

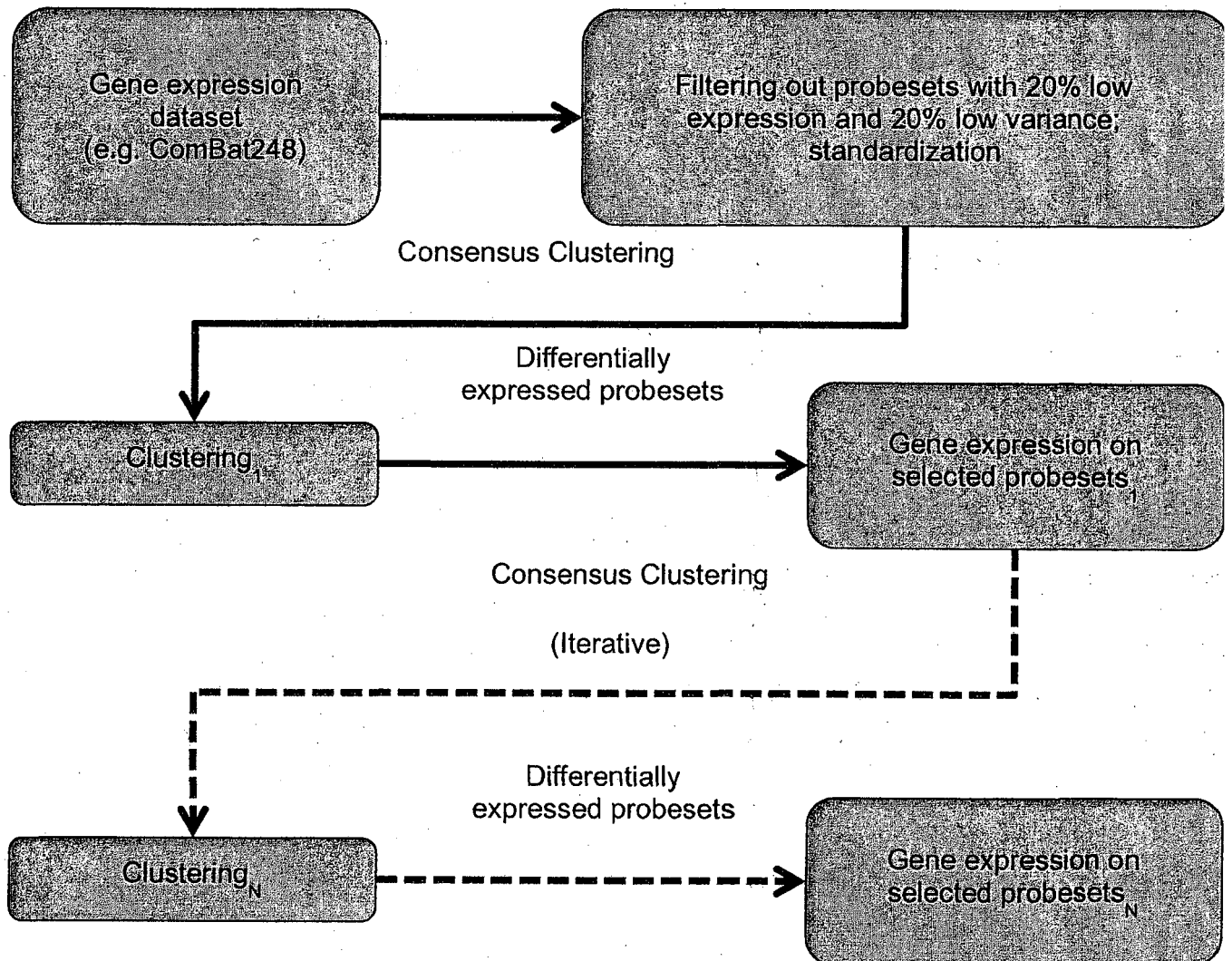


Figure 1

SG248

SG201

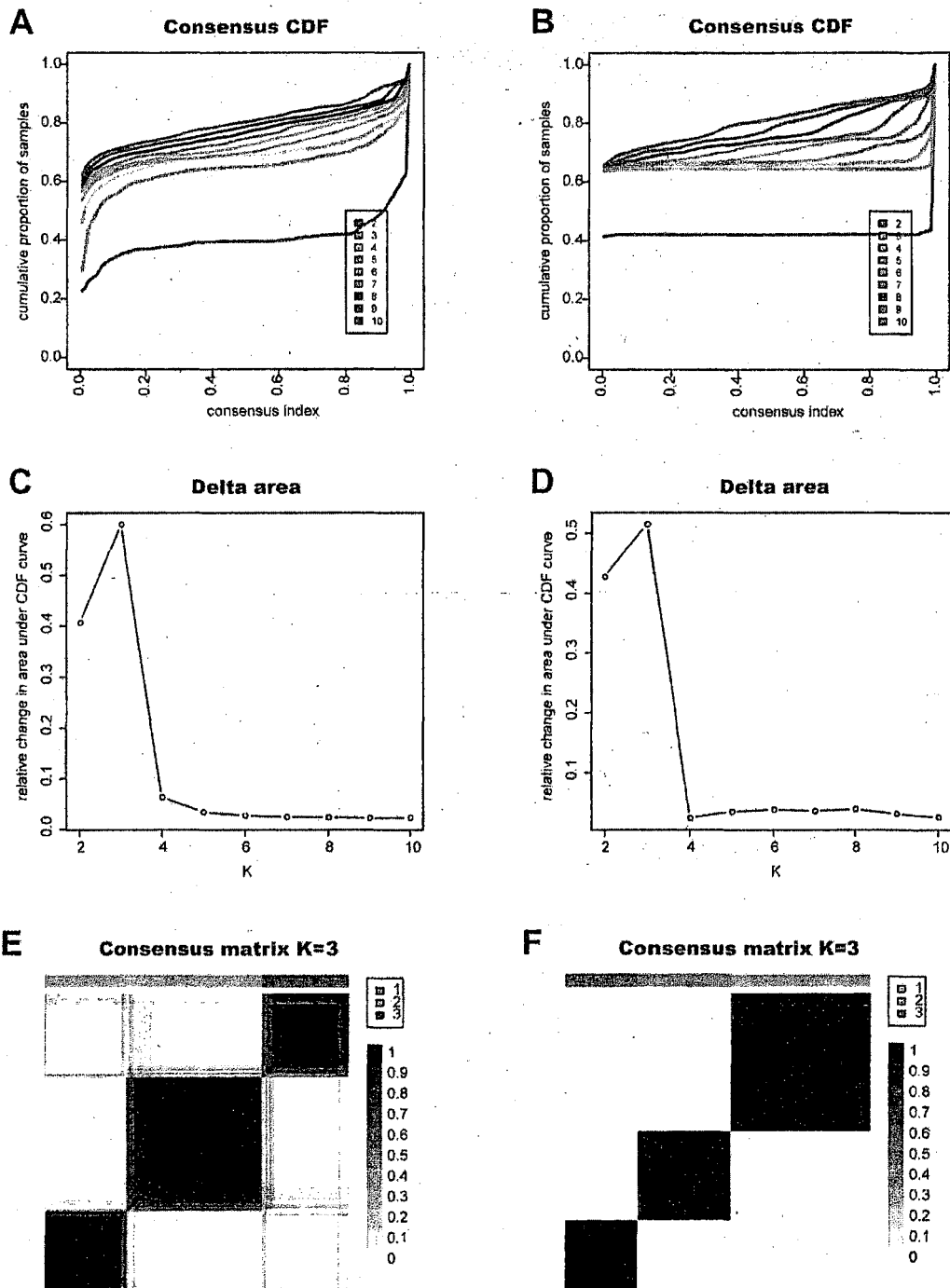


Figure 2

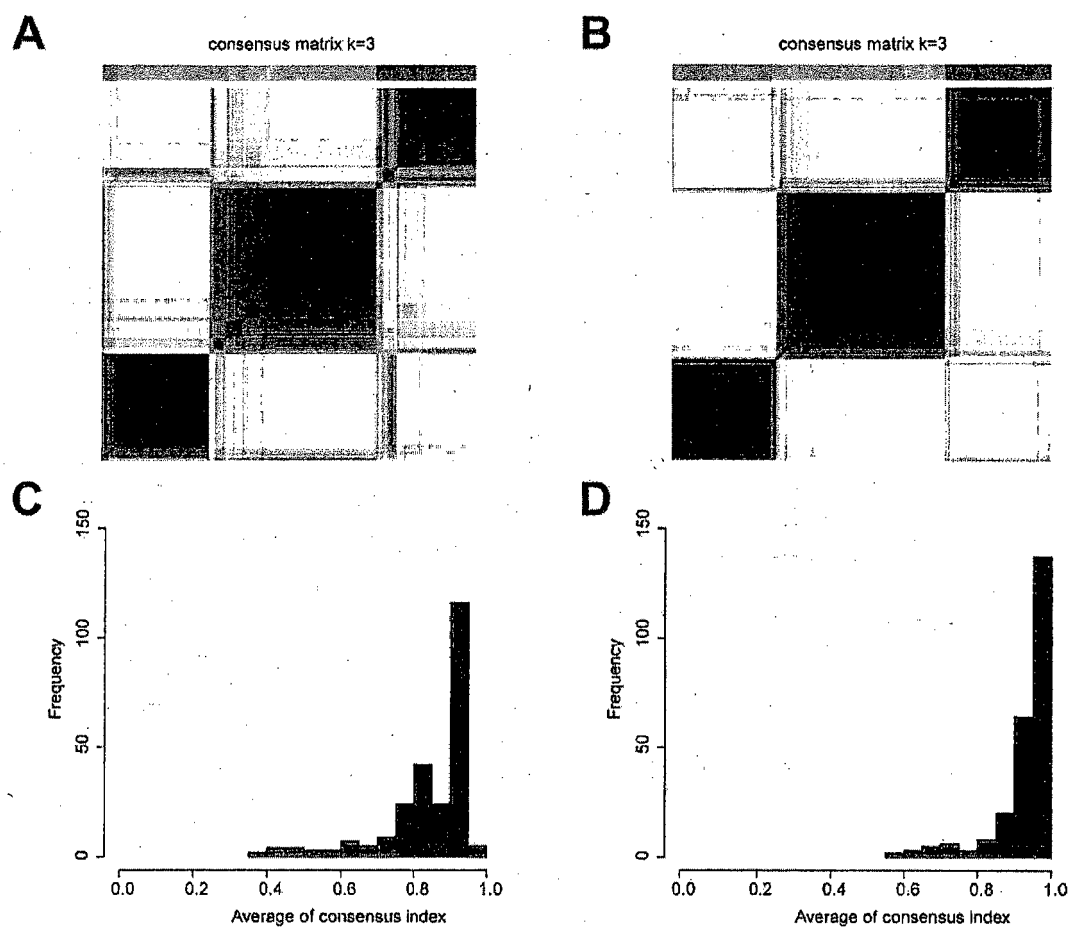
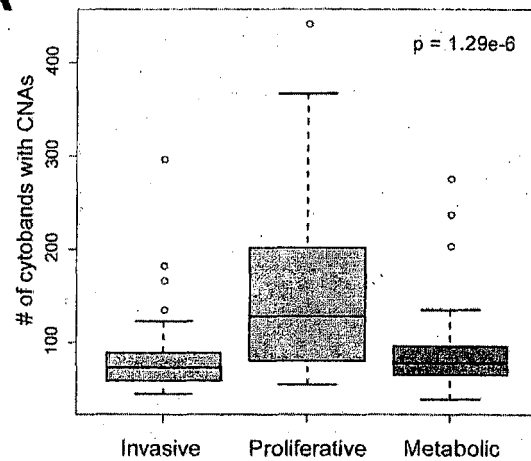


