GLRX5 deficiency causes sideroblastic anemia by specifically impairing heme biosynthesis and depleting cytosolic iron in erythroblasts

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Supplemental data

Supplemental Figure 1

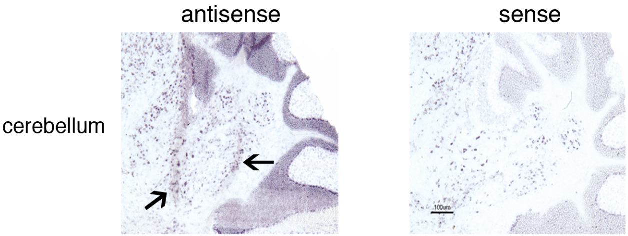
In situ hybridization of GLRX5 in adult mouse tissues reveals high expression in cerebellum. The hybridization by anti-sense probe indicates the expression of GLRX5 *in vivo*, whereas hybridization by sense probe is negative control. It shows a higher magnification of the cerebellum, where arrows point to deep cerebellar nuclei.

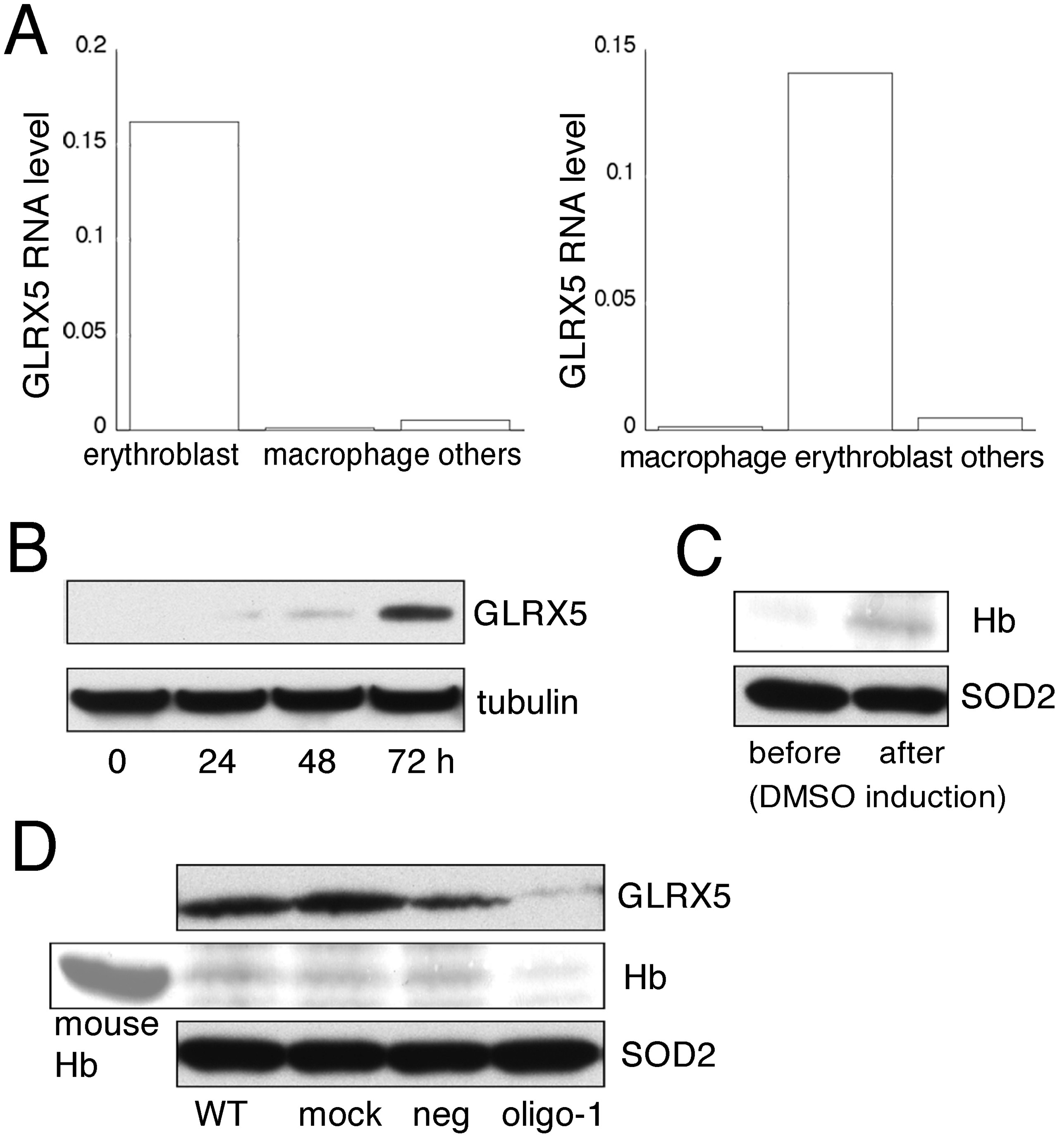
Supplemental Figure 2

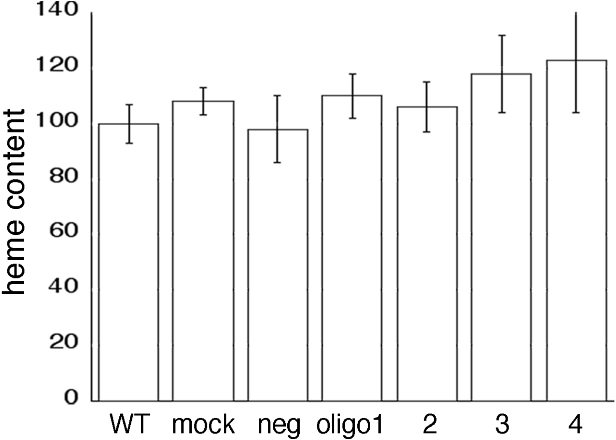
GLRX5 has an additional role in erythropoiesis. (**A**) GLRX5 is highly expressed in erythroblast cells in mouse bone marrow. Mouse bone marrow cells were sorted using Ter119 (for erythroid) and CD11b (for macrophage) coated beads (ref. 50). Ferroportin transcript levels were quantified by qRT-PCR. The order of cell sorting did not affect the results, comparing the two panels. (**B**) GLRX5 protein levels were upregulated (as shown by western blot) during DMSO-induced differentiation of MEL cells. Samples were collected at 24-72 hours post the induction by 2% DMSO. (**C**) Hemoglobin level was increased (as shown by Ponceau S staining) after DMSO induction. SOD2 was used as loading control in the western blot. (**D**) The GLRX5 deficiency could potentially impair the formation of hemoglobin. The GLRX5 oligo-1, which is complementary to the mouse sequence, was used to knockdown mouse GLRX5 in MEL cells. WT, mock and neg were used as negative RNAi controls (as described in Fig. 2 and Fig. 4). All cells were subsequently induced by 2% DMSO three days post-siRNA treatment. Hemoglobin (Hb) level was decreased in the GLRX5 deficient cell that was treated by oligo-1. A hemoglobin protein purified from mouse blood was used as positive control. SOD2 was loading control for western blot.

Supplemental Figure 3

Heme levels were not significantly changed in GLRX5 siRNA treated HeLa S3 cells. Oligos and controls were as described in Fig. 2.


antisense
sense
cerebellum
100um


A
GLRX5 RNA level
0.2
0.15
0.1
0.05
0
erythroblast
macrophage
others
GLRX5 RNA level
0.15
0.1
0.05
0
macrophage
erythroblast
others
B
GLRX5
tubulin
0
24
48
72 h
C
Hb
SOD2
before
after
(DMSO induction)
D
GLRX5
Hb
SOD2
mouse Hb
WT
mock
neg
oligo-1


heme content
140
120
100
80
60
40
20
0
WT
mock
neg
oligo1
2
3
4

Supplemental Table 1

Microarray analysis of transcriptome derived from the GLRX5 deficient patient fibroblasts revealed that 2017 genes in the patient cells were significantly altered. Total mRNA was isolated with Trizol reagent (Invitrogen). RNA quality was assessed using the Agilent Bioanalyzer. RNA samples were processed and hybridized on GeneChip Human Genome U133 Plus 2.0 arrays (Affymetrix). The array was operated and data analyzed by the Genomics Core Laboratory at NIDDK. A human fibroblast cell line (ATCC) was used as control. Results represent averages of three replicates. 2-fold change of gene expression was cutoff. P-values less than 0.05 were considered significant. The data were presented in an order from the most decreased gene to the most increased gene.

Primer use	Oligonucleotide	5’-3’ sequence
RT-PCR (mouse)	mmGRX5-F	ACTATGCGGCCTACAACGTGCTG
	mmGRX5-R	CAAACTCGCCGTTGAGGTACACTTG
	mmACTIN-F	CTGAGAGGGAAATCGTGCGTGAC
	mmACTIN-R	GCTCGTTGCCAATAGTGATGACCTG
RT-PCR (human)	GRX5-F	CAGTTGGACGCGCTGGTGAAGAAG
	GRX5-R	CAGCACGTTGTAGGCCGCGTAATC
	ACTIN-F	GCCATGTACGTTGCTATCCAGGCTG
	ACTIN-R	CGTAGATGGGCACAGTGTGGGTGAC
	DMT1-F	CACCATGACAGGAACCTATTCTGGC
	DMT1-R	AACCACTCGGGCAAAGCGTGAC
	Dcytb-F	ACAGTACATTCCCGCCAGAAGGTG
	Dcytb-R	GGCTCCTTAGGACGTTTCCATTGC
	FTMT-F	GAACAGGACGACTGGGAAAGCG
	FTMT-R	AGAGCGTGCAATTCCAGCAACG
	HO1-F	CCGCATGAACTCCCTGGAGATG
	HO1-R	CTGGATGTTGAGCAGGAACGCAG
	FTL-F	GCGATGATGTGGCTCTGGAAGG
	FTL-R	TGCATCTTCAGGAGACGCTCGTAG
	FPN1-F	GAGCCTACTTGTGCCTCCCAGATG
	FPN1-R	TGCAGTCAAAGCCCAGGACAGTC
Clone in pET28	mGRX5-F	ATATGAATTCGCGGGCTCGGGCGCGG
	mGRX5-R	TTGTCTCGAGTCACTTGGAGTCTTGGTC
Site-directed mutagenesis	K59Q-sense	GTGGTCTTCCTCCAGGGGACGCCGG
	K59Q-antisense	CCGGCGTCCCCTGGAGGAAGACCAC
	C67S-sense	GAGCAGCCCCAGAGCGGCTTCAGCA
	C67S-antisense	TGCTGAAGCCGCTCTGGGGCTGCTC
	T108V-sense	ACTATTCCAACTGGCCCGTCATCCCGCAAGTGTACC
	T108V-antisense	GGTACACTTGCGGGATGACGGGCCAGTTGGAATAGT
	D123N-sense	CGAGTTTGTAGGGGGCTGTAACATTCTTCTGCAGA
	D123N-antisense	TCTGCAGAAGAATGTTACAGCCCCCTACAAACTCG

Supplemental Table 2. Sequences of primers used for quantitative RT-PCR, cloning mature sequence of human GRX5 into pET28 vector, and site-directed mutagenesis.

1. Probeset	Gene Title	Gene Sym	p-value(P vs. WT)
1562736_a	LIM homeobox 9	LHX9	5.54E-06
224588_at	X (inactive)-specific transcript (non-protei	XIST	6.16E-07
227671_at	X (inactive)-specific transcript (non-protei	XIST	6.88E-07
214218_s_	X (inactive)-specific transcript (non-protei	XIST	8.49E-07
230147_at	coagulation factor II (thrombin) receptor-li	F2RL2	1.98E-06
214587_at	collagen, type VIII, alpha 1	COL8A1	2.60E-06
221728_x_	X (inactive)-specific transcript (non-protei	XIST	7.03E-05
226237_at	MRNA full length insert cDNA clone EUR	---	1.64E-05
205523_at	hyaluronan and proteoglycan link protein	HAPLN1	0.000257152
212314_at	KIAA0746 protein /// serine incorporator 2	KIAA0746 /	3.65E-08
230204_at	Transcribed locus	---	0.000177558
224590_at	X (inactive)-specific transcript (non-protei	XIST	8.08E-06
205524_s_	hyaluronan and proteoglycan link protein	HAPLN1	0.000297437
209189_at	v-fos FBJ murine osteosarcoma viral onc	FOS	4.21E-07
1565406_a	LIM homeobox 9	LHX9	1.79E-06
206326_at	gastrin-releasing peptide	GRP	7.28E-05
203881_s_	dystrophin (muscular dystrophy, Duchenn	DMD	5.60E-05
210869_s_	melanoma cell adhesion molecule	MCAM	0.00034992
230895_at	Transcribed locus	---	0.000171629
201843_s_	EGF-containing fibulin-like extracellular m	EFEMP1	4.77E-06
225275_at	EGF-like repeats and discoidin I-like dom	EDIL3	0.0248466
226244_at	C-type lectin domain family 14, member A	CLEC14A	0.00012404
209087_x_	melanoma cell adhesion molecule	MCAM	0.000341686
1555778_a	periostin, osteoblast specific factor	POSTN	3.75E-05
212311_at	KIAA0746 protein /// serine incorporator 2	KIAA0746 /	1.42E-05
209875_s_	secreted phosphoprotein 1 (osteopontin,	SPP1	5.35E-05
236044_at	phosphatidic acid phosphatase type 2 do	PPAPDC1	0.000273468
201842_s_	EGF-containing fibulin-like extracellular m	EFEMP1	1.41E-05
228407_at	signal peptide, CUB domain, EGF-like 3	SCUBE3	2.40E-05
227705_at	transcription elongation factor A (SII)-like	TCEAL7	4.27E-06
236029_at	FAT tumor suppressor homolog 3 (Drosop	FAT3	6.02E-05
239218_at	phosphodiesterase 1C, calmodulin-depen	PDE1C	0.00180773
203184_at	fibrillin 2 (congenital contractural arachno	FBN2	6.74E-05
210809_s_	periostin, osteoblast specific factor	POSTN	3.77E-06
219523_s_	odz, odd Oz/ten-m homolog 3 (Drosophila	ODZ3	0.000276593
204529_s_	thymocyte selection-associated high mobi	TOX	1.03E-06
221933_at	neuroligin 4, X-linked	NLGN4X	5.70E-05
204931_at	transcription factor 21	TCF21	0.00045285
236344_at	phosphodiesterase 1C, calmodulin-depen	PDE1C	0.00136532
204653_at	transcription factor AP-2 alpha (activating	TFAP2A	0.00226603
211340_s_	melanoma cell adhesion molecule	MCAM	0.000396363
242488_at	CDNA FLJ38396 fis, clone FEBRA20079	---	4.57E-05
224559_at	metastasis associated lung adenocarcino	MALAT1	0.00168468
205381_at	leucine rich repeat containing 17	LRRC17	1.25E-05
215717_s_	fibrillin 2 (congenital contractural arachno	FBN2	0.0010191
207379_at	EGF-like repeats and discoidin I-like dom	EDIL3	0.000440456
226789_at	embigin homolog (mouse) pseudogene	LOC64712	0.00047661
201195_s_	solute carrier family 7 (cationic amino acid	SLC7A5	0.000186641
1558643_s	EGF-like repeats and discoidin I-like dom	EDIL3	0.0011071
242138_at	distal-less homeobox 1	DLX1	0.000605682
223062_s_	phosphoserine aminotransferase 1	PSAT1	0.000355409
203989_x_	coagulation factor II (thrombin) receptor	F2R	8.27E-05

1552367_a	scinderin	SCIN	0.000133081
206481_s_	LIM domain binding 2	LDB2	7.49E-06
236734_at	SLIT and NTRK-like family, member 1	SLITRK1	0.000305948
228640_at	protocadherin 7	PCDH7	0.00117564
201650_at	keratin 19	KRT19	5.28E-05
213222_at	phospholipase C, beta 1 (phosphoinositid	PLCB1	2.04E-05
220892_s_	phosphoserine aminotransferase 1	PSAT1	0.000104878
211981_at	collagen, type IV, alpha 1	COL4A1	0.00158765
209763_at	chordin-like 1	CHRDL1	2.91E-06
229529_at	transcription factor 21	TCF21	0.000779233
207147_at	distal-less homeobox 2	DLX2	0.000810542
224589_at	X (inactive)-specific transcript (non-protei	XIST	0.000110039
225548_at	shroom family member 3	SHROOM3	0.000120568
1552365_a	scinderin	SCIN	0.000352057
206825_at	oxytocin receptor	OXTR	0.00642599
235171_at	Transcribed locus	---	5.18E-05
205047_s_	asparagine synthetase	ASNS	0.000305796
1559277_a	hypothetical protein FLJ35700	FLJ35700	0.00172746
209652_s_	placental growth factor	PGF	0.000407512
205475_at	scrapie responsive protein 1	SCRG1	3.22E-05
201694_s_	early growth response 1	EGR1	0.000471091
235591_at	somatostatin receptor 1	SSTR1	0.000692229
211276_at	transcription elongation factor A (SII)-like	TCEAL2	0.00051435
201596_x_	keratin 18	KRT18	0.00174456
237206_at	myocardin	MYOCD	0.00136373
223614_at	chromosome 8 open reading frame 57	C8orf57	6.60E-06
236088_at	netrin G1	NTNG1	0.000239743
203440_at	cadherin 2, type 1, N-cadherin (neuronal)	CDH2	0.000190002
227498_at	CDNA FLJ11723 fis, clone HEMBA10053	---	0.000691144
221467_at	melanocortin 4 receptor	MC4R	0.000555748
1553972_a	cystathionine-beta-synthase	CBS	0.000160925
244623_at	potassium voltage-gated channel, KQT-lik	KCNQ5	0.000575537
228737_at	TOX high mobility group box family memb	TOX2	6.44E-05
229963_at	BEX family member 5	BEX5	2.21E-05
227889_at	lysophosphatidylcholine acyltransferase 2	LPCAT2	0.00247943
229339_at	Transcribed locus	---	0.00147676
210004_at	oxidized low density lipoprotein (lectin-like	OLR1	0.000531613
227404_s_	Early growth response 1	EGR1	0.00271994
228400_at	shroom family member 3	SHROOM3	0.000142977
217901_at	Desmoglein 2	DSG2	0.00406452
1552701_a	caspase-1 dominant-negative inhibitor ps	COP1	0.0036708
201693_s_	early growth response 1	EGR1	0.000510276
205990_s_	wingless-type MMTV integration site famil	WNT5A	0.00379476
203441_s_	cadherin 2, type 1, N-cadherin (neuronal)	CDH2	0.00032693
228582_x_	Metastasis associated lung adenocarcino	MALAT1	0.0068474
211980_at	collagen, type IV, alpha 1	COL4A1	0.00169676
205893_at	neuroligin 1	NLGN1	0.00144391
209631_s_	G protein-coupled receptor 37 (endothelin	GPR37	2.54E-05
237248_at	phosphodiesterase 11A	PDE11A	5.86E-06
222668_at	potassium channel tetramerisation domai	KCTD15	0.00109329
206456_at	gamma-aminobutyric acid (GABA) A rece	GABRA5	0.0129774
206918_s_	copine I	CPNE1	2.24E-06
210794_s_	maternally expressed 3	MEG3	0.00067983

