SUPPLEMENTAL DATA

PHENOTYPIC DIFFERENCES BETWEEN HEALTHY EFFECTOR CTL AND LEUKEMIC LGL CELLS SUPPORT THE NOTION OF ANTIGEN-TRIGGERED CLONAL TRANSFORMATION IN T-LGL LEUKEMIA.

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List of transcripts concordantly up- and downregulated in all three LGL patients vs. healthy effector CD8+CD57+ population (pages 2-14).

FC indicates foldchange in transcript expression in patient sample when compared to control CD57+ cells; I/D, increase/decrease in transcript expression; A, absent signal; NC, no change in signal ratio.

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
AFFX-r2-Bs-dap-5_at	---	---	256.00	I	207.94	I	1176.27	I
AFFX-DapX-M_at	---	---	147.03	I	111.43	I	630.35	I
AFFX-DapX-5_at	---	---	90.51	I	103.97	I	315.17	I
AFFX-r2-Bs-dap-M_at	---	---	84.45	I	48.50	I	388.02	I
AFFX-r2-Bs-dap-3_at	---	---	59.71	I	48.50	I	362.04	I
204533_at	CXCL10/IP-10/SCYB10	chemokine (C-X-C motif) ligand 10	48.50	I	137.19	I	9.24	I
AFFX-ThrX-3_at	---	---	45.25	I	51.98	I	415.87	I
AFFX-DapX-3_at	---	---	45.25	I	39.40	I	256.00	I
241343_at	RNASEH1	Ribonuclease H1	45.25	I	22.63	I	34.30	I
228266_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	36.76	I	25.99	I	34.30	I
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	34.30	I	51.98	I	8.00	I
205461_at	RAB35	RAB35, member RAS oncogene family	34.30	I	39.40	I	19.70	I
227404_s_at	EGR1	Early growth response 1	29.86	I	17.15	I	14.93	I
202411_at	IFI27	interferon, alpha-inducible protein 27	29.86	I	59.71	I	11.79	I
1570541_s_at	LOC400759	Similar to calpain (EC 3.4.22.17) light chain - bovine	21.11	I	39.40	I	7.46	I
231819_at	CEBPZ	CCAAT/enhancer binding protein zeta	19.70	I	14.93	I	24.25	I
201551_s_at	LAMP1	lysosomal-associated membrane protein 1	19.70	I	22.63	I	6.50	I
205249_at	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	18.38	I	9.19	I	2.00	I
AFFX-r2-Bs-thr-M_s_at	---	---	17.15	I	10.56	I	29.86	I
209480_at	HLA-DQB1	Major histocompatibility complex, class II, DQ beta 1	17.15	I	17.15	I	3.48	I
AFFX-r2-Bs-thr-5_s_at	---	---	14.93	I	17.15	I	48.50	I
210077_s_at	SFRS5	splicing factor, arginine/serine-rich 5	14.93	I	34.30	I	4.00	I
AFFX-HUMISGF3A/M97935_5_at	STAT1	signal transducer and activator of transcription 1, 91kDa	14.93	I	16.00	I	2.30	I
202672_s_at	ATF3	activating transcription factor 3	13.93	I	25.99	I	10.56	I
236203_at	HLA-DQA1	Major histocompatibility complex, class II, DQ alpha 1	13.93	I	42.22	I	7.46	I
200796_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	13.93	I	17.15	I	3.48	I
238850_at	---	CDNA FLJ30810 fis, clone FEBRA2001440	12.13	I	6.96	I	39.40	I
1558214_s_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	12.13	I	10.56	I	3.03	I
201694_s_at	EGR1	early growth response 1	12.13	I	8.00	I	2.83	I
210354_at	IFNG	interferon, gamma	12.13	I	13.00	I	25.99	I
211506_s_at	IL8 (CXCL8)	interleukin 8	12.13	I	34.30	I	1.74	I
233406_at	KIAA0256	KIAA0256 gene product	11.31	I	14.93	I	5.28	I
1553176_at	SH2D1B	SH2 domain containing 1B	11.31	I	5.66	I	11.31	I
210895_s_at	CD86 (CD28 ligand)	CD86 molecule	10.56	I	29.86	I		NC
238900_at	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	10.56	I	39.40	I	2.83	I
AFFX-r2-Bs-phe-5_at	---	---	9.85	I	13.93	I	48.50	I
AFFX-LysX-3_at	---	---	9.85	I	8.00	I	27.86	I
1562836_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	9.85	I	5.66	I	2.14	I
212999_x_at	HLA-DQB1	Major histocompatibility complex, class II, DQ beta 1	9.85	I	17.15	I	2.14	I
216901_s_at	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)	9.85	I	13.00	I	3.03	I
AFFX-ThrX-M_at	---	---	9.19	I	7.46	I	45.25	I
230272_at	---	CDNA FLJ30810 fis, clone FEBRA2001440	9.19	I	4.59	I	21.11	I
205685_at	CD86 (CD28 ligand)	CD86 molecule	9.19	I	16.00	I	4.70	I
201422_at	IFI30	nterferon, gamma-inducible protein 30	9.19	I	19.70	I		NC
232352_at	ISL2	ISL2 transcription factor, LIM/homeodomain, (islet-2)	9.19	I	6.50	I	6.96	I
212099_at	RHOB	ras homolog gene family, member B	9.19	I	18.38	I	3.25	I
205727_at	TEP1	telomerase-associated protein 1	9.19	I	14.93	I	6.96	I
201044_x_at	DUSP1	dual specificity phosphatase 1	8.57	I	19.70	I	2.14	I

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
204006_s_at	FCGR3A	Fc fragment of IgG, low affinity IIIa/iiiB, receptor (CD16a/CD16b)	8.57	I	10.56	I	3.25	I
206917_at	GNA13	guanine nucleotide binding protein (G protein), alpha 13	8.57	I	13.93	I	4.00	I
200628_s_at	WARS	tryptophanyl-tRNA synthetase	8.57	I	19.70	I	2.30	I
223383_at	ZNRF1	zinc and ring finger 1	8.57	I	5.28	I	12.13	I
1555594_a_at	MBNL1	muscleblind-like (Drosophila)	8.00	I	7.46	I	2.83	I
204834_at	FGL2	fibrinogen-like 2	7.46	I	13.00	I	3.03	I
231578_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	7.46	I	9.85	I	6.50	I
1555628_a_at	HAVCR2	hepatitis A virus cellular receptor 2	7.46	I	5.28	I	6.96	I
242587_at	SLC9A9	solute carrier family 9, member 9	7.46	I	7.46	I	3.03	I
217853_at	TENS1	Tensin 3	7.46	I	16.00	I	19.70	I
201693_s_at	EGR1	early growth response 1	6.96	I	5.28	I	2.30	I
217202_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	6.96	I	9.19	I	2.30	I
200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	6.96	I	9.85	I	2.30	I
236244_at	HNRPU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	6.96	I	21.11	I	4.29	I
1554508_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	6.96	I	6.96	I	3.73	I
202859_x_at	IL8 (CXCL8)	interleukin 8	6.50	I	16.00	I	A	NC
218850_s_at	LIMD1	LIM domains containing 1	6.50	I	4.00	I	2.83	I
231576_at	---	MRNA; cDNA DKFZp566C034 (from clone DKFZp566C034)	6.06	I	4.92	I	4.92	I
241869_at	APOL6	apolipoprotein L, 6	6.06	I	7.46	I	9.19	I
208116_s_at	MAN1A1	mannosidase, alpha, class 1A, member 1	6.06	I	3.25	I	4.29	I
1557637_at	PPP3CA	Protein phosphatase 3, catalytic subunit, alpha isoform (calcineurin A alpha)	6.06	I	11.31	I	8.57	I
AFFX-HUMISGF3A/M97935_MA_at	STAT1	signal transducer and activator of transcription 1, 91kDa	6.06	I	5.28	I	3.03	I
1569003_at	TMEM49	transmembrane protein 49	6.06	I	9.19	I	4.59	I
203915_at	CXCL9/MIG	chemokine (C-X-C motif) ligand 9	5.89	I	18.38	I	NC	NC
211559_s_at	CCNG2	cyclin G2	5.66	I	3.73	I	2.00	I
213548_s_at	H41	hypothetical protein H41	5.66	I	8.00	I	2.83	I
208949_s_at	LGALS3 /// GALIG	lectin, galactoside-binding, soluble, 3 (galectin 3) /// galectin-3 internal gene	5.66	I	10.56	I	3.73	I
238013_at	PLEKHA2	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	5.66	I	4.92	I	5.66	I
206221_at	RASA3	RAS p21 protein activator 3	5.66	I	4.29	I	6.06	I
213435_at	SATB2	SATB family member 2	5.66	I	2.46	I	18.38	I
1552928_s_at	TAB3	TAK1-binding protein 3	5.66	I	6.96	I	3.73	I
AFFX-PheX-3_at	---	---	5.28	I	6.06	I	14.93	I
207794_at	CCR2	chemokine (C-C motif) receptor 2	5.28	I	3.48	I	-39.40	D
1554279_a_at	CXorf34	chromosome X open reading frame 34	5.28	I	3.48	I	4.00	I
206582_s_at	GPR56	G protein-coupled receptor 56	5.28	I	4.00	I	8.57	I
203293_s_at	LMAN1	lectin, mannose-binding, 1	5.28	I	4.29	I	4.29	I
224917_at	MIRN21	microRNA 21	5.28	I	8.57	I	3.73	I
238421_at	MNAB	Membrane associated DNA binding protein	5.28	I	4.00	I	3.03	I
217095_x_at	NCR1	natural cytotoxicity triggering receptor 1	5.28	I	3.03	I	4.29	I
214971_s_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	5.28	I	4.29	I	2.00	I
206307_s_at	FOXD1	forkhead box D1	4.92	I	2.14	I	6.96	I
221185_s_at	IQCG	IQ motif containing G	4.92	I	2.30	I	2.83	I
200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15	4.92	I	13.00	I	2.00	I
216915_s_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12	4.92	I	4.00	I	4.00	I
244043_at	TFDP2	Transcription factor Dp-2 (E2F dimerization partner 2)	4.92	I	3.48	I	9.85	I
207536_s_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	4.92	I	2.00	I	8.00	I
218832_x_at	ARRB1	arrestin, beta 1	4.59	I	6.06	I	2.83	I
207686_s_at	CASP8	caspase 8, apoptosis-related cysteine peptidase	4.59	I	3.73	I	2.83	I
205238_at	CXorf34	chromosome X open reading frame 34	4.59	I	5.28	I	4.92	I
211395_x_at	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	4.59	I	16.00	I	4.00	I
238585_at	GTDC1	glycosyltransferase-like domain containing 1	4.59	I	3.48	I	2.00	I
209526_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	4.59	I	4.92	I	9.19	I
201466_s_at	JUN	v-jun sarcoma virus 17 oncogene homolog (avian)	4.59	I	18.38	I	4.59	I
215415_s_at	LYST	lysosomal trafficking regulator	4.59	I	4.92	I	4.29	I
207659_s_at	MOBP	myelin-associated oligodendrocyte basic protein	4.59	I	8.00	I	9.85	I
215233_at	PTDSR	phosphatidylserine receptor	4.59	I	6.06	I	9.85	I
214697_s_at	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	4.59	I	3.48	I	2.00	I
238420_at	---	CDNA clone IMAGE:4285619	4.29	I	4.59	I	2.30	I
1568768_s_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	4.29	I	8.57	I	2.83	I
233009_at	C10orf118	Chromosome 10 open reading frame 118	4.29	I	9.19	I	8.00	I
203799_at	CD302	CD302 molecule	4.29	I	8.57	I		NC
202902_s_at	CTSS	cathepsin S	4.29	I	6.96	I	2.00	I

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212107_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	4.29	I	3.03	I	2.46	I
229450_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	4.29	I	2.83	I	2.83	I
200906_s_at	KIAA0992	palladin	4.29	I	2.64	I	3.25	I
225408_at	MBP	myelin basic protein	4.29	I	3.03	I	3.03	I
225742_at	MDM4	Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse)	4.29	I	6.06	I	4.92	I
200604_s_at	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	4.29	I	4.00	I	2.46	I
227824_at	PRKCB1	Protein kinase C, beta 1	4.29	I	3.48	I	2.00	I
206220_s_at	RASA3	RAS p21 protein activator 3	4.29	I	3.48	I	3.25	I
AFFX-HUMISGF3A/M97935_MB_at	STAT1	signal transducer and activator of transcription 1, 91kDa	4.29	I	3.73	I	2.46	I
211786_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	4.29	I	3.73	I	4.00	I
222563_s_at	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	4.29	I	4.59	I	2.00	I
200629_at	WARS	tryptophanyl-tRNA synthetase	4.29	I	10.56	I	2.00	I
205153_s_at	CD40(TNFRSF5)	CD40 molecule, TNF receptor superfamily member 5	4.01	I	8.57	I	A	NC
1569106_s_at	FLJ10707	hypothetical protein FLJ10707	4.00	I	3.48	I	2.00	I
216693_x_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	4.00	I	4.59	I	5.66	I
218280_x_at	HIST2H2AA	histone 2, H2aa	4.00	I	5.66	I	3.25	I
214290_s_at	HIST2H2AA	histone 2, H2aa	4.00	I	5.28	I	3.03	I
241716_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	4.00	I	12.13	I	147.03	I
214007_s_at	PTK9	PTK9 protein tyrosine kinase 9	4.00	I	6.06	I	2.83	I
202388_at	RGS2	regulator of G-protein signalling 2, 24kDa	4.00	I	5.66	I	4.29	I
244377_at	SLC1A4	Solute carrier family 1, member 4	4.00	I	3.03	I	4.59	I
223131_s_at	TRIM8	tripartite motif-containing 8	4.00	I	2.83	I	2.64	I
201337_s_at	VAMP3	vesicle-associated membrane protein 3 (cellubrevin)	4.00	I	6.06	I	2.46	I
AFFX-LysX-5_at	---	---	3.73	I	3.25	I	9.85	I
243495_s_at	---	CDNA FLJ36515 fis, clone TRACH2001810	3.73	I	3.25	I	2.83	I
239536_at	AF1Q	Myeloid/lymphoid or mixed-lineage leukemia	3.73	I	2.83	I	3.03	I
205099_s_at	CCR1	chemokine (C-C motif) receptor 1	3.73	I	4.92	I	-3.25	D
227609_at	EPSTI1	epithelial stromal interaction 1 (breast)	3.73	I	4.59	I	2.46	I
242422_at	G3BP	Ras-GTPase-activating protein SH3-domain-binding protein	3.73	I	3.25	I	2.83	I
217502_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	3.73	I	9.19	I	2.64	I
222860_s_at	PDGFD	platelet derived growth factor D	3.73	I	3.03	I	4.59	I
208447_s_at	PRPS1	phosphoribosyl pyrophosphate synthetase 1	3.73	I	2.64	I	2.00	I
1553177_at	SH2D1B	SH2 domain containing 1B	3.73	I	2.00	I	6.50	I
223340_at	SPG3A	spastic paraplegia 3A (autosomal dominant)	3.73	I	3.73	I	6.06	I
229067_at	---	Similar to Formin binding protein 2 (srGAP2)	3.48	I	4.29	I	3.73	I
1555419_a_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	3.48	I	4.92	I	2.46	I
208653_s_at	CD164	CD164 antigen, sialomucin	3.48	I	3.03	I	2.14	I
205686_s_at	CD86 (CD28 ligand)	CD86 molecule	3.48	I	8.57	I	A	NC
229746_x_at	CEBPZ	CCAAT/enhancer binding protein zeta	3.48	I	3.25	I	4.59	I
209524_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	3.48	I	3.48	I	6.50	I
221581_s_at	LAT2	linker for activation of T cells family, member 2	3.48	I	3.25	I	3.48	I
209199_s_at	MEF2C	MADS box transcription enhancer factor 2, polypeptide C	3.48	I	4.59	I	3.48	I
208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)	3.48	I	3.03	I	3.03	I
225738_at	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	3.48	I	3.25	I	2.46	I
202129_s_at	RIOK3	RIO kinase 3 (yeast) /// RIO kinase 3 (yeast)	3.48	I	5.28	I	2.00	I
224836_at	TP53INP2	tumor protein p53 inducible nuclear protein 2	3.48	I	5.28	I	3.48	I
231152_at	---	MRNA; cDNA DKFZp686D22106 (from clone DKFZp686D22106)	3.25	I	6.96	I	4.92	I
1556545_at	---	CDNA FLJ32379 fis, clone SKMUS1000030	3.25	I	7.46	I	4.29	I
208002_s_at	ACOT7	acyl-CoA thioesterase 7	3.25	I	3.25	I	2.64	I
206513_at	AIM2	absent in melanoma 2	3.25	I	2.14	I	2.30	I
211022_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog)	3.25	I	3.03	I	3.03	I
229733_s_at	CBX6	Chromobox homolog 6	3.25	I	4.00	I	2.30	I
217208_s_at	DLG1	discs, large homolog 1 (Drosophila)	3.25	I	3.48	I	2.14	I
208092_s_at	FAM49A	family with sequence similarity 49, member A	3.25	I	3.25	I	2.83	I
204562_at	IRF4	interferon regulatory factor 4	3.25	I	1.74	I	2.83	I
210184_at	ITGAX	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	3.25	I	6.50	I	4.29	I
201464_x_at	JUN	v-jun sarcoma virus 17 oncogene homolog (avian)	3.25	I	8.57	I	2.64	I
223584_s_at	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	3.25	I	4.00	I	2.46	I
1558937_s_at	LOC153561	Hypothetical protein LOC153561	3.25	I	5.28	I	3.48	I
209200_at	MEF2C	MADS box transcription enhancer factor 2, polypeptide C	3.25	I	3.25	I	4.00	I
237158_s_at	MPHOSPH9	M-phase phosphoprotein 9	3.25	I	2.64	I	2.14	I
203574_at	NFIL3	nuclear factor, interleukin 3 regulated	3.25	I	4.92	I	5.28	I

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227204_at	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	3.25	I	2.64	I	3.48	I
226279_at	PRSS23	protease, serine, 23	3.25	I	2.30	I	4.00	I
216899_s_at	SCAP2	src family associated phosphoprotein 2	3.25	I	3.48	I	3.25	I
212811_x_at	SLC1A4	Solute carrier family 1, member 4	3.25	I	2.00	I	6.96	I
201167_x_at	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	3.03	I	3.03	I	2.46	I
206133_at	BIRC4BP	XIAP associated factor-1	3.03	I	2.46	I	3.25	I
221222_s_at	C1orf56	chromosome 1 open reading frame 56	3.03	I	2.83	I	2.83	I
200935_at	CALR	calreticulin	3.03	I	4.59	I	3.03	I
207319_s_at	CDC2L5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	3.03	I	2.46	I	2.00	I
200764_s_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	3.03	I	3.03	I	2.64	I
221417_x_at	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	3.03	I	2.00	I	2.46	I
46947_at	GNL3L	Guanine nucleotide binding protein-like 3 (nucleolar)-like	3.03	I	3.48	I	2.46	I
202438_x_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	3.03	I	2.30	I	3.25	I
218295_s_at	NUP50	nucleoporin 50kDa	3.03	I	2.64	I	2.14	I
201835_s_at	PRKAB1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	3.03	I	2.14	I	2.30	I
226389_s_at	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	3.03	I	2.30	I	3.73	I
222660_s_at	RNF38	ring finger protein 38	3.03	I	3.73	I	2.00	I
219892_at	TM6SF1	transmembrane 6 superfamily member 1	3.03	I	4.92	I	3.48	I
226825_s_at	TPARL	TPA regulated locus	3.03	I	3.48	I	4.59	I
1555978_s_at	---	LOC440476	2.83	I	3.73	I	2.00	I
229309_at	ADRB1	Adrenergic, beta-1-, receptor	2.83	I	4.92	I	13.93	I
213872_at	C6orf62	Chromosome 6 open reading frame 62	2.83	I	2.83	I	3.48	I
1555827_at	CCNL1	Cyclin L1	2.83	I	5.28	I	4.00	I
210844_x_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	2.83	I	2.64	I	3.03	I
202416_at	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	2.83	I	3.48	I	2.14	I
225834_at	FAM72A	family with sequence similarity 72, member A	2.83	I	3.48	I	3.25	I
204747_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	2.83	I	2.64	I	4.00	I
209653_at	KPNA4	karyopherin alpha 4 (importin alpha 3)	2.83	I	3.03	I	2.00	I
221695_s_at	MAP3K2	mitogen-activated protein kinase kinase kinase 2	2.83	I	3.73	I	2.46	I
233072_at	NTNG2	netrin G2	2.83	I	3.73	I	3.48	I
243296_at	PBEF1	Pre-B-cell colony enhancing factor 1	2.83	I	8.57	I	4.59	I
202458_at	PRSS23	protease, serine, 23	2.83	I	2.14	I	3.48	I
202085_at	TJP2	tight junction protein 2 (zona occludens 2)	2.83	I	2.46	I	4.92	I
242776_at	ZCCHC6	zinc finger, CCHC domain containing 6	2.83	I	2.64	I	2.83	I
201971_s_at	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	2.64	I	3.73	I	2.00	I
204908_s_at	BCL3	B-cell CLL/lymphoma 3	2.64	I	4.59	I	4.00	I
200765_x_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	2.64	I	2.64	I	3.48	I
243388_at	DKFZP564O0463	WD repeats and SOF1 domain containing	2.64	I	3.03	I	3.48	I
224642_at	FYTTD1	forty-two-three domain containing 1	2.64	I	2.00	I	2.14	I
225116_at	HIPK2	Homeodomain interacting protein kinase 2	2.64	I	2.30	I	4.59	I
215779_s_at	HIST1H2BG	histone 1, H2bg	2.64	I	2.83	I	5.66	I
228196_s_at	KIAA0217	La ribonucleoprotein domain family, member 5	2.64	I	2.30	I	2.46	I
231874_at	MGC39518	hypothetical protein MGC39518	2.64	I	2.14	I	4.29	I
210756_s_at	NOTCH2	Notch homolog 2 (Drosophila) /// Notch homolog 2 (Drosophila)	2.64	I	3.73	I	2.46	I
204589_at	NUAK1	NUAK family, SNF1-like kinase, 1	2.64	I	2.00	I	2.14	I
236495_at	PBEF1	Pre-B-cell colony enhancing factor 1	2.64	I	9.19	I	3.73	I
214487_s_at	RAP2A /// RAP2B	RAP2A, member of RAS oncogene family /// RAP2B, member of RAS oncogene family	2.64	I	2.30	I	3.48	I
228996_at	RC3H1	ring finger and CCCH-type zinc finger domains 1	2.64	I	4.29	I	4.92	I
209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	2.64	I	4.29	I	3.25	I
204361_s_at	SCAP2	src family associated phosphoprotein 2	2.64	I	2.83	I	2.64	I
235069_at	TATDN3	TatD DNase domain containing 3	2.64	I	2.83	I	2.64	I
219679_s_at	WAC	WW domain containing adaptor with coiled-coil	2.64	I	2.30	I	2.30	I
242020_s_at	ZBP1	Z-DNA binding protein 1	2.64	I	3.03	I	2.00	I
200868_s_at	ZNF313	zinc finger protein 313	2.64	I	3.25	I	2.00	I
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	2.54	I	9.19	I	A	NC
228642_at	---	Homo sapiens, clone IMAGE:5019307, mRNA	2.46	I	2.46	I	2.30	I
227745_at	---	CDNA FLJ90571 fis, highly similar to Homo sapiens patched related protein TRC8	2.46	I	4.92	I	4.92	I
227260_at	ANKRD10	Ankyrin repeat domain 10	2.46	I	4.92	I	2.83	I
222458_s_at	C1orf108	chromosome 1 open reading frame 108	2.46	I	3.48	I	2.14	I
1553338_at	C1orf55	chromosome 1 open reading frame 55	2.46	I	3.25	I	2.14	I
205692_s_at	CD38	CD38 antigen (p45)	2.46	I	2.83	I	5.66	I
223585_x_at	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	2.46	I	2.00	I	2.46	I

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
229676_at	PAPD1	PAP associated domain containing 1	2.46	I	2.83	I	2.30	I
1554089_s_at	SBDS	Shwachman-Bodian-Diamond syndrome	2.46	I	3.03	I	3.25	I
243797_at	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	2.46	I	4.00	I	2.00	I
217741_s_at	ZA20D2	zinc finger, A20 domain containing 2	2.46	I	5.28	I	2.14	I
242433_at	ZBTB11	Zinc finger and BTB domain containing 11	2.46	I	7.46	I	3.25	I
242836_at	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	2.30	I	8.00	I	6.96	I
227699_at	C14orf149	chromosome 14 open reading frame 149	2.30	I	3.25	I	3.73	I
211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase	2.30	I	2.30	I	2.30	I
236191_at	CD38	CD38 antigen (p45)	2.30	I	6.06	I	9.19	I
200862_at	DHCR24	24-dehydrocholesterol reductase	2.30	I	2.14	I	2.64	I
202430_s_at	PLSCR1	phospholipid scramblase 1	2.30	I	3.25	I	2.00	I
209051_s_at	RALGDS	ral guanine nucleotide dissociation stimulator	2.30	I	2.64	I	2.46	I
221430_s_at	RNF146	ring finger protein 146 /// ring finger protein 146	2.30	I	2.00	I	2.64	I
201311_s_at	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	2.30	I	2.64	I	2.30	I
1552656_s_at	UHMK1	U2AF homology motif (UHM) kinase 1	2.30	I	3.25	I	2.46	I
1559227_s_at	VHL	von Hippel-Lindau tumor suppressor	2.30	I	3.73	I	2.30	I
220494_s_at	---	---	2.14	I	2.00	I	2.30	I
1556676_a_at	---	CDNA clone IMAGE:4793171	2.14	I	2.64	I	3.03	I
225557_at	AXUD1	AXIN1 up-regulated 1	2.14	I	4.92	I	3.25	I
241740_at	CREM	CAMP responsive element modulator	2.14	I	4.59	I	2.30	I
232617_at	CTSS	cathepsin S	2.14	I	3.48	I	2.00	I
212975_at	DENND3	DENN/MADD domain containing 3	2.14	I	2.64	I	2.14	I
209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, beta	2.14	I	3.73	I	2.14	I
231918_s_at	GFM2	G elongation factor, mitochondrial 2	2.14	I	2.00	I	2.83	I
226160_at	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	2.14	I	3.03	I	2.46	I
235458_at	HAVCR2	hepatitis A virus cellular receptor 2	2.14	I	2.14	I	4.59	I
200798_x_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	2.14	I	2.46	I	2.00	I
209519_at	NCBP1	nuclear cap binding protein subunit 1, 80kDa	2.14	I	2.30	I	3.73	I
1559052_s_at	PAK2	p21 (CDKN1A)-activated kinase 2	2.14	I	2.30	I	2.83	I
208982_at	PECAM1	Platelet/endothelial cell adhesion molecule (CD31 antigen)	2.14	I	2.14	I	3.03	I
232392_at	SFRS3	Splicing factor, arginine/serine-rich 3	2.14	I	2.64	I	2.64	I
1564962_at	ZNF92	zinc finger protein 92 (HTF12)	2.14	I	4.00	I	3.73	I
242691_at	---	CDNA FLJ41369 fis, clone BRCAN2006117	2.00	I	3.73	I	5.28	I
230580_at	---	CDNA clone IMAGE:5312086	2.00	I	2.30	I	2.64	I
205010_at	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	2.00	I	2.30	I	2.64	I
202625_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	2.00	I	3.25	I	2.30	I
202446_s_at	PLSCR1	phospholipid scramblase 1	2.00	I	3.25	I	2.30	I
226436_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	2.00	I	2.64	I	3.48	I
1559582_at	RHOQ	ras homolog gene family, member Q	2.00	I	5.66	I	2.64	I
226272_at	---	Full length insert cDNA clone ZD79H10	-2.00	D	-3.25	D	-6.96	D
1556821_x_at	---	Full length insert cDNA YR33G07	-2.00	D	-5.66	D	-2.64	D
232038_at	C6orf170	chromosome 6 open reading frame 170	-2.00	D	-2.30	D	-2.14	D
212400_at	C9orf132	chromosome 9 open reading frame 132	-2.00	D	-2.83	D	-3.48	D
209933_s_at	CD300A	CD300A antigen	-2.00	D	-2.00	D	-68.59	D
205213_at	CENTB1	centaurin, beta 1	-2.00	D	-2.83	D	-4.59	D
213317_at	CLIC5	Chloride intracellular channel 5	-2.00	D	-2.00	D	-3.73	D
203385_at	DGKA	diacylglycerol kinase, alpha 80kDa	-2.00	D	-2.64	D	-2.30	D
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	-2.00	D	-3.25	D	-11.31	D
201769_at	ENTH	enthoprotin	-2.00	D	-2.14	D	-2.30	D
231832_at	GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4)	-2.00	D	-2.00	D	-2.46	D
235306_at	GIMAP8	GTPase, IMAP family member 8	-2.00	D	-3.73	D	-2.00	D
214677_x_at	IGL@	immunoglobulin lambda locus /// immunoglobulin lambda constant 1	-2.00	D	-4.92	D	-5.66	D
227686_at	MGC15763	hypothetical protein BC008322	-2.00	D	-2.64	D	-5.28	D
242770_at	MGC72104	Chromosome 20 open reading frame 80	-2.00	D	-2.00	D	-3.03	D
214771_x_at	M-RIP	myosin phosphatase-Rho interacting protein	-2.00	D	-2.00	D	-2.00	D
204951_at	RHOH	ras homolog gene family, member H	-2.00	D	-6.06	D	-2.00	D
230058_at	SDCCAG3	serologically defined colon cancer antigen 3	-2.00	D	-2.00	D	-2.46	D
219765_at	ZNF329	zinc finger protein 329	-2.00	D	-3.25	D	-2.14	D
229765_at	---	Transcribed locus	-2.14	D	-2.30	D	-2.00	D
212413_at	SEPT6	septin 6	-2.14	D	-2.46	D	-4.29	D
239679_at	ACTR6	ARP6 actin-related protein 6 homolog (yeast)	-2.14	D	-3.73	D	-2.14	D
AFFYMETRIX PROBE SET ID	**GENE SYMBOL**	**GENE TITLE**	**FC#22**	**I/D**	**FC#2**	**I/D**	**FC#26**	**I/D**

