

Supplementary Table 1. Gene-regulations (log₂-folds) in CD8+ cells from 25 patients dosed with IL-21. For each probeset the Affymetrix identifier (Affy ID), Gene symbol (Symbol), Gene name (Name), False Discovery Rate corrected P-value (fdrP), and log₂-folds (Day 5 versus Day 1) for individual patients from both regimens (5+9 and 3x/wk) are listed.

affyID	Symbol	Name	fdrP	1 µg/kg (3 x w.)	1 µg/kg (3 x w.)	1 µg/kg (5+9)	1 µg/kg (5+9)	3 µg/kg (3 x w.)	3 µg/kg (3 x w.)	3 µg/kg (5+9)	3 µg/kg (5+9)	10 µg/kg (3 x w.)	10 µg/kg (3 x w.)	10 µg/kg (5+9)	10 µg/kg (5+9)	30 µg/kg (3 x w.)	30 µg/kg (3 x w.)	30 µg/kg (5+9)	30 µg/kg (5+9)	50 µg/kg (3 x w.)	50 µg/kg (3 x w.)	50 µg/kg (5+9)	50 µg/kg (5+9)	100 µg/kg (3 x w.)	100 µg/kg (3 x w.)	100 µg/kg (5+9)	100 µg/kg (5+9)	
203764_at	DLG7	discs, large homolog 7 (Drosophila)	0.000389932	-0.2	-0.2	0.4	2.0	0.0	-0.5	2.7	3.7	1.9	2.9	4.2	5.4	4.4	5.1	3.6	4.2	4.3	2.6	4.2	5.1	4.7	5.4	3.2	3.5	3.4
210354_at	IFNG	interferon, gamma	0.000211352	0.6	0.7	-0.4	0.3	1.1	2.6	1.7	2.3	2.4	1.2	5.3	5.5	4.5	5.5	2.9	4.7	4.8	3.0	2.8	4.2	5.1	5.3	3.1	4.0	3.3
209773_s_at	RRM2	ribonucleotide reductase M2 polypeptide	0.00172172	-0.1	0.5	-0.5	1.9	1.0	0.2	2.6	4.1	1.7	3.0	3.3	5.6	4.4	4.2	3.4	3.4	3.2	4.2	4.0	4.8	5.1	4.8	2.2	2.8	3.1
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.000400172	0.1	-0.3	0.6	1.7	0.3	0.4	2.7	3.0	0.9	2.4	3.7	5.3	3.8	4.0	3.3	3.8	3.6	2.6	3.5	4.7	4.7	5.3	3.0	3.9	3.1
218585_s_at	DTL	denticleless homolog (Drosophila)	0.000403636	-0.1	-0.3	0.9	2.0	-0.7	-0.8	3.0	3.8	1.7	2.8	4.3	5.1	4.1	4.4	2.8	4.0	3.8	3.2	3.7	4.8	3.9	5.0	2.6	2.9	3.7
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.000437438	0.5	0.4	0.5	2.0	-0.4	-0.3	2.6	3.8	1.5	2.8	3.7	4.8	3.8	3.6	3.8	3.5	4.2	3.9	4.2	5.0	4.1	4.4	2.4	2.4	3.4
214710_s_at	CCNB1	cyclin B1	0.000356177	-0.1	-0.5	0.1	1.1	0.3	-0.3	2.5	2.7	1.0	1.9	3.1	4.3	3.6	4.1	3.4	3.5	3.8	2.2	3.1	4.6	4.8	5.0	3.3	4.0	2.9
218542_at	C10orf3	chromosome 10 open reading frame 3	0.000564283	0.3	0.2	0.0	0.9	0.0	0.0	2.4	2.8	1.8	2.0	4.0	4.5	3.7	4.2	3.5	4.7	4.1	2.6	3.5	4.6	4.0	4.4	2.7	3.8	2.4
219148_at	PBK	PDZ binding kinase	0.000506686	0.0	-0.1	0.1	1.5	-0.2	0.6	2.9	2.3	1.9	1.5	3.7	4.9	3.2	4.3	3.3	4.5	3.6	1.7	3.2	4.8	4.0	4.9	3.5	3.8	3.3
201890_at	RRM2	ribonucleotide reductase M2 polypeptide	0.000345458	0.8	0.8	1.7	1.3	1.5	0.8	2.2	3.6	1.6	2.8	3.4	4.8	4.4	4.0	3.9	3.1	3.3	3.7	3.9	3.8	4.0	4.6	2.1	2.3	2.9
222680_s_at	DTL	denticleless homolog (Drosophila)	0.000628774	0.6	0.0	0.9	1.7	-0.2	0.1	2.3	3.2	1.4	1.4	3.5	4.3	3.6	4.3	3.0	3.6	3.7	1.9	3.2	4.3	3.5	4.6	3.4	3.2	2.5
204444_at	KIF11	kinesin family member 11	0.000808707	0.3	0.0	0.2	1.3	-0.1	-0.2	2.0	3.4	1.4	2.2	3.5	4.0	3.7	4.1	3.0	4.0	3.3	2.6	3.1	4.7	4.0	4.2	2.0	2.6	2.5
202589_at	TYMS	thymidylate synthetase	0.000387781	0.8	-0.2	1.2	2.0	1.1	-0.1	2.1	3.6	1.8	3.1	3.4	5.0	4.2	4.2	3.6	3.1	2.9	3.6	3.6	3.9	4.1	4.0	1.9	2.1	2.7
201292_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.000484828	0.4	-0.4	-0.2	1.0	0.0	-0.1	1.9	3.2	1.9	2.6	3.4	3.7	2.9	3.8	2.8	3.4	4.2	2.5	3.2	4.2	3.7	4.6	2.6	2.8	2.5
203213_at	CDC2	cell division cycle 2, G1 to S and G2 to M	0.000504302	0.7	0.1	-0.2	1.0	1.4	1.2	1.9	3.1	1.6	2.4	3.1	4.6	3.3	4.1	2.6	3.6	3.5	3.4	3.5	4.2	4.0	3.9	1.9	2.4	2.9
202870_s_at	CDC20	CDC20 cell division cycle 20 homolog (S. cerevisiae)	0.000360717	-0.1	-0.5	0.5	1.4	-0.4	0.5	1.9	2.5	1.4	2.1	3.0	4.0	3.4	4.1	2.1	3.6	3.2	2.1	2.7	3.7	4.0	4.8	2.8	3.7	2.7
202705_at	CCNB2	cyclin B2	0.000398993	0.0	-0.2	-0.3	0.5	0.3	0.7	2.3	3.0	1.3	2.1	3.1	3.8	3.7	4.1	2.7	3.1	3.4	2.3	2.7	4.3	4.2	4.1	2.6	3.4	2.2
205768_s_at	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	0.000390859	0.0	-0.4	-0.1	0.8	0.6	0.4	1.1	1.3	1.1	1.0	3.4	4.4	2.5	4.0	2.4	4.2	3.3	1.0	2.9	4.0	4.2	4.6	2.5	3.8	3.2
205394_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	0.000855369	0.4	-0.3	0.0	0.6	-0.2	0.4	2.2	2.6	1.4	1.6	3.3	4.4	3.3	4.2	1.8	4.2	3.3	1.4	3.1	3.8	3.4	4.5	3.2	3.6	2.8
225655_at	UHRF1	ubiquitin-like, containing PHD and RING finger domains, 1	0.000173096	0.4	-0.2	0.4	1.3	-0.6	0.7	1.9	2.9	1.7	1.7	3.1	4.9	3.2	3.7	2.9	3.3	3.5	3.1	3.3	3.5	3.6	4.0	3.1	2.4	2.7
219306_at	KIF15	kinesin family member 15	0.000935053	-0.3	0.7	-0.2	0.7	-0.1	0.4	2.7	3.2	1.5	2.3	3.6	4.1	3.4	4.2	3.0	3.5	3.6	2.3	3.0	3.5	3.1	4.1	2.7	3.7	2.2
202503_s_at	KIAA0101	KIAA0101	0.00043743	-0.7	0.7	0.2	1.5	0.0	0.1	1.6	3.3	1.4	3.1	3.0	5.1	3.7	4.1	4.8	2.3	2.6	3.5	3.3	3.8	4.2	3.7	1.7	1.7	2.4
219918_s_at	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0.000625439	0.6	0.5	0.4	1.1	-0.7	0.6	2.1	3.1	1.4	2.0	3.2	4.5	3.6	3.2	2.8	3.5	3.1	2.4	3.3	3.7	3.3	4.7	2.2	2.9	2.7
204026_s_at	ZWINT	ZW10 interactor	0.000179478	0.5	0.5	0.5	1.0	1.4	1.4	1.7	2.6	1.2	1.8	3.1	4.0	2.7	3.5	3.7	2.8	3.2	3.5	2.7	4.3	3.6	3.7	2.0	2.2	2.9
209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	0.005558575	-0.3	0.0	-0.3	0.5	-0.3	0.3	2.6	1.1	0.4	0.3	3.1	5.2	4.3	0.8	1.1	0.5	1.7	4.3	3.6	3.4	4.7	4.4	4.7	1.3	6.0
205769_at	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	0.000440672	0.2	-0.3	0.0	0.4	0.0	0.6	1.3	1.4	1.0	0.6	3.1	3.8	2.4	3.9	2.8	4.0	3.4	1.0	2.4	3.5	4.0	4.4	1.9	3.7	3.0
204146_at	RAD51AP1	RAD51 associated protein 1	0.000440052	1.0	0.7	0.9	1.4	1.6	0.5	1.6	2.4	1.1	1.8	2.9	3.3	3.2	2.9	3.3	3.6	3.5	3.2	2.0	4.7	3.1	3.0	1.9	2.6	3.0
204825_at	MELK	maternal embryonic leucine zipper kinase	0.000391422	0.4	0.5	0.8	1.9	0.6	-0.5	1.9	2.9	1.2	2.0	3.1	4.2	3.5	3.6	2.9	3.0	3.1	2.5	2.7	4.2	3.6	3.9	1.8	2.3	2.6
202095_s_at	BIRC5	baculoviral IAP repeat-containing 5 (survivin)	0.000560101	0.1	0.2	0.2	0.8	-0.3	1.1	1.3	2.0	1.1	1.6	3.5	3.3	3.5	3.9	2.9	3.9	3.8	2.0	2.2	3.8	3.6	3.2	2.4	2.6	1.9
220651_s_at	MCM10	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)	0.000743536	0.0	-1.0	0.0	0.5	0.2	0.5	1.8	2.9	1.6	1.5	3.6	4.2	3.6	3.9	2.5	3.9	2.9	1.2	2.8	3.3	2.8	4.0	2.9	3.3	2.2
203755_at	BUB1B	BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast)	0.00043174	0.7	0.8	0.4	0.2	-0.1	-0.3	1.6	2.1	1.4	1.9	3.0	3.6	3.3	3.2	3.1	3.4	3.1	1.7	3.0	3.8	3.3	3.9	2.0	2.8	2.3
209642_at	BUB1	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	0.000335066	-0.1	-0.7	0.1	0.0	0.3	0.2	1.3	1.8	0.8	1.9	3.0	3.8	2.9	2.9	2.2	3.5	3.0	1.5	2.8	3.2	2.6	4.3	3.3	4.2	2.3
218883_s_at	MLF1IP	MLF1 interacting protein	0.001183206	1.1	-0.4	0.6	1.6	0.4	0.1	1.5	2.9	1.2	2.0	2.9	5.2	3.1	3.4	2.0	3.0	3.7	2.6	2.3	4.4	3.6	3.8	1.8	2.1	2.6
223381_at	CDCA1	cell division cycle associated 1	0.000426273	-0.5	-0.1	0.2	0.3	0.2	0.1	1.0	2.1	1.0	1.0	3.1	2.1	3.0	3.8	2.2	3.8	3.1	0.9	2.5	3.8	2.7	4.0	2.8	3.4	2.2
221521_s_at	Pfs2	NA	0.001074754	0.8	-0.2	-0.5	1.3	-0.5	0.1	2.3	2.6	1.4	1.9	3.1	3.7	3.4	4.1	2.2	3.4	3.0	1.9	2.1	3.7	3.3	3.5	2.4	2.8	2.4
228033_at	E2F7	E2F transcription factor 7	0.001267566	0.4	0.1	0.3	0.9	0.3	0.4	2.1	2.4	1.4	1.1	3.2	3.6	2.2	3.4	2.7	3.8	3.8	1.3	2.5	3.9	3.0	3.5	2.9	3.0	2.2
210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	0.000803009	0.6	-0.3	-0.7	0.4	0.3	0.1	0.9	2.1	1.3	1.7	2.8	3.5	2.6	3.7	2.2	3.4	3.0	1.6	2.7	3.0	2.9	3.6	1.8	4.1	2.0
212021_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.001018131	-0.4	0.6	1.2	1.1	-0.5	0.2	1.6	2.4	1.4	1.7	2.8	3.0	2.7	3.6	2.8	2.9	3.2	1.6	1.8	4.0	3.2	3.9	2.1	2.6	1.8
203560_at	GGH	gamma-glutamyl hydrolase (conjugase, folypolyglutammaglutamyl hydrolase)	0.00058379	-0.7	0.4	-0.2	0.8	-0.6	-0.9	2.0	1.9	0.9	1.4	2.6	3.4	2.3	2.5	3.1	3.1	3.2	2.7	2.2	3.7	2.6	3.6	2.5	2.7	2.1
1554696_s_at	TYMS	thymidylate synthetase	0.001837299	0.3	-0.4	-0.7	1.7	0.2	-0.1	0.5	2.2	1.1	1.2	3.6	3.8	2.9	4.2	2.1	3.8	3.2	1.8	2.8	3.1	3.3	3.3	1.4	2.8	1.4
209709_s_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.000917669	-0.2	0.2	-0.4	0.6	-0.2	0.4	1.6	1.8	0.7	1.4	3.1	3.0	3.1	3.3	2.5	3.4	2.3	1.0	2.0	3.3	2.7</				

210559_s_at	CDC2	cell division cycle 2, G1 to S and G2 to M	0.002906855	0.4	0.2	0.3	0.6	0.7	-0.6	1.8	1.9	0.6	0.9	2.9	3.6	2.1	3.1	2.1	3.9	3.5	1.1	2.2	3.5	3.1	3.9	2.6	2.8	1.9
206102_at	PSF1	NA	0.000512553	-1.6	0.2	0.9	0.7	0.1	0.0	1.5	2.7	1.0	1.2	3.2	4.7	2.7	2.9	2.1	2.7	3.3	1.5	2.1	3.0	3.5	3.9	2.1	3.4	2.3
209714_s_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	0.001836717	-0.2	0.2	-0.4	1.3	0.5	0.1	1.5	2.5	0.9	1.9	3.0	3.4	2.9	3.4	1.5	3.6	3.0	1.3	2.4	3.4	3.2	3.8	2.4	3.2	1.4
228069_at	FAM54A	family with sequence similarity 54, member A	0.000682278	0.2	1.0	-1.0	0.5	0.1	0.1	1.0	1.6	0.8	1.1	2.5	2.7	2.1	2.7	2.6	3.0	3.5	1.7	1.8	4.0	2.5	3.8	2.7	3.1	2.1
204962_s_at	CENPA	centromere protein A, 17kDa	0.000443504	0.0	0.0	0.4	0.5	-0.3	0.1	1.8	2.5	0.9	1.3	2.9	2.9	2.8	2.6	2.4	3.3	2.8	1.4	2.5	2.9	2.2	3.5	3.2	3.6	2.1
205034_at	CCNE2	cyclin E2	0.001265705	0.3	0.3	0.1	1.0	-0.6	-0.7	1.4	1.7	1.0	1.1	3.3	3.9	2.5	2.3	2.2	3.5	3.1	0.9	2.2	3.5	3.2	3.8	2.1	3.4	2.3
219990_at	E2F8	E2F transcription factor 8	0.001955979	-0.1	0.4	0.0	0.4	0.0	0.1	1.5	2.9	1.0	1.3	3.3	3.9	2.5	3.6	2.3	3.4	2.3	0.4	2.7	3.3	2.6	4.0	2.8	3.2	2.1
1555758_a_at	CDKN3	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	0.000921274	-0.5	-0.4	-0.2	0.5	0.1	-0.1	0.9	2.2	1.2	1.2	3.2	2.9	2.8	3.4	2.2	4.0	2.8	0.8	2.3	3.3	2.7	3.7	2.5	3.3	1.5
