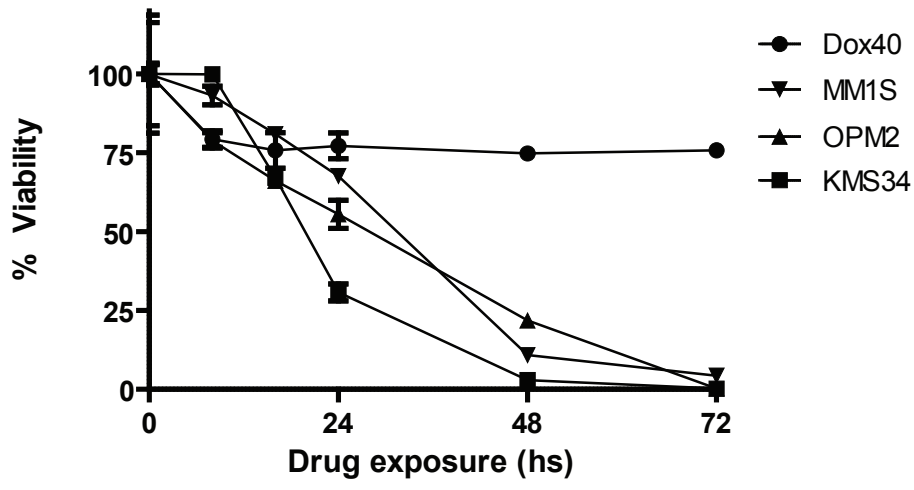
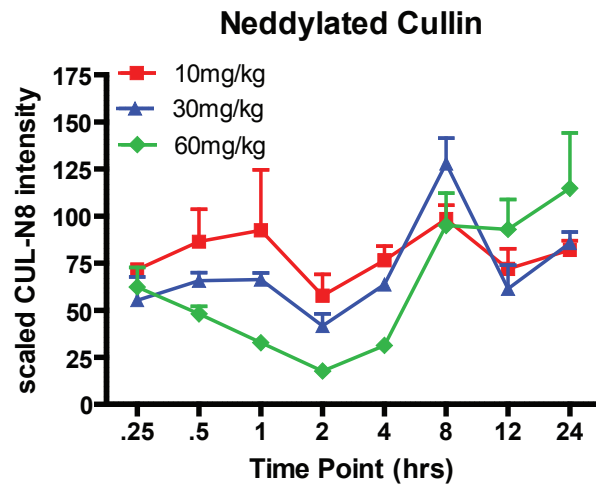


Supplemental Figure 1

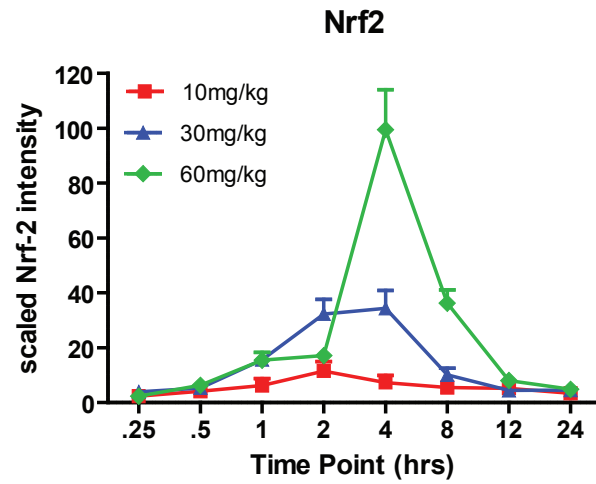


Supplemental Figure 2

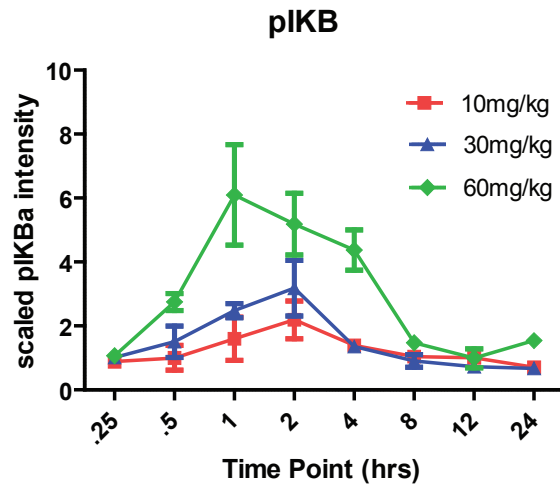
A



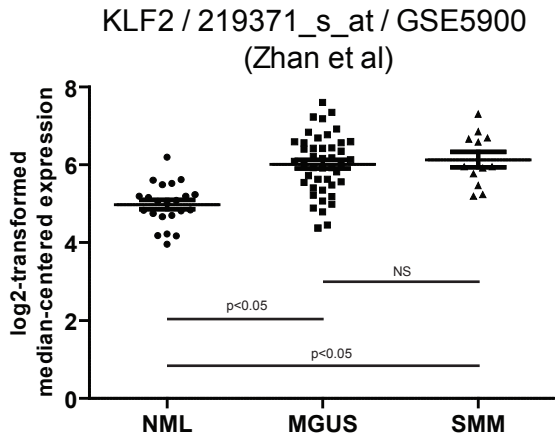
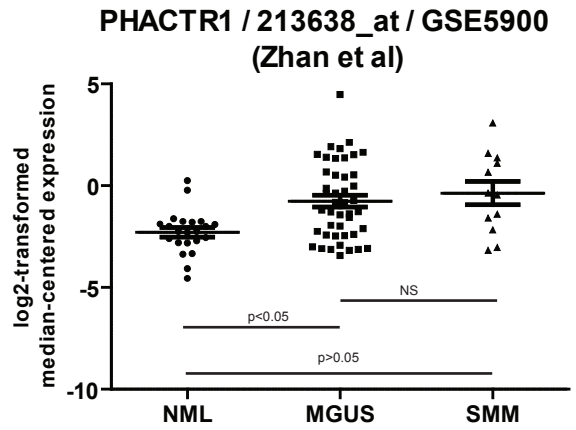
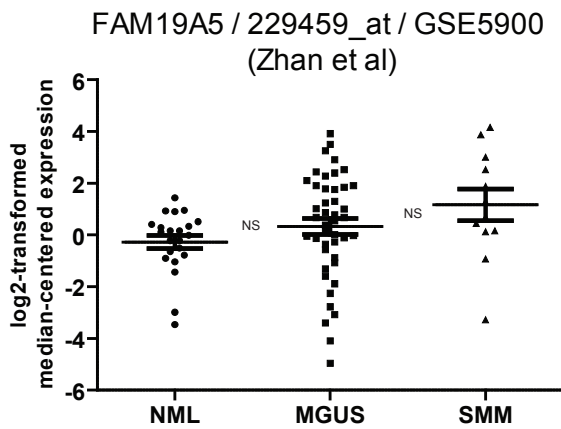
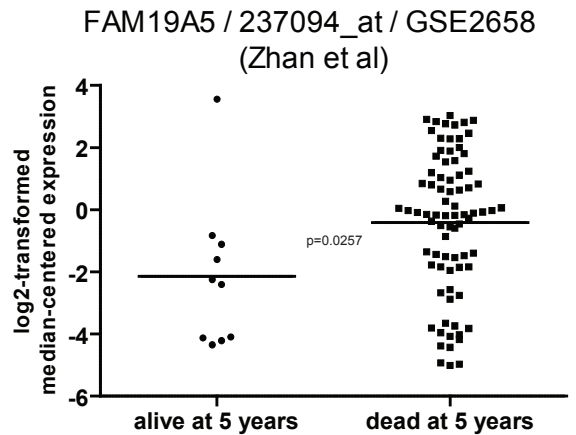
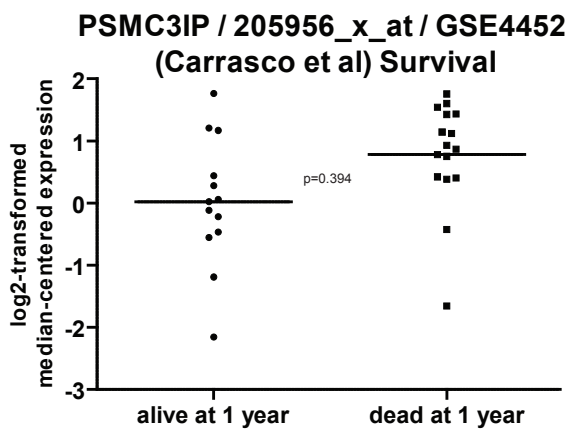
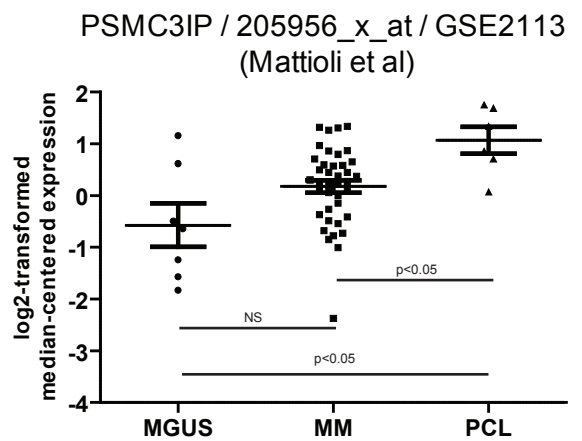
B



C



Supplemental Figure 3

A**B****C****D****E****F**

Supplemental Figure Legends

Supplemental Figure 1. Cell death commitment assays of MLN4924 treatment. Dox40, MM.1S, OPM2 and KMS34 cells were exposed to MLN4924 (500nM) for up to 72hrs, followed by drug washout and incubation in drug-free medium for an additional 72hrs. MLN4924 treatment for 48hrs resulted in commitment to death in KMS34, OPM2 and MM.1S cells, suggesting that molecular events initiating cell death can occur as early as <48hrs of MLN4924 treatment. Dox40 cells remained insensitive to MLN4924 killing when exposed up to 72hrs.