Figure 3

■ Invasive ■ Proliferative ■ Metabolic

A



B

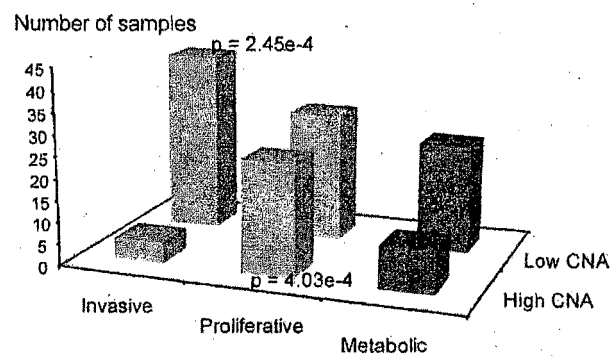


Figure 4

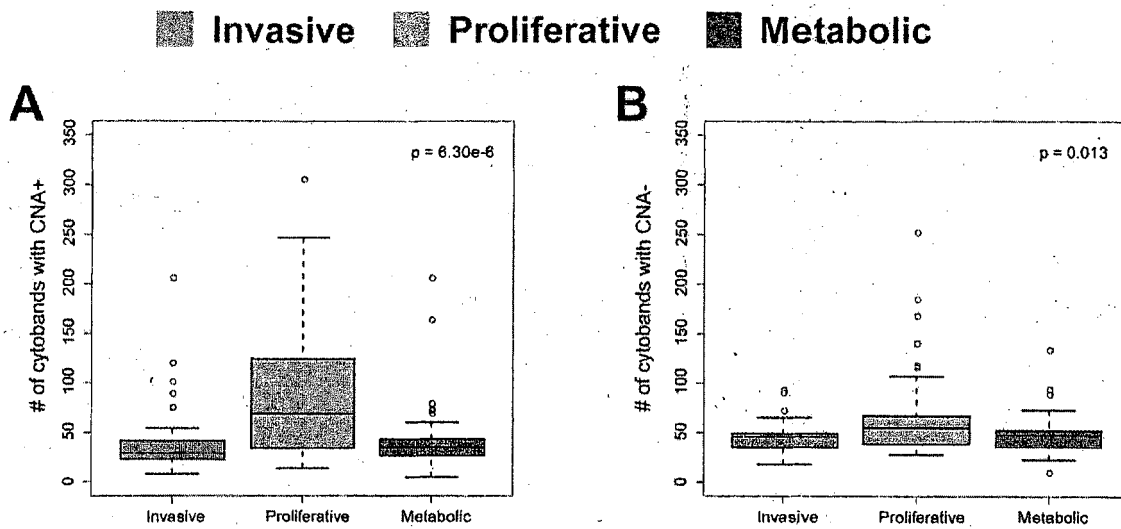


Figure 5

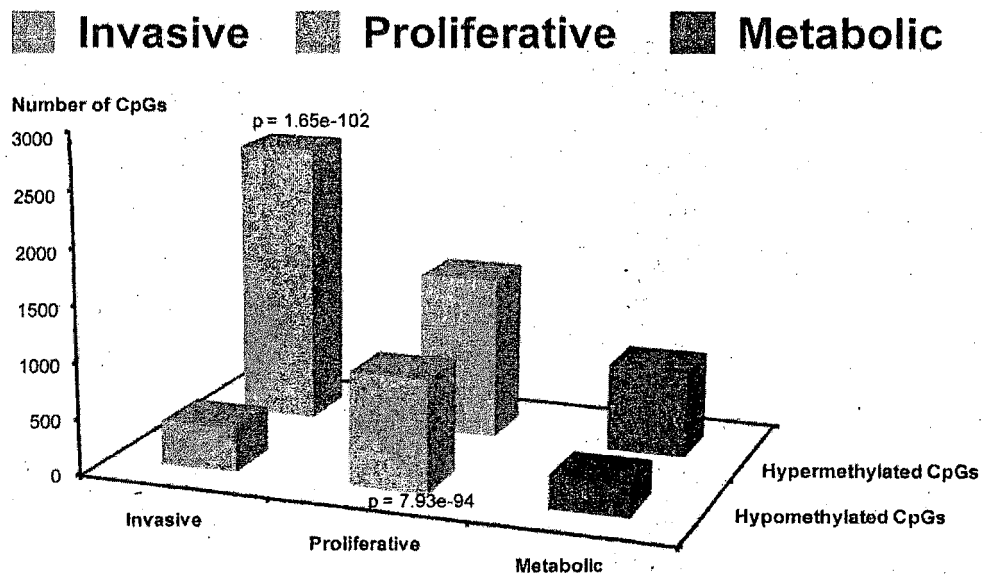


Figure 6

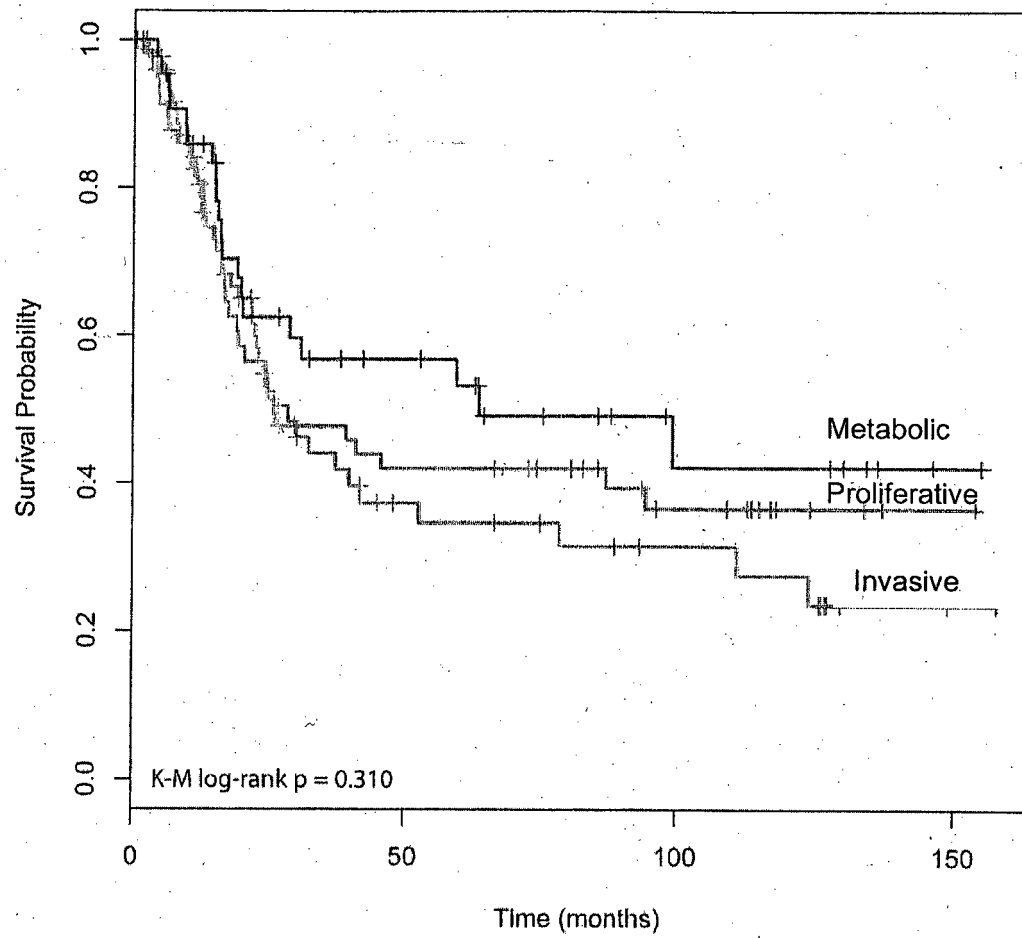


Figure 7

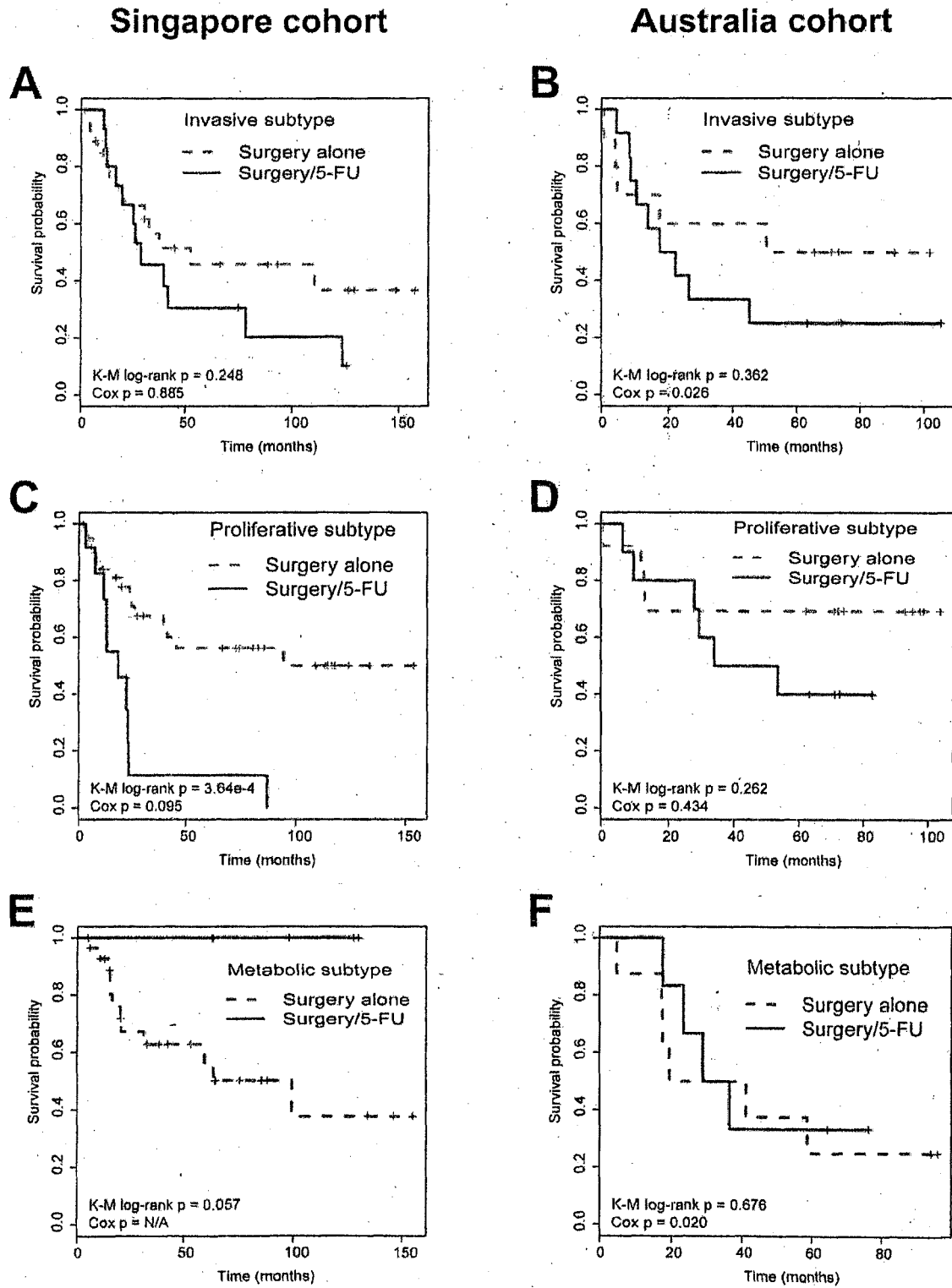


Figure 8

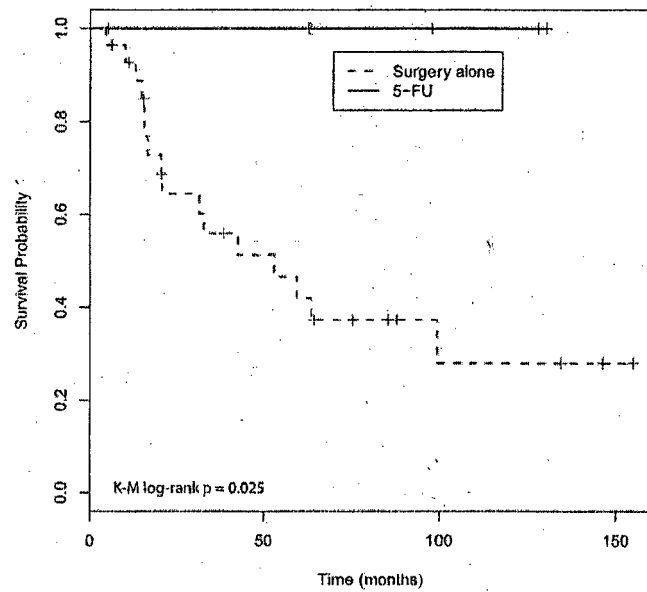


Figure 9

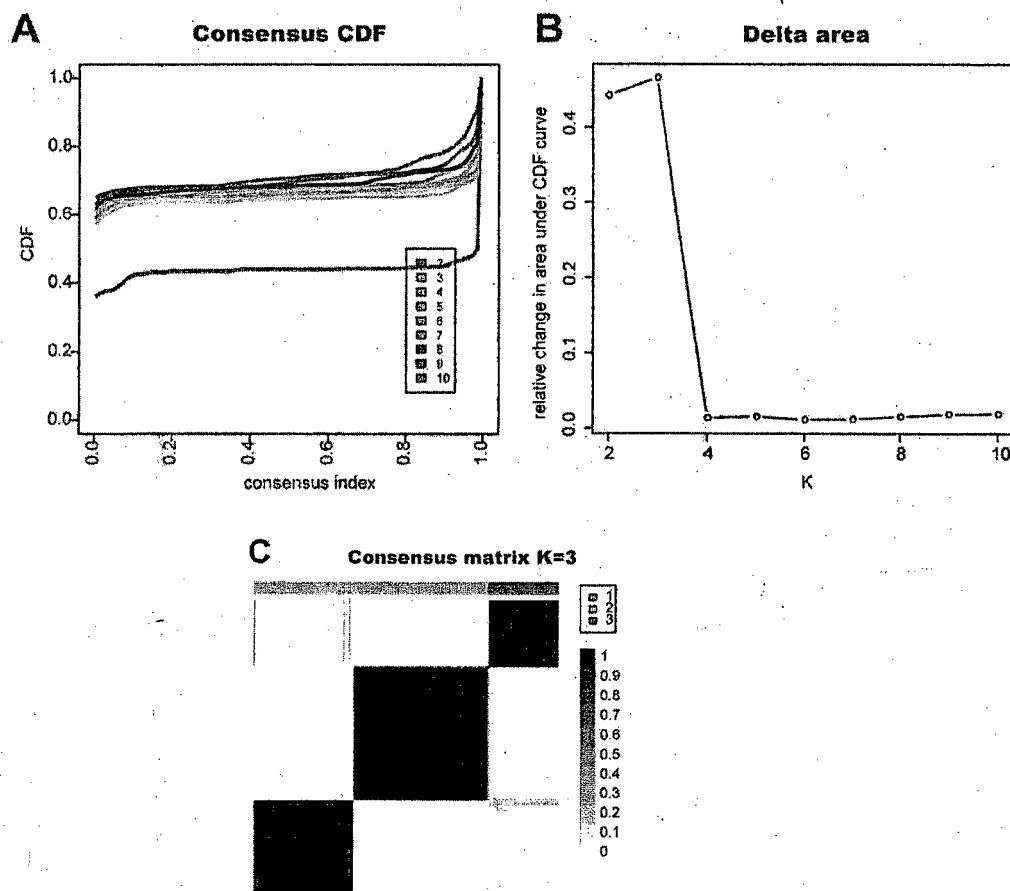


Figure 10

Figure 11

Invasive-subtype up-regulated genes

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	Gene Symbol	Gene Title	GeneBank_ACC
201496_x_at	4.46611	8.657672	16.72513	5.94E-40	7.10E-38	80.22799	MYH11	myosin, heavy chain 11, smooth	S67238
222722_at	4.43418	7.801124	14.69817	1.03E-33	6.09E-32	65.95349	OGN	osteoglycin	AV700059
218730_s_at	4.38619	6.976393	16.70224	6.98E-40	8.28E-38	80.06808	OGN	osteoglycin	NM_014057
212730_at	4.30441	9.232903	17.74241	4.85E-43	8.55E-41	87.29363	SYNM	synemin, intermediate filament	AK026420
223623_at	4.26627	8.345447	14.74234	7.48E-34	4.51E-32	66.26623	C2orf40	chromosome 2 open reading frame	AF325503
228202_at	4.25499	7.672782	17.55792	1.75E-42	2.77E-40	86.01853	PLN	clone MGC:12311 IMAGE:3934199)	AI969945
225894_at	4.25063	6.961195	18.45422	3.54E-45	9.03E-43	92.18378	SYNPO2	synaptopodin 2	AL589603
202992_at	4.23224	8.237806	16.20989	2.24E-38	2.15E-36	76.61985	C7	complement component 7	NM_000587
202222_s_at	4.21065	9.021531	15.77789	4.76E-37	3.99E-35	73.58222	DES	desmin	NM_001927
225720_at	4.16222	9.032289	16.1986	2.43E-38	2.31E-36	76.54063	SYNPO2	synaptopodin 2	AW009747
204938_s_at	4.15237	6.921919	17.74289	4.84E-43	8.55E-41	87.29688	PLN	phospholamban	M60411
205475_at	4.1381	7.281679	16.59946	1.44E-39	1.61E-37	79.34956	SCRG1	scrapie responsive protein 1	NM_007281
209613_s_at	4.1123	7.103251	12.36232	1.71E-26	5.36E-25	49.43285	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	M21692
225895_at	4.11157	9.700421	14.82482	4.16E-34	2.58E-32	66.8502	SYNPO2	synaptopodin 2	AI634580
227662_at	4.01523	8.855335	14.81787	4.37E-34	2.70E-32	66.80104	SYNPO2	synaptopodin 2	AA541622
226303_at	3.97332	8.245437	18.50881	2.43E-45	6.54E-43	92.55684	PGM5	phosphoglucomutase 5	AA706788
204940_at	3.97307	7.209882	17.51777	2.32E-42	3.58E-40	85.74067	PLN	phospholamban	NM_002667
228133_s_at	3.95985	7.565001	19.37629	6.49E-48	2.79E-45	98.44347	MYH11	myosin, heavy chain 11, smooth	BF732767
210299_s_at	3.90935	8.707861	17.28138	1.20E-41	1.68E-39	84.10183	FHL1	four and a half LIM domains 1	AF063002
228504_at	3.86309	5.367591	23.49515	1.27E-59	1.15E-55	125.2017			AI828648
232298_at	3.85047	6.021718	20.82539	3.92E-52	3.45E-49	108.0917	hCG_1806 964	hCG1806964	AK026494
204939_s_at	3.8236	8.516444	16.23601	1.86E-38	1.81E-36	76.80321	PLN	phospholamban	NM_002667
220595_at	3.81573	5.411518	22.02228	1.54E-55	3.37E-52	115.8725	PDZRN4	PDZ domain containing ring finger	NM_013377
227827_at	3.77786	7.058929	14.70821	9.54E-34	5.68E-32	66.0246			AW138143
209612_s_at	3.74611	7.573837	12.13815	8.32E-26	2.47E-24	47.85977	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	M24317
228750_at	3.72159	6.947949	17.21713	1.89E-41	2.58E-39	83.65567			AI693516
227826_s_at	3.70167	7.399725	14.71597	9.03E-34	5.40E-32	66.07951			AW138143
203951_at	3.69162	9.869379	16.29294	1.25E-38	1.23E-36	77.20261	CNN1	calponin 1, basic, smooth muscle	NM_001299
231773_at	3.67989	6.988941	21.53536	3.67E-54	5.56E-51	112.7283	ANGPTL1	angiopoietin-like 1	BF002046
225721_at	3.67398	9.920749	17.39996	5.27E-42	7.63E-40	84.92451	SYNPO2	synaptopodin 2	AI658662
205433_at	3.66121	5.394964	18.08569	4.50E-44	9.36E-42	89.65794	BCH	butyrylcholinesterase	NM_000555
1556325_at	3.61073	5.205348	23.99143	5.67E-61	1.03E-56	128.2829	FILIP1	filamin A interacting protein 1	AL832009
203766_s_at	3.60858	8.668048	18.12345	3.46E-44	7.48E-42	89.91736	LMOD1	leiomodin 1 (smooth muscle)	NM_012134
225381_at	3.59367	7.120351	17.41255	4.82E-42	7.04E-40	85.01182	LOC39995 9	hypothetical gene supported by BX647608	AW162210
218087_s_at	3.58816	9.084772	16.56506	1.83E-39	2.03E-37	79.10897	SORBS1	sorbin and SH3 domain containing	NM_015385
204719_at	3.57985	7.334852	13.40144	1.06E-29	4.37E-28	56.76547	ABCA8	ATP-binding cassette, sub-family A (ABC1), member 8	NM_007168
202037_s_at	3.57139	7.249162	15.61877	1.47E-36	1.18E-34	72.46085	SFRP1	secreted frizzled-related protein 1	NM_003012
235183_at	3.56598	6.358684	21.33019	1.41E-53	1.79E-50	111.3947			AI479277
201539_s_at	3.5533	8.025944	19.32024	9.50E-48	3.96E-45	98.06552	FHL1	four and a half LIM domains 1	U29538
202274_at	3.53734	11.08798	13.62459	2.17E-30	9.39E-29	58.34569	ACTG2	actin, gamma 2, smooth muscle, enteric	NM_001615
243278_at	3.5128	6.068288	18.94615	1.21E-46	4.04E-44	95.53439	FOX2	forkhead box P2	AW291402
203296_s_at	3.51085	6.182715	21.44869	6.47E-54	9.05E-51	112.1656	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	NM_000702
205357_s_at	3.50397	5.583619	20.00804	9.13E-50	5.54E-47	102.6793	AGTR1	angiotensin II receptor, type 1	NM_000685
214505_s_at	3.49662	8.870532	18.27283	1.23E-44	2.92E-42	90.94218	FHL1	four and a half LIM domains 1	AF220153
236141_at	3.48442	5.151952	21.31887	1.51E-53	1.88E-50	111.321	NBLA0030 1	Nbla00301	AA156933
210298_x_at	3.45901	8.036793	18.25167	1.43E-44	3.31E-42	90.7972	FHL1	four and a half LIM domains 1	AF098518
209763_at	3.45328	7.010251	14.89974	2.44E-34	1.56E-32	67.38052	CHRD1	chordin-like 1	AL049176
229461_x_at	3.44015	6.704902	19.88261	2.12E-49	1.21E-46	101.8418	NEGR1	neuronal growth regulator 1	AI123532
237206_at	3.43041	7.462402	15.70139	8.18E-37	6.68E-35	73.04325	MYOCD	myocardin	AI452798
206201_s_at	3.41909	5.236089	19.27966	1.25E-47	4.99E-45	97.79168	MEOX2	mesenchyme homeobox 2	NM_005924
201497_x_at	3.41001	11.24294	14.38587	9.50E-33	5.06E-31	63.74089	MYH11	myosin, heavy chain 11, smooth muscle	NM_022844
212805_at	3.40927	7.914765	16.42392	4.95E-39	5.18E-37	78.12077	PRUNE2	prune homolog 2 (Drosophila)	AB002365
219772_s_at	3.39519	5.749739	14.82772	4.07E-34	2.53E-32	66.87073	SMPX	small muscle protein, X-linked	NM_014332
227061_at	3.38682	7.325075	14.65788	1.37E-33	7.98E-32	65.66813			AI088063
214027_x_at	3.36877	9.57456	16.47128	3.54E-39	3.79E-37	78.45249	DES /// FAM48A	desmin /// family with sequence similarity 48, member A	AA889653

228885_at	3.35944	5.724101	18.84896	2.36E-46	7.45E-44	94.87437	MAMDC2	MAM domain containing 2	AI862120
202036_s_at	3.32746	6.573212	15.84168	3.03E-37	2.60E-35	74.03136	SFRP1	secreted frizzled-related protein 1	AF017987
238751_at	3.32632	6.711581	14.80041	4.95E-34	3.05E-32	66.6774			AI343000
209687_at	3.32041	8.417815	14.19452	3.72E-32	1.89E-30	62.38473	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	U19495
226304_at	3.3143	6.870106	20.00462	9.34E-50	5.60E-47	102.6565	HSPB6	heat shock protein, alpha-crystallin-related, B6	AA563621
235759_at	3.30209	5.636883	19.81628	3.32E-49	1.81E-46	101.3983			AI095542
229649_at	3.30192	6.949164	15.57245	2.04E-36	1.61E-34	72.13418	NRXN3	neurixin 3	AI129949
224339_s_at	3.29628	5.961536	22.97062	3.50E-58	1.91E-54	121.9109	ANGPTL1	angiopoietin-like 1	AB056476
202920_at	3.29216	6.895931	16.64185	1.07E-39	1.22E-37	79.64602	ANK2	ankyrin 2, neuronal	BF726212
221584_s_at	3.27246	8.6846	17.23282	1.69E-41	2.33E-39	83.76466	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	U11058
201495_x_at	3.2664	6.809016	19.38841	5.98E-48	2.59E-45	98.52518	MYH11	myosin, heavy chain 11, smooth muscle	AI889739
219230_at	3.24824	6.902625	16.60046	1.43E-39	1.60E-37	79.35655	TMEM100	transmembrane protein 100	NM_018286
1552309_a_at	3.24601	8.236314	17.63053	1.06E-42	1.72E-40	86.52076	NEXN	nexilin (F actin binding protein)	NM_144573
244745_at	3.24421	5.869817	21.14253	4.83E-53	5.38E-50	110.1704	RERG	RAS-like, estrogen-regulated, growth inhibitor	BG484193
201058_s_at	3.23295	10.25905	16.79424	3.65E-40	4.42E-38	80.71053	MYL9	myosin, light chain 9, regulatory	NM_006097
233496_s_at	3.23001	6.838514	19.12227	3.65E-47	1.31E-44	96.72789	CFL2	cofilin 2 (muscle)	AV726166
221276_s_at	3.22159	7.074287	17.44446	3.86E-42	5.71E-40	85.23292	SYNC	syncollin, intermediate filament protein	NM_030786
211276_at	3.21989	6.459007	15.26814	1.77E-35	1.25E-33	69.98584	TCEAL2	transcription elongation factor A (SII)-like 2	AF063606
226103_at	3.208	8.45266	17.93477	1.28E-43	2.51E-41	88.6198	NEXN	nexilin (F actin binding protein)	AF114264
225782_at	3.20323	9.129725	17.55006	1.85E-42	2.91E-40	85.96416	MSRB3	methionine sulfoxide reductase B3	AW027333
206577_at	3.19884	4.703406	15.14679	4.20E-35	2.89E-33	69.12814	VIP	vasoactive intestinal peptide	NM_003381
1570515_a_at	3.19721	5.414671	21.07207	7.68E-53	8.24E-50	109.7096	FILIP1	filamin A interacting protein 1	BC029425
206552_s_at	3.19166	4.628721	14.91967	2.12E-34	1.37E-32	67.52162	TAC1	tachykinin, precursor 1	NM_003182
235201_at	3.17461	7.301157	19.24228	1.61E-47	6.25E-45	97.53925	FOXP2	forkhead box P2	AW167727
219791_s_at	3.17112	5.413723	20.2625	1.66E-50	1.16E-47	104.3727	NBLA00301	Nbla00301	NM_024748
239183_at	3.16996	4.897173	22.84564	7.77E-58	3.54E-54	121.1216	ANGPTL1	angiopoietin-like 1	W67461
227727_at	3.16706	8.029761	18.47811	3.00E-45	7.88E-43	92.34712	MRGPRF	MAS-related GPR, member F	H15920
209541_at	3.16433	7.781679	13.57866	3.00E-30	1.28E-28	58.02037	IGF1	insulin-like growth factor 1 (somatomedin C)	AI972496
221667_s_at	3.15548	8.792806	17.7571	4.38E-43	7.80E-41	87.39499	HSPB8	heat shock 22kDa protein 8	AF133207
218934_s_at	3.14695	7.097171	18.77492	3.92E-46	1.18E-43	94.37093	HSPB7	heat shock 27kDa protein family, member 7 (cardiovascular)	NM_014424
212806_at	3.14386	5.449666	18.15132	2.86E-44	6.27E-42	90.10869	PRUNE2	prune homolog 2 (Drosophila)	AL138349
213371_at	3.14107	5.738425	18.46772	3.23E-45	8.34E-43	92.27608	LDB3	LIM domain binding 3	AI803302
223235_s_at	3.1404	9.410422	14.54797	2.99E-33	1.68E-31	64.88949	SMOC2	SPARC related modular calcium binding 2	AB014737
222717_at	3.13771	7.11739	18.3535	7.08E-45	1.76E-42	91.49476	SDPR	serum deprivation response (phosphatidylserine binding protein)	BF982174
235503_at	3.13449	4.26175	15.55786	2.27E-36	1.77E-34	72.03123	ASB5	ankyrin repeat and SOCS box-containing 5	BF589787
230130_at	3.1279	6.467858	17.4115	4.86E-42	7.08E-40	85.00453			AI692523
212865_s_at	3.12399	7.658179	15.74845	5.86E-37	4.87E-35	73.37483	COL14A1	collagen, type XIV, alpha 1	BF449063
229288_at	3.1079	6.328096	15.92199	1.72E-37	1.50E-35	74.5966	EPHA7	EPH receptor A7	BF439579
202555_s_at	3.1056	10.93662	17.31169	9.75E-42	1.37E-39	84.31229	MYLK	myosin light chain kinase	NM_005965
209540_at	3.10118	7.473901	13.99417	1.55E-31	7.45E-30	60.96463	IGF1	insulin-like growth factor 1 (somatomedin C)	AU144912
1569956_at	3.08236	4.882876	19.32129	9.43E-48	3.96E-45	98.0726	MYLK	myosin light chain kinase	BC033713
204776_at	3.0816	8.484523	14.32388	1.48E-32	7.72E-31	63.3016	THBS4	thrombospondin 4	NM_003248
219685_at	3.0553	5.68044	19.23257	1.72E-47	6.63E-45	97.47372	TMEM35	transmembrane protein 35	NM_021637
238533_at	3.03983	4.75161	16.40182	5.78E-39	5.99E-37	77.96592	EPHA7	EPH receptor A7	AA651750
215306_at	3.03735	6.359377	23.22169	7.13E-59	4.87E-55	123.4905			AL049443
209948_at	3.02102	8.052314	17.14675	3.09E-41	4.17E-39	83.16647	KCNMB1	potassium large conductance calcium-activated channel, subfamily M, beta member 1	U61536
228854_at	3.01755	6.556662	14.6143	1.86E-33	1.07E-31	65.35939			AI492388

204793_at	3.01436	6.335273	21.8916	3.60E-55	7.28E-52	115.0315	GPRASP1	G protein-coupled receptor associated sorting protein 1	NM_014710
207390_s_at	3.01246	8.438623	19.20738	2.05E-47	7.71E-45	97.30351	SMTN	smoothelin	NM_006932
213791_at	3.01027	5.926308	14.74453	7.37E-34	4.45E-32	66.28177	PENK	proenkephalin	NM_006211
237169_at	2.99208	5.103125	17.3244	8.92E-42	1.27E-39	84.40049			AI266750
224396_s_at	2.98163	8.143239	12.98678	2.03E-28	7.45E-27	53.83305	ASPN	asporin	AF316824
204796_at	2.97089	6.728461	19.9545	1.31E-49	7.68E-47	102.3221	EML1	echinoderm microtubule associated protein like 1	AI825937
227758_at	2.95826	8.225402	20.00141	9.54E-50	5.66E-47	102.6351	RERG	RAS-like, estrogen-regulated, growth inhibitor	AW294092
201957_at	2.95582	8.870409	18.81158	3.05E-46	9.35E-44	94.62029	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	AF324888
223395_at	2.95009	8.635636	12.99738	1.89E-28	6.92E-27	53.90795	ABI3BP	ABI family, member 3 (NESH) binding protein	AB056106
204894_s_at	2.94495	8.291444	18.26824	1.27E-44	2.99E-42	90.91073	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	NM_003734
225242_s_at	2.9446	8.747961	13.03179	1.48E-28	5.48E-27	54.15103	CCDC80	colled-coil domain containing 80	AW303375
223122_s_at	2.93637	9.988297	9.094907	9.17E-17	1.16E-15	27.21988	SFRP2	secreted frizzled-related protein 2	AF311912
1558828_s_at	2.93484	6.097414	19.74997	5.18E-49	2.67E-46	100.9544	LOC72826	CDNA FLJ36638 fis, clone TRACH2018950	AL703532
206070_s_at	2.93126	6.845231	15.04043	8.96E-35	5.97E-33	68.37602	EPHA3	EPH receptor A3	AF213459
206898_at	2.92282	5.555763	15.10913	5.49E-35	3.71E-33	68.86188	CDH19	cadherin 19, type 2	NM_021153
222877_at	2.91916	7.26028	17.78732	3.55E-43	6.51E-41	87.60352			AK024680
226834_at	2.91851	7.8539	16.3795	6.77E-39	6.97E-37	77.80957			BG112263
202437_s_at	2.9176	8.205118	11.85832	5.98E-25	1.67E-23	45.90236	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	NM_000104
213413_at	2.91596	7.538241	19.26292	1.40E-47	5.51E-45	97.67869	STON1	stonin 1	BG434174
227197_at	2.91302	6.636782	16.36933	7.27E-39	7.46E-37	77.73828	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	AI989530
217967_s_at	2.90558	9.400218	19.37208	6.68E-48	2.85E-45	98.41512	FAM129A	family with sequence similarity 129, member A	AF288391
229504_at	2.90392	7.811682	18.08951	4.38E-44	9.16E-42	89.68417			AI810826
214767_s_at	2.90253	6.859038	19.05292	5.86E-47	2.01E-44	96.25832	HSPB6	heat shock protein, alpha-crystallin-related, B6	AL551046
209283_at	2.90073	8.396469	19.76391	4.72E-49	2.48E-46	101.0478	CRYAB	crystallin, alpha B	AF007162
227529_s_at	2.89796	5.82031	18.47175	3.14E-45	8.16E-43	92.30362	AKAP12	A kinase (PRKA) anchor protein 12	BF511276
201540_at	2.89623	10.9466	14.35667	1.17E-32	6.19E-31	63.53399	FHL1	four and a half LIM domains 1	NM_001449
213438_at	2.89118	6.033712	17.78214	3.68E-43	6.64E-41	87.56777	NFASC	neurofascin homolog (chicken)	AA995925
230595_at	2.89015	6.924564	20.60491	1.69E-51	1.40E-48	106.6394	LOC57255	hypothetical locus LOC572558	BF677651
209170_s_at	2.88717	6.818002	16.14475	3.55E-38	3.31E-36	76.16252	GPM6B	glycoprotein M6B	AF016004
1554127_s_at	2.88464	7.753836	20.59815	1.77E-51	1.44E-48	106.5948	MSRB3	methionine sulfoxide reductase B3	BC040053
209242_at	2.87855	5.944133	20.92468	2.03E-52	1.98E-49	108.7438	PEG3	paternally expressed 3	AL042588
210198_s_at	2.87839	5.125747	16.86975	2.15E-40	2.67E-38	81.23739	PLP1	proteolipid protein 1	BC002665
221583_s_at	2.8737	6.106001	16.53636	2.24E-39	2.46E-37	78.90813	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	AI129381
204284_at	2.86455	7.816425	15.97003	1.22E-37	1.09E-35	74.93454	PPP1R3C	protein phosphatase 1, regulatory (inhibitor) subunit 3C	N26005
222043_at	2.86333	7.120228	14.48009	4.85E-33	2.66E-31	64.40855	CLU	clusterin	AI982754
211562_s_at	2.8555	6.144933	20.91161	2.21E-52	2.09E-49	108.658	LMOD1	leiomodulin 1 (smooth muscle)	BC001755
205907_s_at	2.85331	5.954815	14.27764	2.06E-32	1.06E-30	62.97383	OMD	osteomodulin	AI765819
205782_at	2.85058	6.693452	17.47856	3.04E-42	4.59E-40	85.4692	FGF7	fibroblast growth factor 7 (keratinocyte growth factor)	NM_002009
225790_at	2.85038	7.120504	20.29472	1.34E-50	9.48E-48	104.5865	MSRB3	methionine sulfoxide reductase B3	AL048386
224663_s_at	2.84369	8.883324	17.74932	4.63E-43	8.20E-41	87.34131	CFL2	cofilin 2 (muscle)	BF576053
228107_at	2.84319	6.412272	19.31287	9.99E-48	4.09E-45	98.01578	LOC10012	hypothetical protein LOC100127983	BF510533
219778_at	2.83969	6.075468	18.89546	1.72E-46	5.52E-44	95.19028	ZFPM2	zinc finger protein, multitype 2	NM_012082
225328_at	2.83851	8.538954	17.5781	1.52E-42	2.43E-40	86.1582			N21643
205498_at	2.83637	5.696498	18.0732	4.90E-44	1.01E-41	89.57212	GHR	growth hormone receptor	NM_000163