228323_at	CASC5	cancer susceptibility candidate 5	0.000336758	0.5	-0.7	1.1	0.7	0.1	0.7	1.6	2.1	1.3	1.7	2.6	3.3	2.8	3.1	2.5	2.9	2.8	1.9	2.1	3.6	3.0	3.7	1.5	2.7	2.6
228729_at	CCNB1	cyclin B1	0.000857631	-0.3	-0.8	0.4	0.1	-1.0	-0.4	2.0	2.0	0.6	1.1	3.3	3.1	2.7	2.9	2.3	3.6	2.8	0.9	2.6	2.9	3.0	3.7	2.1	4.2	1.3
226980_at	DEPDC1B	DEP domain containing 1B	0.004385442	0.0	0.2	-0.2	0.5	-0.1	-0.1	1.4	2.4	0.7	0.8	3.2	2.9	2.6	2.8	2.0	4.2	3.2	0.8	2.1	3.4	2.5	3.6	2.5	3.8	1.4
236641_at	KIF14	kinesin family member 14	0.001419132	1.0	-0.3	0.3	0.6	-0.1	0.1	1.2	0.8	0.9	1.3	2.3	3.7	2.9	3.1	2.0	3.9	2.8	1.6	2.6	2.5	2.0	3.5	2.6	3.7	1.5
205909_at	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	0.001310864	0.6	-0.3	1.0	1.2	-0.5	0.6	1.7	2.3	1.2	1.2	3.0	3.8	2.5	3.6	2.4	3.2	2.8	1.2	2.0	3.1	2.9	3.4	2.1	3.5	2.0
222036_s_at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	0.000550412	0.0	-0.6	0.4	1.5	0.2	-0.4	0.4	2.2	1.5	1.8	3.1	3.3	2.7	3.5	2.5	3.0	2.8	1.9	2.0	4.0	2.6	3.7	1.6	2.2	2.1
223062_s_at	PSAT1	phosphoserine aminotransferase 1	0.000504571	0.3	-0.8	-0.3	0.9	-0.1	-0.5	1.2	1.3	0.6	0.6	2.8	2.7	2.0	2.6	3.1	3.3	2.3	0.5	2.3	3.2	3.4	3.6	2.1	3.3	2.5
209891_at	SPBC25	spindle pole body component 25 homolog (S. cerevisiae)	0.008699351	0.3	0.5	0.0	0.3	0.3	0.0	1.7	1.9	0.8	1.1	2.7	3.4	2.6	3.1	1.7	4.0	3.3	0.9	1.4	3.2	2.3	4.0	2.4	3.6	1.5
218662_s_at	HCAP-G	NA	0.00096649	0.1	1.1	0.6	0.6	-0.5	-0.3	1.7	2.3	0.9	1.5	2.7	3.1	2.7	3.4	1.5	3.2	2.5	1.7	2.2	3.1	3.1	3.5	1.9	3.1	2.4
203362_s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.000871445	0.0	0.6	-0.8	1.0	-0.3	-0.1	0.3	1.7	0.8	0.8	2.4	2.0	1.6	3.2	4.1	3.2	2.6	1.7	1.8	4.4	3.1	2.5	1.5	1.9	2.3
229305_at	MLF1IP	MLF1 interacting protein	0.00203952	-0.1	0.6	-0.3	1.0	-0.3	-0.1	0.5	2.7	1.4	1.4	2.8	3.9	2.2	3.8	1.9	3.5	3.9	1.6	1.4	3.6	2.8	3.1	1.8	2.2	2.0
212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.00125826	0.7	0.4	-0.1	0.7	0.0	-0.1	1.6	2.0	0.8	1.4	2.5	3.2	2.9	3.6	2.0	3.1	2.8	1.3	1.8	2.8	2.8	3.4	2.1	3.1	1.7
218009_s_at	PRC1	protein regulator of cytokinesis 1	0.001726014	1.3	0.9	-0.2	0.5	-0.3	-0.1	1.6	2.2	0.8	1.2	2.5	2.7	2.3	2.9	2.0	3.4	2.9	1.7	2.6	3.2	3.0	3.9	1.3	2.2	1.9
222608_s_at	ANLN	anillin, actin binding protein (scraps homolog, Drosophila)	0.002380275	0.3	0.4	0.1	-0.1	-0.4	-0.1	1.0	1.9	0.8	0.7	2.5	3.1	3.0	2.9	1.3	3.9	2.9	0.9	2.2	3.3	2.2	3.4	2.6	3.5	1.3
204822_at	TTK	TTK protein kinase	0.002812918	0.1	0.0	-0.1	0.8	0.2	0.6	1.5	2.5	0.7	1.4	3.1	3.3	2.1	1.9	1.7	3.6	2.9	0.7	2.2	3.4	2.8	3.9	2.4	3.8	1.9
206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	0.00275001	0.1	0.0	0.4	1.6	0.6	-0.2	1.8	3.0	1.0	1.5	2.5	3.0	3.4	-0.3	0.8	4.3	3.6	2.2	2.4	3.3	2.2	4.1	2.0	2.9	2.4
218350_s_at	GMNN	germin, DNA replication inhibitor	0.001036168	1.0	0.8	0.1	0.8	1.4	0.4	1.3	1.8	1.0	1.1	2.4	2.4	2.3	2.3	2.5	2.8	2.7	2.3	2.0	4.0	3.3	3.1	1.5	2.2	2.0
224428_s_at	CDCA7	cell division cycle associated 7	0.001257701	-0.4	0.4	-0.6	1.2	1.4	0.8	0.8	2.5	1.3	2.1	3.0	4.6	3.0	3.7	3.6	2.8	2.3	2.0	2.1	2.9	3.5	3.4	0.7	1.3	1.6
203418_at	CCNA2	cyclin A2	0.00145773	-0.2	-0.6	0.7	0.5	0.8	-0.1	1.4	1.9	1.0	1.2	3.1	3.9	2.2	3.0	2.2	3.5	2.8	0.8	2.0	3.0	2.3	3.3	2.4	3.3	2.0
204170_s_at	CKS2	CDC28 protein kinase regulatory subunit 2	0.000422178	-1.8	0.6	0.0	0.7	-0.9	-0.6	1.5	1.4	0.2	1.7	1.7	2.2	2.0	1.9	3.6	2.6	2.8	2.3	2.1	3.2	3.7	3.1	1.3	2.4	1.6
218663_at	HCAP-G	NA	0.002675296	0.6	0.1	0.2	0.6	-0.5	0.1	2.0	1.1	1.2	0.6	2.7	2.7	2.2	2.5	1.6	4.1	2.9	0.7	2.5	2.2	2.7	2.8	2.6	3.9	1.8
223556_at	HELLS	helicase, lymphoid-specific	0.000559386	0.5	0.2	0.3	0.2	0.6	-0.4	0.6	1.6	0.3	1.0	2.9	2.9	1.8	3.1	2.4	2.8	2.8	1.1	2.0	3.6	2.9	3.7	1.5	2.5	2.2
204240_s_at	SMC2L1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	0.001570119	-0.2	0.9	0.1	0.5	0.7	0.2	1.2	1.8	0.5	1.3	2.0	2.3	1.8	3.1	2.6	2.6	2.6	1.6	1.7	4.1	2.8	2.9	1.9	2.4	1.8
205393_s_at	CHEK1	CHK1 checkpoint homolog (S. pombe)	0.001597267	-0.2	0.0	-0.1	0.7	-0.1	-0.1	1.0	1.4	0.9	1.1	2.3	3.4	2.5	3.0	1.0	3.5	2.8	1.4	2.5	3.0	2.2	3.2	2.2	3.4	0.9
222740_at	ATAD2	ATPase family, AAA domain containing 2	0.000567095	1.2	0.6	0.8	0.5	1.0	0.4	1.3	2.1	0.7	0.9	2.6	2.5	1.9	2.9	3.4	2.7	2.2	1.9	1.5	3.9	3.2	3.3	1.2	1.9	1.8
201014_s_at	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	0.001236157	0.6	1.0	0.4	0.6	-0.5	0.8	0.5	1.1	0.7	0.7	2.2	2.1	1.7	2.5	1.8	2.5	2.7	1.8	2.1	4.2	2.8	2.7	2.3	2.7	1.9
202107_s_at	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae)	0.000866363	-0.1	0.1	-0.3	1.4	0.5	-0.3	1.4	2.2	1.1	1.3	2.8	3.2	2.3	3.8	1.4	2.7	2.4	1.8	1.8	3.3	3.2	3.1	1.6	2.2	2.1
205024_s_at	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	0.003741101	0.2	1.0	0.1	0.8	0.2	-0.1	1.5	1.9	1.1	1.3	3.0	3.1	2.6	2.9	1.7	2.9	2.5	1.3	1.7	3.0	2.8	3.2	2.5	2.6	1.5
219000_s_at	DCC1	NA	0.00148201	0.2	-1.2	0.2	0.1	0.4	0.5	1.6	1.1	0.5	0.3	2.5	2.1	2.2	2.7	1.8	3.2	2.9	0.3	1.7	2.9	2.6	3.0	2.1	4.0	1.5
219493_at	SHCBP1	SHC SH2-domain binding protein 1	0.000511035	0.2	-0.5	0.3	0.4	-0.1	0.1	1.3	1.3	0.6	1.3	2.5	2.6	2.3	2.4	1.7	3.2	2.6	1.1	1.6	2.6	2.1	3.6	2.4	3.4	1.8
207828_s_at	CENPF	centromere protein F, 350/400ka (mitosin)	0.002097985	0.4	0.7	0.2	1.0	0.1	0.8	1.3	1.9	0.7	1.4	2.7	3.3	2.4	3.3	2.2	2.8	2.7	1.3	1.5	2.3	3.0	3.1	1.6	2.8	1.8
208079_s_at	STK6	serine/threonine kinase 6	0.002862325	0.7	0.6	0.6	0.3	-0.2	-0.4	2.1	1.4	0.6	0.6	1.6	3.0	2.6	2.3	1.0	2.7	2.3	1.8	2.0	3.1	2.7	3.4	2.1	3.3	1.3
204768_s_at	FEN1	flap structure-specific endonuclease 1	0.003422132	0.6	0.2	0.2	0.9	0.8	0.5	0.6	2.0	0.7	1.1	2.4	2.6	2.3	3.1	1.3	3.2	2.6	1.5	2.1	3.0	2.3	2.8	1.7	2.7	1.9
213226_at	EXOSC9	exosome component 9	0.000822653	-0.1	0.0	-0.9	1.0	0.4	-0.5	1.7	1.6	0.7	1.2	2.5	2.6	2.2	2.8	2.6	2.9	2.4	1.1	1.9	3.3	2.2	3.3	1.3	2.4	2.1
219258_at	FLJ20516	NA	0.000615548	-0.1	-0.4	-1.2	0.4	0.2	-1.0	0.5	1.4	0.6	0.8	1.9	2.4	1.7	2.2	2.1	2.8	2.8	1.3	1.6	3.7	2.7	2.7	2.1	2.7	

224753_at	CDCA5	cell division cycle associated 5	0.000554356	-0.6	-0.6	0.5	0.5	-0.3	0.1	1.3	1.7	0.8	1.1	2.3	3.4	2.2	3.0	1.5	2.7	2.4	1.4	2.0	2.5	2.3	2.6	1.7	2.7	1.6
225520_at	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	0.000173538	0.1	-0.3	-0.2	0.5	-0.1	0.4	0.1	1.1	0.4	0.6	1.9	2.4	1.8	2.1	2.1	2.1	2.3	1.0	2.2	3.1	3.1	2.2	1.6	2.6	2.2
226661_at	CDCA2	cell division cycle associated 2	0.007444254	0.4	0.0	-0.6	0.8	0.5	0.0	0.7	1.7	0.8	1.0	2.9	2.6	2.1	2.3	1.3	3.6	2.7	0.7	1.6	2.6	1.6	3.1	2.3	3.6	0.9
210164_at	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	0.004479197	1.6	0.6	0.3	0.6	4.5	1.5	2.0	1.2	1.2	1.0	3.2	1.9	2.0	2.5	2.4	3.1	2.2	0.4	1.3	1.2	3.2	3.3	1.3	2.9	2.5
200783_s_at	STMN1	stathmin 1/oncoprotein 18	0.002233007	0.6	0.8	0.1	0.9	0.9	-0.5	0.9	2.2	0.7	1.1	2.5	2.7	2.0	3.3	2.5	2.5	2.5	1.8	1.3	2.7	2.8	2.0	1.1	1.7	2.0
225834_at	LOC440687	NA	0.000684359	-0.6	-0.2	1.0	1.4	-0.7	0.0	1.7	0.9	0.8	1.1	1.3	2.7	1.9	0.7	1.8	2.2	3.2	2.6	1.9	3.5	1.6	2.4	2.1	2.8	1.6
218875_s_at	FBXO5	F-box protein 5	0.002457801	-0.1	0.5	-0.4	0.9	1.2	0.6	0.9	1.4	0.7	0.7	2.1	2.1	1.3	2.2	2.7	2.6	3.0	1.6	1.2	3.2	2.8	2.4	1.6	2.0	1.5
208103_s_at	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	0.004595121	0.5	0.4	-0.8	0.5	-0.5	-0.4	0.8	1.3	0.8	1.0	1.8	1.7	1.9	2.8	3.4	2.4	2.8	1.1	1.1	3.1	2.1	2.1	1.6	1.9	1.5
218355_at	KIF4A	kinesin family member 4A	0.004912846	0.1	-0.6	0.8	0.3	-0.5	0.4	1.0	1.5	0.7	0.5	1.9	3.1	1.8	3.3	1.3	3.0	2.0	0.7	1.7	2.7	1.9	3.0	1.9	3.7	0.5
204709_s_at	KIF23	kinesin family member 23	0.008598149	0.2	0.2	0.3	0.5	0.0	-0.3	1.4	1.3	0.7	0.6	1.7	2.7	1.9	1.5	1.1	3.0	2.9	0.9	2.0	3.2	2.1	2.3	1.9	3.6	1.2
204162_at	KNTC2	kinetochore associated 2	0.000484134	0.5	0.6	-1.4	0.1	1.1	0.3	0.4	2.0	0.4	0.9	2.7	2.5	2.1	3.1	2.4	3.0	2.4	1.1	1.5	2.3	2.8	2.8	0.5	1.6	2.1
232238_at	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0.00375038	0.3	0.4	-0.1	-0.2	-0.6	0.4	1.3	1.8	0.4	0.7	1.8	1.9	1.2	2.5	1.2	2.9	3.1	0.7	1.4	2.9	1.9	3.2	2.1	3.0	1.2
226456_at	MGC24665	NA	0.000335847	-0.1	0.2	0.1	0.4	0.8	-0.2	1.0	1.9	1.2	1.3	2.4	1.7	2.0	2.8	2.1	1.5	2.8	1.2	1.9	2.5	2.1	2.4	2.0	2.1	2.0
203968_s_at	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	0.003276811	-0.3	0.1	-0.2	0.5	-0.2	-0.1	0.8	0.9	0.4	1.1	2.7	2.3	2.5	2.6	0.6	3.6	2.2	0.6	2.3	2.5	2.1	2.4	2.1	3.0	0.5
220085_at	HELLS	helicase, lymphoid-specific	0.000925707	0.8	0.8	-0.4	0.7	0.7	0.3	0.6	2.4	-0.1	0.7	2.2	2.7	2.2	2.7	1.6	1.9	2.5	0.5	1.8	3.1	2.6	3.3	1.1	1.6	2.4
213008_at	FLJ10719	NA	0.000943116	0.2	0.3	0.0	0.5	0.0	0.2	0.6	1.6	0.2	0.8	2.3	2.9	1.8	2.5	1.8	2.7	2.2	1.3	1.7	2.7	2.6	2.8	0.8	1.9	2.4
209408_at	KIF2C	kinesin family member 2C	0.000503551	-0.1	0.2	-0.5	0.8	-0.8	0.6	0.9	1.6	0.8	0.8	1.7	2.4	1.6	2.7	1.7	2.4	2.3	1.3	2.5	2.2	2.4	2.6	1.6	2.1	1.6
201202_at	PCNA	proliferating cell nuclear antigen	0.001263863	-0.5	1.4	-1.0	0.6	1.1	-0.3	1.1	1.8	0.8	1.0	2.0	2.0	1.7	2.3	4.2	2.4	1.9	1.5	1.4	2.4	2.4	2.4	1.1	1.5	1.5
219555_s_at	BM039	NA	0.001047884	-0.1	-0.7	-0.2	0.8	-0.1	0.2	1.0	1.5	0.9	1.1	2.0	2.4	1.8	2.4	1.2	3.4	3.0	0.8	1.4	2.4	1.9	2.6	1.7	2.9	1.3
213523_at	CCNE1	cyclin E1	0.001906785	0.2	0.7	-0.1	0.4	0.1	0.9	0.7	1.2	1.1	0.5	2.4	1.9	1.6	2.5	1.3	1.9	2.6	1.9	1.1	2.7	2.6	2.8	1.4	2.8	1.6