Supplemental Figure 2. Tumor levels of neddylated cullin, Nrf2 and pIKB in mice treated with MLN4924. Mice injected subcutaneously with 2×10^7 RPMI8226/S cell were treated with a single dose of 10, 30 or 60 mg/kg MLN4924. Levels of neddylated cullins (A), Nrf2 (B) and pIKB (C) were measured in tumor samples at time points up to 24hrs (N=3 per group).

Supplemental Figure 3. Biological and clinical relevance of distinct transcripts down-regulated by MLN4924. Gene expression profiling was performed on treated MM1S cells (250nM) at 8, 16 and 24hrs. In publically available GEO datasets, we evaluated the association of transcripts suppressed by MLN4924 with clinical outcome and expression in various stages of plasma cell dyscrasias. Panels A-F show examples of these associations, namely the higher level expression of the transcripts KLF2 (A), PHACTR1 (B), or FAM1985 (C) in smoldering myeloma or MGUS compared to normal plasma cells; the higher expression of FAM1985 in myeloma patients who have died within 5 years of study entry vs. those alive at 5 years (D); the higher level of expression of PSMCI3P in patients who have died within 1 year of diagnosis vs. alive after 1 year of diagnosis (E); as well as higher level expression of PSMCI3P in PCL vs. MM vs. MGUS (F).

Supplemental table: gene expression profiling changes triggered by MLN4924 treatment

probe set	gene	MM1S MLN4924 8H	MM1S MLN4924 16H	MM1S MLN4924 24H
1053_at	RFC2: replication factor C (activator 1) 2, 40kDa	-1.18	-1.78	-2.16
1405_i_at	CCL5: chemokine (C-C motif) ligand 5	-1.41	-2.01	-1.85
1552409_a_at	ODF4: outer dense fiber of sperm tails 4	2.08	2.07	2.07
1553856_s_at	P2RY10: purinergic receptor P2Y, G-protein coupled, 10	1.9	2.6	2.76
1553989_a_at	ATP6V1C2: ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C2	-1.57	-1.82	-1.94
1554343_a_at	BRDG1: BCR downstream signaling 1	-1.07	1.75	1.69
1554438_at	KIAA1217: KIAA1217	-1.22	1.88	1.67
1554572_a_at	SUV39H2: suppressor of variegation 3-9 homolog 2 (Drosophila)	-1.11	-1.53	-1.56
1554696_s_at	TYMS: thymidylate synthetase	-1.05	-1.51	-1.73
1555083_at	MGC34774: ribosomal protein L13A-like	1.31	2.07	1.85
1555561_a_at	UGCGL2: UDP-glucose ceramide glucosyltransferase-like 2	-1.4	-1.97	-1.73
1555618_s_at	SAE1: SUMO-1 activating enzyme subunit 1	-1.06	-1.56	-1.51
1555759_a_at	CCL5: chemokine (C-C motif) ligand 5	-1.39	-1.64	-1.69
1555772_a_at	CDC25A: cell division cycle 25A	-1.25	-2.15	-2.14
1555851_s_at	SEPW1: selenoprotein W, 1	-1.17	-1.52	-1.56
1556095_at	UNC13C: unc-13 homolog C (C. elegans)	-1.73	-1.77	-1.91
1556096_s_at	UNC13C: unc-13 homolog C (C. elegans)	-1.6	-1.51	-1.69
1556121_at	NAP1L1: Nucleosome assembly protein 1-like 1	-1.15	-1.72	-1.66
1556347_at	RP11-19J3.3: Hypothetical protein MGC88047	1.09	-2.1	-1.55
1556643_at	LOC93343: Hypothetical protein BC011840	-1.09	1.59	1.59
1556821_x_at	DLEU2: deleted in lymphocytic leukemia, 2	-1.23	-2.27	-1.78
1557128_at	FAM111B: family with sequence similarity 111, member B	-1.2	-2.25	-1.76
1557129_a_at	FAM111B: family with sequence similarity 111, member B	-1.11	-2.46	-1.71
1557267_s_at	LOC284952: hypothetical protein LOC284952	-1.51	-2.44	-1.63
1557383_a_at	CDNA FLJ38112 fis, clone D3OST2002272	1.18	1.92	2.26
1558292_s_at	PIGW: phosphatidylinositol glycan anchor biosynthesis, class W	-1.3	-1.85	-1.89
1559584_a_at	C16orf54 /// LOC653141: chromosome 16 open reading frame 54 /// similar to chromosome 16 open reading frame 54	-1.26	1.72	1.84
1559675_at	gb:BC033513.1 /DB_XREF=gi:23273194 /TID=Hs2.208347.1 /CNT=5 /FEA=mRNA /TIER=ConsEnd /STK=0 /UG=Hs.208347 /UG_TITLE=Homo sapiens, clone IMAGE:5172161, mRNA, partial cds /DEF=Homo sapiens, clone IMAGE:5172161, mRNA, partial cds.	4.46	6.11	3.55
1561690_at	SSBP2: Single-stranded DNA binding protein 2	-1.64	-2.21	-1.24
1563209_a_at	C20orf133: chromosome 20 open reading frame 133	1.06	1.93	2.56
1564064_a_at	ATP11B: ATPase, Class VI, type 11B	1.12	1.54	1.54
1566989_at	ARID1B: AT rich interactive domain 1B (SWI1-like)	1.31	1.68	1.83

1566990_x_at	ARID1B: AT rich interactive domain 1B (SWI1-like)	1.36	1.6	1.81
1567081_x_at	CLN6: ceroid-lipofuscinosis, neuronal 6, late infantile, variant	-1.12	-1.58	-1.53
1568592_at	RNF36: ring finger protein 36	-1.01	1.82	1.64
1569345_at	P2RX1: Purinergic receptor P2X, ligand-gated ion channel, 1	1.15	1.65	1.76
1569346_a_at	P2RX1: Purinergic receptor P2X, ligand-gated ion channel, 1	-1.05	1.64	1.82
1569969_a_at	UNC13C: unc-13 homolog C (C. elegans)	-1.64	-1.76	-1.93
200664_s_at	DNAJB1: DnaJ (Hsp40) homolog, subfamily B, member 1	1.18	-1.8	-1.6
200666_s_at	DNAJB1: DnaJ (Hsp40) homolog, subfamily B, member 1	1.19	-1.78	-1.66
200715_x_at	RPL13A: ribosomal protein L13a	1.22	1.73	1.82
200748_s_at	FTH1: ferritin, heavy polypeptide 1	1.53	1.74	1.4
200762_at	DPYSL2: dihydropyrimidinase-like 2	-1.41	-1.69	-1.68
200799_at	HSPA1A: heat shock 70kDa protein 1A	1.58	-1.89	-2.05
200800_s_at	HSPA1A /// HSPA1B: heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	1.51	-2.4	-1.58
200862_at	DHCR24: 24-dehydrocholesterol reductase	1.43	-1.52	-1.72
200878_at	EPAS1: endothelial PAS domain protein 1	1.78	2.3	2.13
200920_s_at	BTG1: B-cell translocation gene 1, anti-proliferative	-1.09	1.53	1.84
200951_s_at	CCND2: cyclin D2	-1.78	-1.74	-1.72
200952_s_at	CCND2: cyclin D2	-2.13	-1.73	-1.73
200953_s_at	CCND2: cyclin D2	-1.58	-1.59	-1.6
201026_at	EIF5B: eukaryotic translation initiation factor 5B	3.66	1.9	3.15
201266_at	TXNRD1: thioredoxin reductase 1	2.77	2.12	2.06
201324_at	EMP1: epithelial membrane protein 1	1.4	2.08	2.23
201384_s_at	NBR1 /// LOC653347: neighbor of BRCA1 gene 1 /// similar to neighbor of BRCA1 gene 1	-1.02	1.86	1.77
201412_at	LRP10: low density lipoprotein receptor-related protein 10	1.18	1.73	1.9
201417_at	SOX4: SRY (sex determining region Y)-box 4	-1.63	-1.49	-1.65
201427_s_at	SEPP1: selenoprotein P, plasma, 1	1.03	2.48	2.29
201467_s_at	NQO1: NAD(P)H dehydrogenase, quinone 1	3.05	3.57	3.07
201468_s_at	NQO1: NAD(P)H dehydrogenase, quinone 1	4.14	3.37	2.95
201494_at	PRCP: prolylcarboxypeptidase (angiotensinase C)	1.08	1.54	1.61
201555_at	MCM3: MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	-1.09	-1.73	-2
201579_at	FAT: FAT tumor suppressor homolog 1 (Drosophila)	-1.06	1.61	1.8
201667_at	GJA1: gap junction protein, alpha 1, 43kDa (connexin 43)	-1.15	-1.54	-1.75
201755_at	MCM5: MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	-1.14	-2.14	-2.34
201818_at	AYTL2: acyltransferase like 2	-1.28	-1.56	-1.69