218678_at	nestin	NES	4.33E-05
216379_x_	CD24 molecule	CD24	0.004601
215175_at	pecanex homolog (Drosophila)	PCNX	0.000386674
202834_at	angiotensinogen (serpin peptidase inhibit	AGT	0.000371352
224841_x_	growth arrest-specific 5	GAS5	2.69E-07
209086_x_	melanoma cell adhesion molecule	MCAM	0.000613146
266_s_at	CD24 molecule	CD24	0.00661964
224741_x_	growth arrest-specific 5	GAS5	5.02E-08
227198_at	AF4/FMR2 family, member 3	AFF3	0.00081379
238617_at	CDNA FLJ38181 fis, clone FCBBF100012	---	0.000389
1560253_a	LIM homeobox 9	LHX9	0.000198589
206018_at	forkhead box G1	FOXG1	0.00248896
202363_at	sparc/osteonectin, cwcv and kazal-like do	SPOCK1	9.34E-05
208502_s_	paired-like homeodomain 1	PITX1	3.67E-05
200965_s_	actin binding LIM protein 1	ABLIM1	9.16E-05
211538_s_	heat shock 70kDa protein 2	HSPA2	0.00634093
209771_x_	CD24 molecule	CD24	0.00258252
205515_at	protease, serine, 12 (neurotrypsin, motops	PRSS12	7.77E-05
227006_at	protein phosphatase 1, regulatory (inhibit	PPP1R14A	0.0101482
1556583_a	solute carrier family 8 (sodium/calcium ex	SLC8A1	0.0112289
242100_at	chondroitin sulfate synthase 3	CHSY3	0.000294289
229748_x_	similar to hypothetical protein MGC27019	LOC10013	0.00144537
205132_at	actin, alpha, cardiac muscle 1	ACTC1	0.0056546
203638_s_	fibroblast growth factor receptor 2 (bacteri	FGFR2	0.00385216
212344_at	sulfatase 1	SULF1	0.00144115
216869_at	phosphodiesterase 1C, calmodulin-depen	PDE1C	3.18E-05
241879_at	Transcribed locus	---	0.00461726
227330_x_	similar to hypothetical protein MGC27019	LOC10013	0.000523107
232355_at	CDNA FLJ10247 fis, clone HEMBB10007	---	0.00541505
1553705_a	cholinergic receptor, muscarinic 3	CHRM3	0.0001078
204337_at	regulator of G-protein signaling 4	RGS4	0.00204765
217678_at	solute carrier family 7, (cationic amino aci	SLC7A11	0.000240024
205594_at	zinc finger protein 652	ZNF652	8.86E-05
230388_s_	hypothetical protein LOC644246	LOC64424	7.99E-05
231867_at	odz, odd Oz/ten-m homolog 2 (Drosophila	ODZ2	3.68E-06
231227_at	Transcribed locus	---	0.00140694
208442_s_	ataxia telangiectasia mutated	ATM	0.000707613
209373_at	mal, T-cell differentiation protein-like	MALL	0.000281652
226279_at	protease, serine, 23	PRSS23	9.19E-05
213425_at	wingless-type MMTV integration site famil	WNT5A	0.0122525
227870_at	neighbor of Punc E11	NOPE	0.000670815
228121_at	CDNA FLJ11812 fis, clone HEMBA10063	---	0.000237289
202997_s_	lysyl oxidase-like 2 /// ectonucleoside triph	ENTPD4 ///	0.00287869
212816_s_	cystathionine-beta-synthase	CBS	0.000744778
1569603_a	Transcribed locus	---	0.00337008
209921_at	solute carrier family 7, (cationic amino aci	SLC7A11	0.000334379
242856_at	Transcribed locus, strongly similar to XP_	---	0.00768573
239336_at	Thrombospondin 1	THBS1	0.00458493
235077_at	maternally expressed 3	MEG3	0.0034597
235696_at	CDNA clone IMAGE:4837650	---	2.02E-05
1559633_a	cholinergic receptor, muscarinic 3	CHRM3	0.000824581
212353_at	sulfatase 1	SULF1	0.00315909
238931_at	methyltransferase 10 domain containing	METT10D	0.000801705

228740_at	CDNA clone IMAGE:5276765	---	0.00190399
214803_at	Transcribed locus, weakly similar to NP_6	---	0.00487012
208241_at	neuregulin 1	NRG1	0.000304664
213802_at	Transcribed locus, strongly similar to NP_	---	3.17E-05
206070_s_	EPH receptor A3	EPHA3	0.000271521
214043_at	protein tyrosine phosphatase, receptor typ	PTPRD	0.00167825
219937_at	thyrotropin-releasing hormone degrading	TRHDE	0.00122363
201859_at	serglycin	SRGN	0.00539589
201858_s_	serglycin	SRGN	0.00712456
226558_at	similar to CG32820-PA, isoform A	LOC65307	0.000385192
208650_s_	CD24 molecule	CD24	0.0030149
223315_at	netrin 4	NTN4	0.00311429
231798_at	noggin	NOG	0.0463918
239598_s_	lysophosphatidylcholine acyltransferase 2	LPCAT2	9.99E-05
214156_at	myosin VIIA and Rab interacting protein	MYRIP	0.000116365
223541_at	hyaluronan synthase 3	HAS3	0.00146167
220115_s_	cadherin 10, type 2 (T2-cadherin)	CDH10	0.000691471
210372_s_	tumor protein D52-like 1	TPD52L1	0.00121533
241872_at	Transcribed locus	---	0.0026217
223672_at	SH3-domain GRB2-like (endophilin) intera	SGIP1	0.00115015
238013_at	pleckstrin homology domain containing, fa	PLEKHA2	0.00513899
202998_s_	lysyl oxidase-like 2 /// ectonucleoside triph	ENTPD4 ///	0.000989267
238133_at	Transcribed locus	---	0.000361469
219073_s_	oxysterol binding protein-like 10	OSBPL10	0.000215729
241473_at	Transcribed locus	---	0.00109065
201261_x_	biglycan	BGN	5.75E-05
209529_at	phosphatidic acid phosphatase type 2C	PPAP2C	3.20E-05
227618_at	CDNA FLJ30378 fis, clone BRACE20079	---	0.000132163
240083_at	Transcribed locus	---	0.0041749
218380_at	NLR family, pyrin domain containing 1	NLRP1	0.000695939
226614_s_	chromosome 8 open reading frame 13	C8orf13	0.00279062
213905_x_	biglycan	BGN	0.00142588
239624_at	Transcribed locus	---	0.000121514
216268_s_	jagged 1 (Alagille syndrome)	JAG1	2.25E-05
206382_s_	brain-derived neurotrophic factor	BDNF	0.0106648
202016_at	mesoderm specific transcript homolog (m	MEST	0.021014
211966_at	collagen, type IV, alpha 2	COL4A2	0.00429517
204464_s_	endothelin receptor type A	EDNRA	6.18E-05
243065_at	Transcribed locus	---	0.000545646
228214_at	Transcribed locus	---	0.00375323
205715_at	bone marrow stromal cell antigen 1	BST1	0.000320887
239367_at	brain-derived neurotrophic factor	BDNF	0.00853212
203889_at	secretogranin V (7B2 protein)	SCG5	0.000649098
227828_s_	transmembrane protein 166	TMEM166	0.00299674
242447_at	hypothetical gene supported by AK09145	LOC28538	0.00263082
206795_at	coagulation factor II (thrombin) receptor-li	F2RL2	0.000681655
207012_at	matrix metallopeptidase 16 (membrane-in	MMP16	0.000130258
213496_at	plasticity related gene 1	LPPR4	8.26E-05
204338_s_	regulator of G-protein signaling 4	RGS4	0.00471129
231361_at	Neuroligin 1	NLGN1	0.000311745
207303_at	phosphodiesterase 1C, calmodulin-depen	PDE1C	0.000198083
212354_at	sulfatase 1	SULF1	0.00219426
238512_at	Transcribed locus	---	0.0004284

211964_at	collagen, type IV, alpha 2	COL4A2	0.00191885
239591_at	Transcribed locus	---	0.000147757
230700_at	reticulon 4 receptor-like 1	RTN4RL1	0.000356083
220389_at	coiled-coil domain containing 81	CCDC81	0.00125261
231175_at	chromosome 6 open reading frame 65	C6orf65	0.00025166
225864_at	family with sequence similarity 84, membe	FAM84B	0.0103338
1569629_x	similar to Serine/threonine-protein kinase	LOC38990	0.000757351
1568878_a	Transcribed locus, strongly similar to XP_	---	0.00187283
240382_at	hypothetical protein LOC100131914	LOC10013	0.000384757
242691_at	CDNA FLJ41369 fis, clone BRCAN20061	---	0.0125694
237423_at	R-spondin family, member 4	RSPO4	0.000734538
231592_at	X (inactive)-specific transcript, antisense	TSIX	0.000506402
1555978_s	CDNA FLJ33153 fis, clone UTERU20003	---	0.00711423
209772_s_	CD24 molecule	CD24	0.00327599
201107_s_	thrombospondin 1	THBS1	0.00474168
203325_s_	collagen, type V, alpha 1	COL5A1	0.000276987
236675_at	replication protein A1, 70kDa	RPA1	0.000221684
212488_at	collagen, type V, alpha 1	COL5A1	0.00072081
226517_at	branched chain aminotransferase 1, cytos	BCAT1	0.000534745
230290_at	signal peptide, CUB domain, EGF-like 3	SCUBE3	8.91E-05
203499_at	EPH receptor A2	EPHA2	0.00267747
212611_at	deltex 4 homolog (Drosophila)	DTX4	0.000186433
209990_s_	gamma-aminobutyric acid (GABA) B rece	GABBR2	0.000210418
212489_at	collagen, type V, alpha 1	COL5A1	0.000681789
222173_s_	TBC1 domain family, member 2	TBC1D2	2.32E-05
214596_at	cholinergic receptor, muscarinic 3	CHRM3	0.000451656
1555673_a	keratin associated protein 2-1 /// keratin a	KAP2.1B //	0.0169396
234994_at	transmembrane protein 200A	TMEM200	1.90E-05
204114_at	nidogen 2 (osteonidogen)	NID2	0.00111923
219371_s_	Kruppel-like factor 2 (lung)	KLF2	0.00404703
236224_at	Ras-like without CAAX 1	RIT1	0.000673507
243688_at	hypothetical protein LOC285431	LOC28543	5.03E-05
226211_at	maternally expressed 3	MEG3	0.0125115
229557_at	maternally expressed 3	MEG3	0.0125719
1568868_a	cytochrome P450, family 27, subfamily C,	CYP27C1	0.0031025
235442_at	chromosome X open reading frame 56	CXorf56	0.000768091
209871_s_	amyloid beta (A4) precursor protein-bindin	APBA2	6.70E-05
218660_at	dysferlin, limb girdle muscular dystrophy 2	DYSF	0.00032045
206197_at	non-metastatic cells 5, protein expressed	NME5	0.00112545
210858_x_	ataxia telangiectasia mutated	ATM	0.0020914
228949_at	G protein-coupled receptor 177	GPR177	9.43E-05
236300_at	CDNA FLJ37884 fis, clone BRSTN20124	---	0.000684478
205581_s_	nitric oxide synthase 3 (endothelial cell)	NOS3	0.000784329
237465_at	ubiquitin specific peptidase 53	USP53	0.000393369
209098_s_	jagged 1 (Alagille syndrome)	JAG1	5.87E-05
224763_at	Ribosomal protein L37	RPL37	0.000264538
203217_s_	ST3 beta-galactoside alpha-2,3-sialyltrans	ST3GAL5	0.00104915
226733_at	6-phosphofructo-2-kinase/fructose-2,6-bip	PFKFB2	2.07E-05
223435_s_	protocadherin alpha 9 /// protocadherin al	PCDHA1 //	0.00121022
230214_at	murine retrovirus integration site 1 homol	MRVI1	3.76E-05
204517_at	peptidylprolyl isomerase C (cyclophilin C)	PPIC	0.00204242
235309_at	Ribosomal protein S15a	RPS15A	0.000417974
239297_at	chromosome 8 open reading frame 79	C8orf79	0.000871263

228537_at	GLI-Kruppel family member GLI2	GLI2	0.000964301
209099_x_	jagged 1 (Alagille syndrome)	JAG1	2.76E-06
208651_x_	CD24 molecule	CD24	0.00918148
219270_at	ChaC, cation transport regulator homolog	CHAC1	0.0102706
228221_at	solute carrier family 44, member 3	SLC44A3	2.18E-05
212732_at	maternally expressed 3	MEG3	0.0357738
209016_s_	keratin 7	KRT7	0.0209149
212256_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT10	0.00143238
227929_at	CDNA clone IMAGE:5277945	---	0.000541212
232861_at	pyruvate dehydrogenase phosphatase iso	PDP2	0.00250399
228645_at	small nucleolar RNA host gene (non-prote	SNHG9	0.000615775
228360_at	hypothetical protein LOC130576	LOC13057	0.0008511
218145_at	tribbles homolog 3 (Drosophila)	TRIB3	0.000544417
221152_at	collagen, type VIII, alpha 1	COL8A1	8.86E-05
222664_at	potassium channel tetramerisation domai	KCTD15	0.00119878
235367_at	myopalladin	MYPN	0.001998
200606_at	desmoplakin	DSP	0.000149349
203381_s_	apolipoprotein E	APOE	0.000160038
227497_at	CDNA FLJ11723 fis, clone HEMBA10053	---	0.000364478
231202_at	Aldehyde dehydrogenase 1 family, memb	ALDH1L2	0.000822907
201761_at	methylenetetrahydrofolate dehydrogenas	MTHFD2	4.32E-06
231183_s_	Jagged 1 (Alagille syndrome)	JAG1	0.00014303
225240_s_	musashi homolog 2 (Drosophila)	MSI2	0.00176813
208078_s_	SNF1-like kinase	SNF1LK	0.00232061
227875_at	kelch-like 13 (Drosophila)	KLHL13	0.00045221
205624_at	carboxypeptidase A3 (mast cell)	CPA3	0.000563859
230498_at	melanin-concentrating hormone receptor	MCHR1	0.000818801
226210_s_	maternally expressed 3	MEG3	0.014719
213524_s_	G0/G1switch 2	G0S2	0.00282556
202254_at	Signal-induced proliferation-associated 1	SIPA1L1	0.00147772
222315_at	Transcribed locus	---	0.00285927
203608_at	aldehyde dehydrogenase 5 family, memb	ALDH5A1	2.65E-05
219700_at	plexin domain containing 1	PLXDC1	0.00144845
209765_at	ADAM metallopeptidase domain 19 (meltr	ADAM19	0.00724169
228238_at	growth arrest-specific 5	GAS5	0.00182189
228632_at	CDNA FLJ37243 fis, clone BRAMY20043	---	0.00493527
1567575_a	Trapped 3' terminal exon, clone C2C4	---	0.0360154
216933_x_	adenomatous polyposis coli	APC	0.00456111
232535_at	MRNA; cDNA DKFZp434L201 (from clone	---	0.000141103
202458_at	protease, serine, 23	PRSS23	1.55E-05
219791_s_	Nbla00301	NBLA0030	0.000304044
212099_at	ras homolog gene family, member B	RHOB	0.00533292
230560_at	syntaxin binding protein 6 (amisyn)	STXBP6	0.0115352
206595_at	cystatin E/M	CST6	0.0142301
202311_s_	collagen, type I, alpha 1	COL1A1	0.00274769
206373_at	Zic family member 1 (odd-paired homolog	ZIC1	0.00193157
1555788_a	tribbles homolog 3 (Drosophila)	TRIB3	0.000104561
230611_at	synaptophysin-like 2	SYPL2	0.00300849
203786_s_	tumor protein D52-like 1	TPD52L1	0.00390304
207528_s_	solute carrier family 7, (cationic amino aci	SLC7A11	0.000629414
1555976_s	CDNA FLJ33153 fis, clone UTERU20003	---	0.00873877
219694_at	family with sequence similarity 105, mem	FAM105A	6.80E-05
207419_s_	ras-related C3 botulinum toxin substrate 2	RAC2	0.0115297

238129_s_	---	---	0.00333693
241902_at	mohawk homeobox	MKX	8.11E-06
236636_at	Transcribed locus	---	0.00943119
211005_at	linker for activation of T cells /// spinster h	LAT /// SPN	3.40E-05
236123_at	Suppression of tumorigenicity 7 like	ST7L	0.00145662
242239_at	CDNA clone IMAGE:5314281	---	0.00039481
213506_at	coagulation factor II (thrombin) receptor-li	F2RL1	0.00144501
226415_at	KIAA1576 protein	KIAA1576	0.0026648
205439_at	glutathione S-transferase theta 2	GSTT2	0.00158021
1569311_a	Transcribed locus, weakly similar to XP_0	---	0.000300731
203159_at	glutaminase	GLS	0.00214915
225285_at	branched chain aminotransferase 1, cytos	BCAT1	1.09E-05
209082_s_	collagen, type XVIII, alpha 1	COL18A1	0.00894283
1561615_s	solute carrier family 8 (sodium/calcium ex	SLC8A1	0.00386922
229566_at	similar to WDNM1-like protein	LOC64563	2.37E-05
209287_s_	CDC42 effector protein (Rho GTPase bin	CDC42EP3	0.000812881
204463_s_	endothelin receptor type A	EDNRA	0.000191836
228297_at	Transcribed locus	---	0.00730662
213030_s_	plexin A2	PLXNA2	0.000355889
205493_s_	dihydropyrimidinase-like 4	DPYSL4	0.00923372
204339_s_	regulator of G-protein signaling 4	RGS4	0.00231032
213603_s_	ras-related C3 botulinum toxin substrate 2	RAC2	0.00700589
224224_s_	phosphodiesterase 11A	PDE11A	0.00041178
213135_at	T-cell lymphoma invasion and metastasis	TIAM1	0.00781281
215483_at	A kinase (PRKA) anchor protein (yotiao) 9	AKAP9	0.00456299
209120_at	nuclear receptor subfamily 2, group F, me	NR2F2	0.00839252
218729_at	latexin	LXN	0.00022474
223629_at	protocadherin beta 5	PCDHB5	0.000110326
244726_at	Transcribed locus	---	0.000453372
206924_at	interleukin 11	IL11	0.0119882
225168_at	FERM domain containing 4A	FRMD4A	0.00720211
224724_at	sulfatase 2	SULF2	0.00322664
213519_s_	laminin, alpha 2 (merosin, congenital mus	LAMA2	9.35E-05
240402_at	kin of IRRE like 3 (Drosophila)	KIRREL3	0.0167378
225163_at	FERM domain containing 4A	FRMD4A	0.00428515
241752_at	solute carrier family 8 (sodium/calcium ex	SLC8A1	0.0127006
239043_at	zinc finger protein 404	ZNF404	0.00186648
1565743_a	CDNA FLJ37648 fis, clone BRHIP200053	---	0.00247766
214293_at	Septin 11	11-Sep	0.000595458
209710_at	GATA binding protein 2	GATA2	5.31E-05
203397_s_	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT3	0.00820309
214452_at	branched chain aminotransferase 1, cytos	BCAT1	0.00252425
220296_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT10	0.00100194
209031_at	cell adhesion molecule 1	CADM1	0.00456704
228049_x_	Transcribed locus, strongly similar to XP_	---	0.0130221
244503_at	Transcribed locus	---	0.0389328
1555977_a	CDNA FLJ33153 fis, clone UTERU20003	---	0.00124303
206638_at	5-hydroxytryptamine (serotonin) receptor	HTR2B	0.0183522
206343_s_	neuregulin 1	NRG1	0.00941007
236738_at	Similar to LOC166075	LOC40109	0.00123422
203811_s_	DnaJ (Hsp40) homolog, subfamily B, mem	DNAJB4	0.00308668
226591_at	CDNA FLJ33569 fis, clone BRAMY20103	---	0.00712602
232231_at	runt-related transcription factor 2	RUNX2	0.000155609

209870_s_	amyloid beta (A4) precursor protein-bindin	APBA2	3.04E-05
222272_x_	scinderin	SCIN	0.000424098
219260_s_	chromosome 17 open reading frame 81	C17orf81	0.00162739
223578_x_	metastasis associated lung adenocarcinor	MALAT1	0.0246916
1558430_a	CDNA FLJ36648 fis, clone UTERU10001	---	0.000648866
225136_at	pleckstrin homology domain containing, fa	PLEKHA2	0.00821285
201064_s_	poly(A) binding protein, cytoplasmic 4 (ind	PABPC4	0.00279775
211071_s_	myeloid/lymphoid or mixed-lineage leuken	MLLT11	0.000182562
216147_at	MRNA; cDNA DKFZp761L23121 (from clo	---	0.0283949
204364_s_	receptor accessory protein 1	REEP1	3.48E-05
211679_x_	gamma-aminobutyric acid (GABA) B recep	GABBR2	0.000211993
227798_at	SMAD family member 1	SMAD1	0.00109891
230071_at	septin 11	11-Sep	0.0152236
203382_s_	apolipoprotein E	APOE	0.00134314
211042_x_	melanoma cell adhesion molecule	MCAM	0.000247871
210220_at	frizzled homolog 2 (Drosophila)	FZD2	6.33E-05
222931_s_	threonine synthase-like 1 (S. cerevisiae)	THNSL1	0.000583554
230449_x_	Transcribed locus	---	0.00110346
219179_at	dapper, antagonist of beta-catenin, homol	DACT1	0.00241645
223627_at	mex-3 homolog B (C. elegans)	MEX3B	0.00258605
202743_at	phosphoinositide-3-kinase, regulatory sub	PIK3R3	0.00561588
224550_s_	murine retrovirus integration site 1 homolo	MRVI1	0.000954119
1564339_a	cholinergic receptor, muscarinic 3	CHRM3	0.00039689
220147_s_	family with sequence similarity 60, membe	FAM60A	0.00133698
223795_at	tetraspanin 10	TSPAN10	0.00349036
227666_at	doublecortin-like kinase 2	DCLK2	0.00428373
219090_at	solute carrier family 24 (sodium/potassium	SLC24A3	0.00376293
208476_s_	FERM domain containing 4A	FRMD4A	0.0125492
1557197_a	lectin, galactoside-binding, soluble, 3	LGALS3	0.0134151
220786_s_	solute carrier family 38, member 4	SLC38A4	0.000166422
229843_at	Family with sequence similarity 82, memb	FAM82B	1.38E-05
205010_at	guanine nucleotide binding protein-like 3 (	GNL3L	0.00051665
242751_at	Transcribed locus	---	0.00042944
1558508_a	chromosome 1 open reading frame 53	C1orf53	0.000587727
206118_at	signal transducer and activator of transcrip	STAT4	0.000891315
205321_at	eukaryotic translation initiation factor 2, su	EIF2S3	0.0204818
200845_s_	peroxiredoxin 6	PRDX6	1.65E-05
208228_s_	fibroblast growth factor receptor 2 (bacteri	FGFR2	0.00426039
220167_s_	TP53TG3 protein /// similar to TP53TG3 p	LOC72935	0.00125688
202796_at	synaptopodin	SYNPO	0.00558512
1560048_a	CDNA FLJ30026 fis, clone 3NB69200112	---	0.000830972
205832_at	carboxypeptidase A4	CPA4	2.28E-05
241883_x_	---	---	0.0133536
218625_at	neuritin 1	NRN1	3.71E-06
203810_at	DnaJ (Hsp40) homolog, subfamily B, mem	DNAJB4	0.00445441
231467_at	Transcribed locus	---	0.0037524
1557779_a	Homo sapiens, clone IMAGE:4400004, ml	---	0.0184072
1560741_a	small nuclear ribonucleoprotein polypeptid	SNRPN	0.0050358
237075_at	---	---	0.000799447
1568604_a	Ca2+-dependent secretion activator	CADPS	0.00203251
227282_at	protocadherin 19	PCDH19	0.000968102
239153_at	hypothetical gene supported by AK123741	FLJ41747	0.00437761
219506_at	chromosome 1 open reading frame 54	C1orf54	0.000673613