208002_s_at	ACOT7	acyl-CoA thioesterase 7	0.000706439	-0.9	-0.3	0.6	0.5	-0.5	0.4	0.3	1.8	0.7	1.0	2.4	2.7	1.6	2.8	0.6	3.1	2.6	1.5	1.7	2.6	2.7	3.0	0.9	1.7	2.0
225285_at	BCAT1	branched chain aminotransferase 1, cytosolic	0.000771874	-1.0	0.1	0.6	0.7	-0.1	-1.0	1.2	0.3	1.1	1.6	0.1	1.7	1.5	0.2	1.0	1.5	3.0	3.2	1.1	3.6	1.3	2.7	3.1	3.7	0.7
223382_s_at	ZNRF1	zinc and ring finger 1	4.654E-05	-0.3	-0.2	1.0	0.5	0.1	0.6	1.0	0.2	0.7	0.5	0.9	3.1	1.4	0.9	0.2	0.9	2.9	2.6	2.3	3.0	1.8	2.3	3.0	3.3	2.0
226936_at	C6orf173	chromosome 6 open reading frame 173	0.003579145	-0.7	0.2	0.4	0.8	-1.1	0.2	1.6	1.2	0.8	1.3	1.8	2.6	1.8	1.7	0.7	2.4	3.3	1.4	0.8	3.6	1.6	2.8	2.5	2.9	0.9
227350_at	NA	NA	0.002049989	0.9	0.1	0.7	0.2	0.9	-0.2	0.2	2.1	0.3	0.8	2.5	1.8	1.8	3.1	2.3	2.2	2.1	0.2	1.7	2.8	2.0	2.5	1.2	2.1	2.2
222037_at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	0.00350161	0.1	0.1	-0.1	0.7	-0.1	0.3	0.2	1.6	0.7	1.2	2.8	2.7	2.2	3.1	1.0	3.0	2.4	0.7	1.7	2.2	1.8	2.5	1.6	2.6	1.2
235117_at	ASB3	ankyrin repeat and SOCS box-containing 3	0.001092469	-0.3	-0.3	-0.1	0.0	0.4	-0.1	1.2	1.2	0.3	0.0	2.1	1.8	1.1	1.4	2.6	2.7	1.3	0.2	1.5	2.8	2.6	2.8	1.5	3.4	1.9
202338_at	TK1	thymidine kinase 1, soluble	0.002168592	0.2	-0.5	0.3	0.5	-0.7	0.0	1.2	2.0	0.4	1.2	1.7	2.5	1.7	2.7	1.8	2.5	2.8	1.0	1.6	2.6	2.3	2.1	1.0	2.1	1.4
212023_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.007092728	1.1	-0.3	0.1	0.5	0.6	0.0	1.1	0.9	0.4	0.9	1.6	1.6	1.3	3.8	0.8	3.1	2.5	1.2	1.0	2.8	1.8	2.2	0.9	2.9	1.4
204092_s_at	STK6	serine/threonine kinase 6	0.003708764	0.4	0.1	0.3	0.1	-0.4	0.0	1.3	1.2	0.4	0.6	1.6	2.3	1.8	2.1	2.0	2.9	1.5	1.3	1.8	2.7	1.6	2.7	1.4	3.2	0.6
226287_at	NY-REN-41	NA	0.002422994	0.1	0.2	-0.3	0.5	-0.1	0.2	0.3	1.6	-0.3	0.9	2.0	1.6	1.2	2.5	2.6	2.6	1.6	0.2	1.7	2.7	2.0	2.4	1.9	2.6	1.7
223307_at	CDCA3	cell division cycle associated 3	0.001796275	-0.4	0.7	0.1	0.3	-0.3	-1.0	1.4	1.5	0.6	1.2	2.0	2.2	2.0	2.4	1.5	2.2	1.8	1.1	1.7	2.1	2.0	2.3	2.3	2.7	1.4
218782_s_at	ATAD2	ATPase family, AAA domain containing 2	0.003760225	0.0	0.3	0.5	0.3	0.6	1.0	0.8	1.3	0.2	0.6	1.7	2.3	1.8	2.0	0.7	2.7	2.4	0.5	1.5	2.7	1.8	2.7	2.3	2.7	1.6
203358_s_at	EZH2	enhancer of zeste homolog 2 (Drosophila)	0.003727511	1.5	1.9	1.0	0.7	1.8	1.2	0.6	1.7	0.7	1.3	2.2	2.0	1.9	2.3	2.1	2.4	2.3	1.4	1.5	3.2	2.7	2.4	0.2	1.1	2.1
204531_s_at	BRCA1	breast cancer 1, early onset	0.006198034	-0.7	1.1	0.4	0.8	0.8	0.4	1.2	1.6	0.4	0.7	1.8	2.6	1.4	1.7	0.8	2.4	2.8	1.0	2.0	2.8	1.5	2.8	1.8	2.9	1.4
1554408_a_at	TK1	thymidine kinase 1, soluble	0.002699727	0.2	0.8	-0.4	0.3	0.2	-0.2	0.5	1.3	0.4	1.2	0.9	1.8	1.6	3.1	1.1	2.2	3.2	1.3	1.5	2.5	2.3	1.7	0.7	2.7	1.3
218741_at	C22orf18	chromosome 22 open reading frame 18	0.002167868	0.9	0.1	-0.2	0.5	0.2	0.1	0.9	1.7	1.0	1.4	2.2	2.0	2.1	3.1	1.4	2.6	1.9	0.5	1.9	2.5	1.7	2.6	1.3	2.3	1.2
201897_s_at	CKS1B	CDC28 protein kinase regulatory subunit 1B	0.001047451	-0.4	0.6	0.0	0.6	-0.4	0.8	0.9	1.5	0.8	0.8	1.8	1.9	1.4	1.9	1.1	2.5	2.7	1.6	1.1	2.6	2.3	2.7	1.4	2.1	1.6
203344_s_at	RBBP8	retinoblastoma binding protein 8	0.00047826	-0.7	-0.2	0.6	0.7	-0.2	-0.5	1.7	0.7	0.6	1.4	1.1	2.8	1.9	1.1	1.1	1.8	2.6	2.6	1.2	3.3	1.8	2.4	1.8	2.5	0.9
230165_at	SGOL2	shugoshin-like 2 (S. pombe)	0.000685764	-0.1	-0.2	0.7	0.0	0.1	0.3	0.5	1.0	0.4	0.5	2.2	2.4	1.7	1.2	1.8	2.6	1.8	0.9	1.2	2.4	2.1	2.8	1.7	3.2	1.6
222958_s_at	DEPDC1	DEP domain containing 1	0.008634125	0.4	-0.2	0.5	0.4	-0.7	0.4	0.8	0.9	0.4	0.6	2.1	2.1	2.0	2.2	0.7	3.4	1.9	0.6	1.1	2.3	1.3	2.9	2.3	3.6	0.7
201663_s_at	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	0.002749799	0.0	0.6	-1.0	1.1	-1.2	-0.1	0.5	1.5	0.2	0.8	1.9	1.9	1.3	1.6	1.8	2.4	2.6	1.6	1.3	2.7	1.9	3.1	0.8	2.1	1.7
225959_s_at	ZNRF1	zinc and ring finger 1	0.000485093	-1.6	-1.2	-1.0	0.5	0.8	3.7	1.4	0.1	0.9	0.3	1.0	2.8	1.5	0.4	1.0	0.7	2.6	2.3	2.3	2.4	1.7	2.2	2.3	3.2	2.1
203554_x_at	PTTG1	pituitary tumor-transforming 1	0.001949125	0.0	0.2	-0.2	0.6	-0.2	0.2	1.3	1.6	0.8	1.1	2.5	2.6	2.0	3.0	1.7	2.8	2.3	0.7	1.2	2.1	2.4	2.8	0.8	1.8	1.3
209053_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.001723023	0.9	0.1	-0.1	0.6	-0.5	-0.1	0.0	1.4	0.8	1.1	2.0	1.7	1.4	2.5	1.5	2.4	2.9	1.4	0.9	2.8	1.9	2.2	1.0	2.0	1.6
1554572_a_at	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0.004081008	0.2	0.0	0.1	0.0	-0.4	0.3	1.0	1.2	0.8	0.5	2.3	2.3	1.5	3.2	1.3	2.9	2.0	0.3	1.3	2.0	1.9	2.7	1.6	2.6	0.9
201930_at	MCM6	MCM6 minichromosome maintenance deficient 6 (MIS6 homolog, S. pombe) (S. cerevisiae)	0.009250897	1.9	0.5	-0.4	1.1	1.5	0.4	0.8	1.9	0.2	1.0	1.9	2.2	1.4	2.8	1.8	1.8	1.9	1.2	1.3	2.7	2.2	2.2	1.1	2.1	1.9
218349_s_at	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	0.003454916	0.0	0.8	-0.7	0.4	-0.2	0.1	0.7	1.4	0.1	0.5	2.0	2.2	1.3	2.1	1.8	2.5	2.2	0.1	1.3	2.5	2.1	2.7	1.4	2.6	1.7
238075_at	NA	NA	0.00894746																									

212141_at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	0.002237843	-0.4	0.0	0.2	0.3	0.6	0.2	0.9	1.1	0.7	0.9	2.4	2.7	2.2	2.3	0.5	3.2	1.9	0.9	1.3	2.0	1.6	2.6	1.9	2.5	1.1
204127_at	RFC3	replication factor C (activator 1) 3, 38kDa	0.00375617	-0.3	1.2	-0.2	0.6	0.6	0.7	0.7	1.0	0.5	0.7	1.7	2.4	1.3	1.9	2.3	1.8	2.3	1.4	1.1	3.6	1.4	2.3	1.5	2.2	1.1
235609_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.003025186	0.2	-0.4	0.5	0.3	0.5	0.2	1.2	1.9	0.4	0.9	2.4	2.5	2.6	2.5	2.2	2.9	2.0	0.8	1.3	1.5	1.2	2.4	0.8	2.5	1.2
206974_at	CXCR6	chemokine (C-X-C motif) receptor 6	0.001365622	-0.5	0.2	0.4	-0.3	-0.3	0.9	1.8	1.7	0.8	-0.5	2.3	1.8	1.6	2.8	2.4	2.2	0.7	0.1	1.7	1.7	2.3	1.8	1.4	3.1	1.9
212281_s_at	MAC30	NA	0.001094262	-0.5	-0.1	-1.8	0.3	0.2	0.1	0.1	1.2	0.0	0.5	1.9	1.6	1.0	2.2	0.8	2.1	2.0	0.3	0.8	3.0	2.7	2.8	1.5	2.4	2.1
205436_s_at	H2AFX	H2A histone family, member X	0.00687856	-0.4	1.0	-0.3	0.1	0.0	-0.1	0.7	1.1	0.5	0.8	1.8	2.1	1.5	1.3	0.6	2.3	2.5	1.1	1.3	3.1	2.0	2.4	1.5	2.4	1.6
200832_s_at	SCD	stearyl-CoA desaturase (delta-9-desaturase)	0.001511382	0.4	-0.1	1.1	1.0	-0.2	-0.2	0.0	0.7	0.6	0.4	1.7	2.3	1.3	2.5	1.1	2.3	2.2	0.9	1.7	2.5	1.7	1.9	1.6	2.2	1.6
229551_x_at	ZNF367	zinc finger protein 367	0.001094658	1.3	0.8	0.6	0.7	1.8	0.0	0.1	1.9	0.6	0.2	2.3	1.7	1.3	2.1	2.6	1.6	2.1	0.9	1.3	2.9	1.5	2.5	0.8	1.1	2.3
204886_at	PLK4	polo-like kinase 4 (Drosophila)	0.004180373	0.0	0.2	-0.2	0.8	-0.3	0.2	0.3	1.2	0.9	1.0	2.1	2.2	1.5	2.0	1.0	2.7	2.6	0.8	0.9	2.6	1.9	2.6	0.8	2.4	1.0
213454_at	CORT	cortistatin	0.000695036	-0.5	0.5	0.4	0.3	0.1	-0.1	0.7	1.5	0.5	0.9	1.7	2.1	1.6	2.4	1.7	2.3	1.4	0.8	1.5	1.9	1.8	2.1	1.6	2.3	1.6
219510_at	POLQ	polymerase (DNA directed), theta	0.00224861	0.9	-0.3	0.0	0.8	0.3	0.1	0.8	1.2	0.7	0.8	1.9	2.5	1.7	2.0	1.9	2.1	1.9	1.3	1.1	1.7	1.5	2.6	1.6	2.5	1.0
201714_at	TUBG1	tubulin, gamma 1	0.000626019	-0.1	-0.4	-0.2	0.2	0.3	0.9	0.9	0.4	0.1	0.7	1.5	1.6	1.3	2.0	0.4	2.2	2.1	0.8	1.3	2.2	2.3	2.4	1.4	2.6	1.9
228361_at	E2F2	E2F transcription factor 2	0.002991634	-0.3	-0.3	0.6	0.1	0.3	0.2	0.9	1.4	0.5	0.5	1.6	2.1	1.4	1.9	0.6	1.6	2.6	1.7	0.7	2.2	2.0	2.5	1.6	2.8	1.3
222039_at	LOC146909	NA	0.002017699	0.5	0.0	0.4	0.7	0.3	0.3	1.1	1.3	0.6	1.0	2.0	2.0	1.9	2.4	1.9	1.8	1.7	1.5	1.2	2.0	1.4	2.7	1.3	2.3	0.8
202580_x_at	FOXM1	forkhead box M1	0.008164063	-0.3	0.5	0.4	0.8	0.0	-0.2	0.6	1.1	0.3	0.6	1.5	3.1	1.5	1.7	1.1	2.6	2.2	1.3	1.3	2.7	2.5	2.0	0.7	2.4	0.8
203145_at	SPAG5	sperm associated antigen 5	0.001271199	-0.4	-0.6	-0.5	0.3	-0.7	-0.4	0.7	1.2	0.2	0.4	1.3	2.4	1.3	2.0	1.0	2.2	1.9	1.1	1.4	2.1	1.6	2.4	1.3	3.1	1.1
204023_at	RFC4	replication factor C (activator 1) 4, 37kDa	0.003415462	0.5	1.5	-0.6	0.3	1.1	0.5	0.5	1.3	0.3	0.2	2.0	1.6	1.3	2.3	1.4	2.2	1.8	0.5	0.8	2.6	2.1	2.4	1.5	2.1	1.5
226517_at	BCAT1	branched chain aminotransferase 1, cytosolic	0.001643697	-1.6	0.4	0.9	1.6	-1.3	-1.4	1.8	0.2	1.5	1.6	0.1	1.7	1.2	0.2	1.0	1.2	2.3	2.3	0.9	2.5	1.2	2.8	2.8	3.5	0.7
201577_at	NME1	non-metastatic cells 1, protein (NM23A) expressed in	0.000774185	-1.0	0.1	-0.5	0.0	-0.2	0.4	0.3	0.7	0.8	0.6	1.2	1.9	1.2	1.9	0.8	2.0	1.8	1.1	1.6	2.7	2.2	2.4	1.6	2.1	1.1
203046_s_at	TIMELESS	timeless homolog (Drosophila)	0.002965918	-0.1	0.1	-0.5	0.6	0.9	0.8	0.7	1.7	1.1	1.0	2.0	2.0	2.0	2.1	1.4	2.1	2.1	0.9	1.3	2.0	1.7	2.1	1.0	2.2	1.6
212481_s_at	TPM3	tropomyosin 3	0.00179387	-0.8	0.0	0.4	0.7	1.3	-0.2	1.0	1.0	0.7	0.6	1.2	2.5	1.6	1.5	0.2	2.0	2.2	1.1	1.5	2.7	1.7	1.8	1.8	2.1	2.0
242890_at	HELLS	helicase, lymphoid-specific	0.001956415	0.0	-0.2	0.6	0.2	0.4	0.1	0.7	0.9	0.3	0.7	1.9	1.7	1.4	1.6	1.3	2.2	2.4	0.8	1.2	2.5	1.4	3.0	0.9	2.0	1.2
212949_at	BRRN1	barren homolog (Drosophila)	0.005565762	0.1	0.6	0.2	0.3	-0.1	0.3	1.0	1.2	0.8	0.6	1.8	2.3	1.3	2.2	1.1	2.6	2.1	0.7	1.3	2.2	1.5	1.7	1.1	2.6	1.3
219588_s_at	LUZP5	leucine zipper protein 5	0.00254477	0.5	0.6	0.3	0.3	0.2	0.3	0.7	1.7	0.6	0.8	1.7	2.4	1.7	1.9	1.5	2.7	1.8	0.8	1.5	1.5	1.8	2.0	1.0	1.7	1.7
204887_s_at	PLK4	polo-like kinase 4 (Drosophila)	0.002045026	0.3	-0.4	0.1	0.4	0.0	0.0	1.1	1.2	0.4	0.8	1.9	2.0	1.4	2.0	1.6	2.4	1.8	0.7	0.7	2.3	1.7	2.2	1.1	2.6	1.3
203967_at	CDC6	CDC6 cell division cycle 6 homolog (S. cerevisiae)	0.008167871	-0.4	0.4	-0.1	0.4	-0.2	0.1	0.4	0.5	0.6	0.1	2.5	2.2	1.6	2.5	0.8	3.1	1.4	0.5	1.2	0.9	1.4	2.6	1.7	3.3	0.8
