

[illegible]

Protein ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 POS	Mean log2 intensity for 21 NEG	422 FDR <0.2 1-YES	Log2 Ratio 21POS/21NEG	Fold-Change 21POS/21NEG	p-value	FDR
244733_at	---	---	4.65	4.78	1	-0.12	-1.09	0.10	0.194
205966_at	TAF13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa	3.67	3.92	1	-0.25	-1.19	0.01	0.086
225954_s_at	MDM1	MDM1, Mad1 domain containing	4.67	4.87	1	-0.31	-1.24	0.03	0.121
205731_s_at	NCOA2	nuclear receptor coactivator 2	4.50	4.71	1	-0.22	-1.16	0.08	0.175
224540_x_at	---	---	10.53	10.27	1	0.26	1.19	0.01	0.090
210800_at	TIMMBA	translocase of inner mitochondrial membrane 8 homolog A (yeast)	5.78	5.61	1	0.17	1.13	0.08	0.170
220771_at	LOC003728	long intergenic non-protein coding RNA 328	2.58	2.46	1	0.12	1.08	0.09	0.177
230064_at	OC00537606	uncharacterized LOC00537606	5.92	5.79	1	0.13	1.09	0.02	0.092
231886_at	OC00134822	uncharacterized LOC00134822	5.48	5.21	1	0.27	1.21	0.00	0.050
1561893_at	---	---	3.28	3.11	1	0.18	1.13	0.00	0.056
236560_at	---	---	4.78	4.66	1	0.12	1.08	0.11	0.199
1564430_at	---	---	5.60	5.46	1	0.14	1.10	0.05	0.132
1553185_at	RASEF	RAS and EF-hand domain containing	11.10	10.92	1	0.17	1.13	0.02	0.099
239963_at	---	---	3.45	3.30	1	0.15	1.11	0.04	0.129
1553461_at	---	---	3.15	3.04	1	0.11	1.08	0.08	0.170
1570505_at	ABCB4	ATP binding cassette subfamily B member 4	5.26	5.12	1	0.14	1.10	0.08	0.173
236728_at	LNPEP	leucyl/cystinyl aminopeptidase	5.13	5.00	1	0.13	1.09	0.04	0.124
239798_at	PKD1	pyruvate dehydrogenase kinase, isozyme 1	3.43	3.33	1	0.11	1.08	0.07	0.157
1564003_at	NEK1	NIMA-related kinase 1	4.48	4.24	1	0.24	1.18	0.01	0.085
208575_at	HIST3H3A	histone cluster 1, H3a	3.67	3.49	1	0.17	1.13	0.09	0.179
240015_at	PRKCO-AS1	PRKCO antisense RNA 1	4.86	4.76	1	0.10	1.07	0.07	0.167
1561092_at	---	---	3.10	2.98	1	0.12	1.09	0.03	0.111
215161_at	RALGAP1A	Raf GAP activating protein, alpha subunit 1 (catalytic)	4.78	4.66	1	0.12	1.09	0.11	0.198
232161_s_at	PTPN4	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	3.11	2.94	1	0.17	1.13	0.02	0.100
1562457_at	NCKAP5L	NCK-associated protein 5-like	3.23	3.15	1	0.08	1.06	0.08	0.173
1556461_at	KIF12	---	2.55	2.48	1	0.07	1.05	0.09	0.179
1570145_at	PP12708	---	2.19	2.12	1	0.07	1.05	0.05	0.138
228056_s_at	NAP5B	napsin B aspartic peptidase, pseudogene	5.68	5.56	1	0.12	1.08	0.01	0.085
1560142_at	GRIK2	glutamate receptor, ionotropic, kainate 2	2.20	2.14	1	0.07	1.05	0.01	0.088
228393_at	---	---	2.42	2.31	1	0.11	1.08	0.00	0.072
237877_at	---	---	2.80	2.79	1	0.11	1.08	0.01	0.088
1560755_at	---	---	2.22	2.12	1	0.09	1.07	0.03	0.113
237784_at	SUB1	SUB1 homolog, transcriptional regulator	3.27	3.17	1	0.10	1.07	0.03	0.115
216373_at	TAPT1	transmembrane anterior posterior transformation 1	2.47	2.31	1	0.11	1.08	0.05	0.137
1561600_at	SSH2	---	2.13	2.02	1	0.11	1.08	0.05	0.137
219797_at	MGAT4A	mannosyl (alpha-1,3)-glycosylprotein beta-4-N-acetylglucosaminyltransferase, isozyme A	5.64	5.54	1	0.11	1.08	0.09	0.175
1553776_s_at	TBC1D32	TBC1 domain family, member 32	2.56	2.40	1	0.17	1.12	0.00	0.058
1557077_x_at	OC00537286	uncharacterized LOC00537286	3.01	2.91	1	0.10	1.07	0.03	0.111
201689_s_at	TPD52	tumor protein D52	6.22	6.12	1	0.09	1.07	0.04	0.125
206398_s_at	CD19	CD19 molecule	7.45	7.33	1	0.12	1.08	0.01	0.085
232181_at	PPARGC1B	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	3.67	3.55	1	0.12	1.08	0.03	0.111
242228_at	BRC1	bicaudal D homolog 1 (Drosophila)	2.75	2.58	1	0.17	1.13	0.00	0.060
1564970_at	SETD82	SET domain, bifurcated 2	3.84	3.73	1	0.11	1.08	0.10	0.192
224151_s_at	AK3	adenylate kinase 3	4.03	3.88	1	0.15	1.11	0.01	0.085
228055_at	NAP5B	napsin B aspartic peptidase, pseudogene	7.25	7.14	1	0.11	1.08	0.06	0.152
1570022_at	---	---	2.40	2.31	1	0.09	1.07	0.09	0.174
1552633_at	ZNF101	zinc finger protein 101	6.36	6.26	1	0.10	1.07	0.04	0.126
236985_at	---	---	2.84	2.81	1	0.13	1.09	0.04	0.125
1562161_at	---	---	2.69	2.57	1	0.12	1.09	0.07	0.169
232121_at	ZBTB20	zinc finger and BTB domain containing 20	5.31	5.15	1	0.16	1.12	0.15	0.198
229513_at	STRBP	spermatid perinuclear RNA binding protein	6.52	6.37	1	0.14	1.10	0.11	0.199
228905_at	PCM1	pericentriolar material 1	4.18	4.00	1	0.18	1.13	0.04	0.123
1564972_x_at	SETD82	SET domain, bifurcated 2	4.06	3.83	1	0.23	1.18	0.01	0.093
239867_at	---	---	4.07	3.88	1	0.19	1.14	0.01	0.085
1560225_at	CNR1	cannabinoid receptor 1 (brain)	2.95	2.81	1	0.15	1.11	0.08	0.170
211934_x_at	GANAB	glucosylase, alpha; neutral AB	6.79	6.69	1	0.11	1.08	0.09	0.179
1565692_at	---	---	4.75	4.58	1	0.17	1.12	0.03	0.116
217701_x_at	---	---	3.26	3.04	1	0.22	1.17	0.02	0.098
241723_at	IQGAP2	IQ motif containing GTPase activating protein 2	3.12	3.01	1	0.12	1.08	0.11	0.198
1555317_at	POKX	polymerase (DNA directed) kappa	2.57	2.40	1	0.17	1.13	0.05	0.141
1555139_at	GOSR1	golgi SNAP receptor complex member 1	2.81	2.60	1	0.20	1.15	0.02	0.100
1563077_at	OC00028905	uncharacterized LOC00028905	4.13	3.99	1	0.14	1.10	0.06	0.146
1560662_s_at	WHAMMP2	WAS protein homolog associated with actin, golgi membranes and microtubules pseudogene 2	5.13	4.93	1	0.21	1.15	0.00	0.056
1559201_s_at	---	---	6.18	6.05	1	0.13	1.09	0.02	0.092
1566101_at	SUZ12	SUZ12 polycomb repressive complex 2 subunit	3.32	3.14	1	0.18	1.14	0.00	0.071
1560048_at	---	---	2.68	2.62	1	0.06	1.04	0.08	0.171
243910_x_at	CAND1	cullin-associated and neddylation-dissociated 1	5.52	5.39	1	0.12	1.09	0.04	0.126
1561154_at	---	---	2.37	2.21	1	0.16	1.12	0.01	0.077
244766_at	N/PNPS1	putative uncharacterized protein LOC641298 /// putative uncharacterized protein LOC641298 /// putative uncharacterized protein LOC641298	6.58	6.45	1	0.13	1.10	0.02	0.091
207115_x_at	MBTD1	mbt domain containing 1	4.02	3.82	1	0.20	1.15	0.00	0.050
232665_x_at	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	4.57	4.34	1	0.23	1.17	0.00	0.056
215070_x_at	R21 /// RABG1	G protein-coupled receptor 21 /// RAS GTPase activating protein 1	3.57	3.41	1	0.15	1.11	0.02	0.095
1560206_at	---	---	2.10	1.94	1	0.16	1.11	0.00	0.056
1558698_at	ZNF264	zinc finger protein 264	3.19	3.07	1	0.12	1.09	0.03	0.114
1564640_at	MGA	MGA, MAX dimerization protein	2.18	2.08	1	0.09	1.07	0.03	0.118
238075_at	TPN43	transposon 3	2.80	2.65	1	0.09	1.06	0.11	0.199
236660_at	METTL14	methyltransferase like 14	3.18	3.01	1	0.18	1.13	0.01	0.086
1559731_x_at	MACROD1	MACRO domain containing 1	2.85	2.69	1	0.16	1.11	0.03	0.115
234112_at	CBIL8	---	2.93	2.80	1	0.13	1.09	0.07	0.166
232055_at	---	---	5.40	5.22	1	0.18	1.14	0.02	0.096
216527_x_at	HCG18	HLA complex group 18 (non-protein coding)[HCG18]	6.52	6.29	1	0.23	1.17	0.00	0.058
217653_x_at	---	---	5.97	5.69	1	0.28	1.21	0.00	0.050
207286_at	CEP135A	centrosomal protein 135kDa	2.78	2.54	1	0.24	1.18	0.00	0.050
1569573_at	---	---	2.69	2.69	1	0.26	1.20	0.00	0.056
1570415_at	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	2.86	2.59	1	0.27	1.20	0.00	0.064
215900_at	---	---	2.99	2.86	1	0.13	1.09	0.08	0.170
1558418_at	PIAS1	---	3.52	3.38	1	0.14	1.10	0.03	0.121
243899_at	L17A /// ARL4	ADP-ribosylation factor like GTPase 17A /// ADP-ribosylation factor like GTPase 17B	6.12	6.02	1	0.16	1.11	0.01	0.086
1560112_at	WDRF2	WD repeat and FVWL domain containing 2	3.13	2.98	1	0.16	1.11	0.01	0.092
1558828_at	---	---	2.52	2.39	1	0.13	1.10	0.01	0.092
1560349_at	---	---	2.75	2.55	1	0.21	1.15	0.00	0.064
1564438_at	---	---	2.95	2.84	1	0.11	1.08	0.09	0.179
1559580_at	LRR3C	leucine rich repeat containing 39	3.11	2.95	1	0.16	1.12	0.01	0.085
222319_at	---	---	3.91	3.78	1	0.13	1.09	0.09	0.175
1563364_at	---	---	3.22	2.96	1	0.26	1.20	0.00	0.058
217701_x_at	---	---	3.45	3.21	1	0.24	1.18	0.00	0.050
1559039_at	DXH36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	5.19	5.02	1	0.17	1.13	0.01	0.085
215128_at	---	---	4.24	4.02	1	0.22	1.16	0.00	0.072
222036_at	FAR5B	phenylalanyl-tRNA synthetase beta subunit	2.46	2.32	1	0.14	1.10	0.02	0.095
242126_at	---	---	2.93	2.77	1	0.16	1.12	0.01	0.085
235551_at	---	---	3.32	3.08	1	0.25	1.19	0.00	0.058
220216_at	C8orf44	chromosome 8 open reading frame 44	4.36	4.18	1	0.19	1.14	0.02	0.092
237377_at	---	---	3.64	3.50	1	0.14	1.10	0.04	0.122
1568508_at	---	---	2.77	2.63	1	0.14	1.10	0.03	0.121
1561128_at	---	---	3.40	3.24	1	0.16	1.12	0.05	0.132
211459_at	---	---	2.43	2.26	1	0.17	1.13	0.06	0.147
232834_at	RBM43	RNA binding motif protein 43	4.29	4.08	1	0.21	1.16	0.02	0.094
243655_x_at	---	---	2.69	2.54	1	0.15	1.11	0.04	0.126
233239_at	---	---	4.84	4.61	1	0.23	1.18	0.04	0.123
208077_at	---	---	3.78	3.61	1	0.17	1.12	0.09	0.177
206160_x_at	ZC3H7B	zinc finger CCHC-type containing 7B	8.89	8.57	1	0.32	1.25	0.00	0.072
1567892_x_at	AP2A1	adaptor-related protein complex 2, alpha 1 subunit	6.05	5.70	1	0.35	1.27	0.00	0.056
1569472_x_at	TTG3	tetratricopeptide repeat domain 3	5.80	5.53	1	0.27	1.20	0.04	0.126
1571917_x_at	LGA53	lectin, galactoside-binding, soluble, 3	3.15	2.86	1	0.29	1.22	0.02	0.099
215175_at	PCNK	pectenex homology (Drosophila)	5.17	4.92	1	0.25	1.19	0.08	0.172
215648_at	---	---	4.68	4.34	1	0.34	1.27	0.01	0.085
234148_at	---	---	4.53	4.19	1	0.34	1.27	0.02	0.099
1561733_at	---	---	3.74	3.42	1	0.32	1.25	0.00	0.072
206080_at	37A2 /// LRR1	leucine rich repeat containing 37, member A3	4.14	3.78	1	0.36	1.29	0.00	0.072
240246_at	FRG1P	FSHD region gene 1 family member 1, pseudogene	4.54	4.26	1	0.27	1.21	0.01	0.085
237322_at	---	---	3.39	3.12	1	0.28	1.21	0.01	0.085
244010_at	---	---	5.34	5.04	1	0.30	1.23	0.03	0.113
233554_at	---	---	3.93	3.62	1	0.31	1.24	0.02	0.094