201862_s_at	LRRFIP1: leucine rich repeat (in FLII) interacting protein 1	-1.55	-1.58	-1.36
201930_at	MCM6: MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>)	-1.18	-1.82	-2.06
201939_at	PLK2: polo-like kinase 2 (<i>Drosophila</i>)	1.04	1.93	1.87
201969_at	NASP: nuclear autoantigenic sperm protein (histone-binding)	-1.18	-1.93	-2.02
201970_s_at	NASP: nuclear autoantigenic sperm protein (histone-binding)	-1.25	-1.87	-1.95
202085_at	TJP2: tight junction protein 2 (zona occludens 2)	-2.05	-2.4	-2.56
202105_at	IGBP1: immunoglobulin (CD79A) binding protein 1	1.11	1.65	1.78
202107_s_at	MCM2: MCM2 minichromosome maintenance deficient 2, mitotin (<i>S. cerevisiae</i>)	-1.12	-1.98	-2.08
202119_s_at	CPNE3: copine III	1.15	1.59	1.59
202188_at	NUP93: nucleoporin 93kDa	-1.16	-1.66	-1.51
202241_at	TRIB1: tribbles homolog 1 (<i>Drosophila</i>)	1.11	1.71	1.69
202284_s_at	CDKN1A: cyclin-dependent kinase inhibitor 1A (p21, Cip1)	-1.21	-1.59	-2.07
202308_at	SREBF1: sterol regulatory element binding transcription factor 1	-1.24	-1.53	-1.52
202336_s_at	PAM: peptidylglycine alpha-amidating monooxygenase	1.25	1.64	1.65
202364_at	MXI1: MAX interactor 1 /// MAX interactor 1	1.47	1.75	1.59
202412_s_at	USP1: ubiquitin specific peptidase 1	-1.31	-1.72	-1.62
202430_s_at	PLSCR1: phospholipid scramblase 1	-1.42	-1.51	-1.54
202478_at	TRIB2: tribbles homolog 2 (<i>Drosophila</i>)	1.26	1.67	1.51
202479_s_at	TRIB2: tribbles homolog 2 (<i>Drosophila</i>)	1.2	1.91	1.62
202533_s_at	DHFR /// LOC643509 /// LOC653874: dihydrofolate reductase /// similar to Dihydrofolate reductase /// similar to Dihydrofolate reductase	-1.05	-1.72	-1.84
202551_s_at	CRIM1: cysteine rich transmembrane BMP regulator 1 (chordin-like)	1.45	1.66	1.6
202581_at	HSPA1B: heat shock 70kDa protein 1B	1.26	-2.23	-1.51
202636_at	RNF103: ring finger protein 103	1.11	1.6	1.6
202730_s_at	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)	1.21	2.12	2.02
202731_at	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)	1.1	2.03	2.01
202769_at	CCNG2: cyclin G2	1.18	2.22	2.17
202770_s_at	CCNG2: cyclin G2	1.15	2.2	2.17
202869_at	OAS1: 2',5'-oligoadenylate synthetase 1, 40/46kDa	-1.03	1.67	2.01
202903_at	LSM5: LSM5 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	-1.16	-1.68	-1.77
202904_s_at	LSM5: LSM5 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	-1.14	-1.55	-1.87
202971_s_at	DYRK2: dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-1.48	-1.73	-2.1

202988_s_at	RGS1: regulator of G-protein signalling 1	-1.11	2.63	3.43
203209_at	RFC5: replication factor C (activator 1) 5, 36.5kDa	-1.09	-1.64	-1.92
203226_s_at	TSPAN31: tetraspanin 31	-1.06	1.59	1.8
203286_at	RNF44: ring finger protein 44	1.65	2.22	2
203394_s_at	HES1: hairy and enhancer of split 1, (Drosophila)	-2.4	-2.07	-2.43
203395_s_at	HES1: hairy and enhancer of split 1, (Drosophila)	-3.39	-2.29	-2.35
203404_at	ARMCX2: armadillo repeat containing, X-linked 2	-1.06	1.76	1.52
203408_s_at	SATB1: special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating DNA's)	-1.39	1.95	2.26
203476_at	TPBG: trophoblast glycoprotein	1.34	2.74	2.73
203658_at	SLC25A20: solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-1.02	1.55	1.63
203685_at	BCL2: B-cell CLL/lymphoma 2	-1.06	1.54	1.57
203705_s_at	FZD7: frizzled homolog 7 (Drosophila)	1.31	2.23	2.57
203706_s_at	FZD7: frizzled homolog 7 (Drosophila)	1.62	3.17	3.19
203708_at	PDE4B: phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	1.31	2.23	2.77
203729_at	EMP3: epithelial membrane protein 3	1.06	1.75	1.74
203733_at	DEXI: dexamethasone-induced transcript	1.2	1.73	1.58
203810_at	DNAJB4: DnaJ (Hsp40) homolog, subfamily B, member 4	1.71	1.29	1.57
203836_s_at	MAP3K5: mitogen-activated protein kinase kinase kinase 5	-2.04	-1.71	-1.59
203837_at	MAP3K5: mitogen-activated protein kinase kinase kinase 5	-2.02	-1.95	-1.52
203853_s_at	GAB2: GRB2-associated binding protein 2	1.24	1.73	1.54
203904_x_at	CD82: CD82 molecule	-1.55	-1.48	-1.54
203917_at	CXADR: coxsackie virus and adenovirus receptor	-1.22	-1.67	-1.78
203925_at	GCLM: glutamate-cysteine ligase, modifier subunit	2.84	1.59	1.33
203935_at	ACVR1: activin A receptor, type I	1.16	1.56	1.64
203939_at	NT5E: 5'-nucleotidase, ecto (CD73)	1.16	2.49	2.86
203964_at	NMI: N-myc (and STAT) interactor	-2.14	-1.68	-1.39
203967_at	CDC6: CDC6 cell division cycle 6 homolog (S. cerevisiae)	-1.1	-1.87	-1.99
203968_s_at	CDC6: CDC6 cell division cycle 6 homolog (S. cerevisiae)	-1.2	-2.26	-2.12
204033_at	TRIP13: thyroid hormone receptor interactor 13	-1.26	-1.66	-1.73
204045_at	TCEAL1: transcription elongation factor A (SII)-like 1	1.2	1.68	1.85
204059_s_at	ME1: malic enzyme 1, NADP(+)-dependent, cytosolic	1.61	1.48	1.6
204084_s_at	CLN5: ceroid-lipofuscinosis, neuronal 5	1.29	1.64	1.63
204103_at	CCL4: chemokine (C-C motif) ligand 4	-1.58	1.34	1.9
204126_s_at	CDC45L: CDC45 cell division cycle 45-like (S. cerevisiae)	-1.02	-1.62	-2
204127_at	RFC3: replication factor C (activator 1) 3, 38kDa	-1.07	-1.63	-1.74

204128_s_at	RFC3: replication factor C (activator 1) 3, 38kDa	-1.14	-1.76	-2.03
204142_at	ENOSF1: enolase superfamily member 1	-1.45	-1.88	-1.76
204143_s_at	ENOSF1: enolase superfamily member 1	-1.36	-1.71	-1.71
204146_at	RAD51AP1: RAD51 associated protein 1	-1.1	-1.78	-1.65
204151_x_at	AKR1C1: aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.7	2.76	2.67
204195_s_at	PKNOX1: PBX/knotted 1 homeobox 1	-1.24	-1.51	-1.55
204200_s_at	PDGFB: platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog)	1.2	1.73	1.68
204285_s_at	PMAIP1: phorbol-12-myristate-13-acetate-induced protein 1	-1.35	-2	-2.34
204286_s_at	PMAIP1: phorbol-12-myristate-13-acetate-induced protein 1	-1.29	-2.12	-2.26
204418_x_at	GSTM2: glutathione S-transferase M2 (muscle)	1.28	1.7	1.71
204432_at	SOX12: SRY (sex determining region Y)-box 12	1.68	1.74	1.65
204531_s_at	BRCA1: breast cancer 1, early onset	-1.1	-1.7	-1.74
204550_x_at	GSTM1: glutathione S-transferase M1	1.29	1.72	1.56
204655_at	CCL5: chemokine (C-C motif) ligand 5 /// chemokine (C-C motif) ligand 5	-1.42	-2.14	-1.98
204686_at	IRS1: insulin receptor substrate 1	1.1	1.51	1.67
204695_at	CDC25A: cell division cycle 25A	-1.01	-1.6	-1.72
204698_at	ISG20: interferon stimulated exonuclease gene 20kDa	-1.53	-1.65	-1.17
204734_at	KRT15: keratin 15	1.74	1.78	2.08
204768_s_at	FEN1: flap structure-specific endonuclease 1	-1.08	-1.56	-1.89
204775_at	CHAF1B: chromatin assembly factor 1, subunit B (p60)	-1.11	-1.54	-1.79
204798_at	MYB: v-myb myeloblastosis viral oncogene homolog (avian)	1.03	-1.71	-1.79
204805_s_at	H1FX: H1 histone family, member X	-2.27	-1.54	-1.61
204820_s_at	BTN3A3 /// BTN3A2: butyrophilin, subfamily 3, member A3 /// butyrophilin, subfamily 3, member A2	-1.02	1.57	1.52
204840_s_at	EEA1: early endosome antigen 1, 162kD	-1.41	-2.66	-1.6
204894_s_at	AOC3: amine oxidase, copper containing 3 (vascular adhesion protein 1)	1.03	1.74	1.52
204976_s_at	AMMECR1: Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	-1.29	-1.69	-1.55
204979_s_at	SH3BGR: SH3 domain binding glutamic acid-rich protein	1.04	1.58	1.66
204992_s_at	PFN2: profilin 2	-1.44	-1.62	-1.77
205024_s_at	RAD51: RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	-1.2	-2.08	-2.39
205073_at	CYP2J2: cytochrome P450, family 2, subfamily J, polypeptide 2	1.22	1.62	1.65
205085_at	ORC1L: origin recognition complex, subunit 1-like (yeast)	1.06	-1.67	-1.85