227165_at	C13orf3	chromosome 13 open reading frame 3	0.002909623	0.0	-0.2	-0.1	1.0	0.9	0.7	1.3	1.0	0.4	0.9	1.7	2.4	1.1	2.4	1.6	2.3	1.6	0.8	1.5	1.9	1.4	2.1	1.1	2.7	1.0
206486_at	LAG3	lymphocyte-activation gene 3	0.001513928	0.6	0.8	-1.1	0.3	1.0	1.2	0.6	1.0	0.4	0.0	1.9	1.6	1.4	2.6	1.2	2.5	2.0	0.2	1.3	1.3	2.4	1.4	1.2	1.7	2.4
205376_at	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	0.002793464	1.0	1.2	-0.8	0.1	0.7	0.2	-0.5	1.4	0.2	0.2	2.2	1.3	1.0	3.9	1.3	2.4	1.2	0.2	1.1	2.1	1.9	2.2	0.9	1.1	2.4
210439_at	ICOS	inducible T-cell co-stimulator	0.008899344	1.5	-0.1	-0.4	0.0	2.7	0.8	-0.5	1.3	0.2	0.0	2.3	1.4	1.1	3.6	2.0	1.9	1.8	0.5	1.4	2.1	2.9	1.0	0.4	0.0	2.8
208955_at	DUT	dUTP pyrophosphatase	0.0018691	-0.8	0.7	-1.1	0.6	1.3	1.2	0.3	1.3	0.6	0.5	2.0	1.8	1.1	2.7	1.2	2.0	2.2	0.9	1.4	2.2	1.8	1.6	1.3	1.6	1.6
223274_at	TCF19	transcription factor 19 (SC1)	0.001800816	0.6	-1.0	0.3	0.2	-0.6	0.2	0.8	1.7	0.1	0.5	2.1	2.0	1.0	2.3	1.6	2.2	1.7	0.9	0.8	2.0	2.1	1.8	1.2	2.1	1.7
202534_x_at	DHFR	dihydrofolate reductase	0.000389393	-0.5	-0.1	-0.2	0.4	0.9	0.3	0.7	1.7	0.2	0.7	2.0	2.0	1.3	2.2	3.2	1.8	1.5	1.0	0.9	2.1	1.4	1.8	1.0	1.7	1.3
202468_s_at	CTNNA1	catenin (cadherin-associated protein), alpha-like 1	0.002917179	-0.1	0.3	0.1	0.3	0.6	0.1	0.4	1.7	0.9	0.6	2.4	1.9	1.5	2.5	0.7	1.6	2.1	1.0	1.6	2.3	2.0	2.0	1.0	2.2	0.8
38158_at	ESPL1	extra spindle poles like 1 (S. cerevisiae)	0.001001897	-0.1	0.3	0.1	0.2	-0.2	0.4	0.7	1.0	0.5	0.7	1.6	2.3	1.0	1.7	1.6	2.1	2.0	1.0	1.1	1.9	1.8	1.9	1.5	2.4	1.3
222077_s_at	RACGAP1	Rac GTPase activating protein 1	0.001372515	-0.5	0.0	0.1	0.4	0.1	-0.4	1.0	1.6	0.2	0.3	1.6	2.3	1.4	1.7	2.9	2.2	1.8	0.9	1.0	1.9	1.6	2.0	1.0	1.8	1.1
45633_at	FLJ13912	NA	0.007098673	0.3	0.1	0.4	0.6	0.3	0.0	1.1	0.9	0.5	0.2	1.8	1.8	1.6	1.6	0.9	2.5	2.0	0.4	1.2	1.7	1.1	2.1	1.6	2.8	1.5
201830_s_at	NET1	neuroepithelial cell transforming gene 1	0.007092673	-0.6	-0.3	-0.6	0.5	-1.4	-0.2	-0.3	0.5	0.0	0.4	1.3	1.9	0.8	2.0	0.6	2.3	2.2	0.6	1.4	2.0	1.8	2.3	1.4	2.9	0.9
211714_x_at	TUBB	tubulin, beta polypeptide	0.00573696	-0.7	-0.1	-0.7	0.3	-0.4	-0.4	0.2	0.9	0.2	0.8	1.5	2.0	1.1	1.9	-0.3	2.2	1.7	1.3	1.6	2.4	1.9	2.2	1.1	1.9	1.9
221677_s_at	DONSON	downstream neighbor of SON	0.003558464	-0.3	-0.1	0.1	0.4	0.6	0.1	0.1	1.3	0.4	0.5	1.7	1.3	1.3	1.9	0.8	2.5	1.8	0.5	1.6	2.1	1.4	2.0	1.4	2.3	1.2
1555274_a_at	SELI	NA	0.00392176	0.7	0.1	0.0	0.4	-0.7	-0.1	0.2	0.5	0.6	0.3	1.0	1.4	0.8	2.6	1.2	2.1	2.5	0.4	0.9	2.7	2.0	1.5	1.6	1.4	1.1
225686_at	FAM33A	family with sequence similarity 33, member A	0.002503509	0.2	0.0	0.2	0.3	0.0	-0.1	0.6	1.0	0.4	1.0	1.9	1.7	1.6	2.5	1.9	2.7	1.8	0.9	1.3	1.7	1.3	1.7	0.8	1.7	0.8
222777_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.00382407	0.6	-0.8	-1.1	0.9	1.1	0.0	0.1	1.1	0.5	0.7	1.7	1.9	1.3	2.9	0.9	2.3	2.5	0.7	1.4	1.9	1.2	2.2	1.1	1.6	0.4
213253_at	SMC2L1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	0.008821169	0.1	0.3	0.2	0.9	-0.2	0.5	0.9	1.4	0.3	0.4	1.9	1.4	1.4	1.3	1.4	2.1	2.0	0.2	1.2	2.8	1.4	1.9	1.2	2.3	1.4
204558_at	RAD54L	RAD54-like (S. cerevisiae)	0.004089217	-0.5	-0.1	0.8	0.3	0.1	1.2	0.8	1.1	0.3	0.4	1.1	2.1	0.9	1.8	1.3	2.1	1.5	1.3	1.0	1.8	1.8	2.0	1.0	3.1	0.7
201755_at	MCM5	MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	0.003479846	-0.2	-0.5	-0.4	0.6	0.2	0.0	1.0	0.6	0.5	1.0	1.2	2.2	1.4	1.7	-0.3	2.1	2.2	1.4	0.9	2.9	1.6	1.9	1.1	1.7	1.5
234464_s_at	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	0.000439423	-0.5	-0.2	-0.3	0.8	0.2	-0.3	0.6	0.5	0.8	0.2	1.2	2.0	1.3	1.5	0.5	1.6	1.9	1.2	1.2	2.4	1.5	2.0	1.8	2.4	1.1
217755_at	HN1	hematological and neurological expressed 1	0.002427772	0.3	0.2	-0.5	0.4	0.4	0.4	0.9	0.5	0.3	0.9	0.9	1.7	1.2	1.2	0.0	1.9	2.2	1.4	1.2	2.7	2.0	1.8	1.0	2.0	1.4
226319_s_at	THOC4	THO complex 4	0.006109661	0.4	0.3	-0.5	0.																					

201761_at	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methylenetetrahydrofolate cyclohydrolase	0.000279439	-1.0	0.2	-0.1	0.8	2.1	0.7	1.1	-0.1	0.5	0.8	0.3	2.1	1.2	0.4	1.8	0.7	2.4	2.6	1.2	2.2	1.3	1.7	1.6	1.6	1.0
204159_at	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0.000766077	-0.3	-0.4	-0.1	0.3	-0.5	0.0	0.6	1.0	0.4	1.2	1.2	1.6	1.4	1.7	1.8	1.8	2.8	1.1	1.1	3.0	0.9	1.0	0.8	1.4	1.0
200806_s_at	HSPD1	heat shock 60kDa protein 1 (chaperonin)	0.000372547	-0.3	-0.3	-0.5	0.1	-0.9	-0.4	0.4	0.7	-0.2	0.1	1.3	1.6	0.9	1.1	0.5	1.9	1.5	0.4	1.6	2.5	2.0	1.9	1.2	2.5	1.6
202309_at	MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	0.002128876	-0.3	-0.9	-0.1	0.3	-0.1	-0.2	0.7	1.0	0.5	0.7	1.3	1.9	1.1	2.2	0.8	1.8	1.9	1.2	1.1	2.5	1.8	1.8	1.2	1.6	0.8
222402_at	C13orf12	chromosome 13 open reading frame 12	0.00026348	-1.1	-0.1	0.0	0.4	-0.3	0.4	1.3	-0.2	0.3	0.5	0.4	1.7	0.8	0.6	2.4	1.4	1.7	1.9	0.6	2.3	1.9	1.7	1.7	2.1	0.5
202069_s_at	IDH3A	isocitrate dehydrogenase 3 (NAD+) alpha	0.000563351	-0.6	0.7	0.1	0.9	0.3	1.0	1.1	-0.1	0.2	0.4	0.5	1.2	0.6	0.3	1.6	0.7	2.2	1.6	1.3	3.1	1.0	1.6	1.7	2.3	1.4
222500_at	PP1L1	peptidylprolyl isomerase (cyclophilin)-like 1	0.003281824	0.4	0.9	-0.9	-0.3	0.3	-0.9	0.2	0.8	0.2	0.0	1.1	0.9	0.9	1.3	2.2	1.7	1.3	0.0	1.1	1.9	2.0	1.6	1.4	2.6	1.3
217777_s_at	HSPC121	NA	0.006570993	0.3	0.5	-0.6	0.6	-0.8	-0.1	0.9	0.7	0.5	0.4	1.4	1.1	0.8	1.4	1.6	2.4	1.6	0.3	1.3	2.2	1.9	2.2	0.6	1.8	1.4
213092_x_at	MRPS16	mitochondrial ribosomal protein S16	0.002068205	0.0	-0.2	-0.9	-0.1	1.0	0.3	0.1	1.3	0.5	0.4	1.8	1.6	1.1	2.2	1.1	1.9	1.5	0.6	0.8	2.2	1.7	1.9	1.4	1.7	1.3
48808_at	DHFR	dihydrofolate reductase	0.001045072	0.1	0.1	-0.1	0.3	0.1	0.4	0.4	1.4	0.0	0.5	2.1	2.3	1.3	1.9	1.4	1.9	1.6	1.2	1.2	2.2	1.3	1.6	1.0	1.5	1.2
201476_s_at	RRM1	ribonucleotide reductase M1 polypeptide	0.002810389	0.4	-0.2	-1.0	0.0	-1.1	0.4	0.4	1.1	0.5	0.4	1.7	1.2	1.1	1.7	1.0	2.7	1.6	0.7	1.4	1.8	1.1	1.5	1.0	2.4	1.2
221685_s_at	FLJ20364	NA	0.001142373	-0.3	0.2	0.4	0.2	0.9	0.3	0.6	0.7	0.1	0.0	1.7	0.5	0.6	1.6	1.0	1.9	1.8	0.2	0.8	2.4	1.7	1.8	1.2	2.8	1.4
222154_s_at	DNAPT6	NA	0.003349845	-0.6	0.5	-1.7	0.7	-0.9	0.6	0.7	0.7	-0.2	0.1	0.5	2.3	1.4	1.6	1.0	1.3	1.8	1.1	0.7	2.1	1.8	1.8	0.9	2.2	1.5
155698_a_at	LOC285513	NA	0.002323694	0.3	-0.1	-0.6	0.3	-0.3	0.3	0.7	0.6	0.6	0.5	1.9	1.7	1.5	2.0	1.5	2.0	1.6	0.3	1.7	0.6	1.1	1.6	1.1	1.8	2.3
228559_at	NA	NA	0.00285918	0.2	-0.2	0.4	0.0	-0.1	-0.6	1.0	0.9	0.0	0.8	1.5	2.0	1.3	2.1	1.0	2.2	1.5	0.7	1.2	1.6	1.1	1.8	1.2	2.8	0.8
202886_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	0.002422219	0.0	0.0	0.3	-0.3	-0.7	0.5	0.7	0.6	0.4	0.5	1.6	2.0	1.3	1.9	1.3	1.9	1.5	0.2	1.1	1.2	1.3	2.2	1.4	2.6	1.1
203405_at	DSCR2	Down syndrome critical region gene 2	0.000508344	0.1	-0.4	0.3	0.2	0.4	0.1	0.5	0.7	0.1	0.3	1.2	1.6	0.9	1.0	3.0	1.7	1.3	0.8	0.8	2.7	1.2	1.7	0.9	2.0	1.0
242939_at	TFDP1	transcription factor Dp-1	0.00423533	0.5	0.4	-0.3	0.6	0.2	0.3	0.2	0.6	0.6	0.8	0.9	1.8	1.1	1.8	0.9	2.1	2.2	1.0	1.1	2.5	1.7	1.4	1.1	1.3	0.7
234944_s_at	FAM54A	family with sequence similarity 54, member A	0.001834909	-0.2	0.0	0.1	0.1	0.0	0.2	0.8	1.1	0.3	0.0	1.3	1.3	0.9	1.3	0.5	2.2	1.7	0.5	0.7	1.3	1.6	2.6	1.5	2.6	1.5
203432_at	TMPO	thymopoietin	0.000706999	-0.4	0.3	0.1	0.4	1.2	-1.0	0.6	0.4	0.2	0.8	0.6	1.5	0.7	1.2	1.2	1.6	2.1	1.3	0.8	3.0	1.1	1.5	1.3	2.0	1.0
205085_at	ORC1L	origin recognition complex, subunit 1-like (yeast)	0.007423189	0.1	-0.2	-0.1	0.4	0.1	-0.1	0.5	0.6	0.6	0.7	1.8	1.7	0.9	2.5	1.2	2.7	1.6	0.3	0.9	1.3	0.9	1.5	0.6	3.4	0.9
223700_at	GAJ	NA	0.009923674	0.0	0.1	-0.4	0.0	-0.2	-0.2	0.7	0.8	0.9	0.7	2.2	1.9	1.8	1.1	0.6	3.2	0.9	0.2	1.4	1.5	0.6	2.5	1.3	2.9	0.8
215629_s_at	KIAA1799	NA	0.002426175	-0.3	0.8	0.6	0.6	0.3	0.6	0.1	0.8	0.8	0.5	1.4	1.1	1.5	1.3	2.7	2.3	1.7	0.8	0.7	2.2	0.8	1.1	0.6	1.6	1.6
200615_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit	0.002462582	-0.2	-0.1	-0.3	1.0	-0.2	0.5	0.8	0.2	0.2	0.5	0.4	2.2	1.0	1.5	0.2	1.4	1.5	1.1	0.9	3.1	1.7	1.6	1.1	2.0	1.4
213088_s_at	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	0.002150635	-0.6	0.5	-1.2	0.1	1.8	-0.5	0.1	1.2	0.4	0.5	1.8	1.1	1.1	2.4	1.6	1.9	1.5	0.2	0.8	2.2	1.6	1.6	0.7	1.6	1.5
231772_x_at	CENPH	centromere protein H	0.001265493	0.4	-0.7	-0.1	0.4	0.0	0.0	0.2	1.0	0.6	0.9	1.9	1.5	1.6	2.2	1.5	2.1	1.8	0.6	1.0	1.9	1.2	1.0	0.6	1.9	1.1
204510_at	CDC7	CDC7 cell division cycle 7 (S. cerevisiae)	0.002874976	0.5	1.2	0.2	0.0	0.8	0.7	0.5	1.5	0.6	0.1	1.6	0.5	1.0	2.0	3.5	2.0	1.1	-0.2	0.8	1.4	1.7	1.9	0.2	1.2	1.8
227212_s_at	PHF19	PHD finger protein 19	0.009813728	-0.3	-0.2	-1.3	0.6	0.2	0.0	0.9	0.7	0.6	0.6	1.3	1.6	1.0	1.6	0.3	1.7	2.0	1.2	1.0	2.2	1.5	1.7	0.8	2.1	1.3
226694_at	PALM2-AKAP2	NA	0.005749339	0.8	-0.3	-0.2	0.5	0.5	-0.5	0.5	1.2	0.0	1.2	1.7	2.3	1.8	2.0	1.5	1.6	1.6	0.5	0.9	1.3	1.7	2.5	-0.1	0.9	2.2
212282_at	MAC30	NA	0.004231731	0.3	0.2	-0.2	0.8	0.3	0.5	0.2	1.1	0.2	0.5	1.3	1.3	1.0	2.0	0.6	1.8	1.4	0.0	0.7	2.2	1.8	2.2	1.3	2.1	1.4
204728_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.008680525	-0.2	0.1	0.6	-0.3	0.1	0.1	0.2	0.9	0.2	0.3	1.7	1.7	1.4	1.7	1.7	2.8	1.4	0.4	0.9	1.0	0.9	1.5	1.4	2.6	0.6
227478_at	SETBP1	SET binding protein 1	0.002749911	0.6	0.4	-0.6	-0.6	0.9	-0.3	2.0	0.8	0.8	0.9	2.2	2.5	2.2	1.3	1.4	1.3	1.7	0.8	0.7	1.4	1.3	1.8	1.3	1.4	1.8
209825_s_at	UCK2	uridine-cytidine kinase 2	0.003618914	0.2	-0.3	-0.4	0.2	-0.7	0.5	0.4	0.5	0.5	0.2	1.3	1.3	1.1	1.3	0.3	2.1	1.4	0.5	0.7	2.1	1.7	2.1	1.6	2.7	0.7