1554948_at	---	---	4.32	3.98	1	0.34	1.27	0.02	0.092
233824_at	---	---	4.31	4.04	1	0.27	1.21	0.04	0.123
1560800_at	---	---	2.91	2.67	1	0.23	1.17	0.03	0.111
232365_at	SIAM1	siyah E3 ubiquitin protein ligase 1	2.78	2.55	1				

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 PEST	Mean log2 intensity for 21 PHE	422 Fold <0.2 1-YES	Log2 Ratio Z1POST vs Z1PHE	Fold-Change Z1POST vs Z1PHE	p-value	FDR
1557409_at	---	---	5.20	5.03	1	0.16	1.12	0.05	0.137
215462_at	PLK3	polo-like kinase 3	5.73	5.50	1	0.23	1.18	0.01	0.086
215474_at	PLK2	---	3.60	3.32	1	0.28	1.21	0.01	0.085
239008_at	---	---	4.17	3.90	1	0.27	1.20	0.03	0.116
233231_at	---	---	3.64	3.44	1	0.20	1.15	0.08	0.170
214740_at	POLR2J3	polymerase (RNA) II (DNA directed) polypeptide J3	4.33	4.13	1	0.20	1.15	0.09	0.179
242540_at	PRK03	protein kinase D3	4.51	4.29	1	0.21	1.16	0.08	0.170
1559139_at	NOX2L	NOX2-like nuclear associated transcriptional repressor	4.60	4.38	1	0.22	1.17	0.11	0.199
235061_at	PPM1K	protein phosphatase, Mg2+/Mn2+ dependent, 1K	7.12	6.85	1	0.28	1.21	0.00	0.072
213650_at	gABA /// GOL	golgin A8 family, member A /// golgin A8 family, member B	7.50	7.29	1	0.21	1.16	0.10	0.187
205154_at	---	---	3.14	2.80	1	0.34	1.27	0.01	0.083
1570248_at	---	---	3.44	3.19	1	0.25	1.19	0.08	0.170
232330_at	COA1	cytochrome c oxidase assembly factor 1 homolog	6.84	6.46	1	0.39	1.31	0.01	0.083
1562255_at	SYTL3	synaptotagmin-like 3	4.91	4.72	1	0.19	1.14	0.10	0.195
244412_at	---	---	3.51	3.24	1	0.17	1.13	0.09	0.182
242176_at	MEF2A	myocyte enhancer factor 2A	3.47	3.32	1	0.15	1.11	0.06	0.146
234643_x_at	---	---	5.13	4.90	1	0.23	1.17	0.01	0.085
231400_at	---	---	4.63	4.45	1	0.19	1.14	0.10	0.185
236151_at	---	---	4.59	4.39	1	0.14	1.11	0.05	0.132
239661_at	---	---	4.16	3.98	1	0.18	1.13	0.04	0.121
233713_at	---	---	5.71	5.55	1	0.16	1.12	0.03	0.113
1555812_x_at	ABHD18	Rho GTP dissociation inhibitor (GDI) beta	9.00	8.87	1	0.13	1.09	0.08	0.170
215115_s_at	IGH	immunoglobulin heavy locus	6.19	6.02	1	0.17	1.13	0.03	0.113
219980_at	ABHD18	abhydrolase domain containing 18	5.12	4.91	1	0.21	1.16	0.05	0.132
232346_at	LOC388692	uncharacterized LOC388692	6.17	5.94	1	0.23	1.17	0.07	0.168
1568940_at	GABPB1-AS1	GABPB1 antisense RNA 1(GABPB1-AS1)	5.47	5.23	1	0.24	1.18	0.06	0.144
1560814_s_at	C15orf57	chromosome 15 open reading frame 57	4.16	3.80	1	0.26	1.20	0.05	0.146
220467_at	---	---	7.64	7.32	1	0.32	1.25	0.01	0.085
217671_at	---	---	6.49	6.31	1	0.19	1.14	0.05	0.138
242341_x_at	---	---	4.96	4.71	1	0.25	1.19	0.00	0.064
215626_at	---	---	3.45	3.29	1	0.16	1.12	0.09	0.179
215659_at	GSDMB	gasdermin B	3.09	2.88	1	0.20	1.15	0.02	0.103
1560391_at	PICL	phosphatidylinositol glycan anchor biosynthesis class I	3.41	3.27	1	0.13	1.10	0.09	0.179
1557360_at	LRRP6C	leucine-rich pentatricopeptide repeat containing	6.37	6.24	1	0.13	1.09	0.09	0.179
243796_at	---	---	5.65	5.54	1	0.10	1.07	0.11	0.197
1555379_at	FAM159A	family with sequence similarity 159, member A	3.27	3.14	1	0.13	1.09	0.05	0.137
242423_x_at	ZNF782	zinc finger protein 782	3.32	3.16	1	0.16	1.12	0.03	0.117
1554753_at	---	---	4.35	4.14	1	0.21	1.16	0.02	0.109
1569041_at	---	---	4.92	4.70	1	0.22	1.17	0.04	0.126
233630_at	CD52	CDP-diacylglycerol synthase 2	4.57	4.40	1	0.17	1.12	0.08	0.171
243876_at	---	---	5.06	4.86	1	0.20	1.15	0.06	0.145
1554769_at	ZNF785	zinc finger protein 785	3.75	3.54	1	0.21	1.16	0.06	0.143
239649_at	---	---	5.29	5.13	1	0.16	1.12	0.08	0.170
1563051_at	OSBP	oxysterol binding protein	3.82	3.64	1	0.18	1.13	0.07	0.168
1559392_at	TECR	trans-2,3-enoyl-CoA reductase	2.27	2.10	1	0.18	1.13	0.06	0.143
1556849_at	---	---	2.56	2.37	1	0.18	1.14	0.08	0.170
241207_at	---	---	2.74	2.54	1	0.20	1.15	0.04	0.130
242490_at	---	---	5.08	4.87	1	0.21	1.16	0.08	0.171
217594_at	ZCCHC11	zinc finger, CCHC domain containing 11	1.64	1.38	1	0.26	1.19	0.03	0.113
1560441_at	SMCHD3	---	6.38	6.08	1	0.31	1.24	0.02	0.093
232338_at	ZNF431	zinc finger protein 431	4.35	4.11	1	0.25	1.19	0.07	0.159
221191_s_at	G3L1 /// STAG3	stromal antigen 3-like 1 (pseudogene) /// stromal antigen 3-like 3 (pseudogene)	5.76	5.54	1	0.22	1.16	0.08	0.171
1557996_at	---	---	6.54	6.34	1	0.30	1.23	0.03	0.112
1558230_at	---	---	5.62	5.30	1	0.32	1.25	0.03	0.121
241860_at	---	---	4.92	4.68	1	0.24	1.18	0.10	0.187
1560013_at	2724985 /// P	pyridoxal-dependent decarboxylase domain-containing protein 1 /// pyridoxal-dependent decarboxylase domain co	4.12	3.92	1	0.20	1.15	0.09	0.181
239652_at	---	---	5.98	5.77	1	0.25	1.19	0.08	0.172
239652_at	---	---	6.03	5.77	1	0.26	1.20	0.06	0.152
1558802_at	TM2D1	TM2 domain containing 1	3.29	3.07	1	0.22	1.16	0.06	0.146
1559490_at	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	6.58	6.29	1	0.28	1.22	0.04	0.123
239931_at	ZNF207	zinc finger protein 207	6.76	6.49	1	0.23	1.17	0.04	0.122
215012_at	ZNF451	zinc finger protein 451	6.56	6.33	1	0.23	1.17	0.05	0.132
231848_x_at	ZNF207	zinc finger protein 207	8.16	7.91	1	0.25	1.19	0.04	0.125
238760_at	---	---	5.29	5.03	1	0.26	1.20	0.09	0.176
232521_at	PCSK7	proprotein convertase subtilisin/kexin type 7	6.15	5.80	1	0.25	1.19	0.09	0.179
1559527_at	---	---	4.09	3.81	1	0.29	1.22	0.06	0.152
242772_x_at	---	---	4.82	4.43	1	0.40	1.32	0.01	0.086
216981_s_at	ZNF224	zinc finger protein 224	5.40	5.16	1	0.24	1.18	0.08	0.170
1569180_at	---	---	5.80	5.43	1	0.37	1.29	0.02	0.093
218362_s_at	D1S3	D1S3 homolog, exosome endoribonuclease and 3'-5' exoribonuclease	4.86	4.61	1	0.25	1.19	0.02	0.111
1557580_at	---	---	3.42	3.15	1	0.28	1.21	0.01	0.088
242527_at	---	---	4.20	4.00	1	0.20	1.15	0.06	0.155
215375_s_at	LRRP1	leucine-rich repeat (in FLII) interacting protein 1	5.15	4.95	1	0.20	1.15	0.05	0.141
1562412_at	GPR898	G protein-coupled receptor 898	4.30	4.05	1	0.25	1.19	0.03	0.117
232759_at	---	---	3.98	3.65	1	0.34	1.26	0.01	0.085
217695_at	MAP2K5	mitogen-activated protein kinase kinase 5	4.14	3.89	1	0.25	1.19	0.04	0.122
1562038_at	CDC03	cyclin D3	5.57	5.26	1	0.31	1.24	0.02	0.094
232002_at	---	---	4.84	4.58	1	0.26	1.20	0.01	0.092
240720_at	---	---	3.54	3.31	1	0.24	1.18	0.01	0.085
1562238_at	USP11	ubiquitin specific peptidase like 1	3.16	2.89	1	0.28	1.21	0.00	0.062
1557541_s_at	---	---	2.88	2.62	1	0.26	1.20	0.02	0.095
231979_at	GABPB1-AS1	GABPB1 antisense RNA 1(GABPB1-AS1)	3.45	3.24	1	0.21	1.16	0.01	0.088
215170_s_at	CEP152	centrosomal protein 152kDa	3.44	3.16	1	0.28	1.22	0.01	0.079
210858_x_at	ATM	ATM serine/threonine kinase	7.12	6.81	1	0.31	1.16	0.05	0.141
208442_s_at	ATM	ATM serine/threonine kinase	5.78	5.42	1	0.36	1.28	0.03	0.113
242974_at	CD47	CD47 molecule(CD47)	5.79	5.45	1	0.34	1.27	0.00	0.074
205594_at	ZNF652	zinc finger protein 652	4.95	4.63	1	0.32	1.25	0.02	0.095
215020_at	AKR1N1	akrin 1	4.58	4.27	1	0.31	1.24	0.10	0.191
239405_at	---	---	4.29	4.04	1	0.25	1.19	0.08	0.170
215558_at	UBR2	ubiquitin protein ligase E3 component 1-recognition 2	4.26	3.87	1	0.39	1.31	0.01	0.088
242797_x_at	---	---	4.14	3.75	1	0.40	1.32	0.01	0.079
207474_at	SNRK	SNF-related kinase	4.57	4.53	1	0.34	1.27	0.05	0.132
1557270_at	---	---	4.82	4.36	1	0.46	1.37	0.00	0.056
1570571_at	CCDC91	coiled-coil domain containing 91	5.04	4.61	1	0.43	1.34	0.01	0.079
211941_at	CLN8	ceroid-lipofuscinosis, neuronal 8	1.94	1.65	1	0.29	1.22	0.01	0.088
239261_at	---	---	5.47	5.18	1	0.29	1.22	0.07	0.161
1569312_at	---	---	4.69	4.38	1	0.30	1.23	0.06	0.141
207735_at	RNF125	ring finger protein 125, E3 ubiquitin protein ligase	6.05	5.75	1	0.31	1.24	0.07	0.167
243134_at	---	---	5.58	5.14	1	0.44	1.36	0.02	0.094
240691_at	---	---	4.36	4.10	1	0.27	1.20	0.08	0.172
232412_at	FBXL20	F-box and leucine-rich repeat protein 20	3.62	3.27	1	0.35	1.27	0.03	0.113
1565743_at	NABP2L2	NEDD4 binding protein 2-like 2	4.24	3.70	1	0.54	1.45	0.00	0.056
1562283_at	---	---	2.58	2.38	1	0.39	1.31	0.01	0.085
222412_s_at	SSR3	signal sequence receptor, gamma (translocin-associated protein gamma)	6.30	5.95	1	0.35	1.28	0.05	0.136
1566658_at	---	---	6.19	5.77	1	0.42	1.34	0.01	0.085
1559449_x_at	ZNF254	zinc finger protein 254	4.83	4.32	1	0.51	1.42	0.00	0.056
1569538_at	---	---	3.77	3.34	1	0.43	1.36	0.00	0.056
235030_at	NXPE3	neurexophilin and PC-esterase domain family, member 3	4.71	4.40	1	0.30	1.24	0.03	0.111
1566657_at	---	---	5.32	5.03	1	0.30	1.23	0.01	0.092
1557737_s_at	NKTR	natural killer cell triggering receptor	4.68	4.22	1	0.46	1.37	0.00	0.064
1553867_at	---	---	3.13	2.82	1	0.31	1.24	0.06	0.153
216766_at	---	---	4.34	4.00	1	0.34	1.27	0.05	0.132
220458_at	---	---	3.64	3.28	1	0.36	1.28	0.02	0.092
232295_at	GFM1	G elongation factor, mitochondrial 1	3.09	2.81	1	0.28	1.21	0.01	0.083
221771_s_at	MPHO5B6	M phase phosphoprotein B	6.94	6.66	1	0.28	1.22	0.11	0.199
239635_at	RBM14	RNA binding motif protein 14	5.85	5.51	1	0.34	1.26	0.05	0.141
216022_at	---	---	5.30	5.02	1	0.28	1.21	0.10	0.195
1568943_at	INP50/SHIP	inositol triphosphate-5-phosphatase D	6.00	5.56	1	0.44	1.36	0.01	0.077
215392_at	---	---	4.77	4.42	1	0.35	1.27	0.10	0.185
1557551_at	---	---	6.30	5.94	1	0.36	1.28	0.08	0.173
1558515_at	FTX	FTX transcript, XIST regulator (non-protein coding)	6.22	5.79	1	0.43	1.34	0.07	0.164
215123_at	IPK3 /// NR	nuclear pore complex-interacting protein family member B4-like /// uncharacterized LOC105376851 /// nuclear pore	7.07	6.58	1	0.49	1.40	0.02	0.099
1558710_at	ABIN1	ABIN1	4.73	4.43	1	0.30	1.23	0.09	0.179
210556_at	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	5.03	4.62	1	0.41	1.33	0.04	0.125
216811_at	---	---	5.39	4.86	1	0.53	1.44	0.03	0.113
235050_at	---	---	7.11	6.67	1	0.			