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
203865_s_at	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	-2.14	D	-2.64	D	-2.83	D
212930_at	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	-2.14	D	-2.14	D	-3.48	D
220059_at	BRDG1	BCR downstream signaling 1	-2.14	D	-4.92	D	-2.14	D
205831_at	CD2	CD2 antigen (p50), sheep red blood cell receptor	-2.14	D	-3.48	D	-3.03	D
205212_s_at	CENTB1	centaurin, beta 1	-2.14	D	-2.46	D	-2.64	D
236649_at	DTWD1	DTW domain containing 1	-2.14	D	-3.25	D	-2.30	D
236816_at	FLJ13089	hypothetical protein FLJ13089	-2.14	D	-2.00	D	-2.00	D
233085_s_at	FLJ22833	hypothetical protein FLJ22833	-2.14	D	-2.14	D	-2.46	D
222872_x_at	FLJ22833	hypothetical protein FLJ22833	-2.14	D	-2.14	D	-2.64	D
1552315_at	GIMAP1	GTPase, IMAP family member 1	-2.14	D	-3.03	D	-2.00	D
209255_at	KIAA0265	KIAA0265 protein	-2.14	D	-2.46	D	-2.64	D
212675_s_at	KIAA0582	KIAA0582	-2.14	D	-2.14	D	-3.03	D
222603_at	KIAA1815	KIAA1815	-2.14	D	-2.83	D	-2.14	D
1564776_at	LENG10	leukocyte receptor cluster (LRC) member 10	-2.14	D	-5.28	D	-5.66	D
212913_at	MSH5	mutS homolog 5 (E. coli)	-2.14	D	-2.30	D	-4.59	D
212594_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	-2.14	D	-2.64	D	-2.46	D
220954_s_at	PILRB	paired immunoglobin-like type 2 receptor beta	-2.14	D	-2.30	D	-3.03	D
209884_s_at	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-2.14	D	-4.00	D	-2.30	D
201320_at	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	-2.14	D	-2.14	D	-2.00	D
229723_at	TAGAP	T-cell activation GTPase activating protein	-2.14	D	-4.92	D	-2.14	D
214785_at	VPS13A	vacuolar protein sorting 13A (yeast)	-2.14	D	-2.00	D	-2.46	D
214823_at	ZNF204	zinc finger protein 204	-2.14	D	-13.00	D	-10.56	D
242289_at	---	---	-2.30	D	-7.46	D	-2.46	D
236198_at	---	Transcribed locus	-2.30	D	-3.03	D	-4.29	D
228049_x_at	---	Transcribed locus	-2.30	D	-2.14	D	-3.73	D
212414_s_at	SEPT6	septin 6 /// cytokine-like nuclear factor n-pac	-2.30	D	-2.64	D	-3.73	D
212543_at	AIM1	absent in melanoma 1	-2.30	D	-2.46	D	-2.83	D
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-2.30	D	-3.73	D	-3.73	D
1569607_s_at	ANKRD20A1	ankyrin repeat domain 20 family, member A1	-2.30	D	-5.28	D	-6.50	D
209829_at	C6orf32	chromosome 6 open reading frame 32	-2.30	D	-3.73	D	-2.64	D
205467_at	CASP10	caspase 10, apoptosis-related cysteine peptidase	-2.30	D	-2.83	D	-3.03	D
244599_at	CERKL	Ceramide kinase-like	-2.30	D	-2.14	D	-4.59	D
216060_s_at	DAAM1	dishevelled associated activator of morphogenesis 1	-2.30	D	-2.83	D	-2.30	D
230180_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-2.30	D	-2.14	D	-2.30	D
203693_s_at	E2F3	E2F transcription factor 3	-2.30	D	-2.64	D	-4.92	D
1554067_at	FLJ32549	hypothetical protein FLJ32549	-2.30	D	-2.00	D	-3.73	D
1552316_a_at	GIMAP1	GTPase, IMAP family member 1	-2.30	D	-3.25	D	-2.30	D
236862_at	GOPC	Golgi associated PDZ and coiled-coil motif containing	-2.30	D	-2.30	D	-2.00	D
213170_at	GPX7	glutathione peroxidase 7	-2.30	D	-2.46	D	-9.85	D
241036_at	HPS3	Hermansky-Pudlak syndrome 3	-2.30	D	-3.25	D	-2.14	D
1556061_at	LOC283012	hypothetical protein LOC283012	-2.30	D	-2.64	D	-2.00	D
230245_s_at	LOC283663	hypothetical protein LOC283663	-2.30	D	-4.92	D	-4.29	D
213908_at	LOC339005	hypothetical protein LOC339005	-2.30	D	-2.30	D	-21.11	D
235469_at	MGC40405	hypothetical protein MGC40405 /// similar to RIKEN cDNA 5830415L20	-2.30	D	-2.46	D	-2.64	D
226876_at	MGC45871	hypothetical protein MGC45871	-2.30	D	-2.14	D	-8.57	D
242239_at	NSUN6	NOL1/NOP2/Sun domain family, member 6	-2.30	D	-2.30	D	-2.30	D
210448_s_at	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-2.30	D	-4.59	D	-4.29	D
216945_x_at	PASK	PAS domain containing serine/threonine kinase	-2.30	D	-2.14	D	-2.46	D
225295_at	SLC39A10	solute carrier family 39 (zinc transporter), member 10	-2.30	D	-2.14	D	-2.14	D
229253_at	THEM4	thioesterase superfamily member 4	-2.30	D	-3.25	D	-4.92	D
238468_at	TNRC6B	trinucleotide repeat containing 6B	-2.30	D	-2.83	D	-2.30	D
215796_at	TRAV20	T cell receptor alpha variable 20	-2.30	D	-3.25	D	-16.00	D
1559949_at	TRPS1	Trichorhinophalangeal syndrome I	-2.30	D	-2.30	D	-2.83	D
236401_at	---	Full-length cDNA clone CS0DI016YI23	-2.46	D	-3.73	D	-2.30	D
242498_x_at	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	-2.46	D	-2.64	D	-2.30	D
241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	-2.46	D	-5.66	D	-21.11	D
227900_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	-2.46	D	-2.46	D	-2.14	D
206545_at	CD28	CD28 antigen (Tp44)	-2.46	D	-8.57	D	-256.00	D
232063_x_at	FARSLB	phenylalanine-tRNA synthetase-like, beta subunit	-2.46	D	-2.30	D	-2.30	D
208054_at	HERC4	hect domain and RLD 4	-2.46	D	-2.14	D	-8.00	D
209374_s_at	IGHM	immunoglobulin heavy constant mu	-2.46	D	-3.73	D	-3.73	D
212592_at	IGJ	Immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	-2.46	D	-5.66	D	-7.46	D

237733_at	KIAA0564	KIAA0564 protein	-2.46	D	-9.85	D	-2.14	D
53968_at	KIAA1698	KIAA1698 protein	-2.46	D	-3.03	D	-2.00	D
212944_at	MRPS6	Mitochondrial ribosomal protein S6	-2.46	D	-4.00	D	-3.03	D
214177_s_at	PBXIP1	pre-B-cell leukemia transcription factor interacting protein 1	-2.46	D	-3.25	D	-2.00	D
225321_s_at	PILRB	paired immunoglobin-like type 2 receptor beta	-2.46	D	-2.83	D	-2.30	D
211748_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-2.46	D	-2.14	D	-5.28	D
232963_at	RFWD2	Ring finger and WD repeat domain 2	-2.46	D	-2.14	D	-2.00	D
206181_at	SLAMF1	signaling lymphocytic activation molecule family member 1	-2.46	D	-2.46	D	-8.00	D
219156_at	SYNJ2BP	synaptojanin 2 binding protein	-2.46	D	-2.14	D	-2.46	D
235735_at	TNFSF8	Tumor necrosis factor (ligand) superfamily, member 8	-2.46	D	-2.30	D	-6.96	D
237208_at	WDR61	WD repeat domain 61	-2.46	D	-3.48	D	-2.83	D
236583_at	---	Transcribed locus	-2.64	D	-4.92	D	-3.25	D
233219_at	---	---	-2.64	D	-3.25	D	-2.14	D
231247_s_at	---	LOC440667	-2.64	D	-3.73	D	-3.73	D
1557733_a_at	---	MRNA; cDNA DKFZp667K2218	-2.64	D	-4.00	D	-9.19	D
216563_at	ANKRD12	Ankyrin repeat domain 12	-2.64	D	-4.59	D	-6.50	D
238549_at	CBFA2T2	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	-2.64	D	-2.64	D	-2.00	D
238480_at	CHR18 ORF50	Chromosome 18 open reading frame 50	-2.64	D	-2.83	D	-4.00	D
201278_at	DAB2	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-2.64	D	-2.30	D	-68.59	D
64064_at	GIMAP5	GTPase, IMAP family member 5	-2.64	D	-4.59	D	-2.14	D
210425_x_at	GOLGA8B	golgi autoantigen, golgin subfamily a, 8B	-2.64	D	-2.46	D	-3.03	D
225386_s_at	HNRPLL	heterogeneous nuclear ribonucleoprotein L-like	-2.64	D	-2.30	D	-2.30	D
221790_s_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	-2.64	D	-3.25	D	-4.59	D
235811_at	MBNL1	Muscleblind-like (Drosophila)	-2.64	D	-5.28	D	-2.46	D
227354_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-2.64	D	-3.48	D	-3.48	D
239808_at	PITPNC1	Phosphatidylinositol transfer protein, cytoplasmic 1	-2.64	D	-4.59	D	-2.46	D
213093_at	PRKCA	protein kinase C, alpha	-2.64	D	-2.83	D	-2.64	D
233314_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-2.64	D	-4.00	D	-2.46	D
1557081_at	RBM25	RNA binding motif protein 25	-2.64	D	-2.14	D	-2.14	D
232525_at	SND1	Staphylococcal nuclease domain containing 1	-2.64	D	-8.00	D	-2.00	D
230789_at	SUHW2	suppressor of hairy wing homolog 2 (Drosophila)	-2.64	D	-2.14	D	-2.64	D
230779_at	TNRC6B	trinucleotide repeat containing 6B	-2.64	D	-3.48	D	-2.64	D
222180_at	YES1	V-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	-2.64	D	-3.73	D	-2.30	D
228661_s_at	---	CDNA FLJ11489 fis, clone HEMBA1001915	-2.83	D	-3.73	D	-2.30	D
1569482_at	---	CDNA clone IMAGE:5285066	-2.83	D	-4.92	D	-2.83	D
1568780_at	---	Hypothetical LOC497257	-2.83	D	-2.46	D	-3.03	D
239017_at	---	Transcribed locus, moderately similar to XP_497913.1	-2.83	D	-3.73	D	-2.00	D
244035_at	BCL2	B-cell CLL/lymphoma 2	-2.83	D	-3.48	D	-4.29	D
220243_at	BTBD15	BTB (POZ) domain containing 15	-2.83	D	-13.93	D	-2.14	D
213596_at	CASP4	caspase 4, apoptosis-related cysteine peptidase	-2.83	D	-2.30	D	-2.14	D
244413_at	DCAL1	dendritic cell-associated lectin-1	-2.83	D	-3.48	D	-42.22	D
225656_at	EFHC1	EF-hand domain (C-terminal) containing 1	-2.83	D	-3.03	D	-2.00	D
218532_s_at	FLJ20152	hypothetical protein FLJ20152	-2.83	D	-3.25	D	-13.00	D
226218_at	IL7R	Interleukin 7 receptor	-2.83	D	-9.85	D	-11.31	D
1557261_at	LOC339005	hypothetical protein LOC339005	-2.83	D	-3.03	D	-16.00	D
234970_at	MTAC2D1	membrane targeting (tandem) C2 domain containing 1	-2.83	D	-4.59	D	-8.00	D
240829_at	PEX3	Peroxisomal biogenesis factor 3	-2.83	D	-5.66	D	-2.14	D
229553_at	PGM2L1	phosphoglucomutase 2-like 1	-2.83	D	-3.73	D	-2.83	D
1569597_at	PITPNC1	Phosphatidylinositol transfer protein, cytoplasmic 1	-2.83	D	-2.64	D	-2.30	D
242388_x_at	TAGAP	T-cell activation GTPase activating protein	-2.83	D	-8.00	D	-3.25	D
238277_at	TNKS	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-2.83	D	-11.31	D	-4.59	D
235761_at	TPST2	Tyrosylprotein sulfotransferase 2	-2.83	D	-2.14	D	-4.59	D
201369_s_at	ZFP36L2	zinc finger protein 36, C3H type-like 2	-2.83	D	-2.30	D	-2.64	D
238970_at	ZFR	Zinc finger RNA binding protein	-2.83	D	-2.46	D	-2.64	D
228393_s_at	ZNF302	zinc finger protein 302	-2.83	D	-3.25	D	-2.00	D
233169_at	ZNF350	zinc finger protein 350	-2.83	D	-2.30	D	-4.29	D
244422_at	---	Transcribed locus	-3.03	D	-5.66	D	-4.59	D
241365_at	---	CDNA FLJ42259 fis, clone TKIDN2011289	-3.03	D	-5.28	D	-2.46	D
201674_s_at	AKAP1	A kinase (PRKA) anchor protein 1	-3.03	D	-2.83	D	-2.30	D
215907_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-3.03	D	-2.64	D	-2.00	D
1556451_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-3.03	D	-2.83	D	-8.00	D
212560_at	C11orf32	chromosome 11 open reading frame 32	-3.03	D	-3.03	D	-24.25	D
AFFYMETRIX PROBE SET ID	**GENE SYMBOL**	**GENE TITLE**	**FC#22**	**I/D**	**FC#2**	**I/D**	**FC#26**	**I/D**

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
211208_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-3.03	D	-2.64	D	-11.31	D
206337_at	CCR7	chemokine (C-C motif) receptor 7 /// chemokine (C-C motif) receptor 7	-3.03	D	-6.06	D	-9.85	D
205250_s_at	Cep290	centrosome protein cep290	-3.03	D	-4.00	D	-2.30	D
218805_at	GIMAP5	GTPase, IMAP family member 5 /// GTPase, IMAP family member 5	-3.03	D	-6.06	D	-2.00	D
238880_at	GTF3A	general transcription factor IIIA	-3.03	D	-3.73	D	-2.30	D
217022_s_at	IGHA1	immunoglobulin heavy constant alpha 1	-3.03	D	-29.86	D	-21.11	D
212677_s_at	KIAA0582	KIAA0582	-3.03	D	-2.83	D	-2.30	D
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	-3.03	D	-2.83	D	-5.28	D
238722_x_at	NAPE-PLD	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D	-3.03	D	-4.00	D	-2.30	D
203413_at	NELL2	NEL-like 2 (chicken) /// NEL-like 2 (chicken)	-3.03	D	-3.73	D	-11.31	D
203939_at	NT5E	5'-nucleotidase, ecto (CD73)	-3.03	D	-7.46	D	-14.93	D
237456_at	RYBP	RING1 and YY1 binding protein	-3.03	D	-2.64	D	-3.03	D
218346_s_at	SESN1	sestrin 1	-3.03	D	-2.14	D	-2.14	D
203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-3.03	D	-3.03	D	-13.93	D
225583_at	UXS1	UDP-glucuronate decarboxylase 1	-3.03	D	-2.00	D	-4.92	D
205883_at	ZBTB16	zinc finger and BTB domain containing 16	-3.03	D	-3.03	D	-8.57	D
238378_at	---	Transcribed locus	-3.25	D	-4.59	D	-2.14	D
235046_at	---	Transcribed locus	-3.25	D	-11.31	D	-2.14	D
1556889_s_at	---	CDNA FLJ37963 fis, clone CTONG2009689	-3.25	D	-6.06	D	-13.00	D
228416_at	ACVR2A	activin A receptor, type IIA	-3.25	D	-2.83	D	-2.46	D
1555372_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	-3.25	D	-4.59	D	-2.14	D
224367_at	BEX2	brain expressed X-linked 2 /// brain expressed X-linked 2	-3.25	D	-4.00	D	-12.13	D
207996_s_at	C18orf1	chromosome 18 open reading frame 1	-3.25	D	-2.46	D	-3.73	D
230489_at	CD5	CD5 antigen (p56-62)	-3.25	D	-2.64	D	-5.28	D
222620_s_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	-3.25	D	-2.64	D	-2.00	D
218885_s_at	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	-3.25	D	-3.03	D	-2.14	D
210095_s_at	IGFBP3	insulin-like growth factor binding protein 3	-3.25	D	-3.73	D	-18.38	D
205798_at	IL7R	interleukin 7 receptor	-3.25	D	-7.46	D	-7.46	D
240613_at	JAK1	Janus kinase 1 (a protein tyrosine kinase)	-3.25	D	-4.00	D	-2.30	D
243030_at	MAP3K1	Mitogen-activated protein kinase kinase kinase 1	-3.25	D	-2.00	D	-2.14	D
1556306_at	MLL5	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	-3.25	D	-3.03	D	-2.14	D
241155_at	PIP5K2A	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	-3.25	D	-5.28	D	-2.83	D
213222_at	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	-3.25	D	-2.83	D	-6.96	D
220418_at	UBASH3A	ubiquitin associated and SH3 domain containing, A	-3.25	D	-5.66	D	-2.64	D
242819_at	---	---	-3.48	D	-4.92	D	-3.03	D
238875_at	---	Transcribed locus	-3.48	D	-4.00	D	-2.30	D
214298_x_at	SEPT6	septin 6	-3.48	D	-2.64	D	-3.73	D
241705_at	ABCA5	ATP-binding cassette, sub-family A (ABC1), member 5	-3.48	D	-3.25	D	-4.00	D
223961_s_at	CISH	cytokine inducible SH2-containing protein	-3.48	D	-3.25	D	-8.00	D
204720_s_at	DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	-3.48	D	-4.59	D	-27.86	D
230923_at	FAM19A1	family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	-3.48	D	-9.85	D	-6.06	D
243709_at	FLJ90709	hypothetical protein FLJ90709	-3.48	D	-4.00	D	-2.14	D
239533_at	GPR155	G protein-coupled receptor 155	-3.48	D	-2.00	D	-6.06	D
204793_at	GPRASP1	G protein-coupled receptor associated sorting protein 1	-3.48	D	-6.50	D	-10.56	D
228793_at	JMJD1C	jumonji domain containing 1C	-3.48	D	-4.29	D	-2.83	D
239442_at	KIAA0582	KIAA0582	-3.48	D	-2.83	D	-2.46	D
213457_at	MFHAS1	malignant fibrous histiocytoma amplified sequence 1	-3.48	D	-2.83	D	-16.00	D
225626_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-3.48	D	-4.59	D	-2.46	D
215175_at	PCNX	pecanex homolog (Drosophila)	-3.48	D	-2.00	D	-2.00	D
222392_x_at	PERP	PERP, TP53 apoptosis effector	-3.48	D	-2.14	D	-5.66	D
1557738_at	RAB6IP2	RAB6 interacting protein 2	-3.48	D	-3.73	MD	-3.73	D
232231_at	RUNX2	runt-related transcription factor 2	-3.48	D	-4.00	D	-24.25	D
203580_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-3.48	D	-3.25	D	-3.48	D
1556839_s_at	SPTBN5	Spectrin, beta, non-erythrocytic 5	-3.48	D	-2.83	D	-4.00	D
232077_s_at	YPEL3	yippee-like 3 (Drosophila)	-3.48	D	-3.48	D	-2.30	D
228208_x_at	ZNF354C	Zinc finger protein 354C	-3.48	D	-2.14	D	-29.86	D
AFFX-HUMRGE/M10098_M_at	---	---	-3.73	D	-2.64	D	-5.66	D
241838_at	---	Transcribed locus	-3.73	D	-3.25	D	-2.83	D
239833_at	---	Transcribed locus	-3.73	D	-3.48	D	-2.46	D
239798_at	---	Transcribed locus	-3.73	D	-2.83	D	-2.14	D
237768_x_at	---	---	-3.73	D	-4.00	D	-2.14	D
230913_at	---	Full length insert cDNA clone ZE12B03	-3.73	D	-4.59	D	-5.28	D

227663_at	---	CDNA FLJ40901 fis, clone UTERU2003704	-3.73	D	-5.28	D	-2.00	D
1558605_at	---	CDNA FLJ41817 fis, clone NT2RI2013345	-3.73	D	-4.29	D	-2.30	D
205434_s_at	AAK1	AP2 associated kinase 1	-3.73	D	-3.48	D	-2.46	D
239579_at	ABHD7	abhydrolase domain containing 7	-3.73	D	-3.73	D	-22.63	D
240568_at	AKT3	Serologically defined colon cancer antigen 8	-3.73	D	-3.03	D	-3.73	D
215386_at	AUTS2	Autism susceptibility candidate 2	-3.73	D	-27.86	D	-21.11	D
221234_s_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-3.73	D	-3.73	D	-4.92	D
1557239_at	BBX	Bobby sox homolog (Drosophila)	-3.73	D	-4.92	D	-2.14	D
203685_at	BCL2	B-cell CLL/lymphoma 2	-3.73	D	-7.46	D	-5.28	D
239014_at	CCAR1	Cell division cycle and apoptosis regulator 1	-3.73	D	-2.46	D	-2.00	D
208806_at	CHD3	chromodomain helicase DNA binding protein 3	-3.73	D	-3.48	D	-2.00	D
229193_at	CROP	Cisplatin resistance-associated overexpressed protein	-3.73	D	-4.59	D	-2.14	D
240971_x_at	CUL4A	Cullin 4A	-3.73	D	-2.64	D	-2.14	D
232466_at	CUL4A	Cullin 4A	-3.73	D	-3.48	D	-2.83	D
209570_s_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	-3.73	D	-4.29	D	-59.71	D
222621_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	-3.73	D	-2.83	D	-3.03	D
212642_s_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	-3.73	D	-4.59	D	-8.00	D
211548_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-3.73	D	-4.92	D	-4.29	D
223681_s_at	INADL	InaD-like (Drosophila)	-3.73	D	-25.99	D	-8.00	D
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	-3.73	D	-5.66	D	-13.00	D
228046_at	LOC152485	Hypothetical protein LOC152485	-3.73	D	-3.48	D	-24.25	D
222306_at	MGC61571	Hypothetical protein MGC61571	-3.73	D	-2.00	D	-2.00	D
203956_at	MORC2	MORC family CW-type zinc finger 2	-3.73	D	-5.66	D	-2.46	D
1561657_at	NCAM1	Neural cell adhesion molecule 1	-3.73	D	-27.86	D	-12.13	D
241786_at	PPP3R1	Protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa	-3.73	D	-3.48	D	-2.14	D
1561687_a_at	ZNF382	zinc finger protein 382	-3.73	D	-4.00	D	-16.00	D
237747_at	---	---	-4.00	D	-3.73	D	-2.30	D
227394_at	---	CDNA FLJ30008 fis, clone 3NB692000029	-4.00	D	-4.59	D	-32.00	D
225444_at	---	Transcribed locus	-4.00	D	-3.48	D	-2.00	D
244027_at	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-4.00	D	-4.00	D	-2.46	D
232500_at	C20orf74	chromosome 20 open reading frame 74	-4.00	D	-4.59	D	-2.30	D
1565868_at	CD44	CD44 antigen (homing function and Indian blood group system)	-4.00	D	-4.00	D	-4.29	D
205288_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-4.00	D	-2.83	D	-3.73	D
235721_at	DTX3	deltex 3 homolog (Drosophila)	-4.00	D	-2.46	D	-5.28	D
244535_at	FOXP1	Forkhead box P1	-4.00	D	-3.25	D	-4.00	D
201656_at	ITGA6	integrin, alpha 6	-4.00	D	-13.93	D	-10.56	D
236999_at	KIAA0073	Peptidylprolyl isomerase domain and WD repeat containing 1	-4.00	D	-2.00	D	-2.00	D
241790_at	KLHL7	Kelch-like 7 (Drosophila)	-4.00	D	-10.56	D	-2.30	D
244357_at	LOC64744	Stromal membrane-associated protein 1-like	-4.00	D	-3.25	D	-2.64	D
211596_s_at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	-4.00	D	-4.29	D	-4.92	D
234148_at	LRRC5	Leucine rich repeat containing 8 family, member D	-4.00	D	-4.29	D	-2.14	D
225478_at	MFHAS1	Malignant fibrous histiocytoma amplified sequence 1	-4.00	D	-4.29	D	-9.19	D
1552343_s_at	PDE7A	phosphodiesterase 7A	-4.00	D	-6.06	D	-3.03	D
213939_s_at	RIPX	rap2 interacting protein x	-4.00	D	-2.30	D	-2.83	D
244226_s_at	SUPT4H1	Suppressor of Ty 4 homolog 1 (S. cerevisiae)	-4.00	D	-4.00	D	-2.30	D
202478_at	TRIB2	tribbles homolog 2 (Drosophila)	-4.00	D	-5.28	D	-3.73	D
226344_at	ZMAT1	zinc finger, matrin type 1	-4.00	D	-2.30	D	-4.59	D
222368_at	---	CDNA FLJ39459 fis, clone PROST2011439	-4.29	D	-2.30	D	-2.14	D
212764_at	---	---	-4.29	D	-3.03	D	-9.85	D
1561763_at	---	Clone TM029 mRNA sequence	-4.29	D	-4.00	D	-2.83	D
242876_at	AKT3	Serologically defined colon cancer antigen 8	-4.29	D	-3.73	D	-2.64	D
242563_at	FCHSD2	FCH and double SH3 domains 2	-4.29	D	-5.66	D	-2.83	D
241917_at	FCHSD2	FCH and double SH3 domains 2	-4.29	D	-3.03	D	-2.46	D
215221_at	FOXP1	Forkhead box P1	-4.29	D	-3.73	D	-6.06	D
238000_at	KIAA0265	KIAA0265 protein	-4.29	D	-6.96	D	-2.30	D
228974_at	MGC48625	Zinc finger protein 677	-4.29	D	-13.00	D	-6.06	D
214582_at	PDE3B	phosphodiesterase 3B, cGMP-inhibited	-4.29	D	-2.83	D	-12.13	D
225147_at	PSCD3	pleckstrin homology, Sec7 and coiled-coil domains 3	-4.29	D	-4.29	D	-24.25	D
241775_at	SCFD1	Sec1 family domain containing 1	-4.29	D	-2.83	D	-2.46	D
244579_at	TRPS1	Trichorhinophalangeal syndrome I	-4.29	D	-2.64	D	-2.46	D
1557260_a_at	ZNF382	zinc finger protein 382	-4.29	D	-8.57	D	-128.00	D
239819_at	---	Transcribed locus	-4.59	D	-2.83	D	-2.46	D
AFFYMETRIX PROBE SET ID	**GENE SYMBOL**	**GENE TITLE**	**FC#22**	**I/D**	**FC#2**	**I/D**	**FC#26**	**I/D**