209507_at	RPA3	replication protein A3, 14kDa	0.006979976	0.0	0.2	-0.4	0.4	0.6	0.2	0.8	0.8	0.8	0.4	1.5	1.2	1.1	2.1	1.0	2.4	1.7	0.6	0.8	1.8	1.8	1.6	0.9	1.5	1.0
203276_at	LMNB1	lamin B1	0.000320533	-0.7	-0.2	-0.3	0.4	-0.2	0.3	0.9	-0.1	-0.2	0.7	0.7	1.6	1.0	1.0	-0.4	1.3	2.0	1.8	1.5	1.9	1.1	2.0	1.7	2.6	0.8
1554768_a_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.009467545	0.0	0.1	-0.3	0.3	-0.1	-0.2	0.7	1.2	0.7	0.5	2.6	1.0	1.6	1.0	1.1	3.4	1.1	0.4	1.2	1.4	0.9	1.6	1.4	2.4	0.7
201664_at	SMC4L1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	0.002609889	0.3	1.7	0.2	0.5	1.2	-0.6	0.4	1.1	0.1	0.6	1.5	1.6	1.1	1.6	1.7	1.7	1.7	0.6	0.9	1.9	1.7	1.8	0.5	1.6	1.3
205692_s_at	CD38	CD38 antigen (p45)	0.007072048	-0.2	-0.1	0.1	1.3	-0.3	0.5	1.3	1.5	-0.2	1.5	1.2	1.8	1.2	1.0	0.1	2.7	1.6	1.5	0.9	2.4	1.4	2.2	0.6	1.3	1.4
208791_at	CLU	clusterin (complement lysis inhibitor, SP-40, 40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	0.008853436	-0.6	0.7	0.0	0.4	0.2	-0.2	-0.3	-0.2	0.0	0.5	2.1	1.4	1.2	1.5	-0.9	-2.2	2.0	3.2	2.3	2.8	0.2	1.0	1.5	3.4	2.1
228468_at	MASTL	microtubule associated serine/threonine kinase-like	0.001833404	0.4	0.5	-0.4	0.0	-0.5	-0.4	0.5	0.8	0.5	0.4	0.8	0.5	0.8	1.2	1.9	1.6	1.9	1.1	1.0	2.7	0.8	1.2	1.1	1.8	0.9
204817_at	ESPL1	extra spindle poles like 1 (S. cerevisiae)	0.001535675	0.4	0.1	0.0	0.0	-0.1	0.4	0.4	1.0	0.6	0.6	1.3	1.4	1.6	1.5	1.4	2.2	1.2	1.2	1.2	1.6	0.9	1.0	0.8	2.5	1.0
211519_s_at	KIF2C	kinesin family member 2C	0.002043771	-0.1	-0.3	0.5	0.2	0.4	-0.1	0.5	0.8	0.4	0.1	0.8	1.2	1.0	1.2	0.9	2.5	1.8	0.8	0.9	1.4	1.0	1.8	0.7	3.0	0.9
238462_at	STS-1	NA	0.003805382	0.1	0.7	-0.1	0.0	0.1	0.4	1.0	1.1	0.7	0.5	1.0	0.9	1.5	1.2	1.5	0.3	0.7	1.7	1						

203960_s_at	C1orf41	chromosome 1 open reading frame 41	0.008793181	0.9	0.3	0.2	0.3	-0.1	0.5	0.5	0.7	0.7	0.9	1.6	2.3	1.2	1.1	1.1	2.8	1.4	1.2	1.0	2.1	1.7	1.3	0.4	1.6	0.9
218073_s_at	TMEM48	transmembrane protein 48	0.004216947	0.1	0.7	-0.3	0.1	-0.1	0.0	0.5	1.1	0.3	0.2	1.1	0.5	1.3	1.0	0.8	1.7	1.7	0.4	0.9	2.0	1.5	1.9	1.5	2.3	0.9
213646_x_at	K-ALPHA-1	NA	0.001870799	-1.1	0.3	-0.4	0.6	0.5	-0.3	1.3	0.8	0.4	0.8	1.0	1.4	1.2	1.2	0.1	1.6	1.5	1.4	1.2	1.9	1.6	1.6	1.4	1.7	1.3
212320_at	TUBB	tubulin, beta polypeptide	0.002466281	-1.7	0.2	-1.0	0.0	2.7	-0.7	0.7	1.0	0.2	0.6	1.3	2.2	1.0	1.5	1.2	1.6	1.4	1.0	1.3	1.5	1.6	1.5	0.9	1.5	1.4
219159_s_at	SLAMF7	SLAM family member 7	0.001323831	-0.4	0.2	0.1	0.3	-0.9	0.5	1.6	0.6	0.0	-0.5	1.8	1.1	1.3	1.9	0.7	2.4	0.7	0.2	0.1	1.2	2.3	2.7	0.0	0.9	2.9
231577_s_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.00431454	-0.8	0.4	-1.3	0.3	1.2	-0.1	1.2	0.7	0.2	0.0	1.4	2.1	1.1	1.6	2.3	1.2	1.2	1.7	1.6	0.4	2.4	1.7	0.5	0.3	1.3
222192_s_at	FLJ21820	NA	0.001861826	0.4	-0.3	-0.1	0.8	-0.5	-0.1	0.3	0.7	0.1	0.1	0.8	0.6	0.7	1.4	2.2	1.7	1.1	-0.2	1.0	2.1	1.7	1.5	0.5	1.9	1.6
218493_at	C16orf33	chromosome 16 open reading frame 33	0.002577407	-0.5	-0.8	-0.8	0.3	0.2	-0.6	1.2	0.4	0.6	0.3	0.9	0.8	0.9	1.0	-0.1	1.8	1.8	1.3	1.3	3.0	1.3	1.4	1.1	1.6	0.8
206316_s_at	KNTC1	kinetochore associated 1	0.005123178	0.4	0.1	0.5	0.6	0.5	1.0	0.3	1.3	0.5	0.4	1.6	1.4	1.1	1.6	0.6	1.7	1.7	0.7	0.4	2.1	1.1	1.8	1.0	1.9	1.5
201111_at	CSE1L	CSE1 chromosome segregation 1-like (yeast)	0.001831697	0.0	-0.2	0.4	0.4	0.1	0.2	1.2	0.6	-0.2	-0.2	1.1	1.2	0.8	0.5	2.2	1.2	1.3	0.8	0.9	1.7	1.8	1.7	1.4	2.3	0.6
209911_x_at	HIST1H2BD	histone 1, H2bd	0.001960426	0.1	-0.3	-0.1	0.7	-0.2	0.2	0.9	1.1	0.3	0.5	2.4	1.4	1.6	1.5	0.7	1.1	1.5	0.7	1.1	1.7	1.1	1.9	1.2	1.2	1.8
211072_x_at	K-ALPHA-1	NA	0.003617325	-1.0	0.7	-0.7	0.5	0.9	-0.5	1.1	0.8	0.4	0.7	1.1	1.4	1.2	1.2	0.3	1.4	1.4	1.4	1.1	1.8	1.4	1.6	1.3	1.7	1.3
218156_s_at	FLJ10534	NA	0.001090471	-0.7	0.1	-1.0	1.0	-0.2	0.5	-0.2	0.2	0.4	0.0	0.5	1.1	0.8	0.7	1.4	1.5	1.2	1.0	1.0	2.1	1.4	1.6	1.1	2.0	1.2
218049_s_at	MRPL13	mitochondrial ribosomal protein L13	0.006628611	-0.2	-0.1	0.1	0.3	-1.0	0.1	1.4	0.6	0.2	0.5	0.8	1.3	0.9	1.0	0.3	1.9	2.0	0.9	0.9	2.5	1.6	1.4	1.3	1.8	0.7
202532_s_at	DHFR	dihydrofolate reductase	0.003838161	0.2	0.0	0.0	0.3	0.0	0.3	0.9	1.3	0.6	0.3	2.3	1.2	1.1	1.7	1.2	1.7	1.4	0.7	1.1	1.7	0.9	1.5	1.1	2.3	0.4
202330_s_at	UNG	uracil-DNA glycosylase	0.00281218	-0.2	0.0	0.3	0.0	0.9	0.5	0.3	1.4	0.3	0.2	1.7	1.2	1.1	2.1	0.9	1.7	1.4	0.0	1.1	1.8	1.7	1.7	0.6	1.6	1.3
200987_x_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.000438067	-0.9	-0.8	-0.7	0.4	0.7	0.2	0.9	0.4	0.2	0.8	0.6	1.6	0.9	0.8	-0.4	1.6	2.1	1.2	1.1	2.5	1.3	1.4	1.4	1.9	1.1
203022_at	RNASEH2A	ribonuclease H2, large subunit	0.000196999	-0.3	-0.2	-0.3	0.1	-0.3	0.1	0.5	0.7	0.5	0.6	1.3	1.0	1.0	1.3	0.9	1.8	1.4	0.7	1.1	1.5	1.5	1.6	0.9	2.1	1.2
212639_x_at	K-ALPHA-1	NA	0.001793747	-1.0	0.3	-0.9	0.7	1.5	-0.5	1.0	0.8	0.4	0.8	1.0	1.2	1.1	1.1	0.1	1.3	1.5	1.5	1.2	1.9	1.4	1.6	1.1	1.8	1.2
208977_x_at	TUBB2	NA	0.000694921	-0.7	-0.5	-1.1	0.0	0.3	-1.1	1.0	0.6	0.4	0.8	1.0	1.5	1.2	1.1	-0.3	1.5	2.2	0.8	0.9	1.9	1.6	1.7	0.8	2.1	1.2
203211_s_at	MTMR2	myotubularin related protein 2	0.005471748	-0.1	0.2	0.6	0.6	0.4	0.3	0.6	1.0	-0.1	0.3	1.4	1.3	1.1	2.2	1.8	1.6	0.8	0.0	0.8	1.8	1.9	1.6	0.5	1.7	0.9
211058_x_at	K-ALPHA-1	NA	0.001698604	-1.2	0.8	-0.2	0.5	0.9	-0.4	1.1	0.8	0.3	0.6	1.0	1.4	1.2	1.1	0.2	1.4	1.4	1.4	1.1	1.7	1.4	1.5	1.4	1.7	1.2
202647_s_at	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	0.002633075	0.0	0.3	-0.6	0.8	0.1	-1.0	0.8	0.4	0.5	0.8	0.5	1.4	0.7	0.6	1.4	1.2	1.8	1.6	0.9	2.8	1.4	1.1	1.1	1.3	0.8
211747_s_at	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.004239581	-0.2	0.3	-0.5	0.3	1.2	-0.6	-0.2	0.7	0.5	0.5	0.9	0.4	0.5	1.0	3.5	1.4	1.7	0.1	0.8	2.6	1.3	0.9	0.9	1.2	0.7
211713_x_at	KIAA0101	KIAA0101	0.007908176	-0.9	0.2	1.4	0.2	-0.4	0.2	0.7	1.3	0.8	0.1	1.6	2.3	1.7	1.5	1.9	1.2	1.2	0.5	0.8	2.5	2.0	1.2	0.6	1.9	-0.3
206110_at	HIST1H3H	histone 1, H3h	0.008566668	-0.3	0.3	0.1	0.4	-0.2	-0.3	-0.9	-0.5	-0.9	-0.5	1.7	1.4	1.4	1.2	1.7	-1.4	1.3	2.6	1.9	2.9	0.0	0.8	0.4	1.9	1.9
204173_at	MLC1SA	NA	0.003765738	-0.2	-0.2	-0.2	1.0	0.2	-0.1	0.2	0.8	1.1	1.1	1.2	1.7	1.2	1.6	0.5	2.0	1.6	0.6	1.0	1.9	1.5	1.4	1.2	1.4	0.7
227545_at	BARD1	BRCA1 associated RING domain 1	0.00317397	0.3	-0.2	0.1	-0.3	1.2	0.6	0.5	1.2	0.4	0.6	1.8	1.5	0.5	0.8	1.3	1.5	1.0	0.9	1.2	1.9	1.5	2.4	0.7	1.6	1.1
209715_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	0.000939527	-0.5	0.3	-0.5	-0.2	0.3	-0.3	0.4	0.5	0.3	0.3	1.5	1.0	1.3	1.9	0.7	1.8	1.7	0.0	1.2	1.9	1.3	1.0	0.5	1.4	1.8
213726_x_at	TUBB2	NA	0.001268362	-0.8	0.4	-1.1	0.0	0.1	-0.9	0.4	0.7	0.2	0.6	1.1	1.4	1.1	0.9	-0.4	1.5	2.0	0.7	1.0	1.7	1.6	1.8	1.0	2.2	1.3
218392_x_at	SFXN1	sideroflexin 1	0.003073746	0.8	-0.3	0.3	0.2	0.4	0.1	-0.1	0.8	0.0	0.0	1.4	1.5	0.9	1.8	1.1	2.0	1.6	-0.1	1.4	1.3	1.2	1.4	1.0	1.6	1.2
208795_s_at	MCM7	MCM7 minichromosome maintenance deficient 7 (S. cerevisiae)	0.002740675	0.0	0.5	-0.4	0.2	0.2	0.3	0.5	1.0	0.4	0.4	1.6	1.3	1.1	2.0	0.5	2.0	1.3	0.5	0.8	1.6	1.5	1.5	0.9	1.6	1.1
244519_at	ASXL1	additional sex combs like 1 (Drosophila)	0.000766415	0.9	-0.4	0.0	0.0	0.9	-0.4	-0.3	0.6	0.3	0.1	1.0	1.4	0.9	1.8	0.3	1.4	1.5	0.5	0.6	2.3	1.4	1.0	1.4	1.8	1.5
228955_at	NA	NA	0.001978564	0.3	0.8	0.2	0.2	0.1	0.5	0.0	0.7	0.5	0.2	1.4	0.8	1.0	1.2	1.8	1.5	1.6	0.4	1.0	1.9	1.1	1.4	0.4	1.4	1.7
204835_at	POLA	polymerase (DNA directed), alpha	0.002061147	-0.3	-0.3	-0.5	0.3	0.2	0.2	0.3	1.1	0.3	0.5	1.2	1.9	0.9	1.9	1.3	1.6	1.6	0.3	0.5	2.1	1.4	1.8	1.0	1.3	0.9
213984_at	SCC-112	NA	0.004094219	0.4	0.0	0.3	0.6	0.2	-0.4	-0.1	0.3	1.0	0.6	0.3	1.1	1.0	1.7	1.3	1.9	1.3	0.6	1.0	1.8	1.6	1.3	0.5	1.5	0.7
201555_at	MCM3	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	0.002167649	-0.1	0.2	-0.4	0.1	0.6	0.2	0.2	1.1	0.0	0.3	1.5	1.2	1.0	2.0	0.0	1.9	1.5	0.4	0.8	1.9	1.5	1.6	0.7	1.7	1.3
203716_s_at	DPP4	dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2)	0.007863659	0.5	0.2	-0.6	0.1	-0.5	0.5	0.2	1.0	0.4	0.1	1.2	-0.3	0.5	2.7	0.8	1.6	0.7	0.1	1.4	1.9	1.4	0.9	0.8	2.4	1.0
202269_x_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.007583677	-0.6	-0.3	-1.6	0.3	1.8	0.8	1.2	0.8	0.4	0.1	1.4	2.6	1.1	1.4	0.7	1.4	1.3	1.7	1.6	0.6	2.3	1.6	0.8	0.2	1.6
227211_at	PHF19	PHD finger protein 19	0.001631715	0.5	-0.3	-0.3	0.3	0.0	-0.6	0.5	0.8	0.6	0.5	1.2	1.6	0.9	1.3	0.5	1.5	1.7	1.1	0.7	2.0	1.4	1.5	1.2	1.8	0.8
204186_s_at	PPID	peptidylprolyl isomerase D (cyclophilin D)	0.001232219	-0.6	0.2	-0.1	0.4	0.7	-0.3	0.0	0.7	-0.1	0.3	0.7	0.8	0.4	0.9	2.5	1.6	1.4	0.2	0.9	1.9	1.2	1.5	1.1	1.7	1.1
225765_at	TNPO1	transportin 1	0.001238231	0.5	-0.4	0.0	0.1	0.0	-0.1	0.3	0.7	0.0	0.1	1.1	1.2	0.7	1.5	1.7	1.4	1.3	0.0	1.0	2.0	1.4	1.3	1.0	1.8	1.2
227291_s_at	BOLA3	bolA-like 3 (E. coli)	0.005228626	-0.8	0.3	-1.3	0.2	0.5	0.5	-0.1	0.9	0.4	0.1	1.5	0.8	0.9	1.9	1.1	2.3	1.0	-0.2	0.9	1.7	1.8	1.4	0.8	1.6	1.1
205053_at	PRIM1	primase, polypeptide 1, 49kDa	0.008376158	0.2	0.3	-1.0	0.3	0.8	0.7	0.0	1.2	0.3	0.1	1.8	1.4	0.6	1.9	1.4	1.8	1.2	0.4	0.9	1.8	1.5	1.0	0.9	1.5	1.3
201490_s_at	PPIF	peptidylprolyl isomerase F (cyclophilin F)	0.006652014	1.3	-0.5	0.1	0.3	-0.4	0.1	0.2	-0.7	0.1	0.4	-0.2	1.2	0.4	0.7	0.0	1.4	1.9	1.7	0.7	2.0	1.8	1.4	1.0	2.4	0.7