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 PRE	Mean log2 intensity for 21 PRE	422 FDR	Log2 Ratio 21POST vs 21PRE	Fold-Change 21POST vs 21PRE	p value	FDR
222693_at	FNDC3B	fibronectin type III domain containing 3B	5.94	6.06	0	-0.12	-1.08	0.20	0.265
200600_s_at	NR1P1	nuclear receptor interacting protein 1	8.00	8.08	0	-0.08	-1.05	0.37	0.350
221802_s_at	SHY1A1	shyoin 1	5.68	5.81	0	-0.13	-1.10	0.15	0.228
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	5.20	5.31	0	-0.11	-1.08	0.29	0.311
1559910_at	---	---	8.97	9.14	0	-0.18	-1.13	0.11	0.201
1553313_s_at	SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	5.90	6.05	0	-0.15	-1.11	0.13	0.213
218871_s_at	3A /// APOB	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A /// APOBEC3A and APOBEC3B deletion hybrid	7.68	7.80	0	-0.11	-1.08	0.11	0.201
206028_s_at	MEK1K	MEK proto-oncogene, tyrosine kinase	2.57	2.70	0	-0.12	-1.09	0.17	0.247
207697_x_at	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	7.00	7.09	0	-0.09	-1.07	0.14	0.224
219788_at	PLRA	paired immunoglobulin-like type 2 receptor alpha	6.03	6.13	0	-0.10	-1.07	0.14	0.220
201360_at	CS13	cystatin C	7.30	7.38	0	-0.09	-1.06	0.12	0.202
215767_at	ZNFR04A	zinc finger protein 804A	3.57	3.64	0	-0.07	-1.05	0.38	0.351
227632_at	TBC1D24	TBC1 domain family, member 24	2.90	3.00	0	-0.10	-1.07	0.13	0.214
1569431_at	PAFAH1B2	platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	2.55	2.62	0	-0.07	-1.05	0.22	0.276
241955_at	HECTD1	HECT domain containing E3 ubiquitin protein ligase 1	7.48	7.55	0	-0.07	-1.05	0.15	0.221
200628_s_at	WARS	tryptophanyl-tRNA synthetase	8.78	8.85	0	-0.07	-1.05	0.35	0.339
218228_s_at	TNKS2	tankyrase, TRF1-interacting ankyrin-related ADP-ribosyl polymerase 2	7.80	7.83	0	-0.03	-1.02	0.45	0.378
200668_s_at	SCAMP1	secretory carrier membrane protein 1	5.52	5.47	0	0.05	1.03	0.19	0.256
211298_at	RDX	radixin	6.86	6.91	0	-0.05	-1.04	0.47	0.389
230466_s_at	RASSF3	Ras association (RafGDS/AF-6) domain family member 3	6.99	7.12	0	-0.13	-1.09	0.12	0.202
239871_at	CLTC	clathrin, heavy chain (Hc)	2.33	2.40	0	-0.08	-1.05	0.15	0.232
155442_at	BEST1	bestrophin 1	5.87	5.94	0	-0.07	-1.05	0.28	0.305
200730_s_at	PTPA11	protein tyrosine phosphatase type IVA, member 1	7.96	8.02	0	-0.06	-1.04	0.40	0.361
205809_s_at	WASL	Wiskott-Aldrich syndrome-like	6.26	6.39	0	-0.13	-1.09	0.14	0.219
237332_at	MON2	MON2 homolog, regulator of endosome-to-Golgi trafficking	4.34	4.47	0	-0.13	-1.09	0.13	0.215
238470_at	SYSL	Syl1 golgi trafficking protein	4.49	4.40	0	0.09	1.06	0.21	0.274
156556_at	---	---	3.95	3.88	0	0.07	1.05	0.27	0.304
234459_at	PHILN1	periplin 1	3.41	3.33	0	0.08	1.05	0.32	0.328
1559762_at	---	---	2.26	2.19	0	0.07	1.05	0.21	0.271
1554639_at	OC10029132	uncharacterized LOC100291323	3.09	3.06	0	0.04	1.03	0.40	0.359
232527_s_at	---	---	4.20	4.05	0	0.15	1.11	0.14	0.219
241863_x_at	TTC14	tetratricopeptide repeat domain 14	4.10	4.02	0	0.08	1.06	0.21	0.270
2003940_s_at	VASH1	vasohibin 1	4.96	4.85	0	0.11	1.08	0.22	0.276
239378_at	BCAS4	breast carcinoma amplified sequence 4	5.28	5.14	0	0.13	1.10	0.23	0.283
1559455_at	---	---	4.20	3.99	0	0.21	1.16	0.12	0.208
1569263_at	---	---	4.49	4.33	0	0.17	1.12	0.12	0.207
238778_at	---	---	4.85	4.76	0	0.08	1.06	0.20	0.265
200983_at	CCR6	chemokine (C-C motif) receptor 6	4.49	4.42	0	0.07	1.05	0.30	0.319
241680_at	---	---	4.50	4.42	0	0.08	1.05	0.27	0.302
205267_at	POUZAF1	POU class 2 associating factor 1	8.99	8.93	0	0.07	1.05	0.33	0.333
214705_at	INADL	INAD-like (Drosophila)	3.09	2.96	0	0.13	1.09	0.13	0.214
202940_at	3539660 ///	uncharacterized LOC105269600 /// WNK lysine deficient protein kinase 1	4.95	4.82	0	0.14	1.10	0.14	0.224
217534_at	FAM49B	family with sequence similarity 49, member B	5.24	5.04	0	0.21	1.15	0.20	0.265
224031_at	STK17A	---	4.06	3.92	0	0.15	1.11	0.12	0.203
155390_at	---	---	4.72	4.49	0	0.24	1.18	0.14	0.222
14051_s_at	CCL5	chemokine (C-C motif) ligand 5	10.63	10.61	0	0.02	1.02	0.67	0.454
1552417_x_at	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	5.70	5.70	0	0.00	-1.00	0.98	0.540
1552621_at	R212 /// POL	polymerase (RNA) II (DNA directed) polypeptide 12 /// polymerase (RNA) II (DNA directed) polypeptide 13	8.10	7.80	0	0.30	1.23	0.12	0.202
1552627_x_at	ARHGAP5	Rho GTPase activating protein 5	4.05	4.14	0	-0.10	-1.07	0.13	0.216
1552702_at	HELB	helix-loop-helix (DNA) B	4.54	4.40	0	0.14	1.10	0.23	0.281
1552788_a_at	HELB	helix-loop-helix (DNA) B	5.44	5.39	0	0.05	1.03	0.44	0.377
1552978_x_at	SCAMP1	secretory carrier membrane protein 1	6.22	6.20	0	0.03	1.02	0.73	0.468
1553252_s_at	BRWD3	bromodomain and WD repeat domain containing 3	6.99	6.98	0	0.01	1.01	0.85	0.502
1553265_at	SLC23A3	solute carrier family 23, member 3	2.75	2.68	0	0.07	1.05	0.15	0.227
1553267_a_at	CNO1G6	CCR4-NOT transcription complex subunit 6-like	4.44	4.47	0	-0.03	-1.02	0.73	0.468
1553396_a_at	CDC13	coiled-coil domain containing 13	4.46	4.58	0	-0.12	-1.09	0.19	0.259
1553575_at	NDE	NADH dehydrogenase, subunit 6 (complex I)	10.35	10.31	0	0.04	1.03	0.81	0.492
1554007_at	ASH1L-AS1	ASH1L antisense RNA 1	5.79	5.77	0	0.03	1.02	0.65	0.450
1554152_a_at	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	4.00	3.86	0	0.14	1.10	0.25	0.293
1554250_s_at	TRIM73	tripartite motif containing 73	6.54	6.39	0	0.16	1.11	0.24	0.292
1554306_at	ITPR8	inositol triphosphate 3-kinase B	2.95	2.91	0	0.03	1.02	0.51	0.409
1554478_x_at	HEATR3	HEAT repeat containing 3	3.61	3.63	0	-0.02	-1.01	0.66	0.451
1554503_a_at	OSCAR	osteoclast associated, immunoglobulin-like receptor	3.71	3.77	0	-0.06	-1.04	0.59	0.435
1554670_at	GGA1	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	4.58	4.42	0	0.16	1.12	0.27	0.303
1554770_x_at	ZNFR5	zinc finger protein 785	3.17	3.04	0	0.13	1.10	0.31	0.321
1554910_at	PRKD3	protein kinase D3	3.41	3.43	0	-0.02	-1.02	0.77	0.481
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	8.36	8.44	0	-0.08	-1.06	0.65	0.450
1555116_s_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1	2.89	2.83	0	0.06	1.04	0.26	0.299
1555167_s_at	NAMPT	nicotinamide phosphoribosyltransferase	8.88	8.95	0	-0.07	-1.05	0.29	0.315
1555594_a_at	MBNL1	muscleblind like splicing regulator 1	6.26	6.27	0	-0.01	-1.01	0.91	0.523
1555730_x_at	CLF1	cofilin 1 (non-muscle)	8.30	8.05	0	0.25	1.19	0.29	0.315
1555773_s_at	AP153	adaptor-related protein complex 1 sigma 3 subunit	5.21	5.23	0	-0.02	-1.01	0.85	0.504
1555917_at	MYL12A	myosin light chain 12A	6.03	6.00	0	0.04	1.03	0.43	0.374
1556202_at	SRGAP2	SUP-RBDO Rho GTPase activating protein 2	4.11	4.23	0	-0.12	-1.09	0.41	0.365
1556226_at	---	---	4.88	4.82	0	0.06	1.04	0.69	0.457
1556313_s_at	CAND1	cullin-associated and neddylation-dissociated 1	3.45	3.31	0	0.14	1.10	0.27	0.276
1556336_at	RBMX	RNA binding motif protein, X-linked	5.76	5.77	0	-0.01	-1.01	0.88	0.512
1556423_at	VASH1	vasohibin 1	3.25	3.33	0	-0.08	-1.06	0.56	0.424
1556462_a_at	---	---	3.45	3.53	0	-0.08	-1.06	0.29	0.313
1556471_at	SCML4	sex comb on midleg-like 4 (Drosophila)	5.04	5.04	0	-0.01	-1.01	0.83	0.499
1556621_a_at	---	---	4.34	4.25	0	0.09	1.06	0.29	0.315
1556750_at	LOC153577	uncharacterized LOC153577	3.68	3.74	0	-0.06	-1.04	0.58	0.434
1556832_a_at	---	---	4.76	4.78	0	-0.02	-1.01	0.81	0.492
1556931_at	CCDC4-IT1	CCDC4 intronic transcript 1	4.72	4.64	0	0.08	1.06	0.34	0.338
1557065_at	YLPW1	YLP motif containing 1	6.20	6.16	0	0.04	1.03	0.69	0.457
1557113_at	83588 /// RPS	uncharacterized LOC283588 /// ribosomal protein S6 kinase, 90kDa, polypeptide 5	4.11	4.07	0	0.04	1.03	0.65	0.450
1557145_at	STK38	serine/threonine kinase 38	4.42	4.27	0	0.15	1.11	0.34	0.338
1557227_s_at	TPR	translocated promoter region, nuclear basket protein	6.80	6.68	0	0.11	1.08	0.20	0.265
1557236_at	AROL6	apolipoprotein L 6	5.25	5.25	0	0.00	1.00	0.97	0.535
1557238_s_at	---	---	5.32	5.26	0	0.06	1.04	0.65	0.450
1557287_s_at	GEN1	GEN1 Holliday junction 5' flap endonuclease	4.69	4.77	0	-0.08	-1.06	0.62	0.445
1557278_s_at	TNPO1	transposon 1	4.11	4.21	0	-0.10	-1.02	0.68	0.456
1557289_s_at	RD2 /// GTF2	GTTF2 repeat domain containing 2B	5.27	5.11	0	0.16	1.12	0.16	0.236
1557293_at	LINC00969	long intergenic non-protein coding RNA 969	5.72	5.46	0	0.26	1.20	0.13	0.216
1557436_at	XKR6	X-linked K blood group related 6	1.92	1.92	0	0.00	1.00	0.98	0.538
1557512_at	---	---	3.40	3.39	0	0.01	1.01	0.88	0.515
1557519_at	---	---	3.18	3.19	0	-0.01	-1.01	0.85	0.502
1557527_at	---	---	5.19	4.98	0	0.22	1.16	0.16	0.236
1557529_at	HECTD4	HECT domain containing E3 ubiquitin protein ligase 4	5.30	5.28	0	0.02	1.02	0.74	0.468
1557538_at	---	---	4.51	4.20	0	0.31	1.24	0.13	0.214
1557562_at	---	---	3.19	3.00	0	0.19	1.14	0.17	0.243
1557626_at	---	---	4.35	4.26	0	0.09	1.06	0.58	0.432
1557826_x_at	CSOF2B	chromosome 5 open reading frame 2B	6.00	5.77	0	0.24	1.18	0.12	0.204