226134_s_	Transcribed locus	---	9.46E-05
203238_s_	Notch homolog 3 (Drosophila)	NOTCH3	0.000704296
1560359_a	Pelota homolog (Drosophila)	PELO	0.00121337
228507_at	CDNA FLJ37884 fis, clone BRSTN20124	---	0.0011863
204639_at	adenosine deaminase	ADA	0.00766183
244524_at	Transcribed locus	---	0.00136168
214741_at	zinc finger protein 131	ZNF131	0.00113833
229158_at	WNK lysine deficient protein kinase 4	WNK4	9.38E-05
1553275_s	---	---	0.00803195
1561689_a	Transcribed locus	---	0.000379147
1558794_a	Hypothetical protein LOC728190	LOC72819	0.000339805
242260_at	Matrin 3	MATR3	0.00220488
223854_at	protocadherin beta 10	PCDHB10	0.0167487
217967_s_	family with sequence similarity 129, memb	FAM129A	0.0318524
210674_s_	protocadherin alpha 9 /// protocadherin al	PCDHA1 //	0.00378179
230906_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT10	0.00115195
225220_at	small nucleolar RNA host gene (non-prote	SNHG8	0.000225119
232955_at	hypothetical LOC440200	FLJ41170	0.0134435
222809_x_	chromosome 14 open reading frame 65	C14orf65	0.000471835
228310_at	enabled homolog (Drosophila)	ENAH	0.00184187
213640_s_	lysyl oxidase	LOX	0.000558007
229189_s_	CDNA FLJ90295 fis, clone NT2RP200024	---	0.00767527
230737_s_	patched domain containing 3 pseudogene	LOC38764	0.000906829
1558964_a	FAT tumor suppressor homolog 3 (Drosop	FAT3	0.000951332
214436_at	F-box and leucine-rich repeat protein 2	FBXL2	0.00170351
243134_at	Transcribed locus	---	0.0173384
204079_at	tyrosylprotein sulfotransferase 2	TPST2	0.00176298
219829_at	integrin beta 1 binding protein (melusin) 2	ITGB1BP2	1.16E-05
218724_s_	TGFB-induced factor homeobox 2	TGIF2	0.00268879
243087_at	WD repeat domain 63	WDR63	0.00249173
1568765_a	serpin peptidase inhibitor, clade E (nexin,	SERPINE1	0.00592745
1557224_a	CDNA FLJ30981 fis, clone HHDPC20002	---	0.000247861
212667_at	secreted protein, acidic, cysteine-rich (ost	SPARC	0.00050079
200962_at	ribosomal protein L31	RPL31	0.00531492
243564_at	phosphodiesterase 1C, calmodulin-depen	PDE1C	0.0015511
232544_at	CDNA FLJ11572 fis, clone HEMBA10033	---	0.00433428
209433_s_	phosphoribosyl pyrophosphate amidotran	PPAT	0.0056082
224002_s_	FK506 binding protein 7	FKBP7	0.000732305
207357_s_	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT10	0.0145784
222787_s_	transmembrane protein 106B	TMEM106	6.19E-05
229441_at	Protease, serine, 23	PRSS23	0.00101375
218974_at	sine oculis binding protein homolog (Dros	SOBP	0.00075915
213110_s_	collagen, type IV, alpha 5 (Alport syndrom	COL4A5	0.00351878
230083_at	ubiquitin specific peptidase 53	USP53	0.00507306
235518_at	solute carrier family 8 (sodium/calcium ex	SLC8A1	0.0229971
1552867_a	---	---	0.00527235
1555777_a	periostin, osteoblast specific factor	POSTN	7.25E-05
225167_at	FERM domain containing 4A	FRMD4A	0.00442128
205590_at	RAS guanyl releasing protein 1 (calcium a	RASGRP1	0.00189141
1554743_x	PMS1 postmeiotic segregation increased	PMS1	5.48E-05
1563414_a	Full length insert cDNA clone YW28F05	---	0.0119895
229092_at	nuclear receptor subfamily 2, group F, me	NR2F2	0.000285392
215073_s_	nuclear receptor subfamily 2, group F, me	NR2F2	0.0136849

224364_s_	peptidylprolyl isomerase (cyclophilin)-like :	PPIL3	9.79E-05
219636_s_	armadillo repeat containing 9	ARMC9	0.00727078
211330_s_	hemochromatosis	HFE	0.00615076
217427_s_	HIR histone cell cycle regulation defective	HIRA	0.0104472
236321_at	---	---	0.000541527
222833_at	lysophosphatidylcholine acyltransferase 2	LPCAT2	0.000968836
237305_at	Transcribed locus	---	0.00169395
226995_at	Chromosome 21 open reading frame 86	C21orf86	0.00231094
228255_at	amyotrophic lateral sclerosis 2 (juvenile) c	ALS2CR4	6.46E-05
209119_x_	nuclear receptor subfamily 2, group F, mei	NR2F2	0.0138491
235236_at	Transcribed locus	---	0.0402
238774_at	---	---	0.00977583
217430_x_	collagen, type I, alpha 1	COL1A1	0.00205736
231829_at	virus-induced signaling adapter	VISA	0.00731946
212812_at	CDNA: FLJ22642 fis, clone HSI06970	---	0.00225567
218472_s_	pelota homolog (Drosophila)	PELO	0.00141667
241788_x_	Transcribed locus	---	0.00224935
225237_s_	musashi homolog 2 (Drosophila)	MSI2	0.00134055
235228_at	coiled-coil domain containing 85A	CCDC85A	0.0175704
224767_at	Ribosomal protein L37	RPL37	5.44E-06
206103_at	ras-related C3 botulinum toxin substrate 3	RAC3	0.00509197
221139_s_	cysteine sulfinic acid decarboxylase	CSAD	0.00259053
201162_at	insulin-like growth factor binding protein 7	IGFBP7	0.00153563
211106_at	---	---	0.000387377
222750_s_	steroid 5 alpha-reductase 3	SRD5A3	0.00100605
211681_s_	PDZ and LIM domain 5	PDLIM5	0.00928287
212774_at	zinc finger protein 238	ZNF238	0.00107222
233555_s_	sulfatase 2	SULF2	0.036308
210749_x_	discoidin domain receptor tyrosine kinase	DDR1	0.00263542
221974_at	small nuclear ribonucleoprotein polypeptic	SNRPN	0.00195389
243599_at	Transcribed locus	---	0.0310228
232369_at	Clone IMAGE:119716, mRNA sequence	---	0.00846396
205359_at	A kinase (PRKA) anchor protein 6	AKAP6	0.000289145
205939_at	cytochrome P450, family 3, subfamily A, p	CYP3A7	0.00564182
239008_at	CDNA clone IMAGE:4328048	---	3.07E-05
228618_at	platelet endothelial aggregation receptor 1	PEAR1	3.74E-05
209576_at	guanine nucleotide binding protein (G prot	GNAI1	0.00157956
216975_x_	neuronal PAS domain protein 1	NPAS1	0.00103505
237183_at	UDP-N-acetyl-alpha-D-galactosamine:poly	GALNT5	0.0213478
212686_at	protein phosphatase 1H (PP2C domain co	PPM1H	0.00176301
230935_at	---	---	0.000113786
215767_at	zinc finger protein 804A	ZNF804A	0.001373
1556102_x	hypothetical protein LOC286434	LOC28643	0.00106986
204506_at	protein phosphatase 3 (formerly 2B), regu	PPP3R1 ///	0.0226133
222347_at	hypothetical protein LOC644450	LOC64445	0.000902555
57588_at	solute carrier family 24 (sodium/potassium	SLC24A3	0.00383921
203157_s_	glutaminase	GLS	0.00242084
233528_s_	TBC1 domain family, member 10A /// hypo	LOC65296	0.0111175
235061_at	protein phosphatase 1K (PP2C domain co	PPM1K	0.0364727
205943_at	tryptophan 2,3-dioxygenase	TDO2	0.00588613
239302_s_	MRNA; cDNA DKFZp686P18215 (from clo	---	0.000758917
213238_at	ATPase, class V, type 10D	ATP10D	0.000121319
1554689_a	neuroligin 4, X-linked	NLGN4X	0.000494173

226523_at	Transgelin	TAGLN	0.0096339
204897_at	prostaglandin E receptor 4 (subtype EP4)	PTGER4	0.00345902
219629_at	family with sequence similarity 118, memb	FAM118A	1.57E-05
242423_x_	CDNA clone IMAGE:6576427	---	0.0104842
242396_at	Similar to hCG1774772	LOC10013	0.00651973
243444_at	Transcribed locus	---	0.000476481
1564639_a	Hypothetical protein LOC441528	LOC38990	0.0187659
205934_at	phospholipase C-like 1	PLCL1	0.00195141
206993_at	ATP synthase, H+ transporting, mitochon	ATP5S	0.000128943
201468_s_	NAD(P)H dehydrogenase, quinone 1	NQO1	0.00241638
238546_at	solute carrier family 8 (sodium/calcium ex	SLC8A1	0.0199854
230933_at	Destrin (actin depolymerizing factor)	DSTN	0.00331696
212699_at	secretory carrier membrane protein 5	SCAMP5	0.00037326
222288_at	Transcribed locus, weakly similar to NP_0	---	0.0107408
229518_at	family with sequence similarity 46, memb	FAM46B	0.00649599
214954_at	sushi domain containing 5	SUSD5	0.00201664
239503_at	CDNA clone IMAGE:5301910	---	0.00519016
208396_s_	phosphodiesterase 1A, calmodulin-depen	PDE1A	0.0204547
221016_s_	transcription factor 7-like 1 (T-cell specific,	TCF7L1	0.00402175
227863_at	cathepsin D	CTSD	0.000156712
219956_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT6	0.0105223
223038_s_	family with sequence similarity 60, memb	FAM60A	0.000262792
221823_at	chromosome 5 open reading frame 30	C5orf30	0.00305751
208025_s_	high mobility group AT-hook 2	HMGA2	0.0100089
214095_at	serine hydroxymethyltransferase 2 (mitoc	SHMT2	0.00101638
213995_at	ATP synthase, H+ transporting, mitochon	ATP5S	5.79E-06
205646_s_	paired box 6	PAX6	0.00326232
1557275_a	CDNA FLJ20031 fis, clone ADSU02180	---	0.0271313
214657_s_	Trophoblast-derived noncoding RNA	TncRNA	0.00307797
241722_x_	Transcribed locus	---	0.00307775
210567_s_	S-phase kinase-associated protein 2 (p45	SKP2	0.0261429
209440_at	phosphoribosyl pyrophosphate synthetas	PRPS1	0.0157677
234875_at	similar to rCG45476	LOC72992	0.0223369
239468_at	mohawk homeobox	MKX	0.00767122
217208_s_	discs, large homolog 1 (Drosophila)	DLG1	0.00954221
236657_at	hypothetical protein LOC100130506	LOC10013	0.00286123
232287_at	piggyBac transposable element derived 3	PGBD3	0.00154139
211998_at	H3 histone, family 3A /// H3 histone, famil	H3F3A /// H	0.000221293
206713_at	netrin G1	NTNG1	0.000915343
212215_at	prolyl endopeptidase-like	PREPL	0.000693047
210255_at	RAD51-like 1 (S. cerevisiae)	RAD51L1	0.0158752
212543_at	absent in melanoma 1	AIM1	0.0348827
204518_s_	peptidylprolyl isomerase C (cyclophilin C)	PPIC	0.000724262
202178_at	protein kinase C, zeta	PRKCZ	0.00595273
222062_at	interleukin 27 receptor, alpha	IL27RA	0.00942767
228722_at	protein arginine methyltransferase 2	PRMT2	0.0032695
204365_s_	receptor accessory protein 1	REEP1	0.0010883
214595_at	potassium voltage-gated channel, subfam	KCNG1	0.0001878
244187_at	Transcribed locus	---	0.038349
205880_at	protein kinase D1	PRKD1	0.00605251
228370_at	Small nuclear ribonucleoprotein polypepti	SNRPN	4.91E-05
1569191_a	zinc finger protein 826	ZNF826	0.00246711
209841_s_	leucine rich repeat neuronal 3	LRRN3	0.00754353

1553962_s	ras homolog gene family, member B	RHOB	0.017432
227996_at	FERM, RhoGEF (ARHGEF) and pleckstri	FARP1	0.0010239
217373_x_	Mdm2 p53 binding protein homolog (mous	MDM2	0.0403874
200844_s_	peroxiredoxin 6	PRDX6	0.000216855
244066_at	Transcribed locus	---	6.75E-05
205826_at	myomesin (M-protein) 2, 165kDa	MYOM2	9.30E-05
202959_at	methylmalonyl Coenzyme A mutase	MUT	9.44E-05
227410_at	family with sequence similarity 43, membe	FAM43A	0.00851296
227556_at	non-metastatic cells 7, protein expressed	NME7	0.0316949
226587_at	CDNA FLJ33569 fis, clone BRAMY20103	---	0.00150072
227699_at	chromosome 14 open reading frame 149	C14orf149	0.00157685
227623_at	CDNA FLJ30478 fis, clone BRAWH10001	---	0.00275759
228881_at	presenilin associated, rhomboid-like	PARL	0.0350367
217077_s_	gamma-aminobutyric acid (GABA) B rece	GABBR2	0.000421733
224973_at	family with sequence similarity 46, membe	FAM46A	0.00140012
202887_s_	DNA-damage-inducible transcript 4	DDIT4	0.00331628
241359_at	CDNA FLJ20031 fis, clone ADSU02180	---	0.0287714
203639_s_	fibroblast growth factor receptor 2 (bacteri	FGFR2	0.00222826
223136_at	androgen-induced 1	AIG1	0.000190871
226907_at	protein phosphatase 1, regulatory (inhibito	PPP1R14C	0.0196496
204984_at	glypican 4	GPC4	0.00786091
202923_s_	glutamate-cysteine ligase, catalytic subuni	GCLC	0.00137735
218589_at	purinergic receptor P2Y, G-protein couple	P2RY5	0.0026272
226731_at	Pelota homolog (Drosophila)	PELO	0.00635851
204920_at	carbamoyl-phosphate synthetase 1, mitoc	CPS1	0.00731356
204136_at	collagen, type VII, alpha 1 (epidermolysis	COL7A1	0.000318558
224495_at	transmembrane protein 107	TMEM107	0.00524828
1554737_a	fibrillin 2 (congenital contractural arachno	FBN2	0.000984776
235561_at	Transcribed locus	---	0.00156954
227370_at	KIAA1946	KIAA1946	2.36E-05
1568603_a	Ca2+-dependent secretion activator	CADPS	0.00016651
203242_s_	PDZ and LIM domain 5	PDLIM5	0.00323841
244631_at	hypothetical gene supported by AK12340	LOC38983	0.00119019
221330_at	cholinergic receptor, muscarinic 2	CHRM2	0.0250183
232315_at	zinc finger-like	LOC40071	0.00557766
203394_s_	hairy and enhancer of split 1, (Drosophila)	HES1	0.00121744
231784_s_	WD repeats and SOF1 domain containing	WDSOF1	0.0393314
226223_at	Transcribed locus	---	0.000466468
229190_at	CDNA FLJ90295 fis, clone NT2RP200024	---	0.00330441
231470_at	Transcribed locus	---	0.000356132
242321_at	Full length insert cDNA clone ZE03F06	---	0.0336066
227559_at	Transcribed locus	---	7.54E-06
204983_s_	glypican 4	GPC4	0.00769718
218258_at	polymerase (RNA) I polypeptide D, 16kDa	POLR1D	0.000818899
203642_s_	COBL-like 1	COBLL1	0.0039832
210078_s_	potassium voltage-gated channel, shaker-	KCNAB1	0.00485898
205164_at	glycine C-acetyltransferase (2-amino-3-ke	GCAT	0.000283944
1554575_a	3'(2'), 5'-bisphosphate nucleotidase 1	BPNT1	0.00692689
227764_at	LY6/PLAUR domain containing 6	LYPD6	0.00378357
216804_s_	PDZ and LIM domain 5	PDLIM5	0.00194217
221923_s_	nucleophosmin (nucleolar phosphoprotein	NPM1	0.000730868
216840_s_	laminin, alpha 2 (merosin, congenital mus	LAMA2	4.69E-05
212654_at	tropomyosin 2 (beta)	TPM2	0.015327

1560402_a	growth arrest-specific 5	GAS5	0.0023256
236647_at	Transcribed locus	---	0.00210841
203626_s_	S-phase kinase-associated protein 2 (p45	SKP2	0.0175315
205116_at	laminin, alpha 2 (merosin, congenital mus	LAMA2	5.87E-05
206215_at	opioid binding protein/cell adhesion molec	OPCML	0.00136125
229555_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT5	0.000656893
238026_at	ribosomal protein L35a	RPL35A	2.17E-05
202342_s_	tripartite motif-containing 2	TRIM2	0.000250531
235085_at	homolog of rat pragma of Rnd2	PRAGMIN	0.00427198
204992_s_	profilin 2	PFN2	4.26E-05
1556657_a	CDNA FLJ36459 fis, clone THYMU20147	---	0.0201907
1552487_a	basonuclin 1	BNC1	0.000446923
231881_at	caldesmon 1	CALD1	0.00136225
201163_s_	insulin-like growth factor binding protein 7	IGFBP7	0.00419759
224936_at	eukaryotic translation initiation factor 2, su	EIF2S3	0.00536002
209081_s_	collagen, type XVIII, alpha 1	COL18A1	0.00122461
218844_at	acyl-CoA synthetase family member 2	ACSF2	0.0126943
216342_x_	ribosomal protein S4, X-linked /// similar to	LOC10012	4.94E-05
215531_s_	gamma-aminobutyric acid (GABA) A rece	GABRA5	0.0204113
237624_at	Transcribed locus	---	0.00456314
213684_s_	PDZ and LIM domain 5	PDLIM5	0.00381645
216247_at	ribosomal protein S20	RPS20	0.00305072
203243_s_	PDZ and LIM domain 5	PDLIM5	0.00537608
222844_s_	serine racemase	SRR	0.00193303
202289_s_	transforming, acidic coiled-coil containing	TACC2	0.00269636
1556346_a	Partial mRNA; ID YG39-1A	---	0.0248865
215775_at	Thrombospondin 1	THBS1	0.0232776
215177_s_	integrin, alpha 6	ITGA6	0.0148982
239028_at	LY6/PLAUR domain containing 6	LYPD6	0.00494641
244650_at	CDNA FLJ43660 fis, clone SYNOV40048	---	0.00218408
235256_s_	galactose mutarotase (aldose 1-epimeras	GALM	0.000226794
210993_s_	SMAD family member 1	SMAD1	0.00166009
203763_at	dynein, cytoplasmic 2, light intermediate c	DYNC2LI1	0.000419281
219295_s_	procollagen C-endopeptidase enhancer 2	PCOLCE2	0.0250952
242414_at	quinolinate phosphoribosyltransferase (ni	QPRT	0.036379
236047_at	chromosome 8 open reading frame 5	C8orf5	0.000233217
235428_at	Transcribed locus, strongly similar to NP_	---	0.000375253
1556658_a	CDNA FLJ36459 fis, clone THYMU20147	---	0.0431771
228124_at	abhydrolase domain containing 12	ABHD12	0.00012529
217466_x_	ribosomal protein S2	RPS2	0.0023219
239201_at	PFTAIRE protein kinase 2	PFTK2	0.00688632
228481_at	CDNA FLJ13419 fis, clone PLACE100211	---	0.000833385
207570_at	short stature homeobox	SHOX	0.00319762
227708_at	eukaryotic translation elongation factor 1	EEF1A1	0.000431841
239069_s_	Transcribed locus, weakly similar to NP_0	---	0.000276107
208763_s_	TSC22 domain family, member 3	TSC22D3	0.00260247
230228_at	hypothetical LOC284297	LOC28429	0.00400877
1567361_a	brain-derived neurotrophic factor opposite	BDNFOS	0.0101898
239884_at	Ca2+-dependent secretion activator	CADPS	0.0108788
219894_at	MAGE-like 2	MAGEL2	0.000528378
208482_at	somatostatin receptor 1	SSTR1	0.00158605
206448_at	zinc finger protein 365	ZNF365	0.00746362
215009_s_	SEC31 homolog A (S. cerevisiae)	SEC31A	0.00296686