221520_s_at	CDCA8	cell division cycle associated 8	0.002395175	0.2	-0.2	0.4	-0.1	-0.1	0.2	0.8	0.6	0.4	0.2	1.1	1.7	0.9	1.4	1.0	2.0	1.2	0.3	1.1	1.2	1.2	1.4	0.9	2.6	0.9
211750_x_at	TUBA6	NA	0.001868341	-1.2	-0.1	-0.7	0.6	0.4	-0.1	1.1	0.7	0.3	0.8	1.0	1.2	0.9	1.0	-0.1	1.4	1.5	1.4	1.2	1.8	1.4	1.5	1.2	1.8	1.1
202483_s_at	RANBP1	RAN binding protein 1	0.005854666	-0.1	-0.6	-1.4	0.4	1.4	0.0	0.4	0.5	0.2	0.4	1.3	0.8	0.8	1.7	0.5	1.8	1.7	0.7	0.9	1.9	1.5	1.2	0.9	1.5	1.0
212378_at	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	0.006444																									

202533_s_at	DHFR	dihydrofolate reductase	0.005636185	-0.1	-0.3	-0.2	0.8	0.2	0.1	0.5	0.4	0.5	0.3	1.8	1.5	0.7	1.4	0.5	2.2	1.3	0.3	0.9	1.7	0.9	1.5	0.7	2.6	1.1
209853_s_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.005555842	-0.5	0.5	-0.5	0.1	-0.3	0.5	0.8	0.3	0.2	0.6	0.8	1.6	1.0	1.0	-0.1	1.7	1.4	1.2	0.6	1.7	1.1	1.6	1.4	2.1	1.2
209251_x_at	TUBA6	NA	0.000702205	-1.4	0.1	-0.6	0.5	1.2	-0.4	1.2	0.6	0.2	0.7	1.0	1.2	1.0	1.0	0.0	1.3	1.4	1.4	1.2	1.6	1.4	1.4	1.3	1.8	1.2
205933_at	SETBP1	SET binding protein 1	0.000436685	0.6	-1.0	-0.1	-0.2	0.1	-0.2	1.4	0.5	0.4	0.6	1.1	2.1	1.8	1.6	1.1	1.2	0.9	0.5	0.5	1.1	1.3	1.5	1.1	1.7	1.5
212590_at	RRAS2	related RAS viral (r-ras) oncogene homolog 2	0.006112531	0.2	0.0	-0.5	0.2	-0.2	0.1	-0.2	0.6	0.9	0.4	2.1	0.8	1.1	2.4	0.5	1.9	1.6	-0.7	0.4	2.2	1.7	1.9	0.8	1.0	1.2
205449_at	SAC3D1	SAC3 domain containing 1	0.000933105	-1.0	-0.2	-0.3	0.4	0.0	0.1	0.6	0.6	0.1	0.3	0.8	1.0	0.9	1.1	0.1	0.8	2.2	1.6	0.9	2.5	0.9	1.3	1.1	1.6	1.0
1554080_at	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	0.002577155	0.5	0.0	-0.2	0.4	0.9	-0.2	-0.1	0.4	0.6	0.1	1.1	0.9	0.8	1.6	1.6	1.8	1.4	0.2	0.8	1.9	1.5	1.2	0.8	1.2	1.0
212810_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.001412824	-0.2	-0.4	0.0	0.4	0.3	0.4	0.8	0.7	0.0	0.5	0.8	1.3	0.9	1.3	0.0	1.7	1.7	0.9	0.9	1.3	1.5	2.2	0.8	1.8	0.8
225114_at	AGPS	alkylglycerone phosphate synthase	0.00230326	0.7	-0.2	-0.4	0.7	0.2	0.1	-0.2	0.0	0.4	0.4	0.3	1.2	0.7	0.2	3.4	1.0	1.7	1.3	0.7	2.9	0.6	0.8	0.9	1.0	0.8
221987_s_at	SRR	serine racemase	0.003937638	-0.3	1.0	-0.6	0.9	-0.2	0.4	0.2	0.3	0.2	0.0	1.0	1.2	0.9	0.6	0.6	1.2	1.5	0.4	0.8	1.9	1.2	1.8	1.3	2.3	1.1
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.006990843	-1.1	0.6	-0.4	0.5	-0.2	-0.2	0.8	0.7	0.5	0.9	1.2	1.9	1.2	1.6	0.1	2.2	1.7	1.1	0.7	1.5	1.2	1.6	0.5	1.0	1.2
201016_at	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	0.001595638	-0.2	-0.2	-0.4	0.4	0.1	-0.5	-0.1	0.3	0.0	0.2	0.5	0.5	0.6	0.7	2.9	1.6	1.4	0.6	0.8	2.5	1.1	1.0	0.9	0.9	0.5
216870_x_at	DLEU2	deleted in lymphocytic leukemia, 2	0.001647263	-0.3	0.5	0.0	0.7	-0.4	-0.1	0.4	0.6	0.5	0.6	1.0	0.7	1.3	0.9	2.9	1.6	1.2	0.6	0.5	1.6	0.4	1.3	0.7	1.4	1.2
222646_s_at	ERO1L	ERO1-like (S. cerevisiae)	0.000969921	-0.4	0.7	-1.1	0.3	0.4	-0.8	0.0	0.4	0.2	0.4	0.9	1.4	0.7	0.6	2.0	1.0	1.4	1.2	0.6	2.5	1.2	0.9	1.3	1.4	0.8
202154_x_at	TUBB3	tubulin, beta 3	0.000865202	-0.3	-0.2	-0.7	0.0	-1.1	-0.9	0.3	0.2	0.1	0.5	1.0	1.3	0.9	1.0	0.0	1.5	1.2	0.6	1.0	1.9	1.7	1.8	0.9	2.0	1.0
225647_s_at	CTSC	cathepsin C	0.001139245	-1.0	-0.5	-0.4	0.5	0.0	0.3	0.9	0.4	0.3	0.8	0.9	0.4	1.2	0.8	0.8	1.4	1.4	1.0	0.5	2.0	1.6	1.4	0.7	1.2	1.5
205733_at	BLM	Bloom syndrome	0.006107336	0.3	0.2	-0.4	0.2	-0.1	1.0	0.4	0.9	0.2	0.3	0.7	1.3	0.9	1.5	1.4	1.8	0.8	0.2	0.6	1.3	1.4	1.5	1.0	2.0	1.2
218069_at	XTP3TPA	NA	0.000481722	-0.6	-0.3	-0.4	0.1	0.2	0.3	0.1	0.5	0.3	0.2	1.1	1.0	0.6	1.4	0.9	1.5	1.3	0.4	1.0	1.6	1.6	1.4	1.2	1.7	0.9
209398_at	HIST1H1C	histone 1, H1c	0.003906921	-0.9	0.6	-0.3	0.5	0.2	0.0	-0.3	0.5	0.6	0.8	1.4	1.5	0.8	1.7	0.3	2.0	2.0	0.8	0.4	1.6	1.5	1.3	0.4	0.3	2.3
214437_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	0.00711052	-0.4	-0.3	-1.2	0.7	1.1	0.4	0.1	0.5	0.3	0.6	0.7	0.5	0.8	0.7	0.1	1.4	1.7	1.3	1.0	2.0	0.9	1.9	0.9	1.7	1.0
217294_s_at	ENO1	enolase 1, (alpha)	0.001823707	-1.1	0.4	0.3	0.9	0.3	0.4	0.1	-0.5	0.3	0.6	0.6	0.5	0.4	0.3	-0.7	2.1	2.1	1.5	1.7	1.9	1.0	1.4	1.0	1.5	1.1
210691_s_at	CACYBP	calyculin binding protein	0.005520571	-0.7	0.6	0.1	0.3	0.5	-0.1	-0.1	0.7	0.3	0.4	0.9	1.0	0.9	1.1	1.6	1.9	1.5	-0.1	0.8	2.4	1.1	1.5	0.6	1.2	0.9
209849_s_at	RAD51C	RAD51 homolog C (S. cerevisiae)	0.001636043	-1.4	-0.2	0.1	0.4	1.3	0.2	0.7	0.7	0.0	0.0	1.0	1.5	0.7	1.3	1.1	1.4	1.1	0.0	0.6	1.6	1.8	1.8	1.1	2.4	0.4
208792_s_at	CLU	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	0.009842365	-0.3	-0.8	0.7	0.2	0.4	0.9	0.1	-0.2	-0.3	0.4	1.8	1.0	1.2	0.8	-0.4	-2.1	1.4	3.0	2.0	2.6	0.4	1.0	1.2	2.6	1.6
220239_at	KLHL7	kelch-like 7 (Drosophila)	0.00093305	-0.6	0.7	-0.2	0.7	-0.1	-0.2	0.4	0.1	0.5	0.6	0.9	2.0	0.9	1.5	0.4	1.8	2.1	1.3	0.8	2.6	1.1	1.2	0.8	0.8	0.1
202854_at	HPRT1	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	0.006308164	-1.1	0.4	-1.1	0.3	0.0	-0.1	0.2	0.5	0.4	0.5	0.7	1.3	1.0	1.0	1.7	1.3	1.6	1.0	0.6	2.2	1.1	1.1	0.6	1.3	0.8
222011_s_at	ACAT2	acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase)	0.000697794	-0.1	0.5	0.3	0.6	0.0	-0.7	-0.1	0.4	0.3	0.5	0.7	0.9	0.8	1.5	2.4	1.0	1.3	0.6	0.5	2.5	1.0	1.1	0.5	0.9	1.2
227916_x_at	EXOSC3	exosome component 3	0.008487963	-1.5	0.8	-0.4	0.5	0.0	-1.0	1.3	0.3	-0.1	0.0	0.8	1.3	0.8	1.2	0.4	1.5	0.8	0.8	1.1	1.3	1.1	1.8	1.5	2.2	0.8
219819_s_at	MRPS28	mitochondrial ribosomal protein S28	0.001794538	-0.1	0.3	-0.3	-0.2	-0.6	0.4	0.4	0.5	0.5	-0.1	0.8	0.7	0.9	0.6	0.7	1.7	1.4	1.1	0.7	2.1	1.3	1.4	1.2	1.7	0.5
222404_x_at	HSPC121	NA	0.005628209	-0.1	-0.7	-1.1	0.0	0.5	0.3	0.8	0.5	0.3	-0.2	1.4	1.1	0.7	1.3	0.4	2.1	1.4	0.0	1.2	1.7	1.8	1.4	0.6	1.7	1.0
201489_at	PPIF	peptidylprolyl isomerase F (cyclophilin F)	0.003593293	1.0	-0.2	-0.4	0.4	0.4	0.0	0.7	-0.4	0.7	0.7	0.2	1.2	0.4	0.7	-0.9	0.7	2.4	2.0	0.5	2.4	1.5	1.6	1.3	2.1	0.7
203465_at	MRPL19	mitochondrial ribosomal protein L19	0.002698054	-0.1	-0.1	-0.4	0.2	-0.4	-0.2	0.6	0.4	0.2	0.4	0.7	0.9	1.0	1.2	1.8	1.6	1.4	0.6	0.8	1.6	0.9	1.0	0.8	1.6	1.1
201829_at	NET1	neuroepithelial cell transforming gene 1	0.008267211	0.9	0.9	0.0	0.2	-0.3	-0.2	0.0	0.9	-0.1	0.1	1.2	1.0	0.6	1.0	1.0	1.3	1.7	0.6	0.2	1.9	0.7	1.6	1.5	2.0	1.1
224320_s_at	MCM8	MCM8 minichromosome maintenance deficient 8 (S. cerevisiae)	0.002101713	0.1	-0.3	0.2	0.0	0.6	-0.4	0.4	1.2	-0.1	-0.1	1.7	1.0	1.0	1.5	1.4	1.8	1.4	-0.5	0.4	1.4	1.0	1.9	1.0	1.9	1.1
218549_s_at	FAM82B	family with sequence similarity 82, member B	0.004308557	-0.4	0.7	-0.8	0.5	1.8	1.0	0.7	0.2	0.5	0.7	0.7	1.0	0.9	0.4	2.3	1.3	1.5	1.1	0.5	2.1	1.0	1.0	1.1	1.3	0.8
1555618_s_at	SAE1	NA	0.00434193	-0.6	0.7	0.3	0.3	0.1	0.8	0.4	0.1	0.3	0.6	0.6	1.3	0.3	1.9	1.7	2.0	1.5	0.8	1.3	1.7	1.1	0.6	0.6	1.4	0.4
208910_s_at	C1QBP	complement component 1, q subcomponent binding protein	0.002808335	-1.2	0.2	-0.3	0.0	0.2	0.3	0.1	0.7	0.4	0.5	0.7	-0.1	0.6	1.1	0.9	1.6	1.4	0.4	1.1	2.4	0.9	1.1	1.2	1.5	0.8
217834_s_at	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	0.000398543	-2.7	-0.5	-0.3	0.4	-0.2	-0.9	0.6	0.2	0.1	0.0	0.5	1.4	0.6	0.6	1.6	0.9	1.7	0.9	0.8	2.2	0.9	1.3	1.3	1.8	0.5
209231_s_at	DCTN5	dynalectin 5 (p25)	0.002342813	0.6	-0.7	-0.3	0.4	-0.4	-0.1	0.7	0.7	0.1	0.3	0.8	1.2	1.0	1.0	0.2	2.1	0.6	0.6	1.3	1.0	1.5	1.1	1.2	2.4	1.2
201614_s_at	RUVBL1	RuvB-like 1 (E. coli)	0.002999358	-1.0	-0.4	-0.4	0.5	-1.0	0.3	0.2	0.8	0.4	0.5	1.6	0.7	1.0	2.0	1.3	1.9	1.1	0.1	0.9	2.0	1.2	1.1	0.3	1.4	0.7
222962_s_at	MCM10	MCM10 minichromosome maintenance deficient 10 (S. cerevisiae)	0.00704105	-0.2	-0.3	0.1	0.1	0.5	0.3	0.5	0.8	0.5	0.2	1.6	1.1	0.9	1.5	1.1	2.0	0.8	0.1	0.5	1.2	0.8	1.8	0.7	2.7	0.7
202760_s_at	PALM2-AKAP2	NA	0.003909305	0.5	0.3	0.1	0.4	-0.1	-0.1	0.7	1.3	-0.2	1.4	1.5	1.9	1.5	1.6	-0.4	1.5	1.3	0.5	0.6	0.9	1.5	2.7	0.0	1.4	2.0
223515_s_at	COQ3	coenzyme Q3 homolog, methyltransferase (yeast)	0.005326161	-0.1	-0.1	-0.5	0.2	0.1	-0.4	0.4	0.9	0.2	0.2	1.4	0.7	0.7	1.8	1.6	2.0	0.8	-0.2	1.0	1.5	1.3	1.2	0.5	1.7	1.1
226118_at	ADCY3	adenylate cyclase 3	0.001492116	0.3	-0.1	-0.2	-0.2	1.2	0.3	0.9	1.0	0.2	0.4	1.3	1.2	1.4	1.5	0.8	1.6	1.6	0.3	0.9	0.9	1.2	1.8	0.3	1.5	1.1
204252_at	CDK2	cyclin-dependent kinase 2	0.002564403	0.3	-0.3	-0.1	0.1	0.1	0.4	0.0	0.8	0.1	0.4	1.5	1.3	0.6	1.4	0.8	1.5	1.7	0.2	1.3	1.3	1.0	0.9	1.1	2.0	1.2
211767_at	SLD5	NA	0.007971561	-0.6	-0.3	0.2	0.5	0.3	0.2	0.3	1.3	0.5	0.7	0.8	1.5	0.8	2.2	0.6	1.8	1.2	0.1	0.2	1.6	0.9	1.2	1.4	2.0	0.9
202872_at	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C, isoform 1	3.99879E-05	-1.0	-0.2	0.3	0.2	0.1	0.0	1.3	-0.5	0.1	0.6	-0.1	0.8	0.5	-0.4	1.7	0.9	1.2	2.2	0.8	1.6	0.9	1.1	1.6	1.7	1.0
203023_at	HSPC111	NA	0.000588742	-0.3	-0.5	-0.3	0.2	-0.5	0.6	0.3	0.3	0.4	0.4	0.9	-0.2	0.7	0.9	1.0	1.6	0.7	0.3	1.4	1.6	1.0	1.1	1.0	2.2	1.3
34764_at																												

222209_s_at	FLJ22104	NA	0.006654147	1.1	0.8	-0.7	-0.1	-0.2	-0.9	0.2	0.8	0.3	0.4	1.4	0.6	0.8	1.4	2.5	1.4	0.8	0.6	0.9	1.8	1.1	1.2	0.4	1.1	0.8
219785_s_at	FBXO31	F-box protein 31	0.002443336	-0.2	-0.6	0.4	0.7	0.4	0.1	0.1	0.7	0.2	0.7	1.0	1.0	0.7	1.4	1.2	1.6	0.6	0.2	0.6	1.5	1.2	2.1	1.3	1.6	0.7
217919_s_at	MRPL42	mitochondrial ribosomal protein L42	0.000341417	-0.8	-0.4	-0.3	0.0	-0.5	-0.4	1.0	0.8	0.3	0.4	0.8	0.6	0.8	0.8	0.6	1.8	1.2	1.1	1.1	1.5	1.4	1.4	0.8	1.6	0.7