212554_at	2.83076	7.270157	18.08526	4.51E-44	9.36E-42	89.655	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	N90755
213993_at	2.82871	7.240722	16.04465	7.20E-38	6.51E-36	75.45922	SPON1	spondin 1, extracellular matrix protein	AI885290
204364_s_at	2.82362	7.45188	12.66869	1.95E-27	6.59E-26	51.58871	REEP1	receptor accessory protein 1	BE535746
204083_s_at	2.82359	10.74753	16.65427	9.77E-40	1.13E-37	79.73279	TPM2	tropomyosin 2 (beta)	NM_003289
203980_at	2.81126	7.891874	10.21731	5.17E-20	9.08E-19	34.62723	FABP4	fatty acid binding protein 4, adipocyte	NM_001442
202995_s_at	2.81081	8.836875	12.93976	2.84E-28	1.03E-26	53.50102	FBLN1	fibulin 1	NM_006486
238592_at	2.80662	5.346711	19.06034	5.57E-47	1.94E-44	96.30859	PDLIM3	Actinin-associated LIM protein	BE840636
221747_at	2.80326	8.400148	21.25074	2.37E-53	2.87E-50	110.8769	TNS1	tensin 1	AL046979
204457_s_at	2.80284	8.317512	12.87364	4.54E-28	1.62E-26	53.0342	GAS1	growth arrest-specific 1	NM_002048
223468_s_at	2.80219	8.184743	18.32245	8.77E-45	2.13E-42	91.28217	RGMA	RGM domain family, member A	AL136826
207961_x_at	2.79827	9.855164	15.46163	4.49E-36	3.41E-34	71.35229	MYH11	myosin, heavy chain 11, smooth muscle	NM_022870
213068_at	2.79329	6.697782	11.43386	1.17E-23	2.91E-22	42.94893	DPT	dermatopontin	AI146848
229339_at	2.79302	6.98674	17.38594	5.81E-42	8.37E-40	84.8273			AI093327
236038_at	2.78191	5.536256	24.13409	2.33E-61	6.37E-57	129.1627			N50714
201431_s_at	2.77989	9.054213	17.3535	7.28E-42	1.04E-39	84.60233	DPYSL3	dihydropyrimidinase-like 3	NM_001387
204749_at	2.77853	5.86153	18.23363	1.62E-44	3.71E-42	90.67347	NAP1L3	nucleosome assembly protein 1-like 3	NM_004538
214724_at	2.77786	8.282261	18.78811	3.58E-46	1.09E-43	94.46069	DIXDC1	DIX domain containing 1	AF070621
224352_s_at	2.77633	8.801548	18.02175	7.00E-44	1.43E-41	89.21837	CFL2	cofilin 2 (muscle)	AF134802
1557961_s_at	2.7732	5.16377	20.87731	2.78E-52	2.53E-49	108.4328	LOC100127983	hypothetical protein LOC100127983	BG492376
229800_at	2.7707	6.434779	15.7713	4.99E-37	4.16E-35	73.53579	DCLK1	KIAA0369 gene	AI129626
205795_at	2.77063	6.249706	15.10985	5.47E-35	3.70E-33	68.86696	NRXN3	neurexin 3	NM_004796
228728_at	2.76926	9.206439	17.93356	1.29E-43	2.52E-41	88.6115	C7orf58	chromosome 7 open reading frame 58	BF724137
242447_at	2.76773	7.528898	13.83519	4.82E-31	2.22E-29	59.8379	C3orf70	chromosome 3 open reading frame 70	AI656180
227526_at	2.75965	5.708335	22.36577	1.68E-56	5.08E-53	118.0727	CDON	Cdon homolog (mouse)	AU151222
221748_s_at	2.75951	10.06455	17.09367	4.48E-41	5.92E-39	82.79728	TNS1	tensin 1	AL046979
209209_s_at	2.75654	7.56625	18.34847	7.33E-45	1.80E-42	91.46033	FERMT2	fermitin family homolog 2 (Drosophila)	AW469573
204154_at	2.75402	5.520705	19.81131	3.43E-49	1.84E-46	101.3651	CDO1	cysteine dioxygenase, type I	NM_001801
209167_at	2.74994	6.566977	16.06708	6.14E-38	5.59E-36	75.61685	GPM6B	glycoprotein M6B	AI19030
228640_at	2.74975	8.251108	12.62755	2.61E-27	8.74E-26	51.29891	PCDH7	protocadherin 7	BE644809
202291_s_at	2.73946	11.30812	13.68954	1.36E-30	6.02E-29	58.80581	MGP	matrix Gla protein	NM_000900
201645_at	2.73806	9.445293	12.9521	2.60E-28	9.44E-27	53.58814	TNC	tenascin C	NM_002160
213994_s_at	2.73663	7.897401	13.99866	1.50E-31	7.24E-30	60.99645	SPON1	spondin 1, extracellular matrix protein	AI885290
229530_at	2.73415	8.598756	17.78685	3.57E-43	6.51E-41	87.60029	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	BF002625
209621_s_at	2.73375	9.506097	16.45408	4.00E-39	4.25E-37	78.33206	PDLIM3	PDZ and LIM domain 3	AF002280
243357_at	2.72449	6.131152	21.80875	6.17E-55	1.20E-51	114.4973	NEGR1	neuronal growth regulator 1	AA115106
221207_s_at	2.72281	6.703207	17.49573	2.70E-42	4.10E-40	85.58806	NBEA	neurobeachin	NM_015678
212915_at	2.722	8.277904	16.19993	2.40E-38	2.30E-36	76.54998	PDZRN3	PDZ domain containing ring finger 3	AL569804
205399_at	2.72128	6.971874	19.71211	6.69E-49	3.32E-46	100.7007	DCLK1	doublecortin-like kinase 1	NM_004734
227705_at	2.71639	6.401139	17.53465	2.06E-42	3.23E-40	85.85754	TCEAL7	transcription elongation factor A (SII)-like 7	BF591534
244108_at	2.71211	6.956233	18.81512	2.97E-46	9.23E-44	94.64436	SYNPO2	synaptopodin 2	AL552450
228827_at	2.71151	6.766852	17.30151	1.05E-41	1.47E-39	84.24161			AI217416
202436_s_at	2.70468	8.608955	11.93401	3.51E-25	9.98E-24	46.43108	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	AU144855
204955_at	2.70328	8.096871	13.92191	2.60E-31	1.22E-29	60.45245	SRPX	sushi-repeat-containing protein, X-linked	NM_006307
239349_at	2.7026	5.372172	17.89566	1.68E-43	3.20E-41	88.35041	C1QTNF7	C1q and tumor necrosis factor related protein 7	BE856929
232119_at	2.70071	5.821738	19.60429	1.39E-48	6.58E-46	99.97735	SYNPO2	synaptopodin 2	BF984227
238481_at	2.70036	4.856324	16.63803	1.10E-39	1.25E-37	79.6193	MGP	matrix Gla protein	AW512787
213714_at	2.70011	5.763513	18.46449	3.30E-45	8.46E-43	92.25397	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	AI040163
208131_s_at	2.69501	8.16686	14.64204	1.53E-33	8.88E-32	65.55593	PTGIS	prostaglandin I2 (prostacyclin) synthase	NM_000961
203881_s_at	2.69032	7.481809	15.3596	9.26E-36	6.79E-34	70.63193	DMD	dystrophin	NM_004010
210170_at	2.68962	5.844269	18.99929	8.45E-47	2.85E-44	95.89489	PDLIM3	PDZ and LIM domain 3	BC001017
231067_s_at	2.68667	5.487069	19.55304	1.96E-48	9.07E-46	99.63302			BF114967
223519_at	2.68339	8.823156	18.47331	3.10E-45	8.11E-43	92.31429	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	AW069181
205908_s_at	2.68319	5.546589	15.43922	5.26E-36	3.97E-34	71.19407	OMD	osteomodulin	NM_005014

223121_s_at	2.6797	8.599996	9.984685	2.49E-19	4.11E-18	33.06709	SFRP2	secreted frizzled-related protein 2	AW003584
201843_s_at	2.6772	7.797962	12.8872	4.13E-28	1.48E-26	53.12991	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	NM_004105
204359_at	2.67286	7.625554	14.75217	6.98E-34	4.22E-32	66.33588	FLRT2	fibronectin leucine rich transmembrane protein 2	NM_013231
229127_at	2.67008	6.71954	17.99982	8.15E-44	1.65E-41	89.06755	JAM2	junctional adhesion molecule 2	BF195118
228802_at	2.66439	7.493258	17.65831	8.71E-43	1.46E-40	86.71273	RBPMS2	RNA binding protein with multiple splicing 2	BE348466
225990_at	2.66371	7.967676	20.96318	1.57E-52	1.62E-49	108.9964	BOC	Boc homolog (mouse)	W72626
227084_at	2.66176	6.52048	16.21503	2.16E-38	2.07E-36	76.65598	DTNA	dystrobrevin, alpha	AW339310
202035_s_at	2.66139	5.171603	15.62249	1.43E-36	1.16E-34	72.48707	SFRP1	secreted frizzled-related protein 1	AI332407
235570_at	2.65589	7.253751	19.6255	1.20E-48	5.75E-46	100.1197			AW298235
238447_at	2.65034	7.795591	16.71763	6.26E-40	7.47E-38	80.17559	RBMS3	RNA binding motif, single stranded interacting protein	AA428240
243140_at	2.64537	5.366144	20.19722	2.57E-50	1.69E-47	103.939	ACTA2	Actin, alpha 2, smooth muscle, aorta (ACTA2), transcript variant 1, mRNA	AI917901
229024_at	2.644	6.20891	22.82802	8.69E-58	3.65E-54	121.0102			BF056892
228224_at	2.63762	8.027022	18.76158	4.29E-46	1.28E-43	94.28015	PRELP	proline/arginine-rich end leucine-rich repeat protein	AA573140
235182_at	2.63545	6.078074	14.5477	3.00E-33	1.68E-31	64.8876	ISM1	isthmin 1 homolog (zebrafish)	AI816793
210875_s_at	2.63006	5.313211	22.09782	9.46E-56	2.46E-52	116.3577	ZEB1	zinc finger E-box binding homeobox 1	U12170
212713_at	2.62623	8.351586	15.9331	1.59E-37	1.39E-35	74.67476	MFAP4	microfibrillar-associated protein 4	R72286
217966_s_at	2.62187	8.622041	20.04057	7.34E-50	4.55E-47	102.8962	FAM129A	family with sequence similarity 129, member A	NM_022083
204424_s_at	2.61883	6.964695	18.07532	4.83E-44	9.99E-42	89.58664	LMO3	LIM domain only 3 (rhombotin-like 2)	AL050152
225996_at	2.61713	4.94979	17.45351	3.62E-42	5.38E-40	85.29567	LONRF2	LON peptidase N-terminal domain and ring finger 2	AV709727
222924_at	2.61035	6.65112	17.71808	5.75E-43	1.00E-40	87.1256	SLMAP	sarcolemma associated protein	BF526855
236304_at	2.60968	4.898065	16.14734	3.48E-38	3.26E-36	76.18069			AI127700
218711_s_at	2.60948	6.435919	21.39984	8.90E-54	1.22E-50	111.848	SDPR	serum deprivation response (phosphatidylserine binding protein)	NM_004657
238478_at	2.60852	6.552558	20.51573	3.06E-51	2.39E-48	106.0504	BNC2	basonuclin 2	H97386
228406_at	2.60688	4.775135	14.31936	1.53E-32	7.96E-31	63.26952	SMYD1	SET and MYND domain containing 1	BF060984
225442_at	2.60604	8.379568	16.85931	2.31E-40	2.85E-38	81.16459	DDR2	discoidin domain receptor tyrosine kinase 2	AI799915
226824_at	2.60227	8.1434	19.53821	2.17E-48	9.86E-46	99.53333	CPXM2	carboxypeptidase X (M14 family), member 2	AW513612
209406_at	2.60225	8.243755	13.11649	8.08E-29	3.06E-27	54.74967	BAG2	BCL2-associated athanogene 2	AF095192
1554547_at	2.60192	6.942818	17.63076	1.05E-42	1.72E-40	86.52235	FAM13C1	family with sequence similarity 13, member C1	BC036453
201525_at	2.5992	8.935022	11.08668	1.31E-22	2.97E-21	40.55001	APOD	apolipoprotein D	NM_001647
213974_at	2.59801	5.934203	20.91908	2.11E-52	2.02E-49	108.7071	ADAMTSL3	ADAMTS-like 3	AB033059
227006_at	2.59645	7.805965	15.21446	2.60E-35	1.81E-33	69.60648	PPP1R14A	protein phosphatase 1, regulatory (inhibitor) subunit 14A	AA156998
238919_at	2.59455	4.534201	16.5778	1.67E-39	1.86E-37	79.19807			R49295
212764_at	2.59332	9.166978	18.5877	1.41E-45	4.00E-43	93.09535	ZEB1	zinc finger E-box binding homeobox 1	AI806174
228507_at	2.59329	7.698511	19.41368	5.04E-48	2.20E-45	98.69539			AI742043
243864_at	2.59232	6.16463	17.88791	1.77E-43	3.37E-41	88.29705	CCDC80	coiled-coil domain containing 80	AA994712
223987_at	2.59092	7.329087	12.63971	2.39E-27	8.04E-26	51.38452	CHRD2	chordin-like 2	AF332891
210221_at	2.5906	5.939616	14.80029	4.95E-34	3.05E-32	66.67661	CHRNA3	cholinergic receptor, nicotinic, alpha 3	BC000513
224823_at	2.58977	11.48324	15.26549	1.81E-35	1.28E-33	69.96711	MYLK	myosin light chain kinase	AA526844
201616_s_at	2.58102	10.17159	19.26316	1.40E-47	5.51E-45	97.68028	CALD1	caldesmon 1	AL577531
204797_s_at	2.58065	7.867944	17.94308	1.21E-43	2.38E-41	88.67702	EML1	echinoderm microtubule associated protein like 1	NM_004434
223475_at	2.57665	6.733743	12.40301	1.28E-26	4.07E-25	49.71881	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1	AF142573

205529_s_at	2.57331	6.924329	16.86123	2.28E-40	2.82E-38	81.17797	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	NM_004349
1553102_a_at	2.57033	7.169499	16.53469	2.27E-39	2.48E-37	78.89641	CCDC69	coiled-coil domain containing 69	BC016647
230087_at	2.57018	7.20832	16.63247	1.14E-39	1.30E-37	79.58042	PRIMA1	proline rich membrane anchor 1	AI823645
227478_at	2.56707	7.017973	16.42178	5.02E-39	5.25E-37	78.10582	SETBP1	SET binding protein 1	BF739885
209210_s_at	2.5596	9.956498	16.4375	4.50E-39	4.74E-37	78.21591	FERMT2	fermitin family homolog 2 (Drosophila)	Z24725
220955_x_at	2.5576	7.262624	16.29675	1.21E-38	1.20E-36	77.22937	RAB23	RAB23, member RAS, oncogene family	NM_016277
209894_at	2.55617	7.768083	14.15855	4.80E-32	2.40E-30	62.12975	LEPR	leptin receptor	U50748
208335_s_at	2.55442	7.800061	12.20138	5.32E-26	1.61E-24	48.30309	DARC	Duffy blood group, chemokine receptor	NM_002036
235489_at	2.55136	6.481088	17.97873	9.43E-44	1.88E-41	88.92242	RHOJ	ras homolog gene family, member J	AI583530
202435_s_at	2.54626	8.160928	12.26725	3.34E-26	1.03E-24	48.76521	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	AU154504
225662_at	2.54414	9.573112	17.39669	5.39E-42	7.78E-40	84.90186	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	H28667
207957_s_at	2.543	6.45836	15.72867	6.75E-37	5.55E-35	73.23548	PRKCB	protein kinase C, beta	NM_002738
212233_at	2.54099	8.411962	17.87272	1.97E-43	3.73E-41	88.19234	MAP1B	microtubule-associated protein 1B	AL523076
241789_at	2.53997	5.77738	22.93085	4.51E-58	2.24E-54	121.6599			AW338699
219654_at	2.53774	7.34968	12.95009	2.64E-28	9.57E-27	53.57391	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	NM_014241
232113_at	2.53051	5.794045	15.55676	2.28E-36	1.78E-34	72.02349			N90870
204753_s_at	2.52942	5.566674	18.55375	1.79E-45	4.95E-43	92.86371	HLF	hepatic leukemia factor	AI810712
205330_at	2.52927	6.678483	17.57584	1.55E-42	2.46E-40	86.14255	MN1	meningioma (disrupted in balanced translocation) 1	NM_002430
201430_s_at	2.52835	7.615667	15.50795	3.23E-36	2.50E-34	71.67914	DPYSL3	dihydropyrimidinase-like 3	W72516
1555724_s_at	2.52617	11.62804	14.30909	1.64E-32	8.54E-31	63.19676	TAGLN	transgelin	BC010946
209897_s_at	2.52493	7.68872	17.64391	9.63E-43	1.59E-40	86.61322	SLIT2	slit homolog 2 (Drosophila)	AF055585
213746_s_at	2.52134	9.589974	17.63954	9.92E-43	1.63E-40	86.58305	FLNA	filamin A, alpha (actin binding protein 280)	AW051856
222513_s_at	2.51757	9.018322	17.13698	3.31E-41	4.45E-39	83.09851	SORBS1	sorbin and SH3 domain containing 1	N21458
227561_at	2.51485	8.522165	17.70097	6.47E-43	1.11E-40	87.00749	DDR2	discoidin domain receptor tyrosine kinase 2	W73819
201617_x_at	2.5147	9.38674	17.10921	4.02E-41	5.32E-39	82.90539	CALD1	caldesmon 1	NM_004342
212992_at	2.51319	7.695114	12.42747	1.08E-26	3.44E-25	49.89079	AHNAK2	AHNAK nucleoprotein 2	AI935123
203698_s_at	2.50971	8.117531	15.30022	1.41E-35	1.01E-33	70.2125	FRZB	frizzled-related protein	NM_001463
225946_at	2.50086	6.548295	18.89965	1.67E-46	5.39E-44	95.21877	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	BG484552
1560359_at	2.49794	5.361428	21.02474	1.05E-52	1.10E-49	109.3998	PELO	Pelota major mRNA, complete cds; alternatively spliced	BG619261
206638_at	2.49777	5.442787	13.07797	1.06E-28	3.98E-27	54.47741	HTR2B	5-hydroxytryptamine (serotonin) receptor 2B	NM_000867
231098_at	2.49775	5.908517	15.77672	4.80E-37	4.01E-35	73.57397			BF939996
227530_at	2.49713	8.311157	17.43087	4.24E-42	6.25E-40	85.13877	AKAP12	A kinase (PRKA) anchor protein 12	BF511276
227971_at	2.49637	4.858858	16.55618	1.95E-39	2.15E-37	79.04683	NRK	Nik related kinase	AI653107
208096_s_at	2.49007	6.69772	18.19544	2.11E-44	4.73E-42	90.41153	COL21A1	collagen, type XXI, alpha 1	NM_030820
202994_s_at	2.48643	9.374801	13.3074	2.08E-29	8.35E-28	56.09988	FBLN1	fibulin 1	Z95331
225665_at	2.48574	9.877591	18.02767	6.72E-44	1.37E-41	89.25909	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	AI129320
239262_at	2.48427	5.733473	18.90597	1.60E-46	5.19E-44	95.26164			AI498395
211737_x_at	2.4829	8.084313	17.99382	8.49E-44	1.70E-41	89.02625	PTN	pleiotrophin	BC005916
224149_x_at	2.4813	7.598227	16.41467	5.28E-39	5.50E-37	78.05597	SLMAP	sarcolemma associated protein	AF304450
227719_at	2.47505	7.911053	13.82076	5.35E-31	2.45E-29	59.73561	SMAD9	SMAD family member 9	AA934610
221942_s_at	2.47468	8.899361	16.25455	1.63E-38	1.60E-36	76.93333	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	AI719730
201615_x_at	2.47353	9.696538	18.09641	4.18E-44	8.80E-42	89.7316	CALD1	caldesmon 1	AI685060
227235_at	2.47179	8.820861	15.88981	2.15E-37	1.87E-35	74.37014	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	AI758408
1552848_a_at	2.47165	4.894569	14.26861	2.19E-32	1.13E-30	62.90984	PTCHD1	patched domain containing 1	NM_173495
228228_at	2.47063	8.394414	20.86808	2.95E-52	2.64E-49	108.3722	DACT3	dapper, antagonist of beta-catenin, homolog 3 (Xenopus laevis)	AI809234

