253_s_at</td>
<td>LRP12 low density lipoprotein-related protein 12</td>
<td>Hs.654804</td>
<td>2.6</td>
<td>2.2</td>
<td></td>
</tr>
<tr>
<td>215707_s_at</td>
<td>PRNP prion protein</td>
<td>Hs.472010</td>
<td>2.5</td>
<td>2.1</td>
<td></td>
</tr>
<tr>
<td>225956_at</td>
<td>CSorf41 chromosome 5 open reading frame 41</td>
<td>Hs.484195</td>
<td>2.5</td>
<td>2.0</td>
<td></td>
</tr>
<tr>
<td>223178_at</td>
<td>NT5DC1 5' nucleotidase domain containing 1</td>
<td>Hs.520341</td>
<td>2.5</td>
<td>2.3</td>
<td></td>
</tr>
<tr>
<td>1558254_s_at</td>
<td>SRPK2 SFRS protein kinase 2</td>
<td>Hs.285197</td>
<td>2.3</td>
<td>2.7</td>
<td></td>
</tr>
<tr>
<td>218748_s_at</td>
<td>EXOC5 exocyst complex component 5</td>
<td>Hs.655158</td>
<td>2.3</td>
<td>2.3</td>
<td></td>
</tr>
<tr>
<td>241933_at</td>
<td>QRSL1 Glutamyl-tRNA synthase (glutamine-hydrolyzing)-like 1</td>
<td>Hs.406917</td>
<td>2.2</td>
<td>2.1</td>
<td></td>
</tr>
<tr>
<td>238860_at</td>
<td>C6orf130 chromosome 6 open reading frame 130</td>
<td>Hs.227457</td>
<td>2.1</td>
<td>2.2</td>
<td></td>
</tr>
<tr>
<td>221350_at</td>
<td>HOXC8 homeobox C8</td>
<td>Hs.664500</td>
<td>-2</td>
<td>-2.4</td>
<td></td>
</tr>
<tr>
<td>221660_at</td>
<td>MYLC2PL myosin light chain 2. precursor lymphocyte-specific</td>
<td>Hs.247831</td>
<td>-2.1</td>
<td>-2.1</td>
<td></td>
</tr>
<tr>
<td>1554428_s_at</td>
<td>NLGN2 neurogin 2</td>
<td>Hs.26229</td>
<td>-2.1</td>
<td>-2.4</td>
<td></td>
</tr>
<tr>
<td>209057_x_at</td>
<td>CDC5L CDC5 cell division cycle 5-like (S. pombe)</td>
<td>Hs.485471</td>
<td>-2.3</td>
<td>-2.1</td>
<td></td>
</tr>
<tr>
<td>1567913_at</td>
<td>--- ---</td>
<td>Hs.621508</td>
<td>-2.3</td>
<td>-2.9</td>
<td></td>
</tr>
<tr>
<td>228312_at</td>
<td>PI16 peptidase inhibitor 16</td>
<td>Hs.25391</td>
<td>-2.3</td>
<td>-2.3</td>
<td></td>
</tr>
<tr>
<td>224375_at</td>
<td>--- ---</td>
<td>Hs.25110</td>
<td>-2.5</td>
<td>-2.1</td>
<td></td>
</tr>
<tr>
<td>234225_at</td>
<td>--- ---</td>
<td>Hs.25391</td>
<td>-2.6</td>
<td>-4.2</td>
<td></td>
</tr>
<tr>
<td>216246_at</td>
<td>--- ---</td>
<td>Hs.25391</td>
<td>-2.6</td>
<td>-2.8</td>
<td></td>
</tr>
<tr>
<td>201205_at</td>
<td>--- ---</td>
<td>Hs.25391</td>
<td>-2.8</td>
<td>-2.9</td>
<td></td>
</tr>
<tr>
<td>228208_x_at</td>
<td>ZNF354C zinc finger protein 354C</td>
<td>Hs.709873</td>
<td>-2.8</td>
<td>-3.3</td>
<td></td>
</tr>
<tr>
<td>1563431_x_at</td>
<td>--- ---</td>
<td>Hs.713288</td>
<td>-2.8</td>
<td>-3.6</td>
<td></td>
</tr>
<tr>
<td>218565_at</td>
<td>C9orf114 chromosome 9 open reading frame 114</td>
<td>Hs.224137</td>
<td>-2.9</td>
<td>-2.7</td>
<td></td>
</tr>
<tr>
<td>213048_s_at</td>
<td>--- ---</td>
<td>Hs.593218</td>
<td>-2.9</td>
<td>-2.6</td>
<td></td>
</tr>
<tr>
<td>213002_at</td>
<td>MARCKS myristoylated alanine-rich protein kinase C substrate</td>
<td>---</td>
<td>-3.1</td>
<td>-2.9</td>
<td></td>
</tr>
<tr>
<td>211454_x_at</td>
<td>FKS G49 FKSG49</td>
<td>---</td>
<td>-3.2</td>
<td>-2.4</td>
<td></td>
</tr>
<tr>
<td>212952_at</td>
<td>--- ---</td>
<td>Hs.446522</td>
<td>-3.3</td>
<td>-7.7</td>
<td></td>
</tr>
<tr>
<td>219138_at</td>
<td>RPL14 ribosomal protein L14</td>
<td>Hs.406620</td>
<td>-3.5</td>