239660_at	C20orf74	chromosome 20 open reading frame 74	-4.59	D	-4.00	D	-3.73	D
223377_x_at	CISH	cytokine inducible SH2-containing protein	-4.59	D	-4.92	D	-7.46	D
212977_at	CMKOR1	chemokine orphan receptor 1	-4.59	D	-29.86	D	-6.06	D
232874_at	DOCK9	Dedicator of cytokinesis 9	-4.59	D	-3.25	D	-2.14	D
225864_at	FAM84B	family with sequence similarity 84, member B	-4.59	D	-3.03	D	-119.43	D
55872_at	GM632	KIAA1196 protein	-4.59	D	-3.48	D	-29.86	D
1569041_at	JMJD1C	Hypothetical protein MGC14425	-4.59	D	-2.83	D	-2.83	D
1563455_at	KIAA0999	KIAA0999 protein	-4.59	D	-3.73	D	-2.14	D
1556462_a_at	KLF12	Kruppel-like factor 12	-4.59	D	-6.06	D	-3.03	D
209840_s_at	LRRN3	leucine rich repeat neuronal 3	-4.59	D	-27.86	D	-45.25	D
222771_s_at	MYEF2	myelin expression factor 2	-4.59	D	-3.03	D	-36.76	D
239585_at	PCAF	P300/CBP-associated factor	-4.59	D	-5.66	D	-2.14	D
244633_at	PIAS2	Protein inhibitor of activated STAT, 2	-4.59	D	-4.29	D	-2.14	D
244181_at	PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-4.59	D	-4.59	D	-8.00	D
214917_at	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	-4.59	D	-2.00	D	-2.64	D
239784_at	SMYD3	SET and MYND domain containing 3	-4.59	D	-3.48	D	-2.30	D
202524_s_at	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	-4.59	D	-2.46	D	-5.28	D
212071_s_at	SPTBN1	spectrin, beta, non-erythrocytic 1	-4.59	D	-4.59	D	-2.83	D
230970_at	SSH2	Slingshot homolog 2 (Drosophila)	-4.59	D	-7.46	D	-2.64	D
228818_at	TPD52	Tumor protein D52	-4.59	D	-4.92	D	-7.46	D
230713_at	ZCCHC11	Zinc finger, CCHC domain containing 11	-4.59	D	-3.73	D	-2.14	D
212655_at	ZCCHC14	zinc finger, CCHC domain containing 14	-4.59	D	-3.73	D	-2.64	D
243729_at	---	CDNA FLJ37931 fis, clone CTONG2004397	-4.92	D	-4.29	D	-157.59	D
242492_at	---	---	-4.92	D	-4.59	D	-2.00	D
204567_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	-4.92	D	-3.73	D	-9.85	D
219315_s_at	C16orf30	chromosome 16 open reading frame 30	-4.92	D	-6.50	D	-4.29	D
233241_at	C20orf19	chromosome 20 open reading frame 19	-4.92	D	-4.59	D	-4.29	D
239545_at	CAS1	O-acetyltransferase	-4.92	D	-5.66	D	-2.00	D
222996_s_at	CXXC5	CXXC finger 5	-4.92	D	-3.48	D	-10.56	D
204642_at	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	-4.92	D	-6.06	D	-5.28	D
206965_at	KLF12	Kruppel-like factor 12	-4.92	D	-10.56	D	-2.64	D
239091_at	LOC152185	Hypothetical protein AY099107	-4.92	D	-4.92	D	-2.14	D
1569484_s_at	MDN1	MDN1, midasin homolog (yeast)	-4.92	D	-4.92	D	-2.64	D
213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	-4.92	D	-7.46	D	-6.06	D
243997_x_at	PSPC1	Paraspeckle component 1	-4.92	D	-3.03	D	-2.30	D
205139_s_at	UST	uronyl-2-sulfotransferase	-4.92	D	-2.46	D	-8.00	D
209156_s_at	COL6A2	collagen, type VI, alpha 2	-5.28	D	-3.03	D	-2.00	D
238032_at	DHRS3	Dehydrogenase/reductase (SDR family) member 3	-5.28	D	-4.29	D	-4.92	D
236921_at	EMB	Embigin homolog (mouse)	-5.28	D	-8.00	D	-2.00	D
236379_at	EPB41	Erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	-5.28	D	-4.92	D	-2.14	D
230415_at	FOXP1	Forkhead box P1	-5.28	D	-4.29	D	-16.00	D
211202_s_at	JARID1B	Jumonji, AT rich interactive domain 1B (RBP2-like)	-5.28	D	-2.00	D	-2.30	D
243473_at	KIAA0999	KIAA0999 protein	-5.28	D	-2.30	D	-4.29	D
234645_at	MAML2	Mastermind-like 2 (Drosophila)	-5.28	D	-3.03	D	-2.30	D
205259_at	NR3C2	nuclear receptor subfamily 3, group C, member 2	-5.28	D	-6.06	D	-2.64	D
222371_at	PIAS1	Protein inhibitor of activated STAT, 1	-5.28	D	-4.29	D	-2.00	D
236621_at	RPS27	ribosomal protein S27 (metallopanstimulin 1)	-5.28	D	-3.03	D	-2.30	D
241460_at	RPS6KA3	Ribosomal protein S6 kinase, 90kDa, polypeptide 3	-5.28	D	-10.56	D	-2.14	D
229513_at	STRBP	Spermatid perinuclear RNA binding protein	-5.28	D	-6.50	D	-5.28	D
236978_at	THRAP1	Thyroid hormone receptor associated protein 1	-5.28	D	-3.73	D	-3.73	D
1556595_at	WWOX	WW domain containing oxidoreductase	-5.28	D	-5.28	D	-4.29	D
234032_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-5.28	D	-4.92	D	-2.00	D
206448_at	ZNF365	zinc finger protein 365	-5.28	D	-7.46	D	-4.92	D
244636_at	---	Transcribed locus	-5.66	D	-2.46	D	-2.46	D
227576_at	---	CDNA FLJ43311 fis, clone NT2RI2009855	-5.66	D	-5.28	D	-2.14	D
1559496_at	---	---	-5.66	D	-4.59	D	-4.29	D
1558409_at	---	LOC441276	-5.66	D	-2.30	D	-6.06	D
239449_at	ANKH	Ankylosis, progressive homolog (mouse)	-5.66	D	-4.29	D	-2.30	D
236796_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-5.66	D	-2.00	D	-2.30	D
1557240_a_at	BBX	Bobby sox homolog (Drosophila)	-5.66	D	-5.66	D	-2.64	D
233955_x_at	CXXC5	CXXC finger 5	-5.66	D	-3.73	D	-9.19	D
224516_s_at	CXXC5	CXXC finger 5 /// CXXC finger 5	-5.66	D	-3.48	D	-8.57	D
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201280_s_at	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	-5.66	D	-3.03	D	-22.63	D
233995_at	KIAA0372	KIAA0372	-5.66	D	-4.29	D	-2.46	D
239646_at	KIAA1961	KIAA1961 gene	-5.66	D	-5.66	D	-2.14	D
236846_at	LOC284757	hypothetical protein LOC284757	-5.66	D	-12.13	D	-4.92	D
218259_at	MKL2	MKL/myocardin-like 2	-5.66	D	-2.46	D	-2.30	D
225688_s_at	PHLDB2	pleckstrin homology-like domain, family B, member 2	-5.66	D	-6.50	D	-3.03	D
234196_at	TMCC3	Transmembrane and coiled-coil domain family 3	-5.66	D	-4.29	D	-2.30	D
239348_at	USP31	Ubiquitin specific peptidase 31	-5.66	D	-4.00	D	-2.14	D
237383_at	---	Transcribed locus	-6.06	D	-3.73	D	-3.48	D
232929_at	---	CDNA FLJ13240 fis, clone OVARC1000496	-6.06	D	-9.85	D	-3.25	D
227747_at	---	---	-6.06	D	-5.66	D	-2.30	D
229725_at	ACSL6	Acyl-CoA synthetase long-chain family member 6	-6.06	D	-8.57	D	-6.50	D
244061_at	ARHGAP15	Rho GTPase activating protein 15	-6.06	D	-6.96	D	-2.30	D
235333_at	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	-6.06	D	-7.46	D	-64.00	D
217523_at	CD44	CD44 antigen (homing function and Indian blood group system)	-6.06	D	-3.73	D	-4.29	D
1561166_a_at	FOXP1	Forkhead box P1	-6.06	D	-5.28	D	-5.28	D
215385_at	FTO	Fatso	-6.06	D	-4.59	D	-2.30	D
237388_at	GLMN	Glomulin, FKBP associated protein	-6.06	D	-5.28	D	-2.14	D
208798_x_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	-6.06	D	-5.28	D	-3.73	D
215316_at	HIBADH	3-hydroxyisobutyrate dehydrogenase	-6.06	D	-18.38	D	-2.83	D
242920_at	KIAA0999	KIAA0999 protein	-6.06	D	-3.03	D	-2.14	D
235956_at	KIAA1377	KIAA1377 protein	-6.06	D	-4.92	D	-4.00	D
1569181_x_at	LOC51326	ADP-ribosylation factor-like	-6.06	D	-2.83	D	-2.30	D
1569180_at	LOC51326	ADP-ribosylation factor-like	-6.06	D	-3.25	D	-2.64	D
232369_at	MBNL2	Muscleblind-like 2 (Drosophila)	-6.06	D	-6.50	D	-2.00	D
243233_at	PAN3	PABP1-dependent poly A-specific ribonuclease subunit PAN3	-6.06	D	-3.73	D	-2.14	D
220952_s_at	PLEKHA5	pleckstrin homology domain containing, family A member 5	-6.06	D	-2.30	D	-2.30	D
230707_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-6.06	D	-4.92	D	-18.38	D
230651_at	THOC2	THO complex 2	-6.06	D	-4.92	D	-2.64	D
237895_at	TNRC6B	Trinucleotide repeat containing 6B	-6.06	D	-4.00	D	-2.00	D
1556543_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-6.06	D	-9.19	D	-2.00	D
236474_at	ZNF395	Zinc finger protein 395	-6.06	D	-3.73	D	-6.06	D
1556952_at	---	CDNA FLJ37890 fis, clone BRTHA2000574	-6.50	D	-4.00	D	-3.03	D
215388_s_at	CFH /// CFHL1	complement factor H /// complement factor H-related 1	-6.50	D	-6.06	D	-6.50	D
237778_at	DIAPH2	Early lymphoid activation protein	-6.50	D	-4.00	D	-2.14	D
206618_at	IL18R1	interleukin 18 receptor 1	-6.50	D	-9.19	D	-3.25	D
1570021_at	LOC360030	homeobox C14	-6.50	D	-6.50	D	-2.00	D
240824_at	OBFC1	Chromosome 21 open reading frame 53	-6.50	D	-8.57	D	-2.64	D
244726_at	PLCB1	Phospholipase C, beta 1 (phosphoinositide-specific)	-6.50	D	-6.50	D	-90.51	D
219700_at	PLXDC1	plexin domain containing 1	-6.50	D	-5.66	D	-5.66	D
239619_at	ZNF395	Zinc finger protein 395	-6.50	D	-4.29	D	-10.56	D
233037_at	---	Clone FLB2932 mRNA sequence	-6.96	D	-6.96	D	-2.00	D
215528_at	---	MRNA; cDNA DKFZp586O1318 (from clone DKFZp586O1318)	-6.96	D	-2.83	D	-2.83	D
1562245_a_at	---	MRNA; cDNA DKFZp686H1629	-6.96	D	-29.86	D	-22.63	D
242110_at	ARHGAP5	Rho GTPase activating protein 5	-6.96	D	-3.73	D	-5.28	D
215846_at	CDC42SE2	CDC42 small effector 2	-6.96	D	-4.92	D	-3.73	D
229055_at	GPR68	G protein-coupled receptor 68	-6.96	D	-3.48	D	-6.06	D
206666_at	GZMK	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	-6.96	D	-10.56	D	-16.00	D
244774_at	PHACTR2	Phosphatase and actin regulator 2	-6.96	D	-3.03	D	-42.22	D
229483_at	UBE2H	Ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	-6.96	D	-5.66	D	-2.30	D
222357_at	ZBTB20	zinc finger and BTB domain containing 20	-6.96	D	-5.66	D	-2.46	D
1558410_s_at	---	LOC441276	-7.46	D	-3.25	D	-4.29	D
232210_at	BCL2	B-cell CLL/lymphoma 2	-7.46	D	-25.99	D	-6.96	D
243509_at	BTG1	B-cell translocation gene 1, anti-proliferative	-7.46	D	-5.28	D	-2.46	D
243640_x_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-7.46	D	-4.29	D	-4.29	D
243089_at	KLF12	Kruppel-like factor 12	-7.46	D	-13.00	D	-2.83	D
1557578_at	PHLDB2	Pleckstrin homology-like domain, family B, member 2	-7.46	D	-5.66	D	-4.59	D
239264_at	SEC8L1	SEC8-like 1 (S. cerevisiae)	-7.46	D	-4.29	D	-2.46	D
232686_at	SIGLECP3	sialic acid binding Ig-like lectin, pseudogene 3	-7.46	D	-6.50	D	-10.56	D
220485_s_at	SIRPB2	signal-regulatory protein beta 2	-7.46	D	-13.00	D	-10.56	D
244568_at	SYNE2	Spectrin repeat containing, nuclear envelope 2	-7.46	D	-10.56	D	-2.83	D
206150_at	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	-7.46	D	-13.93	D	-45.25	D
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240254_at	TNIK	TRAF2 and NCK interacting kinase	-7.46	D	-6.96	D	-3.03	D
218149_s_at	ZNF395	zinc finger protein 395	-7.46	D	-4.59	D	-12.13	D
236558_at	MBNL1	Muscleblind-like (Drosophila)	-8.00	D	-13.00	D	-2.83	D
205826_at	MYOM2	myomesin (M-protein) 2, 165kDa /// myomesin (M-protein) 2, 165kDa	-8.00	D	-3.48	D	-9.19	D
222317_at	PDE3B	Phosphodiesterase 3B, cGMP-inhibited	-8.00	D	-6.06	D	-18.38	D
226765_at	SPTBN1	Spectrin, beta, non-erythrocytic 1	-8.00	D	-5.66	D	-6.50	D
206828_at	TXK	TXK tyrosine kinase	-8.00	D	-7.46	D	-13.93	D
241391_at	---	Transcribed locus	-8.57	D	-3.25	D	-2.83	D
240865_at	---	---	-8.57	D	-11.31	D	-4.92	D
232583_at	---	CDNA FLJ11435 fis, clone HEMBA1001208	-8.57	D	-18.38	D	-6.50	D
210742_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-8.57	D	-6.96	D	-6.06	D
219895_at	FAM70A	family with sequence similarity 70, member A	-8.57	D	-2.83	D	-36.76	D
228423_at	FLJ21159	ASAP	-8.57	D	-6.96	D	-19.70	D
220467_at	FLJ21272	hypothetical protein FLJ21272	-8.57	D	-8.57	D	-2.83	D
240061_at	LOC54103	Hypothetical protein LOC54103	-8.57	D	-5.28	D	-2.30	D
223543_at	PDZK4	PDZ domain containing 4	-8.57	D	-3.48	D	-6.06	D
239102_s_at	PICALM	Phosphatidylinositol binding clathrin assembly protein	-8.57	D	-6.96	D	-4.92	D
1566608_at	SAMD3	Sterile alpha motif domain containing 3	-8.57	D	-8.57	D	-2.64	D
244878_at	---	Transcribed locus	-9.19	D	-8.00	D	-2.64	D
242874_at	---	CDNA FLJ37931 fis, clone CTONG2004397	-9.19	D	-5.66	D	-8.00	D
236685_at	---	Transcribed locus	-9.19	D	-7.46	D	-5.66	D
243450_at	AKAP13	A kinase (PRKA) anchor protein 13	-9.19	D	-11.31	D	-2.64	D
233690_at	C21orf96	Chromosome 21 open reading frame 96	-9.19	D	-11.31	D	-2.14	D
1558971_at	C6orf190	chromosome 6 open reading frame 190	-9.19	D	-19.70	D	-42.22	D
1562067_at	CERKL	Ceramide kinase-like	-9.19	D	-5.66	D	-2.14	D
236210_at	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	-9.19	D	-3.03	D	-2.46	D
244592_at	FLI1	Friend leukemia virus integration 1	-9.19	D	-9.85	D	-2.00	D
243874_at	FLJ42393	FLJ42393 protein	-9.19	D	-4.59	D	-2.14	D
232974_at	HDHD1A	Haloacid dehalogenase-like hydrolase domain containing 1A	-9.19	D	-6.96	D	-2.14	D
203914_x_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-9.19	D	-2.83	D	-2.14	D
244414_at	MAML2	Mastermind-like 2 (Drosophila)	-9.19	D	-6.50	D	-3.73	D
243810_at	---	Transcribed locus	-9.85	D	-27.86	D	-39.40	D
243791_at	---	Transcribed locus	-9.85	D	-6.06	D	-2.30	D
234865_at	---	T-cell receptor rearranged beta-chain V-region (V-D-J) mRNA, clone ph15 /clone ph21	-9.85	D	-7.46	D	-42.22	D
228854_at	---	Transcribed locus	-9.85	D	-7.46	D	-11.31	D
244548_at	ARHGAP26	Rho GTPase activating protein 26	-9.85	D	-6.50	D	-2.30	D
225792_at	HOOK1	Hook homolog 1 (Drosophila)	-9.85	D	-4.59	D	-2.46	D
232333_at	MAML2	Mastermind-like 2 (Drosophila)	-9.85	D	-6.96	D	-4.59	D
1559882_at	SAMHD1	SAM domain and HD domain 1	-9.85	D	-2.64	D	-2.14	D
219423_x_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-9.85	D	-6.06	D	-13.00	D
220917_s_at	WDR19	WD repeat domain 19	-9.85	D	-8.00	D	-3.73	D
236617_at	WWOX	WW domain containing oxidoreductase	-9.85	D	-5.66	D	-4.29	D
230332_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-9.85	D	-8.00	D	-4.00	D
240758_at	CENTG2	Centaurin, gamma 2	-10.56	D	-27.86	D	-4.59	D
202481_at	DHRS3	dehydrogenase/reductase (SDR family) member 3	-10.56	D	-22.63	D	-90.51	D
242216_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	-10.56	D	-6.50	D	-4.29	D
241692_at	HNRPLL	Heterogeneous nuclear ribonucleoprotein L-like	-10.56	D	-6.06	D	-2.46	D
239946_at	KIAA0922	KIAA0922 protein	-10.56	D	-8.57	D	-2.00	D
239673_at	NR3C2	Nuclear receptor subfamily 3, group C, member 2	-10.56	D	-9.19	D	-5.28	D
222330_at	PDE3B	Phosphodiesterase 3B, cGMP-inhibited	-10.56	D	-14.93	D	-19.70	D
232629_at	PROK2	prokineticin 2	-10.56	D	-3.03	D	-59.71	D
AFFX-HUMRGE/M10098_5_at	---	---	-11.31	D	-11.31	D	-18.38	D
242827_x_at	---	Transcribed locus	-11.31	D	-14.93	D	-2.30	D
212187_x_at	PTGDS	prostaglandin D2 synthase 21kDa (brain)	-11.31	D	-4.92	D	-6.06	D
242801_at	---	Similar to 40S ribosomal protein S3	-12.13	D	-2.46	D	-11.31	D
228623_at	---	Transcribed locus, weakly similar to XP_517454.1	-12.13	D	-8.00	D	-2.64	D
232882_at	FOXO1A	Forkhead box O1A (rhabdomyosarcoma)	-12.13	D	-8.00	D	-3.48	D
207072_at	IL18RAP	interleukin 18 receptor accessory protein	-12.13	D	-27.86	D	-14.93	D
1560562_a_at	MGC48625	Zinc finger protein 677	-12.13	D	-24.25	D	-17.15	D
242737_at	RAD51L1	RAD51-like 1 (S. cerevisiae)	-12.13	D	-8.00	D	-2.83	D
AFFX-HUMRGE/M10098_3_at	SRP68	signal recognition particle 68kDa	-12.13	D	-9.85	D	-11.31	D
239448_at	---	---	-13.00	D	-3.73	D	-7.46	D
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207681_at	CXCR3	chemokine (C-X-C motif) receptor 3	-13.00	D	-7.46	D	-16.00	D
1569477_at	FOXO3A	Forkhead box O3A	-13.00	D	-4.92	D	-3.25	D
242405_at	MAML2	Mastermind-like 2 (Drosophila)	-13.00	D	-6.06	D	-4.92	D
235763_at	SLC44A5	solute carrier family 44, member 5	-13.00	D	-14.93	D	-18.38	D
233614_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	-13.93	D	-9.85	D	-6.06	D
202806_at	DBN1	drebrin 1	-13.93	D	-29.86	D	-3.48	D
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	-13.93	D	-51.98	D	-194.01	D
214705_at	INADL	InaD-like (Drosophila)	-13.93	D	-4.29	D	-29.86	D
243310_at	---	Transcribed locus, weakly similar to XP_209041.2	-14.93	D	-24.25	D	-2.30	D
237201_at	---	Transcribed locus	-14.93	D	-6.50	D	-2.00	D
1558972_s_at	C6orf190	chromosome 6 open reading frame 190	-14.93	D	-24.25	D	-27.86	D
212843_at	NCAM1	neural cell adhesion molecule 1	-14.93	D	-19.70	D	-9.85	D
210612_s_at	SYNJ2	synaptojanin 2	-14.93	D	-22.63	D	-5.28	D
237035_at	WWOX	WW domain containing oxidoreductase	-14.93	D	-3.25	D	-2.30	D
244239_at	ANKH	Ankylosis, progressive homolog (mouse)	-16.00	D	-11.31	D	-2.00	D
204066_s_at	CENTG2	centaurin, gamma 2	-17.15	D	-7.46	D	-16.00	D
209686_at	S100B	S100 calcium binding protein, beta (neural)	-17.15	D	-51.98	D	-9.19	D
1561195_at	TM7SF1	Transmembrane 7 superfamily member 1 (upregulated in kidney)	-18.38	D	-32.00	D	-4.00	D
221123_x_at	ZNF395	zinc finger protein 395	-18.38	D	-6.96	D	-9.85	D
240666_at	FOXP1	Forkhead box P1	-19.70	D	-16.00	D	-3.48	D
239862_at	TPD52	Tumor protein D52	-19.70	D	-27.86	D	-3.25	D
1563460_at	---	Similar to 40S ribosomal protein S3	-21.11	D	-9.19	D	-13.93	D
1558569_at	MAML2	Mastermind-like 2 (Drosophila)	-21.11	D	-51.98	D	-6.06	D
244625_at	RERE	Arginine-glutamic acid dipeptide (RE) repeats	-21.11	D	-3.73	D	-3.25	D
206366_x_at	XCL2	chemokine (C motif) ligand 2	-21.11	D	-5.66	D	-14.93	D
232951_at	---	CDNA FLJ10136 fis, clone HEMBA1003129	-22.63	D	-11.31	D	-3.73	D
203608_at	ALDH5A1	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)	-24.25	D	-6.50	D	-2.00	D
232614_at	BCL2	B-cell CLL/lymphoma 2	-24.25	D	-19.70	D	-6.96	D
1559723_s_at	C9orf3	Chromosome 9 open reading frame 3	-24.25	D	-4.00	D	-3.03	D
226764_at	LOC152485	hypothetical protein LOC152485	-24.25	D	-22.63	D	-32.00	D
214567_s_at	XCL1 /// XCL2	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	-24.25	D	-6.06	D	-24.25	D
222162_s_at	ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	-25.99	D	-34.30	D	-16.00	D
203628_at	IGF1R	insulin-like growth factor 1 receptor	-27.86	D	-6.06	D	-68.59	D
244860_at	KIAA0999	KIAA0999 protein	-29.86	D	-3.48	D	-2.30	D
223216_x_at	ZNF395 / FBXO16	zinc finger protein 395 /F-box protein 16	-29.86	D	-25.99	D	-59.71	D
244845_at	---	CDNA FLJ45435 fis, clone BRHIP3042817	-32.00	D	-9.19	D	-9.19	D
236963_at	---	Transcribed locus, weakly similar to XP_371841.1	-32.00	D	-78.79	D	-6.06	D
232565_at	RAB6IP2	RAB6 interacting protein 2	-36.76	D	-13.93	D	-2.64	D
214295_at	KIAA0485	KIAA0485 protein	-39.40	D	-13.00	D	-2.46	D
232693_s_at	ZNF395 /FBXO16	zinc finger protein 395 /F-box protein 16	-42.22	D	-24.25	D	-45.25	D
234402_at	---	T-cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AE212	-45.25	D	-16.00	D	-24.25	D
240347_at	BTG1	B-cell translocation gene 1, anti-proliferative	-45.25	D	-4.59	D	-2.14	D
237839_at	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)	-59.71	D	-17.15	D	-34.30	D
1564139_at	LOC144571	hypothetical protein LOC144571	-59.71	D	-5.66	D	-39.40	D
232752_at	---	CDNA FLJ10302 fis, clone NT2RM2000042	-64.00	D	-4.00	D	-5.28	D
209160_at	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	-222.9	D	-294.1	D	-776.05	D

List of transcripts concordantly up- and downregulated in all three LGL patients vs. healthy noneffector CD8+CD57- population. (page 15-38)

FC indicates foldchange in transcript expression in patient sample when compared to control CD57+ cells; I/D, increase/decrease in transcript expression.

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
1556545_at	---	CDNA FLJ32379 fis, clone SKMUS1000030	2.30	I	6.50	I	4.00	I
1556676_a_at	---	CDNA clone IMAGE:4793171	2.14	I	2.30	I	4.00	I
1557051_s_at	---	Homo sapiens, clone IMAGE:5019307, mRNA	3.73	I	4.59	I	2.30	I
1559067_a_at	---	Transcribed locus	3.48	I	2.46	I	4.00	I
1562289_at	---	MRNA; cDNA DKFZp434N0220 (from clone DKFZp434N0220)	3.25	I	2.14	I	11.31	I
1562634_at	---	Homo sapiens, clone IMAGE:5169164, mRNA	9.19	I	59.71	I	8.00	I
1570541_s_at	---	Homo sapiens, clone IMAGE:4042735, mRNA	21.11	I	39.40	I	8.57	I
225791_at	---	---	2.14	I	2.46	I	3.03	I
227396_at	---	Homo sapiens, clone IMAGE:4454331, mRNA	3.48	I	3.03	I	4.59	I
227745_at	---	CDNA FLJ90571 fis, clone OVARC1001725	3.03	I	4.29	I	4.92	I
228108_at	---	CDNA clone IMAGE:5263177	2.46	I	2.30	I	6.50	I
228273_at	---	Transcribed locus	5.28	I	6.50	I	2.83	I
228333_at	---	Full length insert cDNA clone YT94E02	5.66	I	2.30	I	6.96	I
228457_at	---	CDNA clone IMAGE:5263177	3.48	I	2.14	I	3.48	I
228642_at	---	Homo sapiens, clone IMAGE:5019307, mRNA	4.00	I	4.00	I	4.29	I
229309_at	---	Beta-1 adrenergic receptor mRNA, 3' UTR	6.96	I	10.56	I	29.86	I
229450_at	---	---	8.57	I	5.66	I	5.28	I
229506_at	---	CDNA clone IMAGE:5263177	5.28	I	4.59	I	5.66	I
230741_at	---	Full length insert cDNA clone YX74D05	2.46	I	4.00	I	3.03	I
230917_at	---	CDNA FLJ45450 fis, clone BRSTN2002691	8.57	I	4.00	I	6.50	I
235122_at	---	CDNA clone IMAGE:6254031	3.03	I	3.03	I	4.59	I
235171_at	---	Full-length cDNA clone CS0DM012YE14 of Fetal liver of Homo sapiens (human)	6.96	I	3.25	I	9.19	I
235293_at	---	CDNA FLJ37816 fis, clone BRSSN2003093	4.92	I	4.29	I	2.30	I
235539_at	---	---	2.00	I	2.30	I	2.46	I
235919_at	---	Transcribed locus, weakly similar to NP_055301.1	3.73	I	2.00	I	5.66	I
237542_at	---	Transcribed locus	3.25	I	5.66	I	3.25	I
238725_at	---	---	2.14	I	3.25	I	4.29	I
242181_at	---	CDNA FLJ33489 fis, clone BRAMY2003585	8.57	I	4.29	I	14.93	I
AFFX-DapX-3_at	---	---	103.97	I	97.01	I	294.07	I
AFFX-DapX-5_at	---	---	59.71	I	59.71	I	181.02	I
AFFX-DapX-M_at	---	---	27.86	I	19.70	I	119.43	I
AFFX-LysX-3_at	---	---	8.57	I	6.06	I	18.38	I
AFFX-PheX-3_at	---	---	3.73	I	4.92	I	12.13	I
AFFX-r2-Bs-dap-3_at	---	---	294.07	I	274.37	I	2352.00	I
AFFX-r2-Bs-dap-5_at	---	---	477.71	I	388.02	I	2194.00	I
AFFX-r2-Bs-dap-M_at	---	---	34.30	I	21.11	I	111.43	I
AFFX-r2-Bs-phe-5_at	---	---	64.00	I	68.59	I	477.71	I
AFFX-r2-Bs-thr-5_s_at	---	---	4.29	I	4.29	I	8.57	I
AFFX-r2-Bs-thr-M_s_at	---	---	6.96	I	5.28	I	13.93	I
AFFX-ThrX-3_at	---	---	59.71	I	78.79	I	512.00	I
AFFX-ThrX-M_at	---	---	3.73	I	2.83	I	13.93	I
212895_s_at	ABR	active BCR-related gene	2.00	I	2.30	I	2.83	I
214671_s_at	ABR	active BCR-related gene	3.03	I	3.73	I	2.00	I
208002_s_at	ACOT7	acyl-CoA thioesterase 7	6.96	I	5.66	I	4.92	I
205180_s_at	ADAM8	ADAM metallopeptidase domain 8	2.83	I	2.64	I	4.29	I
206513_at	AIM2	absent in melanoma 2	3.03	I	2.30	I	2.30	I
201590_x_at	ANXA2	annexin A2	2.30	I	3.48	I	2.83	I
210427_x_at	ANXA2	annexin A2	2.14	I	3.25	I	2.64	I
213503_x_at	ANXA2	annexin A2	2.30	I	3.48	I	2.83	I
201301_s_at	ANXA4	annexin A4	2.83	I	5.28	I	2.30	I