236223_s_	Ras-like without CAAX 1	RIT1	0.00568633
233724_at	aryl hydrocarbon receptor nuclear transloc	ARNT	0.00011545
202341_s_	tripartite motif-containing 2	TRIM2	0.000717869
221593_s_	ribosomal protein L31	RPL31	0.00382118
238790_at	CLR pseudogene	LOC37444	0.0104784
209840_s_	leucine rich repeat neuronal 3	LRRN3	0.0337277
1558507_a	chromosome 1 open reading frame 53	C1orf53	0.0113804
210602_s_	cadherin 6, type 2, K-cadherin (fetal kidne	CDH6	0.000374597
230144_at	glutamate receptor, ionotrophic, AMPA 3	GRIA3	0.0175592
201212_at	legumain	LGMN	0.00777154
243629_x_	CDNA clone IMAGE:4819488	---	0.00170786
236453_at	similar to hCG1993567	LOC10013	0.00181364
229712_at	small nuclear RNA activating complex, pol	SNAPC3	0.00482155
227270_at	hypothetical protein LOC285550	LOC28555	0.0363495
1553191_a	dystonin	DST	0.00160956
230903_s_	Chromosome 8 open reading frame 42	C8orf42	0.00161105
1558680_s	phosphodiesterase 1A, calmodulin-depen	PDE1A	0.00532731
238868_at	uveal autoantigen with coiled-coil domains	UACA	0.00395051
230894_s_	Transcribed locus	---	0.00060825
227963_at	Transcribed locus	---	0.00096522
225321_s_	paired immunoglobin-like type 2 receptor	PILRB	0.000802382
1553973_a	serine peptidase inhibitor, Kazal type 6	SPINK6	0.0115221
211700_s_	trophinin	TRO	0.000832649
228885_at	MAM domain containing 2	MAMDC2	0.0285184
1558882_a	similar to HIV TAT specific factor 1; cofact	LOC40123	0.0011601
236834_at	sec1 family domain containing 2	SCFD2	0.00814066
236141_at	Nbla00301	NBLA0030	0.00261967
211701_s_	trophinin	TRO	0.000340755
227421_at	chromosome 21 open reading frame 57	C21orf57	0.0011354
239058_at	Transcribed locus	---	0.0226797
226597_at	receptor accessory protein 6	REEP6	0.000186125
217234_s_	ezrin	EZR	0.00575661
214472_at	histone cluster 1, H3d	HIST1H3D	0.00671245
208447_s_	phosphoribosyl pyrophosphate synthetase	PRPS1	0.020786
226637_at	Ubiquitin-conjugating enzyme E2H (UBC8	UBE2H	0.0235328
227088_at	phosphodiesterase 5A, cGMP-specific	PDE5A	0.0141196
229649_at	neurexin 3	NRXN3	0.0119676
218816_at	leucine rich repeat containing 1	LRRC1	0.000481716
1560477_a	sterile alpha motif domain containing 11	SAMD11	0.00438872
243084_at	caldesmon 1	CALD1	0.00253261
232138_at	Muscleblind-like 2 (Drosophila)	MBNL2	0.0265504
235944_at	hemicentin 1	HMCN1	0.00179148
201397_at	phosphoglycerate dehydrogenase	PHGDH	9.10E-05
233588_x_	prefoldin subunit 6	PFDN6	0.00496367
212706_at	RAS p21 protein activator 4 /// hypothetica	FLJ21767 /	0.00368121
228908_s_	Chromosome 21 open reading frame 86	C21orf86	0.00305891
222890_at	coiled-coil domain containing 113	CCDC113	0.00217833
227655_at	CDNA FLJ38512 fis, clone HCHON20005	---	0.00147767
210882_s_	trophinin	TRO	0.00644535
214182_at	hypothetical LOC100132430	LOC10013	0.000509073
230605_at	Transcribed locus, strongly similar to XP_	---	0.000959288
225667_s_	family with sequence similarity 84, membe	FAM84A ///	0.000916375
216983_s_	zinc finger protein 224	ZNF224	0.00455574

215945_s_	tripartite motif-containing 2	TRIM2	0.000499513
231130_at	Transcribed locus	---	6.25E-05
229218_at	collagen, type I, alpha 2	COL1A2	0.00100839
206806_at	diacylglycerol kinase, iota	DGKI	0.00332868
238824_at	CDNA FLJ30581 fis, clone BRAWH20070	---	0.00165779
242888_at	Transcribed locus, strongly similar to NP_	---	0.00103458
212236_x_	keratin 17	KRT17	0.00483058
222027_at	Nuclear casein kinase and cyclin-depend	NUCKS1	0.0451345
210654_at	tumor necrosis factor receptor superfamily	TNFRSF10	0.020917
207264_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reti	KDELR3	0.000235989
239708_at	Transcribed locus	---	9.03E-05
216724_at	Doublecortin-like kinase 2	DCLK2	0.0252306
236656_s_	hypothetical protein LOC100130506	LOC10013	0.000477594
213248_at	hypothetical LOC730101	LOC73010	0.0220444
227510_x_	metastasis associated lung adenocarcino	MALAT1	0.0106351
237116_at	hypothetical LOC646903	LOC64690	0.00156789
209991_x_	gamma-aminobutyric acid (GABA) B rece	GABBR2	0.000287455
214390_s_	branched chain aminotransferase 1, cytos	BCAT1	3.62E-05
223606_x_	KIAA1704	KIAA1704	0.00433666
215199_at	caldesmon 1	CALD1	0.0212083
1559500_a	vacuolar protein sorting 8 homolog (S. cer	VPS8	0.0349615
204203_at	CCAAT/enhancer binding protein (C/EBP)	CEBPG	0.00208589
222991_s_	ubiquilin 1	UBQLN1	0.00133085
235545_at	DEP domain containing 1	DEPDC1	0.04245
221436_s_	cell division cycle associated 3	CDCA3	0.0317984
1560049_a	CDNA FLJ36973 fis, clone BRACE20062	---	0.00694902
202307_s_	transporter 1, ATP-binding cassette, sub-f	TAP1	0.00237416
219028_at	homeodomain interacting protein kinase 2	HIPK2	0.0245757
1565830_a	MRNA; cDNA DKFZp686D0673 (from clo	---	0.00352624
209324_s_	regulator of G-protein signaling 16	RGS16	0.0264567
214374_s_	PTPRF interacting protein, binding protein	PPFIBP1	0.00183054
204255_s_	vitamin D (1,25- dihydroxyvitamin D3) rec	VDR	0.000496519
227910_at	X-prolyl aminopeptidase (aminopeptidase	XPNPEP3	0.000531799
1554199_a	protein tyrosine phosphatase, receptor typ	PTPRO	0.00774996
223452_s_	atlastin 3	ATL3	0.000301274
238756_at	Growth arrest-specific 2 like 3	GAS2L3	0.0243823
239661_at	Transcribed locus	---	0.00212272
225987_at	STEAP family member 4	STEAP4	0.000131012
238429_at	transmembrane protein 71	TMEM71	0.00394941
205782_at	fibroblast growth factor 7 (keratinocyte gro	FGF7	0.0130771
227486_at	5'-nucleotidase, ecto (CD73)	NT5E	0.0032241
210612_s_	synaptojanin 2	SYNJ2	0.00646163
212914_at	chromobox homolog 7	CBX7	0.00656661
1556667_a	hypothetical protein LOC348751	LOC34875	0.00794807
238183_at	Transcribed locus	---	0.00140737
227383_at	hypothetical protein LOC727820	LOC72782	0.000434651
206157_at	pentraxin-related gene, rapidly induced by	PTX3	0.00527993
201120_s_	progesterone receptor membrane compo	PGRMC1	0.00251107
244779_at	CDNA FLJ34038 fis, clone FCBBF200564	---	0.0223655
211006_s_	potassium voltage-gated channel, Shab-r	KCNB1	0.00549076
206449_s_	mannan-binding lectin serine peptidase 1	MASP1	0.00102548
223502_s_	tumor necrosis factor (ligand) superfamily,	TNFSF13B	0.0352629
1557765_a	hypothetical protein LOC643401	LOC64340	0.0277557

1556328_a	CDNA clone IMAGE:5301690	---	0.00811923
239519_at	Transcribed locus	---	0.0041749
224924_at	tetratricopeptide repeat domain 7A	TTC7A	0.00898601
202240_at	polo-like kinase 1 (Drosophila)	PLK1	0.0123483
227503_at	CDNA FLJ43100 fis, clone CTONG20031	---	0.000637211
212486_s_	FYN oncogene related to SRC, FGR, YES	FYN	0.00527953
243743_at	Transcribed locus	---	0.00224638
224623_at	THO complex 3 /// similar to THO complex	LOC72855	5.51E-05
210073_at	ST8 alpha-N-acetyl-neuraminide alpha-2,	ST8SIA1	0.00391018
213309_at	phospholipase C-like 2	PLCL2	0.000479046
230536_at	pre-B-cell leukemia homeobox 4	PBX4	0.0011233
208607_s_	serum amyloid A1 /// serum amyloid A2	SAA1 /// SA	0.001805
1559663_a	Clone HQ0312	---	0.000163752
204817_at	extra spindle pole bodies homolog 1 (S. c	ESPL1	0.00544796
219360_s_	transient receptor potential cation channel	TRPM4	0.00258385
1555759_a	chemokine (C-C motif) ligand 5	CCL5	0.00886597
231969_at	storkhead box 2	STOX2	0.00374809
228771_at	adrenergic, beta, receptor kinase 2	ADRBK2	0.00332196
213348_at	cyclin-dependent kinase inhibitor 1C (p57,	CDKN1C	0.0402722
209807_s_	nuclear factor I/X (CCAAT-binding transcri	NFIX	0.00644624
225458_at	hypothetical LOC25845	LOC25845	0.0188841
221211_s_	chromosome 21 open reading frame 7	C21orf7	0.000683374
207521_s_	ATPase, Ca++ transporting, ubiquitous	ATP2A3	0.00466231
230744_at	Transcribed locus	---	0.00263098
241701_at	Rho GTPase activating protein 21	ARHGAP2	0.0408766
236184_at	Transcribed locus	---	0.011077
210821_x_	centromere protein A	CENPA	0.00955683
213134_x_	BTG family, member 3	BTG3	9.10E-05
244427_at	Kinesin family member 23	KIF23	0.00518695
208702_x_	amyloid beta (A4) precursor-like protein 2	APLP2	0.00334448
227243_s_	early B-cell factor 3	EBF3	0.00193281
234033_at	Clone IMAGE:110218 mRNA sequence	---	0.000174678
204641_at	NIMA (never in mitosis gene a)-related kin	NEK2	0.0270446
202531_at	interferon regulatory factor 1	IRF1	0.0385044
241399_at	family with sequence similarity 19 (chemo	FAM19A2	0.0154216
201762_s_	proteasome (prosome, macropain) activat	PSME2	0.000587907
209281_s_	ATPase, Ca++ transporting, plasma mem	ATP2B1	0.0245949
204115_at	guanine nucleotide binding protein (G prot	GNG11	0.000936917
242657_at	Transcribed locus	---	0.000206984
225895_at	synaptopodin 2	SYNPO2	0.00033625
210026_s_	caspase recruitment domain family, mem	CARD10	0.0465648
1555826_a	effector cell peptidase receptor 1	EPR1	0.00216507
1566284_a	PA4=candidate oncogene (3' region) [hum	---	0.0184409
235117_at	ChaC, cation transport regulator homolog	CHAC2	0.00527058
200884_at	creatine kinase, brain	CKB	0.0131339
234973_at	solute carrier family 38, member 5	SLC38A5	0.000355319
203698_s_	frizzled-related protein	FRZB	0.0148814
230972_at	ankyrin repeat domain 9	ANKRD9	0.0114429
218782_s_	ATPase family, AAA domain containing 2	ATAD2	0.0080714
243198_at	testis expressed 9	TEX9	0.00353931
225033_at	hypothetical LOC286167	LOC28616	0.00481295
224806_at	tripartite motif-containing 25	TRIM25	0.000530741
215245_x_	fragile X mental retardation 1	FMR1	0.00042664

206140_at	LIM homeobox 2	LHX2	0.00633551
214433_s_	selenium binding protein 1	SELENBP1	0.0127032
224701_at	poly (ADP-ribose) polymerase family, mem	PARP14	0.00639609
209436_at	spondin 1, extracellular matrix protein	SPON1	0.00186765
203939_at	5'-nucleotidase, ecto (CD73)	NT5E	0.000357811
205253_at	pre-B-cell leukemia homeobox 1	PBX1	0.00206388
239808_at	Transcribed locus	---	0.0129045
211080_s_	NIMA (never in mitosis gene a)-related kin	NEK2	0.0397446
241210_at	Transcribed locus	---	0.000831782
208178_x_	triple functional domain (PTPRF interactin	TRIO	0.0213907
222651_s_	trichorhinophalangeal syndrome I	TRPS1	0.00013798
201188_s_	inositol 1,4,5-triphosphate receptor, type 3	ITPR3	0.0324162
209753_s_	thymopoietin	TMPO	0.0137963
230026_at	mitochondrial ribosomal protein L43	MRPL43	0.000496507
240419_at	solute carrier family 6, member 15	SLC6A15	0.00606883
215078_at	superoxide dismutase 2, mitochondrial	SOD2	0.037908
215471_s_	microtubule-associated protein 7	MAP7	0.000666755
213537_at	major histocompatibility complex, class II,	HLA-DPA1	0.000780635
48808_at	dihydrofolate reductase	DHFR	0.0392313
230434_at	phosphatase, orphan 2	PHOSPHO	0.00263303
222450_at	prostate transmembrane protein, androge	PMEPA1	0.0164803
221903_s_	cylindromatosis (turban tumor syndrome)	CYLD	2.72E-05
207345_at	follistatin	FST	0.00231912
211813_x_	decorin	DCN	0.00267348
235368_at	ADAM metallopeptidase with thrombospo	ADAMTS5	0.0239587
244506_at	transmembrane and tetratricopeptide repe	TMTC1	0.00195276
1568999_a	pregnancy specific beta-1-glycoprotein 4	PSG4	0.006146
213069_at	HEG homolog 1 (zebrafish)	HEG1	2.51E-05
209676_at	tissue factor pathway inhibitor (lipoprotein-	TFPI	0.00303351
220155_s_	bromodomain containing 9	BRD9	0.000139877
204655_at	chemokine (C-C motif) ligand 5	CCL5	0.010017
225263_at	heparan sulfate 6-O-sulfotransferase 1	HS6ST1	0.0263961
223125_s_	chromosome 1 open reading frame 21	C1orf21	0.00769811
209258_s_	structural maintenance of chromosomes 3	SMC3	0.00108916
203636_at	midline 1 (Opitz/BBB syndrome)	MID1	0.00353679
205961_s_	PC4 and SFRS1 interacting protein 1	PSIP1	0.0120482
1554334_a	DnaJ (Hsp40) homolog, subfamily A, mem	DNAJA4	0.000445768
205960_at	pyruvate dehydrogenase kinase, isozyme	PDK4	0.00152565
1559141_s	family with sequence similarity 87, membe	FAM87A ///	0.00311701
209040_s_	proteasome (prosome, macropain) subuni	PSMB8	0.00344857
239002_at	asp (abnormal spindle) homolog, microce	ASPM	0.0171798
228439_at	basic leucine zipper transcription factor, A	BATF2	0.0186186
1554544_a	myelin basic protein	MBP	0.0263774
1565579_a	CDNA clone IMAGE:3689276	---	0.00052742
212582_at	oxysterol binding protein-like 8	OSBPL8	0.000238024
224944_at	thymopoietin	TMPO	0.00752739
205383_s_	zinc finger and BTB domain containing 20	ZBTB20	0.000705915
214822_at	family with sequence similarity 5, member	FAM5B	0.0132876
1554473_a	SLIT-ROBO Rho GTPase activating prote	SRGAP1	0.00223873
242671_at	---	---	0.00149203
208928_at	P450 (cytochrome) oxidoreductase	POR	0.000453783
213285_at	transmembrane protein 30B	TMEM30B	0.000653159
242677_at	Neuropilin 1	NRP1	0.0278456

205174_s_	glutaminyl-peptide cyclotransferase (gluta	QPCT	0.000535343
208191_x_	pregnancy specific beta-1-glycoprotein 4	PSG4	0.0016988
213156_at	Homo sapiens, clone IMAGE:4214654, ml	---	0.00103638
244075_at	Transcribed locus	---	0.0125896
201690_s_	tumor protein D52	TPD52	0.0359947
239108_at	Male sterility domain containing 1	MLSTD1	0.0121029
238767_at	Transcribed locus	---	0.0013542
225062_at	hypothetical gene supported by AL713796	LOC10013	0.00548779
232346_at	CDNA FLJ13580 fis, clone PLACE100885	---	0.00130698
218856_at	tumor necrosis factor receptor superfamily	TNFRSF21	0.00727603
229912_at	sidekick homolog 1, cell adhesion molecul	SDK1	0.000233232
220326_s_	hypothetical protein FLJ10357	FLJ10357	0.00237207
235643_at	sterile alpha motif domain containing 9-like	SAMD9L	0.0159327
221081_s_	DENN/MADD domain containing 2D	DENND2D	0.000243708
238619_at	CDNA FLJ26188 fis, clone ADG04821	---	0.000109128
227367_at	Transcribed locus	---	0.00482609
213008_at	Fanconi anemia, complementation group I	FANCI	0.0246859
1556053_a	DnaJ (Hsp40) homolog, subfamily C, mem	DNAJC7	0.00563423
203882_at	interferon regulatory factor 9	IRF9	0.0010377
225056_at	signal-induced proliferation-associated 1 li	SIPA1L2	0.00638832
214012_at	endoplasmic reticulum aminopeptidase 1	ERAP1	0.00415463
224339_s_	angiopoietin-like 1	ANGPTL1	0.00055538
204731_at	transforming growth factor, beta receptor I	TGFBR3	0.000984653
227230_s_	KIAA1211 protein	KIAA1211	0.00927698
217889_s_	cytochrome b reductase 1	CYBRD1	0.000779523
1555167_s	nicotinamide phosphoribosyltransferase	NAMPT	0.0138576
209257_s_	structural maintenance of chromosomes 3	SMC3	0.000111823
218627_at	damage-regulated autophagy modulator	DRAM	0.00234151
205560_at	proprotein convertase subtilisin/kexin type	PCSK5	0.021114
207978_s_	nuclear receptor subfamily 4, group A, me	NR4A3	5.01E-06
203213_at	cell division cycle 2, G1 to S and G2 to M	CDC2	0.0490276
225941_at	eukaryotic translation initiation factor 4E fa	EIF4E3	0.0185073
238297_at	---	---	0.000654522
216033_s_	FYN oncogene related to SRC, FGR, YES	FYN	0.00556831
216952_s_	lamin B2	LMNB2	0.00389515
205548_s_	BTG family, member 3	BTG3	9.57E-05
206187_at	prostaglandin I2 (prostacyclin) receptor (IF	PTGIR	0.00149576
230163_at	Hypothetical protein LOC143381	LOC14338	0.0389595
230963_at	empty spiracles homeobox 2 opposite stra	EMX2OS	0.00756209
203963_at	carbonic anhydrase XII	CA12	0.0034245
220340_at	KIAA1772	KIAA1772	0.000476926
223340_at	spastic paraplegia 3A (autosomal dominar	SPG3A	0.0177732
1568680_s	YTH domain containing 2	YTHDC2	0.0126049
223220_s_	poly (ADP-ribose) polymerase family, men	PARP9	0.0228993
221872_at	retinoic acid receptor responder (tazarotei	RARRES1	0.00179306
205602_x_	pregnancy specific beta-1-glycoprotein 7	PSG7	0.000458197
229350_x_	poly (ADP-ribose) polymerase family, men	PARP10	0.00180346
1560318_a	Rho GTPase activating protein 29	ARHGAP2	0.0106493
231403_at	Triple functional domain (PTPRF interactir	TRIO	0.0113654
216237_s_	minichromosome maintenance complex co	MCM5	0.00757297
241457_at	Transcribed locus	---	0.0184144
1554825_a	---	---	0.000452395
219441_s_	leucine-rich repeat kinase 1	LRRK1	0.000399362