1557910_at	HS90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	11.15	11.19	0	-0.03	-1.02	0.62	0.445
1557987_at	---	---	7.16	6.85	0	0.31	1.24	0.12	0.202
1558078_at	---	---	5.77	5.45	0	0.32	1.25	0.14	0.224
1558093_s_at	MATR3	matrin 3	8.06	8.14	0	-0.08	-1.06	0.19	0.256
1558105_a_at	SLC3A7	solute carrier family 9, subfamily A (NH2, cation proton antiporter 7), member 7	5.14	5.14	0	0.00	1.00	0.97	0.535
1558111_at	MBNL1	muscleblind like splicing regulator 1	8.62	8.59	0	0.02	1.02	0.63	0.448
1558279_a_at	KDOR	3-ketodihydroxyglutamine reductase	4.05	4.03	0	0.03	1.02	0.76	0.477
1558669_at	OC10013154	uncharacterized LOC100131541	7.39	7.13	0	0.26	1.20	0.18	0.252
1558679_at	105371215 ///	uncharacterized LOC642691 /// uncharacterized LOC105379432	3.78	3.66	0	0.12	1.09	0.30	0.317
1558641_at	SPATA24	spermatogenesis associated 24	7.31	7.32	0	-0.01	-1.01	0.74	0.469
1558678_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	12.67	12.66	0	0.02	1.11	0.65	0.450
1558691_a_at	DOC14	dedicator of cytokinesis 4	4.40	4.49	0	-0.09	-1.06	0.63	0.449
1558702_at	TEX10	testis expressed 10	3.96	3.95	0	0.01	1.01	0.81	0.492
1558719_s_at	RPAIN	RPA interacting protein	3.27	3.10	0	0.17	1.12	0.14	0.219
1558747_at	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	8.88	8.86	0	0.02	1.01	0.79	0.484
1558922_at	---	---	5.59	5.49	0	0.11	1.08	0.53	0.415
1558971_at	THEMIS	thymocyte selection associated	5.56	5.56	0				

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 POST	Mean log2 intensity for 21 PRE	422 FDR	Log2 Ratio Z1POST/Z2PRE	Fold-Change Z1POST/Z1PRE	p value	FDR
1562031_at	JAK2	Janus kinase 2	4.72	4.60	0	0.12	1.09	0.17	0.247
1562230_at	---	---	2.86	2.88	0	-0.02	-1.01	0.76	0.474
1562290_at	---	---	3.59	3.41	0	0.19	1.14	0.25	0.292
1562307_at	---	---	2.32	2.27	0	0.04	1.03	0.44	0.377
1562316_at	---	---	2.34	2.26	0	0.07	1.05	0.18	0.255
1562364_at	GVINP1	GTPase, very large interferon inducible pseudogene 1	4.74	4.62	0	0.12	1.09	0.36	0.343
1562443_at	SSBP1	single-stranded DNA binding protein 1, mitochondrial	5.16	5.22	0	-0.06	-1.04	0.38	0.354
1562481_at	---	---	2.46	2.45	0	0.01	1.01	0.92	0.526
1562527_at	LOC441666	zinc finger protein 91 pseudogene	2.92	2.88	0	0.04	1.03	0.71	0.463
1562836_at	DDX6	DEAD (Asp-Glu-Ala-Asp) box helicase 6	5.62	5.73	0	-0.11	-1.08	0.27	0.304
1563173_at	---	---	2.24	2.21	0	0.03	1.02	0.58	0.434
1563431_x_at	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)	4.66	4.74	0	-0.08	-1.05	0.23	0.280
1563445_x_at	CTSLP8	cathepsin L pseudogene 8	5.35	5.40	0	-0.04	-1.03	0.62	0.445
1563460_at	---	---	2.15	2.12	0	0.03	1.02	0.46	0.383
1563724_at	---	---	2.23	2.16	0	0.07	1.05	0.14	0.224
1564002_a_at	AK9	adenylate kinase 9	5.82	5.88	0	-0.06	-1.04	0.19	0.256
1564053_a_at	YTHDF3	YTH N(6)-methyladenosine RNA binding protein 3	7.07	7.09	0	-0.02	-1.01	0.75	0.472
1564424_at	OC1057975;uncharacterized LOC105379752	---	5.27	5.18	0	0.09	1.06	0.46	0.384
1564789_at	---	---	2.85	2.82	0	0.03	1.02	0.61	0.445
1565436_s_at	KMT2A	lysine (K)-specific methyltransferase 2A	6.51	6.52	0	-0.01	-1.01	0.93	0.526
1565598_at	---	---	5.24	5.33	0	-0.09	-1.06	0.48	0.395
1565810_at	---	---	2.42	2.36	0	0.06	1.04	0.24	0.292
1565875_at	---	---	2.45	2.48	0	-0.02	-1.02	0.60	0.441
1565886_at	---	---	6.85	6.84	0	0.01	1.00	0.94	0.528
1565887_at	---	---	4.29	4.38	0	-0.09	-1.06	0.38	0.355
1565913_at	---	---	5.29	5.23	0	0.06	1.05	0.47	0.392
1566040_at	OC1002865;ankyrin repeat domain 20 family, member A2 pseudogene	---	3.19	3.14	0	0.05	1.03	0.31	0.234
1566603_s_at	RPUSD3	RNA pseudouridylylate synthase domain containing 3	3.06	2.97	0	0.09	1.06	0.41	0.364
1566825_at	---	---	5.57	5.49	0	0.08	1.05	0.62	0.445
1566966_at	---	---	3.07	3.03	0	0.04	1.02	0.69	0.457
1566980_at	---	---	4.37	4.11	0	0.05	1.04	0.51	0.408
1568865_at	FNTB	farnesyltransferase, CAAX box, beta	3.22	3.12	0	0.10	1.07	0.31	0.325
1569128_at	Chlorf8	chromosome 3 open reading frame 38(Chlorf8)	2.14	2.06	0	0.08	1.06	0.18	0.254
1569129_s_at	Chlorf8	chromosome 3 open reading frame 38(Chlorf8)	5.21	5.26	0	-0.07	-1.05	0.59	0.438
1569142_at	TRIM13	tripartite motif containing 13	4.68	4.54	0	0.13	1.10	0.35	0.342
1569189_at	TTC9C	tetratricopeptide repeat domain 9C	4.13	3.98	0	0.15	1.11	0.23	0.285
1569311_at	---	---	2.93	2.86	0	0.08	1.05	0.17	0.243
1569320_at	GPBP1L	GC-rich promoter binding protein 1-like 1	5.74	5.57	0	0.17	1.12	0.30	0.319
1569352_at	FNIP2	folliculin interacting protein 2	6.56	6.53	0	0.03	1.02	0.77	0.481
1569578_at	---	---	4.52	4.39	0	0.13	1.09	0.24	0.290
1569583_at	EREG	epiregulin	5.69	5.78	0	-0.09	-1.06	0.48	0.399
1569706_at	MYSL1	Myb-like, SWIRM and MPN domains 1	2.41	2.28	0	0.02	1.02	0.61	0.443
1569773_at	ATP8A1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	3.67	3.64	0	0.02	1.01	0.81	0.492
1569791_at	STK4	serine/threonine kinase 4	5.70	5.75	0	-0.05	-1.03	0.55	0.423
1569830_at	PTPNC	protein tyrosine phosphatase, receptor type, C	5.08	5.16	0	-0.08	-1.06	0.45	0.381
1569864_at	SERAC1	serine active site containing 1	2.64	2.57	0	0.08	1.05	0.30	0.320
1569948_at	---	---	2.65	2.60	0	0.05	1.04	0.54	0.418
1570021_at	---	---	3.72	3.81	0	-0.09	-1.07	0.44	0.375
1570213_at	---	---	2.44	2.40	0	0.03	1.02	0.57	0.428
1570251_s_at	ANKRD20A3	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A12, pseudogene /// ant	3.50	3.32	0	0.18	1.13	0.26	0.319
1570338_at	---	---	2.97	2.93	0	0.03	1.02	0.54	0.419
1570364_at	ZNF709	zinc finger protein 709	2.54	2.58	0	-0.04	-1.03	0.62	0.445
1570373_s_at	EPT1	ethanodiaminephosphotransferase 1	3.45	3.47	0	-0.02	-1.01	0.82	0.495
1570409_s_at	---	---	2.86	2.83	0	0.03	1.02	0.74	0.469
1570507_at	SCAF11	SR-related CTD-associated factor 11	5.42	5.28	0	0.13	1.10	0.20	0.268
200607_s_at	RAD21	RAD21 cohesin complex component	8.60	8.62	0	-0.03	-1.02	0.44	0.375
200671_s_at	SPYB1	spectrin, beta, non-erythrocytic 1	4.90	4.95	0	-0.05	-1.03	0.20	0.319
200806_s_at	HSPD1	heat shock 70kDa protein 1 (chaperonin)	10.39	10.36	0	0.02	1.02	0.33	0.333
200832_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	5.35	5.37	0	-0.02	-1.01	0.74	0.471
200928_s_at	RAB14	RAB14, member RAS oncogene family	2.97	2.88	0	0.09	1.07	0.22	0.276
200951_s_at	CNO2	cyclin D2	6.28	6.27	0	0.01	1.01	0.83	0.499
201008_s_at	TXNP	thioredoxin interacting protein	10.22	10.17	0	0.05	1.03	0.69	0.457
201043_s_at	ANP32A	acidic nuclear phosphoprotein 32 family member A	6.30	6.32	0	-0.03	-1.02	0.86	0.507
201065_s_at	GT32P1	general transcription factor III /// general transcription factor III pseudogene 1 /// general transcription factor III, pse	8.36	8.31	0	0.05	1.03	0.40	0.363
201070_s_at	SFB1	serpin, fibronectin type 3, subunit 1, 155kDa	8.44	8.46	0	-0.02	-1.01	0.67	0.454
201073_s_at	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	5.94	5.91	0	0.03	1.02	0.66	0.452
201083_s_at	BCLAF1	BCL2-associated transcription factor 1	8.07	8.07	0	0.00	1.00	0.99	0.540
201085_s_at	SON	SON DNA binding protein	9.59	9.56	0	0.02	1.02	0.43	0.375
201292_s_at	MOB1A	MOB kinase activator 1A	8.76	8.80	0	-0.05	-1.03	0.48	0.395
201324_s_at	EMP1	epithelial membrane protein 1	10.11	10.19	0	-0.07	-1.05	0.12	0.204
201325_s_at	EMP1	epithelial membrane protein 1	8.49	8.58	0	-0.09	-1.07	0.17	0.247
201340_s_at	ENCL1	ectodermal-neural cortex 1 (with BTB domain)	5.77	5.87	0	-0.10	-1.07	0.12	0.205
201446_s_at	TIA1	TIA1 cytosolic granule-associated RNA binding protein	8.77	8.73	0	0.03	1.02	0.54	0.419
201450_s_at	TIA1	TIA1 cytosolic granule-associated RNA binding protein	8.31	8.21	0	0.09	1.07	0.24	0.290
201490_s_at	PRF	peptidylglycyl isomerase F	10.05	10.00	0	0.04	1.03	0.70	0.457
201631_s_at	IER3	immediate early response 3	11.47	11.53	0	-0.06	-1.04	0.47	0.390
201635_s_at	FRK1	Fragile X mental retardation, autosomal homolog 1	8.54	8.53	0	0.01	1.00	0.92	0.526
201668_x_at	MARCKS	myristoylated alanine-rich protein kinase C substrate	7.33	7.33	0	0.00	1.00	0.99	0.542
201694_s_at	EGR1	early growth response 1	7.95	7.98	0	-0.02	-1.02	0.78	0.483
201711_s_at	RANBP2	RAN binding protein 2	10.18	10.2	0	-0.03	-1.02	0.54	0.418
201732_s_at	CLCN3	chloride channel, voltage-sensitive 3	5.23	5.32	0	-0.10	-1.07	0.18	0.256
201743_s_at	CD14	CD14 molecule	7.14	7.40	0	-0.26	-1.20	0.13	0.216
201868_s_at	TBL1X	transducin (beta)-like 1X-linked	5.39	5.38	0	0.01	1.00	0.95	0.532
201975_at	ARH1	aridine RBR E3 ubiquitin protein ligase 1	6.86	6.88	0	-0.02	-1.02	0.63	0.449
202118_s_at	CPEB3	copine III	7.07	7.07	0	0.00	1.00	0.98	0.539
202195_s_at	TMED5	transmembrane p24 trafficking protein 5	7.28	7.33	0	-0.05	-1.04	0.40	0.361
202241_at	TRB1	tribbles pseudokinase 1	8.02	8.05	0	-0.03	-1.02	0.65	0.450
202388_at	RCG2	regulator of G-protein signaling 2	10.87	10.88	0	-0.05	-1.03	0.31	0.325
202412_s_at	USP1	ubiquitin specific peptidase 1	7.42	7.47	0	-0.05	-1.03	0.31	0.323