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
201302_at	ANXA4	annexin A4	2.64	I	4.92	I	2.14	I
205639_at	AOAH	acyloxyacyl hydrolase (neutrophil)	4.59	I	4.29	I	6.06	I
209546_s_at	APOL1	apolipoprotein L, 1	3.25	I	2.00	I	2.46	I
225171_at	ARHGAP18	Rho GTPase activating protein 18	2.00	I	2.30	I	2.30	I
201334_s_at	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	3.03	I	2.00	I	3.25	I
226914_at	ARPC5L	actin related protein 2/3 complex, subunit 5-like	2.64	I	2.00	I	4.59	I
218832_x_at	ARRB1	arrestin, beta 1	34.30	I	36.76	I	17.15	I
222756_s_at	ARRB1	arrestin, beta 1	3.03	I	4.00	I	2.30	I
222912_at	ARRB1	arrestin, beta 1	3.03	I	4.92	I	2.64	I
1555419_a_at	ASAH1	N-acylsphingosine amidohydrolase (acid ceramidase) 1	3.03	I	4.29	I	2.30	I
202672_s_at	ATF3	activating transcription factor 3	11.31	I	32.00	I	8.00	I
208836_at	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	2.64	I	3.03	I	3.73	I
201818_at	AYTL2	acyltransferase like 2	3.25	I	2.14	I	4.59	I
219521_at	B3GAT1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	59.71	I	25.99	I	68.59	I
221485_at	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	2.83	I	2.14	I	2.30	I
204908_s_at	BCL3	B-cell CLL/lymphoma 3	2.46	I	3.73	I	4.00	I
206746_at	BFSP1	beaded filament structural protein 1, filensin	27.86	I	18.38	I	78.79	I
201170_s_at	BHLHB2	basic helix-loop-helix domain containing, class B, 2	3.03	I	3.03	I	2.30	I
229437_at	BIC	BIC transcript	4.00	I	3.03	I	3.03	I
230722_at	BNC2	Basonuclin 2	4.29	I	2.83	I	19.70	I
238478_at	BNC2	Basonuclin 2	3.25	I	3.25	I	18.38	I
203502_at	BPGM	2,3-bisphosphoglycerate mutase	4.59	I	2.64	I	2.30	I
1568768_s_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	6.06	I	11.31	I	3.48	I
205548_s_at	BTG3	BTG family, member 3	2.46	I	2.83	I	4.29	I
213134_x_at	BTG3	BTG family, member 3	2.46	I	3.25	I	4.00	I
205839_s_at	BZRAP1	benzodiazapine receptor (peripheral) associated protein 1	3.03	I	2.46	I	2.30	I
227699_at	C14orf149	chromosome 14 open reading frame 149	2.14	I	3.03	I	2.46	I
226901_at	C17orf58	chromosome 17 open reading frame 58	4.29	I	4.00	I	5.28	I
1557016_a_at	C1orf177	chromosome 1 open reading frame 177	5.28	I	2.30	I	6.96	I
221272_s_at	C1orf21	chromosome 1 open reading frame 21	4.00	I	3.48	I	9.85	I
223125_s_at	C1orf21	chromosome 1 open reading frame 21	6.06	I	3.73	I	11.31	I
223126_s_at	C1orf21	chromosome 1 open reading frame 21	5.66	I	3.25	I	13.93	I
1553338_at	C1orf55	chromosome 1 open reading frame 55	2.30	I	3.48	I	2.30	I
217835_x_at	C20orf24	chromosome 20 open reading frame 24	2.00	I	2.46	I	2.00	I
206656_s_at	C20orf3	chromosome 20 open reading frame 3	2.30	I	2.00	I	3.25	I
209906_at	C3AR1	complement component 3a receptor 1	3.73	I	3.48	I	2.64	I
1554486_a_at	C6orf114	chromosome 6 open reading frame 114	4.29	I	4.29	I	5.66	I
206011_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.46	I	2.14	I	2.14	I
209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.14	I	2.30	I	2.46	I
211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.14	I	2.30	I	2.64	I
211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.64	I	2.46	I	2.30	I
211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	2.00	I	2.14	I	2.30	I
205114_s_at	CCL3	chemokine (C-C motif) ligand 3	2.00	I	8.00	I	9.85	I
204103_at	CCL4	chemokine (C-C motif) ligand 4	4.00	I	2.00	I	3.48	I
1555827_at	CCNL1	Cyclin L1	2.30	I	4.29	I	3.03	I
220307_at	CD244	CD244 molecule, natural killer cell receptor 2B4	4.00	I	2.30	I	4.92	I
205692_s_at	CD38	CD38 molecule	6.06	I	5.28	I	9.85	I
236191_at	CD38	CD38 molecule	3.48	I	9.19	I	10.56	I
205173_x_at	CD58	CD58 molecule	2.30	I	2.64	I	2.83	I
211744_s_at	CD58	CD58 molecule /// CD58 molecule	2.46	I	2.83	I	2.83	I
216942_s_at	CD58	CD58 molecule	2.46	I	3.03	I	2.46	I
200663_at	CD63	CD63 molecule	2.83	I	3.48	I	3.25	I
209644_x_at	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	8.57	I	4.92	I	2.46	I
204039_at	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	4.00	I	10.56	I	3.25	I
219150_s_at	CENTA1	centaurin, alpha 1	3.48	I	3.73	I	2.46	I
90265_at	CENTA1	centaurin, alpha 1	3.03	I	3.73	I	3.48	I
1557985_s_at	CEP78	centrosomal protein 78kDa	4.29	I	2.83	I	6.96	I
228774_at	CEP78	centrosomal protein 78kDa	3.73	I	2.64	I	8.00	I
213385_at	CHN2	chimerin (chimaerin) 2	2.64	I	2.83	I	5.28	I
218927_s_at	CHST12	carbohydrate (chondroitin 4) sulfotransferase 12	3.73	I	2.30	I	2.83	I
219529_at	CLIC3	chloride intracellular channel 3	4.92	I	3.25	I	2.30	I
1552701_a_at	COP1	caspase-1 dominant-negative inhibitor pseudo-ICE	2.14	I	3.25	I	2.46	I

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
210688_s_at	CPT1A	carnitine palmitoyltransferase 1A (liver)	3.25	I	4.00	I	3.03	I
209833_at	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	2.83	I	2.46	I	2.30	I
210140_at	CST7	cystatin F (leukocystatin)	2.83	I	2.46	I	4.59	I
225525_at	CTA-221G9.4	KIAA1671 protein	8.00	I	4.59	I	13.00	I
201220_x_at	CTBP2	C-terminal binding protein 2	4.59	I	4.59	I	8.00	I
210554_s_at	CTBP2	C-terminal binding protein 2	4.00	I	4.00	I	4.92	I
210835_s_at	CTBP2	C-terminal binding protein 2	4.59	I	4.29	I	6.96	I
201218_at	CTBP2	C-terminal binding protein 2	6.50	I	4.00	I	4.92	I
201219_at	CTBP2	C-terminal binding protein 2	6.96	I	5.28	I	6.50	I
200764_s_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	6.50	I	5.66	I	5.28	I
200765_x_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	5.28	I	5.28	I	6.96	I
210844_x_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	7.46	I	6.96	I	8.57	I
232617_at	CTSS	cathepsin S	2.30	I	3.73	I	2.14	I
219079_at	CYB5R4	cytochrome b5 reductase 4	2.00	I	2.64	I	2.14	I
212975_at	DENND3	DENN/MADD domain containing 3	4.59	I	6.06	I	3.73	I
200862_at	DHCR24	24-dehydrocholesterol reductase	6.06	I	4.92	I	9.19	I
222154_s_at	DNAPTP6	DNA polymerase-transactivated protein 6	2.14	I	2.14	I	2.83	I
227018_at	DPP8	dipeptidyl-peptidase 8	2.46	I	2.14	I	2.83	I
215501_s_at	DUSP10	dual specificity phosphatase 10	5.28	I	4.59	I	2.83	I
221563_at	DUSP10	dual specificity phosphatase 10	3.48	I	3.03	I	3.73	I
209457_at	DUSP5	dual specificity phosphatase 5	3.25	I	9.19	I	7.46	I
221417_x_at	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	8.57	I	6.06	I	6.96	I
230464_at	EDG8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	5.28	I	3.25	I	8.00	I
217992_s_at	EFHD2	EF-hand domain family, member D2	4.29	I	4.59	I	4.92	I
222483_at	EFHD2	EF-hand domain family, member D2	4.00	I	4.92	I	6.50	I
219190_s_at	EIF2C4	eukaryotic translation initiation factor 2C, 4	2.64	I	2.46	I	2.46	I
1554309_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	8.00	I	9.19	I	5.66	I
201935_s_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	2.00	I	2.00	I	4.59	I
201341_at	ENC1	ectodermal-neural cortex (with BTB-like domain)	3.25	I	3.73	I	6.96	I
227609_at	EPSTI1	epithelial stromal interaction 1 (breast)	3.25	I	4.00	I	2.00	I
216836_s_at	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2	3.48	I	3.03	I	4.29	I
203989_x_at	F2R	coagulation factor II (thrombin) receptor	6.06	I	2.83	I	3.73	I
221766_s_at	FAM46A	family with sequence similarity 46, member A	2.30	I	3.25	I	5.66	I
224973_at	FAM46A	Family with sequence similarity 46, member A	2.83	I	2.64	I	3.03	I
208092_s_at	FAM49A	family with sequence similarity 49, member A	8.57	I	8.57	I	6.96	I
209683_at	FAM49A	Family with sequence similarity 49, member A	4.59	I	3.73	I	8.57	I
203206_at	FAM53B	family with sequence similarity 53, member B	4.92	I	2.83	I	7.46	I
210889_s_at	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	2.83	I	9.85	I	27.86	I
211395_x_at	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	8.00	I	27.86	I	5.66	I
204006_s_at	FCGR3A/B	Fc fragment of IgG, low affinity IIIa/IIIb, receptor (CD16a/CD16b)	22.63	I	27.86	I	7.46	I
204007_at	FCGR3B	Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	11.31	I	9.85	I	6.06	I
238452_at	FCRLM2	Fc receptor-like and mucin-like 2	3.73	I	2.30	I	8.00	I
204834_at	FGL2	fibrinogen-like 2	8.00	I	14.93	I	3.48	I
208438_s_at	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	4.59	I	5.66	I	4.29	I
1555486_a_at	FLJ14213	hypothetical protein FLJ14213	4.00	I	2.83	I	5.28	I
219383_at	FLJ14213	hypothetical protein FLJ14213	4.00	I	2.14	I	6.06	I
227168_at	FLJ25967	hypothetical gene supported by AK098833	5.66	I	2.64	I	8.00	I
236487_at	FLJ30655	Hypothetical protein FLJ30655	2.83	I	2.14	I	2.64	I
225262_at	FOSL2	FOS-like antigen 2	3.48	I	4.92	I	2.30	I
206307_s_at	FOXD1	forkhead box D1	21.11	I	11.31	I	27.86	I
242586_at	FSD1L	Fibronectin type III and SPRY domain containing 1-like	5.28	I	2.64	I	3.03	I
200959_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	2.30	I	2.46	I	2.00	I
209304_x_at	GADD45B	growth arrest and DNA-damage-inducible, beta	2.14	I	3.73	I	2.64	I
231578_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	2.83	I	2.46	I	2.46	I
229625_at	GBP5	Guanylate binding protein 5	3.03	I	3.48	I	2.64	I
205505_at	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	3.48	I	2.14	I	2.64	I
219821_s_at	GFOD1	glucose-fructose oxidoreductase domain containing 1	3.48	I	2.46	I	17.15	I
200648_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	9.85	I	13.00	I	2.83	I
215001_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	4.29	I	4.59	I	3.25	I
217202_s_at	GLUL	glutamate-ammonia ligase (glutamine synthetase)	8.57	I	9.85	I	2.30	I
235139_at	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	4.00	I	3.48	I	4.00	I
238002_at	GOLPH4	golgi phosphoprotein 4	6.50	I	6.06	I	5.28	I

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211977_at	GPR107	G protein-coupled receptor 107	2.00	I	2.64	I	3.25	I
206582_s_at	GPR56	G protein-coupled receptor 56	19.70	I	13.93	I	21.11	I
212070_at	GPR56	G protein-coupled receptor 56	7.46	I	5.28	I	19.70	I
210164_at	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	4.92	I	3.48	I	9.85	I
210321_at	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	6.06	I	5.28	I	9.19	I
1554285_at	HAVCR2	hepatitis A virus cellular receptor 2	7.46	I	8.00	I	6.50	I
1555628_a_at	HAVCR2	hepatitis A virus cellular receptor 2	6.06	I	4.59	I	5.66	I
235458_at	HAVCR2	hepatitis A virus cellular receptor 2	5.28	I	4.29	I	8.57	I
209524_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	3.73	I	3.48	I	6.50	I
209526_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	3.48	I	3.48	I	6.06	I
216693_x_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	3.48	I	3.48	I	4.92	I
228266_s_at	HDGFRP3	hepatoma-derived growth factor, related protein 3	2.30	I	3.48	I	3.03	I
212822_at	HEG1	HEG homolog 1 (zebrafish)	2.14	I	2.00	I	5.28	I
239988_at	HERC6	Hect domain and RLD 6	2.46	I	2.14	I	2.00	I
202814_s_at	HEXIM1	hexamethylene bis-acetamide inducible 1	2.30	I	2.00	I	2.64	I
225116_at	HIPK2	Homeodomain interacting protein kinase 2	2.14	I	2.00	I	3.48	I
214290_s_at	HIST2H2AA	histone 2, H2aa	4.29	I	5.66	I	2.83	I
218280_x_at	HIST2H2AA	histone 2, H2aa	4.00	I	5.66	I	3.48	I
211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	5.28	I	8.00	I	2.14	I
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	51.98	I	84.45	I	17.15	I
209480_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	24.25	I	34.30	I	4.92	I
211654_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	8.57	I	16.00	I	2.46	I
212999_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	11.31	I	27.86	I	4.92	I
204670_x_at	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	3.73	I	4.59	I	2.00	I
236203_at	HLA-DRB1	Major histocompatibility complex, class II, DR beta 1	18.38	I	48.50	I	11.31	I
238900_at	HLA-DRB1	Major histocompatibility complex, class II, DR beta 1	24.25	I	97.01	I	7.46	I
211597_s_at	HOP	homeodomain-only protein /// homeodomain-only protein	2.00	I	2.14	I	3.03	I
206194_at	HOXC4	homeobox C4	5.28	I	4.59	I	5.66	I
209581_at	HRASLS3	HRAS-like suppressor 3	6.50	I	4.29	I	8.00	I
201193_at	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	2.00	I	2.64	I	2.64	I
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	2.46	I	2.14	I	2.46	I
202438_x_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	2.30	I	2.14	I	2.64	I
206342_x_at	IDS	iduronate 2-sulfatase (Hunter syndrome)	2.83	I	3.25	I	3.03	I
217502_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	3.25	I	9.19	I	2.00	I
226757_at	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	2.83	I	4.92	I	3.73	I
204747_at	IFIT3	interferon-induced protein with tetratricopeptide repeats 3	4.29	I	4.59	I	5.66	I
210354_at	IFNG	interferon, gamma	45.25	I	45.25	I	78.79	I
201393_s_at	IGF2R	insulin-like growth factor 2 receptor	2.14	I	2.14	I	2.64	I
244261_at	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	3.03	I	2.30	I	5.66	I
221185_s_at	IQCG	IQ motif containing G	6.96	I	3.48	I	4.29	I
204562_at	IRF4	interferon regulatory factor 4	3.48	I	2.46	I	4.92	I
232352_at	ISL2	ISL2 transcription factor, LIM/homeodomain, (islet-2)	16.00	I	13.93	I	14.93	I
210184_at	ITGAX	integrin, alpha X (complement component 3 receptor 4 subunit)	6.06	I	9.85	I	6.96	I
238600_at	JAKMIP1	janus kinase and microtubule interacting protein 1	3.48	I	2.00	I	3.25	I
201464_x_at	JUN	v-jun sarcoma virus 17 oncogene homolog (avian)	3.48	I	8.57	I	2.46	I
201466_s_at	JUN	v-jun sarcoma virus 17 oncogene homolog (avian)	3.48	I	14.93	I	2.83	I
227265_at	KIAA1505	KIAA1505 protein	6.06	I	6.96	I	3.25	I
202393_s_at	KLF10	Kruppel-like factor 10	2.46	I	9.19	I	2.83	I
207723_s_at	KLRC3	killer cell lectin-like receptor subfamily C, member 3	5.28	I	3.25	I	8.57	I
207795_s_at	KLRD1	killer cell lectin-like receptor subfamily D, member 1	4.00	I	2.46	I	6.06	I
210606_x_at	KLRD1	killer cell lectin-like receptor subfamily D, member 1	3.73	I	2.14	I	6.06	I
223836_at	KSP37	Ksp37 protein	8.00	I	7.46	I	12.13	I
206486_at	LAG3	lymphocyte-activation gene 3	3.48	I	2.30	I	4.00	I
221581_s_at	LAT2	linker for activation of T cells family, member 2	6.96	I	6.50	I	6.50	I
202068_s_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	4.59	I	4.00	I	5.66	I
201105_at	LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	4.29	I	4.59	I	3.48	I
208949_s_at	LGALS3 /// GALIG	lectin, galactoside-binding, soluble, 3 (galectin 3) / galectin-3 internal gene	4.00	I	8.00	I	2.64	I
211336_x_at	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	3.48	I	8.00	I	3.03	I
207104_x_at	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	5.28	I	14.93	I	4.29	I
229937_x_at	LILRB1	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	9.19	I	14.93	I	9.19	I
209205_s_at	LMO4	LIM domain only 4	2.14	I	2.14	I	2.00	I
236717_at	LOC165186	similar to RIKEN cDNA 4632412N22 gene	6.06	I	4.92	I	13.00	I

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1557411_s_at	LOC203427	similar to solute carrier family 25 , member 16	2.46	I	2.14	I	2.30	I
230727_at	LOC284106	hypothetical protein LOC284106	3.73	I	2.46	I	3.25	I
227478_at	LOC284262	hypothetical protein LOC284262	8.00	I	4.29	I	12.13	I
230179_at	LOC285812	hypothetical protein LOC285812	4.59	I	2.83	I	11.31	I
230272_at	LOC645323	Hypothetical protein LOC645323	147.03	I	78.79	I	388.02	I
238850_at	LOC645323	Hypothetical protein LOC645323	39.40	I	8.57	I	90.51	I
239494_at	LOC646725	hypothetical protein LOC646725	3.73	I	11.31	I	2.83	I
225834_at	LOC652689	hypothetical protein LOC652689	3.25	I	3.73	I	2.64	I
229067_at	LOC653464	Similar to SLIT-ROBO Rho GTPase-activating protein 2 (srGAP2)	2.46	I	2.83	I	2.30	I
202625_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	5.66	I	8.00	I	6.06	I
202626_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	4.92	I	8.00	I	10.56	I
210754_s_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	4.92	I	7.46	I	9.19	I
203518_at	LYST	lysosomal trafficking regulator	2.64	I	2.00	I	4.59	I
215415_s_at	LYST	lysosomal trafficking regulator	3.73	I	3.73	I	2.00	I
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	2.64	I	4.29	I	2.30	I
208116_s_at	MAN1A1	mannosidase, alpha, class 1A, member 1	4.59	I	2.46	I	3.03	I
225408_at	MBP	myelin basic protein	2.83	I	2.14	I	2.30	I
230110_at	MCOLN2	mucolipin 2	3.03	I	2.30	I	3.03	I
220603_s_at	MCTP2	multiple C2 domains, transmembrane 2	2.46	I	2.14	I	2.30	I
209200_at	MEF2C	MADS box transcription enhancer factor 2, polypeptide A	3.03	I	2.64	I	3.25	I
212830_at	MEGF9	multiple EGF-like-domains 9	2.30	I	3.73	I	2.64	I
225955_at	METRNL	meteorin, glial cell differentiation regulator-like	6.96	I	6.06	I	8.00	I
228606_at	MGC33212	hypothetical protein MGC33212	2.30	I	2.14	I	2.64	I
224917_at	MIRN21	microRNA 21	4.00	I	5.28	I	2.46	I
213395_at	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	4.29	I	5.66	I	10.56	I
209928_s_at	MSC	musculin (activated B-cell factor-1)	6.96	I	3.25	I	4.29	I
201761_at	MTHFD2	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2	2.46	I	3.03	I	2.14	I
212509_s_at	MXRA7	matrix-remodelling associated 7	3.03	I	4.29	I	4.59	I
227326_at	MXRA7	matrix-remodelling associated 7	4.29	I	5.28	I	6.50	I
213733_at	MYO1F	myosin IF	2.30	I	2.64	I	2.46	I
203216_s_at	MYO6	myosin VI	6.06	I	2.64	I	8.57	I
210480_s_at	MYO6	myosin VI	5.28	I	2.64	I	9.19	I
228062_at	NAP1L5	nucleosome assembly protein 1-like 5	2.83	I	2.46	I	2.46	I
228063_s_at	NAP1L5	nucleosome assembly protein 1-like 5	2.64	I	2.64	I	3.03	I
207860_at	NCR1	natural cytotoxicity triggering receptor 1	7.46	I	5.66	I	5.28	I
217095_x_at	NCR1	natural cytotoxicity triggering receptor 1	17.15	I	24.25	I	21.11	I
203574_at	NFIL3	nuclear factor, interleukin 3 regulated	9.19	I	13.93	I	13.93	I
213915_at	NKG7	natural killer cell group 7 sequence	2.46	I	2.30	I	2.83	I
210756_s_at	NOTCH2	Notch homolog 2 (Drosophila)	2.83	I	4.00	I	2.64	I
204589_at	NUAK1	NUAK family, SNF1-like kinase, 1	45.25	I	36.76	I	36.76	I
205660_at	OASL	2'-5'-oligoadenylate synthetase-like	3.73	I	3.25	I	5.28	I
210797_s_at	OASL	2'-5'-oligoadenylate synthetase-like	3.48	I	2.83	I	3.25	I
223464_at	OSBPL5	oxysterol binding protein-like 5	3.48	I	2.64	I	3.48	I
200897_s_at	PALLD	palladin, cytoskeletal associated protein	5.66	I	4.59	I	14.93	I
200906_s_at	PALLD	palladin, cytoskeletal associated protein	5.28	I	4.00	I	4.00	I
200907_s_at	PALLD	palladin, cytoskeletal associated protein	8.57	I	4.59	I	21.11	I
227204_at	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	17.15	I	13.93	I	19.70	I
243296_at	PBEF1	Pre-B-cell colony enhancing factor 1	2.14	I	6.50	I	3.48	I
218676_s_at	PCTP	phosphatidylcholine transfer protein	2.46	I	2.46	I	3.48	I
204735_at	PDE4A	phosphodiesterase 4A, cAMP-specific	3.73	I	4.00	I	6.50	I
219304_s_at	PDGFD	platelet derived growth factor D	3.73	I	3.48	I	13.00	I
222860_s_at	PDGFD	platelet derived growth factor D	4.92	I	2.83	I	6.50	I
202273_at	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	4.29	I	3.25	I	13.00	I
208690_s_at	PDLIM1	PDZ and LIM domain 1 (elfin)	9.19	I	4.59	I	14.93	I
200788_s_at	PEA15	phosphoprotein enriched in astrocytes 15	2.30	I	5.28	I	2.83	I
1554508_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	6.06	I	5.66	I	3.03	I
226459_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	4.59	I	4.00	I	7.46	I
204613_at	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)	5.28	I	2.46	I	6.96	I
203470_s_at	PLEK	pleckstrin	2.64	I	4.92	I	4.29	I
203471_s_at	PLEK	pleckstrin	3.03	I	3.03	I	4.59	I
204436_at	PLEKHQ1	pleckstrin homology domain containing, family Q member 1	2.46	I	2.30	I	4.00	I
202446_s_at	PLSCR1	phospholipid scramblase 1	2.00	I	3.03	I	2.00	I

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204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.64	I	6.50	I	3.03	I
218009_s_at	PRC1	protein regulator of cytokinesis 1	3.03	I	4.00	I	4.59	I
217192_s_at	PRDM1	PR domain containing 1, with ZNF domain	2.30	I	2.30	I	2.00	I
201858_s_at	PRG1	proteoglycan 1, secretory granule	2.00	I	2.00	I	3.03	I
202458_at	PRSS23	protease, serine, 23	19.70	I	14.93	I	24.25	I
226279_at	PRSS23	protease, serine, 23	24.25	I	19.70	I	32.00	I
202006_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12	3.25	I	2.30	I	4.59	I
216915_s_at	PTPN12	protein tyrosine phosphatase, non-receptor type 12	3.48	I	2.83	I	3.25	I
203555_at	PTPN18	protein tyrosine phosphatase, non-receptor type 18	3.25	I	3.25	I	2.14	I
213521_at	PTPN18	protein tyrosine phosphatase, non-receptor type 18	2.14	I	2.30	I	2.00	I
210879_s_at	RAB11FIP5	RAB11 family interacting protein 5 (class I)	3.48	I	3.25	I	4.92	I
209514_s_at	RAB27A	RAB27A, member RAS oncogene family	3.73	I	3.03	I	2.14	I
210951_x_at	RAB27A	RAB27A, member RAS oncogene family	3.73	I	3.03	I	2.30	I
228113_at	RAB37	RAB37, member RAS oncogene family	2.30	I	2.30	I	3.48	I
230405_at	RAD50	RAD50 homolog (S. cerevisiae)	2.46	I	2.00	I	4.59	I
209050_s_at	RALGDS	ral guanine nucleotide dissociation stimulator	2.83	I	2.46	I	4.29	I
209051_s_at	RALGDS	ral guanine nucleotide dissociation stimulator	3.25	I	2.83	I	2.83	I
221830_at	RAP2A	RAP2A, member of RAS oncogene family	4.00	I	2.64	I	8.57	I
225585_at	RAP2A	RAP2A, member of RAS oncogene family	6.96	I	4.00	I	8.57	I
214487_s_at	RAP2A	RAP2A, member of RAS oncogene family	3.73	I	3.25	I	5.28	I
225738_at	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	4.92	I	4.92	I	3.73	I
226389_s_at	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	4.00	I	3.73	I	5.28	I
204346_s_at	RASSF1	Ras association (RalGDS/AF-6) domain family 1	3.03	I	2.83	I	3.03	I
226436_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	6.96	I	9.85	I	10.56	I
49306_at	RASSF4	Ras association (RalGDS/AF-6) domain family 4	5.66	I	6.96	I	14.93	I
1554602_at	RBM8A	RNA binding motif protein 8A	3.25	I	5.28	I	2.64	I
204759_at	RCBTB2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	2.64	I	2.00	I	2.83	I
226021_at	RDH10	retinol dehydrogenase 10 (all-trans)	3.03	I	2.83	I	3.25	I
202388_at	RGS2	regulator of G-protein signalling 2, 24kDa	3.48	I	5.28	I	3.73	I
219202_at	RHBDF2	rhomboid 5 homolog 2 (Drosophila)	2.46	I	2.83	I	2.64	I
212099_at	RHOB	ras homolog gene family, member B	21.11	I	48.50	I	8.57	I
212120_at	RHOQ	ras homolog gene family, member Q	2.00	I	3.03	I	2.00	I
209545_s_at	RIPK2	receptor-interacting serine-threonine kinase 2	2.46	I	4.00	I	3.25	I
1556874_a_at	RKHD2	ring finger and KH domain containing 2	4.00	I	8.57	I	3.73	I
223592_s_at	RNF135	ring finger protein 135	2.46	I	4.59	I	2.00	I
221430_s_at	RNF146	ring finger protein 146 /// ring finger protein 146	2.14	I	2.14	I	2.83	I
204900_x_at	SAP30	Sin3A-associated protein, 30kDa	6.50	I	5.66	I	3.48	I
213435_at	SATB2	SATB family member 2	7.46	I	3.73	I	32.00	I
204361_s_at	SCAP2	src family associated phosphoprotein 2	3.03	I	3.25	I	3.25	I
204362_at	SCAP2	src family associated phosphoprotein 2	2.83	I	2.83	I	4.92	I
216899_s_at	SCAP2	src family associated phosphoprotein 2	4.00	I	4.29	I	3.48	I
213572_s_at	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	2.14	I	2.14	I	2.14	I
219382_at	SERTAD3	SERTA domain containing 3	4.59	I	4.29	I	2.00	I
205933_at	SETBP1	SET binding protein 1	5.66	I	2.64	I	13.00	I
1553176_at	SH2D1B	SH2 domain containing 1B	12.13	I	6.06	I	12.13	I
1553177_at	SH2D1B	SH2 domain containing 1B	13.00	I	5.66	I	19.70	I
207351_s_at	SH2D2A	SH2 domain protein 2A	2.30	I	2.00	I	3.25	I
209370_s_at	SH3BP2	SH3-domain binding protein 2	2.83	I	2.64	I	2.30	I
211250_s_at	SH3BP2	SH3-domain binding protein 2	2.64	I	4.92	I	3.48	I
222838_at	SLAMF7	SLAM family member 7	2.83	I	2.00	I	4.29	I
219386_s_at	SLAMF8	SLAM family member 8	3.48	I	7.46	I	4.00	I
225043_at	SLC15A4	solute carrier family 15, member 4	2.46	I	2.30	I	3.25	I
225057_at	SLC15A4	Solute carrier family 15, member 4	3.03	I	2.14	I	2.83	I
209610_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	16.00	I	5.66	I	34.30	I
212810_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	8.00	I	8.57	I	32.00	I
212811_x_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	7.46	I	4.59	I	18.38	I
235875_at	SLC1A4	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	9.19	I	4.29	I	32.00	I
244377_at	SLC1A4	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	8.00	I	6.06	I	9.19	I
243623_at	SLC1A7	solute carrier family 1 (glutamate transporter), member 7	9.19	I	12.13	I	11.31	I
222217_s_at	SLC27A3	solute carrier family 27 (fatty acid transporter), member 3	2.64	I	3.73	I	2.83	I
216236_s_at	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	3.25	I	5.28	I	2.30	I
209921_at	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	17.15	I	12.13	I	13.00	I