243805_at	collagen and calcium binding EGF domair	CCBE1	0.000403749
203637_s_	midline 1 (Opitz/BBB syndrome)	MID1	0.00345671
209053_s_	Wolf-Hirschhorn syndrome candidate 1	WHSC1	0.0127483
214086_s_	poly (ADP-ribose) polymerase family, men	PARP2	0.000700864
211744_s_	CD58 molecule	CD58	0.015311
209408_at	kinesin family member 2C	KIF2C	0.00898389
1552538_a	kinesin family member 6	KIF6	0.00301494
204168_at	microsomal glutathione S-transferase 2	MGST2	0.00591914
222802_at	endothelin 1	EDN1	0.00976339
229357_at	ADAM metallopeptidase with thrombospor	ADAMTS5	0.0357176
225564_at	spermatogenesis associated 13	SPATA13	0.00207152
232530_at	phospholipase D1, phosphatidylcholine-sp	PLD1	0.00677896
227461_at	stonin 2	STON2	0.00557381
228469_at	Peptidylprolyl isomerase D (cyclophilin D)	PPID	0.00155343
207785_s_	recombination signal binding protein for in	RBPJ	0.00058792
228340_at	transducin-like enhancer of split 3 (E(sp1)	TLE3	0.0019207
214285_at	fatty acid binding protein 3, muscle and he	FABP3	0.0474258
201984_s_	epidermal growth factor receptor (erythrob	EGFR	0.00081917
210052_s_	TPX2, microtubule-associated, homolog (	TPX2	0.0474811
211792_s_	cyclin-dependent kinase inhibitor 2C (p18,	CDKN2C	0.00600526
219197_s_	signal peptide, CUB domain, EGF-like 2	SCUBE2	0.00106948
227769_at	Transcribed locus	---	0.047604
1556283_s	FGFR1 oncogene partner 2	FGFR1OP2	0.000547132
203910_at	Rho GTPase activating protein 29	ARHGAP29	0.0022702
218541_s_	chromosome 8 open reading frame 4	C8orf4	0.00565336
1558924_s	CAP-GLY domain containing linker protein	CLIP1	0.000842785
220466_at	coiled-coil domain containing 15	CCDC15	0.00540087
208535_x_	collagen, type XIII, alpha 1	COL13A1	0.00023635
229228_at	cAMP responsive element binding protein	CREB5	0.00309407
1556754_a	CDNA FLJ33712 fis, clone BRAWH20082	---	0.000324928
216361_s_	MYST histone acetyltransferase (monocyt	MYST3	0.0236688
226129_at	family with sequence similarity 83, membe	FAM83H	0.00490381
235308_at	zinc finger and BTB domain containing 20	ZBTB20	0.00318242
214727_at	breast cancer 2, early onset	BRCA2	0.00312773
228692_at	CDNA FLJ13569 fis, clone PLACE100836	---	0.0369332
225896_at	CDNA FLJ34018 fis, clone FCBBF200280	---	0.00639199
220615_s_	male sterility domain containing 1	MLSTD1	0.00669967
214077_x_	Meis homeobox 3 pseudogene 1	MEIS3P1	0.00478961
210832_x_	prostaglandin E receptor 3 (subtype EP3)	PTGER3	0.0218093
243404_at	Transcribed locus	---	0.000659837
229001_at	protein phosphatase 1, regulatory (inhibitc	PPP1R3E	0.00217001
221521_s_	GINS complex subunit 2 (Psf2 homolog)	GINS2	0.0268209
223657_at	chromosome 1 open reading frame 90	C1orf90	0.00241299
205327_s_	activin A receptor, type IIA	ACVR2A	0.00798863
236962_at	Transcribed locus	---	0.0220475
222001_x_	family with sequence similarity 91, membe	FAM91A2	0.000370128
204444_at	kinesin family member 11	KIF11	0.0447389
210105_s_	FYN oncogene related to SRC, FGR, YES	FYN	0.000464347
227948_at	FYVE, RhoGEF and PH domain containin	FGD4	0.00625616
223076_s_	NOL1/NOP2/Sun domain family, member	NSUN2	0.000122943
227717_at	FLJ41603 protein	FLJ41603	0.00629284
213103_at	StAR-related lipid transfer (START) domai	STARD13	0.000276323
1558199_a	fibronectin 1	FN1	0.0240023

209149_s_	transmembrane 9 superfamily member 1	TM9SF1	0.000289357
205205_at	v-rel reticuloendotheliosis viral oncogene	RELB	0.0204081
235836_at	matrix-remodelling associated 7	MXRA7	0.00287732
222680_s_	denticleless homolog (Drosophila)	DTL	0.0378051
222847_s_	egl nine homolog 3 (C. elegans)	EGLN3	0.0449545
243050_at	Transcribed locus	---	0.00022237
203052_at	complement component 2	C2	0.00456488
209355_s_	phosphatidic acid phosphatase type 2B	PPAP2B	0.00316815
1555009_a	synaptojanin 2	SYNJ2	0.00671642
243495_s_	MRNA; cDNA DKFZp686E18224 (from cl	---	0.0100761
221696_s_	serine/threonine/tyrosine kinase 1	STYK1	0.000637874
204442_x_	latent transforming growth factor beta bin	LTBP4	0.0344271
210665_at	tissue factor pathway inhibitor (lipoprotein-	TFPI	0.00864921
232653_at	CDNA FLJ14044 fis, clone HEMBA10061	---	0.00584141
211432_s_	TYRO3 protein tyrosine kinase	TYRO3	0.000345807
236561_at	Transforming growth factor, beta receptor	TGFBR1	0.00933279
210367_s_	prostaglandin E synthase	PTGES	0.00122889
201502_s_	nuclear factor of kappa light polypeptide g	NFKBIA	0.00853645
222740_at	ATPase family, AAA domain containing 2	ATAD2	0.0240478
215485_s_	intercellular adhesion molecule 1 (CD54),	ICAM1	0.00319124
209891_at	SPC25, NDC80 kinetochore complex com	SPC25	0.0226146
204170_s_	CDC28 protein kinase regulatory subunit	CKS2	0.0125299
205663_at	poly(rC) binding protein 3	PCBP3	0.000335666
228493_at	NFKB activating protein	NKAP	0.00172814
202637_s_	intercellular adhesion molecule 1 (CD54),	ICAM1	0.00911978
201957_at	protein phosphatase 1, regulatory (inhibit	PPP1R12B	0.013232
210285_x_	Wilms tumor 1 associated protein	WTAP	0.0492635
202338_at	thymidine kinase 1, soluble	TK1	0.0165735
203967_at	cell division cycle 6 homolog (S. cerevisia	CDC6	0.0458925
222848_at	centromere protein K	CENPK	0.0286041
225152_at	zinc finger protein 622	ZNF622	0.000717508
231786_at	homeobox A13	HOXA13	0.002978
228919_at	---	---	0.00917453
238736_at	REV3-like, catalytic subunit of DNA polym	REV3L	0.00576459
205330_at	meningioma (disrupted in balanced transl	MN1	0.00015087
1554741_s	fibroblast growth factor 7 (keratinocyte gro	FGF7 /// KC	0.0110418
1555355_a	v-ets erythroblastosis virus E26 oncogene	ETS1	0.00266208
234992_x_	epithelial cell transforming sequence 2 on	ECT2	0.000267813
242418_at	Chromosome 2 open reading frame 27	C2orf27	0.00725504
217914_at	two pore segment channel 1	TPCN1	0.0109694
227915_at	ankyrin repeat and SOCS box-containing	ASB2	0.00181851
222958_s_	DEP domain containing 1	DEPDC1	0.021006
218741_at	centromere protein M	CENPM	0.0282392
228494_at	protein phosphatase 1, regulatory (inhibit	PPP1R9A	0.0191307
203528_at	sema domain, immunoglobulin domain (Ig	SEMA4D	0.00536963
218574_s_	LIM and cysteine-rich domains 1	LMCD1	0.00669257
225721_at	synaptopodin 2	SYNPO2	0.000286263
219918_s_	asp (abnormal spindle) homolog, microce	ASPM	0.0385763
229304_s_	MLF1 interacting protein	MLF1IP	0.0100431
229247_at	fibulin 7	FBLN7	0.00311415
210831_s_	prostaglandin E receptor 3 (subtype EP3)	PTGER3	0.0305503
220295_x_	DEP domain containing 1	DEPDC1	0.028664
212021_s_	antigen identified by monoclonal antibody	MKI67	0.00715138

203927_at	nuclear factor of kappa light polypeptide g	NFKBIE	0.00570549
214269_at	major facilitator superfamily domain conta	MFSD7	0.000427833
206324_s_	death-associated protein kinase 2	DAPK2	0.00185704
226718_at	adhesion molecule with Ig-like domain 1	AMIGO1	0.00663372
231513_at	Transcribed locus	---	0.000427466
209940_at	poly (ADP-ribose) polymerase family, men	PARP3	0.00690249
226185_at	CDNA: FLJ23044 fis, clone LNG02454	---	0.000741352
200632_s_	N-myc downstream regulated gene 1	NDRG1	0.00446294
206472_s_	transducin-like enhancer of split 3 (E(sp1)	TLE3	0.0136456
228365_at	copine VIII	CPNE8	0.00390905
218739_at	abhydrolase domain containing 5	ABHD5	0.000969317
202896_s_	signal-regulatory protein alpha	SIRPA	0.00260366
203716_s_	dipeptidyl-peptidase 4 (CD26, adenosine	DPP4	0.00024628
230800_at	adenylate cyclase 4	ADCY4	0.000358644
228593_at	hypothetical LOC339483	LOC33948	0.00152384
209054_s_	Wolf-Hirschhorn syndrome candidate 1	WHSC1	0.00720933
222449_at	prostate transmembrane protein, androge	PMEPA1	0.0110207
242890_at	CDNA FLJ34225 fis, clone FCBBF302337	---	0.0355081
216269_s_	elastin (supravalvular aortic stenosis, Willi	ELN	0.0337884
225373_at	chromosome 10 open reading frame 54	C10orf54	0.00931731
201189_s_	inositol 1,4,5-triphosphate receptor, type 3	ITPR3	0.000992158
238032_at	Transcribed locus	---	0.00421664
213258_at	tissue factor pathway inhibitor (lipoprotein	TFPI	0.00308828
208436_s_	interferon regulatory factor 7	IRF7	0.00397684
203418_at	cyclin A2	CCNA2	0.00861051
227550_at	hypothetical protein LOC143381	LOC14338	0.0346862
208696_at	chaperonin containing TCP1, subunit 5 (e	CCT5	1.43E-05
218691_s_	PDZ and LIM domain 4	PDLIM4	0.000590542
209660_at	transthyretin (prealbumin, amyloidosis typ	TTR	0.000362599
216005_at	Tenascin C (hexabrachion)	TNC	0.000601879
201508_at	insulin-like growth factor binding protein 4	IGFBP4	0.0123115
206908_s_	claudin 11 (oligodendrocyte transmembra	CLDN11	0.0307397
213994_s_	spondin 1, extracellular matrix protein	SPON1	0.0042351
237426_at	SP100 nuclear antigen	SP100	0.000720286
239448_at	Transcribed locus	---	0.000373071
219858_s_	FLJ20160 protein	FLJ20160	0.000967433
226869_at	multiple EGF-like-domains 6	MEGF6	0.0167423
230165_at	shugoshin-like 2 (S. pombe)	SGOL2	0.016266
220783_at	matrix metallopeptidase 27	MMP27	0.0044869
203214_x_	cell division cycle 2, G1 to S and G2 to M	CDC2	0.0412158
239979_at	---	---	0.0217112
223556_at	helicase, lymphoid-specific	HELLS	0.00747912
204680_s_	Rap guanine nucleotide exchange factor (	RAPGEF5	0.0396291
224184_s_	Boc homolog (mouse)	BOC	0.000599366
217436_x_	major histocompatibility complex, class I,	HLA-J	0.00056912
205193_at	v-maf musculoaponeurotic fibrosarcoma o	MAFF	0.000923528
210374_x_	prostaglandin E receptor 3 (subtype EP3)	PTGER3	0.0310417
200814_at	proteasome (prosome, macropain) activat	PSME1	0.000565822
205891_at	adenosine A2b receptor	ADORA2B	0.00152529
206796_at	WNT1 inducible signaling pathway protein	WISP1	0.000224668
209654_at	KIAA0947 protein	KIAA0947	0.000383936
202947_s_	glycophorin C (Gerbich blood group)	GYPC	0.00205149
211564_s_	PDZ and LIM domain 4	PDLIM4	0.00227312

201292_at	topoisomerase (DNA) II alpha 170kDa	TOP2A	0.0352924
201736_s_	membrane-associated ring finger (C3HC4	6-Mar	0.000129912
218943_s_	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX58	0.0228156
221207_s_	neurobeachin	NBEA	0.00330863
232392_at	Splicing factor, arginine/serine-rich 3	SFRS3	0.00968276
215184_at	death-associated protein kinase 2	DAPK2	0.00897605
211974_x_	recombination signal binding protein for im	RBPJ	0.00113786
203414_at	monocyte to macrophage differentiation-a	MMD	0.00932319
208394_x_	endothelial cell-specific molecule 1	ESM1	0.00596685
207334_s_	transforming growth factor, beta receptor I	TGFBR2	0.0221049
219168_s_	proline rich 5 (renal)	PRR5	0.0120608
239014_at	Cell division cycle and apoptosis regulator	CCAR1	0.00774426
201645_at	tenascin C (hexabrachion)	TNC	0.00101263
226299_at	protein kinase N3	PKN3	0.000139449
225531_at	Cdk5 and Abl enzyme substrate 1	CABLES1	0.0011324
1552680_a	cancer susceptibility candidate 5	CASC5	0.00369917
1559117_a	CDNA FLJ34664 fis, clone LIVER200059	---	0.00060772
204908_s_	B-cell CLL/lymphoma 3	BCL3	0.00319308
228044_at	stress-associated endoplasmic reticulum	SERP2	0.00382643
205696_s_	GDNF family receptor alpha 1	GFRA1	0.0143426
208614_s_	filamin B, beta (actin binding protein 278)	FLNB	0.000122279
224061_at	indolethylamine N-methyltransferase	INMT	0.000875298
226474_at	NLR family, CARD domain containing 5	NLRC5	0.00132903
1553778_a	Williams Beuren syndrome chromosome r	WBSCR27	0.000236394
1561775_a	---	---	0.0494676
226252_at	CDNA FLJ34585 fis, clone KIDNE200875	---	0.00168384
241762_at	F-box protein 32	FBXO32	0.0140194
228152_s_	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX60L	0.0125638
232396_at	MRNA full length insert cDNA clone EUR	---	0.00243484
205034_at	cyclin E2	CCNE2	0.0268632
213822_s_	ubiquitin protein ligase E3B	UBE3B	0.000357856
36711_at	v-maf musculoaponeurotic fibrosarcoma o	MAFF	2.27E-05
219203_at	chromosome 14 open reading frame 122	C14orf122	0.00300456
227376_at	GLI-Kruppel family member GLI3 (Greig c	GLI3	0.00431039
243296_at	Nicotinamide phosphoribosyltransferase	NAMPT	0.00454309
225894_at	synaptopodin 2	SYNPO2	0.000398436
210375_at	prostaglandin E receptor 3 (subtype EP3)	PTGER3	0.00594996
211799_x_	major histocompatibility complex, class I,	HLA-C	0.000643785
229026_at	Transcribed locus	---	0.0194307
218066_at	solute carrier family 12 (potassium/chlorid	SLC12A7	0.00216525
228617_at	XIAP associated factor 1	XAF1	0.0105359
234095_at	CDNA FLJ13274 fis, clone OVARC10010	---	0.00560518
204580_at	matrix metallopeptidase 12 (macrophage	MMP12	0.00219174
204159_at	cyclin-dependent kinase inhibitor 2C (p18,	CDKN2C	0.0064833
213556_at	similar to R28379_1	LOC39094	0.000276456
232263_at	solute carrier family 6, member 15	SLC6A15	0.00201564
222830_at	grainyhead-like 1 (Drosophila)	GRHL1	0.0010831
238069_at	CDNA: FLJ21968 fis, clone HEP05670	---	0.000712602
242363_at	Transcribed locus	---	0.000693045
230036_at	sterile alpha motif domain containing 9-lik	SAMD9L	0.00360549
214022_s_	interferon induced transmembrane protein	IFITM1	0.00250266
219488_at	alpha 1,4-galactosyltransferase (globotria	A4GALT	0.00585711
226743_at	schlafen family member 11	SLFN11	0.00429035

203689_s_	fragile X mental retardation 1	FMR1	0.000248765
206364_at	kinesin family member 14	KIF14	0.0364379
202589_at	thymidylate synthetase	TYMS	0.00846862
217482_at	CDNA FLJ11925 fis, clone HEMBB10003	---	0.000703807
208944_at	transforming growth factor, beta receptor I	TGFBR2	0.00279613
222303_at	---	---	0.00236147
220941_s_	chromosome 21 open reading frame 91	C21orf91	0.000494978
208079_s_	aurora kinase A	AURKA	0.0272562
228766_at	---	---	0.0165698
238669_at	prostaglandin-endoperoxide synthase 1 (	PTGS1	0.00248779
210735_s_	carbonic anhydrase XII	CA12	0.00163227
204603_at	exonuclease 1	EXO1	0.0074071
220639_at	transmembrane 4 L six family member 20	TM4SF20	0.0140962
38158_at	extra spindle pole bodies homolog 1 (S. c	ESPL1	0.00350355
204254_s_	vitamin D (1,25- dihydroxyvitamin D3) rec	VDR	1.02E-05
223842_s_	scavenger receptor class A, member 3	SCARA3	0.0256031
222101_s_	dachsous 1 (Drosophila)	DCHS1	0.00430393
228462_at	iroquois homeobox 2	IRX2	0.000504559
240815_at	Transcribed locus	---	0.00298998
218663_at	non-SMC condensin I complex, subunit G	NCAPG	0.0334103
1559063_a	EST from clone 79282, full insert	---	0.000109731
214710_s_	cyclin B1	CCNB1	0.0284429
213931_at	inhibitor of DNA binding 2, dominant nega	ID2 /// ID2B	0.0180288
209182_s_	chromosome 10 open reading frame 10	C10orf10	0.00564215
214329_x_	tumor necrosis factor (ligand) superfamily,	TNFSF10	0.0105991
227384_s_	hypothetical protein LOC727820	LOC72782	0.000617803
225955_at	meteorin, glial cell differentiation regulator	LOC65350	8.83E-05
204709_s_	kinesin family member 23	KIF23	0.0302267
235594_at	Small inducible cytokine subfamily E, men	SCYE1	0.000688533
215723_s_	phospholipase D1, phosphatidylcholine-s	PLD1	0.00405365
238226_at	family with sequence similarity 70, membe	FAM70B	0.000863432
218039_at	nucleolar and spindle associated protein 1	NUSAP1	0.04283
233425_at	---	---	0.000289015
208116_s_	mannosidase, alpha, class 1A, member 1	MAN1A1	0.00398682
226055_at	arrestin domain containing 2	ARRDC2	0.000213668
1558636_s	ADAM metallopeptidase with thrombospo	ADAMTS5	0.0322906
209493_at	PDZ domain containing 2	PDZD2	0.0492541
227082_at	MRNA; cDNA DKFZp586K1922 (from clo	---	0.00313456
212949_at	non-SMC condensin I complex, subunit H	NCAPH	0.00941409
229656_s_	similar to echinoderm microtubule associa	FLJ42562	0.0102358
225720_at	synaptopodin 2	SYNPO2	0.000179037
211896_s_	decorin	DCN	0.00482066
230864_at	hypothetical protein MGC42105	MGC42105	0.00655412
238800_s_	Zinc finger, CCHC domain containing 6	ZCCHC6	0.000308323
201140_s_	RAB5C, member RAS oncogene family	RAB5C	0.000449323
202895_s_	signal-regulatory protein alpha	SIRPA	0.0140593
219200_at	FAST kinase domains 3	FASTKD3	0.000137704
223092_at	ankylosis, progressive homolog (mouse)	ANKH	0.000138874
235190_at	Transcribed locus	---	0.000443004
203888_at	thrombomodulin	THBD	0.0103742
212770_at	transducin-like enhancer of split 3 (E(sp1)	TLE3	0.00101754
209234_at	kinesin family member 1B	KIF1B	0.000245038
209011_at	triple functional domain (PTPRF interactin	LOC10013	0.00173918