<td>-3.7</td>
<td></td>
</tr>
<tr>
<td>214001_x_at</td>
<td>--- ---</td>
<td>Hs.707453</td>
<td>-3.5</td>
<td>-2.6</td>
<td></td>
</tr>
<tr>
<td>Gene Symbol</td>
<td>Gene Name</td>
<td>Hs.</td>
<td>log2 Fold Change 1</td>
<td>log2 Fold Change 2</td>
<td></td>
</tr>
<tr>
<td>-------------------</td>
<td>-----------------------------</td>
<td>------</td>
<td>-------------------</td>
<td>-------------------</td>
<td></td>
</tr>
<tr>
<td>212953_x_at</td>
<td>CALR</td>
<td></td>
<td>-3.7</td>
<td>-3.2</td>
<td></td>
</tr>
<tr>
<td>209972_s_at</td>
<td>JTV1</td>
<td></td>
<td>-3.9</td>
<td>-3.9</td>
<td></td>
</tr>
<tr>
<td>228204_at</td>
<td>PSMB4</td>
<td></td>
<td>-4.6</td>
<td>-4.6</td>
<td></td>
</tr>
<tr>
<td>201774_s_at</td>
<td>NCAPD2</td>
<td></td>
<td>-2.8</td>
<td>-2.8</td>
<td></td>
</tr>
<tr>
<td>213979_s_at</td>
<td>CTBP1</td>
<td></td>
<td>-2.6</td>
<td>-2.6</td>
<td></td>
</tr>
<tr>
<td>202648_at</td>
<td></td>
<td></td>
<td>-5.6</td>
<td>-5.6</td>
<td></td>
</tr>
<tr>
<td>201171_at</td>
<td>ATP6V0E1</td>
<td></td>
<td>-5.9</td>
<td>-5.9</td>
<td></td>
</tr>
<tr>
<td>221995_s_at</td>
<td></td>
<td></td>
<td>-3.7</td>
<td>-3.7</td>
<td></td>
</tr>
<tr>
<td>214315_x_at</td>
<td>CALR</td>
<td></td>
<td>-6.7</td>
<td>-6.7</td>
<td></td>
</tr>
<tr>
<td>216554_s_at</td>
<td></td>
<td></td>
<td>-5.3</td>
<td>-5.3</td>
<td></td>
</tr>
<tr>
<td>222027_at</td>
<td>NUCKS1</td>
<td></td>
<td>-5.6</td>
<td>-10</td>
<td></td>
</tr>
<tr>
<td>212044_s_at</td>
<td>RPL27A</td>
<td></td>
<td>-5.6</td>
<td>-5.6</td>
<td></td>
</tr>
<tr>
<td>213813_x_at</td>
<td></td>
<td></td>
<td>-2.4</td>
<td>-2.4</td>
<td></td>
</tr>
<tr>
<td>213736_at</td>
<td>COX5B</td>
<td></td>
<td>-2.4</td>
<td>-2.4</td>
<td></td>
</tr>
<tr>
<td>229420_at</td>
<td></td>
<td></td>
<td>-5.9</td>
<td>-5</td>
<td></td>
</tr>
<tr>
<td>202028_s_at</td>
<td>RPL38</td>
<td></td>
<td>-6.3</td>
<td>-6.3</td>
<td></td>
</tr>
<tr>
<td>221943_x_at</td>
<td>RPL38</td>
<td></td>
<td>-5.3</td>
<td>-5.3</td>
<td></td>
</tr>
<tr>
<td>222966_at</td>
<td></td>
<td></td>
<td>-10</td>
<td>-10</td>
<td></td>
</tr>
<tr>
<td>231387_at</td>
<td></td>
<td></td>
<td>-5.9</td>
<td>-5.9</td>
<td></td>
</tr>
<tr>
<td>213642_at</td>
<td></td>
<td></td>
<td>-8.3</td>
<td>-8.3</td>
<td></td>
</tr>
<tr>
<td>214041_x_at</td>
<td>RPL37A</td>
<td></td>
<td>-4.4</td>
<td>-4.4</td>
<td></td>
</tr>
<tr>
<td>213875_x_at</td>
<td>C6orf62</td>
<td></td>
<td>-10</td>
<td>-10</td>
<td></td>
</tr>
<tr>
<td>234464_s_at</td>
<td>EME1</td>
<td></td>
<td>-4.4</td>
<td>-4.4</td>
<td></td>
</tr>
<tr>
<td>224321_at</td>
<td>TMEFF2</td>
<td></td>
<td>-8.3</td>
<td>-8.3</td>
<td></td>
</tr>
<tr>
<td>230750_at</td>
<td></td>
<td></td>
<td>-2.6</td>
<td>-2.6</td>
<td></td>
</tr>
<tr>
<td>224346_at</td>
<td></td>
<td></td>
<td>-12.5</td>
<td>-12.5</td>
<td></td>
</tr>
<tr>
<td>1556316_s_at</td>
<td>LOC284889</td>
<td></td>
<td>-33.3</td>
<td>-33.3</td>
<td></td>
</tr>
<tr>
<td>213350_at</td>
<td>RPS11</td>
<td></td>
<td>-20</td>
<td>-20</td>
<td></td>
</tr>
<tr>
<td>229538_s_at</td>
<td>IQGAP3</td>
<td></td>
<td>-4.6</td>
<td>-4.6</td>
<td></td>
</tr>
</tbody>
</table>
Figure S1. MSC morphology and phenotype.