212330_at	TFDP1	transcription factor Dp-1	0.000867781	-1.7	-1.0	0.4	0.8	-0.4	0.1	0.4	0.9	0.5	0.5	1.0	1.9	0.8	1.5	1.1	1.4	1.6	1.1	0.7	1.9	0.8	1.1	0.9	1.3	0.5
226686_at	LOC493856	NA	0.000170816	-0.3	-0.7	0.2	0.2	-0.5	0.3	0.3	0.1	0.0	0.4	0.6	1.4	0.7	0.8	2.1	1.4	1.5	0.8	0.8	1.4	1.2	1.0	1.1	1.2	0.6
222701_s_at	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	0.008484873	0.0	1.0	-1.0	0.2	-0.4	0.5	0.4	0.4	0.3	0.5	0.7	1.2	1.1	0.7	0.4	1.2	0.9	1.1	1.1	2.0	1.2	1.2	1.0	1.6	1.1
201060_x_at	STOM	stomatin	0.007787746	-0.1	0.6	-1.0	0.1	2.5	0.3	1.0	0.6	0.1	-0.1	1.2	2.0	1.1	1.2	2.0	1.1	1.3	0.1	0.8	1.0	1.4	1.4	0.9	1.3	1.2
201764_at	MGC5576	NA	0.003179941	-0.3	0.2	-0.3	0.3	0.2	0.4	0.0	0.9	0.3	0.1	1.8	1.3	0.5	2.1	0.6	2.0	1.1	0.2	0.6	1.4	1.4	1.4	0.8	1.8	0.6
212568_s_at	DLAT	dihydropyrimidine S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	0.006073581	0.2	-0.1	-0.3	0.5	0.0	0.1	0.5	1.0	0.3	0.1	1.0	1.6	0.6	0.8	2.6	1.4	1.1	0.7	0.8	1.4	0.7	1.0	1.2	1.6	0.6
218982_s_at	MRPS17	mitochondrial ribosomal protein S17	0.003343766	0.1	-0.9	-0.1	0.4	-0.3	0.9	0.7	0.5	0.3	0.1	0.9	1.4	0.8	1.3	0.4	1.3	1.3	0.5	0.9	1.9	1.5	1.4	1.0	1.9	0.6
212811_x_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	0.005603682	-0.5	0.2	0.4	0.7	0.6	0.6	0.1	0.6	0.1	0.6	0.8	1.7	1.0	0.8	0.1	1.9	1.4	0.7	0.8	1.3	1.3	1.4	1.3	1.9	0.6
203564_at	FANCG	Fanconi anemia, complementation group G	0.00681653	0.7	0.3	0.1	0.0	1.4	0.4	0.2	1.4	0.4	0.0	1.5	1.5	1.1	1.7	1.0	1.6	1.2	0.2	0.4	1.2	1.3	1.5	0.6	1.3	1.3
220094_s_at	C6orf79	chromosome 6 open reading frame 79	0.003218959	-0.6	0.1	0.1	0.3	0.4	0.2	0.1	0.8	0.1	0.6	1.2	1.4	1.2	1.2	0.0	0.9	1.7	0.8	0.9	2.4	0.9	1.2	0.9	1.3	1.0
205687_at	UBPH	NA	0.001820533	-0.3	0.3	0.3	0.2	0.1	0.5	0.2	0.2	-0.1	0.3	0.5	0.9	0.8	0.8	0.7	1.4	0.6	0.2	0.8	1.7	1.2	1.9	1.0	2.2	1.1
213320_at	HRMT1L3	HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae)	0.007856649	0.9	0.6	-0.7	0.3	0.7	0.1	0.0	0.4	0.4	-0.1	0.5	0.9	0.6	0.8	2.3	1.2	1.3	0.4	0.9	2.3	1.3	0.7	0.8	1.2	0.6
212533_at	WEE1	WEE1 homolog (S. pombe)	0.00081113	-0.1	0.1	-0.4	0.0	0.7	0.7	0.3	1.0	0.0	0.0	1.7	2.1	1.3	1.5	2.5	1.4	0.6	0.1	0.4	0.8	1.2	2.0	0.3	1.0	1.2
1557910_at	HSPCB	heat shock 90kDa protein 1, beta	0.005139608	-0.6	0.0	-1.5	0.1	0.2	0.2	0.4	0.6	0.5	0.2	0.4	1.4	0.7	1.0	0.4	1.3	1.5	0.1	1.5	1.8	1.2	1.4	0.6	1.5	1.3
210448_s_at	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	0.005875197	-0.2	0.8	0.0	0.3	1.4	1.0	-0.1	1.1	0.9	0.5	1.6	0.1	0.9	1.2	0.2	-0.4	0.8	1.5	1.4	1.5	1.8	1.6	0.8	1.1	2.0
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa	0.00050976	-1.1	0.2	0.1	0.3	2.2	1.1	0.9	0.4	-0.1	0.0	1.0	2.0	0.7	1.0	3.1	0.7	1.2	1.7	0.9	0.2	1.9	1.3	0.6	-0.1	1.0
206991_s_at	CCR5	chemokine (C-C motif) receptor 5	0.00176931	-0.2	-0.7	-0.2	-0.2	0.9	0.9	1.4	1.1	-0.1	-0.3	1.2	1.1	1.6	2.4	1.5	1.6	-0.1	0.1	0.9	0.5	1.5	1.1	0.1	1.8	1.2
209080_x_at	TXNL2	thioredoxin-like 2	0.001141766	-0.4	0.1	-0.1	0.2	0.0	-0.4	0.8	0.3	0.4	0.3	0.8	0.7	0.8	0.8	0.9	1.6	1.4	0.8	0.9	2.0	1.0	1.0	0.7	1.2	1.1
202068_s_at	LDLR	low density lipoprotein receptor (familial hypercholesterolemia)	0.002006672	0.3	-0.6	-1.2	0.5	1.3	0.6	0.7	-0.4	0.3	-0.3	-0.3	1.9	0.7	1.2	0.3	0.4	1.7	1.4	0.4	1.2	1.9	1.2	1.2	1.3	1.3
202759_s_at	PALM2-AKAP2	NA	0.004919508	-0.9	0.2	-0.4	0.6	-0.8	-0.1	0.3	0.8	0.3	1.4	1.5	1.7	1.3	1.7	1.0	1.7	1.1	0.1	1.0	0.4	1.4	1.7	0.1	1.1	1.6
204128_s_at	RFC3	replication factor C (activator 1) 3, 38kDa	0.009283647	0.3	0.1	-0.2	0.3	0.0	0.1	0.0	0.8	0.5	0.8	0.7	1.3	0.4	0.8	0.8	2.3	1.1	0.5	1.3	0.7	0.9	1.4	0.8	2.5	0.7
205345_at	BARD1	BRCA1 associated RING domain 1	0.006453447	0.2	0.6	0.5	-0.2	2.1	0.2	0.8	1.1	0.2	0.3	1.4	0.6	0.8	1.2	-0.4	1.7	1.2	0.8	0.8	1.9	1.4	1.5	0.6	1.4	1.3
239002_at	ASPM	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0.002933488	-0.5	-0.4	0.1	0.6	-0.4	-0.5	0.8	1.1	0.5	0.5	0.8	1.2	0.9	1.0	0.5	1.7	1.2	0.3	0.3	1.1	1.0	2.0	1.0	2.4	0.8
231769_at	FBXO6	F-box protein 6	0.000935744	-0.1	-1.5	-0.1	0.6	0.9	0.7	0.9	-0.1	0.0	0.4	0.4	1.3	0.7	0.4	0.7	1.1	1.5	1.6	0.8	1.2	1.4	1.4	1.0	0.6	1.6
228931_at	COQ4	coenzyme Q4 homolog (yeast)	0.001599183	-0.7	0.1	0.0	0.0	-0.9	0.3	0.0	0.9	0.5	0.2	1.1	0.9	0.7	1.5	0.9	1.7	1.0	0.5	0.8	1.2	0.9	1.4	0.9	1.9	0.7
212038_s_at	VDAC1	voltage-dependent anion channel 1	0.003617036	-0.8	-0.2	-1.1	0.5	0.5	-0.5	0.3	0.2	0.4	0.5	0.4	0.5	0.7	0.7	1.5	1.1	1.5	0.8	0.8	2.1	1.0	1.2	0.7	1.4	0.7
209218_at	SQLE	squalene epoxidase	0.001620482	-0.6	0.4	-0.1	0.4	0.1	0.1	0.6	0.1	0.2	0.1	0.4	1.9	0.9	0.8	0.9	0.3	0.0	1.3	0.4	1.4	1.3	2.0	0.9	1.8	2.1
200039_s_at	PSMB2	proteasome (prosome, macropain) subunit, beta type, 2	0.008088016	-1.4	-0.5	-1.7	0.3	0.8	0.0	0.6	0.3	0.5	0.5	0.8	0.6	0.7	1.0	0.2	1.6	1.6	0.9	0.5	1.9	1.4	1.2	0.8	1.5	0.8
202085_at	TJP2	tight junction protein 2 (zona occludens 2)	0.00164002	-0.8	-1.9	-0.6	0.8	0.3	-2.0	1.4	-0.6	-0.7	0.7	0.0	2.4	1.3	-1.0	0.5	-0.5	2.8	2.9	0.2	2.3	0.5	1.3	1.4	1.7	0.9
216705_s_at	ADA	adenosine deaminase	0.004458413	-0.2	0.4	-0.8	0.5	0.9	0.2	0.7	0.9	0.4	0.5	1.5	1.1	1.1	2.1	0.0	1.6	1.3	0.5	0.9	1.1	1.9	1.5	-0.5	0.8	1.9
215380_s_at	C7orf24	chromosome 7 open reading frame 24	0.001581867	-1.6	-0.9	-0.8	0.2	1.3	1.5	0.2	0.6	0.3	0.5	1.0	1.1	0.8	1.1	0.7	1.5	1.6	0.5	1.0	1.9	1.0	1.3	0.9	1.4	0.4
1558292_s_at	PIGW	phosphatidylinositol glycan, class W	0.002017947	-1.3	0.5	-0.2	0.4	-0.2	-0.3	-0.1	0.4	0.5	0.1	0.9	0.8	0.7	1.3	2.5	0.9	1.1	-0.3	1.0	1.3	1.1	1.1	1.1	1.2	0.9
209520_s_at	NCBP1	nuclear cap binding protein subunit 1, 80kDa	0.002473953	0.0	-0.2	0.1	0.5	-0.3	-0.2	1.2	0.1	0.1	0.3	0.8	1.0	0.8	0.8	0.4	1.4	1.0	0.7	0.9	1.2	1.0	1.4	0.8	2.4	1.4
1556283_s_at	FGFR1OP2	FGFR1 oncogene partner 2	0.003051754	-0.8	0.1	-0.4	1.0	0.1	-1.1	0.5	-0.3	0.2	1.0	0.3	1.7	0.6	0.4	-0.1	1.2	1.9	2.4	0.6	2.7	0.8	1.1	0.7	1.4	0.4
235256_s_at	GALM	galactose mutarotase (aldose 1-epimerase)	0.001869262	-0.6	0.0	-0.3	0.0	0.4	0.0	0.1	1.0	-0.1	0.2	1.5	0.6	0.7	2.1	1.0	2.5	1.1	0.1	0.9	1.1	0.9	1.0	0.3	1.4	0.9
228286_at	FLJ40869	NA	0.002531505	0.4	0.0	-0.5	0.3	0.4	-0.4	0.4	0.7	0.1	0.3	1.0	0.6	1.2	0.6	1.8	1.5	0.9	0.5	0.4	1.4	0.6	1.3	0.6	1.8	1.4
209186_at	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.00342191	-0.1	1.2	-0.1	0.3	0.7	-0.2	0.9	0.0	0.6	0.2	0.5	1.4	0.5	0.6	0.9	1.1	1.4	0.7	1.1	1.8	1.5	1.3	1.0	1.4	0.6
212527_at	D15Wsu75e	NA	0.00050975	-0.2	0.9	-0.5	0.0	-0.1	-0.1	0.2	0.2	0.2	0.5	0.5	0.8	0.6	0.6	0.9	0.8	1.0	0.9	1.3	0.9	1.4	1.2	1.3	2.0	1.2
219017_at	ETNK1	ethanolamine kinase 1	0.002836563	0.6	-0.9	0.8	0.8	0.0	0.3	1.3	0.0	0.1	0.5	0.6	1.0	1.0	0.4	2.6	1.0	0.7	1.5	0.9	1.6	1.0	1.2	0.5	0.8	0.6
212295_s_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	0.001057772	0.1	-0.1	-2.0	-0.3	1.8	0.4	0.2	0.6	0.2	0.1	1.3	0.9	0.7	1.7	1.2	1.5	1.0	-0.3	0.9	1.2	1.6	1.5	0.6	1.8	0.7
226269_at	GDAP1	ganglioside-induced differentiation-associated protein 1	0.007056168	0.6	0.9	-0.8	-0.2	-0.4	0.0	0.4	0.2	0.9	0.6	1.1	1.2	1.2	0.8	1.2	1.4	0.9	0.5	1.3	1.6	0.9	1.5	0.8	1.4	0.4
214426_x_at	CHAF1A	chromatin assembly factor 1, subunit A (p150)	0.006116278	0.2	-0.2	0.4	0.3	0.8	0.0	1.0	0.2	0.3	0.1	-0.1	1.7	1.1	1.3	0.7	1.4	1.4	0.9	0.4	1.7	1.0	0.9	1.0	1.5	0.6
218817_at	SPCS3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	0.000449329	-1.3	-0.3	-0.6	0.4	0.3	0.0	0.3	-0.1	0.1	0.5	0.3	1.8	0.5	0.4	1.7	0.8	1.5	1.3	0.3	2.6	0.9	1.2	1.0	1.1	0.7
201277_s_at	HNRPAB	heterogeneous nuclear ribonucleoprotein A/B	0.000389452	-0.6	-0.4	-0.2	0.1	2.5	-0.2	0.8	0.5	0.2	0.4	0.8	1.0	0.8	0.9	0.2	1.3	1.5	0.7	0.8	1.8	1.2	1.2	1.0	1.9	0.8
213476_x_at	TUBB3	tubulin, beta 3	0.001973278	-0.1	0.4	-0.9	0.3	-0.2	-0.2	0.5	0.3	0.2	0.6	0.9	0.8	1.0	1.0	-0.6	1.3	1.5	0.7	0.7	1.7	1.6	1.4	0.8	2.0	0.7

219386_s_at	SLAMF8	SLAM family member 8	0.00561512	-0.1	-0.5	-0.8	0.6	-0.5	0.7	2.1	0.0	0.4	0.8	1.2	2.8	1.7	0.7	-0.5	1.0	0.6	1.7	0.2	0.3	2.4	2.7	0.8	0.2	2.1
214155_s_at	LARP4	La ribonucleoprotein domain family, member 4	0.003240371	0.1	-0.2	0.3	0.3	-0.3	-0.5	0.6	0.1	-0.1	0.3	0.9	1.2	1.2	0.5	1.3	1.2	1.2	0.1	0.8	1.0	0.7	1.5	1.3	2.2	0.9
213849_s_at	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	0.004851537	0.9	0.8	-0.4	-0.1	1.3	0.0	0.4	0.9	0.0	-0.1	1.7	1.1	0.9	2.8	2.0	1.6	0.4	-0.9	0.1	0.6	1.4	1.8	0.3	1.4	1.4
218911_at	YEATS4	YEATS domain containing 4	0.007636508	0.1	0.0	-0.5	0.1	-0.4	0.2	-0.2	0.8	0.6	0.3	1.0	0.9	0.8	2.0	1.4	2.1	1.6	0.0	0.6	1.4	0.7	1.0	0.2	1.3	0.6
201946_s_at	CCT2	chaperonin containing TCP1, subunit 2 (beta)	0.001721301	-0.5	0.0	0.0	0.0	-0.2	-0.1	0.1	0.7	0.6	0.3	0.9	0.8	0.8	0.9	-0.2	1.6	1.3	0.2	1.6	1.7	1.4	1.3	0.2	1.3	1.7
1564520_s_at	SKB1	SKB1 homolog (S. pombe)	0.00069822	-1.1	0.2	-1.1	0.2	0.1	0.8	-0.5	0.0	0.4	-0.2	0.8	0.4	0.5	0.7	0.3	0.9	1.6	1.1	0.9	2.0	0.8	0.9	1.2	1.7	1.1
212828_at	SYNJ2	synaptojanin 2	0.005675929	1.5	0.0	-0.2	0.2	-0.1	-0.8	-0.5	1.1	0.1	0.1	1.2	-0.2	0.4	2.1	1.3	0.1	1.3	-0.2	1.0	2.1	0.9	0.9	0.7	1.2	1.9
200650_s_at	LDHA	lactate dehydrogenase A	0.000405127	-1.1	0.5	-0.9	0.3	3.1	0.2	0.4	0.4	0.5	0.5	0.6	1.3	0.8	1.0	0.9	1.0	1.2	0.8	1.0	1.5	1.1	1.2	1.1	1.3	1.1
225253_s_at	FLJ12760	NA	0.001377796	-0.4	0.4	0.2	0.1	0.0	0.4	0.0	0.6	0.0	0.6	0.7	0.7	0.9	0.8	0.5	1.4	1.1	0.4	1.0	1.8	1.1	1.5	0.5	1.7	1.1