205235_s_at	MPHOSPH1: M-phase phosphoprotein 1	-1.19	-3.05	-1.63
205257_s_at	AMPH: amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen)	-1.22	-1.81	-1.64
205281_s_at	PIGA: phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria) /// phosphatidylinositol glycan anchor biosynthesis, class A (paroxysmal nocturnal hemoglobinuria)	-1.13	-1.52	-1.66
205296_at	gb:AL365505 /DB_XREF=gi:11558572 /FEA=FLmRNA /CNT=36 /TID=Hs.87.0 /TIER=ConsEnd /STK=4 /UG=Hs.87 /LL=5933 /UG_GENE=RBL1 /UG_TITLE=retinoblastoma-like 1 (p107) /DEF=Human DNA sequence from clone RP11-382A12 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the 5 part of the gene for a 72.1 KDa protein (DKFZP564A032, SBB188) similar to mouse IFN-gamma induced MG11 and the 3 part of the RBL... /FL=gb:L14812.1 gb:NM_002895.1	-1.17	-1.72	-1.57
205352_at	SERPINI1: serpin peptidase inhibitor, clade I (neuroserpin), member 1	1	1.95	2.44
205393_s_at	CHEK1: CHK1 checkpoint homolog (S. pombe)	1.01	-1.66	-1.86
205436_s_at	H2AFX: H2A histone family, member X	-1.28	-1.57	-1.73
205519_at	WDR76: WD repeat domain 76	1.04	-1.68	-1.91
205544_s_at	CR2: complement component (3d/Epstein Barr virus) receptor 2	-1.26	-1.76	-1.9
205552_s_at	OAS1: 2',5'-oligoadenylate synthetase 1, 40/46kDa	-1.18	1.94	2.37
205632_s_at	PIP5K1B: phosphatidylinositol-4-phosphate 5-kinase, type I, beta	1.14	1.51	1.54
205677_s_at	DLEU1 /// SPANXC: deleted in lymphocytic leukemia, 1 /// SPANX family, member C	1.55	1.54	1.35
205733_at	BLM: Bloom syndrome	-1.02	-1.74	-1.74
205770_at	GSR: glutathione reductase	2.89	1.76	1.73
205909_at	POLE2: polymerase (DNA directed), epsilon 2 (p59 subunit)	-1.16	-1.84	-2
205943_at	TDO2: tryptophan 2,3-dioxygenase	1.18	1.77	2.22
205956_x_at	PSMC3IP: PSMC3 interacting protein	-1.38	-1.76	-1.84
206003_at	CEP135: centrosomal protein 135kDa	-1.3	-1.8	-1.58
206118_at	STAT4: signal transducer and activator of transcription 4	-1.01	1.94	1.85
206121_at	AMPD1: adenosine monophosphate deaminase 1 (isoform M)	-1.09	2.17	2.63
206185_at	CRYBB1: crystallin, beta B1	-1.37	-2.98	-3.83
206301_at	TEC: tec protein tyrosine kinase	1.2	1.51	1.52
206316_s_at	KNTC1: kinetochore associated 1	-1.15	-1.59	-1.51
206369_s_at	PIK3CG: phosphoinositide-3-kinase, catalytic, gamma polypeptide	1.24	1.98	2.24
206370_at	PIK3CG: phosphoinositide-3-kinase, catalytic, gamma polypeptide	1.21	2.01	2.27

206385_s_at	ANK3: ankyrin 3, node of Ranvier (ankyrin G)	-2.18	-2.25	-1.85
206414_s_at	DDEF2: development and differentiation enhancing factor 2	-1.53	-1.6	-1.63
206513_at	AIM2: absent in melanoma 2	-1.05	1.88	1.84
206698_at	XK: X-linked Kx blood group (McLeod syndrome)	-1.5	-1.6	-1.62
206828_at	TXK: TXK tyrosine kinase	-1.02	1.56	1.92
206949_s_at	RUSC1: RUN and SH3 domain containing 1	1.56	1.6	1.28
206978_at	CCR2: chemokine (C-C motif) receptor 2 /// chemokine (C-C motif) receptor 2	-1.58	1.75	2.26
207332_s_at	TFRC: transferrin receptor (p90, CD71)	1.66	1.42	1.52
207485_x_at	BTN3A1: butyrophilin, subfamily 3, member A1	1.04	1.51	1.58
207543_s_at	P4HA1: procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide I	1.19	1.67	1.69
207655_s_at	BLNK: B-cell linker	1.13	1.58	1.68
207681_at	CXCR3: chemokine (C-X-C motif) receptor 3	1.52	2.66	3.18
207734_at	LAX1: lymphocyte transmembrane adaptor 1	1.25	1.6	1.66
207826_s_at	ID3: inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	-1.55	-1.8	-2.14
208319_s_at	RBM3: RNA binding motif (RNP1, RRM) protein 3	-1.39	-2.52	-1.88
208373_s_at	P2RY6: pyrimidinergic receptor P2Y, G-protein coupled, 6	1.3	1.71	2.12
208699_x_at	TKT: transketolase (Wernicke-Korsakoff syndrome)	1.91	1.77	1.53
208700_s_at	TKT: transketolase (Wernicke-Korsakoff syndrome)	2	1.86	1.59
208763_s_at	TSC22D3: TSC22 domain family, member 3	-1.08	1.51	1.52
208791_at	CLU: clusterin	1.14	1.58	1.71
208792_s_at	CLU: clusterin	1.1	1.62	1.73
208795_s_at	MCM7: MCM7 minichromosome maintenance deficient 7 (<i>S. cerevisiae</i>)	-1.08	-1.69	-1.95
208891_at	DUSP6: dual specificity phosphatase 6	1.18	1.55	1.54
208893_s_at	DUSP6: dual specificity phosphatase 6	1.15	1.58	1.54
208955_at	DUT: dUTP pyrophosphatase	-1.08	-1.91	-2.42
209034_at	PNRC1: proline-rich nuclear receptor coactivator 1	1.13	1.78	1.81
209043_at	PAPSS1: 3'-phosphoadenosine 5'-phosphosulfate synthase 1	1.33	1.62	1.59
209102_s_at	HBP1: HMG-box transcription factor 1	1.19	1.99	2.28
209160_at	AKR1C3: aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	3.2	6.14	6.17
209184_s_at	IRS2: insulin receptor substrate 2	1.3	1.54	1.53
209276_s_at	GLRX: glutaredoxin (thioltransferase)	1.32	1.52	1.75
209360_s_at	RUNX1: runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	1.81	1.85	1.54

209398_at	HIST1H1C: histone 1, H1c	-1.2	-1.88	-1.77
209479_at	CCDC28A: coiled-coil domain containing 28A	1.13	1.66	1.54
209530_at	CACNB3: calcium channel, voltage-dependent, beta 3 subunit	1.13	1.79	1.73
209538_at	ZNF32: zinc finger protein 32	1.26	1.73	1.76
209541_at	IGF1: insulin-like growth factor 1 (somatomedin C)	-1.54	-1.54	1.07
209636_at	NFKB2: nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	-1.7	-1.52	-1.45
209699_x_at	AKR1C2: aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	2.17	3.83	3.79
209708_at	MOXD1: monooxygenase, DBH-like 1	-1.03	1.99	1.75
209715_at	CBX5: chromobox homolog 5 (HP1 alpha homolog, Drosophila)	-1.16	-1.68	-1.84
209732_at	CLEC2B: C-type lectin domain family 2, member B	1.2	1.99	2.13
209764_at	CDNA FLJ43371 fis, clone NTONG2005969	1.23	1.69	1.51
209806_at	HIST1H2BK: histone 1, H2bk	-1.14	1.83	3.25
209832_s_at	CDT1: chromatin licensing and DNA replication factor 1	1.01	-1.6	-2.17
209846_s_at	BTN3A2: butyrophilin, subfamily 3, member A2	1.03	1.63	1.59
209864_at	FRAT2: frequently rearranged in advanced T-cell lymphomas 2	1.21	1.68	1.85
209933_s_at	CD300A: CD300a molecule	1.23	1.52	1.6
209949_at	NCF2: neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)	1.08	1.92	1.73
210253_at	HTATIP2: HIV-1 Tat interactive protein 2, 30kDa	1.17	1.64	1.51
210370_s_at	LY9: lymphocyte antigen 9	1.07	1.8	1.98
210432_s_at	SCN3A: sodium channel, voltage-gated, type III, alpha	1.2	2.56	3.46
210448_s_at	P2RX5: purinergic receptor P2X, ligand-gated ion channel, 5	-1.31	-1.51	-1.61
210519_s_at	NQO1: NAD(P)H dehydrogenase, quinone 1	3.07	3.66	3.26
210567_s_at	SKP2: S-phase kinase-associated protein 2 (p45)	-1.11	-1.72	-1.64
210983_s_at	MCM7: MCM7 minichromosome maintenance deficient 7 (<i>S. cerevisiae</i>)	-1.07	-1.87	-2.03
211138_s_at	KMO: kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	-1.06	1.57	2.12
211450_s_at	MSH6: mutS homolog 6 (<i>E. coli</i>)	1.02	-1.56	-1.6
211458_s_at	GABARAPL1 /// GABARAPL3: GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3	2.06	2.47	2.27
211597_s_at	HOP: homeodomain-only protein /// homeodomain-only protein	1.13	2.42	2.22