213749_at	mannan-binding lectin serine peptidase 1	MASP1	0.0029105
202889_x_	microtubule-associated protein 7	MAP7	2.11E-05
215240_at	integrin, beta 3 (platelet glycoprotein IIIa,	ITGB3	8.53E-05
1560680_a	Transcribed locus, moderately similar to N	---	0.00312443
201348_at	glutathione peroxidase 3 (plasma)	GPX3	0.0164575
205303_at	potassium inwardly-rectifying channel, sub	KCNJ8	0.0109176
228143_at	ceruloplasmin (ferroxidase) /// similar to C	CP /// LOC	0.00992146
211502_s_	PFTAIRE protein kinase 1	PFTK1	0.000999222
203435_s_	membrane metallo-endopeptidase	MME	0.000401529
223467_at	RAS, dexamethasone-induced 1	RASD1	6.95E-05
229641_at	Transcribed locus	---	0.000501155
228323_at	cancer susceptibility candidate 5	CASC5	0.0285055
208070_s_	REV3-like, catalytic subunit of DNA polym	REV3L	0.00155584
1553313_s	solute carrier family 5 (inositol transporter	SLC5A3	0.00829315
222608_s_	anillin, actin binding protein	ANLN	0.0476344
219493_at	SHC SH2-domain binding protein 1	SHCBP1	0.0206835
206765_at	potassium inwardly-rectifying channel, sub	KCNJ2	1.01E-05
229534_at	acyl-CoA thioesterase 4	ACOT4	0.00386098
230372_at	Hyaluronan synthase 2	HAS2	0.0170597
225415_at	deltex 3-like (Drosophila)	DTX3L	0.00692013
215509_s_	BUB1 budding uninhibited by benzimidazo	BUB1	0.0247553
212020_s_	antigen identified by monoclonal antibody	MKI67	0.00406333
225173_at	Rho GTPase activating protein 18	ARHGAP1	0.00139237
1557810_a	Clone HEA5 Cri-du-chat critical region mR	---	0.000159554
222731_at	zinc finger, DHHC-type containing 2	ZDHHC2	0.000227827
226250_at	CDNA FLJ34585 fis, clone KIDNE200875	---	1.01E-05
215172_at	protein tyrosine phosphatase, non-recepto	PTPN20A /	5.26E-07
205003_at	dedicator of cytokinesis 4	DOCK4	0.00102142
231773_at	angiopoietin-like 1	ANGPTL1	0.00113519
202412_s_	ubiquitin specific peptidase 1	USP1	0.00114846
219902_at	betaine-homocysteine methyltransferase	BHMT2	0.00036062
234269_at	CDNA FLJ20012 fis, clone ADKA03438	---	0.000336755
201272_at	aldo-keto reductase family 1, member B1	AKR1B1	0.0045023
236000_s_	Transcribed locus	---	6.58E-06
229429_x_	family with sequence similarity 91, membe	FAM91A2	0.00177902
1556606_a	neuron navigator 2	NAV2	0.00268994
227959_at	Transcribed locus, weakly similar to XP_0	---	0.00977339
225946_at	Ras association (RalGDS/AF-6) domain fa	RASSF8	2.40E-05
219403_s_	heparanase	HPSE	6.70E-05
203434_s_	membrane metallo-endopeptidase	MME	8.38E-05
201329_s_	v-ets erythroblastosis virus E26 oncogene	ETS2	0.00548814
228523_at	nanos homolog 1 (Drosophila)	NANOS1	0.0188903
203764_at	discs, large homolog 7 (Drosophila)	DLG7	0.0251932
202446_s_	phospholipid scramblase 1	PLSCR1	0.0156625
207828_s_	centromere protein F, 350/400ka (mitosin)	CENPF	0.0236116
203765_at	grancalcin, EF-hand calcium binding prote	GCA	0.00416875
204508_s_	carbonic anhydrase XII	CA12	0.00177206
202954_at	ubiquitin-conjugating enzyme E2C	UBE2C	0.0154838
220651_s_	minichromosome maintenance complex c	MCM10	0.0465039
224534_at	kringle containing transmembrane protein	KREMEN1	0.00235893
209013_x_	triple functional domain (PTPRF interactin	TRIO	0.00138919
209193_at	pim-1 oncogene	PIM1	0.0080629
219594_at	ninjurin 2	NINJ2	0.000159467

202760_s_	PALM2-AKAP2	PALM2-AK	0.00086021
204735_at	phosphodiesterase 4A, cAMP-specific (ph	PDE4A	0.00132608
232238_at	asp (abnormal spindle) homolog, microce	ASPM	0.00787771
229824_at	CDNA FLJ45325 fis, clone BRHIP300671	---	0.0118313
203585_at	zinc finger protein 185 (LIM domain)	ZNF185	0.0049604
201291_s_	topoisomerase (DNA) II alpha 170kDa	TOP2A	0.0458221
205945_at	interleukin 6 receptor	IL6R	0.000201363
236947_at	Transcribed locus	---	0.000240013
226034_at	Homo sapiens, clone IMAGE:3881549, m	---	0.00771801
228573_at	Transcribed locus	---	0.000161695
238751_at	CDNA clone IMAGE:4791597	---	0.012394
227452_at	CDNA FLJ26252 fis, clone DMC03335	---	0.00426557
226636_at	phospholipase D1, phosphatidylcholine-s	PLD1	0.00420614
203865_s_	adenosine deaminase, RNA-specific, B1 (	ADARB1	0.0358167
213131_at	olfactomedin 1	OLFM1	0.00189391
224461_s_	apoptosis-inducing factor, mitochondrion-	AIFM2	0.000495921
207233_s_	microphthalmia-associated transcription f	MITF	0.00890918
241703_at	RUN domain containing 3B	RUNDC3B	0.00124424
209583_s_	CD200 molecule	CD200	0.0317037
232278_s_	DEP domain containing 1	DEPDC1	0.0229393
1554408_a	thymidine kinase 1, soluble	TK1	0.0228817
227259_at	CD47 molecule	CD47	0.000919645
217130_at	chromosome 9 open reading frame 33	C9orf33	0.00379203
204748_at	prostaglandin-endoperoxide synthase 2 (	PTGS2	0.00979448
214091_s_	glutathione peroxidase 3 (plasma)	GPX3	0.0134431
218986_s_	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX60	0.00744437
229797_at	mucolipin 3	MCOLN3	0.0016909
228531_at	sterile alpha motif domain containing 9	SAMD9	0.00231659
202901_x_	cathepsin S	CTSS	0.0133992
212769_at	transducin-like enhancer of split 3 (E(sp1)	TLE3	2.26E-06
212886_at	coiled-coil domain containing 69	CCDC69	0.00040884
1552455_a	prune homolog 2 (Drosophila)	PRUNE2	0.000744871
205289_at	bone morphogenetic protein 2	BMP2	0.0341181
218542_at	centrosomal protein 55kDa	CEP55	0.0299661
239185_at	ATP-binding cassette, sub-family A (ABC1	ABCA9	0.000232482
227265_at	fibrinogen-like 2	FGL2	0.00268432
218662_s_	non-SMC condensin I complex, subunit G	NCAPG	0.0369285
205559_s_	proprotein convertase subtilisin/kexin type	PCSK5	0.0120825
204014_at	dual specificity phosphatase 4	DUSP4	0.00896898
203835_at	leucine rich repeat containing 32	LRRC32	9.84E-05
212392_s_	phosphodiesterase 4D interacting protein	LOC65252	0.000966371
202732_at	protein kinase (cAMP-dependent, catalyti	PKIG	0.0117492
207388_s_	prostaglandin E synthase	PTGES	0.000420517
229068_at	chaperonin containing TCP1, subunit 5 (e	CCT5	8.46E-05
203200_s_	5-methyltetrahydrofolate-homocysteine m	MTRR	3.33E-05
221801_x_	neurofilament, light polypeptide 68kDa	NEFL	0.00059889
224770_s_	neuron navigator 1	NAV1	0.000707851
202241_at	tribbles homolog 1 (Drosophila)	TRIB1	0.00275581
1553589_a	PDZK1 interacting protein 1	PDZK1IP1	0.000666866
240407_at	hypothetical LOC100126784	LOC10012	0.00482287
206133_at	XIAP associated factor 1	XAF1	0.00106923
232120_at	CDNA FLJ14259 fis, clone PLACE100107	---	7.59E-05
213007_at	Fanconi anemia, complementation group	FANCI	0.0122748

209348_s_	v-maf musculoaponeurotic fibrosarcoma o	MAF	0.00439048
205046_at	centromere protein E, 312kDa	CENPE	0.0147943
212822_at	HEG homolog 1 (zebrafish)	HEG1	0.00058387
219011_at	pleckstrin homology domain containing, fa	PLEKHA4	0.00342707
1555758_a	cyclin-dependent kinase inhibitor 3 (CDK2	CDKN3	0.0129636
226433_at	ring finger protein 157	RNF157	0.000467861
202986_at	aryl-hydrocarbon receptor nuclear translo	ARNT2	3.69E-05
219935_at	ADAM metallopeptidase with thrombospo	ADAMTS5	0.0147308
228636_at	basic helix-loop-helix domain containing,	BHLHB5	0.0231697
1561908_a	Heparan sulfate (glucosamine) 3-O-sulfot	HS3ST3B1	0.000435658
219062_s_	zinc finger, CCHC domain containing 2	ZCCHC2	0.000629896
1553102_a	coiled-coil domain containing 69	CCDC69	0.00145579
232618_at	chromosome Y open reading frame 15A	CYorf15A	1.46E-05
204135_at	filamin A interacting protein 1-like	FILIP1L	0.000221374
231218_at	Transcribed locus	---	0.000431423
241897_at	---	---	0.000776008
210155_at	myocilin, trabecular meshwork inducible g	MYOC	0.00269018
209012_at	triple functional domain (PTPRF interactin	TRIO	0.0053525
239786_at	Transcribed locus	---	0.00086576
204315_s_	G-2 and S-phase expressed 1	GTSE1	0.0153006
202094_at	baculoviral IAP repeat-containing 5 (surviv	BIRC5	0.0143053
204015_s_	dual specificity phosphatase 4	DUSP4	0.00649385
205668_at	lymphocyte antigen 75	LY75	0.00513453
225491_at	solute carrier family 1 (glial high affinity gl	SLC1A2	0.0361921
230741_at	Full length insert cDNA clone YX74D05	---	0.00699084
235008_at	CDNA FLJ25241 fis, clone STM02689	---	0.00493345
225990_at	Boc homolog (mouse)	BOC	6.50E-05
239340_at	Transcribed locus	---	0.00820457
213464_at	SHC (Src homology 2 domain containing)	SHC2	0.019237
229432_at	N-acetylglutamate synthase	NAGS	0.00196276
201156_s_	RAB5C, member RAS oncogene family	RAB5C	0.000345023
233607_at	CDNA FLJ11739 fis, clone HEMBA10054	---	0.000568526
207165_at	hyaluronan-mediated motility receptor (R	HMMR	0.0101429
206279_at	protein kinase, Y-linked	PRKY	0.000489479
227419_x_	placenta-specific 9	PLAC9	0.00548045
222817_at	hydroxy-delta-5-steroid dehydrogenase, 3	HSD3B7	0.000215693
205345_at	BRCA1 associated RING domain 1	BARD1	0.0171235
207836_s_	RNA binding protein with multiple splicing	RBPMS	0.00363621
232716_at	CDNA FLJ11971 fis, clone HEMBB10012	---	0.00292192
213375_s_	NEDD4 binding protein 2-like 1	N4BP2L1	0.00116083
222793_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX58	0.0134234
214734_at	exophilin 5	EXPH5	0.00882496
212067_s_	complement component 1, r subcompone	C1R	0.0083799
219044_at	threonine synthase-like 2 (S. cerevisiae)	THNSL2	0.000529659
225524_at	anthrax toxin receptor 2	ANTXR2	0.000154285
240809_at	chromosome 21 open reading frame 121	C21orf121	0.000836321
210087_s_	myelin protein zero-like 1	MPZL1	1.77E-05
202466_at	polymerase (DNA directed) sigma	POLS	0.000317649
225687_at	family with sequence similarity 83, membe	FAM83D	0.0172628
203139_at	death-associated protein kinase 1	DAPK1	0.0337024
231972_at	CDNA: FLJ21028 fis, clone CAE07155	---	0.00171634
223094_s_	ankylosis, progressive homolog (mouse)	ANKH	0.00101912
239167_at	Transcribed locus	---	0.00298781

210454_s_	potassium inwardly-rectifying channel, su	KCNJ6	0.0192892
219588_s_	non-SMC condensin II complex, subunit G	NCAPG2	0.0131429
216261_at	integrin, beta 3 (platelet glycoprotein IIIa,	ITGB3	0.00182203
203755_at	BUB1 budding uninhibited by benzimidaz	BUB1B	0.0124009
1555935_s	hormonally upregulated Neu-associated k	HUNK	0.00140952
220484_at	mucolipin 3	MCOLN3	0.0164271
236243_at	Zinc finger, CCHC domain containing 6	ZCCHC6	2.05E-05
212268_at	serpin peptidase inhibitor, clade B (ovalbu	SERPINB1	4.66E-05
218308_at	transforming, acidic coiled-coil containing	TACC3	0.00380731
235182_at	chromosome 20 open reading frame 82	C20orf82	0.000509876
232027_at	spectrin repeat containing, nuclear envelo	SYNE1	0.00372152
225046_at	hypothetical protein LOC100132181	LOC10013	0.0204583
1560826_a	CDNA clone IMAGE:4151535	---	0.00694149
201983_s_	epidermal growth factor receptor (erythrol	EGFR	0.00365048
219229_at	solute carrier organic anion transporter fa	SLCO3A1	0.00178317
206271_at	toll-like receptor 3	TLR3	0.000863886
227394_at	neural cell adhesion molecule 1	NCAM1	0.010189
219306_at	kinesin family member 15	KIF15	0.00709666
211519_s_	kinesin family member 2C	KIF2C	0.0113515
221760_at	Mannosidase, alpha, class 1A, member 1	MAN1A1	0.0030417
242961_x_	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX58	0.00269403
203145_at	sperm associated antigen 5	SPAG5	0.00575548
244579_at	Transcribed locus	---	1.43E-05
230360_at	gliomedin	GLDN	0.00085012
213125_at	olfactomedin-like 2B	OLFML2B	0.0135399
213256_at	membrane-associated ring finger (C3HC4	LOC10013	0.0022889
218726_at	Holliday junction recognition protein	HJURP	0.00734757
225532_at	Cdk5 and Abl enzyme substrate 1	CABLES1	0.000110911
227083_at	beta 1,3-galactosyltransferase-like	B3GALTL	2.53E-05
217590_s_	transient receptor potential cation channel	TRPA1	0.00371432
243048_at	cat eye syndrome chromosome region, ca	CECR7	0.000115977
1570360_s	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX3Y /// L	0.00102764
233044_at	CDNA FLJ12308 fis, clone MAMMA10019	---	0.000105261
243907_at	Transcribed locus	---	0.0014688
227209_at	Contactin 1	CNTN1	0.0181718
206377_at	forkhead box F2	FOXF2	0.000847709
213757_at	Transcribed locus, weakly similar to XP_0	---	0.00010138
226930_at	fibronectin type III domain containing 1	FNDC1	0.0042484
209714_s_	cyclin-dependent kinase inhibitor 3 (CDK2	CDKN3	0.0132235
220034_at	interleukin-1 receptor-associated kinase 3	IRAK3	0.0018898
218309_at	calcium/calmodulin-dependent protein kin	CAMK2N1	0.00546105
232024_at	GTPase, IMAP family member 2	GIMAP2	0.000792575
204806_x_	major histocompatibility complex, class I,	HLA-F	9.59E-05
221875_x_	major histocompatibility complex, class I,	HLA-F	0.000192881
213909_at	leucine rich repeat containing 15	LRRC15	0.000979521
226955_at	actin filament associated protein 1-like 1	AFAP1L1	0.000223886
206631_at	prostaglandin E receptor 2 (subtype EP2),	PTGER2	0.00158312
205128_x_	prostaglandin-endoperoxide synthase 1 (	PTGS1	6.64E-05
202723_s_	forkhead box O1	FOXO1	0.00538917
216941_s_	TATA box binding protein (TBP)-associate	TAF1B	0.0012758
1556329_a	CDNA clone IMAGE:5301690	---	0.00183823
212946_at	KIAA0564	KIAA0564	0.00655876
213791_at	proenkephalin	PENK	0.0031265

236926_at	T-box 1	TBX1	7.95E-05
235086_at	Thrombospondin 1	THBS1	0.00864128
205304_s_	potassium inwardly-rectifying channel, sub	KCNJ8	0.00215557
226397_s_	CDNA: FLJ21028 fis, clone CAE07155	---	0.00243013
218755_at	kinesin family member 20A	KIF20A	0.0301367
224999_at	Placenta mRNA, clone PL45, partial sequ	---	5.12E-05
228155_at	chromosome 10 open reading frame 58	C10orf58	0.0227382
236114_at	Transcribed locus	---	0.00210214
225380_at	hypothetical protein BC007901	LOC91461	0.00443274
223274_at	transcription factor 19 (SC1)	TCF19	0.00978452
1569342_a	GLI-Kruppel family member GLI3 (Greig c	GLI3	6.43E-05
239587_at	Transcribed locus	---	0.00584814
213071_at	dermatopontin	DPT	0.0355208
203788_s_	sema domain, immunoglobulin domain (Ig	SEMA3C	1.56E-05
230475_at	similar to RIKEN cDNA 6030419C18 gene	LOC38813	0.00221426
208747_s_	complement component 1, s subcompone	C1S	0.00453159
202890_at	microtubule-associated protein 7	MAP7	0.00382323
235019_at	carboxypeptidase M	CPM	0.000516911
204187_at	guanosine monophosphate reductase	GMPR	0.00177779
231973_s_	anaphase promoting complex subunit 1	ANAPC1	0.000269815
211149_at	ubiquitously transcribed tetratricopeptide r	LOC10013	6.67E-05
230319_at	CDNA FLJ36413 fis, clone THYMU20108	---	0.00295311
203886_s_	fibulin 2	FBLN2	0.00190232
209687_at	chemokine (C-X-C motif) ligand 12 (strom	CXCL12	0.000119821
224937_at	prostaglandin F2 receptor negative regula	PTGFRN	0.0133572
235088_at	hypothetical protein LOC201725	LOC20172	0.00031198
229070_at	chromosome 6 open reading frame 105	C6orf105	0.0100242
1553243_a	inter-alpha (globulin) inhibitor H5	ITIH5	0.000270955
1553129_a	sushi, von Willebrand factor type A, EGF a	SVEP1	1.16E-05
236641_at	kinesin family member 14	KIF14	0.0195887
239706_x_	Transcribed locus	---	0.000536394
209709_s_	hyaluronan-mediated motility receptor (RH	HMMR	0.00790852
238577_s_	Teashirt zinc finger homeobox 2	TSHZ2	0.000167512
213122_at	TSPY-like 5	TSPYL5	0.00247258
224341_x_	toll-like receptor 4	TLR4	0.00167171
221841_s_	Kruppel-like factor 4 (gut)	KLF4	0.00168486
209928_s_	musculin (activated B-cell factor-1)	MSC	0.0146815
1552619_a	anillin, actin binding protein	ANLN	0.0202964
204591_at	cell adhesion molecule with homology to L	CHL1	0.00728325
212022_s_	antigen identified by monoclonal antibody	MKI67	0.035627
214131_at	chromosome Y open reading frame 15B	CYorf15B	0.000770431
204858_s_	thymidine phosphorylase	TYMP	1.50E-05
225868_at	tripartite motif-containing 47	TRIM47	0.0181127
225817_at	cingulin-like 1	CGNL1	0.012685
208613_s_	filamin B, beta (actin binding protein 278)	FLNB	0.000459186
239942_at	Transcribed locus	---	0.00460812
231925_at	CDNA: FLJ23006 fis, clone LNG00414	---	0.000379433
210305_at	phosphodiesterase 4D interacting protein	PDE4DIP	0.00472712
211062_s_	carboxypeptidase Z	CPZ	0.00261938
234987_at	Transcribed locus	---	0.011621
202994_s_	fibulin 1	FBLN1	0.00197431
218638_s_	spondin 2, extracellular matrix protein	SPON2	0.00700382
229305_at	MLF1 interacting protein	MLF1IP	0.0261058