202691_at	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	0.004222384	-0.6	-0.1	-0.7	0.4	-0.4	0.7	0.4	0.6	0.2	0.2	0.9	1.3	0.8	1.0	0.5	1.4	1.9	0.5	0.7	1.8	1.0	1.2	0.9	1.3	0.8
201521_s_at	NCBP2	nuclear cap binding protein subunit 2, 20kDa	0.003005511	-0.6	0.7	-0.3	0.6	-0.2	0.0	0.1	0.4	0.4	0.8	0.6	0.7	0.9	0.7	-0.3	1.3	1.1	0.9	0.6	2.0	0.9	1.2	1.5	2.1	1.0
235139_at	GNGT2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	0.009804943	0.2	0.6	-0.1	0.1	-0.3	1.0	0.9	0.9	0.2	0.3	0.9	1.7	1.0	1.6	0.0	1.2	0.6	0.7	0.3	1.3	1.4	1.3	0.9	1.6	1.7
214959_s_at	API5	apoptosis inhibitor 5	0.002050353	-0.3	0.1	-0.1	0.2	-0.1	0.6	0.1	0.0	0.2	0.2	1.0	1.2	0.6	1.1	1.2	2.1	0.8	0.3	1.0	1.3	1.1	1.2	0.3	1.9	0.7
203594_at	RTCD1	RNA terminal phosphate cyclase domain 1	0.002883079	-0.7	1.0	0.0	0.2	0.8	0.7	0.6	0.4	0.3	0.4	0.9	1.2	0.6	0.9	1.2	1.2	0.8	0.8	0.8	2.3	0.9	1.0	0.7	1.6	0.9
213461_at	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.007936817	0.4	0.3	0.4	0.3	0.2	0.4	0.6	0.8	0.3	0.6	0.8	0.6	0.6	1.7	1.0	1.6	1.2	0.7	1.2	1.3	0.4	1.1	0.8	1.3	0.8
228606_at	TM4SF19	transmembrane 4 L six family member 19	0.001632062	-0.3	-1.2	0.0	0.9	-0.9	-0.4	-0.3	1.1	0.4	0.3	1.6	1.1	0.6	1.9	2.2	1.8	0.9	0.2	0.4	1.4	1.1	1.4	0.2	0.7	0.8
205120_s_at	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	0.001424869	-0.4	0.5	-0.2	0.3	0.0	0.8	0.0	0.8	0.4	-0.3	1.6	1.3	0.4	1.6	-0.3	1.9	1.1	0.1	0.7	1.2	1.5	2.1	0.9	1.7	0.7
225766_s_at	TNPO1	transportin 1	0.002752886	-0.4	0.2	0.1	0.2	-0.7	0.7	0.5	0.6	0.1	0.1	0.9	1.1	0.6	1.2	1.2	1.2	1.1	0.0	1.0	1.4	0.8	1.0	1.0	1.6	1.4
204775_at	CHAF1B	chromatin assembly factor 1, subunit B (p60)	0.009844047	-0.1	-0.7	0.8	0.1	-0.1	0.5	0.1	0.6	0.5	0.9	1.5	1.5	0.7	1.7	0.8	1.8	1.2	0.3	1.1	1.0	0.8	1.1	1.2	1.6	0.5
217946_s_at	SAE1	NA	0.009894269	-0.7	0.3	-1.0	0.3	-0.4	-0.7	0.1	0.7	0.3	0.4	0.9	0.8	0.4	1.3	0.5	1.5	1.5	0.6	0.6	2.0	1.2	0.9	0.7	1.3	1.0
202884_s_at	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 65), beta isoform	0.001573357	0.0	0.0	0.3	0.5	0.1	0.3	0.5	0.6	0.3	0.5	1.1	0.9	0.5	1.4	1.3	1.7	1.0	0.6	0.6	1.1	1.1	0.8	0.8	1.7	0.9
221923_s_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.003563087	0.0	0.3	-0.7	0.0	-0.1	0.1	0.0	0.6	0.3	0.3	0.9	0.8	0.5	1.3	1.2	1.5	1.1	0.4	0.9	1.5	1.4	1.0	0.9	1.2	0.5
225723_at	C6orf129	chromosome 6 open reading frame 129	0.005700454	-1.7	0.2	-0.2	0.3	0.3	0.1	0.5	0.7	0.4	0.5	1.3	1.0	0.9	1.6	0.3	2.1	1.2	0.1	0.9	1.9	1.2	1.5	0.5	1.0	0.4
218894_s_at	FLJ10292	NA	0.005317679	-0.2	0.0	0.0	0.2	0.2	-0.2	0.4	0.4	0.4	0.1	1.4	1.1	0.7	1.2	0.5	1.8	1.0	0.0	0.7	1.8	1.1	1.2	0.9	1.6	1.0
239680_at	WDR76	WD repeat domain 76	0.003457751	-0.4	0.1	-0.2	0.0	-0.3	-0.2	-0.2	1.2	0.1	0.2	1.9	1.0	1.2	2.2	1.0	1.5	0.5	0.1	0.9	0.8	0.6	1.5	0.7	1.4	1.1
212185_x_at	MT2A	metallothionein 2A	0.001304317	-0.3	-0.6	0.4	0.5	0.0	0.2	0.4	0.7	0.3	0.6	0.8	1.6	1.0	1.4	0.7	1.7	1.2	0.3	0.7	1.0	1.6	1.5	0.8	0.9	0.8
223151_at	MGC2714	NA	0.009493293	-0.4	1.0	-1.1	0.0	0.0	0.7	0.4	0.2	0.1	0.1	0.8	1.1	0.6	1.2	0.7	1.4	1.3	0.9	0.6	1.8	1.1	1.1	0.5	1.4	0.9
218027_at	MRPL15	mitochondrial ribosomal protein L15	0.004537535	-1.7	0.2	-1.1	0.4	0.3	1.0	0.6	0.0	0.4	0.4	0.2	0.8	0.6	0.4	0.2	1.0	1.5	1.3	0.8	2.0	1.1	1.2	1.2	1.5	0.7
1554020_at	BICD1	bicaudal D homolog 1 (Drosophila)	0.007070109	0.1	-0.3	0.3	-0.3	-0.3	0.5	0.0	1.1	0.4	0.2	1.2	1.1	0.3	1.8	1.3	1.0	1.6	0.2	0.3	1.3	1.2	1.7	0.3	2.0	0.5
221935_s_at	AER61	NA	0.009037592	0.6	0.1	-0.6	0.2	0.5	0.1	-0.1	0.7	0.0	0.4	0.8	0.5	0.8	1.5	2.6	2.5	1.4	-0.5	0.2	2.1	0.8	0.6	-0.3	0.8	1.0
219553_at	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	0.007721258	0.2	0.1	-1.2	0.1	-0.1	0.3	0.0	1.0	0.3	0.2	1.1	0.7	0.6	1.0	1.2	1.4	1.0	0.3	1.0	1.6	1.2	1.4	0.7	1.0	1.2
218219_s_at	LANCL2	LANC lantibiotic synthetase component C-like 2 (bacterial)	0.00619835	0.7	0.2	0.1	0.4	0.4	-0.5	0.4	0.3	0.4	0.6	1.0	0.7	0.9	1.1	-0.2	1.4	1.2	0.8	0.7	1.9	1.2	1.5	0.8	1.5	0.8
210732_s_at	LGALS8	lectin, galactoside-binding, soluble, 8 (galectin 8)	0.000179979	-0.7	-0.4	0.5	0.2	-0.9	0.2	0.4	-0.2	0.3	0.4	0.3	0.6	0.5	0.4	1.0	1.1	1.2	1.7	1.4	1.3	0.5	0.9	1.0	1.5	0.9
225300_at	C15orf23	chromosome 15 open reading frame 23	0.006703183	-0.6	0.1	0.5	0.1	0.0	-0.4	1.0	-0.2	0.2	0.4	0.6	0.7	0.8	0.7	0.5	0.9	1.1	0.3	1.0	1.2	0.9	1.9	1.1	2.8	0.3
225485_at	TSGA14	testis specific, 14	0.003107903	0.2	-0.2	-0.6	0.3	0.9	-0.1	-0.7	1.1	-0.1	0.3	1.4	0.7	0.2	2.6	1.5	1.3	0.7	0.0	0.7	1.4	1.0	0.7	0.4	1.2	1.7
203225_s_at	RFK	riboflavin kinase	3.53103E-05	-1.0	-0.8	0.6	0.4	0.2	0.1	0.4	-0.4	0.0	0.2	0.3	1.5	0.9	0.5	0.6	0.9	1.3	1.3	0.4	1.6	1.2	1.4	1.4	1.1	0.8
208581_x_at	MT1X	metallothionein 1X	0.001097947	-0.6	-0.5	0.2	0.8	0.5	0.3	0.2	0.7	0.4	0.6	0.9	1.0	0.9	1.2	0.2	1.8	1.2	0.3	0.8	1.4	1.4	1.5	0.7	1.0	1.1
205296_at	RBL1	retinoblastoma-like 1 (p107)	0.001457195	0.0	0.0	-0.1	0.3	-0.1	-0.6	0.2	1.0	0.0	0.0	1.2	0.7	1.1	1.6	1.2	1.7	0.8	0.3	1.0	1.5	1.1	1.0	0.1	0.8	1.0
219037_at	CGI-115	NA	0.003488622	0.1	-0.5	-0.2	-0.2	-0.7	-0.2	0.8	0.5	0.2	0.1	0.9	0.4	0.7	0.6	2.7	1.1	1.1	0.0	0.8	0.7	1.6	1.3	0.6	1.5	0.6
213951_s_at	TBPIP	NA	0.003652602	-0.2	-0.3	0.2	0.7	0.3	0.0	0.5	0.6	0.2	-0.1	1.1	1.6	0.9	0.5	0.4	1.4	1.9	0.6	0.6	1.0	1.5	1.2	0.6	2.4	0.5
204639_at	ADA	adenosine deaminase	0.009683159	0.5	0.8	-0.5	0.2	1.7	0.1	0.4	1.1	0.4	0.3	1.8	1.1	1.1	2.1	1.0	1.5	1.1	0.3	0.6	0.8	1.6	1.2	0.0	0.6	1.5
212514_x_at	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	0.000595116	0.5	-0.9	0.0	0.4	-0.1	0.7	0.5	0.4	-0.2	0.3	0.2	1.0	0.4	0.2	1.2	0.7	1.1	0.9	1.1	1.9	0.8	1.0	1.2	1.8	0.8
36830_at	MIPEP	mitochondrial intermediate peptidase	0.004522498	0.2	0.0	-0.4	0.6	0.0	-0.2	-0.1	0.6	0.3	0.1	1.0	0.5	0.9	1.8	1.3	1.7	1.0	0.1	0.8	1.4	0.8	1.2	0.2	1.3	0.9
205401_at	AGPS	alkylglycerone phosphate synthase	0.002266967	0.3	-0.2	-1.3	0.6	0.0	0.4	0.3	0.1	0.3	0.7	0.4	1.0	1.1	0.4	0.0	1.0	1.8	1.3	0.5	2.0	0.9	1.0	0.7	1.8	0.7
214011_s_at	HSPC111	NA	0.00161894	0.0	0.7	0.4	0.2	0.0	0.2	0.7	0.3	0.2	0.3	1.0	0.0	0.7	0.7	0.5	0.9	1.0	0.8	0.7	1.2	1.7	1.4	0.9	1.7	1.0
231862_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	0.000775278	-0.6	-0.4	-0.3	-0.4	0.2	-0.8	-0.1	1.0	0.0	-0.3	1.1	0.4	0.3	1.4	0.7	1.4	1.4	0.3	0.9	1.3	0.5	0.8	1.0	1.8	1.5
200622_x_at	CALM3	calmodulin 3 (phosphorylase kinase, delta)	0.000551764	-1.3	-0.4	0.1	0.5	-0.2	0.5	0.8	0.3	0.3	0.7	0.9	1.1	0.9	1.1	-0.2	1.0	1.6	1.4	0.9	2.0	0.8	0.9	0.8	1.1	1.0
218477_at	TMEM14A	transmembrane protein 14A	0.007142823	0.2	0.9	-1.3	0.1	1.2	-0.5	-0.4	0.9	0.2	0.3	1.7	0.3	0.3	1.8	2.5	1.9	1.2	-0.4	0.5	1.0	1.4	0.9	-0.1	0.9	1.2

225736_at	FBXO22	F-box protein 22	0.001306867	-0.7	-1.0	-0.5	0.2	-0.7	0.7	0.9	0.6	0.1	0.0	0.8	1.1	0.7	0.6	0.4	1.3	0.7	1.3	1.1	1.3	0.9	0.8	1.5	2.2	0.4
232155_at	KIAA1618	KIAA1618	0.005842972	-0.4	-0.2	-0.7	0.1	0.3	-0.5	0.2	1.2	0.5	0.0	0.9	2.1	0.9	1.6	0.4	1.4	0.5	0.0	0.8	0.6	1.3	1.1	0.8	1.7	2.0
225711_at	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	0.001279216	-0.3	-0.5	0.3	0.0	-0.3	0.7	0.9	-0.1	0.4	0.4	0.5	0.8	1.0	1.1	1.6	1.4	1.6	0.5	0.8	1.1	0.6	1.2	0.3	1.6	0.3
226085_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	0.000299248	-1.6	-0.6	0.0	-0.6	-0.9	-0.3	0.2	1.0	0.3	-0.1	1.2	-0.1	0.4	1.5	1.1	0.9	1.2	0.4	0.6	1.6	1.1	0.9	0.8	1.4	1.1
208838_at	CAND1	cullin-associated and neddylation-dissociated 1	0.006955016	0.3	1.0	0.0	0.3	1.2	1.3	0.8	0.5	0.0	0.2	0.7	0.8	0.6	0.9	3.1	1.1	0.8	0.5	0.6	1.2	0.5	1.1	0.9	1.3	0.4
204507_s_at	PPP3R1	protein phosphatase 3 (formerly 2B), regulatory subunit B, 19kDa, alpha isoform (calcineurin B, type I)	0.001837825	0.3	-1.3	0.0	0.3	0.2	-0.3	1.4	-0.1	0.5	0.1	0.3	0.8	0.6	0.0	0.1	1.3	1.6	1.2	0.4	2.0	0.9	1.3	1.1	2.2	0.5
223306_at	EBPL	emopamil binding protein-like	0.008979848	-1.9	0.0	-1.3	0.5	-1.0	1.4	0.1	0.3	0.5	0.2	0.7	1.0	0.2	0.6	1.2	1.2	1.6	0.5	0.8	2.4	0.8	0.7	1.1	1.0	0.7
225614_at	LOC113174	NA	0.001682634	0.3	-0.5	-0.1	0.4	0.2	0.3	0.1	0.8	0.1	0.3	1.1	0.8	0.6	1.2	1.0	1.5	1.3	0.4	0.9	1.3	1.0	0.8	0.4	1.6	1.0
213983_s_at	SCC-112	NA	0.004948176	-0.1	-0.6	0.7	0.4	0.9	0.8	0.1	0.5	0.7	0.1	0.5	1.0	0.1	1.5	0.7	1.8	1.5	0.6	0.9	1.5	1.1	0.8	0.5	1.3	0.7
206237_s_at	NRG1	neuregulin 1	0.003130984	-0.5	-0.1	0.1	1.2	-0.6	0.6	0.3	-1.4	-0.2	-0.1	-2.7	-0.7	-1.4	-1.3	-1.3	-0.1	-0.3	-0.2	-1.0	-0.9	-2.0	-1.7	-0.5	-0.6	-1.7
1562255_at	SYTL3	synaptotagmin-like 3	0.001408293	2.7	0.7	0.7	0.2	0.9	-1.0	-0.8	-0.2	-0.1	-0.8	-2.1	-1.7	-1.1	-2.1	0.4	-1.5	-1.3	-2.6	-1.2	-1.0	-0.6	-0.9	-1.7	-0.9	1.2
227082_at	NA	NA	0.001571023	2.1	0.5	-0.5	0.3	0.0	-0.7	-0.6	0.5	-0.9	-0.3	-0.8	-1.6	-0.5	-1.4	0.4	-1.3	-1.3	-0.8	-0.1	-1.0	-1.0	-1.9	-1.5	-3.0	0.0
1555847_a_at	LOC284454	NA	0.006733493	1.2	-0.6	-0.8	-0.2	0.1	-1.6	-0.2	-0.8	-0.2	-0.1	-2.0	-0.6	-0.4	-0.6	-1.8	-3.4	-0.4	0.8	-1.9	-0.6	-0.1	-1.7	-0.2	-1.1	-2.5
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.009021854	1.9	0.9	0.5	1.7	0.7	-2.6	-3.6	-0.4	1.3	0.8	-3.3	-1.9	-1.0	1.6	-2.5	-1.8	3.3	1.9	-1.8	0.9	0.6	-4.2	-3.4	-5.1	-3.8
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.008556579	1.8	1.0	0.4	1.6	0.7	-2.6	-3.4	-0.6	1.2	0.8	-3.4	-1.6	-1.0	1.5	-2.7	-1.9	2.5	1.4	-1.9	0.2	0.6	-3.8	-2.9	-4.4	-3.8