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222071_s_at	SLCO4C1	solute carrier organic anion transporter family, member 4C1	6.06	I	2.64	I	8.00	I
237246_at	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	2.64	I	4.00	I	3.73	I
223340_at	SPG3A	spastic paraplegia 3A (autosomal dominant)	3.48	I	3.73	I	5.28	I
227649_s_at	SRGAP2	SLIT-ROBO Rho GTPase activating protein 2	3.03	I	3.48	I	3.25	I
223635_s_at	SSBP3	single stranded DNA binding protein 3	2.46	I	4.00	I	2.46	I
223065_s_at	STARD3NL	STARD3 N-terminal like	3.03	I	2.14	I	4.00	I
226390_at	STARD4	START domain containing 4, sterol regulated	2.64	I	2.83	I	5.28	I
235670_at	STX11	Syntaxin 11	6.50	I	6.96	I	4.00	I
226264_at	SUSD1	sushi domain containing 1	3.73	I	3.25	I	3.48	I
209197_at	SYT11	synaptotagmin XI	4.92	I	2.64	I	8.57	I
209198_s_at	SYT11	synaptotagmin XI	5.28	I	2.64	I	7.46	I
232677_at	SYT11	Synaptotagmin XI	3.73	I	8.00	I	11.31	I
1554415_at	TAF5L	TAF5-like RNA polymerase II, p300	2.00	I	3.03	I	4.92	I
220684_at	TBX21	T-box 21	4.29	I	3.25	I	9.19	I
225798_at	tcag7.981	juxtaposed with another zinc finger gene 1	4.00	I	3.25	I	3.48	I
1557945_at	TCTE3	T-complex-associated-testis-expressed 3	3.03	I	3.73	I	3.48	I
203589_s_at	TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	3.25	I	2.64	I	3.48	I
206715_at	TFEC	transcription factor EC	17.15	I	45.25	I	2.64	I
202085_at	TJP2	tight junction protein 2 (zona occludens 2)	6.50	I	5.66	I	11.31	I
219892_at	TM6SF1	transmembrane 6 superfamily member 1	4.00	I	6.50	I	6.50	I
1569003_at	TMEM49	transmembrane protein 49	4.59	I	8.00	I	2.83	I
203508_at	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	2.64	I	4.00	I	4.00	I
207536_s_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	9.85	I	4.00	I	17.15	I
217853_at	TNS3	tensin 3	4.59	I	10.56	I	16.00	I
204529_s_at	TOX	thymus high mobility group box protein TOX	6.50	I	3.48	I	9.85	I
204530_s_at	TOX	thymus high mobility group box protein TOX	7.46	I	3.25	I	6.06	I
224836_at	TP53INP2	tumor protein p53 inducible nuclear protein 2	5.66	I	7.46	I	6.50	I
223131_s_at	TRIM8	tripartite motif-containing 8	3.48	I	2.83	I	2.64	I
228438_at	TRPA1	Transient receptor potential cation channel, subfamily A, member 1	3.25	I	2.30	I	6.96	I
223392_s_at	TSHZ3	teashirt family zinc finger 3	2.83	I	4.00	I	6.06	I
227233_at	TSPAN2	tetraspanin 2	5.28	I	2.83	I	2.64	I
227236_at	TSPAN2	tetraspanin 2	4.59	I	3.48	I	2.00	I
220384_at	TXNDC3	thioredoxin domain containing 3 (spermatozoa)	17.15	I	9.85	I	29.86	I
225787_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	2.64	I	3.03	I	2.46	I
231948_s_at	UBE2F	ubiquitin-conjugating enzyme E2F (putative)	2.30	I	2.83	I	2.00	I
1552678_a_at	USP28	ubiquitin specific peptidase 28	4.00	I	2.14	I	2.83	I
200931_s_at	VCL	vinculin	2.46	I	2.00	I	3.25	I
227899_at	VIT	vitrin	13.00	I	6.50	I	16.00	I
205126_at	VRK2	vaccinia related kinase 2	2.30	I	2.64	I	2.30	I
200629_at	WARS	tryptophanyl-tRNA synthetase	5.66	I	12.13	I	2.64	I
242390_at	WDFY1	WD repeat and FYVE domain containing 1	2.14	I	3.25	I	4.29	I
234157_at	WDFY1	WD repeat and FYVE domain containing 1	2.00	I	3.03	I	3.48	I
218055_s_at	WDR41	WD repeat domain 41	3.03	I	2.00	I	5.28	I
222503_s_at	WDR41	WD repeat domain 41	3.48	I	2.30	I	3.48	I
243087_at	WDR63	WD repeat domain 63	9.85	I	3.25	I	27.86	I
203827_at	WIPI1	WD repeat domain, phosphoinositide interacting 1	3.73	I	3.03	I	3.03	I
213836_s_at	WIPI1	WD repeat domain, phosphoinositide interacting 1	3.73	I	2.46	I	2.64	I
201760_s_at	WSB2	WD repeat and SOCS box-containing 2	2.00	I	2.46	I	2.83	I
225665_at	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	2.46	I	3.73	I	2.14	I
242020_s_at	ZBP1	Z-DNA binding protein 1	3.73	I	4.29	I	2.30	I
230846_at	ZBTB25	Zinc finger and BTB domain containing 25	8.00	I	3.25	I	8.57	I
1557797_a_at	ZFHX1B	Zinc finger homeobox 1b	2.64	I	2.00	I	6.96	I
203603_s_at	ZFHX1B	zinc finger homeobox 1b	8.57	I	8.00	I	7.46	I
233031_at	ZFHX1B	zinc finger homeobox 1b	5.66	I	8.57	I	3.48	I
235593_at	ZFHX1B	zinc finger homeobox 1b	8.00	I	10.56	I	7.46	I
239296_at	ZFHX1B	Zinc finger homeobox 1b	2.46	I	2.30	I	9.85	I
223383_at	ZNRF1	zinc and ring finger 1	16.00	I	8.57	I	21.11	I
212414_s_at	Sep6	septin 6 /// cytokine-like nuclear factor n-pac	-2.46	D	-3.03	D	-4.29	D
228941_at	---	Transcribed locus	-2.00	D	-5.66	D	-2.46	D
239895_at	---	---	-4.29	D	-3.48	D	-2.00	D
232905_at	---	CDNA: FLJ21221 fis, clone COL00570	-4.92	D	-18.38	D	-36.76	D
226806_s_at	---	---	-3.25	D	-4.92	D	-2.64	D

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227274_at	---	Transcribed locus	-2.14	D	-2.46	D	-3.48	D
230987_at	---	Transcribed locus, strongly similar to XP_530134.1	-2.30	D	-3.48	D	-3.03	D
1556889_s_at	---	CDNA FLJ37963 fis, clone CTONG2009689	-8.57	D	-16.00	D	-17.15	D
1558515_at	---	CDNA clone IMAGE:4328048	-6.50	D	-4.29	D	-2.30	D
1558732_at	---	---	-4.92	D	-6.50	D	-2.14	D
1558934_a_at	---	Clone 27609 defective mariner transposon Hsmar2 mRNA sequence	-6.50	D	-3.48	D	-4.29	D
1559205_s_at	---	Homo sapiens, clone IMAGE:5745627, mRNA	-2.83	D	-2.46	D	-9.85	D
1559496_at	---	---	-5.28	D	-5.66	D	-5.66	D
1560637_at	---	CDNA clone IMAGE:5744875	-3.03	D	-3.25	D	-2.46	D
1561004_at	---	Full length insert cDNA clone YY74A01	-2.30	D	-2.64	D	-2.14	D
1561363_a_at	---	CDNA FLJ36285 fis, clone THYMU2003470	-2.83	D	-8.57	D	-2.14	D
1562067_at	---	CDNA clone IMAGE:5312957	-8.00	D	-5.28	D	-2.00	D
1562245_a_at	---	MRNA; cDNA DKFZp686H1629 (from clone DKFZp686H1629)	-5.28	D	-29.86	D	-19.70	D
1563182_at	---	CDNA clone IMAGE:4796641	-5.28	D	-7.46	D	-5.66	D
1564154_at	---	---	-2.64	D	-3.25	D	-6.06	D
1568807_a_at	---	CDNA clone IMAGE:4825606	-4.92	D	-4.29	D	-21.11	D
1569482_at	---	CDNA clone IMAGE:5262617	-4.59	D	-6.06	D	-2.83	D
212675_s_at	---	---	-4.00	D	-4.59	D	-6.06	D
212764_at	---	---	-8.00	D	-5.28	D	-17.15	D
213156_at	---	Homo sapiens, clone IMAGE:4214654, mRNA	-3.25	D	-4.92	D	-2.14	D
213158_at	---	Homo sapiens, clone IMAGE:4214654, mRNA	-2.14	D	-3.48	D	-2.30	D
213750_at	---	Full length insert cDNA YH77E09	-2.30	D	-3.03	D	-4.59	D
214148_at	---	Clone 23641 mRNA sequence	-2.14	D	-2.30	D	-2.14	D
216380_x_at	---	---	-2.83	D	-2.30	D	-2.83	D
216857_at	---	T-cell receptor active beta-chain (V10-D-J-C) mRNA, clone PL3.9	-11.31	D	-4.59	D	-11.31	D
217164_at	---	---	-3.25	D	-3.48	D	-2.00	D
217482_at	---	CDNA FLJ11925 fis, clone HEMBB1000354	-6.50	D	-8.00	D	-3.73	D
220882_at	---	---	-8.00	D	-8.57	D	-2.00	D
222348_at	---	---	-68.59	D	-55.72	D	-21.11	D
223358_s_at	---	CDNA FLJ33024 fis, clone THYMU1000532	-3.73	D	-4.29	D	-5.28	D
225478_at	---	CDNA FLJ39185 fis, clone OCBBF2004418	-3.48	D	-4.00	D	-6.96	D
225611_at	---	---	-7.46	D	-3.48	D	-5.28	D
226218_at	---	MRNA; cDNA DKFZp667P0610 (from clone DKFZp667P0610)	-6.50	D	-22.63	D	-24.25	D
226272_at	---	Full length insert cDNA clone ZD79H10	-10.56	D	-19.70	D	-36.76	D
226333_at	---	---	-3.73	D	-2.30	D	-13.00	D
226458_at	---	CDNA FLJ30340 fis, clone BRACE2007411	-2.14	D	-3.73	D	-2.30	D
226591_at	---	CDNA FLJ33569 fis, clone BRAMY2010317	-2.64	D	-4.59	D	-2.30	D
226765_at	---	CDNA clone IMAGE:3897439	-9.19	D	-6.96	D	-6.06	D
226869_at	---	Full length insert cDNA clone ZD77F06	-64.00	D	-34.30	D	-119.43	D
227082_at	---	MRNA; cDNA DKFZp586K1922 (from clone DKFZp586K1922)	-3.25	D	-6.50	D	-2.00	D
227576_at	---	CDNA FLJ42015 fis, clone SPLEN2032813	-6.50	D	-6.06	D	-2.30	D
227747_at	---	---	-8.57	D	-8.57	D	-4.92	D
227762_at	---	Transcribed locus	-4.92	D	-3.25	D	-13.00	D
228049_x_at	---	Transcribed locus	-4.00	D	-4.59	D	-6.96	D
228091_at	---	Full-length cDNA clone CS0DB009YL20	-3.03	D	-2.83	D	-2.30	D
228190_at	---	---	-2.46	D	-2.46	D	-2.30	D
228242_at	---	---	-2.30	D	-2.64	D	-3.03	D
228314_at	---	---	-3.03	D	-4.29	D	-2.00	D
228390_at	---	CDNA clone IMAGE:5259272	-4.92	D	-8.00	D	-3.48	D
228549_at	---	---	-3.25	D	-2.64	D	-8.57	D
228623_at	---	Transcribed locus, weakly similar to XP_517454.1	-11.31	D	-6.96	D	-2.64	D
228661_s_at	---	CDNA FLJ11489 fis, clone HEMBA1001915	-5.28	D	-6.50	D	-4.29	D
228745_at	---	CDNA FLJ33275 fis, clone ASTRO2008040	-2.64	D	-2.30	D	-4.59	D
228854_at	---	Transcribed locus	-14.93	D	-12.13	D	-16.00	D
228972_at	---	---	-2.30	D	-3.25	D	-3.03	D
229029_at	---	---	-6.50	D	-6.50	D	-32.00	D
229064_s_at	---	---	-6.50	D	-7.46	D	-97.01	D
229072_at	---	CDNA clone IMAGE:5259272	-3.73	D	-4.92	D	-3.03	D
229116_at	---	CDNA clone IMAGE:30721737	-59.71	D	-59.71	D	-29.86	D
229850_at	---	Full length insert cDNA clone YX81F03	-3.73	D	-3.03	D	-3.48	D
230083_at	---	Full length insert cDNA clone YI48C03	-2.83	D	-10.56	D	-14.93	D
230913_at	---	Full length insert cDNA clone ZE12B03	-5.66	D	-6.96	D	-9.19	D

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231247_s_at	---	CDNA FLJ36837 fis, clone ASTRO2011422	-2.30	D	-4.29	D	-3.48	D
231862_at	---	CDNA clone IMAGE:4842353	-2.30	D	-2.14	D	-4.29	D
232125_at	---	CDNA FLJ34585 fis, clone KIDNE2008758	-3.03	D	-4.29	D	-4.92	D
232165_at	---	---	-5.66	D	-14.93	D	-10.56	D
232511_at	---	CDNA clone IMAGE:5310744	-4.00	D	-4.59	D	-2.00	D
232752_at	---	Homo sapiens, clone IMAGE:4095671, mRNA	-73.52	D	-5.66	D	-8.00	D
233401_at	---	CDNA FLJ11892 fis, clone HEMBA1007281	-14.93	D	-42.22	D	-29.86	D
235028_at	---	CDNA FLJ42313 fis, clone TRACH2019425	-13.00	D	-6.06	D	-2.00	D
235046_at	---	Transcribed locus, moderately similar to XP_518244.1	-5.28	D	-19.70	D	-3.48	D
235109_at	---	CDNA FLJ40581 fis, clone THYMU2007729	-4.92	D	-2.83	D	-18.38	D
235436_at	---	---	-3.25	D	-4.92	D	-3.25	D
235888_at	---	Transcribed locus	-29.86	D	-2.00	D	-4.00	D
235890_at	---	Transcribed locus	-2.83	D	-3.73	D	-2.46	D
236198_at	---	Transcribed locus	-6.06	D	-8.57	D	-12.13	D
236220_at	---	Transcribed locus	-27.86	D	-10.56	D	-34.30	D
236595_at	---	---	-2.64	D	-2.00	D	-24.25	D
236685_at	---	Transcribed locus	-17.15	D	-14.93	D	-10.56	D
236858_s_at	---	---	-6.06	D	-6.50	D	-39.40	D
236962_at	---	Transcribed locus	-3.03	D	-3.48	D	-3.48	D
236963_at	---	Transcribed locus, weakly similar to XP_371841.1	-17.15	D	-21.11	D	-4.00	D
237747_at	---	---	-4.00	D	-3.25	D	-2.14	D
238155_at	---	Transcribed locus, weakly similar to NP_787073.2	-3.25	D	-3.73	D	-3.48	D
238673_at	---	Transcribed locus	-10.56	D	-13.93	D	-10.56	D
238861_at	---	MRNA; clone CD 43T7	-2.30	D	-2.00	D	-3.03	D
238918_at	---	CDNA FLJ42015 fis, clone SPLEN2032813	-3.48	D	-2.64	D	-2.46	D
239231_at	---	CDNA FLJ41910 fis, clone PEBLM2007834	-3.03	D	-6.96	D	-2.14	D
239278_at	---	CDNA clone IMAGE:5301129	-4.29	D	-4.29	D	-5.28	D
239301_at	---	Transcribed locus	-3.03	D	-9.19	D	-2.30	D
239726_at	---	---	-3.25	D	-4.29	D	-8.57	D
239888_at	---	---	-3.03	D	-4.00	D	-3.03	D
240865_at	---	---	-8.00	D	-12.13	D	-5.28	D
241365_at	---	CDNA FLJ42259 fis, clone TKIDN2011289	-9.19	D	-14.93	D	-6.06	D
241388_at	---	CDNA FLJ40566 fis, clone THYMU2004733	-2.64	D	-3.48	D	-2.14	D
241505_at	---	Transcribed locus	-21.11	D	-5.66	D	-2.64	D
241819_at	---	---	-8.57	D	-11.31	D	-14.93	D
241936_x_at	---	Transcribed locus, weakly similar to XP_517655.1	-3.25	D	-2.14	D	-2.64	D
242289_at	---	---	-2.46	D	-6.50	D	-2.14	D
242388_x_at	---	---	-3.25	D	-10.56	D	-3.73	D
243791_at	---	Transcribed locus	-11.31	D	-7.46	D	-2.30	D
243810_at	---	Transcribed locus	-14.93	D	-45.25	D	-73.52	D
244422_at	---	Transcribed locus	-6.96	D	-12.13	D	-9.85	D
244636_at	---	Transcribed locus	-4.92	D	-2.30	D	-2.00	D
244798_at	---	---	-36.76	D	-4.29	D	-16.00	D
244860_at	---	Transcribed locus	-36.76	D	-4.59	D	-2.64	D
244881_at	---	Transcribed locus	-4.59	D	-4.92	D	-3.03	D
201737_s_at	MARCH6	membrane-associated ring finger (C3HC4) 6	-2.14	D	-2.64	D	-2.46	D
212413_at	SEPT6	septin 6	-3.03	D	-3.03	D	-4.59	D
213666_at	SEPT6	septin 6	-4.92	D	-2.30	D	-5.28	D
214298_x_at	SEPT6	septin 6	-3.73	D	-2.83	D	-3.48	D
205434_s_at	AAK1	AP2 associated kinase 1	-3.25	D	-3.03	D	-2.14	D
204567_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	-5.66	D	-4.00	D	-14.93	D
238563_at	ABI1	Abl-interactor 1	-2.30	D	-3.03	D	-2.00	D
200965_s_at	ABLIM1	actin binding LIM protein 1	-3.48	D	-5.28	D	-2.46	D
236401_at	ABP1	Amiloride binding protein 1 (amine oxidase (copper-containing))	-3.48	D	-4.92	D	-3.03	D
236583_at	ABP1	Amiloride binding protein 1 (amine oxidase (copper-containing))	-3.73	D	-6.50	D	-4.59	D
211207_s_at	ACSL6	acyl-CoA synthetase long-chain family member 6	-8.00	D	-6.96	D	-6.50	D
229725_at	ACSL6	Acyl-CoA synthetase long-chain family member 6	-8.57	D	-13.93	D	-8.00	D
205942_s_at	ACSM3	acyl-CoA synthetase medium-chain family member 3	-10.56	D	-13.93	D	-3.73	D
208636_at	ACTN1	actinin, alpha 1	-7.46	D	-4.59	D	-14.93	D
208637_x_at	ACTN1	actinin, alpha 1	-6.50	D	-3.73	D	-16.00	D
1552519_at	ACVR1C	activin A receptor, type IC	-7.46	D	-5.66	D	-6.06	D
228416_at	ACVR2A	activin A receptor, type IIA	-4.00	D	-4.00	D	-4.29	D

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203865_s_at	ADARB1	adenosine deaminase, RNA-specific	-2.83	D	-2.64	D	-3.48	D
239171_at	ADD3	Adducin 3 (gamma)	-5.66	D	-6.06	D	-2.14	D
239131_at	ADNP	Activity-dependent neuroprotector	-4.00	D	-6.06	D	-2.14	D
205013_s_at	ADORA2A	adenosine A2a receptor	-3.48	D	-2.83	D	-14.93	D
237383_at	AFF1	AF4/FMR2 family, member 1	-5.28	D	-4.00	D	-4.29	D
227198_at	AFF3	AF4/FMR2 family, member 3	-3.03	D	-4.92	D	-4.92	D
218096_at	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5	-2.46	D	-3.03	D	-2.64	D
212543_at	AIM1	absent in melanoma 1	-2.14	D	-2.30	D	-2.46	D
201674_s_at	AKAP1	A kinase (PRKA) anchor protein 1	-4.00	D	-3.48	D	-3.25	D
201675_at	AKAP1	A kinase (PRKA) anchor protein 1	-3.25	D	-3.03	D	-3.25	D
210625_s_at	AKAP1	A kinase (PRKA) anchor protein 1	-2.83	D	-3.48	D	-17.15	D
243450_at	AKAP13	A kinase (PRKA) anchor protein 13	-12.13	D	-18.38	D	-3.03	D
209160_at	AKR1C3	aldo-keto reductase family 1, member C3	-48.50	D	-64.00	D	-168.90	D
242876_at	AKT3	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	-3.48	D	-3.73	D	-2.14	D
203608_at	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	-42.22	D	-8.57	D	-3.25	D
223318_s_at	ALKBH7	alkB, alkylation repair homolog 7 (E. coli)	-2.83	D	-2.30	D	-6.96	D
226431_at	ALS2CR13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13	-4.00	D	-7.46	D	-6.50	D
226718_at	AMIGO1	adhesion molecule with Ig-like domain 1	-6.06	D	-6.50	D	-6.96	D
207992_s_at	AMPD3	adenosine monophosphate deaminase (isoform E)	-2.46	D	-3.03	D	-24.25	D
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	-4.29	D	-4.92	D	-5.28	D
237839_at	ANK3	Ankyrin 3, node of Ranvier (ankyrin G)	-103.97	D	-29.86	D	-73.52	D
223093_at	ANKH	ankylosis, progressive homolog (mouse)	-2.46	D	-2.46	D	-2.00	D
239449_at	ANKH	Ankylosis, progressive homolog (mouse)	-8.00	D	-6.50	D	-4.00	D
213005_s_at	ANKRD15	ankyrin repeat domain 15	-3.48	D	-4.00	D	-45.25	D
210027_s_at	APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1	-2.64	D	-2.46	D	-3.73	D
203747_at	AQP3	aquaporin 3 (Gill blood group)	-4.29	D	-9.19	D	-5.28	D
39248_at	AQP3	aquaporin 3 (Gill blood group)	-6.50	D	-13.00	D	-14.93	D
244061_at	ARHGAP15	Rho GTPase activating protein 15	-7.46	D	-8.00	D	-2.83	D
217936_at	ARHGAP5	Rho GTPase activating protein 5	-2.83	D	-4.59	D	-12.13	D
233849_s_at	ARHGAP5	Rho GTPase activating protein 5	-3.25	D	-4.00	D	-6.06	D
235635_at	ARHGAP5	Rho GTPase activating protein 5	-5.28	D	-6.06	D	-21.11	D
242110_at	ARHGAP5	Rho GTPase activating protein 5	-10.56	D	-5.28	D	-7.46	D
203404_at	ARMCX2	armadillo repeat containing, X-linked 2	-36.76	D	-6.96	D	-42.22	D
228423_at	ASAP	aster-associated protein	-10.56	D	-6.96	D	-21.11	D
203427_at	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	-2.64	D	-6.06	D	-2.64	D
203428_s_at	ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	-2.14	D	-4.00	D	-2.14	D
228381_at	ATF7IP2	Activating transcription factor 7 interacting protein 2	-2.83	D	-2.46	D	-2.83	D
1553387_at	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	-4.29	D	-3.48	D	-2.64	D
212672_at	ATM	ataxia telangiectasia mutated (includes complementation groups A, C and D)	-2.14	D	-3.73	D	-2.00	D
209281_s_at	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	-3.03	D	-2.00	D	-3.25	D
212930_at	ATP2B1	ATPase, Ca++ transporting, plasma membrane 1	-2.00	D	-2.00	D	-3.25	D
213587_s_at	ATP6V0E2L	ATPase, H+ transporting V0 subunit E2-like (rat)	-2.00	D	-2.00	D	-2.64	D
222696_at	AXIN2	axin 2 (conductin, axil)	-6.06	D	-4.59	D	-6.96	D
210121_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	-5.28	D	-48.50	D	-21.11	D
217452_s_at	B3GALT2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	-10.56	D	-274.37	D	-181.02	D
1556451_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-9.85	D	-8.57	D	-21.11	D
215907_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-7.46	D	-6.50	D	-5.66	D
221234_s_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-13.93	D	-14.93	D	-18.38	D
227173_s_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-18.38	D	-13.00	D	-13.93	D
236307_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-119.43	D	-55.72	D	-137.19	D
236796_at	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	-18.38	D	-7.46	D	-8.57	D
1557239_at	BBX	Bobby sox homolog (Drosophila)	-3.73	D	-4.59	D	-2.00	D
1557240_a_at	BBX	Bobby sox homolog (Drosophila)	-4.92	D	-5.28	D	-2.30	D
203685_at	BCL2	B-cell CLL/lymphoma 2	-4.29	D	-8.57	D	-6.06	D
232210_at	BCL2	B-cell CLL/lymphoma 2	-13.93	D	-45.25	D	-12.13	D
232614_at	BCL2	B-cell CLL/lymphoma 2	-42.22	D	-25.99	D	-14.93	D
244035_at	BCL2	B-cell CLL/lymphoma 2	-7.46	D	-9.19	D	-16.00	D
242819_at	BET1	BET1 homolog (S. cerevisiae)	-5.28	D	-7.46	D	-3.73	D
224367_at	BEX2	brain expressed X-linked 2 /// brain expressed X-linked 2	-6.06	D	-10.56	D	-25.99	D

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215440_s_at	BEXL1	brain expressed X-linked-like 1	-6.96	D	-2.30	D	-32.00	D
210538_s_at	BIRC3	baculoviral IAP repeat-containing 3	-2.30	D	-3.48	D	-2.14	D
201848_s_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	-3.03	D	-2.00	D	-2.46	D
201849_at	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	-2.64	D	-3.25	D	-3.03	D
228570_at	BTBD11	BTB (POZ) domain containing 11	-4.59	D	-4.29	D	-13.00	D
238692_at	BTBD11	BTB (POZ) domain containing 11	-6.50	D	-4.29	D	-9.19	D
240347_at	BTG1	B-cell translocation gene 1, anti-proliferative	-137.19	D	-8.57	D	-4.92	D
243509_at	BTG1	B-cell translocation gene 1, anti-proliferative	-6.50	D	-4.92	D	-2.46	D
217809_at	BZW2	basic leucine zipper and W2 domains 2	-2.14	D	-2.00	D	-2.83	D
212771_at	C10orf38	chromosome 10 open reading frame 38	-4.00	D	-4.00	D	-16.00	D
224435_at	C10orf58	chromosome 10 open reading frame 58	-4.00	D	-2.46	D	-6.50	D
222785_x_at	C11orf1	chromosome 11 open reading frame 1	-2.00	D	-3.03	D	-2.46	D
231530_s_at	C11orf1	chromosome 11 open reading frame 1	-2.30	D	-3.03	D	-2.46	D
212560_at	C11orf32	chromosome 11 open reading frame 32	-3.48	D	-3.25	D	-25.99	D
224759_s_at	C12orf23	chromosome 12 open reading frame 23	-2.14	D	-4.59	D	-2.00	D
236816_at	C12orf30	chromosome 12 open reading frame 30	-2.64	D	-2.30	D	-2.00	D
242874_at	C14orf161	Chromosome 14 open reading frame 161	-21.11	D	-13.93	D	-22.63	D
243729_at	C14orf161	Chromosome 14 open reading frame 161	-4.29	D	-4.29	D	-128.00	D
1559097_at	C14orf64	chromosome 14 open reading frame 64	-4.92	D	-6.50	D	-11.31	D
232094_at	C15orf29	Chromosome 15 open reading frame 29	-3.25	D	-4.92	D	-2.30	D
219315_s_at	C16orf30	chromosome 16 open reading frame 30	-13.93	D	-18.38	D	-11.31	D
223401_at	C17orf48	chromosome 17 open reading frame 48	-2.00	D	-2.83	D	-2.00	D
207996_s_at	C18orf1	chromosome 18 open reading frame 1	-4.92	D	-3.48	D	-4.29	D
1555194_at	C18orf17	Chromosome 18 open reading frame 17	-3.25	D	-6.06	D	-19.70	D
230747_s_at	C18orf17	Chromosome 18 open reading frame 17	-3.03	D	-2.83	D	-8.00	D
238480_at	C18orf17	Chromosome 18 open reading frame 17	-2.46	D	-2.64	D	-3.73	D
232235_at	C18orf4	chromosome 18 open reading frame 4	-24.25	D	-13.00	D	-45.25	D
221648_s_at	C1orf121	chromosome 1 open reading frame 121	-4.59	D	-4.92	D	-4.59	D
208910_s_at	C1QBP	complement component 1, q subcomponent binding protein	-2.00	D	-2.00	D	-3.03	D
214214_s_at	C1QBP	complement component 1, q subcomponent binding protein	-2.00	D	-2.00	D	-4.29	D
233241_at	C20orf19	chromosome 20 open reading frame 19	-6.50	D	-6.50	D	-4.92	D
219570_at	C20orf23	chromosome 20 open reading frame 23	-12.13	D	-2.83	D	-6.06	D
232500_at	C20orf74	chromosome 20 open reading frame 74	-4.92	D	-4.92	D	-2.64	D
239660_at	C20orf74	chromosome 20 open reading frame 74	-5.28	D	-4.92	D	-4.59	D
239208_s_at	C21orf57	Chromosome 21 open reading frame 57	-4.00	D	-2.30	D	-2.00	D
238785_at	C3orf63	Chromosome 3 open reading frame 63	-2.30	D	-2.64	D	-2.83	D
219023_at	C4orf16	chromosome 4 open reading frame 16	-2.00	D	-2.00	D	-2.46	D
218561_s_at	C6orf149	chromosome 6 open reading frame 149	-2.00	D	-2.30	D	-2.64	D
1558971_at	C6orf190	chromosome 6 open reading frame 190	-13.93	D	-29.86	D	-59.71	D
1558972_s_at	C6orf190	chromosome 6 open reading frame 190	-19.70	D	-29.86	D	-36.76	D
226301_at	C6orf192	chromosome 6 open reading frame 192	-3.48	D	-2.83	D	-8.00	D
209829_at	C6orf32	chromosome 6 open reading frame 32	-2.46	D	-4.00	D	-2.83	D
220755_s_at	C6orf48	chromosome 6 open reading frame 48	-2.00	D	-2.00	D	-3.25	D
1552563_a_at	C8orf6	chromosome 8 open reading frame 6	-7.46	D	-13.93	D	-5.66	D
215390_at	C9orf5	Chromosome 9 open reading frame 5	-6.06	D	-4.59	D	-3.48	D
202715_at	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	-2.00	D	-2.30	D	-3.25	D
241871_at	CAMK4	calcium/calmodulin-dependent protein kinase IV	-10.56	D	-21.11	D	-78.79	D
239778_x_at	CAPN7	Calpain 7	-4.29	D	-2.83	D	-2.46	D
239545_at	CASD1	CAS1 domain containing 1	-4.92	D	-5.66	D	-2.00	D
207620_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-3.48	D	-2.00	D	-3.25	D
211208_s_at	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-4.29	D	-3.48	D	-11.31	D
209790_s_at	CASP6	caspase 6, apoptosis-related cysteine peptidase	-3.73	D	-4.29	D	-2.83	D
242323_at	CASP6	Caspase 6, apoptosis-related cysteine peptidase	-3.25	D	-3.25	D	-2.30	D
233614_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	-9.85	D	-7.46	D	-4.29	D
234112_at	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	-3.25	D	-4.00	D	-2.14	D
205379_at	CBR3	carbonyl reductase 3	-3.73	D	-9.85	D	-17.15	D
226287_at	CCDC34	coiled-coil domain containing 34	-2.00	D	-2.83	D	-2.64	D
228122_at	CCDC66	coiled-coil domain containing 66	-2.14	D	-3.03	D	-2.00	D
232489_at	CCDC76	coiled-coil domain containing 76	-2.64	D	-5.28	D	-2.30	D
226521_s_at	CCDC98	coiled-coil domain containing 98	-2.30	D	-2.83	D	-2.14	D
233543_s_at	CCDC98	coiled-coil domain containing 98	-2.30	D	-2.64	D	-3.03	D