226084_at	2.46894	8.646856	17.96981	1.00E-43	1.98E-41	88.86103	MAP1B	microtubule-associated protein 1B	AA554833
202566_s_at	2.46888	8.108167	18.83655	2.57E-46	8.02E-44	94.79007	SVIL	supervillin	AF051851
219647_at	2.46859	5.453507	16.49991	2.90E-39	3.12E-37	78.65299	POPC2	popeye domain containing 2	NM_022135
205528_s_at	2.46832	6.027862	18.81339	3.01E-46	9.29E-44	94.63259	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	X79990
239468_at	2.46574	4.66085	16.15906	3.21E-38	3.03E-36	76.26302	MKX	mohawk homeobox	AW023227
212423_at	2.46534	8.95208	19.65097	1.01E-48	4.98E-46	100.2907	ZCCHC24	zinc finger, CCHC domain containing 24	AK024784
228850_s_at	2.46448	6.329792	19.79871	3.73E-49	1.98E-46	101.2807			AI963304
209243_s_at	2.46218	4.098945	21.59393	2.50E-54	4.02E-51	113.108	PEG3 /// ZIM2	paternally expressed 3 /// zinc finger, imprinted 2	AF208967
205547_s_at	2.46127	11.89622	13.59435	2.69E-30	1.15E-28	58.13147	TAGLN	transgelin	NM_003186
236300_at	2.45611	6.713199	18.27747	1.20E-44	2.86E-42	90.974			BF698797
225968_at	2.45467	6.855082	21.07178	7.69E-53	8.24E-50	109.7077	PRICKLE2	prickle homolog 2 (Drosophila)	BG285881
209469_at	2.45094	4.814681	15.76602	5.18E-37	4.32E-35	73.49856	GPM6A	glycoprotein M6A	BF939489
226047_at	2.44973	9.314874	18.71511	5.90E-46	1.74E-43	93.96382	MRV1	murine retrovirus integration site 1 homolog	N66571
212758_s_at	2.44931	8.35462	19.55768	1.90E-48	8.94E-46	99.66423	ZEB1	zinc finger E-box binding homeobox 1	AI373166
228186_s_at	2.44851	8.023045	10.89862	4.84E-22	1.04E-20	39.25785	RSPO3	R-spondin 3 homolog (Xenopus laevis)	BF589322
212551_at	2.44734	7.294942	17.51641	2.34E-42	3.61E-40	85.73127	CAP2	CAP, adenylate cyclase-associated protein, 2 (yeast)	NM_006366
200930_s_at	2.44588	5.239486	18.61154	1.20E-45	3.43E-43	93.25797	VCL	vinculin	AA156675
221019_s_at	2.4411	7.172875	14.59208	2.18E-33	1.25E-31	65.20198	COLEC12	collectin sub-family member 12	NM_030781
213306_at	2.44019	7.873976	22.51355	6.50E-57	2.37E-53	119.0148	MPDZ	multiple PDZ domain protein	AA917899
203697_at	2.43812	8.40564	14.46348	5.46E-33	2.97E-31	64.29088	FRZB	frizzled-related protein	U91903
204422_s_at	2.4373	5.259813	21.47903	5.30E-54	7.82E-51	112.3627	FGF2	fibroblast growth factor 2 (basic)	NM_002006
213436_at	2.43597	5.0185	13.8829	3.43E-31	1.60E-29	60.17598	CNR1	cannabinoid receptor 1 (brain)	U73304
238441_at	2.43597	4.793702	13.57233	3.14E-30	1.34E-28	57.97552	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	AI928203
219087_at	2.43111	10.62486	11.78891	9.73E-25	2.66E-23	45.418	ASPN	asporin	NM_017680
204069_at	2.42581	8.067465	17.70646	6.23E-43	1.08E-40	87.04536	MEIS1	Meis homeobox 1	NM_002398
230722_at	2.41737	6.685222	20.18388	2.81E-50	1.80E-47	103.8503	BNC2	basonuclin 2	AI377043
203065_s_at	2.41423	10.02434	14.90825	2.30E-34	1.47E-32	67.4408	CAV1	caveolin 1, caveolae protein, 22kDa	NM_001753
225207_at	2.41347	8.734609	10.3321	2.37E-20	4.30E-19	35.40134	PDK4	pyruvate dehydrogenase kinase, isozyme 4	AV707102
220794_at	2.41328	5.803275	10.56663	4.76E-21	9.32E-20	36.99083	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	NM_022469
212886_at	2.41145	7.663406	17.34703	7.62E-42	1.09E-39	84.5575	CCDC69	coiled-coil domain containing 69	AL080169
232067_at	2.40756	5.287252	13.59137	2.74E-30	1.18E-28	58.11038	C6orf168	chromosome 6 open reading frame 168	BC004869
228776_at	2.3951	7.270929	15.93651	1.55E-37	1.36E-35	74.69877	GJC1	gap junction protein, gamma 1, 45kDa	AA430014
209465_x_at	2.39457	6.3402	16.6795	8.19E-40	9.53E-38	79.90914	PTN	pleiotrophin	AL565812
209821_at	2.38978	7.55983	10.18035	6.64E-20	1.16E-18	34.37862	IL33	interleukin 33	AB024518
204223_at	2.38031	7.992651	17.41871	4.62E-42	6.76E-40	85.05451	PRELP	proline/arginine-rich end leucine-rich repeat protein	NM_002725
207876_s_at	2.37689	8.192689	18.90762	1.58E-46	5.17E-44	95.27287	FLNC	filamin C, gamma (actin binding protein 280)	NM_001458
225345_s_at	2.37557	7.135511	16.84174	2.62E-40	3.20E-38	81.04203			AU155376
230214_at	2.37262	7.25937	13.64309	1.90E-30	8.25E-29	58.47675	MRV1	murine retrovirus integration site 1 homolog	AL044056
213071_at	2.36965	7.402967	12.69112	1.66E-27	5.66E-26	51.74683	DPT	dermatopontin	AL049798
214212_x_at	2.36915	8.05044	19.81214	3.41E-49	1.84E-46	101.3706	FERMT2	fermitin family homolog 2 (Drosophila)	AI928241
218468_s_at	2.36823	10.20591	8.267566	1.82E-14	1.80E-13	21.99145	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	AF154054
213904_at	2.36722	4.757181	18.16006	2.69E-44	5.95E-42	90.16871			AL390170
230730_at	2.36583	6.278278	17.65637	8.83E-43	1.47E-40	86.69934	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	AA401248

1554741_s_at	2.36457	7.217109	13.91127	2.80E-31	1.32E-29	60.37702	FGF7 /// KGFLP1 /// KGFLP2	fibroblast growth factor 7 (keratinocyte growth factor) ///	AF523265
								keratinocyte growth factor-like protein 1 /// keratinocyte growth factor-like protein 2	#N/A
219737_s_at	2.35722	6.228158	14.10385	7.10E-32	3.53E-30	61.74207	PCDH9	protocadherin 9	AI524125
210517_s_at	2.35648	9.145568	15.48517	3.80E-36	2.91E-34	71.51842	AKAP12	A kinase (PRKA) anchor protein 12	AB003476
209427_at	2.35351	8.385856	18.55437	1.78E-45	4.95E-43	92.86792	SMTN	smoothelin	AF064238
219845_at	2.35335	6.731241	18.19359	2.13E-44	4.77E-42	90.39885	BARX1	BARX homeobox 1	NM_021570
202363_at	2.34972	7.727734	11.16909	7.42E-23	1.71E-21	41.11796	SPOCK1	sparc/osteonectin, cwcv and kazal- like domains proteoglycan (testican) 1	AF231124
205933_at	2.3443	6.958381	17.12105	3.70E-41	4.94E-39	82.98773	SETBP1	SET binding protein 1	NM_015559
221974_at	2.34176	5.417317	16.30037	1.18E-38	1.18E-36	77.25471	IPW	Imprinted in Prader-Willi syndrome (non-protein coding)	AW770748
235004_at	2.34141	5.473361	15.96605	1.26E-37	1.11E-35	74.90656	RBM24	RNA binding motif protein 24	AI677701
213110_s_at	2.33936	7.395237	11.818	7.93E-25	2.19E-23	45.62098	COL4A5	collagen, type IV, alpha 5	AW052179
229578_at	2.33869	6.561982	17.42146	4.53E-42	6.65E-40	85.07355	JPH2	junctophilin 2	AA716165
232712_at	2.33612	4.16218	17.78631	3.58E-43	6.52E-41	87.59654			AU156306
201842_s_at	2.33564	9.899361	11.78536	9.98E-25	2.73E-23	45.39329	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	AI826799
227236_at	2.33453	7.615028	13.70839	1.19E-30	5.28E-29	58.93939	TSPAN2	tetraspanin 2	AI743596
214348_at	2.3337	6.219487	14.83365	3.90E-34	2.43E-32	66.91275	TACR2	tachykinin receptor 2	NM_001057
209436_at	2.33362	9.507379	14.16556	4.57E-32	2.29E-30	62.17945	SPON1	spondin 1, extracellular matrix protein	AB018305
227297_at	2.32756	7.622771	16.23395	1.89E-38	1.83E-36	76.78874	ITGA9	integrin, alpha 9	AI479176
226322_at	2.32468	7.475432	18.35818	6.86E-45	1.71E-42	91.52684	TMT1	transmembrane and tetratricopeptide repeat containing 1	BF109231
204754_at	2.32454	5.344909	19.63444	1.13E-48	5.46E-46	100.1797	HLF	hepatic leukemia factor	W60800
226931_at	2.32339	6.946548	17.9198	1.42E-43	2.74E-41	88.51669	TMT1	transmembrane and tetratricopeptide repeat containing 1	AU151239
202565_s_at	2.32249	9.453529	17.90797	1.54E-43	2.96E-41	88.43521	SVIL	supervillin	NM_003174
209286_at	2.32166	7.599015	16.04313	7.28E-38	6.57E-36	75.44852	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	AI754416
225241_at	2.31774	8.572521	14.75259	6.96E-34	4.21E-32	66.33881	CCDC80	coiled-coil domain containing 80	AA570507
230109_at	2.3173	7.33862	20.21745	2.24E-50	1.51E-47	104.0734	PDE7B	phosphodiesterase 7B	AI638433
206116_s_at	2.31268	10.61715	16.86878	2.17E-40	2.68E-38	81.23061	TPM1	tropomyosin 1 (alpha)	NM_000366
238906_s_at	2.31254	5.412666	20.93132	1.94E-52	1.93E-49	108.7874	RHOJ	ras homolog gene family, member J	BE218803
238613_at	2.31112	7.679086	17.82499	2.74E-43	5.12E-41	87.86334	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	AI475164
242348_at	2.31038	4.093811	13.49154	5.59E-30	2.35E-28	57.40336	FAM19A4	family with sequence similarity 19 (chemokine (C-C motif)-like), member A4	AA757457
214761_at	2.31021	7.339187	17.69471	6.76E-43	1.15E-40	86.96423	ZNF423	zinc finger protein 423	AW149417
227088_at	2.31006	8.34665	18.57862	1.50E-45	4.21E-43	93.03342	PDE5A	phosphodiesterase 5A, cGMP- specific	BF221547
203305_at	2.30966	7.897255	12.83283	6.07E-28	2.14E-26	52.74618	F13A1	coagulation factor XIII, A1 polypeptide	NM_000129
213992_at	2.30618	6.079946	12.01863	1.93E-25	5.60E-24	47.02285	COL4A6	collagen, type IV, alpha 6	AI889941
209505_at	2.30397	8.068866	14.72594	8.41E-34	5.05E-32	66.15014	NR2F1	Chicken ovalbumin upstream promoter transcription factor (COUP-TF)	AI951185
227657_at	2.30266	6.385043	23.53599	9.81E-60	1.07E-55	125.4564	RNF150	ring finger protein 150	AA722069
229975_at	2.3012	5.724182	11.85542	6.10E-25	1.70E-23	45.88209	BMPRI1B	bone morphogenetic protein receptor, type IB	AI826437
203680_at	2.29848	7.832615	12.1622	7.02E-26	2.10E-24	48.02838	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	NM_002736
225685_at	2.2981	7.975851	15.82568	3.39E-37	2.88E-35	73.91871			AI801777
200795_at	2.29479	11.75564	15.27665	1.67E-35	1.19E-33	70.04593	SPARCL1	SPARC-like 1 (hevin)	NM_004684
219902_at	2.29368	6.214982	20.48173	3.84E-51	2.91E-48	105.8256	BHMT2	betaine-homocysteine methyltransferase 2	NM_017614
218418_s_at	2.29228	9.424473	21.67912	1.43E-54	2.37E-51	113.6596	KANK2	KN motif and ankyrin repeat domains 2	NM_015493
204557_s_at	2.29096	5.304694	19.04678	6.11E-47	2.09E-44	96.21677	DZIP1	DAZ interacting protein 1	NM_014934

206227_at	2.28941	7.736318	11.47703	8.66E-24	2.18E-22	43.24836	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	NM_003613
209651_at	2.28905	9.632494	16.40068	5.83E-39	6.03E-37	77.95799	TGFB111	transforming growth factor beta 1 induced transcript 1	BC001830
215440_s_at	2.2879	7.596097	13.93922	2.30E-31	1.09E-29	60.57517	BEX4	brain expressed, X-linked 4	AL523320
1553194_at	2.28725	4.87617	22.75854	1.35E-57	5.28E-54	120.5704	NEGR1	neuronal growth regulator 1	NM_173808
233857_s_at	2.2833	5.870377	16.25358	1.65E-38	1.61E-36	76.92647	ASB2	ankyrin repeat and SOCS box-containing 2	AK002049
235000_at	2.28326	7.593794	18.51852	2.27E-45	6.21E-43	92.62312			T86629
235173_at	2.28251	8.124001	18.22628	1.70E-44	3.89E-42	90.62309	hCG_1806964	hCG1806964	AA093668
214752_x_at	2.28152	9.896728	17.99075	8.67E-44	1.74E-41	89.00509	FLNA	filamin A, alpha (actin binding protein 280)	AI625550
1554007_at	2.28107	6.920144	16.08655	5.35E-38	4.90E-36	75.75366			BC036488
218820_at	2.27669	7.527755	18.43741	3.97E-45	1.01E-42	92.06887	C14orf132	chromosome 14 open reading frame 132	NM_020215
217897_at	2.27488	8.137306	18.4888	2.79E-45	7.38E-43	92.42012	FXYD6	FXYD domain containing ion transport regulator 6	NM_022003
241879_at	2.27236	9.344173	16.67972	8.17E-40	9.53E-38	79.91071			AW511222
212419_at	2.26945	8.580177	20.41745	5.89E-51	4.41E-48	105.4001	ZCCHC24	zinc finger, CCHC domain containing 24	AA131324
1556427_s_at	2.26744	6.855416	18.0664	5.14E-44	1.05E-41	89.52538	LRRN4CL	LRRN4 C-terminal like	AL834319
238458_at	2.26697	4.747369	20.25538	1.74E-50	1.20E-47	104.3254	EFHA2	EF-hand domain family, member A2	AI868167
236144_at	2.26584	6.645208	20.89122	2.53E-52	2.35E-49	108.5241	CPXM2	carboxypeptidase X (M14 family), member 2	BF726934
219368_at	2.2641	4.750205	19.1815	2.44E-47	9.13E-45	97.12854	NAP1L2	nucleosome assembly protein 1-like 2	NM_021963
227915_at	2.26272	7.192614	15.33119	1.13E-35	8.22E-34	70.43123	ASB2	ankyrin repeat and SOCS box-containing 2	AI872284
227618_at	2.26253	6.669118	21.24528	2.46E-53	2.91E-50	110.8413			AI250910
241255_at	2.25161	4.882082	14.48879	4.56E-33	2.51E-31	64.4702			BF433749
205803_s_at	2.24857	5.806671	22.07877	1.07E-55	2.54E-52	116.2353	TRPC1	transient receptor potential cation channel, subfamily C, member 1	NM_003304
204464_s_at	2.2476	8.657101	14.32153	1.50E-32	7.85E-31	63.28489	EDNRA	endothelin receptor type A	NM_001957
207317_s_at	2.24543	6.751418	14.8703	3.01E-34	1.90E-32	67.17216	CASQ2	calsequestrin 2 (cardiac muscle)	NM_001232
200859_x_at	2.2454	10.04332	17.70791	6.17E-43	1.07E-40	87.05538	FLNA	filamin A, alpha (actin binding protein 280)	NM_001456
226523_at	2.23946	8.130527	17.18666	2.34E-41	3.18E-39	83.44388	TAGLN	SM22 alpha	AI082237
212288_at	2.23658	8.871557	17.15821	2.85E-41	3.87E-39	83.24614	FNBP1	formin binding protein 1	AB011126
227265_at	2.23622	9.785304	14.45186	5.93E-33	3.22E-31	64.20851	FGL2	fibrinogen-like 2	AW135176
204337_at	2.23374	7.337822	12.04976	1.55E-25	4.53E-24	47.24069	RGS4	regulator of G-protein signaling 4	AL514445
227623_at	2.23337	7.887845	12.47524	7.67E-27	2.48E-25	50.2267			H16409
239580_at	2.22861	5.956581	19.55474	1.94E-48	9.05E-46	99.64448	GUCY1A3	guanylate cyclase 1, soluble, alpha 3	BF724601
208396_s_at	2.22667	6.474137	15.34103	1.06E-35	7.68E-34	70.50076	PDE1A	phosphodiesterase 1A, calmodulin-dependent	NM_005019
239708_at	2.22494	4.319915	20.93501	1.90E-52	1.92E-49	108.8116			AA027105
228080_at	2.22447	7.284382	18.59861	1.31E-45	3.73E-43	93.16982	LAYN	layilin	BE856341
218469_at	2.22437	10.59922	8.043297	7.36E-14	6.81E-13	20.61534	GREM1	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)	NM_013372
204463_s_at	2.22241	7.174889	13.87194	3.71E-31	1.72E-29	60.0983	EDNRA	endothelin receptor type A	AU118882
209663_s_at	2.22111	6.71723	17.5525	1.82E-42	2.87E-40	85.98105	ITGA7	integrin, alpha 7	AF072132
225688_s_at	2.22071	9.090631	14.49026	4.51E-33	2.49E-31	64.48066	PHLDB2	pleckstrin homology-like domain, family B, member 2	AK025444
1555229_a_at	2.22027	8.548859	11.37716	1.74E-23	4.24E-22	42.55607	C1S	complement component 1, s subcomponent	BC007010
227997_at	2.21894	6.554555	16.34555	8.60E-39	8.78E-37	77.57153	IL17RD	interleukin 17 receptor D	AW007080
243041_s_at	2.21463	5.029373	25.65416	2.13E-65	1.16E-60	138.3751	RBMS3	RNA binding motif, single stranded interacting protein 3	AI217028
204963_at	2.21445	7.08516	16.3715	7.16E-39	7.36E-37	77.75347	SSPN	sarcospan (Kras oncogene-associated gene)	AL136756
201117_s_at	2.21272	8.287841	10.71286	1.74E-21	3.54E-20	37.98702	CPE	carboxypeptidase E	NM_001873
226225_at	2.21173	7.240358	14.48949	4.54E-33	2.50E-31	64.47515	MCC	mutated in colorectal cancers	BE967311
206510_at	2.21146	6.758271	13.30945	2.05E-29	8.24E-28	56.11443	SIX2	SIX homeobox 2	AF332197
203498_at	2.20987	8.502865	13.71712	1.12E-30	4.97E-29	59.00125	RCAN2	regulator of calcineurin 2	NM_005822
205168_at	2.2092	8.000589	17.84918	2.31E-43	4.37E-41	88.03011	DDR2	discoidin domain receptor tyrosine kinase 2	NM_006182

226932_at	2.20691	8.336133	15.11849	5.14E-35	3.48E-33	68.92802	SSPN	sarcospan (Kras oncogene-associated gene)	AW467136
214071_at	2.20581	5.745847	17.57822	1.52E-42	2.43E-40	86.15901	MPPE1	MRNA; cDNA DKFZp686K2379 (from clone DKFZp686K2379)	AI082827
231213_at	2.20395	5.7818	15.95558	1.35E-37	1.19E-35	74.8329	PDE1A	phosphodiesterase 1A, calmodulin-dependent	AU146305
213933_at	2.20376	6.671989	13.79791	6.29E-31	2.87E-29	59.57369	PTGER3	prostaglandin E receptor 3 (subtype EP3)	AW242315
227892_at	2.20299	5.665074	12.55135	4.47E-27	1.47E-25	50.76229	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	AA855042
218694_at	2.20121	7.98272	16.16164	3.15E-38	2.98E-36	76.28115	ARMCX1	armadillo repeat containing, X-linked 1	NM_016608
209470_s_at	2.20001	4.636919	14.41075	7.95E-33	4.26E-31	63.91723	GPM6A	glycoprotein M6A	D49958
212097_at	2.19878	10.56291	15.37842	8.10E-36	6.00E-34	70.76485	CAV1	caveolin 1, caveolae protein, 22kDa	AU147399
228766_at	2.19799	6.206098	9.418011	1.10E-17	1.53E-16	29.3192	CD36	CD36 molecule (thrombospondin receptor)	AW299226
209292_at	2.19713	6.333243	13.92435	2.55E-31	1.20E-29	60.46978	ID4	Id-related helix-loop-helix protein Id4	AL022726
214660_at	2.19545	6.396582	17.52502	2.20E-42	3.43E-40	85.79087	PELO	Pelota major mRNA, complete cds; alternatively spliced	X68742
218656_s_at	2.19422	8.657965	16.3648	7.51E-39	7.69E-37	77.7065	LHFP	lipoma HMGIC fusion partner	NM_005780
222288_at	2.19407	6.827493	11.47196	8.98E-24	2.26E-22	43.21316			AI004009
230958_s_at	2.19032	8.054187	15.97314	1.19E-37	1.06E-35	74.95641			BE670797
227209_at	2.18931	5.482807	17.64645	9.46E-43	1.57E-40	86.63079	CNTN1	Contactin 2 precursor (CNTN1)	AI091445
227070_at	2.1891	7.635298	13.48514	5.85E-30	2.45E-28	57.35802	GLT8D2	glycosyltransferase 8 domain containing 2	W63754
235723_at	2.18885	4.897414	23.57124	7.86E-60	1.07E-55	125.6762	BNC2	basonuclein 2	AA843242
1559477_s_at	2.18605	7.124735	19.76071	4.82E-49	2.51E-46	101.0263	MEIS1	Meis homeobox 1	AL832770
209737_at	2.18452	6.060707	17.22747	1.76E-41	2.41E-39	83.72747	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	AB014605
1555233_at	2.1843	6.51844	18.48851	2.80E-45	7.38E-43	92.41813	RHOJ	ras homolog gene family, member J	BC025770
228602_at	2.183	6.983374	16.91631	1.55E-40	1.95E-38	81.56204	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	AA479286
209335_at	2.17979	10.00383	12.18626	5.92E-26	1.78E-24	48.19704	DCN	decorin	AI281593
225915_at	2.17818	7.234295	15.49859	3.45E-36	2.66E-34	71.61312	CAB39L	calcium binding protein 39-like	AL138875
224184_s_at	2.17754	7.660657	23.05585	2.04E-58	1.24E-54	122.448	BOC	Boc homolog (mouse)	AY027658
216331_at	2.17313	7.47592	19.29598	1.12E-47	4.50E-45	97.9018	ITGA7	integrin, alpha 7	AK022548
228783_at	2.17107	6.588021	16.65562	9.68E-40	1.12E-37	79.74229	BVES	blood vessel epicardial substance	AA993518
205478_at	2.1701	5.955402	12.30453	2.57E-26	7.94E-25	49.02691	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	NM_006741
209822_s_at	2.16689	6.485229	13.58506	2.87E-30	1.23E-28	58.06565	VLDLR	very low density lipoprotein receptor	L22431
229116_at	2.16657	4.610014	18.1495	2.89E-44	6.32E-42	90.0962	CNKSR2	connector enhancer of kinase suppressor of Ras 2	AI670947
203562_at	2.16611	7.959338	18.22265	1.75E-44	3.97E-42	90.59816	FEZ1	fasciculation and elongation protein zeta 1 (zyglin I)	NM_005103
205407_at	2.16584	7.602816	15.14002	4.41E-35	3.02E-33	69.08026	RECK	reversion-inducing-cysteine-rich protein with kazal motifs	NM_021111
223463_at	2.16495	9.749503	16.46739	3.64E-39	3.89E-37	78.42531	RAB23	RAB23, member RAS oncogene family	AF161486
216887_s_at	2.16316	5.099664	16.62948	1.16E-39	1.32E-37	79.55954	LDB3	LIM domain binding 3	AJ133768
236936_at	2.1594	5.215682	17.65237	9.08E-43	1.51E-40	86.67168			AI672386
228724_at	2.15913	4.763758	17.31472	9.55E-42	1.35E-39	84.3333			N49237
206157_at	2.15869	5.0657	10.12747	9.50E-20	1.63E-18	34.02337	PTX3	pentraxin-related gene, rapidly induced by IL-1 beta	NM_002852
206104_at	2.15573	7.275303	11.8021	8.87E-25	2.45E-23	45.51001	ISL1	ISL LIM homeobox 1	NM_002202
209542_x_at	2.15438	7.362778	14.40458	8.31E-33	4.45E-31	63.87348	IGF1	insulin-like growth factor 1 (somatomedin C)	M29644
235562_at	2.15196	5.925866	14.91895	2.13E-34	1.37E-32	67.51648	C3orf70	chromosome 3 open reading frame 70	AI493909
209288_s_at	2.15074	8.321874	14.9171	2.16E-34	1.39E-32	67.5034	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	AL136842
200906_s_at	2.15036	9.365558	15.92787	1.65E-37	1.44E-35	74.63796	PALLD	palladin, cytoskeletal associated protein	AK025843