211653_x_at	AKR1C2: aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III) /// aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	2.67	4.66	5.19
211697_x_at	LOC56902: putative 28 kDa protein /// putative 28 kDa protein	1.5	1.54	1.65
211856_x_at	CD28: CD28 molecule	1.2	1.63	1.54
211937_at	EIF4B: eukaryotic translation initiation factor 4B	1.09	1.53	1.62
212085_at	SLC25A6: solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	1.22	1.8	1.73
212135_s_at	ATP2B4: ATPase, Ca++ transporting, plasma membrane 4	1.34	1.94	1.63
212136_at	ATP2B4: ATPase, Ca++ transporting, plasma membrane 4	1.14	2.07	1.62
212141_at	MCM4: MCM4 minichromosome maintenance deficient 4 (<i>S. cerevisiae</i>)	1.02	-1.83	-1.99
212142_at	MCM4: MCM4 minichromosome maintenance deficient 4 (<i>S. cerevisiae</i>)	-1.13	-1.76	-2.24
212205_at	H2AFV: H2A histone family, member V	-1.12	-1.57	-1.58
212335_at	GNS: glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)	1.06	1.54	1.52
212382_at	CDNA FLJ37747 fis, clone BRHIP2022986	-1.67	-1.65	-1.24
212383_at	ATP6V0A1: ATPase, H+ transporting, lysosomal V0 subunit a1	1.33	1.75	1.95
212385_at	CDNA FLJ37747 fis, clone BRHIP2022986	-1.64	-1.6	-1.28
212386_at	CDNA FLJ37747 fis, clone BRHIP2022986	-1.64	-1.61	-1.26
212457_at	TFE3: transcription factor binding to IGHM enhancer 3	1.39	1.57	1.54
212593_s_at	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)	1.19	1.85	2
212594_at	PDCD4: programmed cell death 4 (neoplastic transformation inhibitor)	1.1	1.85	1.87
212614_at	ARID5B: AT rich interactive domain 5B (MRF1-like)	1.28	2.08	2.14
212634_at	KIAA0776: KIAA0776	-1.52	-1.69	-1.08
212642_s_at	HIVP2: human immunodeficiency virus type I enhancer binding protein 2	1.12	1.58	1.75
212660_at	PHF15: PHD finger protein 15	1.43	1.74	1.67
212737_at	GM2A: GM2 ganglioside activator	1.11	1.59	1.84
212788_x_at	FTL: ferritin, light polypeptide	1.59	1.66	1.59
212826_s_at	SLC25A6: solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	1.16	1.64	1.56
212843_at	NCAM1: neural cell adhesion molecule 1	3.03	6.63	8.53

212913_at	MSH5 /// C6orf26: mutS homolog 5 (E. coli) /// chromosome 6 open reading frame 26	-1.49	-1.69	-1.68
212920_at	gb:AV682285 /DB_XREF=gi:10284148 /DB_XREF=AV682285 /CLONE=GKBACA04 /FEA=EST /CNT=65 /TID=Hs.227630.1 /TIER=Stack /STK=40 /UG=Hs.227630 /LL=5978 /UG_GENE=REST /UG_TITLE=RE1-silencing transcription factor	-1.55	-1.76	-1.3
213002_at	MARCKS: Myristoylated alanine-rich protein kinase C substrate	-2.82	-1.58	-1.51
213008_at	KIAA1794: KIAA1794	-1.03	-1.64	-1.66
213092_x_at	DNAJC9: DnaJ (Hsp40) homolog, subfamily C, member 9	1.02	-1.7	-1.67
213187_x_at	FTL: ferritin, light polypeptide	1.77	1.87	1.76
213261_at	LBA1: lupus brain antigen 1	-1.06	2.34	2.42
213534_s_at	PASK: PAS domain containing serine/threonine kinase	-1.13	-1.54	-1.96
213606_s_at	ARHGDI1: Rho GDP dissociation inhibitor (GDI) alpha	-1.24	-1.59	-1.66
213638_at	PHACTR1: phosphatase and actin regulator 1	-1.85	-2.04	-1.74
213891_s_at	CDNA FLJ37747 fis, clone BRHIP2022986	-1.6	-1.67	-1.26
213951_s_at	PSMC3IP: PSMC3 interacting protein	-1.5	-2.24	-2.23
214023_x_at	TUBB2B: tubulin, beta 2B	-1.72	-2.33	-2.35
214057_at	MCL1: Myeloid cell leukemia sequence 1 (BCL2-related)	1.67	2.21	2.18
214152_at	CCPG1: cell cycle progression 1	1.61	1.66	2.52
214211_at	FTH1: ferritin, heavy polypeptide 1	2.25	1.65	1.5
214290_s_at	HIST2H2AA3 /// LOC653610 /// HIST2H2AA4: histone 2, H2aa3 /// similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615) /// histone 2, H2aa4	-1.21	-1.57	-1.81
214430_at	GLA: galactosidase, alpha	1.94	2.13	1.73
214582_at	PDE3B: phosphodiesterase 3B, cGMP-inhibited	1.06	1.7	1.7
214615_at	P2RY10: purinergic receptor P2Y, G-protein coupled, 10	1.54	2.02	2.21
214620_x_at	PAM: peptidylglycine alpha-amidating monooxygenase	1.23	1.86	1.82
215071_s_at	HIST1H2AC: histone 1, H2ac	-1.25	1.86	3.13
215111_s_at	TSC22D1: TSC22 domain family, member 1	1.21	2.01	1.98
215136_s_at	EXOSC8: exosome component 8	-1.18	-1.51	-1.58
215137_at	KIAA0508: KIAA0508 protein	-1.26	-1.89	-1.72
215333_x_at	GSTM1: glutathione S-transferase M1	1.31	1.62	1.65
215629_s_at	DLEU2 /// DLEU2L: deleted in lymphocytic leukemia, 2 /// deleted in lymphocytic leukemia 2-like	-1.13	-2.52	-2.26
215967_s_at	LY9: lymphocyte antigen 9	1.05	1.78	1.89
216237_s_at	MCM5: MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	-1.04	-1.97	-2.46

216508_x_at	HMGB1 /// HMG1L1 /// LOC644380: high-mobility group box 1 /// high-mobility group (nonhistone chromosomal) protein 1-like 1 /// similar to High mobility group protein 1-like 10 (HMG-1L10)	-1.18	-1.54	-1.69
216594_x_at	AKR1C1: ald-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	1.63	2.39	2.33
216834_at	RGS1: regulator of G-protein signalling 1	1.02	2.37	2.69
216870_x_at	DLEU2: deleted in lymphocytic leukemia, 2	-1.22	-2.7	-2
216945_x_at	PASK: PAS domain containing serine/threonine kinase	1.03	-1.57	-1.83
217119_s_at	CXCR3: chemokine (C-X-C motif) receptor 3	1.55	2.21	2.26
217147_s_at	TRAT1: T cell receptor associated transmembrane adaptor 1	2.27	2.28	2.74
217678_at	SLC7A11: solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	2.62	-1.02	1.63
217783_s_at	YPEL5: yippee-like 5 (Drosophila)	1.28	1.95	2.06
217846_at	QARS: glutaminyl-tRNA synthetase	1.15	1.57	1.69
217905_at	C10orf119: chromosome 10 open reading frame 119	-1.19	-1.57	-1.57
217914_at	TPCN1: two pore segment channel 1	-1.54	-1.51	-1.51
217967_s_at	C1orf24: chromosome 1 open reading frame 24	-1.2	-1.81	-1.94
217973_at	DCXR: dicarbonyl/L-xylulose reductase	-1.24	-1.61	-1.63
217989_at	DHRS8: dehydrogenase/reductase (SDR family) member 8	1.13	1.96	1.84
218041_x_at	SLC38A2: solute carrier family 38, member 2	1.2	1.55	1.58
218113_at	TMEM2: transmembrane protein 2	1.16	1.52	1.77
218161_s_at	CLN6: ceroid-lipofuscinosis, neuronal 6, late infantile, variant	-1.4	-1.78	-1.67
218285_s_at	BDH2: 3-hydroxybutyrate dehydrogenase, type 2	1.2	1.52	1.61
218358_at	CRELD2: cysteine-rich with EGF-like domains 2	-1.36	-1.97	-1.7
218380_at	NALP1: NACHT, leucine rich repeat and PYD (pyrin domain) containing 1	1.02	1.55	1.65
218585_s_at	DTL: denticleless homolog (Drosophila)	-1.09	-1.6	-1.89
218602_s_at	FAM29A: family with sequence similarity 29, member A	-1.1	-1.93	-1.54
218705_s_at	SNX24: sorting nexin 24	-1.27	-1.94	-1.94
218782_s_at	ATAD2: ATPase family, AAA domain containing 2	1.09	-1.68	-1.57
218802_at	CCDC109B: coiled-coil domain containing 109B	-1.34	-1.75	-1.85
218839_at	HEY1: hairy/enhancer-of-split related with YRPW motif 1	1.39	1.91	1.94
218875_s_at	FBXO5: F-box protein 5	-1.09	-1.74	-1.67
218918_at	MAN1C1: mannosidase, alpha, class 1C, member 1	1.26	1.73	1.57
218951_s_at	PLCXD1: phosphatidylinositol-specific phospholipase C, X domain containing 1	-1.11	-1.55	-1.68