202430_s_at	PLSCR1	phospholipid scramblase 1	7.90	7.88	0	0.02	1.01	0.79	0.488
202581_at	PA1A	/// HSP heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	7.58	7.54	0	0.04	1.03	0.65	0.450
202601_s_at	HTR1F1	HTR 1F1 rat specific factor 1	5.07	5.17	0	-0.10	-1.07	0.26	0.300
202609_at	EPH8	epidermal growth factor receptor pathway substrate 8	7.29	7.28	0	0.00	1.00	0.96	0.535
202759_s_at	2	/// PALM2-FA kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthrough	7.83	7.86	0	-0.03	-1.02	0.52	0.412
202760_s_at	2	/// PALM2-FA kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthrough	8.12	8.13	0	-0.01	-1.00	0.93	0.526
202814_s_at	HEXAM1	hexamethylene bis-actinamide inducible 1	7.80	7.85	0	-0.08	-1.06	0.30	0.317
202855_s_at	SLC16A3	solute carrier family 16 (monocarboxylate transporter), member 3	6.68	6.72	0	-0.04	-1.03	0.84	0.499
202856_s_at	SLC16A3	solute carrier family 16 (monocarboxylate transporter), member 3	7.76	7.84	0	-0.08	-1.05	0.49	0.401
202869_at	OAS1	2'-5'-oligoadenylate synthetase 1	8.44	8.45	0	-0.01	-1.01	0.85	0.502
202976_s_at	PRK2	pre-B-cell leukemia homology 2	6.47	6.64	0	-0.16	-1.12	0.18	0.252
202987_s_at	DDIT4	DNA damage inducible transcript 4	9.93	9.91	0	0.03	1.02	0.79	0.484
202988_s_at	ANPEP	alanyl (membrane) aminopeptidase	8.40	8.51	0	-0.11	-1.08	0.43	0.374
203231_s_at	ATXN1	ataxin 1	5.50	5.51	0	-0.02	-1.01	0.84	0.501
203394_s_at	HES1	hes family bHLH transcription factor 1	8.24	8.20	0	0.05	1.03	0.54	0.417
203607_at	INPP5F	inositol polyphosphate 5-phosphatase F	6.63	6.59	0	0.03	1.02	0.68	0.456
203887_s_at	THBD	thrombomodulin	5.76	5.88	0	-0.13	-1.09	0.36	0.345
203888_at	THBD	thrombomodulin	4.87	4.98	0	-0.11	-1.08	0.37	0.350
203889_at	SCG5	secretogranin V	5.82	5.92	0	-0.11	-1.08	0.45	0.379
203958_s_at	ZBTB40	zinc finger and BTB domain containing 40	6.53	6.57	0	-0.04	-1.03	0.67	0.454
204011_at	SPRY2	sprouty RTK signaling antagonist 2	5.78	5.92	0	-0.14	-1.10	0.17	0.241
204014_at	DUSP4	dual specificity phosphatase 4	8.66	8.62	0	0.04	1.03	0.60	0.441
204015_s_at	DUSP4	dual specificity phosphatase 4	8.39	8.42	0	-0.03	-1.02	0.41	0.365
204088_at	P2RX4	purinergic receptor P2X, ligand gated ion channel, 4	8.66	8.63	0	0.04	1.03	0.78	0.482
204103_at	CCLA	chemokine (C-C motif) ligand 4	11.96	12.08	0	-0.13	-1.09	0.22	0.279
204165_at	WASF1	WASF protein family, member 1	3.77	3.74	0	0.02	1.01	0.70	0.457
204180_s_at	ZBTB43	zinc finger and BTB domain containing 43	6.91	6.95	0	-0.03	-1.02	0.62	0.445
204192_at	CD37	CD37 molecule	7.33	7.09	0	0.24	1.18	0.22	0.278
204270_at	SKI	SKI proto-oncogene	7.63	7.53	0	0.10	1.07	0.39	0.356
204470_at	CK1L3	chemokine (C-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	11.47	11.61	0	-0.11	-1.08	0.39	0.356
204475_at	MMP1	matrix metalloproteinase 1	7.81	7.80	0	0.02	1.01	0.92	0.526
204560_at	FKBP5	FK506 binding protein 5	5.47	5.43	0	0.03	1.03	0.83	0.498
204629_s_at	ITGB3	integrin beta 3	4.83	4.80	0	0.04	1.02	0.69	0.457
204686_at	IRS1	insulin receptor substrate 1	3.51	3.44	0	0.07	1.05	0.41	0.364
204748_at	PTGS2	prostaglandin-endoperoxide synthase							

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for Z1 POST	Mean log2 intensity for Z2 POST	422 FDR <0.2 >YES	Log2 Ratio Z1POST/Z2POST	Fold-Change Z1POST/Z2POST	p value	FDR
206279_at	PRKY	protein kinase, Y-linked, pseudogene	5.28	5.19	0	0.08	1.06	0.46	0.384
206341_at	IL2RA	interleukin 2 receptor, alpha	6.42	6.38	0	0.04	1.03	0.65	0.450
206366_x_at	XCL1	chemokine [C motif] ligand 1	7.33	7.36	0	-0.03	-1.02	0.61	0.441
206500_s_at	MS18BP1	MS18 binding protein 1	7.13	7.23	0	-0.10	-1.07	0.13	0.214
206548_at	---	---	4.39	4.30	0	0.09	1.06	0.63	0.448
206652_at	zinc finger, MYM-type 5	zinc finger, MYM-type 5	6.96	6.98	0	-0.03	-1.02	0.59	0.435
206667_s_at	SCAMP1	secretory carrier membrane protein 1	5.35	5.38	0	-0.02	-1.02	0.72	0.466
206928_at	ZNF124	zinc finger protein 124	4.60	4.55	0	0.06	1.04	0.49	0.400
207038_at	SLC16A6	solute carrier family 16, member 6	5.69	5.78	0	-0.08	-1.06	0.32	0.330
207219_at	ZFP968	ZFP96 zinc finger protein 8	3.46	3.40	0	0.06	1.04	0.50	0.402
207237_at	KCNAB3	potassium channel, voltage gated shaker related subfamily A, member 3	6.00	5.94	0	0.05	1.04	0.60	0.440
207316_at	HAS1	hyaluronan synthase 1	3.05	3.06	0	-0.01	-1.01	0.87	0.508
207334_s_at	TGFB2	transforming growth factor beta receptor II	5.78	5.76	0	0.02	1.01	0.87	0.508
207388_s_at	PTGES	prostaglandin G synthase	5.14	5.17	0	-0.02	-1.02	0.74	0.469
207523_at	CCL1	chemokine [C-C motif] ligand 1	5.26	5.24	0	-0.08	-1.06	0.48	0.399
207545_s_at	11928143	LOC10191928143 /// numb homology (Drosophila)	6.99	7.11	0	-0.11	-1.08	0.21	0.271
207549_x_at	CD46	CD46 molecule, complement regulatory protein	7.58	7.55	0	0.03	1.02	0.52	0.412
207630_s_at	CREM	cAMP responsive element modulator	10.96	10.99	0	-0.04	-1.03	0.36	0.344
207674_at	FCAR	Fc fragment of IgA receptor	6.32	6.44	0	-0.12	-1.09	0.50	0.402
207786_at	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	4.31	4.26	0	0.04	1.03	0.61	0.441
207819_s_at	ARCB4	ATP binding cassette subfamily B member 4	5.02	4.95	0	0.07	1.05	0.21	0.269
207850_at	CXCL3	chemokine [C-X-C motif] ligand 3	11.07	11.15	0	-0.08	-1.06	0.47	0.391
207852_at	CXCL5	chemokine [C-X-C motif] ligand 5	4.64	4.66	0	-0.01	-1.01	0.91	0.524
207907_at	TNFSF14	tumor necrosis factor (ligand) superfamily, member 14	6.01	6.01	0	-0.01	-1.01	0.95	0.532
208067_x_at	UTY	ubiquitously transcribed tetrahydropteridine repeat containing, Y-linked	7.26	7.35	0	-0.08	-1.06	0.24	0.290
208075_s_at	CCL7	chemokine [C-C motif] ligand 7	6.51	6.54	0	-0.04	-1.03	0.81	0.492
208178_x_at	TRIO	trio Rho guanine nucleotide exchange factor	5.51	5.53	0	-0.02	-1.01	0.78	0.484
208198_x_at	105379650	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 /// killer cell immunoglobulin-like rec	4.02	4.03	0	-0.01	-1.01	0.80	0.492
208601_s_at	TUBB1	tubulin, beta 1 class VI	6.44	6.50	0	-0.06	-1.04	0.51	0.408
208621_s_at	E2R	estrin	9.77	9.76	0	0.01	1.01	0.85	0.504
208664_s_at	ITC5	tetratricopeptide repeat domain 3	6.54	6.55	0	0.00	1.00	0.96	0.534
208797_s_at	GOLGA8A	golgin A8 family, member A	6.76	6.65	0	0.11	1.08	0.32	0.328
208830_s_at	ILF3	interleukin enhancer binding factor 3	7.76	7.77	0	-0.01	-1.01	0.89	0.516
208960_s_at	IFI16	interferon, gamma inducible protein 16	10.14	10.10	0	0.04	1.03	0.36	0.343
209013_x_at	TRIO	trio Rho guanine nucleotide exchange factor	5.54	5.53	0	0.02	1.01	0.86	0.507
209060_x_at	NCOA3	nuclear receptor coactivator 3	7.40	7.43	0	-0.03	-1.02	0.36	0.343
209201_s_at	BICD2	bicaudal D homology 2 (Drosophila)	6.25	6.21	0	0.04	1.03	0.65	0.450
209277_at	TPP1	tissue factor pathway inhibitor 2	8.28	8.31	0	-0.03	-1.02	0.83	0.498
209321_s_at	ADCY3	adenylate cyclase 3	5.63	5.52	0	0.11	1.08	0.38	0.354
209446_s_at	---	---	5.92	5.87	0	0.05	1.03	0.74	0.469
209599_s_at	PRUNE	prune exopolyphosphatase	3.76	3.77	0	0.00	-1.00	0.95	0.535
209616_s_at	SSI	5'-phosphoribosyl transferase 1 /// carboxylesterase 1 pseudogene 1	7.04	7.09	0	-0.05	-1.02	0.63	0.449
209675_s_at	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	6.20	6.10	0	0.10	1.07	0.24	0.292
209699_x_at	AKR1C2	aldo-keto reductase family 1, member C2	6.51	6.62	0	-0.11	-1.08	0.14	0.219
209715_at	CBX5	chromobox homology 5	5.27	5.30	0	-0.03	-1.02	0.57	0.428
209760_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	7.79	7.83	0	-0.04	-1.03	0.36	0.344
209774_x_at	CXCL2	chemokine [C-X-C motif] ligand 2	12.80	12.85	0	-0.04	-1.03	0.53	0.416
209790_s_at	CASP6	caspase 6	5.83	5.79	0	0.04	1.03	0.42	0.372
209803_s_at	PHLDA2	pleckstrin homology-like domain, family A, member 2	6.82	6.88	0	-0.06	-1.04	0.44	0.377
209860_s_at	SLC18A3	solute carrier family 13 (LDP-N-acetylglucosamine [UDP-GlcNAc] transporter), member A3	3.74	3.73	0	0.00	-1.00	0.99	0.540
209931_s_at	CD300A	CD300a molecule	7.65	7.65	0	-0.01	-1.01	0.88	0.512
209967_s_at	CREM	cAMP responsive element modulator	10.79	10.84	0	-0.05	-1.03	0.25	0.294
210057_s_at	SMG1	SMG1 phosphatidylinositol 3-kinase-related kinase	4.60	4.51	0	0.10	1.07	0.35	0.342
210118_s_at	IL1A	interleukin 1 alpha	10.03	10.11	0	-0.08	-1.06	0.55	0.422
210119_at	KCN115	potassium channel, inwardly rectifying subfamily 1, member 15	3.91	3.95	0	-0.04	-1.03	0.59	0.438
210140_at	CST7	cystatin F (leukocystatin)	8.48	8.50	0	-0.02	-1.01	0.73	0.468
210216_s_at	SP100	SP100 nuclear antigen	8.22	8.27	0	-0.04	-1.03	0.44	0.377
210251_s_at	RUPY3	RUN and FYVE domain containing 3	5.88	5.85	0	0.03	1.02	0.70	0.457
210282_at	ZMYM2	zinc finger, MYM-type 2	6.48	6.36	0	0.12	1.09	0.29	0.315
210367_s_at	PTGES	prostaglandin G synthase	3.49	3.53	0	-0.04	-1.03	0.56	0.427
210406_at	CC78	chaperonin containing TCP1, subunit B (theta)	3.09	3.09	0	0.01	1.01	0.92	0.526