HD-MSC (n=6) and FL-MSC (n=10) were analyzed at the end of P1.
(a) Phase contrast microscopy of representative HD-MSC (Left panel) and FL-MSC (Right panel) cultures. Magnification x 10 is shown.
(b) Filled histograms represent isotype-matched controls, and full lines the staining with specific antibodies. Shown is one representative phenotype of FL-MSC.
Figure S2. FISH analysis of FL-MSC
Interphase fluorescence in situ hybridization (FISH) was performed according to standard procedures using LSI IGH/BCL2 dual color, dual fusion translocation probe (Vysis-Abbott, Rungis, France) on P1 FL-MSC (Left panels) and on CD19pos B cells purified from autologous invaded lymph nodes (Right panels). After nuclei counterstaining by DAPI (Vector, Burlingame, USA), the cells were viewed using a fluorescent Axioplan II microscope (Zeiss, Le Pecq, France). In a normal nucleus the expected pattern is the two orange, two green signal pattern. In a nucleus harboring a t(14;18), the most common pattern is one orange signal, one green signal, and two orange/green (yellow) fusion signals. FISH patterns were determined by analyzing 100 non-overlapping nuclei. Two representative pairs of FL-MSC/malignant B cells are shown.
Figure S3. Expression of CDKN2A by MSC
RNA was extracted from HD-MSC (n=6) and FL-MSC (n=10) at the end of P1 and CDKN2A expression was determined by RQ-PCR experiments as described¹. Each sample was normalized to 18S, and Saos-2, a human osteosarcoma cell line expressing a high level of CDKN2A due to a homozygous Rb deletion, was used as a standard to calculate the relative CDKN2A expression in MSC.

Figure S4. Subcellular repartition and physiopathological functions of proteins encoded by genes of the FL-MSC signature.

The 408-PS list defining the FL-MSC signature was analyzed by Ingenuity Pathway Analysis software. (a) Subcellular localization of the gene products. Genes coding for membrane or extracellular proteins were subjected to hierarchical clustering using Cluster and TreeView softwares. The relative level of gene expression is depicted according to the shown color scale. (b) Top-3 physiopathological functions highlighted by Ingenuity Pathway.

<table>
<thead>
<tr>
<th>Physiopathological System Development and Function</th>
<th>No of molecules</th>
<th>P values (min-max)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hematological System Development and Function</td>
<td>31</td>
<td>9.95E-05 - 3.26E-02</td>
</tr>
<tr>
<td>Hematopoiesis</td>
<td>22</td>
<td>9.95E-05 - 2.96E-02</td>
</tr>
<tr>
<td>Immune Cell Trafficking</td>
<td>13</td>
<td>4.93E-04 - 3.26E-02</td>
</tr>
</tbody>
</table>
Figure S5. Identification of the genes found in both FL-MSC signature and TNF/LT signature. A Venn diagram revealed the 109 probesets which overlapped between TNF/LT signature and FL-MSC signature including 101 genes which are coordinately up or downregulated in the two signatures.
Figure S6. Inhibition of LPS-induced TNF production in macrophages by MSC
Monocytes were cultured during 7 days with or without HD-MSC, or FL-MSC from grade 1, grade 2, or grade 3a FL patients before stimulation or not by LPS during 18 hours. TNF concentration was then measured in cell supernatants by ELISA. Results are expressed as the percentage of TNF production by LPS-stimulated macrophages alone, arbitrary assigned to 100%.
**Figure S7. Role of TNF in the malignant B cell-driven CCL2 production in HD-MSC**

CCL2 was quantified by ELISA in the supernatants of HD-MSC cocultured or not (CTRL) with RL or VAL for 3 days. When indicated, B-cell lines were separated from HD-MSC by Transwell chambers with 0.4-μm pore filters in the presence or not of recombinant TNFRI-Fc chimera (R&D Systems, 200 ng/mL).