218979_at	RMI1: RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	-1.11	-1.65	-1.66
218999_at	TMEM140: transmembrane protein 140	1.69	3.24	3.17
219002_at	FASTKD1: FAST kinase domains 1	1.36	1.58	1.58
219258_at	TIPIN: TIMELESS interacting protein	-1.05	-1.6	-1.89
219294_at	CENPQ: centromere protein Q	1.02	-1.52	-1.58
219306_at	KIF15 /// C7orf9: kinesin family member 15 /// chromosome 7 open reading frame 9	-1.11	-1.94	-1.71
219319_at	HIF3A: hypoxia inducible factor 3, alpha subunit	-1.47	-1.78	-1.54
219371_s_at	KLF2: Kruppel-like factor 2 (lung)	-2.34	-2.47	-2.62
219410_at	TMEM45A: transmembrane protein 45A	1.07	2.16	2.57
219431_at	ARHGAP10: Rho GTPase activating protein 10	-1.49	-1.68	-1.69
219540_at	ZNF267: zinc finger protein 267	-1.6	-1.97	-1.32
219684_at	RTP4: receptor transporter protein 4	1.03	1.75	1.85
219895_at	FAM70A: family with sequence similarity 70, member A	1.92	2	2.09
220059_at	BRDG1: BCR downstream signaling 1	-1.14	1.67	1.77
220085_at	HELLS: helicase, lymphoid-specific	1.1	-1.88	-1.97
220201_at	MNAB: membrane associated DNA binding protein	1.27	1.76	1.6
220223_at	C17orf41: chromosome 17 open reading frame 41	1.03	-1.99	-1.58
220255_at	FANCE: Fanconi anemia, complementation group E	-1.12	-1.68	-1.76
220277_at	CXXC4: CXXC finger 4	-1.13	1.52	1.78
220466_at	CCDC15: coiled-coil domain containing 15	-1.27	-1.8	-1.59
220651_s_at	MCM10: MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)	1.01	-1.62	-1.93
220924_s_at	SLC38A2: solute carrier family 38, member 2	1.25	1.57	1.63
220969_s_at	gb:NM_030892.1 /DB_XREF=gi:13569855 /GEN=FLJ11786 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900103.84 /TIER=FL /STK=0 /DEF=Homo sapiens hypothetical protein FLJ11786 (FLJ11786), mRNA. /PROD=hypothetical protein FLJ11786 /FL=gb:NM_030892.1	-1.18	-1.58	-1.67
220987_s_at	C11orf17 /// NUA2: chromosome 11 open reading frame 17 /// chromosome 11 open reading frame 17 /// NUA2 family, SNF1-like kinase, 2 /// NUA2 family, SNF1-like kinase, 2	1.16	1.52	1.69
221156_x_at	CCPG1: cell cycle progression 1	1.51	1.36	1.82
221479_s_at	BNIP3L: BCL2/adenovirus E1B 19kDa interacting protein 3-like /// BCL2/adenovirus E1B 19kDa interacting protein 3-like	-1.23	1.62	1.87
221511_x_at	CCPG1: cell cycle progression 1	1.34	1.57	2.25
221521_s_at	GINS2: GINS complex subunit 2 (Psf2 homolog)	-1.08	-1.95	-2.24
221525_at	DKFZp761I2123: hypothetical protein DKFZp761I2123	-1.55	-1.78	-1.88

221530_s_at	BHLHB3: basic helix-loop-helix domain containing, class B, 3	1.49	2.35	2.27
221565_s_at	FAM26B: family with sequence similarity 26, member B	1.48	1.85	1.64
221611_s_at	PHF7: PHD finger protein 7	1.68	1.53	1.36
221677_s_at	DONSON: downstream neighbor of SON	-1.11	-1.53	-1.73
221698_s_at	CLEC7A: C-type lectin domain family 7, member A /// C-type lectin domain family 7, member A	-1.26	1.78	2.09
221703_at	BRIP1: BRCA1 interacting protein C-terminal helicase 1 /// BRCA1 interacting protein C-terminal helicase 1	-1.06	-1.81	-1.67
221756_at	MGC17330: HGFL gene /// HGFL gene	1.2	1.52	1.61
221824_s_at	MARCH8: membrane-associated ring finger (C3HC4) 8	1.12	1.56	1.55
221905_at	CYLD: cylindromatosis (turban tumor syndrome)	-1.68	-1.79	-1.44
221960_s_at	RAB2: RAB2, member RAS oncogene family	1.82	1.73	1.61
221985_at	KLHL24: kelch-like 24 (Drosophila)	1.63	3.02	3.05
221986_s_at	KLHL24: kelch-like 24 (Drosophila)	1.39	2.56	2.94
222037_at	MCM4: MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	-1.02	-1.71	-2.05
222111_at	CDNA clone IMAGE:4794011	-1.69	-2.01	-1.45
222139_at	KIAA1466: KIAA1466 gene	2.3	4.16	6.8
222146_s_at	TCF4: transcription factor 4	-1.67	-1.54	-1.21
222156_x_at	CCPG1: cell cycle progression 1	1.43	1.56	2.23
222201_s_at	CASP8AP2: CASP8 associated protein 2	-1.13	-2.24	-1.58
222309_at	C6orf62: Chromosome 6 open reading frame 62	-1.33	-1.56	-1.58
222317_at	PDE3B: Phosphodiesterase 3B, cGMP-inhibited	1.56	2.67	3.1
222408_s_at	YPEL5: yippee-like 5 (Drosophila)	1.4	2.13	2.08
222680_s_at	DTL: denticleless homolog (Drosophila)	-1.01	-1.59	-1.72
222740_at	ATAD2: ATPase family, AAA domain containing 2	1	-1.59	-1.71
222848_at	CENPK: centromere protein K	-1.22	-2.35	-2.29
222962_s_at	MCM10: MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)	1.12	-1.62	-1.98
223044_at	SLC40A1: solute carrier family 40 (iron-regulated transporter), member 1	1.43	1.94	1.68
223165_s_at	IHPK2: inositol hexaphosphate kinase 2	1.01	1.62	1.58
223248_at	HSDL1: hydroxysteroid dehydrogenase like 1	1.24	1.52	1.54
223318_s_at	ALKBH7: alkB, alkylation repair homolog 7 (E. coli)	1.13	1.66	1.87
223363_at	MGC10911: hypothetical protein MGC10911	-1.21	-1.53	-1.56
223492_s_at	LRRFIP1: leucine rich repeat (in FLII) interacting protein 1	-1.31	-1.6	-2
223493_at	FBXO4: F-box protein 4	-1.51	-1.67	-1.57
223517_at	FBXO44: F-box protein 44	1.5	1.97	1.8

223556_at	HELLS: helicase, lymphoid-specific	-1.13	-1.74	-1.97
223570_at	MCM10: MCM10 minichromosome maintenance deficient 10 (<i>S. cerevisiae</i>)	1.14	-1.51	-1.95
223596_at	SLC12A6: solute carrier family 12 (potassium/chloride transporters), member 6	1.34	2.44	2.36
224320_s_at	MCM8: MCM8 minichromosome maintenance deficient 8 (<i>S. cerevisiae</i>)	1.04	-1.54	-1.71
224428_s_at	CDCA7: cell division cycle associated 7 /// cell division cycle associated 7	-1.7	-3.16	-3.25
224444_s_at	C1orf97: chromosome 1 open reading frame 97 /// chromosome 1 open reading frame 97	-1.11	1.57	1.67
224478_s_at	MGC11257: hypothetical protein MGC11257 /// hypothetical protein MGC11257	-1.22	-1.88	-1.81
224480_s_at	LPAAT-THETA: lysophosphatidic acid acyltransferase theta /// lysophosphatidic acid acyltransferase theta	2.54	1.87	1.6
224596_at	SLC44A1: solute carrier family 44, member 1	-1.01	1.75	1.78
224650_at	MAL2: mal, T-cell differentiation protein 2	-1.35	-2.71	-3.06
224731_at	HMGB1: high-mobility group box 1	-1.14	-1.53	-1.6
224741_x_at	GAS5: growth arrest-specific 5	1.22	1.56	1.73
224772_at	NAV1: neuron navigator 1	-1.73	-1.6	-1.75
224783_at	FAM100B: family with sequence similarity 100, member B	1.18	1.53	1.52
224968_at	CCDC104: coiled-coil domain containing 104	1.05	1.58	1.98
225046_at	MRNA; cDNA DKFZp686H157 (from clone DKFZp686H157)	-1.18	-1.63	-1.87
225047_at	NUPL1: nucleoporin like 1	-1.12	-1.54	-1.83
225074_at	RAB2B: RAB2B, member RAS oncogene family	1.24	1.57	1.6
225107_at	HNRPA2B1: Heterogeneous nuclear ribonucleoprotein A2/B1	-1.41	-1.92	-1.68
225123_at	MRNA; cDNA DKFZp313B1017 (from clone DKFZp313B1017)	1.55	1.82	1.67
225164_s_at	EIF2AK4: eukaryotic translation initiation factor 2 alpha kinase 4	1.16	2.41	2.25
225252_at	SRXN1: sulfiredoxin 1 homolog (<i>S. cerevisiae</i>)	4.57	3.44	2.93
225287_s_at	TMEM55B: transmembrane protein 55B	1.33	1.74	1.58
225540_at	MAP2: microtubule-associated protein 2	1.66	2.12	2.32
225548_at	SHROOM3: shroom family member 3	1.22	1.68	1.58
225564_at	SPATA13: spermatogenesis associated 13	-1.02	-1.62	-1.91
225567_at	LOC388114: Hypothetical LOC388114	-2.37	-1.8	-1.69
225609_at	GSR: glutathione reductase	2.74	1.87	1.83
225655_at	UHRF1: ubiquitin-like, containing PHD and RING finger domains, 1	-1.11	-1.66	-2.04
225662_at	ZAK: sterile alpha motif and leucine zipper containing kinase AZK	-1.13	-1.66	-1.65
225665_at	ZAK: sterile alpha motif and leucine zipper containing kinase AZK	1.04	-1.61	-1.66