210693_at	SPPL28	signal peptide peptidase like 28	5.26	5.24	0	0.02	1.01	0.84	0.499
210717_at	---	---	3.22	3.32	0	-0.10	-1.07	0.46	0.384
210772_at	FP2	formyl peptide receptor 2	4.96	5.04	0	-0.09	-1.06	0.35	0.339
210773_s_at	FP2	formyl peptide receptor 2	4.91	4.79	0	0.12	1.09	0.19	0.256
210807_s_at	SLC16A7	solute carrier family 16 (monocarboxylate transporter), member 7	4.24	4.14	0	0.09	1.07	0.32	0.329
210818_s_at	HS1	GRK1-BTB and CMC homology 1, basic leucine zipper transcription factor 1 /// GRK1 antisense RNA 2	6.74	6.84	0	-0.10	-1.07	0.39	0.357
210887_at	CNCT4	CNCT4-NOT1 transcription complex subunit 4	3.68	3.63	0	0.05	1.04	0.50	0.402
210942_s_at	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	6.90	7.02	0	-0.11	-1.08	0.16	0.234
210965_x_at	CDK13	cyclin-dependent kinase 13	5.23	5.08	0	0.16	1.11	0.12	0.208
210985_s_at	SP100	SP100 nuclear antigen	4.42	4.29	0	0.13	1.09	0.22	0.278
211022_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked	5.75	5.82	0	-0.07	-1.05	0.47	0.391
211074_at	---	---	8.39	8.35	0	0.04	1.03	0.62	0.445
211081_s_at	MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	6.06	6.04	0	0.02	1.02	0.72	0.465
211192_s_at	CD84	CD84 molecule	5.37	5.40	0	-0.03	-1.02	0.70	0.457
211307_s_at	FCAR	Fc fragment of IgA receptor	6.55	6.57	0	-0.02	-1.02	0.90	0.521
211310_at	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit	4.57	4.64	0	-0.07	-1.05	0.65	0.450
211429_s_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiprotease, antitrypsin), member 1	8.58	8.63	0	-0.05	-1.04	0.38	0.354
211538_s_at	HSF2	heat shock 70kDa protein 2	4.49	4.49	0	0.00	1.00	0.97	0.536
211688_at	3DL1	3DL1 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 /// killer cell immunoglobulin-like rec	5.46	5.31	0	0.15	1.11	0.20	0.262
211721_s_at	ZNF551	zinc finger protein 551	4.33	4.27	0	0.06	1.04	0.51	0.409
211751_at	---	LOC6335 phosphodiesterase 4D interacting protein-like /// phosphodiesterase 4D interacting protein-like /// phosphodiesterase	6.08	6.12	0	-0.03	-1.02	0.52	0.412
211794_at	FYB	FYB binding protein	6.71	6.72	0	-0.01	-1.01	0.92	0.526
211816_s_at	FCAR	Fc fragment of IgA receptor	6.71	6.72	0	-0.01	-1.01	0.92	0.526
211821_x_at	GYPA	glycophorin A (MNS blood group)	3.31	3.31	0	0.01	1.00	0.91	0.524
211899_s_at	TRAFA4	TNF receptor-associated factor 4	5.22	5.27	0	-0.05	-1.03	0.73	0.468
211947_s_at	PRRC2C	proline-rich coiled-coil 2C	6.83	6.86	0	-0.03	-1.02	0.64	0.449
211965_at	ZFP36L1	ZFP36 zinc finger protein-like 1	6.65	6.63	0	0.02	1.01	0.81	0.492
211973_at	NUDT3	nucleoside diphosphate kinase 3	5.50	5.56	0	-0.06	-1.04	0.50	0.402
212079_s_at	KMT2A	lysine (K)-specific methyltransferase 2A	7.00	7.00	0	0.00	1.00	0.97	0.536
212105_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box helicase 9	6.06	6.10	0	-0.04	-1.03	0.75	0.474
212107_s_at	DHX9	DEAH (Asp-Glu-Ala-His) box helicase 9	7.04	8.00	0	-0.06	-1.04	0.20	0.263
212172_at	AK2	adenylate kinase 2	3.83	3.78	0	0.05	1.03	0.53	0.415
212182_at	NUDT4	nucleoside diphosphate kinase 4	2.46	2.37	0	0.08	1.06	0.12	0.202
212249_at	CNCR1	phosphoinositide 3-kinase, regulatory subunit 1 (alpha)	7.16	7.18	0	-0.03	-1.02	0.78	0.483
212286_at	ANKRD12	ankyrin repeat domain 12	8.99	9.01	0	-0.02	-1.01	0.64	0.449
212332_at	RBL2	retinoblastoma-like 2	7.23	7.19	0	0.03	1.02	0.64	0.449
212392_s_at	3996724	Pi phosphodiesterase 4D interacting protein-like /// phosphodiesterase 4D interacting protein	5.31	5.37	0	-0.06	-1.04	0.70	0.457
212417_at	SCAMP1	secretory carrier membrane protein 1	8.86	8.88	0	-0.02	-1.02	0.59	0.438
212451_at	SECISBP2	SECIS binding protein 2-like	7.13	7.21	0	-0.08	-1.06	0.18	0.256
212592_at	JCHAIN	joining chain of multimeric IgA and IgM	8.50	8.44	0	0.06	1.04	0.36	0.345
212650_at	EHBP1	EH domain binding protein 1	5.83	5.91	0	-0.08	-1.06	0.24	0.291
212700_at	PARP6A	poly(ADP-ribose) polymerase 6A	6.50	6.47	0	0.03	1.02	0.65	0.450
212758_s_at	ZEB1	zinc finger E-box binding homeobox 1	7.96	7.88	0	0.08	1.06	0.13	0.209
212762_s_at	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	5.46	5.49	0	-0.04	-1.03	0.73	0.468
212979_s_at	TCF41	TRPM8 channel-associated factor 1	5.18	5.06	0	0.12	1.09	0.17	0.243
213005_s_at	KANAL1	Kan motif and ankyrin repeat domains 1	6.53	6.60	0	-0.07	-1.05	0.49	0.402
213266_at	ZFR	zinc finger RNA binding protein	6.75	6.85	0	-0.10	-1.07	0.19	0.256
213355_at	ST3GAL6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	7.08	7.15	0	-0.07	-1.05	0.37	0.350
213430_at	RUPY3	RUN and FYVE domain containing 3	3.69	3.71	0	-0.02	-1.02	0.81	0.492
213436_at	CNR1	cannabinoid receptor 1 (brain)	4.31	4.19	0	0.13	1.10	0.13	0.216
213457_at	MFMAS1	malignant fibrous histiocytoma amplified sequence 1	6.79	6.83	0	-0.04	-1.03	0.66	0.450
213472_at	HNRNP13	heterogeneous nuclear ribonucleoprotein Hs (H)	5.22	5.15	0	0.08	1.06	0.67	0.454
213566_at	RNASE6	ribonuclease, RNase A family, K6	6.43	6.40	0	0.03	1.02	0.75	0.474
213638_at	PHACTR1	phosphatase and actin regulator 1	8.02	7.99	0	0.03	1.02	0.66	0.452
213875_x_at	C6orf62	chromosome 6 open reading frame 62	7.77	7.83	0	-0.05	-1.04	0.55	0.422
213956_at	CEP350	centrosomal protein 350kDa	6.66	6.72	0	-0.06	-1.04	0.52	0.412
213971_s_at	212	LOC6335 phosphodiesterase 4D interacting protein-like /// phosphodiesterase 4D interacting protein	7.51	7.50	0	0.01	1.01	0.84	0.499
214034_at	ERAP1	endoplasmic reticulum aminopeptidase 1	4.61	4.71	0	-0.09	-1.07	0.15	0.228
214041_x_at	RPL37A	ribosomal protein L37a	5.68	5.73	0	-0.05	-1.03	0.78	0.484
214149_s_at	ATP5VD1	ATP							

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 POST	Mean log2 intensity for 21 PRE	422 FDR <0.2 1-YES	Log2 Ratio ZIPOST vs PRE	Fold-Change ZIPOST vs PRE	p value	FDR
215188_at	STK24	serine/threonine kinase 24	5.37	5.22	0	0.15	1.11	0.21	0.269
215191_at	---	---	4.96	4.75	0	0.21	1.16	0.20	0.265
215220_s_at	TPR	translocated promoter region, nuclear basket protein	5.70	5.59	0	0.11	1.08	0.38	0.351
215246_at	---	---	4.86	4.86	0	0.01	1.00	0.96	0.535
215308_at	XRC6C	X-ray repair complementing defective repair in Chinese hamster cells 6	2.56	2.52	0	0.03	1.02	0.52	0.412
215318_at	MINOS1P1	mitochondrial inner membrane organizing system 1 pseudogene 1	5.05	4.80	0	0.25	1.19	0.12	0.206
215330_at	---	---	6.61	6.39	0	0.22	1.17	0.19	0.256
215339_at	NKTR	natural killer cell triggering receptor	4.75	4.74	0	0.01	1.01	0.92	0.526
215342_s_at	RABGAP1L	RAB GTPase activating protein 1-like	6.33	6.27	0	0.06	1.04	0.33	0.333
215352_at	GIMAP5	GTPase, IMAP family member 5	4.82	4.89	0	-0.07	-1.05	0.55	0.422
215434_s_at	NBPFL1	Neuroblastoma breakpoint family member 1 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma bre	9.46	9.53	0	-0.07	-1.05	0.39	0.357
215555_at	---	---	4.88	4.65	0	0.23	1.17	0.23	0.283
215586_at	PPP3C8	---	3.32	3.17	0	0.15	1.11	0.21	0.271
215589_at	SMURF1	---	3.62	3.68	0	-0.06	-1.04	0.42	0.371
215608_at	KDM5A	lysine (K)-specific demethylase 5A	6.16	6.19	0	-0.03	-1.02	0.64	0.450
215761_at	DMXL2	Dmx-like 2	5.17	5.11	0	0.06	1.04	0.74	0.469
215866_at	---	---	3.32	3.21	0	0.11	1.08	0.14	0.225
215893_at	SKIL	SKI-like proto-oncogene	4.44	4.43	0	0.02	1.01	0.86	0.506
215965_at	---	---	2.57	2.45	0	0.11	1.08	0.22	0.276
215991_s_at	EMC1	ER membrane protein complex subunit 1	2.80	2.76	0	0.04	1.03	0.50	0.402
216015_s_at	NLRP3	NLR family, pyrin domain containing 3	4.79	4.97	0	-0.18	-1.13	0.24	0.291
216016_s_at	NLRP3	NLR family, pyrin domain containing 3	2.83	2.73	0	0.09	1.07	0.21	0.275
216050_at	PRMT2	protein arginine methyltransferase 2	6.73	6.69	0	0.04	1.03	0.73	0.468
216101_at	---	---	4.65	4.64	0	0.00	1.00	0.99	0.540
216117_at	EXO5C2	exosome component 2	2.78	2.76	0	0.02	1.02	0.60	0.440
216248_s_at	NRAA2	nuclear receptor subfamily 4, group A, member 2	10.09	10.12	0	-0.03	-1.02	0.33	0.333
216361_s_at	KAT5A	Kluyverdoxyl acetyltransferase 5A	5.20	5.22	0	-0.02	-1.02	0.88	0.515
216370_s_at	TKTL1	transketolase-like 1	4.38	4.50	0	-0.11	-1.08	0.39	0.356
216433_s_at	PRDM2	PR domain containing 2, with ZNF domain	3.61	3.66	0	-0.05	-1.04	0.65	0.450
216594_s_at	AKR1C1	aldo-keto reductase family 1, member C1	6.37	6.45	0	-0.08	-1.06	0.16	0.234
216595_at	FAM188A	family with sequence similarity 186, member A	3.86	3.02	0	0.14	1.10	0.16	0.234
216683_at	---	---	3.00	2.93	0	0.07	1.05	0.42	0.369
216901_s_at	IKZF1	IKAROS family zinc finger 1	5.98	5.84	0	0.14	1.11	0.42	0.372
217234_s_at	E2F8	e2f8	10.23	10.17	0	-0.06	-1.03	0.39	0.357
217507_at	SLC11A1	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1	3.17	3.15	0	0.03	1.02	0.74	0.469
217529_at	ORA2	ORAI calcium release-activated calcium modulator 2	6.46	6.28	0	0.18	1.13	0.21	0.275
217540_at	NKX3	neurexophilin and PC-esterase domain family, member 3	3.85	3.92	0	-0.07	-1.05	0.26	0.301