236029_at	2.14939	5.001856	14.85308	3.40E-34	2.13E-32	67.05028	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	AI283093
230933_at	2.14831	5.59555	19.16227	2.78E-47	1.03E-44	96.99851	DSTN	Actin depolymerizing factor [human, fetal brain, mRNA, 1452 nt]	AA458636
232090_at	2.14817	5.349878	20.53883	2.63E-51	2.08E-48	106.2031	LOC100128178	similar to hCG2041313	AI761578
235649_at	2.14726	7.174463	15.6034	1.64E-36	1.31E-34	72.35244	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8	AW207389
228218_at	2.14648	6.094201	15.32415	1.19E-35	8.59E-34	70.38154			AI858493
228082_at	2.14466	6.576916	17.36675	6.64E-42	9.52E-40	84.69426	ASAM	adipocyte-specific adhesion molecule	BF056275
227688_at	2.14425	5.175733	20.19379	2.63E-50	1.71E-47	103.9161	LRCH2	leucine-rich repeats and calponin homology (CH) domain containing 2	AK022128
205413_at	2.14287	4.596781	19.72454	6.15E-49	3.08E-46	100.784	MPPED2	metallophosphoesterase domain containing 2	NM_001584
204731_at	2.14259	8.140312	13.88707	3.33E-31	1.55E-29	60.20552	TGFB3	transforming growth factor, beta receptor III	NM_003243
225481_at	2.13948	8.624424	14.15704	4.86E-32	2.43E-30	62.11909	FRMD6	FERM domain containing 6	AL040051
205392_s_at	2.13891	8.354795	13.42348	9.08E-30	3.75E-28	56.92149	CCL14 /// CCL15	chemokine (C-C motif) ligand 14 /// chemokine (C-C motif) ligand 15	NM_004166
204755_x_at	2.13854	5.023865	18.49653	2.65E-45	7.08E-43	92.47297	HLF	hepatic leukemia factor	M95585
226425_at	2.13853	7.626377	15.72346	7.00E-37	5.75E-35	73.19873	CLIP4	CAP-GLY domain containing linker protein family, member 4	AU144247
211555_s_at	2.13169	7.027704	18.28758	1.12E-44	2.70E-42	91.0433	GUCY1B3	guanylate cyclase 1, soluble, beta 3	AF020340
211577_s_at	2.13039	7.000245	14.33485	1.37E-32	7.18E-31	63.37936	IGF1	insulin-like growth factor 1 (somatomedin C)	M37484
226439_s_at	2.12976	5.894678	15.85866	2.69E-37	2.32E-35	74.15088	NBEA	neurobeachin	AI246710
204030_s_at	2.12836	7.148075	15.60883	1.58E-36	1.26E-34	72.39075	SCHIP1	schwannomin interacting protein 1	NM_014575
1553243_at	2.1278	6.599245	17.19036	2.28E-41	3.11E-39	83.46964	ITI5	inter-alpha (globulin) inhibitor H5	NM_032817
233364_s_at	2.125	5.153728	18.35185	7.16E-45	1.77E-42	91.4835			AK021804
208790_s_at	2.12364	7.646033	16.91989	1.51E-40	1.90E-38	81.58702	PTRF	polymerase I and transcript release factor	AF312393
203817_at	2.12284	9.144896	17.45538	3.58E-42	5.32E-40	85.30858	GUCY1B3	guanylate cyclase 1, soluble, beta 3	W93728
225567_at	2.11861	7.156806	15.98764	1.08E-37	9.62E-36	75.05841			BE207755
225987_at	2.11762	8.010855	10.99865	2.42E-22	5.31E-21	39.9445	STEAP4	STEAP family member 4	AA650281
202508_s_at	2.11689	5.427871	9.566629	4.10E-18	5.96E-17	30.2944	SNAP25	synaptosomal-associated protein, 25kDa	NM_003081
209168_at	2.11634	5.527223	15.52903	2.78E-36	2.16E-34	71.82784	GPM6B	glycoprotein M6B	AW148844
225801_at	2.11448	5.314152	16.29133	1.26E-38	1.24E-36	77.19134			AW518714
238151_at	2.11374	5.829208	23.2465	6.09E-59	4.75E-55	123.6461			BF511636
203723_at	2.11137	7.715883	19.9498	1.35E-49	7.84E-47	102.2907	ITPKB	Inositol 1,4,5-trisphosphate 3-kinase B	NM_002221
229994_at	2.11108	4.817715	19.08446	4.73E-47	1.68E-44	96.47193	LOC100190890	MRNA; cDNA DKFZp686J23256 (from clone DKFZp686J23256)	R45950
232297_at	2.10655	6.86081	15.72945	6.71E-37	5.53E-35	73.24097			AL049385
223843_at	2.10644	5.046431	16.19039	2.57E-38	2.45E-36	76.48302	SCARA3	scavenger receptor class A, member 3	AB007830
212845_at	2.10634	8.472097	17.28995	1.13E-41	1.59E-39	84.16138	SAMD4A	sterile alpha motif domain containing 4A	AB028976
208561_at	2.10564	4.355965	22.43172	1.10E-56	3.53E-53	118.4935	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	NM_020297
225450_at	2.10443	8.418768	18.72854	5.38E-46	1.60E-43	94.05531	AMOTL1	angiomin like 1	AI433831
235944_at	2.10142	6.241419	12.58237	3.59E-27	1.19E-25	50.9807	HMCN1	hemicentin 1	BF446673
232267_at	2.10122	6.189952	14.7956	5.12E-34	3.14E-32	66.64335	GPR133	G protein-coupled receptor 133	AL162032
204834_at	2.10094	8.629075	12.13117	8.74E-26	2.60E-24	47.81085	FGL2	fibrinogen-like 2	NM_006682
212813_at	2.09873	8.767974	17.64588	9.50E-43	1.57E-40	86.62682	JAM3 /// LOC100133502	junctional adhesion molecule 3 /// hypothetical protein LOC100133502	AA149644
209550_at	2.09793	8.08996	16.28265	1.34E-38	1.32E-36	77.13043	NDN	necdin homolog (mouse)	U35139
226237_at	2.09755	8.921531	8.597407	2.27E-15	2.49E-14	24.04861			AL359062
204052_s_at	2.0973	6.786275	7.369041	4.34E-12	3.20E-11	16.5999	SFRP4	secreted frizzled-related protein 4	NM_003014

226587_at	2.09138	5.444632	16.09638	5.00E-38	4.60E-36	75.82272	SNRPN	small nuclear ribonucleoprotein polypeptide N	BE783065
218974_at	2.09086	7.50075	13.09242	9.59E-29	3.61E-27	54.57951	SOBP	sine oculis binding protein homolog (Drosophila)	NM_018013
227762_at	2.09043	6.651702	15.31972	1.23E-35	8.85E-34	70.3502			AW244016
230179_at	2.08862	7.029039	16.43029	4.73E-39	4.96E-37	78.16545	LOC285812	hypothetical protein LOC285812	N52572
230264_s_at	2.08555	9.130308	18.49008	2.77E-45	7.37E-43	92.42888	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	AA551090
218162_at	2.08553	8.830345	14.71327	9.21E-34	5.49E-32	66.06041	OLFML3	olfactomedin-like 3	NM_020190
204570_at	2.08436	8.51524	18.53343	2.05E-45	5.63E-43	92.72494	COX7A1	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)	NM_001864
52837_at	2.08388	5.280874	14.63176	1.65E-33	9.52E-32	65.48306	LL22NC03-75B3.6	KIAA1644 protein	AL047020
244741_s_at	2.08346	6.213837	18.1528	2.83E-44	6.23E-42	90.11887	MGC9913	hypothetical protein MGC9913	BE855713
228739_at	2.08269	6.181986	14.60589	1.98E-33	1.14E-31	65.29987	CYS1	cystin 1	AI139413
226338_at	2.07797	6.926371	18.11964	3.56E-44	7.65E-42	89.89117	TMEM55A	transmembrane protein 55A	AA604382
204964_s_at	2.07758	7.627294	16.11475	4.39E-38	4.06E-36	75.9518	SSPN	sarcospan (Kras oncogene-associated gene)	NM_005086
203088_at	2.07629	7.89023	14.97718	1.41E-34	9.20E-33	67.92857	FBLN5	fibulin 5	NM_006329
206101_at	2.07531	7.720959	13.83427	4.85E-31	2.24E-29	59.83138	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	NM_001393
226731_at	2.07381	8.154958	18.51562	2.32E-45	6.27E-43	92.60336	PELO	Pelota major mRNA, complete cds; alternatively spliced	AA156873
209466_x_at	2.07187	7.939207	16.98391	9.66E-41	1.24E-38	82.03316	PTN	pleiotrophin	M57399
222918_at	2.07149	6.140241	17.01887	7.56E-41	9.74E-39	82.2766	RAB9B	RAB9B, member RAS oncogene family	AL139228
219728_at	2.06678	4.362536	15.61	1.56E-36	1.25E-34	72.39897	MYOT	myotilin	NM_006790
203688_at	2.06559	8.011148	16.88286	1.96E-40	2.45E-38	81.32884	PKD2	polycystic kidney disease 2 (autosomal dominant)	NM_000297
204688_at	2.06302	8.204453	13.6615	1.66E-30	7.27E-29	58.60717	SGCE	sarcoglycan, epsilon	NM_003919
227646_at	2.05922	7.327237	12.58489	3.53E-27	1.17E-25	50.9984	EBF1	early B-cell factor 1	BG435302
224811_at	2.05842	10.48375	19.54359	2.09E-48	9.59E-46	99.56951			BF112093
220751_s_at	2.05834	7.100044	18.42867	4.22E-45	1.07E-42	92.00911	C5orf4	chromosome 5 open reading frame 4	NM_016348
228813_at	2.05462	6.516549	19.82164	3.20E-49	1.76E-46	101.4341	HDAC4	histone deacetylase 4	AW206037
236600_at	2.05418	5.728162	18.68581	7.21E-46	2.10E-43	93.76426	SPG20	spastic paraplegia 20 (Troyer syndrome)	AI651603
224550_s_at	2.05378	6.735335	15.16161	3.78E-35	2.61E-33	69.23289	MRV1	murine retrovirus integration site 1 homolog	AF081250
226279_at	2.05231	9.406555	14.95071	1.70E-34	1.10E-32	67.74122	PRSS23	protease, serine, 23	AW471145
204051_s_at	2.04927	8.269934	6.906175	6.37E-11	3.97E-10	13.96064	SFRP4	secreted frizzled-related protein 4	AW089415
205883_at	2.04808	5.901935	13.82854	5.06E-31	2.32E-29	59.79074	ZBTB16	zinc finger and BTB domain containing 16	NM_006006
238484_s_at	2.04784	4.342611	21.73384	1.00E-54	1.77E-51	114.0135			AL566553
213675_at	2.04771	7.353574	21.34643	1.26E-53	1.64E-50	111.5005			W61005
219213_at	2.04516	7.427503	15.55851	2.25E-36	1.77E-34	72.03583	JAM2	junctional adhesion molecule 2	NM_021219
205612_at	2.04502	4.996095	10.78181	1.08E-21	2.24E-20	38.45803	MMRN1	multimerin 1	NM_007351
203295_s_at	2.04379	5.710222	16.67214	8.62E-40	1.00E-37	79.85774	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	AW440492
209656_s_at	2.04197	9.819903	13.43613	8.30E-30	3.44E-28	57.01102	TMEM47	transmembrane protein 47	AL136550
226625_at	2.0415	8.650198	14.47495	5.03E-33	2.75E-31	64.37215	TGFR3	transforming growth factor, beta receptor III	AW193698
242033_at	2.0405	4.397364	22.35794	1.77E-56	5.08E-53	118.0227	RNF180	ring finger protein 180	BE672684
212609_s_at	2.03822	7.70709	20.51294	3.12E-51	2.40E-48	106.0319	AKT3	Clones 23920 and 23921 mRNA sequence	U79271
226885_at	2.03797	6.144623	16.65394	9.80E-40	1.13E-37	79.73049			AI743880
244370_at	2.0339	4.121982	15.12003	5.08E-35	3.45E-33	68.93894	KIAA2022	KIAA2022	AI743137
238583_at	2.03292	6.981336	20.33477	1.02E-50	7.45E-48	104.8522	MSRB3	methionine sulfoxide reductase B3	BG023974
1558019_at	2.03261	4.97305	18.91549	1.50E-46	4.96E-44	95.32632			BC020911
225464_at	2.03112	8.447321	14.46519	5.39E-33	2.94E-31	64.303	FRMD6	FERM domain containing 6	N30138
1554966_a_at	2.02865	9.101166	14.86595	3.10E-34	1.96E-32	67.1414	FILIP1L	filamin A interacting protein 1-like	AF329092
204471_at	2.02715	4.520331	14.16848	4.48E-32	2.25E-30	62.20015	GAP43	growth associated protein 43	NM_002045
207177_at	2.02445	5.094745	17.97764	9.50E-44	1.89E-41	88.91489	PTGFR	prostaglandin F receptor (FP)	NM_000959
225524_at	2.02358	9.439136	15.78963	4.38E-37	3.68E-35	73.66487	ANTXR2	anthrax toxin receptor 2	AU152178

209437_s_at	2.0235	7.221026	17.4067	5.02E-42	7.30E-40	84.97127	SPON1	spondin 1, extracellular matrix protein	AB051390
209047_at	2.0221	10.02956	11.60884	3.44E-24	9.03E-23	44.16394	AQP1	aquaporin 1 (Colton blood group)	AL518391
215303_at	2.02121	4.498495	19.26173	1.41E-47	5.51E-45	97.67063	DCLK1	doublecortin-like kinase 1	BE046461
204365_s_at	2.02038	7.018741	12.66799	1.96E-27	6.62E-26	51.58383	REEP1	receptor accessory protein 1	NM_022912
203865_s_at	2.01939	6.843373	19.41722	4.92E-48	2.17E-45	98.71921	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	NM_015833
205079_s_at	2.01937	7.221546	21.96237	2.27E-55	4.78E-52	115.4872	MPDZ	multiple PDZ domain protein	NM_003829
209655_s_at	2.01816	8.291026	15.13572	4.55E-35	3.11E-33	69.04991	TMEM47	transmembrane protein 47	AI803181
205578_at	2.01638	5.812464	18.09947	4.09E-44	8.65E-42	89.75261	ROR2	receptor tyrosine kinase-like orphan receptor 2	NM_004560
207453_s_at	2.01495	5.591444	16.14517	3.54E-38	3.30E-36	76.16549	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	NM_012266
231166_at	2.0148	6.631636	10.16551	7.34E-20	1.27E-18	34.27883	GPR155	G protein-coupled receptor 155	AI733474
235518_at	2.01425	7.228049	15.83545	3.17E-37	2.70E-35	73.98753	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	AI741439
211006_s_at	2.01243	4.719612	16.15761	3.24E-38	3.06E-36	76.25281	KCNB1	potassium voltage-gated channel, Shab-related subfamily, member 1	L02840
215039_at	2.01077	6.278051	17.05881	5.72E-41	7.45E-39	82.55466	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	AK002179
202157_s_at	2.01056	9.163126	15.92344	1.70E-37	1.49E-35	74.60679	CUGBP2	CUG triplet repeat, RNA binding protein 2	U69546
220272_at	2.00971	6.478678	19.05333	5.84E-47	2.01E-44	96.26109	BNC2	basonuclin 2	NM_017637
220765_s_at	2.00548	7.643692	19.21731	1.91E-47	7.25E-45	97.37057	LIMS2	LIM and senescent cell antigen-like domains 2	NM_017980
231721_at	2.00414	5.100337	16.99303	9.06E-41	1.16E-38	82.09665	JAM3	junctional adhesion molecule 3	AF356518
227875_at	2.00272	6.249685	11.51839	6.49E-24	1.65E-22	43.5354	KLHL13	kelch-like 13 (Drosophila)	AB037730
200621_at	2.00168	11.44208	17.77576	3.85E-43	6.87E-41	87.5238	CSRP1	cysteine and glycine-rich protein 1	NM_004078
212793_at	2.00003	7.138155	20.79185	4.89E-52	4.17E-49	107.8711	DAAM2	dishevelled associated activator of morphogenesis 2	BF513244
228554_at	1.99821	5.71365	19.51676	2.51E-48	1.13E-45	99.38911	PGR	progesterone receptor	AI137566
201116_s_at	1.99815	8.527008	10.79841	9.66E-22	2.01E-20	38.5716	CPE	carboxypeptidase E	AI922855
203787_at	1.99791	7.497864	16.60511	1.38E-39	1.56E-37	79.38909	SSBP2	single-stranded DNA binding protein 2	NM_012446
37996_s_at	1.99762	7.028679	17.73127	5.25E-43	9.18E-41	87.21673	DMPK	dystrophin myotonic-protein kinase	L08835
201958_s_at	1.99624	5.860035	17.79639	3.34E-43	6.16E-41	87.66611	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	NM_002481
202156_s_at	1.99605	6.933435	17.31697	9.40E-42	1.33E-39	84.34888	CUGBP2	CUG triplet repeat, RNA binding protein 2	N36839
215146_s_at	1.99598	6.486452	18.2587	1.36E-44	3.18E-42	90.84533	TTC28	tetratricopeptide repeat domain 28	AB028966
222880_at	1.99534	5.791828	17.4406	3.97E-42	5.85E-40	85.2062	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AF135794
209685_s_at	1.99272	7.321429	13.80337	6.05E-31	2.76E-29	59.61237	PRKCB	protein kinase C, beta	M13975
208451_s_at	1.99266	9.354169	13.72861	1.03E-30	4.60E-29	59.0826	C4A /// C4B	complement component 4A (Rodgers blood group) /// complement component 4B (Chido blood group)	NM_000592
228396_at	1.98865	8.185601	19.92155	1.63E-49	9.38E-47	102.1021	PRKG1	protein kinase, cGMP-dependent, type I	AW274503
229976_at	1.98812	5.236657	11.82957	7.31E-25	2.03E-23	45.70168	MORN5	MORN repeat containing 5	AW188190
226769_at	1.98809	7.783425	13.04093	1.38E-28	5.14E-27	54.21561	FIBIN	fin bud initiation factor homolog (zebrafish)	AI802391
227816_at	1.98631	6.273358	15.17929	3.34E-35	2.31E-33	69.3579	NTN1	netrin 1	BF591483
211819_s_at	1.98541	6.380668	18.10655	3.89E-44	8.34E-42	89.80123	SORBS1	sorbin and SH3 domain containing 1	AF136381
205952_at	1.98377	5.642393	11.73101	1.46E-24	3.94E-23	45.01442	KCNK3	potassium channel, subfamily K, member 3	NM_002246
226677_at	1.98321	6.126227	12.86869	4.71E-28	1.67E-26	52.99925	ZNF521	zinc finger protein 521	AF141339
235318_at	1.9826	6.326813	13.42789	8.80E-30	3.64E-28	56.95269	FBN1	fibrillin 1	AW955612
213451_x_at	1.9819	8.145232	13.84515	4.49E-31	2.08E-29	59.90844	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	BE044614

227326_at	1.98091	8.001405	20.63269	1.41E-51	1.18E-48	106.8227	MXRA7	matrix-remodelling associated 7	BE966768
218901_at	1.97513	8.040376	14.67831	1.18E-33	6.95E-32	65.81283	PLSCR4	phospholipid scramblase 4	NM_020353
213001_at	1.97498	8.855443	14.34256	1.29E-32	6.81E-31	63.43395	ANGPTL2	angiotensin-like 2	AF007150
225728_at	1.97447	8.47772	9.752882	1.18E-18	1.81E-17	31.5245	SORBS2	sorbin and SH3 domain containing 2	AI659533
205802_at	1.974	6.472804	19.1207	3.69E-47	1.32E-44	96.71726	TRPC1	transient receptor potential cation channel, subfamily C, member 1	NM_003304
205794_s_at	1.97391	5.451298	15.31616	1.26E-35	9.06E-34	70.32507	NOVA1	neuro-oncological ventral antigen 1	NM_002515
223492_s_at	1.97373	7.931942	17.78505	3.61E-43	6.54E-41	87.58785	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	BC004958
212414_s_at	1.97286	8.012936	15.31292	1.29E-35	9.26E-34	70.30218	N-PAC /// SEPT6	cytokine-like nuclear factor n-pac /// septin 6	D50918
203300_x_at	1.97184	8.564427	18.00454	7.88E-44	1.60E-41	89.09999	AP152	adaptor-related protein complex 1, sigma 2 subunit	NM_003916
236576_at	1.97121	4.271086	14.96986	1.48E-34	9.67E-33	67.87677			N63005
204035_at	1.97113	5.864655	10.04151	1.70E-19	2.85E-18	33.44711	SCG2	secretogranin II (chromogranin C)	NM_003469
204082_at	1.96818	8.45229	17.78157	3.70E-43	6.64E-41	87.56388	PBX3	pre-B-cell leukemia homeobox 3	NM_006195
226545_at	1.96727	7.34211	12.21119	4.97E-26	1.50E-24	48.3719	CD109	CD109 molecule	AL110152
232235_at	1.96698	4.854813	15.48094	3.91E-36	2.99E-34	71.48851	DSEL	dermatan sulfate epimerase-like	AK021539
214930_at	1.9661	5.133346	15.51064	3.17E-36	2.45E-34	71.69811	SLITRK5	SLIT and NTRK-like family, member 5	AW449813
219064_at	1.96603	7.603774	14.90787	2.30E-34	1.47E-32	67.43811	ITIH5	inter-alpha (globulin) inhibitor H5	NM_030569
237301_at	1.96439	5.392394	15.77729	4.78E-37	4.00E-35	73.57793			BF433570
202133_at	1.96275	10.62745	14.72022	8.76E-34	5.25E-32	66.10961	WWTR1	WW domain containing transcription regulator 1	BF674349
213547_at	1.96192	6.615001	18.3713	6.26E-45	1.57E-42	91.61661	CAND2	cullin-associated and neddylation-dissociated 2 (putative)	AB014567
210869_s_at	1.96184	9.362806	15.58713	1.84E-36	1.46E-34	72.23771	MCAM	melanoma cell adhesion molecule	M29277
235371_at	1.96032	7.115058	10.57634	4.45E-21	8.75E-20	37.05685	GLT8D4	glycosyltransferase 8 domain containing 4	AI452595
225243_s_at	1.95897	9.867597	16.03288	7.83E-38	7.04E-36	75.37648	SLMAP	sarcolemma associated protein	AB046821
205935_at	1.95701	8.907335	14.23191	2.85E-32	1.46E-30	62.64972	FOXF1	forkhead box F1	NM_001451
213156_at	1.95586	8.238023	14.9753	1.42E-34	9.32E-33	67.91523			BG251521
211734_s_at	1.95559	5.383309	11.35404	2.05E-23	4.94E-22	42.39596	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	BC005912
228310_at	1.9553	7.040939	14.9602	1.59E-34	1.03E-32	67.80843	ENAH	enabled homolog (Drosophila)	BF223300
209169_at	1.95059	5.04134	14.5353	3.27E-33	1.83E-31	64.79976	GPM68	glycoprotein M68	N63576
228548_at	1.9476	7.226439	19.15294	2.96E-47	1.09E-44	96.93539			AU126086
205382_s_at	1.94605	9.054374	9.549063	4.61E-18	6.67E-17	30.17883	CFD	complement factor D (adipsin)	NM_001928
212607_at	1.94551	8.098546	17.14885	3.04E-41	4.12E-39	83.18105	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	N32526
222379_at	1.94548	7.007771	16.33195	9.46E-39	9.57E-37	77.47617	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	AI002715
205226_at	1.9451	6.572645	12.0784	1.27E-25	3.73E-24	47.44122	PDGFRL	platelet-derived growth factor receptor-like	NM_006207
213764_s_at	1.94442	7.081848	8.057157	6.76E-14	6.27E-13	20.69983	MFAP5	microfibrillar associated protein 5	AW665892
238577_s_at	1.94399	6.613232	17.69998	6.52E-43	1.11E-40	87.00062	TSHZ2	Cell growth-inhibiting protein 7	AA628481
239847_at	1.94384	5.910823	14.68101	1.16E-33	6.83E-32	65.83192			AA631103
216333_x_at	1.94337	8.064076	13.63107	2.07E-30	8.98E-29	58.39161	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	M25813
231031_at	1.94321	6.197454	19.31203	1.00E-47	4.09E-45	98.01015	KGFLP2	keratinocyte growth factor-like protein 2	AI761573
230071_at	1.94206	7.224034	14.76287	6.47E-34	3.92E-32	66.4116	SEPT11	septin 11	AI333326
211896_s_at	1.94161	11.09971	11.18472	6.65E-23	1.54E-21	41.22577	DCN	decorin	AF138302
204400_at	1.94104	6.355471	17.49915	2.64E-42	4.01E-40	85.61175	EF5	embryonal Fyn-associated substrate	NM_005864
229518_at	1.93949	6.396388	12.85746	5.10E-28	1.81E-26	52.91998	FAM46B	family with sequence similarity 46, member B	AA531023