225684_at	FAM33A: family with sequence similarity 33, member A	-1.27	-1.63	-1.51
225686_at	FAM33A: family with sequence similarity 33, member A	-1.26	-1.8	-1.76
225768_at	NR1D2: nuclear receptor subfamily 1, group D, member 2	1.95	1.37	1.51
225793_at	LIX1L: Lix1 homolog (mouse) like	1.17	1.85	1.75
225803_at	FBXO32: F-box protein 32	1.08	2.46	2.25
225809_at	DKFZP564O0823: DKFZP564O0823 protein	-1.34	-1.55	-1.52
225885_at	EEA1: early endosome antigen 1, 162kD	-1.57	-2.64	-1.46
225897_at	Homo sapiens, clone IMAGE:5547644, mRNA	-3.21	-1.99	-1.9
225912_at	TP53INP1: tumor protein p53 inducible nuclear protein 1	1.36	2.22	2.23
225922_at	KIAA1450: KIAA1450 protein	-1.62	-1.55	-1.5
225924_at	KIAA1450: KIAA1450 protein	-1.51	-1.52	-1.51
225956_at	LOC153222: adult retina protein	-1.18	1.75	2.38
225957_at	LOC153222: adult retina protein	-1.03	1.65	2.37
226003_at	KIF21A: kinesin family member 21A	-1.06	-1.94	-1.56
226037_s_at	TAF9B /// LOC653068: TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa /// similar to TBP-associated factor 9L	-1.32	-1.59	-1.75
226085_at	CDNA clone IMAGE:4842353	-1.23	-1.51	-1.78
226140_s_at	OTUD1: OTU domain containing 1	1.42	1.66	1.62
226150_at	PPAPDC1B: Phosphatidic acid phosphatase type 2 domain containing 1B	-1.52	-1.58	-1.29
226158_at	KLHL24: kelch-like 24 (Drosophila)	1.48	2.15	2.97
226208_at	ZSWIM6: zinc finger, SWIM-type containing 6	1.08	1.59	1.62
226308_at	NY-SAR-48: sarcoma antigen NY-SAR-48	-1.17	-1.67	-1.69
226336_at	gb:T62044 /DB_XREF=gi:665287 /DB_XREF=yc66b09.s1 /CLONE=IMAGE:85625 /FEA=EST /CNT=48 /TID=Hs.182937.3 /TIER=Stack /STK=47 /UG=Hs.182937 /LL=5478 /UG_GENE=PPIA /UG_TITLE=peptidylprolyl isomerase A (cyclophilin A)	-1.17	-1.71	-1.8
226363_at	ABCC5: ATP-binding cassette, sub-family C (CFTR/MRP), member 5	1.26	2.13	1.85
226397_s_at	TBC1D7: TBC1 domain family, member 7	-2.07	-1.94	-1.61
226416_at	THEX1: three prime histone mRNA exonuclease 1	-1.06	-1.71	-1.92
226421_at	AMMECR1: Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1	-1.2	-1.57	-1.53
226436_at	RASSF4: Ras association (RalGDS/AF-6) domain family 4	-1.94	-1.83	-1.91
226446_at	HES6: hairy and enhancer of split 6 (Drosophila)	1.04	-1.7	-2.08
226456_at	C16orf75: chromosome 16 open reading frame 75	-1.48	-1.78	-1.9
226530_at	BMF: Bcl2 modifying factor	1.24	1.86	1.76
226619_at	SENP1: SUMO1/sentrin specific peptidase 1	-1.1	-1.57	-1.52

226741_at	SLC12A6: solute carrier family 12 (potassium/chloride transporters), member 6	1.14	1.63	1.53
226821_at	RIF1: RAP1 interacting factor homolog (yeast)	1.01	-2.16	-1.56
226842_at	LOC90110: hypothetical protein LOC90110	1.13	1.59	1.67
226860_at	TMEM19: transmembrane protein 19	1.07	1.6	1.64
226870_at	COMTD1: catechol-O-methyltransferase domain containing 1	-1.3	-1.57	-1.55
226873_at	CDNA clone IMAGE:4794011	-1.55	-1.85	-1.53
227020_at	YPEL2: yippee-like 2 (Drosophila)	1.34	2.1	1.96
227033_at	PDIA3: protein disulfide isomerase family A, member 3	-1.38	-1.82	-1.51
227168_at	FLJ25967: hypothetical gene supported by AK098833	1.83	2.21	2.16
227247_at	PLEKHA8: Pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	1.06	1.96	1.82
227252_at	LRP10: Low density lipoprotein receptor-related protein 10	1.23	1.59	1.52
227312_at	SNTB2: syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	-1.25	-1.66	-1.61
227349_at	gb:AI807356 /DB_XREF=gi:5393922 /DB_XREF=wf47c03.x1 /CLONE=IMAGE:2358724 /FEA=mRNA /CNT=38 /TID=Hs.127797.0 /TIER=Stack /STK=11 /UG=Hs.127797 /UG_TITLE=Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	1.03	-1.61	-1.75
227350_at	HELLS: Helicase, lymphoid-specific	-1.04	-1.94	-1.96
227394_at	NCAM1: Neural cell adhesion molecule 1	3.39	7.91	10.76
227506_at	SLC16A9: solute carrier family 16, member 9 (monocarboxylic acid transporter 9)	-1.15	-1.82	-1.8
227842_at	RAB30: RAB30, member RAS oncogene family	1.1	1.6	1.7
227856_at	C4orf32: chromosome 4 open reading frame 32	-1.55	-1.74	-2.1
227878_s_at	ALKBH7: alkB, alkylation repair homolog 7 (E. coli)	1.13	1.7	1.89
227884_at	TAF15: TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	-1.48	-1.61	-1.54
227894_at	WDR90: WD repeat domain 90	-1.35	-1.65	-1.78
227985_at	gb:AI928513 /DB_XREF=gi:5664477 /DB_XREF=wp02h03.x1 /CLONE=IMAGE:2463701 /FEA=EST /CNT=78 /TID=Hs.59203.0 /TIER=Stack /STK=75 /UG=Hs.59203 /UG_TITLE=ESTs	-1.11	1.64	1.74
228003_at	RAB30: RAB30, member RAS oncogene family	-1.04	1.85	2.18
228084_at	CASP6: Caspase 6, apoptosis-related cysteine peptidase	-1.39	-1.91	-1.53
228151_at	Transcribed locus	1.13	1.67	1.59
228286_at	FLJ40869: hypothetical protein FLJ40869	-1.11	-2.02	-1.65

228287_at	ING5 /// LOC653066 /// LOC653474 /// LOC653494: inhibitor of growth family, member 5 /// similar to inhibitor of growth family, member 5 /// similar to inhibitor of growth family, member 5	-1.12	-1.52	-1.68
228361_at	E2F2: E2F transcription factor 2	-1.31	-1.94	-2.01
228400_at	Transcribed locus	1.32	1.78	1.77
228401_at	ATAD2: ATPase family, AAA domain containing 2	1.04	-1.83	-1.53
228485_s_at	SLC44A1: solute carrier family 44, member 1	1.01	2.01	2.27
228486_at	SLC44A1: solute carrier family 44, member 1	1.11	2.72	3.07
228495_at	CCDC75: Coiled-coil domain containing 75	-1.6	-1.72	-1.44
228557_at	L3MBTL4: L(3)mbt-like 4 (Drosophila)	-1.68	-1.57	-1.57
228597_at	C21orf45: chromosome 21 open reading frame 45	-1.09	-1.56	-1.81
228658_at	C22orf35: chromosome 22 open reading frame 35	1.63	1.92	2
228677_s_at	FLJ21438: hypothetical protein FLJ21438	1.43	1.61	1.53
228702_at	FLJ43663 /// LOC641825 /// LOC647017: hypothetical protein FLJ43663 /// hypothetical protein LOC641825 /// hypothetical protein LOC647017	-1.2	1.78	2.28
228728_at	FLJ21986: hypothetical protein FLJ21986	1.5	1.68	2.26
228774_at	CEP78: centrosomal protein 78kDa	-1.05	-1.6	-1.6
228837_at	CDNA FLJ37747 fis, clone BRHIP2022986	-2.09	-1.75	-1.28
228859_at	LOC91431: prematurely terminated mRNA decay factor-like	-1.23	-1.91	-1.61
228868_x_at	CDT1: DNA replication factor	-1.07	-1.57	-1.92
228993_s_at	LOC92482: hypothetical protein LOC92482	1.32	2.02	2.05
229070_at	C6orf105: chromosome 6 open reading frame 105	-1.81	-1.45	-1.52
229126_at	TMEM19: transmembrane protein 19	1.12	1.66	1.73
229146_at	C7orf31: chromosome 7 open reading frame 31	1.09	1.89	1.97
229147_at	Transcribed locus, strongly similar to NP_958834.1 Ras association (RalGDS/AF-6) domain family 6 isoform b; putative RAS binding protein [Homo sapiens]	1.57	1.5	2.07
229164_s_at	ABTB1: ankyrin repeat and BTB (POZ) domain containing 1	1.15	2.07	1.83
229305_at	MLF1IP: MLF1 interacting protein	-1.18	-2.32	-1.78
229307_at	ANKRD28: ankyrin repeat domain 28	1.27	1.96	2.53
229431_at	RFXAP: regulatory factor X-associated protein	-1.53	-1.47	-1.69
229459_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	-1.52	-2.25	-1.65
229498_at	MRNA; cDNA DKFZp779M2422 (from clone DKFZp779M2422)	-1.17	-2.15	-1.7
229551_x_at	ZNF367: zinc finger protein 367	-1.11	-1.65	-1.84