221523_s_	Ras-related GTP binding D	RRAGD	0.0107573
231118_at	ankyrin repeat domain 35	ANKRD35	0.0039464
1564378_a	CDNA: FLJ21448 fis, clone COL04473	---	0.00238166
203037_s_	metastasis suppressor 1	MTSS1	0.00334503
219528_s_	B-cell CLL/lymphoma 11B (zinc finger prot	BCL11B	6.24E-05
1555989_a	Transcribed locus	---	0.000853571
239583_x_	placenta-specific 7	PLAC7	0.000977265
242055_at	Transcribed locus	---	0.000468911
218400_at	2'-5'-oligoadenylate synthetase 3, 100kDa	OAS3	0.00767941
201890_at	ribonucleotide reductase M2 polypeptide	RRM2	0.020516
239022_at	succinate dehydrogenase complex, subun	SDHALP1	0.00387555
228195_at	hypothetical protein MGC13057	MGC13057	0.000234362
1554966_a	filamin A interacting protein 1-like	FILIP1L	8.97E-05
1554696_s	thymidylate synthetase	TYMS	0.010322
232615_at	CDNA: FLJ22765 fis, clone KAIA1180	---	0.000824632
219209_at	interferon induced with helicase C domain	IFIH1	0.0203932
236901_at	Transcribed locus	---	0.00255182
209959_at	nuclear receptor subfamily 4, group A, me	NR4A3	0.00061914
223687_s_	lymphocyte antigen 6 complex, locus K	LY6K	1.26E-05
202995_s_	fibulin 1	FBLN1	0.00283353
218883_s_	MLF1 interacting protein	MLF1IP	0.0204785
202295_s_	cathepsin H	CTSH	0.0272981
201924_at	AF4/FMR2 family, member 1	AFF1	0.00124803
200923_at	lectin, galactoside-binding, soluble, 3 bind	LGALS3BP	0.00312999
227607_at	STAM binding protein-like 1	STAMBPL1	0.00257627
225540_at	microtubule-associated protein 2	MAP2	0.0499821
202481_at	dehydrogenase/reductase (SDR family) m	DHRS3	0.000300766
233011_at	Annexin A1	ANXA1	0.0010848
227250_at	kringle containing transmembrane protein	KREMEN1	2.68E-05
206632_s_	apolipoprotein B mRNA editing enzyme, c	APOBEC3	0.00529155
204962_s_	centromere protein A	CENPA	0.0112326
227145_at	lysyl oxidase-like 4	LOXL4	0.00398377
201430_s_	dihydropyrimidinase-like 3	DPYSL3	0.00405718
204317_at	G-2 and S-phase expressed 1	GTSE1	0.00196197
229538_s_	IQ motif containing GTPase activating pro	IQGAP3	0.0235131
223484_at	chromosome 15 open reading frame 48	C15orf48	0.00093248
221901_at	KIAA1644 protein	LL22NC03-	6.41E-05
204614_at	serpin peptidase inhibitor, clade B (ovalbu	SERPINB2	0.00241448
219978_s_	nucleolar and spindle associated protein 1	NUSAP1	0.018981
224950_at	prostaglandin F2 receptor negative regula	PTGFRN	0.000396002
242794_at	mastermind-like 3 (Drosophila)	MAML3	0.00102148
241455_at	Transcribed locus	---	0.0039557
231828_at	CDNA clone IMAGE:5218355	---	0.000114137
213457_at	malignant fibrous histiocytoma amplified s	MFHAS1	7.89E-05
205347_s_	thymosin-like 8 /// thymosin beta15b	MGC39900	0.0083217
212843_at	neural cell adhesion molecule 1	NCAM1	0.00442576
219630_at	PDZK1 interacting protein 1	PDZK1IP1	0.000385036
225325_at	FLJ20160 protein	FLJ20160	0.0160941
204273_at	endothelin receptor type B	EDNRB	0.00041345
227995_at	MRNA; cDNA DKFZp564O0862 (from clo	---	0.00535172
229404_at	twist homolog 2 (Drosophila)	TWIST2	0.000188429
206330_s_	SHC (Src homology 2 domain containing)	SHC3	0.00651784
233130_at	CDNA FLJ12202 fis, clone MAMMA10009	---	0.00411807

218355_at	kinesin family member 4A	KIF4A	0.00206756
221524_s_	Ras-related GTP binding D	RRAGD	0.00528731
205100_at	glutamine-fructose-6-phosphate transami	GFPT2	0.00168892
210136_at	myelin basic protein	MBP	0.0441277
207063_at	chromosome Y open reading frame 14	CYorf14	1.11E-05
226066_at	microphthalmia-associated transcription f	MITF	0.0088324
237953_at	---	---	0.000233766
212801_at	citron (rho-interacting, serine/threonine ki	CIT	0.0038381
221087_s_	apolipoprotein L, 3	APOL3	0.00605574
229352_at	NADPH oxidase, EF-hand calcium binding	NOX5 /// S	0.000892555
227949_at	phosphatase and actin regulator 3	PHACTR3	0.0033788
204162_at	NDC80 homolog, kinetochore complex co	NDC80	0.0173635
203571_s_	chromosome 10 open reading frame 116	C10orf116	0.0143633
203823_at	regulator of G-protein signaling 3	RGS3	0.00901786
225207_at	pyruvate dehydrogenase kinase, isozyme	PDK4	0.028869
202870_s_	cell division cycle 20 homolog (S. cerevisi	CDC20	0.0110838
228807_at	Transcribed locus	---	0.000297636
223646_s_	chromosome Y open reading frame 15B	CYorf15B	0.00132998
209354_at	tumor necrosis factor receptor superfamily	TNFRSF14	0.000186203
210557_x_	colony stimulating factor 1 (macrophage)	CSF1	0.00110798
202145_at	lymphocyte antigen 6 complex, locus E	LY6E	0.0034165
244804_at	Sequestosome 1	SQSTM1	0.00352988
211991_s_	major histocompatibility complex, class II,	HLA-DPA1	0.00195874
209140_x_	major histocompatibility complex, class I,	HLA-B /// H	0.000572644
204509_at	carbonic anhydrase XII	CA12	0.000479351
225061_at	DnaJ (Hsp40) homolog, subfamily A, mem	DNAJA4	0.000143203
219778_at	zinc finger protein, multitype 2	ZFPM2	0.000289125
202644_s_	tumor necrosis factor, alpha-induced prot	TNFAIP3	0.00275218
205542_at	six transmembrane epithelial antigen of th	STEAP1	0.000184575
229800_at	Doublecortin-like kinase 1	DCLK1	0.000221206
230588_s_	hypothetical protein LOC285074	LOC28507	0.000778975
212681_at	erythrocyte membrane protein band 4.1-li	EPB41L3	6.25E-06
1557570_a	hypothetical protein LOC285084	LOC28508	0.00426857
203508_at	tumor necrosis factor receptor superfamily	TNFRSF1B	0.000117028
218404_at	sorting nexin 10	SNX10	0.000846844
202869_at	2',5'-oligoadenylate synthetase 1, 40/46k	OAS1	0.0179848
216526_x_	major histocompatibility complex, class I,	HLA-B /// H	8.55E-06
213933_at	prostaglandin E receptor 3 (subtype EP3)	PTGER3	0.0074709
213197_at	astrotactin 1	ASTN1	0.00126877
1553572_a	cytoglobin	CYGB	0.00106032
224374_s_	elastin microfibril interfacer 2	EMILIN2	3.73E-06
202948_at	interleukin 1 receptor, type I	IL1R1	0.00541884
209183_s_	chromosome 10 open reading frame 10	C10orf10	0.00993392
225612_s_	UDP-GlcNAc:betaGal beta-1,3-N-acetylgl	B3GNT5	0.042753
227468_at	carnitine palmitoyltransferase 1C	CPT1C	0.000199378
215813_s_	prostaglandin-endoperoxide synthase 1 (	PTGS1	0.000127229
237372_at	Transcribed locus	---	0.00494459
204683_at	intercellular adhesion molecule 2	ICAM2	0.00697965
52837_at	KIAA1644 protein	LL22NC03-	0.000242922
209773_s_	ribonucleotide reductase M2 polypeptide	RRM2	0.0125776
209642_at	BUB1 budding uninhibited by benzimidaz	BUB1	0.015667
233847_x_	Uncharacterized gastric protein ZA31P	---	0.0294928
1570155_a	Transcribed locus	---	0.00012932

238015_at	hypothetical protein LOC201725	LOC20172	0.00212392
215942_s_	G-2 and S-phase expressed 1	GTSE1	0.00805376
211911_x_	major histocompatibility complex, class I,	FAM20B ///	0.000231708
209785_s_	phospholipase A2, group IVC (cytosolic, c	PLA2G4C	0.000674107
206371_at	folate receptor 3 (gamma)	FOLR3	0.00314118
221886_at	DENN/MADD domain containing 2A	DENND2A	0.000123159
208018_s_	hemopoietic cell kinase	HCK	0.0359005
227826_s_	CDNA clone IMAGE:4791597	---	0.00833954
206432_at	hyaluronan synthase 2	HAS2	0.0107021
232224_at	mannan-binding lectin serine peptidase 1	MASP1	0.000856411
219863_at	hect domain and RLD 5	HERC5	0.00114028
204318_s_	G-2 and S-phase expressed 1	GTSE1	0.0105525
213142_x_	hypothetical protein LOC54103	tcag7.1314	0.000292819
242881_x_	Clone HLS_IMAGE_626842 mRNA seque	---	0.00544382
209821_at	interleukin 33	IL33	0.000710886
202391_at	brain abundant, membrane attached sign	BASP1	6.99E-05
211809_x_	collagen, type XIII, alpha 1	COL13A1	0.000235774
235706_at	carboxypeptidase M	CPM	0.000739037
209897_s_	slit homolog 2 (Drosophila)	SLIT2	0.00475187
227827_at	CDNA clone IMAGE:4791597	---	0.00896038
227084_at	dystrobrevin, alpha	DTNA	0.00855052
238513_at	Proline rich Gla (G-carboxyglutamic acid)	PRRG4	0.000614123
244521_at	Teashirt zinc finger homeobox 2	TSHZ2	3.67E-05
218009_s_	protein regulator of cytokinesis 1	PRC1	0.00620085
216222_s_	myosin X	MYO10	0.00139337
207834_at	fibulin 1	FBLN1	0.0014234
230930_at	hypothetical protein LOC338620	LOC33862	6.62E-05
202709_at	fibromodulin	FMOD	0.0133415
206027_at	S100 calcium binding protein A3	S100A3	0.00553359
212338_at	myosin ID	MYO1D	0.0107
227475_at	forkhead box Q1	FOXQ1	0.000648833
220975_s_	C1q and tumor necrosis factor related pro	C1QTNF1	0.0178947
201427_s_	selenoprotein P, plasma, 1	SEPP1	0.00218086
202859_x_	interleukin 8	IL8	0.018724
213921_at	somatostatin	SST	0.00966379
1558034_s	ceruloplasmin (ferroxidase)	CP	0.00882818
217626_at	aldo-keto reductase family 1, member C1	AKR1C1	0.00332874
209829_at	chromosome 6 open reading frame 32	C6orf32	4.01E-07
208562_s_	ATP-binding cassette, sub-family C (CFTF	ABCC9	0.000304999
209596_at	matrix-remodelling associated 5	MXRA5	0.00318614
210664_s_	tissue factor pathway inhibitor (lipoprotein	TFPI	0.00153224
227606_s_	STAM binding protein-like 1	STAMBPL1	0.000858161
232925_at	CDNA FLJ13503 fis, clone PLACE100483	---	0.000456139
235244_at	coiled-coil domain containing 58	CCDC58	5.18E-05
229872_s_	hypothetical protein LOC100132999	LOC10013	0.0191289
228139_at	receptor-interacting serine-threonine kina	RIPK3	1.21E-05
216250_s_	leupaxin	LPXN	7.70E-08
205756_s_	coagulation factor VIII, procoagulant com	F8	0.000166368
202888_s_	alanyl (membrane) aminopeptidase (amin	ANPEP	0.000245335
204072_s_	furry homolog (Drosophila)	FRY	0.00293426
206376_at	solute carrier family 6, member 15	SLC6A15	0.0121353
223194_s_	solute carrier family 22, member 23	SLC22A23	0.00116854
208729_x_	major histocompatibility complex, class I,	HLA-B	0.000185637

208609_s_	tenascin XB	TNXB	0.00288822
1554897_s	rhomboid, veinlet-like 2 (Drosophila)	RHBDL2	0.000156512
225511_at	G protein-coupled receptor, family C, grou	GPRC5B	0.00546552
209335_at	decorin	DCN	0.00116829
202283_at	serpin peptidase inhibitor, clade F (alpha-	SERPINF1	0.0204348
220416_at	ATPase, class I, type 8B, member 4	ATP8B4	0.0025938
210640_s_	G protein-coupled estrogen receptor 1	GPER	1.86E-06
206093_x_	tenascin XA pseudogene /// tenascin XB	TNXA /// TN	0.0111367
202580_x_	forkhead box M1	FOXM1	0.0095167
225973_at	transporter 2, ATP-binding cassette, sub-f	TAP2	0.000495803
211806_s_	potassium inwardly-rectifying channel, sub	KCNJ15	3.33E-05
203000_at	stathmin-like 2	STMN2	0.00248992
209167_at	glycoprotein M6B	GPM6B	4.16E-05
235272_at	suprabasin	SBSN	0.00873135
211776_s_	erythrocyte membrane protein band 4.1-li	EPB41L3	0.00389709
243940_at	teashirt zinc finger homeobox 2	TSHZ2	0.000138491
235821_at	CDNA FLJ14388 fis, clone HEMBA10027	---	6.79E-05
227816_at	netrin 1	NTN1	0.00650487
204678_s_	potassium channel, subfamily K, member	KCNK1	0.0103511
1556590_s	CDNA FLJ25645 fis, clone SYN00113	---	0.000475738
212070_at	G protein-coupled receptor 56	GPR56	0.00237343
204224_s_	GTP cyclohydrolase 1 (dopa-responsive d	GCH1	0.00586338
241014_at	hypothetical protein LOC339400	LOC33940	0.000288146
218824_at	PNMA-like 1	PNMAL1	0.00174597
209869_at	adrenergic, alpha-2A-, receptor	ADRA2A	0.0116941
229127_at	junctional adhesion molecule 2	JAM2	0.00442345
1561642_a	Full length insert cDNA clone YN62D03	---	2.16E-05
210058_at	mitogen-activated protein kinase 13	MAPK13	4.92E-05
240509_s_	gremlin 2, cysteine knot superfamily, hom	GREM2	0.00043848
220266_s_	Kruppel-like factor 4 (gut)	KLF4	0.00179094
226305_at	Ly6/neurotoxin 1	LYNX1	0.00344036
211343_s_	collagen, type XIII, alpha 1	COL13A1	0.000179433
219747_at	chromosome 4 open reading frame 31	C4orf31	0.00702684
222150_s_	hypothetical protein LOC54103	tcag7.1314	0.000538036
237006_at	Transcribed locus	---	0.000112165
242288_s_	elastin microfibril interfacer 2	EMILIN2	0.00110237
205290_s_	bone morphogenetic protein 2	BMP2	0.0263954
228850_s_	---	---	0.00232394
231963_at	CDNA FLJ13937 fis, clone Y79AA100080	---	0.000685355
223749_at	C1q and tumor necrosis factor related pro	C1QTNF2	0.001957
243813_at	CDNA FLJ31059 fis, clone HSYRA20008	---	0.0022715
1555229_a	complement component 1, s subcompone	C1S	0.00144311
210059_s_	mitogen-activated protein kinase 13	MAPK13	1.02E-06
201328_at	v-ets erythroblastosis virus E26 oncogene	ETS2	0.00457381
204628_s_	integrin, beta 3 (platelet glycoprotein IIIa,	ITGB3	0.00415196
238178_at	Transcribed locus	---	0.00326167
209619_at	CD74 molecule, major histocompatibility c	CD74	0.000345006
211839_s_	colony stimulating factor 1 (macrophage)	CSF1	0.000331939
209277_at	tissue factor pathway inhibitor 2	TFPI2	6.58E-05
216841_s_	superoxide dismutase 2, mitochondrial	SOD2	0.00678525
205476_at	chemokine (C-C motif) ligand 20	CCL20	0.0012139
238623_at	CDNA FLJ37310 fis, clone BRAMY20167	---	0.000115976
240556_at	Decorin	DCN	0.000513922

205016_at	transforming growth factor, alpha	TGFA	4.11E-05
202566_s_	supervillin	SVIL	0.00787531
227072_at	rotatin	RTTN	6.48E-05
235616_at	teashirt zinc finger homeobox 2	TSHZ2	0.000340263
1557919_a	Hypothetical protein LOC100128757	LOC64823	0.00178137
202897_at	signal-regulatory protein alpha	SIRPA	0.00105922
219064_at	inter-alpha (globulin) inhibitor H5	ITIH5	0.00200283
229490_s_	Transcribed locus	---	0.00582016
209278_s_	tissue factor pathway inhibitor 2	TFPI2	2.38E-06
216598_s_	chemokine (C-C motif) ligand 2	CCL2	0.0106541
207835_at	fibulin 1	FBLN1	0.000986635
242715_at	Transcribed locus	---	0.00562954
223645_s_	chromosome Y open reading frame 15B	CYorf15B	7.41E-06
209170_s_	glycoprotein M6B	GPM6B	6.73E-06
209732_at	C-type lectin domain family 2, member B	CLEC2B	0.000221107
217504_at	ATP-binding cassette, sub-family A (ABC1	ABCA6	0.00401691
204041_at	monoamine oxidase B	MAOB	0.00351889
235705_at	Transcribed locus	---	0.000288192
205730_s_	actin binding LIM protein family, member	ABLIM3	9.16E-05
224435_at	chromosome 10 open reading frame 58	C10orf58	0.00540239
216333_x_	tenascin XA pseudogene /// tenascin XB	TNXA /// TN	0.00698274
208561_at	ATP-binding cassette, sub-family C (CFTF	ABCC9	0.000106611
222730_s_	zinc finger, DHHC-type containing 2	ZDHHC2	3.91E-05
232584_at	CDNA FLJ12328 fis, clone MAMMA10021	---	7.19E-05
211829_s_	G protein-coupled estrogen receptor 1	GPER	0.0013038
233771_at	CDNA FLJ13489 fis, clone PLACE100393	---	9.23E-05
210229_s_	colony stimulating factor 2 (granulocyte-m	CSF2	0.000217222
218559_s_	v-maf musculoaponeurotic fibrosarcoma o	MAFB	0.0297622
220898_at	---	---	0.000567881
204625_s_	integrin, beta 3 (platelet glycoprotein IIIa,	ITGB3	0.000449763
218543_s_	poly (ADP-ribose) polymerase family, men	PARP12	0.00157191
232746_at	Chemokine (C-X-C motif) receptor 7	CXCR7	0.0034906
202687_s_	tumor necrosis factor (ligand) superfamily,	TNFSF10	0.00100878
206315_at	cytokine receptor-like factor 1	CRLF1	2.03E-05
213451_x_	tenascin XA pseudogene /// tenascin XB	TNXA /// TN	0.00828914
207977_s_	dermatopontin	DPT	0.017822
232617_at	cathepsin S	CTSS	0.00286672
229377_at	growth hormone regulated TBC protein 1	GRTP1	0.000304086
204033_at	thyroid hormone receptor interactor 13	TRIP13	0.00240766
1552502_s	rhomboid, veinlet-like 2 (Drosophila)	RHBDL2	0.000223712
206404_at	fibroblast growth factor 9 (glia-activating fa	FGF9	0.0424026
204679_at	potassium channel, subfamily K, member	KCNK1	0.00405449
219454_at	EGF-like-domain, multiple 6	EGFL6	0.00310029
204846_at	ceruloplasmin (ferroxidase)	CP	0.00719089
242417_at	hypothetical protein LOC283278	LOC28327	0.00243701
228728_at	chromosome 7 open reading frame 58	C7orf58	0.000164583
213929_at	CDNA clone IMAGE:4733238	---	0.00510193
206100_at	carboxypeptidase M	CPM	0.00194873
215223_s_	superoxide dismutase 2, mitochondrial	SOD2	0.0240192
205225_at	estrogen receptor 1	ESR1	6.75E-06
228772_at	histamine N-methyltransferase	HNMT	0.000992596
203887_s_	thrombomodulin	THBD	0.00160071
205552_s_	2',5'-oligoadenylate synthetase 1, 40/46kD	OAS1	0.0132837