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1562028_at	CCND3	Cyclin D3	-2.64	D	-4.92	D	-2.30	D
238243_at	CCNH	Cyclin H	-3.48	D	-2.64	D	-6.50	D
206337_at	CCR7	chemokine (C-C motif) receptor 7 /// chemokine (C-C motif) receptor 7	-21.11	D	-36.76	D	-84.45	D
205831_at	CD2	CD2 molecule /// CD2 molecule	-2.00	D	-3.48	D	-2.83	D
1560395_at	CD24	CD24 molecule	-13.00	D	-73.52	D	-11.31	D
219025_at	CD248	CD248 molecule, endosialin	-21.11	D	-3.25	D	-8.57	D
206545_at	CD28	CD28 molecule	-7.46	D	-21.11	D	-776.05	D
211861_x_at	CD28	CD28 molecule	-4.29	D	-11.31	D	-51.98	D
1565868_at	CD44	CD44 molecule (Indian blood group)	-9.85	D	-6.50	D	-6.50	D
217523_at	CD44	CD44 molecule (Indian blood group)	-8.00	D	-5.66	D	-6.96	D
230489_at	CD5	CD5 molecule	-3.48	D	-3.73	D	-5.66	D
201925_s_at	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	-3.03	D	-2.00	D	-9.85	D
200984_s_at	CD59	CD59 molecule, complement regulatory protein	-2.30	D	-2.14	D	-3.73	D
200985_s_at	CD59	CD59 molecule, complement regulatory protein	-3.03	D	-2.64	D	-5.28	D
205049_s_at	CD79A	CD79a molecule, immunoglobulin-associated alpha	-2.46	D	-4.29	D	-4.59	D
205288_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-5.66	D	-4.29	D	-5.66	D
210742_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-14.93	D	-13.00	D	-9.19	D
210743_s_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-5.66	D	-5.28	D	-5.66	D
243640_x_at	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-12.13	D	-7.46	D	-8.00	D
215846_at	CDC42SE2	CDC42 small effector 2	-4.92	D	-4.29	D	-3.25	D
234260_at	CDC42SE2	CDC42 small effector 2	-5.66	D	-9.19	D	-2.30	D
225081_s_at	CDCA7L	cell division cycle associated 7-like	-4.29	D	-3.03	D	-5.66	D
243808_at	CDK6	Cyclin-dependent kinase 6	-17.15	D	-3.73	D	-2.46	D
209501_at	CDR2	cerebellar degeneration-related protein 2, 62kDa	-3.48	D	-4.92	D	-4.92	D
204066_s_at	CENTG2	centaurin, gamma 2	-6.50	D	-2.83	D	-5.28	D
207971_s_at	CEP68	centrosomal protein 68kDa	-5.66	D	-5.28	D	-10.56	D
212677_s_at	CEP68	centrosomal protein 68kDa	-6.06	D	-6.06	D	-4.29	D
239442_at	CEP68	Centrosomal protein 68kDa	-7.46	D	-6.50	D	-5.28	D
236327_at	CEPT1	Choline/ethanolamine phosphotransferase 1	-4.59	D	-2.14	D	-2.30	D
215318_at	CG012	hypothetical gene CG012	-5.66	D	-4.59	D	-3.03	D
243751_at	CHD2	Chromodomain helicase DNA binding protein 2	-4.92	D	-5.66	D	-2.00	D
1562673_at	CHES1	Checkpoint suppressor 1	-3.25	D	-2.30	D	-2.00	D
226350_at	CHML	choroideremia-like (Rab escort protein 2)	-2.64	D	-2.14	D	-2.30	D
212313_at	CHMP7	CHMP family, member 7	-3.25	D	-6.96	D	-3.25	D
1557733_a_at	CHRM3	Cholinergic receptor, muscarinic 3	-13.93	D	-21.11	D	-42.22	D
230656_s_at	CIRH1A	cirrhosis, autosomal recessive 1A (cirhin)	-2.00	D	-2.00	D	-2.14	D
221223_x_at	CISH	cytokine inducible SH2-containing protein	-6.96	D	-4.29	D	-14.93	D
223377_x_at	CISH	cytokine inducible SH2-containing protein	-7.46	D	-8.00	D	-11.31	D
223961_s_at	CISH	cytokine inducible SH2-containing protein	-4.92	D	-4.92	D	-13.00	D
213317_at	CLIC5	chloride intracellular channel 5	-2.83	D	-2.83	D	-4.29	D
204085_s_at	CLN5	ceroid-lipofuscinosis, neuronal 5	-2.46	D	-2.46	D	-3.03	D
204576_s_at	CLUAP1	clusterin associated protein 1	-4.92	D	-4.00	D	-18.38	D
212977_at	CMKOR1	chemokine orphan receptor 1	-3.73	D	-19.70	D	-5.66	D
232951_at	CMTM7	CKLF-like MARVEL transmembrane domain containing 7	-29.86	D	-13.93	D	-4.29	D
234562_x_at	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	-3.48	D	-3.25	D	-2.46	D
235099_at	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	-29.86	D	-11.31	D	-10.56	D
228297_at	CNN3	Calponin 3, acidic	-6.50	D	-10.56	D	-29.86	D
222313_at	CNOT2	CCR4-NOT transcription complex, subunit 2	-2.46	D	-2.64	D	-2.30	D
239833_at	COMMD1	Copper metabolism (Murr1) domain containing 1	-5.28	D	-6.06	D	-3.25	D
1560349_at	COMMD10	COMM domain containing 10	-4.92	D	-2.83	D	-2.46	D
1569167_at	COMMD10	COMM domain containing 10	-3.73	D	-2.83	D	-2.14	D
205544_s_at	CR2	complement component (3d/Epstein Barr virus) receptor 2	-19.70	D	-32.00	D	-9.85	D
237502_at	CRLS1	Cardiolipin synthase 1	-2.00	D	-2.46	D	-5.28	D
229193_at	CROP	Cisplatin resistance-associated overexpressed protein	-4.59	D	-5.66	D	-2.46	D
1552347_at	CRYZL1	crystallin, zeta (quinone reductase)-like 1	-2.64	D	-2.46	D	-2.00	D
222819_at	CTPS2	CTP synthase II	-3.25	D	-2.14	D	-3.03	D
240798_at	CUTL1	Cut-like 1, CCAAT displacement protein (Drosophila)	-9.19	D	-2.64	D	-3.25	D
207681_at	CXCR3	chemokine (C-X-C motif) receptor 3	-16.00	D	-8.00	D	-22.63	D
217119_s_at	CXCR3	chemokine (C-X-C motif) receptor 3	-3.48	D	-5.28	D	-34.30	D
206974_at	CXCR6	chemokine (C-X-C motif) receptor 6	-5.28	D	-6.06	D	-22.63	D
222996_s_at	CXXC5	CXXC finger 5	-3.03	D	-2.00	D	-6.06	D
233955_x_at	CXXC5	CXXC finger 5	-3.25	D	-2.00	D	-4.92	D

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209569_x_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	-5.28	D	-4.92	D	-42.22	D
209570_s_at	D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	-5.28	D	-6.06	D	-59.71	D
202806_at	DBN1	drebrin 1	-14.93	D	-29.86	D	-3.25	D
222101_s_at	DCHS1	dachsous 1 (Drosophila)	-8.00	D	-22.63	D	-24.25	D
230180_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-2.83	D	-3.03	D	-3.03	D
236210_at	DDX31	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31	-9.19	D	-3.25	D	-2.83	D
230607_at	DENND4A	DENN/MADD domain containing 4A	-6.06	D	-3.73	D	-2.64	D
203385_at	DGKA	diacylglycerol kinase, alpha 80kDa	-5.28	D	-6.50	D	-5.66	D
211272_s_at	DGKA	diacylglycerol kinase, alpha 80kDa	-4.29	D	-6.96	D	-8.00	D
238032_at	DHRS3	Dehydrogenase/reductase (SDR family) member 3	-8.00	D	-9.85	D	-8.00	D
202481_at	DHRS3	dehydrogenase/reductase (SDR family) member 3	-8.57	D	-19.70	D	-78.79	D
230285_at	DKFZp313A2432	hypothetical protein DKFZp313A2432	-2.46	D	-3.73	D	-2.00	D
235085_at	DKFZp761P0423	homolog of rat pragma of Rnd2	-3.25	D	-6.50	D	-2.00	D
214247_s_at	DKK3	dickkopf homolog 3 (Xenopus laevis)	-4.00	D	-4.59	D	-64.00	D
215629_s_at	DLEU2	deleted in lymphocytic leukemia, 2	-2.14	D	-2.64	D	-2.30	D
224215_s_at	DLL1	delta-like 1 (Drosophila)	-27.86	D	-3.73	D	-5.66	D
222640_at	DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	-2.83	D	-2.14	D	-3.03	D
212538_at	DOCK9	dedicator of cytokinesis 9	-3.25	D	-5.28	D	-3.48	D
232874_at	DOCK9	Dedicator of cytokinesis 9	-9.19	D	-6.06	D	-4.29	D
219590_x_at	DPH5	DPH5 homolog (S. cerevisiae)	-2.30	D	-2.14	D	-3.25	D
222360_at	DPH5	DPH5 homolog (S. cerevisiae)	-3.03	D	-2.46	D	-2.83	D
223671_x_at	DPH5	DPH5 homolog (S. cerevisiae)	-2.46	D	-3.25	D	-3.03	D
224060_s_at	DPH5	DPH5 homolog (S. cerevisiae)	-3.25	D	-3.73	D	-3.73	D
224196_x_at	DPH5	DPH5 homolog (S. cerevisiae)	-2.46	D	-3.03	D	-3.03	D
203716_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-5.28	D	-48.50	D	-13.93	D
203717_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-5.28	D	-19.70	D	-10.56	D
211478_s_at	DPP4	dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-4.92	D	-64.00	D	-42.22	D
237953_at	DPP4	Dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)	-16.00	D	-11.31	D	-13.00	D
226721_at	DPY19L4	Dpy-19-like 4 (C. elegans)	-2.30	D	-3.25	D	-2.14	D
207324_s_at	DSC1	desmocollin 1	-97.01	D	-137.19	D	-137.19	D
219864_s_at	DSCR1L2	Down syndrome critical region gene 1-like 2	-5.28	D	-4.92	D	-73.52	D
236649_at	DTWD1	DTW domain containing 1	-2.46	D	-3.73	D	-2.30	D
1558739_at	DUSP16	Dual specificity phosphatase 16	-3.48	D	-6.96	D	-3.03	D
1558740_s_at	DUSP16	Dual specificity phosphatase 16	-3.03	D	-4.92	D	-2.30	D
224832_at	DUSP16	dual specificity phosphatase 16	-3.73	D	-13.93	D	-5.28	D
202971_s_at	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-3.03	D	-4.59	D	-2.30	D
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)	-3.73	D	-5.28	D	-19.70	D
223623_at	ECRG4	esophageal cancer related gene 4 protein	-4.29	D	-18.38	D	-51.98	D
204642_at	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1	-4.59	D	-6.50	D	-4.00	D
206437_at	EDG6	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 6	-2.46	D	-2.64	D	-2.30	D
238458_at	EFHA2	EF-hand domain family, member A2	-10.56	D	-21.11	D	-45.25	D
225656_at	EFHC1	EF-hand domain (C-terminal) containing 1	-2.46	D	-2.46	D	-2.00	D
1556732_at	EML4	Echinoderm microtubule associated protein like 4	-4.29	D	-4.29	D	-3.03	D
232587_at	EML4	echinoderm microtubule associated protein like 4	-4.00	D	-2.30	D	-2.30	D
233940_at	EML4	Echinoderm microtubule associated protein like 4	-5.28	D	-4.92	D	-3.25	D
236379_at	EPB41	Erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	-6.50	D	-5.66	D	-2.30	D
228948_at	EPHA4	EPH receptor A4	-3.73	D	-5.66	D	-14.93	D
209368_at	EPHX2	epoxide hydrolase 2, cytoplasmic	-3.25	D	-9.85	D	-6.96	D
232164_s_at	EPPK1	epiplakin 1	-4.00	D	-5.66	D	-14.93	D
1557772_at	EXOC4	Exocyst complex component 4	-6.06	D	-2.00	D	-3.03	D
239264_at	EXOC4	Exocyst complex component 4	-5.66	D	-3.25	D	-2.14	D
214734_at	EXPH5	exophilin 5	-6.96	D	-5.28	D	-68.59	D
213506_at	F2RL1	coagulation factor II (thrombin) receptor-like 1	-2.46	D	-2.14	D	-25.99	D
226876_at	FAM101B	family with sequence similarity 101, member B	-4.29	D	-4.00	D	-14.93	D
226905_at	FAM101B	family with sequence similarity 101, member B	-3.48	D	-2.83	D	-17.15	D
212400_at	FAM102A	family with sequence similarity 102, member A	-6.06	D	-8.57	D	-12.13	D
223059_s_at	FAM107B	family with sequence similarity 107, member B	-2.14	D	-2.83	D	-2.14	D
229695_at	FAM107B	Family with sequence similarity 107, member B	-2.64	D	-3.73	D	-3.73	D
228298_at	FAM113B	family with sequence similarity 113, member B	-4.29	D	-6.50	D	-2.14	D
230923_at	FAM19A1	family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	-3.73	D	-9.85	D	-4.92	D
238146_at	FAM82B	Family with sequence similarity 82, member B	-2.83	D	-3.25	D	-2.14	D

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225864_at	FAM84B	family with sequence similarity 84, member B	-4.59	D	-3.48	D	-97.01	D
234758_at	FARS2	Phenylalanine-tRNA synthetase 2 (mitochondrial)	-5.66	D	-4.00	D	-2.00	D
223036_at	FARSLB	phenylalanine-tRNA synthetase-like, beta subunit	-3.25	D	-10.56	D	-3.03	D
232063_x_at	FARSLB	phenylalanine-tRNA synthetase-like, beta subunit	-4.00	D	-3.73	D	-3.25	D
211623_s_at	FBL	fibrillarin /// fibrillarin	-2.14	D	-2.30	D	-2.83	D
203088_at	FBLN5	fibulin 5	-13.00	D	-16.00	D	-8.00	D
227641_at	FBXL16	F-box and leucine-rich repeat protein 16	-3.03	D	-4.92	D	-10.56	D
203240_at	FCGBP	Fc fragment of IgG binding protein	-4.00	D	-3.25	D	-6.50	D
242563_at	FCHSD2	FCH and double SH3 domains 2	-2.83	D	-2.64	D	-2.30	D
235982_at	FCRL1	Fc receptor-like 1	-2.46	D	-14.93	D	-32.00	D
206492_at	FHIT	fragile histidine triad gene	-8.00	D	-8.00	D	-16.00	D
201540_at	FHL1	four and a half LIM domains 1	-2.14	D	-2.83	D	-7.46	D
236520_at	FKBP1A	FK506 binding protein 1A, 12kDa	-5.66	D	-11.31	D	-2.14	D
204560_at	FKBP5	FK506 binding protein 5	-2.14	D	-2.46	D	-9.19	D
224840_at	FKBP5	FK506 binding protein 5	-2.64	D	-4.29	D	-2.46	D
224856_at	FKBP5	FK506 binding protein 5	-2.46	D	-3.25	D	-2.83	D
219871_at	FLJ13197	hypothetical protein FLJ13197	-5.66	D	-4.00	D	-9.19	D
218510_x_at	FLJ20152	hypothetical protein FLJ20152	-18.38	D	-24.25	D	-90.51	D
218532_s_at	FLJ20152	hypothetical protein FLJ20152	-9.85	D	-11.31	D	-42.22	D
220467_at	FLJ21272	hypothetical protein FLJ21272	-6.96	D	-6.50	D	-2.30	D
1552716_at	FLJ23577	KPL2 protein	-7.46	D	-12.13	D	-7.46	D
231252_at	FLJ23861	hypothetical protein FLJ23861	-2.46	D	-5.28	D	-4.59	D
225444_at	FLJ25778	Hypothetical protein FLJ25778	-4.92	D	-3.25	D	-2.00	D
1554067_at	FLJ32549	hypothetical protein FLJ32549	-3.48	D	-4.29	D	-4.59	D
228686_at	FLJ33630	hypothetical protein LOC644873	-2.46	D	-16.00	D	-6.06	D
1557895_at	FLJ35934	FLJ35934 protein	-6.06	D	-6.06	D	-4.59	D
223477_s_at	FLJ38663	hypothetical protein FLJ38663	-2.14	D	-3.73	D	-2.46	D
1569040_s_at	FLJ40330	similar to protein immuno-reactive with anti-PTH polyclonal antibodies	-194.01	D	-4.92	D	-13.00	D
238148_s_at	FLJ46385	FLJ46385 protein	-3.48	D	-3.25	D	-6.96	D
238149_at	FLJ46385	FLJ46385 protein	-4.59	D	-3.25	D	-6.50	D
1562416_at	FLNB	Filamin B, beta (actin binding protein 278)	-2.00	D	-5.28	D	-13.93	D
208614_s_at	FLNB	filamin B, beta (actin binding protein 278)	-36.76	D	-18.38	D	-17.15	D
206980_s_at	FLT3LG	fms-related tyrosine kinase 3 ligand	-6.50	D	-7.46	D	-13.93	D
210607_at	FLT3LG	fms-related tyrosine kinase 3 ligand	-5.28	D	-6.50	D	-8.57	D
243876_at	FNBP1	Formin binding protein 1	-2.30	D	-3.48	D	-6.50	D
202723_s_at	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	-4.00	D	-5.28	D	-2.83	D
202724_s_at	FOXO1A	forkhead box O1A (rhabdomyosarcoma)	-3.73	D	-8.00	D	-2.64	D
232882_at	FOXO1A	Forkhead box O1A (rhabdomyosarcoma)	-19.70	D	-11.31	D	-6.06	D
1569477_at	FOXO3A	Forkhead box O3A	-7.46	D	-2.83	D	-2.14	D
1561166_a_at	FOXP1	Forkhead box P1	-29.86	D	-24.25	D	-22.63	D
215221_at	FOXP1	Forkhead box P1	-6.06	D	-6.50	D	-12.13	D
224838_at	FOXP1	forkhead box P1	-2.46	D	-3.03	D	-2.14	D
230415_at	FOXP1	Forkhead box P1	-9.85	D	-8.57	D	-32.00	D
235444_at	FOXP1	forkhead box P1	-6.96	D	-6.96	D	-2.64	D
240666_at	FOXP1	Forkhead box P1	-17.15	D	-16.00	D	-3.73	D
243291_at	FOXP1	Forkhead box P1	-39.40	D	-11.31	D	-128.00	D
243878_at	FOXP1	Forkhead box P1	-13.00	D	-4.29	D	-24.25	D
244535_at	FOXP1	Forkhead box P1	-13.00	D	-8.57	D	-12.13	D
244845_at	FOXP1	Forkhead box P1	-73.52	D	-22.63	D	-19.70	D
218373_at	FTS	fused toes homolog (mouse)	-2.83	D	-3.48	D	-2.00	D
243498_at	GABPA	GA binding protein transcription factor, alpha subunit 60kDa	-3.25	D	-3.03	D	-2.00	D
218885_s_at	GALNT12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12)	-3.73	D	-3.48	D	-2.30	D
230097_at	GART	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase	-2.64	D	-4.29	D	-2.64	D
224741_x_at	GAS5	growth arrest-specific 5	-3.25	D	-3.48	D	-3.25	D
224841_x_at	GAS5	growth arrest-specific 5	-2.64	D	-3.25	D	-3.73	D
209602_s_at	GATA3	GATA binding protein 3	-2.00	D	-2.46	D	-2.46	D
209603_at	GATA3	GATA binding protein 3	-2.00	D	-2.00	D	-2.83	D
205527_s_at	GEMIN4	gem (nuclear organelle) associated protein 4	-3.03	D	-3.25	D	-2.14	D
1552318_at	GIMAP1	GTPase, IMAP family member 1	-3.25	D	-5.28	D	-3.03	D
1552315_at	GIMAP1	GTPase, IMAP family member 1	-3.03	D	-4.92	D	-3.25	D
1552316_a_at	GIMAP1	GTPase, IMAP family member 1	-3.25	D	-4.29	D	-3.48	D

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218805_at	GIMAP5	GTPase, IMAP family member 5 /// GTPase, IMAP family member 5	-3.73	D	-8.00	D	-2.83	D
64064_at	GIMAP5	GTPase, IMAP family member 5	-3.25	D	-5.66	D	-2.64	D
235306_at	GIMAP8	GTPase, IMAP family member 8	-2.30	D	-4.29	D	-2.14	D
229312_s_at	GKAP1	G kinase anchoring protein 1	-2.00	D	-2.14	D	-2.46	D
55872_at	GM632	KIAA1196 protein	-6.96	D	-5.66	D	-51.98	D
207124_s_at	GNB5	guanine nucleotide binding protein (G protein), beta 5	-2.14	D	-3.03	D	-2.14	D
208798_x_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	-4.92	D	-4.29	D	-3.25	D
213650_at	GOLGA8A	golgi autoantigen, golgin subfamily a, 8A	-7.46	D	-3.03	D	-5.28	D
210425_x_at	GOLGA8B	golgi autoantigen, golgin subfamily a, 8B	-2.64	D	-2.64	D	-3.03	D
236862_at	GOPC	Golgi associated PDZ and coiled-coil motif containing	-2.46	D	-2.46	D	-2.46	D
207926_at	GP5	glycoprotein V (platelet)	-6.50	D	-6.96	D	-4.29	D
1561195_at	GPR137B	G protein-coupled receptor 137B	-24.25	D	-39.40	D	-4.59	D
231166_at	GPR155	G protein-coupled receptor 155	-4.00	D	-4.59	D	-8.00	D
239533_at	GPR155	G protein-coupled receptor 155	-8.00	D	-6.06	D	-16.00	D
204793_at	GPRASP1	G protein-coupled receptor associated sorting protein 1	-11.31	D	-21.11	D	-34.30	D
213170_at	GPX7	glutathione peroxidase 7	-2.46	D	-2.64	D	-13.00	D
224807_at	GRAMD1A	GRAM domain containing 1A	-3.25	D	-2.00	D	-6.06	D
229726_at	GRAP	GRB2-related adaptor protein	-6.06	D	-3.73	D	-32.00	D
205541_s_at	GSPT2	G1 to S phase transition 2 /// G1 to S phase transition 2	-2.00	D	-2.30	D	-5.28	D
238880_at	GTF3A	general transcription factor IIIA	-4.00	D	-4.29	D	-3.25	D
202947_s_at	GYPC	glycophorin C (Gerbich blood group)	-2.46	D	-2.83	D	-2.64	D
206666_at	GZMK	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	-9.85	D	-13.93	D	-21.11	D
1552787_at	HELB	helicase (DNA) B	-3.48	D	-2.46	D	-2.64	D
208054_at	HERC4	hect domain and RLD 4	-2.83	D	-2.83	D	-13.93	D
1559932_at	HEXA	Hexosaminidase A (alpha polypeptide)	-9.19	D	-19.70	D	-25.99	D
215316_at	HIBADH	3-hydroxyisobutyrate dehydrogenase	-6.50	D	-21.11	D	-4.29	D
200093_s_at	HINT1	histidine triad nucleotide binding protein 1 /// histidine triad nucleotide binding protein 1	-2.14	D	-2.00	D	-2.46	D
212641_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	-3.48	D	-4.00	D	-8.00	D
212642_s_at	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	-5.66	D	-6.50	D	-12.13	D
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	-10.56	D	-32.00	D	-147.03	D
225792_at	HOOK1	hook homolog 1 (Drosophila)	-27.86	D	-13.00	D	-9.19	D
203914_x_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-29.86	D	-7.46	D	-6.06	D
211548_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	-9.19	D	-11.31	D	-10.56	D
209657_s_at	HSF2	heat shock transcription factor 2	-2.46	D	-2.14	D	-2.14	D
230718_at	HSF5	heat shock transcription factor family member 5	-5.28	D	-5.66	D	-4.29	D
241299_at	IFT140	Intraflagellar transport 140 homolog (Chlamydomonas)	-13.93	D	-11.31	D	-6.06	D
203628_at	IGF1R	insulin-like growth factor 1 receptor	-29.86	D	-11.31	D	-119.43	D
236934_at	IGF1R	Insulin-like growth factor 1 receptor	-17.15	D	-12.13	D	-16.00	D
217022_s_at	IGHA1 / IGHA2	immunoglobulin heavy constant alpha 1 / alpha 2	-3.48	D	-68.59	D	-27.86	D
209374_s_at	IGHM	immunoglobulin heavy constant mu	-3.03	D	-4.00	D	-5.28	D
212827_at	IGHM	immunoglobulin heavy constant mu	-2.46	D	-7.46	D	-8.00	D
212592_at	IGJ	Immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	-3.73	D	-9.19	D	-8.57	D
214677_x_at	IGL@	immunoglobulin lambda locus	-3.03	D	-8.00	D	-9.19	D
206618_at	IL18R1	interleukin 18 receptor 1	-3.48	D	-4.92	D	-2.14	D
207072_at	IL18RAP	interleukin 18 receptor accessory protein	-9.19	D	-18.38	D	-11.31	D
205945_at	IL6R	interleukin 6 receptor /// interleukin 6 receptor	-4.59	D	-2.14	D	-14.93	D
204863_s_at	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	-3.25	D	-3.25	D	-4.92	D
212195_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	-4.29	D	-3.48	D	-4.59	D
212196_at	IL6ST	Interleukin 6 signal transducer (gp130, oncostatin M receptor)	-2.83	D	-2.64	D	-4.59	D
205798_at	IL7R	interleukin 7 receptor /// interleukin 7 receptor	-8.00	D	-16.00	D	-18.38	D
1555571_at	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	-6.50	D	-9.85	D	-25.99	D
1558409_at	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	-12.13	D	-5.66	D	-10.56	D
1558410_s_at	IMMP2L	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	-14.93	D	-5.66	D	-9.85	D
201892_s_at	IMPDH2	IMP (inosine monophosphate) dehydrogenase 2	-3.03	D	-3.25	D	-4.92	D
214705_at	INADL	InaD-like (Drosophila)	-32.00	D	-21.11	D	-78.79	D
223681_s_at	INADL	InaD-like (Drosophila)	-16.00	D	-128.00	D	-24.25	D
239173_at	INADL	InaD-like (Drosophila)	-6.06	D	-19.70	D	-19.70	D
53968_at	INTS5	integrator complex subunit 5	-2.14	D	-2.83	D	-2.00	D
200995_at	IPO7	Importin 7	-2.14	D	-2.83	D	-2.00	D
235613_at	IQWD1	IQ motif and WD repeats 1	-6.06	D	-2.46	D	-2.00	D
1557174_a_at	IRAK1BP1	Interleukin-1 receptor-associated kinase 1 binding protein 1	-3.73	D	-45.25	D	-2.30	D