217576_s_at	SO2	SOS Ras/Rho guanine nucleotide exchange factor 2	5.74	5.72	0	0.02	1.01	0.76	0.477
217602_at	PP1A	peptidylprolyl isomerase A (cyclophilin A)	3.84	3.81	0	0.03	1.02	0.84	0.500
217644_s_at	SO2	SOS Ras/Rho guanine nucleotide exchange factor 2	5.03	4.91	0	0.13	1.09	0.33	0.332
217656_at	---	---	5.35	5.29	0	0.06	1.04	0.59	0.438
217813_s_at	SPIN1	spinidin 1	4.99	5.13	0	-0.14	-1.10	0.27	0.304
217878_s_at	CDC27	cell division cycle 27	7.66	7.68	0	-0.02	-1.02	0.66	0.451
217951_s_at	PHF3	PHD finger protein 3	6.83	6.87	0	-0.03	-1.02	0.65	0.450
218186_s_at	RSF1	remodeling and spacing factor 1	6.51	6.57	0	-0.06	-1.04	0.33	0.334
218401_at	SKN1D	sorting nexin 10	9.05	9.09	0	-0.04	-1.03	0.44	0.375
218430_s_at	RFK7	regulatory factor X, 7	5.06	4.96	0	0.10	1.07	0.37	0.349
218469_at	GREM1	gremlin 1, DAN family BMP antagonist	4.96	5.07	0	-0.10	-1.07	0.41	0.365
218743_s_at	EXO5C	exocyst complex component 5	5.64	5.71	0	-0.08	-1.06	0.34	0.337
218830_at	HEV1	hes-related family BHLH transcription factor with YRPW motif 1	6.46	6.59	0	-0.12	-1.09	0.19	0.254
218930_s_at	TMEM106B	transmembrane protein 106B	5.65	5.68	0	-0.02	-1.02	0.68	0.456
218967_s_at	PTER	phosphotransferase related	5.72	5.73	0	0.00	-1.00	0.96	0.533
219402_s_at	HPSE	heparanase	6.68	6.69	0	-0.05	-1.04	0.59	0.438
219518_s_at	ELL3	elongation factor RNA polymerase II-like 3	5.75	5.73	0	0.02	1.01	0.73	0.468
219574_at	MARCH3	membrane associated ring finger 1	6.92	6.88	0	0.04	1.03	0.62	0.445
219730_at	MED18	mediator complex subunit 18	2.40	2.31	0	0.08	1.06	0.24	0.292
219844_at	CCDC186	coiled-coil domain containing 186	5.39	5.45	0	-0.06	-1.04	0.43	0.374
219858_s_at	MSD6	major facilitator superfamily domain containing 6	4.89	5.02	0	-0.02	-1.02	0.84	0.501
219864_s_at	RCAN3	RCAN family member 3	4.28	4.27	0	0.01	1.00	0.95	0.533
219922_s_at	LTBP3	latent transforming growth factor beta binding protein 3	5.86	5.67	0	0.19	1.14	0.39	0.357
219960_at	TSLG	tasitin gamma	4.76	4.72	0	0.02	1.01	0.83	0.499
220038_at	144-SGK3	144-SGK3 /// C/EBP44-SGK3 readthrough /// serum/glucocorticoid regulated kinase family, member 3	4.85	4.91	0	-0.06	-1.04	0.60	0.441
220068_at	VPREB3	pre-B lymphocyte 3	5.67	5.69	0	-0.02	-1.01	0.87	0.507
220220_at	171804	171804 /// L1R leucine-rich repeat-containing protein 37A3 pseudogene /// leucine rich repeat containing 37, member A4, pseudog	3.63	3.57	0	0.04	1.03	0.68	0.455
220251_s_at	LRP1	low density lipoprotein receptor related protein 12	5.74	5.52	0	-0.01	-1.01	0.89	0.513
220586_at	CHD9	chromodomain helicase DNA binding protein 9	2.54	2.43	0	0.11	1.08	0.13	0.215
220643_s_at	FAIM5	Fas apoptotic inhibitory molecule 5	5.44	5.45	0	-0.01	-1.01	0.82	0.495
220704_at	IKZF1	IKAROS family zinc finger 1	5.51	5.28	0	0.23	1.17	0.22	0.276
221092_at	IKZF3	IKAROS family zinc finger 3	5.16	4.89	0	0.17	1.12	0.45	0.379
221231_s_at	NRDE2	NRDE-2, necessary for RNA interference, domain containing	2.51	2.49	0	0.03	1.02	0.65	0.450
221345_at	FFAR2	free fatty acid receptor 2	5.08	5.15	0	-0.07	-1.05	0.56	0.424
221496_s_at	TGS2	transducer of ERBB2, 2	5.82	5.87	0	-0.06	-1.04	0.50	0.406
221695_s_at	MARCKS2	mitogen-activated protein kinase kinase kinase 2	7.13	7.15	0	-0.02	-1.02	0.75	0.473
221705_s_at	SIKE1	suppressor of IKKBE1	5.79	5.72	0	0.06	1.04	0.42	0.369
221986_s_at	KHL24	ketch-like family member 24	7.31	7.27	0	0.04	1.03	0.44	0.376
222131_at	---	---	7.39	7.39	0	0.00	1.00	0.99	0.540
222343_at	BCL2L11	BCL2-like 11 (apoptosis factor)	5.88	5.85	0	0.04	1.03	0.64	0.409
222387_s_at	VP535	VP535 retromer complex component	7.59	7.66	0	-0.07	-1.05	0.17	0.247
222406_s_at	PNRC2	proline-rich nuclear receptor coactivator 2	9.01	8.96	0	0.05	1.04	0.38	0.354
222473_s_at	ERBB2IP	erbB2 interacting protein	8.00	8.00	0	0.01	1.00	0.89	0.516
222505_s_at	ARGL1	arginine and glutamate rich 1	7.53	7.45	0	0.07	1.05	0.57	0.429
222527_s_at	RBM22	RNA binding motif protein 22	7.49	7.55	0	-0.06	-1.04	0.51	0.409
222538_s_at	APPL1	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	6.65	6.62	0	0.03	1.02	0.69	0.457
222562_s_at	TNKS2	tenascin, TRF3-interacting ankyrin-related ADP-ribose polymerase 2	8.37	8.31	0	-0.07	-1.05	0.22	0.278
222600_s_at	UBA6	ubiquitin-like modifier activating enzyme 6	7.23	7.31	0	-0.08	-1.06	0.15	0.231
222634_s_at	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	5.90	5.90	0	-0.01	-1.00	0.89	0.518
222670_s_at	MAR8	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog 8	9.28	9.32	0	-0.04	-1.03	0.49	0.401
222679_s_at	DCUN1D1	DCN1, defective in cutin degradation 1, domain containing 1	6.74	6.77	0	-0.04	-1.03	0.43	0.374
222714_s_at	LACTB2	lactamase, beta 2	5.24	5.22	0	0.02	1.02	0.80	0.489
222880_at	AKT3	v-akt murine thymoma viral oncogene homolog 3	4.60	4.62	0	-0.02	-1.01	0.89	0.517
222906_at	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	5.16	5.02	0	0.15	1.11	0.22	0.277
223038_s_at	FAM60A	family with sequence similarity 60, member A	7.95	7.89	0	-0.02	-1.02	0.62	0.445
223079_s_at	GLS	glutaminase	7.79	7.81	0	-0.02	-1.01	0.73	0.468
223254_s_at	G2E3	G2/M-phase specific E3 ubiquitin protein ligase	6.20	6.20	0	0.00	-1.00	0.94	0.528
223314_at	TPSAIN4	tetraspavin 4	6.56	6.49	0	0.07	1.05	0.31	0.324
223465_at	COL4A3BP	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	7.08	7.00	0	-0.02	-1.01	0.73	0.468
223578_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)(MALAT1)	5.72	5.75	0	-0.03	-1.02	0.87	0.507
223681_s_at	INADL	INAD-like (Drosophila)	3.76	3.72	0	0.04	1.03	0.67	0.454
223701_s_at	USP47	ubiquitin specific peptidase 47	8.46	8.45	0	0.01	1.01	0.80	0.489
223771_at	TMEM67A	transmembrane protein 67A	3.18	3.18	0	0.04	1.03	0.67	0.454
223814_at	TRNT1	tRNA nucleotidyl transferase, CCA-adding, 1	4.07	3.98	0	0.09	1.07	0.34	0.338
223890_at	PRO1082	uncharacterized protein PRO1082	3.06	3.10	0	-0.04	-1.03	0.57	0.428
223940_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	9.19	9.14	0	0.19	1.14	0.27	0.302
223984_s_at	NUP58	nucleoporin 58kDa	4.44	4.38	0	0.06	1.04	0.64	0.450
224012_at	20A2	20A2 /// ANK1 ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A2 /// ankyrin repeat do	2.36	2.29	0	0.06	1.05	0.36	0.345
224098_at	---	---	3.91	3.79	0	0.13	1.09	0.15	0.227
224152_s_at	PBBM1	polybrinoma 1	4.40	4.46	0	-0.06	-1.04	0.50	0.402
224227_s_at	BDP1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIb	5.90	5.83	0	-0.03	-1.02	0.72	0.467
224310_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	3.82	3.97	0	-0.16	-1.12	0.29	0.312
224311_s_at	CAB39	calcium binding protein 39	6.71	6.76	0	-0.06	-1.04	0.33	0.333
224435_at	FAM213A	family with sequence similarity 213, member A	3.66	3.60	0	0.07	1.05	0.54	0.421
224568_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	9.84	9.64	0	0.20	1.15	0.17	0.243
224580_at	SLC38A1	solute carrier family 38, member 1	6.63	6.71	0	-0.09	-1.06	0.25	0.293
224618_s_at	PTB3	polypyrimidine tract binding protein 3	7.12	7.03	0	0.09	1.06	0.22	0.276
224775_at	WIS1	WIS1 homolog (S. cerevisiae)	7.16	7.21	0	-0.06	-1.04	0.15	0.228
224875_at	Csor24	chromosome 5 open reading frame 24	5.80	5.70	0	0.10	1.07	0.44	0.376
224940_s_at	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	2.94	2.81	0	0.12	1.09	0.36	0.345
224989_at	SMIM4	small integral membrane protein 14	6.95	7.01	0	-0.06	-1.04	0.55	0.423
224992_at	ASPH	aspartate beta-hydroxylase	6.35	6.47	0	-0.13	-1.09	0.17	0.247
225046_at	724441	724441 /// LOC102723360 /// uncharacterized LOC102724219 /// uncharacterized LOC102724441 /// unchara	4.65	4.55	0	0.10	1.07	0.32	0.331
225237_s_at	MSI2	musashi RNA binding protein 2	5.18	5.21	0	-0.03	-1.02	0.79	0.484
225662_at	ZAK	sterile alpha motif and leucine zipper containing kinase ZAK	7.04	7.13	0	-0.09			

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 PHS	Mean log2 intensity for 21 PHE	422 FDR <0.2 =YES	Log2 Ratio ZIPOST vs PHE	Fold-Change ZIPOST vs PHE	p value	FDR	Mean42 FOS	Mean47 RO TD	Mean30 HHS	Mean44 HHC	PHS1	PHS2	PHS3	PHS4	PHS5	PHS6	PHS7	PHS8	PHS9	PHS10	PHS11	PHS12	PHS13	PHS14	PHS15	PHS16	PHS17	PHS18	PHS19	PHS20	PHS21	PHS22	PHS23	PHS24	PHS25
228170_at	OLIG1	oligodendrocyte transcription factor 1	3.76	3.78	0	-0.03	-1.02	0.76	0.477																													
228188_at	FOSL2	FOS-like antigen 2	8.24	8.28	0	-0.05	-1.03	0.31	0.324																													
228250_at	FNBP1	filiculin interacting protein 1	6.49	6.52	0	-0.03	-1.02	0.69	0.457																													
228478_at	SPPL2A	signal peptide peptidase like 2A	7.20	7.17	0	0.03	1.02	0.69	0.457																													
228549_at	TMEM63A	transmembrane protein 63A	6.83	6.70	0	0.12	1.09	0.27	0.303																													
228654_at	SPIN4	spindlin family, member 4	4.74	4.80	0	-0.06	-1.04	0.25	0.292																													
228986_at	OSBP1B	oxysterol binding protein-like B	8.22	8.28	0	-0.06	-1.05	0.41	0.365																													