204163_at	1.93829	7.999238	16.10651	4.65E-38	4.29E-36	75.8939	EMILIN1	elastin microfibril interfacier 1	NM_007046
204979_s_at	1.93694	6.473579	17.71404	5.91E-43	1.03E-40	87.09776	SH3BGR	SH3 domain binding glutamic acid-rich protein	NM_007341
212135_s_at	1.93673	9.281703	18.79519	3.41E-46	1.04E-43	94.50881	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	AW517686
204591_at	1.93252	5.42971	12.84784	5.46E-28	1.93E-26	52.85211	CHL1	cell adhesion molecule with homology to L1CAM (close homolog of L1)	NM_006614
242245_at	1.9303	6.183819	12.01973	1.92E-25	5.56E-24	47.03052			N90719
222453_at	1.93001	9.960846	12.05779	1.47E-25	4.29E-24	47.29691	CYBRD1	cytochrome b reductase 1	AL136693
222486_s_at	1.92999	6.390629	11.81053	8.36E-25	2.31E-23	45.56885	ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif, 1	AF060152
212993_at	1.92996	8.460915	17.50716	2.49E-42	3.82E-40	85.66721	NACC2	NACC family member 2, BEN and BTB (POZ) domain containing	AA114166
200907_s_at	1.92867	10.99128	16.14318	3.59E-38	3.34E-36	76.1515	PALLD	palladin, cytoskeletal associated protein	AU157932
205280_at	1.92808	4.710197	15.39941	6.98E-36	5.18E-34	70.91305	GLRB	glycine receptor, beta	NM_000824
223393_s_at	1.92767	6.870743	18.76611	4.16E-46	1.25E-43	94.31101	TSHZ3	teashirt zinc finger homeobox 3	AL136805
212148_at	1.92528	8.692131	12.38638	1.44E-26	4.55E-25	49.60195	PBX1	pre-B-cell leukemia homeobox 1	AL049381
205384_at	1.92389	6.993623	17.99739	8.28E-44	1.67E-41	89.05078	FXD1	FXD domain containing ion transport regulator 1	NM_005031
218625_at	1.92374	6.492185	11.63739	2.82E-24	7.45E-23	44.36256	NRN1	neurtin 1	NM_016588
227183_at	1.92353	6.610457	16.53411	2.28E-39	2.48E-37	78.89234	LOC72826	hypothetical protein LOC728264	AI417267
230413_s_at	1.92347	6.405758	16.90391	1.69E-40	2.12E-38	81.47564			AA480858
229302_at	1.92278	5.37344	14.76936	6.17E-34	3.75E-32	66.45758	TMEM178	transmembrane protein 178	AA058832
202821_s_at	1.92267	8.469827	15.42631	5.76E-36	4.31E-34	71.10291	LPP	LIM domain containing preferred translocation partner in lipoma	AL044018
205880_at	1.92193	6.0572	16.17442	2.88E-38	2.73E-36	76.37089	PRKD1	protein kinase D1	NM_002742
232125_at	1.92126	6.041455	16.51598	2.59E-39	2.81E-37	78.76545			AU147419
228376_at	1.91849	7.281996	15.22508	2.41E-35	1.69E-33	69.68154	GGTA1	glycoprotein, alpha-galactosyltransferase 1	AI972498
205303_at	1.91399	7.14248	15.55839	2.26E-36	1.77E-34	72.03497	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	BF514158
201559_s_at	1.91188	8.294229	14.67272	1.23E-33	7.22E-32	65.77324	CLIC4	chloride intracellular channel 4	AF109196
205083_at	1.90924	6.250309	11.38749	1.62E-23	3.96E-22	42.62761	AOX1	aldehyde oxidase 1	NM_001159
209447_at	1.90665	7.406953	16.46693	3.65E-39	3.89E-37	78.42204	SYNE1	spectrin repeat containing, nuclear envelope 1	AF043290
1558102_at	1.90622	6.200105	15.36408	8.97E-36	6.58E-34	70.66353			AK055438
208792_s_at	1.90532	10.09796	9.042001	1.30E-16	1.62E-15	26.87899	CLU	clusterin	M25915
228176_at	1.90441	8.48384	13.10572	8.72E-29	3.29E-27	54.6735	S1PR3	sphingosine-1-phosphate receptor 3	AA534817
205110_s_at	1.90331	6.514316	10.49895	7.57E-21	1.45E-19	36.53105	FGF13	fibroblast growth factor 13	NM_004114
213247_at	1.90253	7.544454	16.29845	1.20E-38	1.19E-36	77.24127	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	AA716107
1561615_s_at	1.90199	5.914474	15.69285	8.70E-37	7.08E-35	72.98301	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	Y12885
230750_at	1.90065	5.746726	17.78112	3.71E-43	6.64E-41	87.56076			AI290475
212526_at	1.89853	7.534005	14.62584	1.72E-33	9.90E-32	65.44115	SPG20	spastic paraplegia 20 (Troyer syndrome)	AK002207
228370_at	1.8981	6.298642	13.05068	1.29E-28	4.81E-27	54.28455	SNRPN	small nuclear ribonucleoprotein polypeptide N	BF114870
209156_s_at	1.89752	9.80903	13.19716	4.55E-29	1.77E-27	55.32002	COL6A2	collagen, type VI, alpha 2	AY029208
206093_x_at	1.89715	8.076512	13.61638	2.30E-30	9.91E-29	58.2875	TNXA /// TNXB	tenascin XA pseudogene /// tenascin XB	NM_007116
218312_s_at	1.89611	8.008638	12.41494	1.18E-26	3.76E-25	49.80269	ZSCAN18	zinc finger and SCAN domain containing 18	NM_023926
228949_at	1.89467	8.753389	13.24581	3.22E-29	1.27E-27	55.66415	GPR177	G protein-coupled receptor 177	AL534095
230309_at	1.89294	5.003096	18.51764	2.29E-45	6.22E-43	92.61711			BE876610
225803_at	1.89291	8.44116	13.87972	3.51E-31	1.63E-29	60.15343	FBXO32	F-box protein 32	AW006123
224061_at	1.89276	7.050228	17.2356	1.66E-41	2.29E-39	83.78397	INMT	indolethylamine N-methyltransferase	AF128846

219440_at	1.8927	7.298415	13.66789	1.59E-30	6.96E-29	58.65243	RAI2	retinoic acid induced 2	NM_021785
228062_at	1.89255	6.598167	11.73842	1.39E-24	3.75E-23	45.066	NAP1L5	nucleosome assembly protein 1-like 5	AW025330
212843_at	1.8924	5.794722	10.78063	1.09E-21	2.26E-20	38.45003	NCAM1	neural cell adhesion molecule 1	AA126505
213800_at	1.89034	8.41733	10.17354	6.95E-20	1.21E-18	34.33285	CFH	complement factor H	X04697
205422_s_at	1.88843	7.110828	7.595879	1.12E-12	8.94E-12	17.92932	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	NM_004791
226018_at	1.88839	6.46355	14.0312	1.19E-31	5.80E-30	61.22712	C7orf41	chromosome 7 open reading frame 41	W73230
211538_s_at	1.88811	7.865833	10.86336	6.17E-22	1.31E-20	39.01617	HSPA2	heat shock 70kDa protein 2	U56725
205960_at	1.88726	6.058411	12.10154	1.08E-25	3.18E-24	47.6033	PDK4	pyruvate dehydrogenase kinase, isozyme 4	NM_002612
210762_s_at	1.88705	8.786834	14.44905	6.05E-33	3.29E-31	64.18861	OLC1	deleted in liver cancer 1	AF026219
215014_at	1.88568	5.015596	15.12893	4.77E-35	3.26E-33	69.00186	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	AL512727
208791_at	1.88286	9.972756	8.864199	4.10E-16	4.87E-15	25.73955	CLU	clusterin	M25915
210036_s_at	1.88011	7.868749	12.81602	6.84E-28	2.40E-26	52.62758	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	AB044806
218651_s_at	1.87918	6.886755	15.61915	1.47E-36	1.18E-34	72.46349	LARP6	La ribonucleoprotein domain family, member 6	NM_018357
207542_s_at	1.87875	9.000913	13.27093	2.69E-29	1.07E-27	55.84184	AQP1	aquaporin 1 (Colton blood group)	NM_000385
227565_at	1.87698	7.12043	14.76598	6.32E-34	3.84E-32	66.43363			BE501881
206757_at	1.87672	5.137631	18.54939	1.84E-45	5.07E-43	92.83393	PDE5A	phosphodiesterase 5A, cGMP-specific	NM_001083
229480_at	1.87506	4.564609	22.43804	1.06E-56	3.53E-53	118.5338			AI341053
238455_at	1.87444	6.653681	11.18652	6.57E-23	1.52E-21	41.23819			AA329676
226069_at	1.87429	6.048127	15.35611	9.49E-36	6.95E-34	70.60728	PRICKLE1	prickle homolog 1 (Drosophila)	AA404269
222162_s_at	1.8738	9.187989	11.29093	3.18E-23	7.56E-22	41.95933	ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif, 1	AK023795
227376_at	1.87267	6.917677	17.84371	2.40E-43	4.51E-41	87.99239	GLI3	GLI-Kruppel family member GLI3	AW021102
226713_at	1.8725	7.702775	19.30798	1.03E-47	4.18E-45	97.98283	CCDC50	coiled-coil domain containing 50	AI247881
221796_at	1.87225	5.234314	9.301025	2.38E-17	3.18E-16	28.55573	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	AA707199
220979_s_at	1.8704	6.012682	9.775688	1.02E-18	1.57E-17	31.67571	ST6GALNA5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	NM_030965
209616_s_at	1.86807	7.862933	9.208496	4.36E-17	5.69E-16	27.95455	CES1	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	S73751
202158_s_at	1.86433	7.245029	16.29111	1.26E-38	1.24E-36	77.18976	CUGBP2	CUG triplet repeat, RNA binding protein 2	NM_006561
202965_s_at	1.86424	7.470814	7.894567	1.84E-13	1.62E-12	19.71343	CAPN6	calpain 6	NM_014289
203000_at	1.86308	6.056431	9.056223	1.18E-16	1.48E-15	26.97055	STMN2	stathmin-like 2	BF967657
213058_at	1.86264	6.999383	18.17292	2.46E-44	5.49E-42	90.25694	TTC28	tetratricopeptide repeat domain 28	AL033538
218502_s_at	1.86256	6.729833	14.47295	5.10E-33	2.79E-31	64.35802	TRPS1	trichorhinophalangeal syndrome I	NM_014112
209526_s_at	1.86099	7.848592	13.23294	3.53E-29	1.39E-27	55.57309	HDGFRP3	hepatoma-derived growth factor, related protein 3	AB029156
210302_s_at	1.86003	4.289681	13.33106	1.75E-29	7.10E-28	56.2673	MAB21L2	mab-21-like 2 (C. elegans)	AF262032
209200_at	1.85331	7.96192	15.4843	3.82E-36	2.92E-34	71.51226	MEF2C	myocyte enhancer factor 2C	AL536517
212413_at	1.85186	5.906884	17.04287	6.39E-41	8.31E-39	82.44376	SEPT6	septin 6	D50918
229404_at	1.85149	6.408464	15.59218	1.78E-36	1.41E-34	72.2733	TWIST2	twist homolog 2 (Drosophila)	AI086614
226806_s_at	1.85108	8.625037	14.36333	1.12E-32	5.91E-31	63.5812			AW022607
205051_s_at	1.85096	7.662744	11.55052	5.18E-24	1.34E-22	43.75859	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	NM_000222
211535_s_at	1.84978	8.468962	18.58433	1.45E-45	4.07E-43	93.07238	FGFR1	fibroblast growth factor receptor 1	M60485
201787_at	1.84851	8.419471	10.82478	8.05E-22	1.69E-20	38.752	FBLN1 /// LOC100133843	fibulin 1 /// similar to Fibulin 1	NM_001996

235631_at	1.84753	5.715423	19.47123	3.41E-48	1.53E-45	99.08287	DDR2	CDNA FLJ35055 fis, clone OCBBF2018563	AA545764
218918_at	1.84639	7.260773	14.72104	8.71E-34	5.22E-32	66.11539	MAN1C1	mannosidase, alpha, class 1C, member 1	NM_020379
209524_at	1.84635	7.987977	13.30067	2.18E-29	8.74E-28	56.05228	HDGFRP3	hepatoma-derived growth factor, related protein 3	AK001280
200897_s_at	1.84622	11.31088	15.65386	1.15E-36	9.29E-35	72.70825	PALLD	palladin, cytoskeletal associated protein	NM_016081
212136_at	1.84557	9.239403	18.70362	6.38E-46	1.86E-43	93.88562	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	AW517686
232060_at	1.84547	7.200012	10.85132	6.71E-22	1.41E-20	38.93374	ROR1	receptor tyrosine kinase-like orphan receptor 1	AK000776
204472_at	1.84491	9.788487	13.81616	5.52E-31	2.53E-29	59.70299	GEM	GTP binding protein overexpressed in skeletal muscle	NM_005261
203404_at	1.84448	8.139985	12.2561	3.62E-26	1.11E-24	48.68694	ARMCX2	armadillo repeat containing, X-linked 2	NM_014782
238419_at	1.84433	5.140826	15.61219	1.54E-36	1.24E-34	72.41441	PHLDB2	pleckstrin homology-like domain, family B, member 2	T68150
244885_at	1.84159	4.66179	14.71723	8.95E-34	5.35E-32	66.08842			AI016316
227202_at	1.8411	3.652717	16.26023	1.57E-38	1.54E-36	76.97316	CNTN1	Contactin 2 precursor (CNTN1)	AW072790
200974_at	1.84039	12.48002	13.58707	2.83E-30	1.21E-28	58.0799	ACTA2	actin, alpha 2, smooth muscle, aorta	NM_001613
236640_at	1.8391	5.269871	19.64479	1.05E-48	5.14E-46	100.2492	LOC399959	Hypothetical gene supported by BX647608, mRNA (cDNA clone IMAGE:5270494)	AI638169
232570_s_at	1.83898	6.317178	19.01207	7.74E-47	2.63E-44	95.98151	ADAM33	ADAM metalloproteinase domain 33	AL356755
235279_at	1.83877	6.783299	22.06119	1.20E-55	2.73E-52	116.1225			AW138886
216693_x_at	1.83847	7.780386	12.99853	1.87E-28	6.87E-27	53.91605	HDGFRP3	hepatoma-derived growth factor, related protein 3	AL133102
227568_at	1.83814	6.963205	16.09508	5.04E-38	4.64E-36	75.81358	HECTD2	HECT domain containing 2	AF131793
202822_at	1.83811	10.13921	17.24621	1.54E-41	2.13E-39	83.85765	LPP	LIM domain containing preferred translocation partner in lipoma	BF221852
219093_at	1.83726	6.861232	11.47922	8.53E-24	2.15E-22	43.26351	PID1	phosphotyrosine interaction domain containing 1	NM_017933
236297_at	1.83724	6.489891	11.15364	8.26E-23	1.89E-21	41.01134			AI420817
229308_at	1.83713	5.40773	13.80389	6.03E-31	2.75E-29	59.61605			AW273796
231762_at	1.83629	4.841115	15.83792	3.11E-37	2.66E-35	74.00491	FGF10	fibroblast growth factor 10	NM_004465
226771_at	1.83539	7.882157	15.40796	6.57E-36	4.89E-34	70.9734	ATP8B2	ATPase, class I, type 8B, member 2	AB032963
228333_at	1.83398	7.0315	13.77931	7.18E-31	3.24E-29	59.44186			AI912571
213364_s_at	1.83395	7.7968	22.0907	9.91E-56	2.46E-52	116.3119	SNX1	sorting nexin 1	AI052536
209614_at	1.83383	5.725594	12.31683	2.35E-26	7.30E-25	49.1133	ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	AF153821
210987_x_at	1.83377	11.52219	16.32059	1.03E-38	1.03E-36	77.39658	TPM1	tropomyosin 1 (alpha)	M19267
203543_s_at	1.83339	8.429189	12.22124	4.63E-26	1.40E-24	48.44238	KLF9	Kruppel-like factor 9	NM_001206
213832_at	1.83322	6.524259	13.79253	6.54E-31	2.98E-29	59.53558	KCND3	potassium voltage-gated channel, Shal-related subfamily, member 3	AA530995
235468_at	1.83313	4.791746	9.882034	4.98E-19	7.92E-18	32.38243	hCG_1776007	hexaribonucleotide binding protein 3	AA531287
227082_at	1.83294	7.87346	15.01111	1.10E-34	7.32E-33	68.16861			AI760356
230291_s_at	1.83109	7.362094	12.3822	1.48E-26	4.68E-25	49.57254	NFIB	HMGIC/NFIB fusion protein (HMGIC/NFIB)	T90642
220108_at	1.83107	6.323074	16.14972	3.43E-38	3.22E-36	76.19744	GNA14	guanine nucleotide binding protein (G protein), alpha 14	NM_004297
204135_at	1.8306	9.826352	14.08968	7.85E-32	3.90E-30	61.64158	FILIP1L	filamin A interacting protein 1-like	NM_014890
228636_at	1.82941	6.332587	15.27367	1.71E-35	1.21E-33	70.02489	BHLHE22	basic helix-loop-helix family, member e22	AI134708
212914_at	1.8291	8.171489	19.21759	1.91E-47	7.25E-45	97.37251	CBX7	chromobox homolog 7	AV648364
230067_at	1.82692	5.591831	17.06255	5.57E-41	7.27E-39	82.58072	FAM124A	CDNA FLJ39045 fis, clone NT2RP7010521	AA151659
229733_s_at	1.8264	7.602793	14.1601	4.75E-32	2.38E-30	62.14077			N54506
1558103_a_at	1.8258	5.613552	17.06808	5.36E-41	7.01E-39	82.61922			AK055438
202132_at	1.82571	8.294051	15.08645	6.46E-35	4.33E-33	68.70149	WWTR1	WW domain containing transcription regulator 1	AA081084
226136_at	1.82559	7.362725	15.27177	1.73E-35	1.22E-33	70.01149	GLIPR1	GLI pathogenesis-related 1	N32834
1557080_s_at	1.82277	7.255418	8.351656	1.08E-14	1.09E-13	22.51224	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	AI753143

205518_s_at	1.82229	6.255728	14.3304	1.41E-32	7.38E-31	63.34779	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene	NM_003570
213924_at	1.82189	6.796985	16.53899	2.20E-39	2.42E-37	78.92655	MPPE1	MRNA; cDNA DKFZp686K2379 (from clone DKFZp686K2379)	BF476502
227198_at	1.82107	5.099799	10.02697	1.88E-19	3.13E-18	33.34983	AFF3	AF4/FMR2 family, member 3	AW085505
202283_at	1.82061	10.18419	11.87983	5.14E-25	1.44E-23	46.05258	SERPINF1	serpin peptidase inhibitor, clade F (alpha-2 antipiasmin, pigment epithelium derived factor), member 1	NM_002615
227550_at	1.81868	6.704863	15.69768	8.40E-37	6.85E-35	73.01706	LOC143381	hypothetical protein LOC143381	AW242720
226930_at	1.81847	6.847298	6.871432	7.76E-11	4.77E-10	13.76673	FNDC1	fibronectin type III domain containing 1	AI345957
213496_at	1.81784	5.533333	13.11285	8.29E-29	3.13E-27	54.72392	LPPR4	plasticity related gene 1	AW592563
227419_x_at	1.81703	7.298896	12.72708	1.29E-27	4.42E-26	52.00033	PLAC9	placenta-specific 9	AW964972
212509_s_at	1.81679	11.29564	16.65664	9.61E-40	1.11E-37	79.74939	MXRA7	matrix-remodelling associated 7	BF968134
220432_s_at	1.81493	4.929094	11.93575	3.47E-25	9.86E-24	46.44325	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	NM_016593
225817_at	1.81464	6.82222	11.79928	9.05E-25	2.49E-23	45.49038	CGNL1	cingulin-like 1	AB051536
227874_at	1.81393	6.893354	13.97255	1.81E-31	8.66E-30	60.81138	EMCN	CDNA FLJ52983 complete cds, highly similar to Endomucin precursor	AI635774
227340_s_at	1.81305	6.903052	12.54811	4.58E-27	1.51E-25	50.73946	RGMB	RGM domain family, member B	AL117590
202242_at	1.81067	7.545106	10.4246	1.26E-20	2.36E-19	36.02698	TSPAN7	tetraspanin 7	NM_004615
218518_at	1.81038	7.823993	18.10139	4.03E-44	8.57E-42	89.76577	FAM13B1	family with sequence similarity 13, member B1	NM_016603
238451_at	1.80961	5.791423	10.82515	8.03E-22	1.68E-20	38.75455	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	BF693302
1557938_s_at	1.80883	8.514623	17.52051	2.27E-42	3.53E-40	85.75963	PTRF	polymerase I and transcript release factor	AL545542
203813_s_at	1.80698	6.71783	13.2901	2.35E-29	9.40E-28	55.97748	SLIT3	slit homolog 3 (Drosophila)	NM_003062
235979_at	1.80576	4.952314	13.6661	1.61E-30	7.04E-29	58.63975	C7	complement component 7	AI697588
235561_at	1.80541	4.923271	16.14109	3.64E-38	3.38E-36	76.13679			T16544
1558680_s_at	1.80476	5.637438	16.23215	1.91E-38	1.85E-36	76.77612	PDE1A	phosphodiesterase 1A, calmodulin-dependent	BQ894022
209074_s_at	1.80255	7.226982	11.45431	1.02E-23	2.53E-22	43.09075	FAM107A	family with sequence similarity 107, member A	AL050264
223749_at	1.79782	6.146709	17.59931	1.31E-42	2.13E-40	86.30484	C1QTNF2	C1q and tumor necrosis factor related protein 2	AF329836
226522_at	1.79778	7.829595	16.14698	3.49E-38	3.27E-36	76.1782	PODN	podocan	AW015571
202729_s_at	1.79728	9.637224	12.83598	5.94E-28	2.10E-26	52.76845	LTBP1	latent transforming growth factor beta binding protein 1	NM_000627
226402_at	1.79728	6.240739	15.61522	1.51E-36	1.21E-34	72.43576	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	AK026498
235051_at	1.79724	6.309785	18.46725	3.24E-45	8.34E-43	92.27285	CCDC50	coiled-coil domain containing 50	BF696931
226492_at	1.79669	6.053945	11.56289	4.75E-24	1.23E-22	43.84453	SEMA6D	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	AL036088
203485_at	1.79575	5.858706	10.54413	5.55E-21	1.08E-19	36.83788	RTN1	reticulin 1	NM_021136
228414_at	1.79522	4.257139	16.05359	6.76E-38	6.14E-36	75.52206	KCNMA1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	AI832576
212358_at	1.79371	7.864308	19.12319	3.63E-47	1.31E-44	96.73415	CLIP3	CAP-GLY domain containing linker protein 3	AL117468
213765_at	1.79279	7.012889	7.776616	3.77E-13	3.19E-12	19.00446	MFAP5	microfibrillar associated protein 5	AW665892
209785_s_at	1.79269	6.965452	13.76937	7.71E-31	3.47E-29	59.37146	PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)	AF065214
219436_s_at	1.78901	6.66658	13.26796	2.75E-29	1.10E-27	55.82086	EMCN	endomucin	NM_016242
210072_at	1.78811	7.922631	7.015712	3.40E-11	2.22E-10	14.57595	CCL19	chemokine (C-C motif) ligand 19	U88321
211340_s_at	1.78798	8.510748	14.65409	1.40E-33	8.19E-32	65.64128	MCAM	melanoma cell adhesion molecule	M28882
209318_x_at	1.7859	8.239753	11.92251	3.80E-25	1.08E-23	46.3507	PLAGL1	pleiomorphic adenoma gene-like 1	BG547855