229655_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	-1.28	-2.04	-1.58
229656_s_at	FLJ42562: similar to echinoderm microtubule associated protein like 5	1.46	1.74	1.54
229713_at	CDNA FLJ13267 fis, clone OVARC1000964	-1.19	-1.56	-1.55
229963_at	NGFRAP1L1: NGFRAP1-like 1	-1.35	-1.71	-1.69
230012_at	C17orf44: chromosome 17 open reading frame 44	1.16	2.91	2.94
230312_at	Transcribed locus	-1.34	-2.56	-2.52
230405_at	RAD50: RAD50 homolog (<i>S. cerevisiae</i>)	1.13	1.65	1.75
230769_at	DENND2C: DENN/MADD domain containing 2C	1.03	1.6	1.52
230968_at	Full-length cDNA clone CS0DF032YA11 of Fetal brain of Homo sapiens (human)	1.11	1.65	1.71
231202_at	ALDH1L2: aldehyde dehydrogenase 1 family, member L2	-1.2	-2.49	-2.09
231259_s_at	Transcribed locus	-1.39	-1.86	-1.96
231431_s_at	LOC388114 /// LOC649557: hypothetical LOC388114 /// hypothetical protein LOC649557	-1.82	-1.52	-1.48
231767_at	HOXB4: homeobox B4	1.18	1.68	1.62
231779_at	IRAK2: interleukin-1 receptor-associated kinase 2	1.34	2	1.66
231807_at	KIAA1217: KIAA1217	-1.15	1.55	1.74
231827_at	CRLS1: Cardiolipin synthase 1	-1.03	-1.65	-1.53
231843_at	DDX55: DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	-1.27	-1.63	-1.7
231862_at	CDNA clone IMAGE:4842353	-1.48	-1.75	-1.82
231871_at	GPR180: G protein-coupled receptor 180	-1.28	-1.59	-1.66
231875_at	KIF21A: kinesin family member 21A	-1.11	-1.7	-1.55
231895_at	SASS6: spindle assembly 6 homolog (<i>C. elegans</i>)	1.02	-1.96	-1.68
232116_at	GRHL3: grainyhead-like 3 (<i>Drosophila</i>)	-2.02	-1.65	-1.81
232291_at	C13orf25: chromosome 13 open reading frame 25	-1.37	-2.02	-1.94
232760_at	TEX15: testis expressed sequence 15	-1.09	-3.35	-1.98
233210_at	FLJ12120: hypothetical LOC388439	-1.11	1.72	1.94
233235_x_at	CDNA: FLJ21443 fis, clone COL04430	1.82	1.58	1.22
233463_at	RASSF6: Ras association (RalGDS/AF-6) domain family 6	1.6	1.33	2.22
233933_s_at	OTUD5: OTU domain containing 5	1.15	1.59	1.52
234863_x_at	FBXO5: F-box protein 5	-1.12	-1.62	-1.7
235142_at	ZBTB8: zinc finger and BTB domain containing 8	-1.62	-1.62	-1.34
235203_at	Homo sapiens, clone IMAGE:3866695, mRNA	-1.13	-1.83	-1.83
235266_at	ATAD2: ATPase family, AAA domain containing 2	-1.03	-1.63	-1.73
235278_at	C20orf133: chromosome 20 open reading frame 133	1.05	1.79	2.7
235310_at	GCET2: germinal center expressed transcript 2	-1.02	1.58	1.6

235542_at	MGC22014: hypothetical protein MGC22014	-1.22	-1.54	-1.61
235556_at	LOC153222: Adult retina protein	1.01	1.64	2.13
235609_at	Transcribed locus	-1.09	-2.02	-1.76
235638_at	RASSF6: Ras association (RalGDS/AF-6) domain family 6	1.49	1.52	2.04
235678_at	GM2A: GM2 ganglioside activator	1	1.63	1.59
235696_at	CDNA clone IMAGE:4837650	1.13	1.58	1.67
235749_at	UGCGL2: UDP-glucose ceramide glucosyltransferase-like 2	-1.1	-2.33	-2.07
235764_at	PRDM5: PR domain containing 5	-1.89	-1.73	-1.24
235803_at	CRLF3: Cytokine receptor-like factor 3	-1.26	-1.69	-1.53
236140_at	GCLM: glutamate-cysteine ligase, modifier subunit	2.89	1.47	1.57
236280_at	Transcribed locus	1.79	2.29	2.41
236546_at	POLA2: Polymerase (DNA directed), alpha 2 (70kD subunit)	-1.32	-1.68	-1.99
236619_at	Transcribed locus	-1.11	-2.39	-1.53
236665_at	CCDC18: coiled-coil domain containing 18	-1.36	-2.6	-1.58
236976_at	FANCA: Fanconi anemia, complementation group A	-1.11	-1.73	-2.08
237003_at	VMD2L3: vitelliform macular dystrophy 2-like 3	-1.46	-1.55	-1.87
237094_at	FAM19A5: family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	-1.84	-2.47	-2.16
237322_at	LOC150271: Hypothetical protein LOC150271	1.4	1.68	1.79
237725_x_at	SMC5: structural maintenance of chromosomes 5	1.02	-2.13	-1.57
238015_at	LOC201725: hypothetical protein LOC201725	-1.29	-1.6	-1.75
238117_at	PPOX: protoporphyrinogen oxidase	-1.18	2.18	2.3
238476_at	LOC153222: adult retina protein	1.02	1.91	2.64
238681_at	GDPD1: glycerophosphodiester phosphodiesterase domain containing 1	1.55	2.93	2.91
238701_x_at	FLJ45803: FLJ45803 protein	1.85	1.67	1.99
238704_at	Homo sapiens, clone IMAGE:3866695, mRNA	-1.09	-1.8	-1.77
238732_at	COL24A1: collagen, type XXIV, alpha 1	2.05	2.63	3.42
238977_at	MCM6: MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae)	-1.33	-2.66	-2.16
239294_at	Transcribed locus	1.17	2.06	2.14
239841_at	C7orf24: Chromosome 7 open reading frame 24	-1.09	-1.59	-1.53
239897_at	BCLAF1: BCL2-associated transcription factor 1	-1.35	-2.5	-1.6
240118_at	TXNDC11: Thioredoxin domain containing 11	-1.44	-2.08	-1.94
240392_at	CARD14: Caspase recruitment domain family, member 14	1.16	2.03	1.87
241360_at	CCDC15: Coiled-coil domain containing 15	-1.23	-1.97	-1.68
241436_at	SCNN1G: sodium channel, nonvoltage-gated 1, gamma	-2.31	-1.83	-1.85
241569_at	LOC146909: Hypothetical protein LOC146909	-1.33	-1.8	-1.91

242269_at	FLJ42875: FLJ42875 protein	2.12	3.05	3.47
242890_at	HELLS: Helicase, lymphoid-specific	-1.04	-1.97	-2.18
242918_at	NASP: Nuclear autoantigenic sperm protein (histone-binding)	-1.34	-1.89	-1.94
243465_at	TMEM140: Transmembrane protein 140	1.92	2.53	3.61
244071_at	LOC345630: similar to fibrillarin	2.21	2.34	2.52
244559_at	VPS52: Vacuolar protein sorting 52 (<i>S. cerevisiae</i>)	1.44	1.53	1.92
244623_at	gb:BF513800 /DB_XREF=gi:11598979 /DB_XREF=UI-H-BW1-amp-c-10-0-UI.s1 /CLONE=IMAGE:3070483 /FEA=EST /CNT=6 /TID=Hs.125304.0 /TIER=ConsEnd /STK=3 /UG=Hs.125304 /UG_TITLE=ESTs	-1.31	-1.71	-1.59
34726_at	CACNB3: calcium channel, voltage-dependent, beta 3 subunit	1.35	1.75	1.63
36711_at	MAFF: v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	1.03	1.72	1.7
49306_at	RASSF4: Ras association (RalGDS/AF-6) domain family 4	-2.28	-1.6	-1.93
56256_at	SIDT2: SID1 transmembrane family, member 2	1.02	1.66	1.6

* Table contains probes determined by analysis through dChip to have a) fold change (up- or down-regulation) of >1.2; b) absolute increase or decrease in signal by >100; c) significant change in at least one of the 3 time points of the analysis; d) fold change (up- or down-regulation) of >1.5 in at least 2 of the time points of the analysis