228988_at	DNF11	zinc finger protein 711	4.65	4.58	0	0.07	1.05	0.25	0.292																													
229075_at	SPATA5	spermatogenesis associated 5	2.68	2.77	0	-0.09	-1.07	0.17	0.243																													
229115_at	DYNC1H1	dynein, cytoplasmic 1, heavy chain 1	6.44	6.35	0	0.09	1.06	0.30	0.319																													
229274_at	GNAS	GNAS complex locus	7.25	7.24	0	0.01	1.01	0.86	0.506																													
229389_at	ATG16L2	autophagy related 16-like 2	6.38	6.42	0	-0.04	-1.03	0.69	0.457																													
229399_at	CCDC186	coiled-coil domain containing 186	6.99	7.07	0	-0.07	-1.05	0.36	0.344																													
229413_s_at	---	---	4.42	4.34	0	0.08	1.06	0.43	0.374																													
229437_at	MIR155HG	MIR155 host gene	11.40	11.38	0	0.02	1.01	0.68	0.455																													
229553_at	PGM2L1	phosphoglucomutase 2-like 1	7.01	7.01	0	0.00	-1.00	0.99	0.542																													
229706_at	TCEG1	transcription elongation regulator 1	3.37	3.47	0	-0.10	-1.07	0.15	0.231																													
229732_at	ZNF823	zinc finger protein 823	3.95	3.92	0	0.03	1.02	0.63	0.448																													
229841_at	---	---	5.91	6.00	0	-0.09	-1.06	0.28	0.309																													
229850_at	KDSR	3-ketodihydroxyglutamate reductase	5.69	5.56	0	0.14	1.10	0.18	0.252																													
229869_at	---	---	4.61	4.59	0	0.02	1.01	0.78	0.483																													
229881_at	KLF12	Kruppel-like factor 12	5.71	5.71	0	-0.01	-1.00	0.96	0.533																													
229966_at	EWSR1	ERW RNA binding protein 1	6.68	6.64	0	0.04	1.03	0.75	0.472																													
230000_at	RNF213	ring finger protein 213	7.43	7.33	0	0.10	1.07	0.34	0.337																													
230014_at	---	---	4.84	4.89	0	-0.06	-1.04	0.44	0.377																													
230026_at	KIAA0907	KIAA0907	5.31	5.26	0	0.05	1.04	0.49	0.402																													
230106_at	ZDOC	ZDO family zinc finger C	5.69	5.73	0	-0.04	-1.03	0.61	0.441																													
230127_at	---	---	5.66	5.65	0	0.01	1.01	0.92	0.526																													
230180_at	DDX17	DEAD (Asp-Glu-Ala-Asp) box helicase 17	8.24	8.19	0	0.05	1.03	0.70	0.457																													
230322_s_at	TMEM45B	transmembrane protein 45B	4.14	4.22	0	-0.08	-1.05	0.37	0.428																													
230352_s_at	PRPS2	phosphoribosyl pyrophosphate synthetase 2	4.05	4.06	0	-0.01	-1.01	0.91	0.523																													
230434_at	PHOSPHO2	phosphatase, orphan 2	4.53	4.59	0	-0.05	-1.04	0.46	0.382																													
230511_at	CREM	cAMP responsive element modulator	8.45	8.48	0	-0.03	-1.02	0.42	0.368																													
230607_at	---	---	5.29	5.43	0	-0.14	-1.11	0.12	0.204																													
230681_at	TBRG1	transforming growth factor beta regulator 1	5.56	5.53	0	0.02	1.02	0.85	0.504																													
230742_at	RBMS5	RNA binding motif protein 5	7.23	7.18	0	0.05	1.03	0.74	0.469																													
230820_at	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	5.57	5.67	0	-0.11	-1.08	0.28	0.306																													
230896_at	BEND4	BEN domain containing 4	4.35	4.27	0	0.08	1.05	0.31	0.323																													
231108_at	FUS	FUS RNA binding protein	7.18	6.90	0	0.28	1.22	0.12	0.208																													
231109_at	---	---	6.31	6.24	0	0.07	1.05	0.51	0.409																													
231235_at	NKTR	natural killer cell triggering receptor	5.64	5.58	0	0.07	1.05	0.53	0.413																													
231370_at	PRK1A	protein phosphatase, Mg ²⁺ /Mn ²⁺ -dependent, 1A	5.02	4.98	0	-0.05	-1.03	0.58	0.423																													
231597_x_at	---	---	8.21	8.06	0	0.15	1.11	0.22	0.276																													
231644_at	---	---	3.30	3.20	0	0.10	1.07	0.27	0.303																													
231697_s_at	---	---	5.80	5.99	0	-0.19	-1.14	0.13	0.209																													
231820_at	MAVS	mitochondrial antiviral signaling protein	3.35	3.34	0	0.02	1.01	0.83	0.499																													
231862_at	CBX5	chromobox homolog 5	4.85	4.78	0	0.08	1.05	0.34	0.338																													
231873_at	BMPRI2	bone morphogenetic protein receptor type II	5.80	5.82	0	-0.02	-1.01	0.88	0.514																													
231934_at	TRIM14	tripartite motif containing 14	4.59	4.62	0	-0.03	-1.02	0.66	0.452																													
231956_at	RNF213	ring finger protein 213	6.64	6.64	0	0.22	1.16	0.19	0.254																													
231995_at	CAAP1	caseinolytic and apoptosis inhibitor 1	3.87	3.82	0	0.05	1.03	0.34	0.338																													
232000_at	TTC39B	tetratricopeptide repeat domain 39B	4.07	4.01	0	0.06	1.04	0.45	0.378																													
232020_at	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	3.83	3.72	0	0.11	1.08	0.40	0.361																													
232179_at	---	---	3.92	3.88	0	0.04	1.03	0.74	0.469																													
232204_at	EBF1	early B-cell factor 1	7.12	7.12	0	0.00	-1.00	0.97	0.535																													
232319_at	---	---	3.87	3.77	0	0.09	1.07	0.31	0.323																													
232386_at	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	3.99	3.97	0	-0.04	-1.03	0.71	0.463																													
232466_at	CUL4A	culin 4A	4.87	4.66	0	0.22	1.16	0.19	0.256																													
232472_at	---	---	4.66																																			

[illegible]

Probeset ID	Gene Symbol	Gene Title	Mean log2 intensity for 21 POST	Mean log2 intensity for 21 PRE	422 FDR <0.2 1=YES 0=NO	Log2 Ratio Z1POST vs Z1PRE	Fold-Change Z1POST vs Z1PRE	p value	FDR
243552_at	MBTD1	mbt domain containing 1	3.99	3.90	0	0.09	1.07	0.12	0.204
243570_at	SPCS2	signal peptidase complex subunit 2	2.70	2.71	0	-0.01	-1.01	0.85	0.504
243631_at	---	---	5.82	5.87	0	-0.05	-1.03	0.39	0.357
243648_at	ZBED6	zinc finger, BED-type containing 6	6.35	6.46	0	-0.12	-1.08	0.26	0.295
243673_at	---	---	3.43	3.39	0	0.04	1.03	0.69	0.457
243739_at	---	---	4.84	4.83	0	0.02	1.01	0.84	0.500
243751_at	CHD2	chromodomain helicase DNA binding protein 2	7.08	6.95	0	0.12	1.09	0.34	0.338
243767_at	---	---	3.80	3.74	0	0.06	1.04	0.49	0.402
243835_at	ZDHHC21	zinc finger, DHHC-type containing 21	5.00	5.00	0	0.00	-1.00	0.97	0.535
243940_at	TSHZ2	teashirt zinc finger homeobox 2	2.70	2.70	0	0.00	-1.00	0.96	0.533
243959_at	---	---	3.11	3.15	0	-0.04	-1.03	0.54	0.419
243996_at	NPR2	natruietic peptide receptor 2	2.94	2.84	0	0.10	1.07	0.24	0.292
244035_at	---	---	6.27	6.23	0	0.04	1.03	0.52	0.412
244055_at	---	---	4.98	4.90	0	0.09	1.06	0.19	0.258
244125_at	---	---	5.44	5.38	0	0.05	1.04	0.52	0.409
244153_at	ZNF207	zinc finger protein 207	5.10	5.15	0	-0.05	-1.03	0.51	0.409
244171_at	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	2.91	2.93	0	-0.02	-1.01	0.86	0.506
244219_at	WTAP	Wilms tumor 1 associated protein	5.02	5.01	0	0.01	1.01	0.93	0.526
244263_at	---	---	3.29	3.36	0	-0.07	-1.05	0.39	0.356
244396_at	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	3.57	3.69	0	-0.12	-1.09	0.11	0.201
244443_at	LINC01578	long intergenic non-protein coding RNA 1578(LINC01578)	4.33	4.34	0	-0.01	-1.00	0.94	0.528
244508_at	SEPT7	septin 7	5.30	5.21	0	0.09	1.07	0.15	0.229
244546_at	CYCS	cytochrome c, somatic	4.37	4.25	0	0.13	1.09	0.22	0.278
244568_at	---	---	4.63	4.64	0	-0.01	-1.01	0.92	0.526
244579_at	---	---	7.11	7.19	0	-0.08	-1.06	0.37	0.349
244669_at	NORD50A	small nucleolar RNA host gene 5 /// small nucleolar RNA, C/D box 50A /// small nucleolar RNA, C/D box 50B	8.41	8.42	0	0.00	-1.00	0.95	0.533
244674_at	---	---	4.63	4.78	0	-0.15	-1.11	0.23	0.286
244737_at	---	---	3.95	3.93	0	0.03	1.02	0.68	0.455
244763_at	MTRF1	mitochondrial translational release factor 1	2.69	2.67	0	0.03	1.02	0.69	0.457
244780_at	SGPP2	sphingosine-1-phosphate phosphatase 2	4.36	4.21	0	0.15	1.11	0.32	0.328
244791_at	---	---	4.82	4.77	0	0.05	1.04	0.64	0.449
244794_at	OC10537487:uncharacterized LOC105374872	---	5.13	5.07	0	0.06	1.04	0.55	0.423
244804_at	SGSTM1	sequestosome 1	9.11	9.07	0	0.05	1.03	0.65	0.450
244840_x_at	DOCK4	dedicator of cytokinesis 4	5.76	5.85	0	-0.09	-1.06	0.45	0.380
244846_at	---	---	4.70	4.83	0	-0.13	-1.10	0.33	0.333
244847_at	---	---	3.71	3.65	0	0.06	1.04	0.37	0.349
244872_at	RBBP4	retinoblastoma binding protein 4	4.05	3.92	0	0.13	1.10	0.16	0.236
33148_at	ZFR	zinc finger RNA binding protein	5.86	5.89	0	-0.02	-1.02	0.70	0.458
37145_at	GNLY	granulysin	10.72	10.67	0	0.05	1.04	0.49	0.400
39402_at	IL1B	interleukin 1 beta	12.38	12.45	0	-0.07	-1.05	0.35	0.342
60794_f_at	ZNF814	zinc finger protein 814	2.94	2.90	0	0.04	1.03	0.66	0.450
60835_at	POUR24	polymerase (RNA) II (DNA directed) polypeptide I4, pseudogene	5.24	5.13	0	0.10	1.07	0.52	0.412