222816_s_	zinc finger, CCHC domain containing 2	ZCCHC2	2.52E-05
202643_s_	tumor necrosis factor, alpha-induced prote	TNFAIP3	0.00128364
204429_s_	solute carrier family 2 (facilitated glucose/f	SLC2A5	2.31E-05
221541_at	cysteine-rich secretory protein LCCL doma	CRISPLD2	0.000711641
219684_at	receptor (chemosensory) transporter prote	RTP4	0.00111387
206837_at	ALX homeobox 1	ALX1	0.00188531
207082_at	colony stimulating factor 1 (macrophage)	CSF1	0.000385938
233822_x_	uncharacterized gastric protein YC12P	LOC57400	0.00404897
220030_at	serine/threonine/tyrosine kinase 1	STYK1	0.000246774
206701_x_	endothelin receptor type B	EDNRB	0.000371155
212096_s_	mitochondrial tumor suppressor 1	MTUS1	0.000296155
203666_at	chemokine (C-X-C motif) ligand 12 (strom	CXCL12	0.000130587
205082_s_	aldehyde oxidase 1	AOX1	0.000342018
214807_at	MRNA; cDNA DKFZp564O0862 (from clo	---	0.000769981
232636_at	SLIT and NTRK-like family, member 4	SLITRK4	0.0160102
227654_at	chromosome 20 open reading frame 175	C20orf175	0.000675947
204415_at	interferon, alpha-inducible protein 6	IFI6	0.00142751
206710_s_	erythrocyte membrane protein band 4.1-lik	EPB41L3	0.000311225
204681_s_	Rap guanine nucleotide exchange factor (	RAPGEF5	0.0115947
206987_x_	fibroblast growth factor 18	FGF18	0.0308301
211732_x_	histamine N-methyltransferase	HNMT	0.000700562
232541_at	CDNA FLJ20099 fis, clone COL04544	---	0.000315551
205083_at	aldehyde oxidase 1	AOX1	0.000496723
218510_x_	family with sequence similarity 134, memb	FAM134B	0.000425191
205207_at	interleukin 6 (interferon, beta 2)	IL6	0.00365583
233314_at	phosphatase and tensin homolog (mutate	PTEN	2.03E-06
235931_at	Transcribed locus	---	3.11E-05
242541_at	ATP-binding cassette, sub-family A (ABC1	ABCA9	0.000532679
212538_at	dedicator of cytokinesis 9	DOCK9	0.000580064
226722_at	family with sequence similarity 20, membe	FAM20C	0.000241291
203185_at	Ras association (RalGDS/AF-6) domain fa	RASSF2	0.000444299
204972_at	2'-5'-oligoadenylate synthetase 2, 69/71kD	OAS2	0.00149122
216594_x_	aldo-keto reductase family 1, member C1	AKR1C1	0.0375871
204271_s_	endothelin receptor type B	EDNRB	0.000597861
219213_at	junctional adhesion molecule 2	JAM2	0.00261955
235059_at	RAB12, member RAS oncogene family	RAB12	2.56E-05
233002_at	KIAA1622	KIAA1622	0.00184606
226950_at	activin A receptor type II-like 1	ACVRL1	0.000166647
202565_s_	supervillin	SVIL	0.00915491
203001_s_	stathmin-like 2	STMN2	0.00132611
207103_at	potassium voltage-gated channel, Shal-rel	KCND2	0.000852938
242605_at	Transcribed locus	---	0.000184829
1568849_a	chromosome 21 open reading frame 135	C21orf135	0.00805186
218332_at	brain expressed, X-linked 1	BEX1	0.0145337
211029_x_	fibroblast growth factor 18	FGF18	0.0250074
227188_at	chromosome 21 open reading frame 63	C21orf63	0.00589391
230472_at	iroquois homeobox 1	IRX1	1.58E-05
239461_at	UDP-N-acetyl-alpha-D-galactosamine:poly	GALNTL2	0.000434892
228176_at	sphingosine-1-phosphate receptor 3	S1PR3	0.00153952
237054_at	ectonucleotide pyrophosphatase/phospho	ENPP5	2.06E-05
209699_x_	aldo-keto reductase family 1, member C2	AKR1C2	0.0490811
213568_at	odd-skipped related 2 (Drosophila)	OSR2	0.00412763
211663_x_	prostaglandin D2 synthase 21kDa (brain)	PTGDS	0.000682314

205830_at	calmegin	CLGN	0.00048939
240397_x_	Transcribed locus	---	0.00110986
209613_s_	alcohol dehydrogenase 1B (class I), beta	ADH1B	0.00959505
235504_at	gremlin 2, cysteine knot superfamily, hom	GREM2	0.000126214
211506_s_	interleukin 8	IL8	0.0246823
209716_at	colony stimulating factor 1 (macrophage)	CSF1	0.000859399
241234_at	similar to hCG1812929	LOC64573	2.52E-05
237383_at	Transcribed locus	---	0.000848083
201787_at	fibulin 1 /// similar to Fibulin 1	FBLN1 /// L	0.00148802
213247_at	sushi, von Willebrand factor type A, EGF	SVEP1	0.00271201
211990_at	major histocompatibility complex, class II,	HLA-DPA1	0.00142259
225728_at	sorbin and SH3 domain containing 2	SORBS2	0.000526469
228752_at	chromosome X open reading frame 10	CXorf10	7.67E-05
223044_at	solute carrier family 40 (iron-regulated tra	SLC40A1	0.0125819
230746_s_	Stanniocalcin 1	STC1	0.000360291
209994_s_	ATP-binding cassette, sub-family B (MDR	ABCB1 ///	0.000609726
218999_at	transmembrane protein 140	TMEM140	0.000844126
230130_at	Transcribed locus	---	0.00317374
236361_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNTL2	0.000789789
1558803_a	CDNA FLJ41560 fis, clone CTONG10000	---	0.000244197
228116_at	Clone IMAGE:120162 mRNA sequence	---	0.0123607
204148_s_	zona pellucida glycoprotein 3 (sperm rece	POMZP3 //	0.000283554
202510_s_	tumor necrosis factor, alpha-induced prote	TNFAIP2	0.00344367
205114_s_	chemokine (C-C motif) ligand 3 /// chemok	CCL3 /// C	0.00940884
228790_at	family with sequence similarity 110, memb	FAM110B	0.00417409
219869_s_	solute carrier family 39 (zinc transporter),	SLC39A8	0.0215109
209598_at	paraneoplastic antigen MA2	PNMA2	0.00168334
213068_at	dermatopontin	DPT	0.0149978
226804_at	family with sequence similarity 20, membe	FAM20A	0.00218497
222895_s_	B-cell CLL/lymphoma 11B (zinc finger prot	BCL11B	1.84E-06
214983_at	testis-specific transcript, Y-linked 15	TTTY15	4.27E-05
205794_s_	neuro-oncological ventral antigen 1	NOVA1	0.000942423
242094_at	Full length insert cDNA clone YR40C10	---	0.000215288
228665_at	cysteine/tyrosine-rich 1	CYYR1	0.000229309
204151_x_	aldo-keto reductase family 1, member C1	AKR1C1	0.0418847
201525_at	apolipoprotein D	APOD	0.000393602
205896_at	solute carrier family 22 (organic cation/erg	SLC22A4	1.65E-05
204994_at	myxovirus (influenza virus) resistance 2 (	MX2	0.00287199
204161_s_	ectonucleotide pyrophosphatase/phospho	ENPP4	0.000230536
204112_s_	histamine N-methyltransferase	HNMT	0.000769256
207542_s_	aquaporin 1 (Colton blood group)	AQP1	0.00107127
210692_s_	solute carrier family 43, member 3	SLC43A3	0.000608964
203407_at	periplakin	PPL	0.00952139
234931_at	AYP1 pseudogene 1	AYP1p1	4.80E-06
207819_s_	ATP-binding cassette, sub-family B (MDR	ABCB4	0.00227175
228302_x_	calcium/calmodulin-dependent protein kin	CAMK2N1	0.0040713
220794_at	gremlin 2, cysteine knot superfamily, hom	GREM2	0.000162832
202411_at	interferon, alpha-inducible protein 27	IFI27	0.00146127
228635_at	protocadherin 10	PCDH10	0.00271245
205828_at	matrix metallopeptidase 3 (stromelysin 1,	MMP3	0.00109077
204470_at	chemokine (C-X-C motif) ligand 1 (melanc	CXCL1	0.0213632
219352_at	hect domain and RLD 6	HERC6	0.00418941
213620_s_	intercellular adhesion molecule 2	ICAM2	0.000637834

224397_s_	transmembrane and tetratricopeptide repe	TMTC1	0.00139684
230760_at	zinc finger protein, Y-linked /// hypothetical	LOC10013	8.26E-05
204288_s_	sorbin and SH3 domain containing 2	SORBS2	0.00163624
214265_at	integrin, alpha 8	ITGA8	1.30E-05
210910_s_	POM (POM121 homolog, rat) and ZP3 fus	POMZP3	1.14E-05
212224_at	aldehyde dehydrogenase 1 family, membe	ALDH1A1	0.00390394
223703_at	chromosome 10 open reading frame 11	C10orf11	8.22E-06
210145_at	phospholipase A2, group IVA (cytosolic, ca	PLA2G4A	0.00226044
220032_at	chromosome 7 open reading frame 58	C7orf58	2.82E-05
202902_s_	cathepsin S	CTSS	0.0119945
231382_at	Fibroblast growth factor 18	FGF18	0.0242361
209546_s_	apolipoprotein L, 1	APOL1	3.98E-05
236694_at	chromosome Y open reading frame 15A	CYorf15A	3.94E-06
203632_s_	G protein-coupled receptor, family C, grou	GPRC5B	0.00202759
209612_s_	alcohol dehydrogenase 1B (class I), beta	ADH1B	0.0226839
209267_s_	solute carrier family 39 (zinc transporter),	SLC39A8	0.0200252
234623_x_	Metastasis related protein (MB2)	---	0.0355407
204389_at	monoamine oxidase A	MAOA	3.72E-05
218532_s_	family with sequence similarity 134, memb	FAM134B	0.000662016
229657_at	thyroid hormone receptor, beta (erythrobla	THRB	0.0138931
221885_at	DENN/MADD domain containing 2A	DENND2A	4.47E-05
225871_at	six transmembrane epithelial antigen of th	STEAP2	9.77E-05
219825_at	cytochrome P450, family 26, subfamily B,	CYP26B1	0.000417031
213113_s_	solute carrier family 43, member 3	SLC43A3	0.000621658
211596_s_	leucine-rich repeats and immunoglobulin-l	LRIG1	0.00148583
213797_at	radical S-adenosyl methionine domain cor	RSAD2	0.0368657
213385_at	chimerin (chimaerin) 2	CHN2	0.000696121
227835_at	Hypothetical protein LOC100132181	LOC10013	7.06E-05
204279_at	proteasome (prosome, macropain) subuni	PSMB9	0.00133423
235666_at	Transcribed locus	---	3.09E-05
202688_at	tumor necrosis factor (ligand) superfamily,	TNFSF10	0.00011889
211748_x_	prostaglandin D2 synthase 21kDa (brain)	PTGDS	0.000827568
217220_at	---	---	4.83E-05
232668_at	CDNA FLJ11528 fis, clone HEMBA10026	---	0.000241004
219908_at	dickkopf homolog 2 (Xenopus laevis)	DKK2	0.0133039
221959_at	family with sequence similarity 110, memb	FAM110B	0.0014445
235044_at	cysteine/tyrosine-rich 1	CYYR1	7.55E-05
217767_at	complement component 3	C3	0.00600744
53991_at	DENN/MADD domain containing 2A	DENND2A	7.03E-07
226632_at	cytoglobin	CYGB	0.00286822
227526_at	Cdon homolog (mouse)	CDON	0.00604267
202409_at	insulin-like growth factor 2 (somatomedin	IGF2	0.0367546
1559254_a	chromosome 21 open reading frame 113	C21orf113	0.00250681
204410_at	eukaryotic translation initiation factor 1A,	EIF1AY	0.000126144
242625_at	radical S-adenosyl methionine domain cor	RSAD2	0.0175426
205001_s_	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX3Y ///	4.34E-06
218885_s_	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT12	0.000615301
206026_s_	tumor necrosis factor, alpha-induced prote	TNFAIP6	0.0204457
243115_at	Transcribed locus	---	0.000554233
219552_at	sushi, von Willebrand factor type A, EGF	SVEP1	0.000130366
210119_at	potassium inwardly-rectifying channel, sul	KCNJ15	1.73E-06
204501_at	nephroblastoma overexpressed gene	NOV	0.00172217
213415_at	chloride intracellular channel 2	CLIC2	0.000383294

217553_at	similar to Six transmembrane epithelial an	MGC87042	2.76E-06
226702_at	cytidine monophosphate (UMP-CMP) kina	CMPK2	0.00196967
228716_at	thyroid hormone receptor, beta (erythrobla	THRB	0.0238919
224414_s_	caspase recruitment domain family, memb	CARD6	4.22E-07
234104_at	CDNA FLJ10198 fis, clone HEMBA10048	---	8.07E-05
207703_at	neuroligin 4, Y-linked	NLGN4Y	3.02E-05
206134_at	ADAM-like, decysin 1	ADAMDEC	0.000451843
202086_at	myxovirus (influenza virus) resistance 1, i	MX1	0.00249716
204430_s_	solute carrier family 2 (facilitated glucose/	SLC2A5	0.00015674
213036_x_	ATPase, Ca++ transporting, ubiquitous	ATP2A3	8.93E-05
228501_at	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNTL2	0.000285685
204719_at	ATP-binding cassette, sub-family A (ABC1	ABCA8	0.000117285
212187_x_	prostaglandin D2 synthase 21kDa (brain)	PTGDS	0.00140484
221916_at	neurofilament, light polypeptide 68kDa	NEFL	0.000113664
203828_s_	interleukin 32	IL32	0.00835039
212670_at	elastin (supravalvular aortic stenosis, Willi	ELN	0.00645962
207375_s_	interleukin 15 receptor, alpha	IL15RA	0.000398392
229802_at	CDNA FLJ14388 fis, clone HEMBA10027	---	5.48E-05
210538_s_	baculoviral IAP repeat-containing 3	BIRC3	0.00246491
217546_at	metallothionein 1M	MT1M	0.000652994
202718_at	insulin-like growth factor binding protein 2,	IGFBP2	0.00106489
202286_s_	tumor-associated calcium signal transduc	TACSTD2	0.0067088
221019_s_	collectin sub-family member 12	COLEC12	0.00214998
238455_at	CDNA FLJ45742 fis, clone KIDNE201632	---	0.000319492
206025_s_	tumor necrosis factor, alpha-induced prote	TNFAIP6	0.0197163
205413_at	metallophosphoesterase domain contain	MPPED2	0.00272346
209392_at	ectonucleotide pyrophosphatase/phospho	ENPP2	0.000467628
225016_at	adenomatosis polyposis coli down-regulat	APCDD1	0.00951759
1555623_a	---	---	0.017568
224354_at	---	---	0.0153011
202037_s_	secreted frizzled-related protein 1	SFRP1	0.000273313
204597_x_	stanniocalcin 1	STC1	0.000121422
227742_at	chloride intracellular channel 6	CLIC6	0.0105607
222773_s_	UDP-N-acetyl-alpha-D-galactosamine:pol	GALNT12	0.00063296
1554163_a	twist homolog 2 (Drosophila)	TWIST2	1.65E-05
205226_at	platelet-derived growth factor receptor-like	PDGFRL	0.00570656
204595_s_	stanniocalcin 1	STC1	0.000141915
204879_at	podoplanin	PDPN	2.64E-05
236297_at	CDNA FLJ45742 fis, clone KIDNE201632	---	9.41E-05
209496_at	retinoic acid receptor responder (tazarote	RARRES2	0.00128032
223235_s_	SPARC related modular calcium binding 2	SMOC2	0.00498447
206700_s_	jumonji, AT rich interactive domain 1D	JARID1D	1.92E-06
204388_s_	monoamine oxidase A	MAOA	0.000174782
209047_at	aquaporin 1 (Colton blood group)	AQP1	0.000135943
226926_at	dermokine	DMKN	0.000794276
206624_at	ubiquitin specific peptidase 9, Y-linked (fat	LOC10013	2.90E-05
226658_at	podoplanin	PDPN	3.44E-05
202036_s_	secreted frizzled-related protein 1	SFRP1	0.000583108
220351_at	chemokine (C-C motif) receptor-like 1	CCRL1	0.0101668
207522_s_	ATPase, Ca++ transporting, ubiquitous	ATP2A3	0.000190227
212741_at	monoamine oxidase A	MAOA	8.42E-05
207386_at	cytochrome P450, family 7, subfamily B, p	CYP7B1	0.000258473
235438_at	Transcribed locus	---	0.00194471

206172_at	interleukin 13 receptor, alpha 2	IL13RA2	0.000298089
226322_at	transmembrane and tetratricopeptide repe	TMTC1	0.0010184
205713_s_	cartilage oligomeric matrix protein	COMP	0.00351414
228450_at	pleckstrin homology domain containing, fa	PLEKHA7	0.00109978
228492_at	ubiquitin specific peptidase 9, Y-linked (fat	LOC10013	4.65E-05
205870_at	bradykinin receptor B2	BDKRB2	0.000290368
214321_at	nephroblastoma overexpressed gene	NOV	0.00107567
204638_at	acid phosphatase 5, tartrate resistant	ACP5	4.31E-06
203180_at	aldehyde dehydrogenase 1 family, membe	ALDH1A3	4.92E-05
226865_at	MRNA; cDNA DKFZp564O0862 (from clo	---	6.39E-05
200986_at	serpin peptidase inhibitor, clade G (C1 inh	SERPING1	7.85E-05
205113_at	neurofilament, medium polypeptide 150kD	NEFM	0.000366269
223121_s_	secreted frizzled-related protein 2	SFRP2	0.00905972
209616_s_	carboxylesterase 1 (monocyte/macrophag	CES1	1.06E-05
213817_at	CDNA FLJ13601 fis, clone PLACE101006	---	5.76E-05
204596_s_	stanniocalcin 1	STC1	4.10E-05
223710_at	chemokine (C-C motif) ligand 26	CCL26	2.80E-05
207761_s_	methyltransferase like 7A	METTL7A	0.00238616
205818_at	deleted in bladder cancer 1	DBC1	0.00111464
204160_s_	ectonucleotide pyrophosphatase/phospho	ENPP4	5.82E-05
212977_at	chemokine (C-X-C motif) receptor 7	CXCR7	0.00162213
204627_s_	integrin, beta 3 (platelet glycoprotein IIIa,	ITGB3	0.000170621
223122_s_	secreted frizzled-related protein 2	SFRP2	0.0071308
209160_at	aldo-keto reductase family 1, member C3	AKR1C3	0.0155996
228057_at	DNA-damage-inducible transcript 4-like	DDIT4L	0.000996522
202291_s_	matrix Gla protein	MGP	0.000378866
210839_s_	ectonucleotide pyrophosphatase/phospho	ENPP2	0.00140031
231804_at	relaxin/insulin-like family peptide receptor	RXFP1	0.000338159
218345_at	transmembrane protein 176A	TMEM176	0.000121887
204932_at	tumor necrosis factor receptor superfamily	TNFRSF11	0.0040407
228186_s_	R-spondin 3 homolog (Xenopus laevis)	RSPO3	0.00257038
238206_at	relaxin/insulin-like family peptide receptor	RXFP1	0.000719292
202035_s_	secreted frizzled-related protein 1	SFRP1	0.000302411
211892_s_	prostaglandin I2 (prostacyclin) synthase	PTGIS	1.52E-06
227803_at	ectonucleotide pyrophosphatase/phospho	ENPP5	2.62E-05
227058_at	chromosome 13 open reading frame 33	C13orf33	3.29E-06
205382_s_	complement factor D (adipsin)	CFD	3.12E-05
221898_at	podoplanin	PDPN	0.000105372
202357_s_	complement factor B	CFB	0.00352611
206030_at	aspartoacylase (Canavan disease)	ASPA	1.20E-05
1552715_a	relaxin/insulin-like family peptide receptor	RXFP1	0.000749799
226931_at	transmembrane and tetratricopeptide repe	TMTC1	6.28E-05
210702_s_	prostaglandin I2 (prostacyclin) synthase	PTGIS	1.64E-05
204409_s_	eukaryotic translation initiation factor 1A,	EIF1AY	2.47E-06
221805_at	neurofilament, light polypeptide 68kDa	NEFL	0.000299767
227276_at	plexin domain containing 2	PLXDC2	5.88E-05
205000_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide	DDX3Y	1.29E-07
220532_s_	transmembrane protein 176B	TMEM176	8.33E-06
205110_s_	fibroblast growth factor 13	FGF13	1.29E-05
205549_at	Purkinje cell protein 4	PCP4	0.00823663
204933_s_	tumor necrosis factor receptor superfamily	TNFRSF11	0.0060495
218723_s_	chromosome 13 open reading frame 15	C13orf15	6.17E-05
205792_at	WNT1 inducible signaling pathway protein	WISP2	1.71E-05

207092_at	leptin	LEP	0.000180351
208131_s_	prostaglandin I2 (prostacyclin) synthase	PTGIS	0.000147476
201909_at	ribosomal protein S4, Y-linked 1 /// hypoth	LOC10013	1.40E-07
232267_at	G protein-coupled receptor 133	GPR133	4.32E-05

GFoldChange(P vs. WT)
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