214428_x_at	1.78302	9.302636	13.67932	1.47E-30	6.44E-29	58.73338	C4A /// C4B	complement component 4A (Rodgers blood group) /// complement component 4B (Chido blood group)	K02403
204042_at	1.78299	7.022843	10.39603	1.53E-20	2.83E-19	35.83358	WASF3	WAS protein family, member 3	AB020707
224975_at	1.7826	8.320978	15.24031	2.16E-35	1.52E-33	69.7892	NFIA	nuclear factor I/A	AB037860
233547_x_at	1.78248	4.648049	17.90755	1.54E-43	2.96E-41	88.43231	PDE1A	phosphodiesterase 1A, calmodulin- dependent	N53248
228546_at	1.78137	4.525945	12.22652	4.46E-26	1.36E-24	48.47942	DPP6	dipeptidyl-peptidase 6	AW071705
203370_s_at	1.78078	7.597217	15.54698	2.45E-36	1.91E-34	71.95448	PDLM7	PDZ and LIM domain 7 (enigma)	NM_005451
207977_s_at	1.77923	6.585707	11.79673	9.21E-25	2.53E-23	45.47256	DPT	dermatopontin	NM_001937
205200_at	1.77893	8.41633	10.25987	3.87E-20	6.88E-19	34.91393	CLEC3B	C-type lectin domain family 3, member B	NM_003278
208016_s_at	1.77622	4.849476	16.3056	1.14E-38	1.14E-36	77.2914	AGTR1	angiotensin II receptor, type 1	NM_004835
226435_at	1.7754	6.575532	11.71934	1.59E-24	4.27E-23	44.93307	PAPLN	papilin, proteoglycan-like sulfated glycoprotein	AU145309
205304_s_at	1.77443	6.92417	16.32856	9.69E-39	9.78E-37	77.45246	KCNJ8	potassium inwardly-rectifying channel, subfamily J, member 8	NM_004982
226865_at	1.77397	7.896279	11.57109	4.49E-24	1.17E-22	43.90153			AW130600
216840_s_at	1.77358	7.157124	15.47824	3.99E-36	3.04E-34	71.4695	LAMA2	laminin, alpha 2	AK026829
213519_s_at	1.77158	6.89754	14.93377	1.91E-34	1.24E-32	67.62137	LAMA2	laminin, alpha 2	AI078169
202202_s_at	1.77103	8.885899	14.29243	1.85E-32	9.60E-31	63.07866	LAMA4	laminin, alpha 4	NM_002290
214577_at	1.76898	5.882916	20.2012	2.50E-50	1.66E-47	103.9654	MAP1B	microtubule-associated protein 1B	BG164365
229584_at	1.76878	5.708193	16.09416	5.07E-38	4.66E-36	75.80713	LRRK2	leucine-rich repeat kinase 2	AK026776
202350_s_at	1.75989	9.04788	8.057189	6.75E-14	6.27E-13	20.70002	MATN2	matrilin 2	NM_002380
218204_s_at	1.75947	8.240163	18.84002	2.51E-46	7.87E-44	94.81361	FYCO1	FYVE and coiled-coil domain containing 1	NM_024513
224976_at	1.7588	8.25798	16.43354	4.62E-39	4.87E-37	78.18819	NFIA	nuclear factor I/A	R37335
236179_at	1.75849	7.051299	10.51225	6.91E-21	1.33E-19	36.62133	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	AI754693
226751_at	1.75807	8.331687	16.69464	7.36E-40	8.69E-38	80.01498	CNRIP1	cannabinoid receptor interacting protein 1	AW193693
205624_at	1.75638	8.66292	7.506071	1.92E-12	1.48E-11	17.40028	CPA3	carboxypeptidase A3 (mast cell)	NM_001870
209191_at	1.75618	9.927171	13.99812	1.51E-31	7.26E-30	60.99265	TUBB6	tubulin, beta 6	BC002654
227091_at	1.75607	6.389933	14.34065	1.31E-32	6.89E-31	63.42046	CCDC146	coiled-coil domain containing 146	AB040938
228693_at	1.75566	7.193802	17.56062	1.72E-42	2.73E-40	86.03725	CCDC50	coiled-coil domain containing 50	AI681307
232054_at	1.75409	5.090695	8.400674	7.90E-15	8.13E-14	22.81699	PCDH20	protocadherin 20	AA040057
227307_at	1.75396	7.32666	14.30942	1.64E-32	8.53E-31	63.19908	TSPAN18	CDNA PSEC0247 fis, clone NT2RP3001613, weakly similar to PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3	AL565381
212067_s_at	1.75098	10.52934	13.15077	6.33E-29	2.42E-27	54.99202	C1R	complement component 1, r subcomponent	AL573058
203789_s_at	1.74961	9.423194	9.813935	7.87E-19	1.22E-17	31.92957	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	NM_006379
226142_at	1.74882	7.517655	14.24867	2.53E-32	1.30E-30	62.76855	GLIPR1	GLI pathogenesis-related 1	AV682252
227692_at	1.74786	7.997418	11.19733	6.09E-23	1.42E-21	41.31275	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	AU153866
218353_at	1.74779	9.720371	10.55301	5.22E-21	1.02E-19	36.89822	RGS5	regulator of G-protein signaling 5	NM_025226
214920_at	1.74702	5.880242	12.28126	3.03E-26	9.33E-25	48.86354	THSD7A	thrombospondin, type I, domain containing 7A	R33964
205609_at	1.74612	6.154715	13.50296	5.15E-30	2.17E-28	57.48423	ANGPT1	angiopoietin 1	NM_001146
211813_x_at	1.74406	11.39163	11.03195	1.92E-22	4.27E-21	40.17339	DCN	decorin	AF138303
235616_at	1.74373	6.484535	17.14398	3.15E-41	4.25E-39	83.14722	TSHZ2	teashirt zinc finger homeobox 2	AI694059
236359_at	1.74214	5.722054	14.82668	4.10E-34	2.55E-32	66.86341	SCN4B	sodium channel, voltage-gated, type IV, beta	AW026241
224822_at	1.74161	8.43231	15.00206	1.18E-34	7.78E-33	68.1046	DLC1	deleted in liver cancer 1	AA524250
228573_at	1.74146	7.839921	13.96522	1.91E-31	9.10E-30	60.75946			BE673665
204823_at	1.7401	6.150206	13.76411	8.01E-31	3.60E-29	59.33419	NAV3	neuron navigator 3	NM_014903

1568760_at	1.73883	5.535789	15.48619	3.77E-36	2.89E-34	71.52557	MYH11	myosin, heavy chain 11, smooth muscle	BF510409
226695_at	1.73874	8.25932	9.673998	2.01E-18	2.99E-17	31.00246	PRRX1	paired related homeobox 1	AA775472
204041_at	1.73846	8.80863	9.657588	2.24E-18	3.33E-17	30.89405	MAOB	monoamine oxidase B	NM_000898
204338_s_at	1.73685	4.995661	11.69709	1.85E-24	4.95E-23	44.77809	RGS4	regulator of G-protein signaling 4	NM_005613
213158_at	1.73683	8.917869	14.20606	3.42E-32	1.74E-30	62.46649			AA045174
225710_at	1.73527	9.384134	14.22875	2.91E-32	1.49E-30	62.62733	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	H99792
222455_s_at	1.73485	7.994218	17.12568	3.58E-41	4.80E-39	83.01997	PARVA	parvin, alpha	AF237771
227399_at	1.73418	6.889147	8.588017	2.41E-15	2.64E-14	23.98952	VGLL3	vestigial like 3 (Drosophila)	AI754423
235497_at	1.73376	5.77881	16.98684	9.46E-41	1.21E-38	82.05353	LOC643837	hypothetical LOC643837	ALO79648
213004_at	1.73346	7.818035	14.0213	1.28E-31	6.20E-30	61.15695	ANGPTL2	angiotensin-like 2	AI074333
206511_s_at	1.73231	5.339492	14.1603	4.75E-32	2.38E-30	62.14216	SIX2	SIX homeobox 2	NM_016932
243584_at	1.73085	4.731314	17.59663	1.34E-42	2.16E-40	86.28637			AW976035
228974_at	1.72921	5.907744	14.41618	7.65E-33	4.10E-31	63.95568			AI816281
219367_s_at	1.72888	6.317275	16.83496	2.75E-40	3.34E-38	80.99469			NM_018534
225604_s_at	1.72885	7.057251	12.79785	7.78E-28	2.72E-26	52.49941	GLIPR2	GLI pathogenesis-related 2	AA284532
218223_s_at	1.72583	8.45779	15.21279	2.63E-35	1.83E-33	69.59468	PLEKHO1	pleckstrin homology domain containing, family O member 1	NM_016274
229218_at	1.72488	7.710894	9.712072	1.56E-18	2.34E-17	31.25423	COL1A2	collagen, type I, alpha 2	AA628535
227233_at	1.72409	5.622824	15.52986	2.76E-36	2.15E-34	71.83376	TSPAN2	tetraspanin 2	AU147132
201150_s_at	1.72349	10.11481	10.69809	1.93E-21	3.90E-20	37.88623	TIMP3	TIMP metalloproteinase inhibitor 3	NM_000362
232204_at	1.72295	6.870996	12.40103	1.30E-26	4.12E-25	49.70491	EBF1	early B-cell factor 1	AF208502
238778_at	1.72274	7.182226	9.213939	4.21E-17	5.51E-16	27.98984	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	AI244661
224560_at	1.72116	10.64015	12.36191	1.71E-26	5.37E-25	49.42995	TIMP2	TIMP metalloproteinase inhibitor 2	BF107565
205934_at	1.72048	5.158926	17.08867	4.64E-41	6.12E-39	82.76248	PLCL1	phospholipase C-like 1	NM_006226
217525_at	1.71847	6.966161	13.55316	3.60E-30	1.53E-28	57.8397	OLFML1	olfactomedin-like 1	AW305097
219427_at	1.71844	6.822645	14.8656	3.11E-34	1.96E-32	67.13892	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	NM_024582
220037_s_at	1.71839	4.587117	9.957967	2.99E-19	4.87E-18	32.88866	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	NM_016164
231384_at	1.71782	3.752455	16.17642	2.84E-38	2.69E-36	76.38491	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	T65537
205132_at	1.71761	7.963255	12.60367	3.09E-27	1.03E-25	51.1307	ACTC1	actin, alpha, cardiac muscle 1	NM_005159
205231_s_at	1.71682	6.24645	17.06845	5.34E-41	7.01E-39	82.62179	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	NM_005670
202732_at	1.71615	9.431636	15.84402	2.98E-37	2.57E-35	74.04785	PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	NM_007066
228185_at	1.71581	6.562667	21.68714	1.36E-54	2.32E-51	113.7115	ZNF25	zinc finger protein 25	N32599
227121_at	1.71568	7.755361	16.82895	2.86E-40	3.48E-38	80.9528			BF476076
205898_at	1.71134	5.600564	11.66842	2.27E-24	6.02E-23	44.57846	CX3CR1	chemokine (C-X3-C motif) receptor 1	U20350
1555725_a_at	1.71026	9.249785	10.48921	8.09E-21	1.54E-19	36.46496	RGS5	regulator of G-protein signaling 5	AF493929
204288_s_at	1.71006	8.040571	10.2217	5.01E-20	8.83E-19	34.65683	SORBS2	sorbin and SH3 domain containing 2	NM_021069
202766_s_at	1.70847	9.746266	10.91727	4.25E-22	9.15E-21	39.38576	FBN1	fibrillin 1	NM_000138
208789_at	1.70823	9.849666	16.44909	4.14E-39	4.39E-37	78.29711	PTRF	polymerase I and transcript release factor	BC004295
231987_at	1.70786	6.502381	16.48089	3.31E-39	3.55E-37	78.51981	LOC728264	hypothetical protein LOC728264	AW081196
207996_s_at	1.7078	6.766308	13.94092	2.27E-31	1.07E-29	60.58722	C18orf1	chromosome 18 open reading frame 1	NM_004338
218824_at	1.70763	5.877473	9.15945	6.02E-17	7.75E-16	27.63688	PNMAL1	PNMA-like 1	NM_018215
206167_s_at	1.70478	7.65589	10.39839	1.50E-20	2.79E-19	35.84954	ARHGAP6	Rho GTPase activating protein 6	NM_001174
242134_at	1.70423	5.585135	14.62897	1.68E-33	9.70E-32	65.46335			AI733194
223599_at	1.70423	5.909227	14.43295	6.79E-33	3.66E-31	64.07451	TRIM6	tripartite motif-containing 6	AF220030
226989_at	1.70313	8.687904	11.89823	4.51E-25	1.27E-23	46.18106	RGMB	RGM domain family, member B	BE855765
205619_s_at	1.7028	6.558129	12.73761	1.19E-27	4.12E-26	52.07455	MEOX1	mesenchyme homeobox 1	NM_004527
204931_at	1.70272	7.014685	12.07042	1.34E-25	3.94E-24	47.38535	TCF21	transcription factor 21	NM_003206

202007_at	1.7008	9.455648	12.41288	1.19E-26	3.81E-25	49.7882	NID1	nidogen 1	BF940043
228108_at	1.69979	6.698322	10.33883	2.26E-20	4.12E-19	35.4468			AW274846
228480_at	1.69947	5.922205	16.69443	7.37E-40	8.69E-38	80.01345	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	AW296039
202765_s_at	1.69876	7.963233	11.12738	9.91E-23	2.26E-21	40.83039	FBN1	fibrillin 1	AI264196
203799_at	1.69871	8.987894	11.90941	4.17E-25	1.18E-23	46.2592	CD302	CD302 molecule	NM_014880
226001_at	1.69808	9.314926	12.53913	4.88E-27	1.60E-25	50.67625	KLHL5	kelch-like 5 (Drosophila)	AK002174
218736_s_at	1.69705	6.84306	12.62942	2.57E-27	8.63E-26	51.31207	PALMD	palmdelphin	NM_017734
200986_at	1.69627	9.574768	12.47187	7.86E-27	2.53E-25	50.203	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	NM_000062
209087_x_at	1.69566	8.686202	14.6639	1.31E-33	7.66E-32	65.71075	MCAM	melanoma cell adhesion molecule	AF089868
216235_s_at	1.69481	6.782975	15.72329	7.01E-37	5.75E-35	73.19751	EDNRA	endothelin receptor type A	S81545
226705_at	1.69373	7.273989	19.13803	3.28E-47	1.20E-44	96.83458	FGFR1	fibroblast growth factor receptor 1	BE467261
209960_at	1.69355	5.728777	11.3324	2.38E-23	5.71E-22	42.24615	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	X16323
203603_s_at	1.69349	7.331936	11.88482	4.96E-25	1.39E-23	46.08744	ZEB2	zinc finger E-box binding homeobox 2	NM_014795
227449_at	1.69349	5.404426	12.55672	4.31E-27	1.42E-25	50.80006	EPHA4	EPH receptor A4	AI799018
226051_at	1.69299	10.1242	14.50863	3.96E-33	2.20E-31	64.61083	SELM	selenoprotein M	BF973568
238861_at	1.69126	5.141481	21.5612	3.10E-54	4.83E-51	112.8959			AI692322
238727_at	1.69064	4.175527	10.99422	2.50E-22	5.47E-21	39.91401			AA031832
214927_at	1.68988	7.529017	8.443673	6.02E-15	6.29E-14	23.08503	ITGBL1	integrin, beta-like 1 (with EGF-like repeat domains)	AL359052
213844_at	1.68895	7.654665	12.67805	1.82E-27	6.18E-26	51.65468	HOXA5	homeobox A5	NM_019102
209488_s_at	1.68769	9.389971	14.061	9.63E-32	4.74E-30	61.43832	RBPMS	RNA binding protein with multiple splicing	D84109
213666_at	1.68692	6.388203	16.22074	2.07E-38	1.99E-36	76.69605	SEPT6	septin 6	AK026589
206117_at	1.68658	7.46161	12.00719	2.10E-25	6.04E-24	46.94281	TPM1	tropomyosin 1 (alpha)	NM_000366
227713_at	1.68558	6.861127	16.1567	3.26E-38	3.07E-36	76.24644	KATNAL1	katanin p60 subunit A-like 1	AI807482
205666_at	1.68506	6.210093	10.61274	3.47E-21	6.87E-20	37.30457	FMO1	flavin containing monooxygenase 1	NM_002021
218864_at	1.68387	7.095284	18.0942	4.24E-44	8.91E-42	89.71643	TNS1	tensin 1	AF116610
203666_at	1.68383	8.05583	12.05818	1.46E-25	4.28E-24	47.29968	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)	NM_000609
212077_at	1.68356	12.02671	14.8503	3.47E-34	2.17E-32	67.0306	CALD1	caldesmon 1	AL583520
205525_at	1.68329	5.501376	16.62557	1.20E-39	1.36E-37	79.53219	CALD1	caldesmon 1	NM_018495
221933_at	1.68283	4.884432	9.448319	8.99E-18	1.26E-16	29.51761	NLGN4X	neuroligin 4, X-linked	AI338338
217890_s_at	1.68152	9.153439	18.33144	8.24E-45	2.02E-42	91.34374	PARVA	parvin, alpha	NM_018222
226591_at	1.68003	4.134523	14.79567	5.12E-34	3.14E-32	66.64385	SNRPN	small nuclear ribonucleoprotein polypeptide N	BG413612
224970_at	1.67951	9.415648	15.34994	9.92E-36	7.24E-34	70.56366	NFIA	nuclear factor I/A	AA419275
229225_at	1.67885	6.729471	15.43314	5.49E-36	4.14E-34	71.15118	NRP2	neuropilin 2	N90777
211726_s_at	1.67856	6.819131	9.834179	6.87E-19	1.08E-17	32.06408	FMO2	flavin containing monooxygenase 2 (non-functional)	BC005894
204165_at	1.67835	6.773003	11.20533	5.76E-23	1.34E-21	41.36796	WASF1	WAS protein family, member 1	NM_003931
236644_at	1.67828	3.690602	22.20708	4.67E-56	1.28E-52	117.0581	RNF180	ring finger protein 180	BF433928
202728_s_at	1.67788	8.210836	15.12173	5.02E-35	3.41E-33	68.95098	LTBP1	latent transforming growth factor beta binding protein 1	AI986120
228905_at	1.67657	5.760483	17.73379	5.15E-43	9.05E-41	87.23408	PCM1	pericentriolar material 1	BE672700
226856_at	1.67607	6.545988	10.00237	2.21E-19	3.66E-18	33.18529	MUSTN1	musculoskeletal, embryonic nuclear protein 1	BF793701
206852_at	1.67397	3.801057	11.39827	1.50E-23	3.68E-22	42.70226	EPHA7	EPH receptor A7	NM_004440
225793_at	1.67394	9.080281	18.12859	3.34E-44	7.27E-42	89.95265	LIX1L	Lix1 homolog (mouse)-like	AW500180
243940_at	1.67356	5.054199	15.2732	1.71E-35	1.21E-33	70.02157	TSHZ2	teashirt zinc finger homeobox 2	AW953679
209686_at	1.67331	5.326209	10.61828	3.34E-21	6.62E-20	37.34226	S100B	S100 calcium binding protein B	BC001766
240509_s_at	1.67304	3.935897	11.1879	6.51E-23	1.51E-21	41.24767	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	BF064262
203662_s_at	1.67288	7.116972	17.3788	6.10E-42	8.77E-40	84.77782	TMOD1	tropomodulin 1	NM_003275
212151_at	1.67288	9.65735	13.48033	6.05E-30	2.53E-28	57.32395	PBX1	pre-B-cell leukemia homeobox 1	BF967998
238546_at	1.67248	5.557393	16.44233	4.35E-39	4.59E-37	78.24974	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	BF344961