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244599_at	ITGA4	Integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	-2.46	D	-2.00	D	-4.92	D
201656_at	ITGA6	integrin, alpha 6	-10.56	D	-34.30	D	-29.86	D
215177_s_at	ITGA6	integrin, alpha 6	-13.93	D	-25.99	D	-548.75	D
244665_at	ITGA6	Integrin, alpha 6	-27.86	D	-90.51	D	-10.56	D
1554306_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	-2.30	D	-2.64	D	-2.00	D
1569041_at	JMJD1C	Jumonji domain containing 1C	-6.96	D	-4.92	D	-4.29	D
228793_at	JMJD1C	jumonji domain containing 1C	-4.29	D	-4.29	D	-3.25	D
241391_at	JMJD1C	Jumonji domain containing 1C	-8.00	D	-3.03	D	-2.30	D
236732_at	JMJD2C	Jumonji domain containing 2C	-10.56	D	-4.29	D	-2.46	D
224870_at	KIAA0114	KIAA0114 gene product	-3.03	D	-2.00	D	-3.73	D
202713_s_at	KIAA0391	KIAA0391	-2.46	D	-2.83	D	-2.00	D
214764_at	KIAA0507	KIAA0507	-5.28	D	-8.57	D	-2.64	D
222920_s_at	KIAA0748	KIAA0748	-4.59	D	-8.57	D	-4.92	D
239946_at	KIAA0922	KIAA0922	-13.00	D	-9.85	D	-2.83	D
205976_at	KIAA0971	KIAA0971	-2.14	D	-2.30	D	-2.00	D
1563455_at	KIAA0999	KIAA0999 protein	-4.29	D	-3.03	D	-2.14	D
225784_s_at	KIAA1166	KIAA1166	-9.85	D	-7.46	D	-12.13	D
235288_at	KIAA1276	KIAA1276 protein	-2.14	D	-2.83	D	-2.00	D
232030_at	KIAA1632	KIAA1632	-2.83	D	-3.25	D	-2.30	D
215750_at	KIAA1659	KIAA1659 protein	-4.29	D	-2.83	D	-2.46	D
235112_at	KIAA1958	KIAA1958	-9.85	D	-9.19	D	-34.30	D
1561763_at	KIAA2026	KIAA2026	-4.59	D	-3.73	D	-2.14	D
203130_s_at	KIF5C	kinesin family member 5C	-2.64	D	-2.30	D	-84.45	D
1556461_at	KLF12	Kruppel-like factor 12	-2.83	D	-8.57	D	-4.92	D
1556462_a_at	KLF12	Kruppel-like factor 12	-4.59	D	-6.50	D	-2.64	D
243089_at	KLF12	Kruppel-like factor 12	-7.46	D	-10.56	D	-3.03	D
221838_at	KLHL22	kelch-like 22 (Drosophila)	-2.00	D	-2.83	D	-2.00	D
1560397_s_at	KLHL6	kelch-like 6 (Drosophila)	-45.25	D	-12.13	D	-8.57	D
228167_at	KLHL6	kelch-like 6 (Drosophila)	-4.00	D	-3.25	D	-7.46	D
214039_s_at	LAPTM4B	lysosomal associated protein transmembrane 4 beta	-5.66	D	-6.06	D	-111.43	D
223161_at	LCHN	LCHN protein	-3.25	D	-3.73	D	-6.50	D
221790_s_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	-8.00	D	-11.31	D	-18.38	D
57082_at	LDLRAP1	low density lipoprotein receptor adaptor protein 1	-6.06	D	-6.50	D	-13.00	D
204454_at	LDOC1	leucine zipper, down-regulated in cancer 1	-2.64	D	-5.28	D	-42.22	D
210948_s_at	LEF1	lymphoid enhancer-binding factor 1	-11.31	D	-18.38	D	-97.01	D
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	-14.93	D	-19.70	D	-51.98	D
1564776_at	LENG10	leukocyte receptor cluster (LRC) member 10	-14.93	D	-27.86	D	-36.76	D
202594_at	LEPROTL1	leptin receptor overlapping transcript-like 1	-2.46	D	-5.28	D	-2.46	D
202595_s_at	LEPROTL1	leptin receptor overlapping transcript-like 1	-2.00	D	-2.64	D	-4.00	D
242722_at	LMO7	LIM domain 7	-3.73	D	-13.00	D	-3.25	D
227867_at	LOC129293	hypothetical protein LOC129293	-13.00	D	-13.93	D	-21.11	D
225469_at	LOC144363	hypothetical protein LOC144363	-2.00	D	-2.83	D	-2.14	D
1564139_at	LOC144571	hypothetical protein LOC144571	-45.25	D	-4.00	D	-29.86	D
226764_at	LOC152485	hypothetical protein LOC152485	-14.93	D	-14.93	D	-34.30	D
228046_at	LOC152485	Hypothetical protein LOC152485	-4.00	D	-3.48	D	-27.86	D
1560703_at	LOC201229	hypothetical protein LOC201229	-3.25	D	-2.64	D	-4.29	D
214945_at	LOC202134	hypothetical protein LOC202134	-12.13	D	-22.63	D	-78.79	D
236832_at	LOC221442	hypothetical LOC221442	-2.64	D	-3.25	D	-2.14	D
235060_at	LOC23117	KIAA0220-like protein	-3.73	D	-2.14	D	-2.46	D
222307_at	LOC282997	hypothetical protein LOC282997	-4.29	D	-3.48	D	-6.96	D
1556061_at	LOC283012	hypothetical protein LOC283012	-2.83	D	-4.00	D	-2.00	D
230245_s_at	LOC283663	hypothetical protein LOC283663	-2.30	D	-4.92	D	-5.28	D
232801_at	LOC375748	RAD26L hypothetical protein	-4.92	D	-7.46	D	-2.00	D
222368_at	LOC389634	Hypothetical LOC389634	-5.28	D	-2.64	D	-2.46	D
239017_at	LOC389634	Hypothetical LOC389634	-3.25	D	-4.59	D	-2.14	D
232001_at	LOC439949	hypothetical gene supported by AY007155	-4.00	D	-13.00	D	-6.50	D
232594_at	LOC440498	Hypothetical gene supported by AK001829	-9.85	D	-6.06	D	-3.48	D
229872_s_at	LOC440667	hypothetical LOC440667	-2.64	D	-2.30	D	-3.73	D
225028_at	LOC550643	hypothetical protein LOC550643	-2.00	D	-2.83	D	-2.00	D
243362_s_at	LOC641518	hypothetical protein LOC641518	-11.31	D	-3.73	D	-11.31	D
240246_at	LOC642236	similar to FRG1 protein (FSHD region gene 1 protein)	-5.66	D	-8.57	D	-2.83	D
242770_at	LOC642236	similar to FRG1 protein (FSHD region gene 1 protein)	-2.14	D	-2.14	D	-3.25	D

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
242577_at	LOC642398	hypothetical protein LOC642398	-3.25	D	-9.19	D	-4.00	D
1559957_a_at	LOC642852	hypothetical protein LOC642852	-3.73	D	-7.46	D	-2.46	D
230064_at	LOC643473	Hypothetical protein LOC643473	-4.59	D	-2.64	D	-3.25	D
241838_at	LOC644112	Similar to splicing factor 3b, subunit 4	-3.48	D	-3.48	D	-3.03	D
1558569_at	LOC645238	hypothetical protein LOC645238	-55.72	D	-97.01	D	-17.15	D
227074_at	LOC646848	hypothetical protein LOC646848	-4.92	D	-3.03	D	-2.14	D
228465_at	LOC646848	Hypothetical protein LOC646848	-2.00	D	-2.30	D	-2.00	D
239819_at	LOC647065	Hypothetical protein LOC647065	-2.64	D	-2.00	D	-2.64	D
237825_x_at	LOC647065	Hypothetical protein LOC647065	-2.46	D	-4.29	D	-3.03	D
234852_at	LOC648859	hypothetical protein LOC648859	-4.29	D	-2.14	D	-13.00	D
227984_at	LOC650392	Hypothetical protein LOC650392	-5.28	D	-16.00	D	-194.01	D
1566040_at	LOC653316	Hypothetical protein LOC653316	-51.98	D	-25.99	D	-34.30	D
213166_x_at	LOC653784	similar to hypothetical protein FLJ14346	-2.00	D	-2.14	D	-2.46	D
228841_at	LOC90624	hypothetical protein LOC90624	-2.30	D	-4.29	D	-2.00	D
232910_at	LOC92482	hypothetical protein LOC92482	-2.64	D	-4.59	D	-2.00	D
233198_at	LOC92497	hypothetical protein LOC92497	-4.92	D	-2.64	D	-2.14	D
211596_s_at	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	-4.29	D	-4.92	D	-6.50	D
230793_at	LRRC16	leucine rich repeat containing 16	-11.31	D	-6.06	D	-12.13	D
1558517_s_at	LRRC8C	Leucine rich repeat containing 8 family, member C	-3.73	D	-4.29	D	-2.64	D
234148_at	LRRC8D	Leucine rich repeat containing 8 family, member D	-4.92	D	-4.29	D	-3.03	D
209840_s_at	LRRN3	leucine rich repeat neuronal 3	-64.00	D	-445.72	D	-891.44	D
209841_s_at	LRRN3	leucine rich repeat neuronal 3	-36.76	D	-59.71	D	-955.43	D
207339_s_at	LTB	lymphotoxin beta (TNF superfamily, member 3)	-4.59	D	-11.31	D	-25.99	D
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	-5.66	D	-4.59	D	-7.46	D
230174_at	LYPLAL1	Lysophospholipase-like 1	-2.00	D	-2.30	D	-2.30	D
244878_at	MAGED1	Melanoma antigen family D, 1	-8.00	D	-6.50	D	-2.46	D
244450_at	MAK	Male germ cell-associated kinase	-16.00	D	-4.00	D	-2.83	D
204777_s_at	MAL	mal, T-cell differentiation protein	-10.56	D	-24.25	D	-24.25	D
1570299_at	MAML2	Mastermind-like 2 (Drosophila)	-3.25	D	-9.19	D	-9.19	D
232333_at	MAML2	Mastermind-like 2 (Drosophila)	-24.25	D	-16.00	D	-9.19	D
234645_at	MAML2	Mastermind-like 2 (Drosophila)	-13.93	D	-7.46	D	-7.46	D
235106_at	MAML2	mastermind-like 2 (Drosophila)	-2.83	D	-2.30	D	-3.03	D
235457_at	MAML2	mastermind-like 2 (Drosophila)	-5.28	D	-4.92	D	-4.59	D
242405_at	MAML2	Mastermind-like 2 (Drosophila)	-22.63	D	-11.31	D	-9.85	D
244414_at	MAML2	Mastermind-like 2 (Drosophila)	-25.99	D	-18.38	D	-12.13	D
218918_at	MAN1C1	mannosidase, alpha, class 1C, member 1	-10.56	D	-5.28	D	-27.86	D
243030_at	MAP3K1	Mitogen-activated protein kinase kinase kinase 1	-5.28	D	-3.25	D	-3.25	D
226190_at	MAP3K13	Mitogen-activated protein kinase kinase kinase 13	-2.83	D	-2.30	D	-4.29	D
1565889_at	MAP3K7IP2	Mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-4.59	D	-3.48	D	-2.14	D
244846_at	MAP4K4	Mitogen-activated protein kinase kinase kinase kinase 4	-2.83	D	-2.83	D	-2.30	D
1556657_at	MBNL1	Muscleblind-like (Drosophila)	-10.56	D	-13.93	D	-2.00	D
1556658_a_at	MBNL1	Muscleblind-like (Drosophila)	-8.57	D	-8.00	D	-2.14	D
235811_at	MBNL1	Muscleblind-like (Drosophila)	-6.06	D	-10.56	D	-4.29	D
236558_at	MBNL1	Muscleblind-like (Drosophila)	-13.00	D	-19.70	D	-4.00	D
238558_at	MBNL1	Muscleblind-like (Drosophila)	-6.06	D	-8.57	D	-2.46	D
226225_at	MCC	mutated in colorectal cancers	-6.96	D	-9.19	D	-16.00	D
233231_at	MCCC2	Methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	-7.46	D	-4.00	D	-2.46	D
1569484_s_at	MDN1	MDN1, midasin homolog (yeast)	-7.46	D	-6.96	D	-2.83	D
1562731_s_at	MDS2	myelodysplastic syndrome 2 translocation associated	-4.29	D	-2.64	D	-5.66	D
239571_at	MEF2A	MADS box transcription enhancer factor 2, polypeptide A	-4.00	D	-2.64	D	-2.46	D
202016_at	MEST	mesoderm specific transcript homolog (mouse)	-9.19	D	-12.13	D	-7.46	D
213457_at	MFHAS1	malignant fibrous histiocytoma amplified sequence 1	-4.59	D	-4.29	D	-17.15	D
1569136_at	MGAT4A	Mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	-2.46	D	-4.59	D	-5.66	D
215528_at	MGAT5	Mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	-11.31	D	-4.59	D	-4.00	D
1554609_at	MGC12965	similar to Cytochrome c, somatic	-2.64	D	-3.48	D	-2.00	D
221756_at	MGC17330	HGFL gene /// HGFL gene	-5.66	D	-5.28	D	-5.66	D
221757_at	MGC17330	HGFL gene /// HGFL gene	-4.59	D	-3.48	D	-9.19	D
225330_at	MGC18216	hypothetical protein MGC18216	-4.29	D	-4.92	D	-7.46	D
238365_s_at	MGC33556	hypothetical LOC339541	-3.25	D	-2.83	D	-9.19	D
242520_s_at	MGC33556	hypothetical LOC339541	-8.57	D	-3.25	D	-59.71	D
1556373_a_at	MGC35361	Hypothetical protein MGC35361	-2.64	D	-2.64	D	-2.00	D

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243602_at	MGC40069	Hypothetical protein MGC40069	-5.28	D	-8.57	D	-12.13	D
237033_at	MGC52498	hypothetical protein MGC52498	-2.64	D	-3.03	D	-2.30	D
222306_at	MGC61571	Hypothetical protein MGC61571	-4.59	D	-3.03	D	-3.03	D
244740_at	MGC9913	hypothetical protein MGC9913	-13.93	D	-11.31	D	-13.00	D
244741_s_at	MGC9913	hypothetical protein MGC9913	-6.50	D	-19.70	D	-12.13	D
213188_s_at	MINA	MYC induced nuclear antigen	-2.83	D	-3.03	D	-3.03	D
213189_at	MINA	MYC induced nuclear antigen	-2.83	D	-3.48	D	-3.48	D
218259_at	MKL2	MKL/myocardin-like 2	-6.50	D	-2.83	D	-2.83	D
233219_at	MKLN1	Muskelin 1, intracellular mediator containing kelch motifs	-3.03	D	-4.00	D	-2.46	D
1569652_at	MLLT3	Myeloid/lymphoid or mixed-lineage leukemia	-3.03	D	-3.03	D	-3.03	D
225157_at	MLXIP	MLX interacting protein	-3.48	D	-2.14	D	-3.48	D
203956_at	MORC2	MORC family CW-type zinc finger 2	-4.59	D	-7.46	D	-2.83	D
216863_s_at	MORC2	MORC family CW-type zinc finger 2	-3.48	D	-5.28	D	-3.03	D
226092_at	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	-6.06	D	-2.30	D	-2.00	D
238451_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-3.73	D	-2.30	D	-13.93	D
238778_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-3.73	D	-2.46	D	-25.99	D
236955_at	MRPS28	Mitochondrial ribosomal protein S28	-9.19	D	-6.96	D	-6.50	D
218654_s_at	MRPS33	mitochondrial ribosomal protein S33	-2.46	D	-2.83	D	-2.00	D
228592_at	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	-2.30	D	-21.11	D	-4.29	D
1553132_a_at	MTAC2D1	membrane targeting (tandem) C2 domain containing 1	-3.03	D	-2.64	D	-16.00	D
234970_at	MTAC2D1	membrane targeting (tandem) C2 domain containing 1	-3.48	D	-4.29	D	-8.57	D
1557965_at	MTERFD2	MTERF domain containing 2	-2.64	D	-2.83	D	-2.83	D
1557966_x_at	MTERFD2	MTERF domain containing 2	-2.46	D	-3.03	D	-2.46	D
230444_at	MTFR1	Mitochondrial fission regulator 1	-4.29	D	-4.29	D	-4.59	D
239846_at	MTHFD1	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1	-3.48	D	-4.29	D	-2.00	D
36920_at	MTM1	myotubularin 1	-2.30	D	-2.00	D	-3.03	D
212096_s_at	MTUS1	mitochondrial tumor suppressor 1	-9.85	D	-4.59	D	-32.00	D
213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	-2.00	D	-3.03	D	-2.30	D
202431_s_at	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	-10.56	D	-27.86	D	-39.40	D
222771_s_at	MYEF2	myelin expression factor 2	-4.92	D	-3.48	D	-39.40	D
231996_at	N4BP2	Nedd4 binding protein 2	-3.25	D	-3.25	D	-2.14	D
208754_s_at	NAP1L1	nucleosome assembly protein 1-like 1	-2.14	D	-2.00	D	-3.25	D
219368_at	NAP1L2	nucleosome assembly protein 1-like 2	-6.50	D	-2.46	D	-2.14	D
204749_at	NAP1L3	nucleosome assembly protein 1-like 3	-2.30	D	-3.48	D	-5.66	D
219378_at	NARG1L	NMDA receptor regulated 1-like	-2.00	D	-2.46	D	-2.30	D
242191_at	NBPF11	neuroblastoma breakpoint family, member 11	-4.59	D	-3.03	D	-4.00	D
203315_at	NCK2	NCK adaptor protein 2	-3.03	D	-3.25	D	-5.66	D
232583_at	NCK2	NCK adaptor protein 2	-12.13	D	-29.86	D	-8.57	D
211352_s_at	NCOA3	nuclear receptor coactivator 3	-2.64	D	-2.30	D	-2.00	D
222423_at	NDFIP1	Nedd4 family interacting protein 1	-2.46	D	-3.03	D	-2.14	D
203413_at	NELL2	NEL-like 2 (chicken) /// NEL-like 2 (chicken)	-18.38	D	-24.25	D	-59.71	D
239876_at	NFKB1	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	-5.66	D	-3.48	D	-3.48	D
217963_s_at	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	-3.48	D	-3.48	D	-22.63	D
229963_at	NGFRAP1L1	NGFRAP1-like 1	-6.96	D	-9.85	D	-194.01	D
231235_at	NKTR	natural killer-tumor recognition sequence	-3.03	D	-3.03	D	-7.46	D
205005_s_at	NMT2	N-myristoyltransferase 2	-2.14	D	-2.46	D	-2.30	D
215743_at	NMT2	N-myristoyltransferase 2	-4.29	D	-5.66	D	-2.83	D
231798_at	NOG	Noggin	-21.11	D	-16.00	D	-294.07	D
1554082_a_at	NOL9	nucleolar protein 9	-2.00	D	-2.14	D	-2.30	D
217950_at	NOSIP	nitric oxide synthase interacting protein	-4.59	D	-4.92	D	-6.06	D
201695_s_at	NP	nucleoside phosphorylase	-2.00	D	-2.64	D	-2.83	D
39549_at	NPAS2	neuronal PAS domain protein 2	-4.00	D	-24.25	D	-22.63	D
235432_at	NPHP3	nephronophthisis 3 (adolescent)	-2.00	D	-2.83	D	-2.64	D
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	-2.30	D	-2.30	D	-2.00	D
1564236_at	NR3C2	Nuclear receptor subfamily 3, group C, member 2	-128.00	D	-103.97	D	-19.70	D
205259_at	NR3C2	nuclear receptor subfamily 3, group C, member 2	-14.93	D	-16.00	D	-7.46	D
239673_at	NR3C2	Nuclear receptor subfamily 3, group C, member 2	-24.25	D	-22.63	D	-14.93	D
204105_s_at	NRCAM	neuronal cell adhesion molecule	-84.45	D	-21.11	D	-5.66	D
202599_s_at	NRIP1	nuclear receptor interacting protein 1	-4.00	D	-2.30	D	-51.98	D
202600_s_at	NRIP1	nuclear receptor interacting protein 1	-5.66	D	-2.00	D	-59.71	D
1569180_at	NSF	N-ethylmaleimide-sensitive factor	-5.28	D	-2.83	D	-2.14	D

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1569181_x_at	NSF	N-ethylmaleimide-sensitive factor	-5.66	D	-2.64	D	-2.14	D
242239_at	NSUN6	NOL1/NOP2/Sun domain family, member 6	-3.03	D	-2.64	D	-2.46	D
223178_s_at	NT5DC1	5'-nucleotidase domain containing 1	-2.00	D	-2.00	D	-2.30	D
1553994_at	NT5E	5'-nucleotidase, ecto (CD73)	-11.31	D	-13.00	D	-78.79	D
1553995_a_at	NT5E	5'-nucleotidase, ecto (CD73)	-25.99	D	-17.15	D	-78.79	D
203939_at	NT5E	5'-nucleotidase, ecto (CD73)	-22.63	D	-45.25	D	-64.00	D
227486_at	NT5E	5'-nucleotidase, ecto (CD73)	-24.25	D	-24.25	D	-25.99	D
240824_at	OBFC1	Oligonucleotide/oligosaccharide-binding fold containing 1	-7.46	D	-10.56	D	-3.25	D
1555890_at	OR2A7	Olfactory receptor, family 2, subfamily A, member 7	-5.28	D	-11.31	D	-25.99	D
1563051_at	OSBP	oxysterol binding protein	-2.30	D	-2.14	D	-2.14	D
215262_at	OXNAD1	Oxidoreductase NAD-binding domain containing 1	-19.70	D	-14.93	D	-119.43	D
227686_at	OXNAD1	oxidoreductase NAD-binding domain containing 1	-9.19	D	-13.00	D	-22.63	D
231502_at	P15RS	Hypothetical protein FLJ10656	-4.00	D	-3.73	D	-2.30	D
210448_s_at	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	-3.73	D	-6.06	D	-7.46	D
206637_at	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	-2.14	D	-3.03	D	-6.96	D
225626_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-6.06	D	-8.00	D	-4.00	D
227354_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	-4.92	D	-6.06	D	-6.50	D
201013_s_at	PAICS	phosphoribosylaminoimidazole carboxylase	-3.25	D	-3.48	D	-4.00	D
239597_at	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-5.66	D	-3.48	D	-2.00	D
243233_at	PAN3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-7.46	D	-4.59	D	-2.83	D
240141_at	PAPD4	PAP associated domain containing 4	-3.25	D	-2.64	D	-3.48	D
227626_at	PAQR8	progestin and adipoQ receptor family member VIII	-5.28	D	-5.66	D	-6.96	D
213534_s_at	PASK	PAS domain containing serine/threonine kinase	-8.57	D	-9.85	D	-12.13	D
216945_x_at	PASK	PAS domain containing serine/threonine kinase	-9.19	D	-10.56	D	-12.13	D
212259_s_at	PBXIP1	pre-B-cell leukemia transcription factor interacting protein 1	-2.14	D	-2.00	D	-2.14	D
214177_s_at	PBXIP1	pre-B-cell leukemia transcription factor interacting protein 1	-3.03	D	-4.00	D	-2.46	D
241956_at	PCGF5	Polycomb group ring finger 5	-3.03	D	-2.30	D	-2.30	D
238902_at	PCMTD1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-3.48	D	-4.00	D	-2.46	D
237577_at	PCNP	PEST proteolytic signal containing nuclear protein	-2.30	D	-2.46	D	-3.73	D
215175_at	PCNX	pecanex homolog (Drosophila)	-4.59	D	-2.64	D	-2.64	D
237459_at	PCTK2	PCTAIRE protein kinase 2	-4.29	D	-2.83	D	-2.00	D
212594_at	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	-2.30	D	-2.83	D	-2.64	D
214582_at	PDE3B	phosphodiesterase 3B, cGMP-inhibited	-13.00	D	-8.57	D	-51.98	D
222317_at	PDE3B	Phosphodiesterase 3B, cGMP-inhibited	-24.25	D	-14.93	D	-42.22	D
222330_at	PDE3B	Phosphodiesterase 3B, cGMP-inhibited	-25.99	D	-36.76	D	-48.50	D
203708_at	PDE4B	phosphodiesterase 4A, cAMP-specific	-5.28	D	-2.46	D	-24.25	D
213388_at	PDE4DIP	phosphodiesterase 4D interacting protein (myomegalin)	-2.30	D	-4.00	D	-2.00	D
1552343_s_at	PDE7A	phosphodiesterase 7A	-6.50	D	-11.31	D	-5.28	D
224046_s_at	PDE7A	phosphodiesterase 7A	-4.00	D	-4.59	D	-6.96	D
226452_at	PDK1	pyruvate dehydrogenase kinase, isozyme 1	-3.73	D	-4.92	D	-4.29	D
239798_at	PDK1	Pyruvate dehydrogenase kinase, isozyme 1	-12.13	D	-9.19	D	-6.50	D
235547_at	PFAAP5	Phosphonoformate immuno-associated protein 5	-3.25	D	-2.30	D	-2.64	D
213302_at	PFAS	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	-3.25	D	-3.73	D	-3.73	D
220576_at	PGAP1	GPI deacylase	-5.66	D	-3.48	D	-3.48	D
229553_at	PGM2L1	phosphoglucomutase 2-like 1	-2.83	D	-3.48	D	-2.64	D
242277_at	PHACTR2	Phosphatase and actin regulator 2	-3.03	D	-2.64	D	-4.92	D
244774_at	PHACTR2	Phosphatase and actin regulator 2	-8.00	D	-4.00	D	-48.50	D
244791_at	PHGDHL1	Phosphoglycerate dehydrogenase like 1	-8.00	D	-6.96	D	-2.46	D
235107_at	PIAS2	Protein inhibitor of activated STAT, 2	-2.83	D	-4.29	D	-2.14	D
244633_at	PIAS2	Protein inhibitor of activated STAT, 2	-4.29	D	-4.29	D	-2.00	D
232262_at	PIGL	phosphatidylinositol glycan, class L	-2.30	D	-3.48	D	-4.29	D
215212_at	PIK3CA	Phosphoinositide-3-kinase, catalytic, alpha polypeptide	-5.28	D	-3.73	D	-3.03	D
212249_at	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-2.64	D	-2.00	D	-2.83	D
244181_at	PIK3R1	Phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	-3.03	D	-4.00	D	-4.92	D
241155_at	PIP5K2A	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	-3.48	D	-5.66	D	-3.03	D
239808_at	PITPNC1	Phosphatidylinositol transfer protein, cytoplasmic 1	-2.14	D	-3.48	D	-2.00	D
1563217_at	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-13.00	D	-36.76	D	-238.86	D
204612_at	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-6.50	D	-6.06	D	-45.25	D
226864_at	PKIA	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	-32.00	D	-3.73	D	-78.79	D
202732_at	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	-3.03	D	-6.96	D	-4.29	D
205372_at	PLAG1	pleiomorphic adenoma gene 1	-4.92	D	-4.92	D	-48.50	D
244726_at	PLCB1	Phospholipase C, beta 1 (phosphoinositide-specific)	-5.28	D	-4.29	D	-45.25	D

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
209504_s_at	PLEKHB1	pleckstrin homology domain containing, family B (evectins) member 1	-4.00	D	-4.29	D	-8.00	D
205871_at	PLGLB2	plasminogen-like B2	-2.30	D	-4.29	D	-3.48	D
205190_at	PLS1	plastin 1 (I isoform)	-6.06	D	-2.00	D	-36.76	D
219700_at	PLXDC1	plexin domain containing 1	-17.15	D	-9.19	D	-9.85	D
222490_at	POLR3E	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	-2.46	D	-2.46	D	-2.83	D
1562280_at	POU2F1	POU domain, class 2, transcription factor 1	-4.29	D	-9.85	D	-2.00	D
37152_at	PPARD	peroxisome proliferative activated receptor, delta	-2.64	D	-2.14	D	-2.46	D
236999_at	PPWD1	Peptidylprolyl isomerase domain and WD repeat containing 1	-3.73	D	-3.03	D	-2.64	D
213093_at	PRKCA	protein kinase C, alpha	-8.00	D	-9.19	D	-7.46	D
216069_at	PRMT2	Protein arginine methyltransferase 2	-4.29	D	-4.00	D	-3.03	D
228722_at	PRMT2	protein arginine methyltransferase 2	-3.25	D	-4.29	D	-3.25	D
231735_s_at	PRO1073	PRO1073 protein	-2.64	D	-2.30	D	-2.00	D
226610_at	PRR6	proline rich 6	-2.64	D	-12.13	D	-6.06	D
226611_s_at	PRR6	proline rich 6	-3.25	D	-4.59	D	-2.64	D
234865_at	PRSS1	Protease, serine, 1 (trypsin 1)	-4.00	D	-4.00	D	-24.25	D
243997_x_at	PSPC1	Paraspeckle component 1	-6.06	D	-3.73	D	-2.64	D
233314_at	PTEN	phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	-3.25	D	-4.59	D	-2.83	D
1568898_at	PTPRK	Protein tyrosine phosphatase, receptor type, K	-36.76	D	-9.19	D	-18.38	D
203038_at	PTPRK	protein tyrosine phosphatase, receptor type, K	-9.19	D	-6.96	D	-7.46	D
218984_at	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	-2.14	D	-4.00	D	-3.48	D
221974_at	PWCR1	Prader-Willi syndrome chromosome region 1	-3.48	D	-4.92	D	-3.73	D
233089_at	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	-2.30	D	-2.64	D	-2.00	D
229398_at	RAB18	RAB18, member RAS oncogene family	-2.64	D	-2.64	D	-2.00	D
213531_s_at	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	-6.06	D	-4.29	D	-9.85	D
223471_at	RAB3IP	RAB3A interacting protein (rabin3)	-5.28	D	-4.59	D	-6.50	D
238853_at	RAB3IP	RAB3A interacting protein (rabin3)	-9.19	D	-8.57	D	-29.86	D
225632_s_at	RAB43	RAB43, member RAS oncogene family	-3.73	D	-3.03	D	-2.83	D
1557738_at	RAB6IP2	RAB6 interacting protein 2	-6.06	D	-5.28	D	-6.96	D
232565_at	RAB6IP2	RAB6 interacting protein 2	-45.25	D	-24.25	D	-4.29	D
242737_at	RAD51L1	RAD51-like 1 (S. cerevisiae)	-10.56	D	-6.50	D	-2.30	D
244813_at	RAD51L1	RAD51-like 1 (S. cerevisiae)	-2.64	D	-2.30	D	-2.46	D
235846_at	RAD54B	RAD54 homolog B (S. cerevisiae)	-4.00	D	-14.93	D	-39.40	D
227224_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-2.30	D	-12.13	D	-24.25	D
227533_at	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	-2.83	D	-4.29	D	-64.00	D
230078_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	-2.30	D	-4.00	D	-2.00	D
239646_at	RAPGEF6	Rap guanine nucleotide exchange factor (GEF) 6	-8.00	D	-9.19	D	-3.03	D
231075_x_at	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	-2.14	D	-2.64	D	-2.46	D
1553185_at	RASEF	RAS and EF-hand domain containing	-4.92	D	-3.25	D	-2.30	D
1553186_x_at	RASEF	RAS and EF-hand domain containing	-3.25	D	-2.46	D	-2.30	D
228109_at	RASGRF2	Ras protein-specific guanine nucleotide-releasing factor 2	-16.00	D	-21.11	D	-9.85	D
212332_at	RBL2	retinoblastoma-like 2 (p130)	-2.30	D	-3.25	D	-2.00	D
238185_at	RBMS1	RNA binding motif, single stranded interacting protein 1	-3.73	D	-5.66	D	-2.30	D
238281_at	RBMS1	RNA binding motif, single stranded interacting protein 1	-4.00	D	-3.03	D	-8.00	D
223447_at	REG4	regenerating islet-derived family, member 4	-16.00	D	-3.48	D	-6.96	D
244625_at	RERE	Arginine-glutamic acid dipeptide (RE) repeats	-19.70	D	-3.73	D	-2.64	D
232963_at	RFWD2	Ring finger and WD repeat domain 2	-3.25	D	-2.64	D	-2.64	D
217671_at	RFX3	Regulatory factor X, 3 (influences HLA class II expression)	-8.00	D	-9.85	D	-2.83	D
232791_at	RFX3	Regulatory factor X, 3 (influences HLA class II expression)	-3.48	D	-51.98	D	-4.92	D
218723_s_at	RGC32	response gene to complement 32	-6.96	D	-4.29	D	-10.56	D
210676_x_at	RGPD5	RANBP2-like and GRIP domain containing 5	-2.46	D	-2.46	D	-2.00	D
204319_s_at	RGS10	regulator of G-protein signalling 10	-3.73	D	-2.83	D	-8.57	D
216166_at	RHOH	Ras homolog gene family, member H	-6.50	D	-4.29	D	-2.00	D
204951_at	RHOH	ras homolog gene family, member H	-3.48	D	-11.31	D	-3.25	D
236293_at	RHOH	Ras homolog gene family, member H	-7.46	D	-6.50	D	-3.03	D
214519_s_at	RLN2	relaxin 2	-4.29	D	-4.59	D	-73.52	D
1565544_at	RNF141	ring finger protein 141	-48.50	D	-32.00	D	-21.11	D
226433_at	RNF157	ring finger protein 157	-3.03	D	-4.00	D	-3.48	D
230776_at	RNF157	Ring finger protein 157	-7.46	D	-25.99	D	-3.25	D
213194_at	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	-4.92	D	-3.25	D	-7.46	D
237733_at	RP11-125A7.3	KIAA0564 protein	-2.83	D	-9.85	D	-2.64	D
215321_at	RPIB9	Rap2-binding protein 9	-3.25	D	-3.03	D	-13.93	D
229590_at	RPL13	Ribosomal protein L13	-3.48	D	-2.14	D	-6.06	D

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221593_s_at	RPL31	ribosomal protein L31	-2.64	D	-2.14	D	-3.73	D
200962_at	RPL31	ribosomal protein L31 /// similar to ribosomal protein L31	-2.14	D	-3.48	D	-7.46	D
238026_at	RPL35A	Ribosomal protein L35a	-3.03	D	-2.64	D	-2.83	D
219762_s_at	RPL36	ribosomal protein L36	-2.30	D	-2.46	D	-2.64	D
224767_at	RPL37	Ribosomal protein L37	-2.46	D	-2.46	D	-3.25	D
224763_at	RPL37	Ribosomal protein L37	-2.46	D	-3.03	D	-4.00	D
214167_s_at	RPLP0	ribosomal protein, large, P0 /// similar to ribosomal protein P0	-2.14	D	-2.00	D	-2.30	D
213427_at	RPP40	ribonuclease P 40kDa subunit	-4.92	D	-3.73	D	-2.30	D
214097_at	RPS21	ribosomal protein S21	-2.30	D	-2.30	D	-2.14	D
227722_at	RPS23	ribosomal protein S23	-4.59	D	-4.00	D	-4.92	D
236621_at	RPS27	ribosomal protein S27 (metallopanstimulin 1)	-6.96	D	-3.03	D	-2.64	D
1568449_at	RPS6KA3	Ribosomal protein S6 kinase, 90kDa, polypeptide 3	-2.14	D	-2.14	D	-3.25	D
209567_at	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	-2.00	D	-2.83	D	-2.64	D
239868_at	RSAFD1	Radical S-adenosyl methionine and flavodoxin domains 1	-2.00	D	-2.14	D	-13.00	D
212018_s_at	RSL1D1	ribosomal L1 domain containing 1	-2.46	D	-2.83	D	-2.83	D
232231_at	RUNX2	runt-related transcription factor 2	-9.19	D	-9.85	D	-64.00	D
236859_at	RUNX2	runt-related transcription factor 2	-48.50	D	-48.50	D	-103.97	D
237456_at	RYBP	RING1 and YY1 binding protein	-2.83	D	-2.00	D	-2.30	D
209686_at	S100B	S100 calcium binding protein, beta (neural)	-36.76	D	-128.00	D	-25.99	D
1559882_at	SAMHD1	SAM domain and HD domain 1	-8.57	D	-2.83	D	-2.46	D
203408_s_at	SATB1	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	-5.28	D	-6.96	D	-3.03	D
244267_at	SATB1	Special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	-9.85	D	-13.00	D	-22.63	D
240326_at	SBF2	SET binding factor 2	-8.57	D	-2.46	D	-4.29	D
237137_at	SCARNA2	small Cajal body-specific RNA 2	-2.14	D	-4.29	D	-4.59	D
235652_at	SCML1	Sex comb on midleg-like 1 (Drosophila)	-6.96	D	-2.14	D	-97.01	D
1556472_s_at	SCML4	sex comb on midleg-like 4 (Drosophila)	-3.03	D	-4.29	D	-2.64	D
230058_at	SDCCAG3	serologically defined colon cancer antigen 3	-2.00	D	-2.46	D	-2.46	D
242064_at	SDK2	sidekick homolog 2 (chicken)	-2.64	D	-25.99	D	-14.93	D
221931_s_at	SEH1L	SEH1-like (S. cerevisiae)	-2.00	D	-3.03	D	-2.14	D
212812_at	SERINC5	Serine incorporator 5	-4.59	D	-2.83	D	-13.93	D
241494_at	SERINC5	Serine incorporator 5	-73.52	D	-17.15	D	-32.00	D
218346_s_at	SESN1	sestrin 1	-3.73	D	-2.83	D	-2.83	D
243546_at	SESN3	Sestrin 3	-8.00	D	-8.00	D	-5.66	D
210172_at	SF1	splicing factor 1	-4.92	D	-2.64	D	-2.00	D
219513_s_at	SH2D3A	SH2 domain containing 3A	-6.06	D	-13.00	D	-6.06	D
204019_s_at	SH3YL1	SH3 domain containing, Ysc84-like 1 (S. cerevisiae)	-4.59	D	-7.46	D	-4.59	D
1560171_at	SHPRH	SNF2 histone linker PHD RING helicase	-2.46	D	-4.00	D	-3.48	D
239600_at	SIPA1L1	Signal-induced proliferation-associated 1 like 1	-7.46	D	-2.30	D	-3.25	D
220485_s_at	SIRPG	signal-regulatory protein gamma	-19.70	D	-42.22	D	-45.25	D
206181_at	SLAMF1	signaling lymphocytic activation molecule family member 1	-4.59	D	-5.66	D	-17.15	D
219915_s_at	SLC16A10	solute carrier family 16 (monocarboxylic acid transporters), member 10	-84.45	D	-45.25	D	-137.19	D
222939_s_at	SLC16A10	solute carrier family 16 (monocarboxylic acid transporters), member 10	-19.70	D	-13.93	D	-11.31	D
207057_at	SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	-2.46	D	-4.00	D	-2.30	D
210807_s_at	SLC16A7	solute carrier family 16 (monocarboxylic acid transporters), member 7	-2.30	D	-2.64	D	-2.64	D
209267_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	-4.29	D	-2.83	D	-5.66	D
223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1	-2.46	D	-4.29	D	-39.40	D
203579_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-2.83	D	-2.14	D	-5.28	D
203580_s_at	SLC7A6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-6.96	D	-6.06	D	-6.50	D
1553055_a_at	SLFN5	schlafen family member 5	-2.14	D	-2.14	D	-2.46	D
243999_at	SLFN5	schlafen family member 5	-2.00	D	-2.30	D	-3.25	D
1558937_s_at	SMA3	SMA3	-3.73	D	-2.14	D	-3.25	D
239448_at	SMAD3	SMAD, mothers against DPP homolog 3 (Drosophila)	-8.00	D	-2.30	D	-4.59	D
244357_at	SMAP1L	Stromal membrane-associated protein 1-like	-6.06	D	-4.29	D	-3.73	D
241620_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	-2.64	D	-2.83	D	-34.30	D
239784_at	SMYD3	SET and MYND domain containing 3	-4.29	D	-2.83	D	-2.14	D
225220_at	SNORA24	Small nucleolar RNA, H/ACA box 24	-3.03	D	-2.14	D	-4.00	D
207474_at	SNRK	SNF related kinase	-5.66	D	-5.66	D	-2.14	D
223027_at	SNX9	sorting nexin 9	-10.56	D	-4.00	D	-238.86	D
223028_s_at	SNX9	sorting nexin 9	-3.03	D	-2.46	D	-9.85	D
203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-4.00	D	-3.48	D	-16.00	D
230707_at	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	-6.06	D	-4.92	D	-21.11	D

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1555882_at	SPIN3	spindlin family, member 3	-2.83	D	-4.59	D	-45.25	D
206310_at	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	-24.25	D	-9.19	D	-22.63	D
202524_s_at	SPOCK2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	-6.96	D	-3.48	D	-7.46	D
200672_x_at	SPTBN1	spectrin, beta, non-erythrocytic 1	-2.64	D	-2.64	D	-4.29	D
212071_s_at	SPTBN1	spectrin, beta, non-erythrocytic 1	-6.50	D	-6.50	D	-4.00	D
1562442_a_at	SSBP1	single-stranded DNA binding protein 1	-2.14	D	-2.14	D	-3.48	D
1557813_at	SSBP2	Single-stranded DNA binding protein 2	-4.29	D	-2.14	D	-13.00	D
1561690_at	SSBP2	Single-stranded DNA binding protein 2	-4.92	D	-2.64	D	-8.57	D
203787_at	SSBP2	single-stranded DNA binding protein 2	-3.48	D	-2.30	D	-34.30	D
1560306_at	SSH2	Slingshot homolog 2 (Drosophila)	-2.14	D	-2.64	D	-2.30	D
230970_at	SSH2	Slingshot homolog 2 (Drosophila)	-7.46	D	-13.00	D	-4.29	D
222557_at	STMN3	stathmin-like 3	-5.66	D	-4.00	D	-8.57	D
223245_at	STRBP	spermatid perinuclear RNA binding protein	-2.83	D	-4.92	D	-5.66	D
229513_at	STRBP	Spermatid perinuclear RNA binding protein	-11.31	D	-14.93	D	-11.31	D
233251_at	STRBP	Spermatid perinuclear RNA binding protein	-73.52	D	-17.15	D	-14.93	D
233252_s_at	STRBP	spermatid perinuclear RNA binding protein	-4.29	D	-6.96	D	-5.66	D
238462_at	STS-1	Cbl-interacting protein Sts-1	-3.73	D	-2.14	D	-3.48	D
238303_at	STT3B	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	-4.29	D	-2.83	D	-2.46	D
227182_at	SUSD3	sushi domain containing 3	-8.00	D	-4.92	D	-59.71	D
202565_s_at	SVIL	supervillin	-4.00	D	-2.30	D	-13.00	D
242245_at	SYDE2	Synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	-42.22	D	-21.11	D	-111.43	D
244568_at	SYNE2	Spectrin repeat containing, nuclear envelope 2	-6.50	D	-6.06	D	-2.14	D
210612_s_at	SYNJ2	synaptojanin 2	-68.59	D	-59.71	D	-18.38	D
212828_at	SYNJ2	synaptojanin 2	-5.28	D	-7.46	D	-4.29	D
219156_at	SYNJ2BP	synaptojanin 2 binding protein	-4.00	D	-3.48	D	-4.00	D
201260_s_at	SYPL1	synaptophysin-like 1	-2.46	D	-2.46	D	-6.96	D
227884_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	-3.03	D	-2.64	D	-2.83	D
241885_at	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	-3.25	D	-4.29	D	-3.03	D
235020_at	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kDa	-6.06	D	-6.06	D	-9.19	D
229723_at	TAGAP	T-cell activation GTPase activating protein	-2.83	D	-6.50	D	-2.83	D
236450_at	TARSL2	Threonyl-tRNA synthetase-like 2	-5.28	D	-13.93	D	-2.14	D
241997_at	TAS2R14	Taste receptor, type 2, member 14	-5.66	D	-3.25	D	-2.30	D
234042_at	TAS2R45	taste receptor, type 2, member 45	-2.46	D	-2.64	D	-2.64	D
203386_at	TBC1D4	TBC1 domain family, member 4	-4.59	D	-2.64	D	-9.19	D
203387_s_at	TBC1D4	TBC1 domain family, member 4	-4.59	D	-2.46	D	-18.38	D
1556054_at	TBC1D8	TBC1 domain family, member 8 (with GRAM domain)	-2.30	D	-3.25	D	-2.83	D
336_at	TBXA2R	thromboxane A2 receptor	-10.56	D	-4.00	D	-34.30	D
226388_at	TCEA3	transcription elongation factor A (SII), 3	-6.06	D	-9.19	D	-32.00	D
204045_at	TCEAL1	transcription elongation factor A (SII)-like 1	-2.64	D	-2.30	D	-6.06	D
224819_at	TCEAL8	transcription elongation factor A (SII)-like 8	-2.00	D	-2.30	D	-2.30	D
229706_at	TCERG1	transcription elongation regulator 1	-3.25	D	-3.03	D	-3.48	D
205254_x_at	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-11.31	D	-12.13	D	-10.56	D
205255_x_at	TCF7	transcription factor 7 (T-cell specific, HMG-box)	-6.96	D	-6.06	D	-5.28	D
210875_s_at	TCF8	transcription factor 8 (represses interleukin 2 expression)	-7.46	D	-3.73	D	-8.57	D
212758_s_at	TCF8	transcription factor 8 (represses interleukin 2 expression)	-4.59	D	-29.86	D	-8.00	D
39318_at	TCL1A	T-cell leukemia/lymphoma 1A	-2.46	D	-6.96	D	-7.46	D
1558702_at	TEX10	Testis expressed sequence 10	-2.46	D	-2.14	D	-3.03	D
233692_at	THADA	Thyroid adenoma associated	-3.25	D	-5.66	D	-2.00	D
1553118_at	THEM4	thioesterase superfamily member 4	-6.50	D	-5.28	D	-9.85	D
229253_at	THEM4	thioesterase superfamily member 4	-4.29	D	-6.50	D	-10.56	D
243492_at	THEM4	Thioesterase superfamily member 4	-6.96	D	-4.92	D	-8.00	D
222931_s_at	THNSL1	threonine synthase-like 1 (bacterial)	-4.00	D	-6.06	D	-6.96	D
230651_at	THOC2	THO complex 2	-5.28	D	-4.00	D	-2.00	D
236978_at	THRAP1	Thyroid hormone receptor associated protein 1	-3.48	D	-2.83	D	-2.14	D
213135_at	TIAM1	T-cell lymphoma invasion and metastasis 1	-3.25	D	-2.14	D	-12.13	D
236524_at	TM2D1	TM2 domain containing 1	-4.59	D	-5.28	D	-2.83	D
218930_s_at	TMEM106B	transmembrane protein 106B	-2.14	D	-3.03	D	-2.83	D
222787_s_at	TMEM106B	transmembrane protein 106B	-3.03	D	-4.29	D	-2.83	D
226529_at	TMEM106B	transmembrane protein 106B	-2.00	D	-3.48	D	-3.03	D
228925_at	TMEM116	Transmembrane protein 116	-2.14	D	-2.00	D	-2.14	D
213285_at	TMEM30B	transmembrane protein 30B	-2.64	D	-3.25	D	-2.64	D
230493_at	TMEM46	transmembrane protein 46	-19.70	D	-13.93	D	-8.57	D

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
214833_at	TMEM63A	transmembrane protein 63A	-6.96	D	-8.00	D	-2.64	D
222988_s_at	TMEM9	transmembrane protein 9	-2.30	D	-2.00	D	-3.48	D
242827_x_at	TNFAIP8	Tumor necrosis factor, alpha-induced protein 8	-12.13	D	-19.70	D	-2.83	D
231775_at	TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a	-5.28	D	-3.48	D	-10.56	D
219423_x_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-19.70	D	-13.00	D	-25.99	D
210847_x_at	TNFRSF25	tumor necrosis factor receptor superfamily, member 25	-4.92	D	-32.00	D	-59.71	D
206150_at	TNFRSF7	tumor necrosis factor receptor superfamily, member 7	-14.93	D	-34.30	D	-90.51	D
207216_at	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	-4.00	D	-3.25	D	-17.15	D
235735_at	TNFSF8	Tumor necrosis factor (ligand) superfamily, member 8	-6.50	D	-6.06	D	-17.15	D
240254_at	TNIK	TRAF2 and NCK interacting kinase	-6.50	D	-8.57	D	-2.14	D
238277_at	TNKS	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-3.03	D	-8.00	D	-3.25	D
230779_at	TNRC6B	trinucleotide repeat containing 6B	-2.46	D	-3.25	D	-2.83	D
237895_at	TNRC6B	Trinucleotide repeat containing 6B	-6.50	D	-4.59	D	-2.14	D
238468_at	TNRC6B	trinucleotide repeat containing 6B	-2.83	D	-3.03	D	-2.30	D
227156_at	TNRC8	trinucleotide repeat containing 8	-8.00	D	-6.06	D	-128.00	D
201689_s_at	TPD52	tumor protein D52	-2.30	D	-5.28	D	-6.96	D
201690_s_at	TPD52	tumor protein D52	-2.14	D	-5.66	D	-4.29	D
228818_at	TPD52	Tumor protein D52	-4.92	D	-6.50	D	-8.57	D
239862_at	TPD52	Tumor protein D52	-22.63	D	-29.86	D	-3.25	D
217394_at	TRA@	T cell receptor alpha locus	-4.59	D	-2.30	D	-18.38	D
234013_at	TRA@	T cell receptor alpha locus /// Clone PSA.S.31 T-cell receptor alpha chain	-6.06	D	-3.48	D	-29.86	D
215411_s_at	TRAF3IP2	TRAF3 interacting protein 2	-4.59	D	-4.59	D	-68.59	D
234964_at	TRDV2	T cell receptor delta variable 2	-4.29	D	-2.00	D	-78.79	D
202478_at	TRIB2	tribbles homolog 2 (Drosophila)	-3.03	D	-4.00	D	-2.83	D
200990_at	TRIM28	tripartite motif-containing 28	-2.00	D	-2.00	D	-4.00	D
205802_at	TRPC1	transient receptor potential cation channel, subfamily C, member 1	-3.73	D	-4.29	D	-5.66	D
225485_at	TSGA14	testis specific, 14	-3.48	D	-2.64	D	-2.64	D
227307_at	TSPAN18	Tetraspanin 18	-4.92	D	-4.00	D	-7.46	D
241060_x_at	TSPAN5	Tetraspanin 5	-9.19	D	-16.00	D	-2.46	D
1569472_s_at	TTC3	tetratricopeptide repeat domain 3	-2.64	D	-2.14	D	-8.00	D
213174_at	TTC9	tetratricopeptide repeat domain 9	-9.85	D	-27.86	D	-48.50	D
226181_at	TUBE1	tubulin, epsilon 1	-2.46	D	-2.64	D	-3.03	D
206828_at	TXK	TXK tyrosine kinase	-19.70	D	-18.38	D	-32.00	D
220418_at	UBASH3A	ubiquitin associated and SH3 domain containing, A	-4.92	D	-8.57	D	-4.29	D
240139_at	UBE2D2	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	-4.00	D	-2.14	D	-3.73	D
215392_at	USP3	Ubiquitin specific peptidase 3	-5.66	D	-2.30	D	-3.25	D
238057_at	USP45	ubiquitin specific peptidase 45	-2.00	D	-3.25	D	-2.64	D
237465_at	USP53	Ubiquitin specific peptidase 53	-2.14	D	-3.73	D	-68.59	D
216775_at	USP53	ubiquitin specific peptidase 53	-3.48	D	-48.50	D	-4.92	D
231817_at	USP53	ubiquitin specific peptidase 53	-3.73	D	-11.31	D	-19.70	D
219675_s_at	UXS1	UDP-glucuronate decarboxylase 1	-5.28	D	-3.25	D	-6.50	D
225583_at	UXS1	UDP-glucuronate decarboxylase 1	-5.66	D	-3.25	D	-9.19	D
205019_s_at	VIPR1	vasoactive intestinal peptide receptor 1	-6.50	D	-3.48	D	-39.40	D
234370_at	VSIG1	V-set and immunoglobulin domain containing 1	-13.93	D	-12.13	D	-55.72	D
243764_at	VSIG1	V-set and immunoglobulin domain containing 1	-8.57	D	-19.70	D	-10.56	D
231495_at	VTI1A	Vesicle transport through interaction with t-SNAREs homolog 1A	-4.92	D	-5.66	D	-2.14	D
233323_at	VTI1A	Vesicle transport through interaction with t-SNAREs homolog 1A	-12.13	D	-3.25	D	-2.00	D
220917_s_at	WDR19	WD repeat domain 19	-14.93	D	-9.85	D	-4.59	D
214662_at	WDR43	WD repeat domain 43	-2.14	D	-2.83	D	-3.03	D
237208_at	WDR61	WD repeat domain 61	-2.64	D	-4.59	D	-3.73	D
1557261_at	WHDC1L1	WAS protein homology region 2 domain containing 1-like 1	-4.92	D	-4.29	D	-16.00	D
213908_at	WHDC1L1	WAS protein homology region 2 domain containing 1-like 1	-3.25	D	-3.73	D	-36.76	D
1556595_at	WWOX	WW domain containing oxidoreductase	-5.66	D	-5.66	D	-4.59	D
1563460_at	WWOX	WW domain containing oxidoreductase	-34.30	D	-14.93	D	-25.99	D
237035_at	WWOX	WW domain containing oxidoreductase	-48.50	D	-5.28	D	-4.00	D
242099_at	WWOX	WW domain containing oxidoreductase	-6.50	D	-2.46	D	-6.06	D
242801_at	WWOX	WW domain containing oxidoreductase	-18.38	D	-4.00	D	-14.93	D
214567_s_at	XCL1 / XCL2	chemokine (C motif) ligand 1 / 2	-9.19	D	-2.46	D	-9.19	D
206366_x_at	XCL2	chemokine (C motif) ligand 2	-9.85	D	-2.83	D	-6.96	D
1557065_at	YLPM1	YLP motif containing 1	-4.59	D	-3.25	D	-2.46	D
243310_at	YLPM1	YLP motif containing 1	-13.00	D	-14.93	D	-3.25	D
205883_at	ZBTB16	zinc finger and BTB domain containing 16	-3.48	D	-2.83	D	-8.57	D

AFFYMETRIX PROBE SET ID	GENE SYMBOL	GENE TITLE	FC#22	I/D	FC#2	I/D	FC#26	I/D
222357_at	ZBTB20	zinc finger and BTB domain containing 20	-8.00	D	-6.06	D	-2.83	D
232929_at	ZBTB20	Zinc finger and BTB domain containing 20	-5.28	D	-8.00	D	-2.83	D
237803_x_at	ZBTB20	Zinc finger and BTB domain containing 20	-6.06	D	-5.28	D	-2.30	D
239955_at	ZBTB20	Zinc finger and BTB domain containing 20	-6.06	D	-6.50	D	-2.14	D
240216_at	ZBTB20	Zinc finger and BTB domain containing 20	-6.06	D	-17.15	D	-2.00	D
1559263_s_at	ZC3H12D	zinc finger CCCH-type containing 12D	-2.64	D	-2.14	D	-2.14	D
238875_at	ZC3H6	Zinc finger CCCH-type containing 6	-4.92	D	-5.66	D	-3.03	D
1565913_at	ZC3HAV1	Zinc finger CCCH-type, antiviral 1	-4.00	D	-3.48	D	-3.25	D
230713_at	ZCCHC11	Zinc finger, CCHC domain containing 11	-4.92	D	-3.48	D	-2.14	D
212655_at	ZCCHC14	zinc finger, CCHC domain containing 14	-5.28	D	-6.06	D	-3.25	D
1556543_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-6.06	D	-9.85	D	-2.14	D
230332_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-9.19	D	-7.46	D	-4.00	D
234032_at	ZCCHC7	Zinc finger, CCHC domain containing 7	-6.96	D	-6.50	D	-2.83	D
242562_at	ZCSL3	Zinc finger, CSL-type containing 3	-2.30	D	-4.00	D	-2.64	D
243528_at	ZDHHC2	Zinc finger, DHHC-type containing 2	-4.00	D	-3.25	D	-3.25	D
1558700_s_at	ZFP260	zinc finger protein 260	-2.14	D	-6.50	D	-2.00	D
235728_at	ZFP3	zinc finger protein 3 homolog (mouse)	-3.48	D	-3.73	D	-3.48	D
238970_at	ZFR	Zinc finger RNA binding protein	-3.25	D	-2.46	D	-2.83	D
226344_at	ZMAT1	zinc finger, matrin type 1	-4.59	D	-2.46	D	-5.66	D
1552634_a_at	ZNF101	zinc finger protein 101	-2.64	D	-5.66	D	-3.48	D
206314_at	ZNF167	zinc finger protein 167	-2.14	D	-3.73	D	-2.30	D
210282_at	ZNF198	zinc finger protein 198	-2.83	D	-2.30	D	-3.73	D
214823_at	ZNF204	zinc finger protein 204	-6.06	D	-36.76	D	-25.99	D
229765_at	ZNF207	Zinc finger protein 207	-2.46	D	-3.03	D	-2.14	D
236075_s_at	ZNF232	Zinc finger protein 232	-2.14	D	-2.83	D	-2.64	D
212774_at	ZNF238	zinc finger protein 238	-3.73	D	-2.30	D	-18.38	D
236659_x_at	ZNF277	Zinc finger protein 277	-2.64	D	-2.30	D	-2.64	D
228392_at	ZNF302	zinc finger protein 302	-2.64	D	-2.46	D	-2.14	D
228393_s_at	ZNF302	zinc finger protein 302	-2.83	D	-3.48	D	-2.30	D
228208_x_at	ZNF354C	Zinc finger protein 354C	-4.59	D	-2.14	D	-32.00	D
1557260_a_at	ZNF382	zinc finger protein 382	-2.83	D	-9.85	D	-194.01	D
1561687_a_at	ZNF382	zinc finger protein 382	-7.46	D	-13.00	D	-29.86	D
218149_s_at	ZNF395	zinc finger protein 395	-6.06	D	-4.00	D	-10.56	D
221123_x_at	ZNF395	zinc finger protein 395	-25.99	D	-8.57	D	-11.31	D
236474_at	ZNF395	Zinc finger protein 395	-7.46	D	-4.92	D	-8.00	D
239619_at	ZNF395	Zinc finger protein 395	-6.96	D	-5.28	D	-9.19	D
223216_x_at	ZNF395	Zinc finger protein 395	-25.99	D	-22.63	D	-36.76	D
232693_s_at	ZNF395	Zinc finger protein 395	-32.00	D	-21.11	D	-45.25	D
233239_at	ZNF407	Zinc finger protein 407	-4.00	D	-2.64	D	-4.92	D
218312_s_at	ZNF447	zinc finger protein 447	-6.96	D	-6.06	D	-34.30	D
215307_at	ZNF529	Zinc finger protein 529	-3.03	D	-3.25	D	-12.13	D
235121_at	ZNF542	zinc finger protein 542	-3.48	D	-9.85	D	-2.46	D
1559401_a_at	ZNF609	Zinc finger protein 609	-9.85	D	-11.31	D	-2.83	D
1566166_at	ZNF650	Zinc finger protein 650	-4.59	D	-3.48	D	-2.14	D
231950_at	ZNF658	zinc finger protein 658	-3.03	D	-17.15	D	-2.30	D
1560562_a_at	ZNF677	Zinc finger protein 677	-19.70	D	-36.76	D	-27.86	D
228974_at	ZNF677	Zinc finger protein 677	-6.96	D	-17.15	D	-6.96	D
1557270_at	ZNF69	Zinc finger protein 69	-2.83	D	-4.59	D	-2.30	D