230121_at	1.67194	6.495325	15.50666	3.26E-36	2.52E-34	71.67005	C1orf133	chromosome 1 open reading frame 133	BF508679
218683_at	1.67026	7.943097	14.0239	1.26E-31	6.09E-30	61.17532	PTBP2	polypyrimidine tract binding protein 2	NM_021190
229487_at	1.66948	6.413159	13.02115	1.59E-28	5.88E-27	54.0759	EBF1	early B-cell factor 1	W73890
225961_at	1.66926	7.743379	14.86485	3.13E-34	1.97E-32	67.13357	KLHDC5	kelch domain containing 5	AI334297
209645_s_at	1.66806	7.568378	13.62037	2.23E-30	9.66E-29	58.31577	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	NM_000692
227227_at	1.66799	7.187625	14.91623	2.17E-34	1.40E-32	67.49726			AI344332
228950_s_at	1.66729	8.556995	12.76491	9.83E-28	3.41E-26	52.2671	GPR177	G protein-coupled receptor 177	AL534095
222434_at	1.6665	6.502562	16.07849	5.67E-38	5.17E-36	75.69706	ENAH	enabled homolog (Drosophila)	AI963713
203710_at	1.66589	7.82352	14.74151	7.53E-34	4.53E-32	66.26037	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	NM_002222
230968_at	1.66381	5.997498	13.13432	7.12E-29	2.71E-27	54.87572			AW953794
209555_s_at	1.66359	6.551309	7.502114	1.97E-12	1.52E-11	17.37705	CD36	CD36 molecule (thrombospondin receptor)	M98399
214085_x_at	1.6624	8.357461	13.64692	1.85E-30	8.04E-29	58.50383	GLIPR1	GLI pathogenesis-related 1	AI912583
204072_s_at	1.66165	7.831258	11.91975	3.88E-25	1.10E-23	46.33144	FRY	furry homolog (Drosophila)	NM_023037
212636_at	1.66082	8.360472	12.7677	9.64E-28	3.35E-26	52.28675	QKI	quaking homolog, KH domain RNA binding (mouse)	AL031781
214298_x_at	1.66021	7.066609	14.95285	1.67E-34	1.09E-32	67.75636	SEPT6	septin 6	AL568374
236704_at	1.65991	6.412211	17.70572	6.26E-43	1.08E-40	87.04026			BG413366
229441_at	1.6599	6.827509	13.25908	2.93E-29	1.16E-27	55.75801	PRSS23	CDNA PSEC0048 fis, clone NT2RP2000028, highly similar to Serine protease 23 precursor (EC 3.4.21.-)	AI569872
229942_at	1.65901	6.504364	18.41569	4.61E-45	1.16E-42	91.92037	BNC2	basonuclein 2	AW024890
216598_s_at	1.65846	8.868475	8.654228	1.58E-15	1.77E-14	24.40678	CCL2	chemokine (C-C motif) ligand 2	S69738
201508_at	1.65825	9.968276	12.27766	3.11E-26	9.55E-25	48.83832	IGFBP4	insulin-like growth factor binding protein 4	NM_001552
205383_s_at	1.65795	8.729092	16.32672	9.82E-39	9.88E-37	77.43954	ZBTB20	zinc finger and BTB domain containing 20	NM_015642
243481_at	1.65768	5.646756	17.82427	2.75E-43	5.13E-41	87.85836	RHOJ	ras homolog gene family, member J	AA181207
206306_at	1.65749	3.938138	13.83253	4.92E-31	2.26E-29	59.81899	RYR3	ryanodine receptor 3	NM_001036
215073_s_at	1.65679	7.515351	13.86306	3.95E-31	1.83E-29	60.03541	NR2F2	nuclear receptor subfamily 2, group F, member 2	AL554245
227261_at	1.65665	7.333683	13.95859	2.00E-31	9.52E-30	60.71242	KLF12	Kruppel-like factor 12	AA020010
1552507_at	1.65605	5.956628	15.81469	3.67E-37	3.10E-35	73.84135	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	NM_080671
220170_at	1.65557	5.219687	9.885227	4.87E-19	7.76E-18	32.40369	FHL5	four and a half LIM domains 5	NM_020482
228266_s_at	1.65483	6.548166	12.76799	9.62E-28	3.34E-26	52.28877	HDGFRP3	hepatoma-derived growth factor, related protein 3	BE703418
212262_at	1.65433	7.63093	14.5202	3.64E-33	2.03E-31	64.69277	QKI	quaking homolog, KH domain RNA binding (mouse)	AA149639
230076_at	1.65423	6.418807	11.42944	1.21E-23	2.99E-22	42.91828	PITPNM3	PITPNM family member 3	BF063164
228071_at	1.6539	7.618089	10.62532	3.18E-21	6.33E-20	37.39018	GIMAP7	GTPase, IMAP family member 7	AA858297
228027_at	1.65359	7.490092	15.4717	4.18E-36	3.18E-34	71.42334	GPRASP2	G protein-coupled receptor associated sorting protein 2	BF732712
226875_at	1.65338	8.227091	13.02211	1.58E-28	5.85E-27	54.08263	DOCK11	dedicator of cytokinesis 11	AI742838
223282_at	1.65148	7.995706	13.94739	2.17E-31	1.03E-29	60.63309	TSHZ1	teashirt zinc finger homeobox 1	W60810
235977_at	1.65079	4.968097	15.12759	4.82E-35	3.29E-33	68.99236	LONRF2	LON peptidase N-terminal domain and ring finger 2	BF433341
223854_at	1.65017	5.555488	11.31792	2.63E-23	6.29E-22	42.14598	PCDHB10	protocadherin beta 10	AF131761
206637_at	1.6501	7.526561	7.870995	2.12E-13	1.85E-12	19.57129	P2RY14	purinergic receptor P2Y, G-protein coupled, 14	NM_014879
205236_x_at	1.64707	8.04899	16.83894	2.67E-40	3.26E-38	81.02248	SOD3	superoxide dismutase 3, extracellular	NM_003102
235556_at	1.64599	6.749474	17.59032	1.40E-42	2.25E-40	86.24272			AL037805
242736_at	1.64494	5.251999	14.12364	6.16E-32	3.07E-30	61.8823			AI377221
225123_at	1.64432	8.124524	11.25488	4.08E-23	9.65E-22	41.71018			BE883841
201108_s_at	1.64294	8.64743	10.66904	2.36E-21	4.73E-20	37.68809	THBS1	thrombospondin 1	BF055462
228368_at	1.64082	5.611451	15.26024	1.88E-35	1.32E-33	69.93005	ARHGAP20	Rho GTPase activating protein 20	AI936560
1555097_a_at	1.64018	4.172187	16.7653	4.48E-40	5.40E-38	80.50847	PTGFR	prostaglandin F receptor (FP)	BC035694
220677_s_at	1.63928	5.610295	14.53066	3.38E-33	1.89E-31	64.76687	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8	NM_007037

1554614_a_at	1.63753	5.142759	13.47547	6.27E-30	2.62E-28	57.2896	PTBP2	polypyrimidine tract binding protein 2	AB051233
212503_s_at	1.63731	7.428017	15.4785	3.98E-36	3.04E-34	71.47131	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N22859
236234_at	1.63712	4.495742	17.69762	6.63E-43	1.13E-40	86.98435	PDE1A	phosphodiesterase 1A, calmodulin-dependent	AW614381
219561_at	1.6365	7.871786	18.90789	1.58E-46	5.17E-44	95.27472	COPZ2	coatamer protein complex, subunit zeta 2	NM_016429
222771_s_at	1.63528	5.841957	8.73503	9.42E-16	1.08E-14	24.91797	MYEF2	myelin expression factor 2	BF224052
224218_s_at	1.63502	6.103109	13.91284	2.77E-31	1.30E-29	60.38821	TRPS1	trichorhinophalangeal syndrome I	AF264784
227486_at	1.63453	5.96653	16.32672	9.82E-39	9.88E-37	77.43954	NT5E	5'-nucleotidase, ecto (CD73)	AI086864
235306_at	1.63446	7.047987	12.4816	7.33E-27	2.37E-25	50.27146	GIMAP8	GTPase, IMAP family member 8	AI611648
205638_at	1.63435	4.117025	14.44227	6.35E-33	3.44E-31	64.14055	BAI3	brain-specific angiogenesis inhibitor 3	NM_001704
203788_s_at	1.63261	6.168582	11.40633	1.42E-23	3.49E-22	42.75811	SEMA3C	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	AI962897
1552767_a_at	1.63255	4.960885	7.657433	7.76E-13	6.29E-12	18.29394	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	NM_147174
209199_s_at	1.63207	8.719757	14.18661	3.93E-32	1.99E-30	62.32866	MEF2C	myocyte enhancer factor 2C	N22468
235521_at	1.63186	7.219419	11.47836	8.58E-24	2.17E-22	43.25759	HOXA3	homeobox A3	AW137982
208430_s_at	1.63112	5.756009	15.31107	1.31E-35	9.37E-34	70.28911	DTNA	dystrobrevin, alpha	NM_001390
212675_s_at	1.63091	8.366744	17.3143	9.57E-42	1.35E-39	84.33036	CEP68	centrosomal protein 68kDa	AB011154
208747_s_at	1.6306	11.30553	11.78422	1.01E-24	2.75E-23	45.38532	C1S	complement component 1, s subcomponent	M18767
227817_at	1.63031	6.044931	15.13582	4.54E-35	3.11E-33	69.0506	PRKCB	protein kinase C, beta	R51324
219197_s_at	1.62991	5.84527	12.63996	2.39E-27	8.03E-26	51.38628	SCUBE2	signal peptide, CUB domain, EGF-like 2	AI424243
206355_at	1.62959	4.38718	17.5044	2.54E-42	3.88E-40	85.64814	GNAL	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	R20102
215506_s_at	1.62845	5.657907	11.4848	8.21E-24	2.07E-22	43.30225	DIRAS3	DIRAS family, GTP-binding RAS-like 3	AK021882
216944_s_at	1.62802	6.961479	16.13756	3.73E-38	3.46E-36	76.11203	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	U23850
207191_s_at	1.62719	7.826108	9.526193	5.37E-18	7.71E-17	30.0285	ISLR	immunoglobulin superfamily containing leucine-rich repeat	NM_005545
228563_at	1.62641	5.946662	15.33864	1.07E-35	7.80E-34	70.48387	GJC1	gap junction protein, gamma 1, 45kDa	BE504215
203131_at	1.62625	10.18165	9.75673	1.15E-18	1.77E-17	31.55	PDGFRA	platelet-derived growth factor receptor, alpha polypeptide	NM_006206
203706_s_at	1.62619	8.124071	10.35253	2.06E-20	3.76E-19	35.53935	FZD7	frizzled homolog 7 (Drosophila)	NM_003507
244050_at	1.62568	7.605361	12.75449	1.06E-27	3.67E-26	52.19355	PTPLAD2	protein tyrosine phosphatase-like A domain containing 2	AI804932
223007_s_at	1.6253	9.255965	15.06936	7.29E-35	4.87E-33	68.58062	C9orf5	chromosome 9 open reading frame 5	AA495988
229130_at	1.62505	5.418058	19.06846	5.27E-47	1.86E-44	96.36361	LOC28553	hypothetical protein LOC285535	AU145323
202388_at	1.62479	10.71222	11.03429	1.89E-22	4.21E-21	40.18947	RGS2	regulator of G-protein signaling 2, 24kDa	NM_002923
228423_at	1.62464	7.109615	9.996887	2.30E-19	3.80E-18	33.14863	MAP9	microtubule-associated protein 9	AI887898
231431_s_at	1.62456	7.651042	16.86598	2.21E-40	2.73E-38	81.21113			AI125670
215707_s_at	1.62316	8.181258	14.98998	1.28E-34	8.43E-33	68.01908	PRNP	prion protein	AV725328
203685_at	1.61822	6.579837	13.6537	1.76E-30	7.66E-29	58.55192	BCL2	B-cell CLL/lymphoma 2	NM_000633
209683_at	1.61715	5.414422	14.18083	4.10E-32	2.07E-30	62.28769	FAM49A	family with sequence similarity 49, member A	AA243659
227444_at	1.6164	5.296918	17.26925	1.31E-41	1.82E-39	84.01765	ARMCX4	Armaddillo repeat containing, X-linked 4, mRNA (cDNA clone IMAGE:5261888)	AW519141
219059_s_at	1.61621	6.174948	9.453173	8.71E-18	1.22E-16	29.54941	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1	AL574194
217504_at	1.61595	4.853102	14.90383	2.37E-34	1.51E-32	67.40952	ABCA6	ATP-binding cassette, sub-family A (ABC1), member 6	AA099357
1555526_a_at	1.61423	6.622803	14.03963	1.12E-31	5.47E-30	61.28684	SEPT6	septin 6	AF403061
229554_at	1.61349	8.006554	9.358916	1.62E-17	2.21E-16	28.93307			AI141861

220988_s_at	1.61347	7.705979	11.56795	4.59E-24	1.19E-22	43.87968	AMACR /// C1QTNF3	alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein 3	NM_030945
241350_at	1.61228	5.329641	15.43036	5.60E-36	4.21E-34	71.13152	FBXL22	F-box and leucine-rich repeat protein 22	AL533913
226280_at	1.61158	7.894845	16.854	2.40E-40	2.94E-38	81.12751			AA133277
209733_at	1.61135	6.513813	18.27461	1.22E-44	2.91E-42	90.95438	LOC28644 0	hypothetical protein LOC286440	AL034399
235836_at	1.60995	5.4502	20.25171	1.78E-50	1.22E-47	104.301	MXRA7	matrix-remodelling associated 7	N51413
213249_at	1.60969	6.875944	21.77911	7.48E-55	1.41E-51	114.3059	FBXL7	F-box and leucine-rich repeat protein 7	AU145127
1564139_at	1.60969	4.979667	18.65207	9.09E-46	2.63E-43	93.53432	LOC14457 1	hypothetical protein LOC144571	AK056852
231118_at	1.60949	6.197241	20.36741	8.23E-51	6.07E-48	105.0686	ANKRD35	ankyrin repeat domain 35	AW511401
206953_s_at	1.60939	7.896576	11.64362	2.70E-24	7.15E-23	44.4059	LPHN2	latrophilin 2	NM_012302
235308_at	1.60857	8.920312	15.61075	1.56E-36	1.25E-34	72.40431	ZBTB20	zinc finger and BTB domain containing 20	AW499525
220327_at	1.60772	4.808664	12.13938	8.25E-26	2.45E-24	47.86839	VGLL3	vestigial like 3 (Drosophila)	NM_016206
205893_at	1.60714	3.862551	14.08721	7.99E-32	3.95E-30	61.62412	NLGN1	neuroligin 1	NM_014932
211071_s_at	1.60647	7.914011	8.792949	6.49E-16	7.54E-15	25.28571	MLLT11	myeloid/lymphoid or mixed- lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	BC006471
230482_at	1.60607	5.959527	11.42787	1.22E-23	3.03E-22	42.90737	ST6GALNA C5	Alpha 2,6-sialyltransferase (ST6GALNAC V gene)	AF131837
204222_s_at	1.60569	7.817163	11.7202	1.58E-24	4.24E-23	44.93911	GLIPR1	GLI pathogenesis-related 1	NM_006851
203323_at	1.60431	8.781798	9.759257	1.13E-18	1.74E-17	31.56676	CAV2	caveolin 2	BF197655
235347_at	1.60388	6.701487	20.01879	8.49E-50	5.21E-47	102.751	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	BF435591
238865_at	1.60383	5.179116	17.52636	2.18E-42	3.40E-40	85.80014	PABPC4L	poly(A) binding protein, cytoplasmic 4-like	AI822134
203477_at	1.60382	10.28711	11.12985	9.74E-23	2.22E-21	40.84735	COL15A1	collagen, type XV, alpha 1	NM_001855
223620_at	1.6025	7.218337	9.984247	2.50E-19	4.12E-18	33.06416	GPR34	G protein-coupled receptor 34	AF039686
209356_x_at	1.60192	8.690772	15.14079	4.39E-35	3.01E-33	69.08569	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	AB030655
205116_at	1.60049	6.890079	15.43261	5.51E-36	4.15E-34	71.14739	LAMA2	laminin, alpha 2	NM_000426
228692_at	1.59949	4.63642	16.75649	4.76E-40	5.73E-38	80.447			N63377
215020_at	1.5994	5.500941	11.54347	5.44E-24	1.40E-22	43.70964	NRXN3	neurexin 3	AF123462
238852_at	1.59869	5.178489	9.15436	6.22E-17	7.99E-16	27.60395			AA424567
228063_s_at	1.59809	7.438616	11.39042	1.59E-23	3.88E-22	42.64789	NAP1L5	nucleosome assembly protein 1- like 5	AW025330
221618_s_at	1.59753	6.254578	11.3112	2.76E-23	6.58E-22	42.09951	LOC72819 8 /// TAF9B	similar to transcription associated factor TAFII31L /// TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	AF220509
232876_at	1.5957	4.679301	18.24391	1.51E-44	3.47E-42	90.74395			#N/A
213262_at	1.59564	7.232268	11.15274	8.31E-23	1.90E-21	41.00515	SACS	spastic ataxia of Charlevoix- Saguenay (sacsin)	AI932370
223764_x_at	1.59534	4.28701	16.95114	1.22E-40	1.54E-38	81.80482	NIPSNAP3 B	nipsnap homolog 3B (C. elegans)	BC005202
212122_at	1.59532	6.506996	14.24861	2.53E-32	1.30E-30	62.76813	RHOQ	ras homolog gene family, member Q	AW771590
241412_at	1.59514	5.917594	8.748309	8.65E-16	9.93E-15	25.00219	BTC	betacellulin	AI620677
212677_s_at	1.59375	7.751659	15.55831	2.26E-36	1.77E-34	72.03443	CEP68	centrosomal protein 68kDa	BG530481
229485_x_at	1.59362	5.477937	9.070665	1.07E-16	1.35E-15	27.06358	SHISA3	shisa homolog 3 (Xenopus laevis)	AI735586
206377_at	1.59311	8.026969	9.030503	1.40E-16	1.73E-15	26.80501	FOXF2	forkhead box F2	NM_001452
236892_s_at	1.59299	5.018018	8.505915	4.06E-15	4.32E-14	23.47417	LOC10013 0740	similar to hCG2042068	BF590528
217767_at	1.59248	11.08289	8.55921	2.90E-15	3.13E-14	23.80844	C3	complement component 3	NM_000064
222651_s_at	1.59176	7.905628	13.87418	3.65E-31	1.70E-29	60.1142	TRPS1	trichorhinophalangeal syndrome I	BF701166
222885_at	1.59163	7.873485	11.46514	9.41E-24	2.36E-22	43.16589	EMCN	endomucin	AF205940
226682_at	1.58919	7.397246	13.16909	5.56E-29	2.14E-27	55.12152	RORA	RAR-related orphan receptor A	AW006185
213543_at	1.58772	6.602345	16.22448	2.02E-38	1.95E-36	76.72229	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	AA570453

203661_s_at	1.58673	6.79753	17.45627	3.56E-42	5.31E-40	85.3148	TMOD1	tropomodulin 1	BC002660
217764_s_at	1.58656	9.959705	13.16041	5.91E-29	2.27E-27	55.06015	RAB31	RAB31, member RAS oncogene family	AF183421
201109_s_at	1.58523	8.931769	9.1493	6.43E-17	8.25E-16	27.57121	THBS1	thrombospondin 1	AV726673
231175_at	1.58518	4.307976	16.60693	1.36E-39	1.54E-37	79.40184	BEND6	BEN domain containing 6	N48613
231945_at	1.58486	5.738128	15.19736	2.93E-35	2.04E-33	69.48565	FILIP1	filamin A interacting protein 1	AK001570
214807_at	1.5847	6.874992	11.65298	2.53E-24	6.70E-23	44.47105			AI278204
214954_at	1.58424	4.280003	10.55962	4.99E-21	9.75E-20	36.94321	SUSD5	sushi domain containing 5	BF977837
243059_at	1.58393	4.773851	15.46806	4.29E-36	3.26E-34	71.39764	LOC283904	hypothetical protein LOC283904	AI680624
209758_s_at	1.58322	8.042189	6.983384	4.10E-11	2.64E-10	14.39374	MFAP5	microfibrillar associated protein 5	U37283
203851_at	1.58272	8.277263	12.64962	2.23E-27	7.52E-26	51.45437	IGFBP6	insulin-like growth factor binding protein 6	NM_002178
207776_s_at	1.58147	5.604722	13.90495	2.93E-31	1.37E-29	60.33223	CACNB2	calcium channel, voltage-dependent, beta 2 subunit	NM_000724
229287_at	1.58125	6.781713	17.3028	1.04E-41	1.46E-39	84.25053	PCNX	pecanex homolog (Drosophila)	BE326214
210829_s_at	1.58086	6.942723	16.38744	6.40E-39	6.61E-37	77.86521	SSBP2	single-stranded DNA binding protein 2	AF077048
228345_at	1.57937	6.393891	12.14373	8.00E-26	2.39E-24	47.8989	CHIC1	cysteine-rich hydrophobic domain 1	AI745136
201893_x_at	1.57929	12.29291	10.63064	3.07E-21	6.11E-20	37.42646	DCN	decorin	AF138300
231001_at	1.57836	6.427454	13.77391	7.47E-31	3.36E-29	59.40361	FIBIN	fin bud initiation factor homolog (zebrafish)	AI755024
203001_s_at	1.57825	5.380475	7.886218	1.93E-13	1.70E-12	19.66306	STMN2	stathmin-like 2	NM_007029
242358_at	1.57715	4.147823	19.46834	3.48E-48	1.54E-45	99.0634			AW024656
223343_at	1.57711	8.383538	9.955501	3.04E-19	4.95E-18	32.8722	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	AI301935
226152_at	1.57681	6.881607	14.91241	2.23E-34	1.43E-32	67.47018	TTC7B	tetratricopeptide repeat domain 7B	BE963437
201300_s_at	1.57654	10.37538	12.34971	1.87E-26	5.82E-25	49.34424	PRNP	prion protein	NM_000311
209291_at	1.57643	8.824764	8.81757	5.54E-16	6.48E-15	25.44235	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	AW157094
203066_at	1.57578	8.982846	12.38383	1.47E-26	4.63E-25	49.58401	GALNAC4S6ST	B cell RAG associated protein	NM_014863
207836_s_at	1.57571	7.789288	14.10917	6.83E-32	3.40E-30	61.77974	RBPMS	RNA binding protein with multiple splicing	NM_006867
202196_s_at	1.5754	7.819507	10.42309	1.27E-20	2.38E-19	36.01676	DKK3	dickkopf homolog 3 (Xenopus laevis)	NM_013253
213658_at	1.57491	6.124665	11.66973	2.25E-24	5.97E-23	44.58762			BE858194
1552508_at	1.57398	6.202181	16.6296	1.16E-39	1.32E-37	79.56032	KCNE4	potassium voltage-gated channel, Isk-related family, member 4	NM_080671
211597_s_at	1.57377	9.600888	8.879934	3.70E-16	4.42E-15	25.83999	HOPX	HOP homeobox	AB059408
230744_at	1.57362	5.99498	18.20143	2.02E-44	4.56E-42	90.45261			N22766
233903_s_at	1.57278	4.162559	15.81228	3.73E-37	3.15E-35	73.82439	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	AK022655
225540_at	1.57273	6.359201	8.957326	2.24E-16	2.74E-15	26.33514	MAP2	microtubule-associated protein 2	BF342661
212372_at	1.57186	9.226594	10.25286	4.06E-20	7.21E-19	34.86669	MYH10	myosin, heavy chain 10, non-muscle	AK026977
213428_s_at	1.57058	10.63533	12.53081	5.18E-27	1.69E-25	50.61773	COL6A1	collagen, type VI, alpha 1	AA292373
209708_at	1.57056	6.912132	11.07178	1.46E-22	3.28E-21	40.44742	MOXD1	monooxygenase, DBH-like 1	AY007239
210139_s_at	1.57036	10.28045	13.19114	4.75E-29	1.84E-27	55.27747	PMP22	peripheral myelin protein 22	L03203
201149_s_at	1.56993	8.639593	10.33667	2.29E-20	4.17E-19	35.43216	TIMP3	TIMP metalloproteinase inhibitor 3	U67195
236262_at	1.56928	6.663262	13.14276	6.70E-29	2.55E-27	54.93541	MMRN2	multimerin 2	AA025351
229014_at	1.56851	6.723919	17.79363	3.40E-43	6.26E-41	87.64706	FLJ42709	hypothetical gene supported by AK124699	AW206234
209493_at	1.56758	6.354227	12.19237	5.67E-26	1.71E-24	48.23988	POZD2	PDZ domain containing 2	AF338650
227059_at	1.56611	8.192549	10.35071	2.08E-20	3.81E-19	35.52709	GPC6	glypican 6	AI651255
213429_at	1.56579	7.173064	10.09937	1.15E-19	1.96E-18	33.83479			AW025579
235362_at	1.56489	4.887365	15.48963	3.68E-36	2.83E-34	71.54984	LOC729970	CDNA FLJ37477 fis, clone BRAWH2013047	AW614589
204225_at	1.56478	7.097538	15.82572	3.39E-37	2.88E-35	73.91902	HDAC4	histone deacetylase 4	NM_006037
235264_at	1.5635	6.78146	16.07929	5.64E-38	5.15E-36	75.70267	HCFC2	host cell factor C2	AW956392
225571_at	1.56308	5.853151	8.516421	3.80E-15	4.06E-14	23.53999	LIFR	leukemia inhibitory factor receptor alpha	AA701657
229802_at	1.56275	6.6801	7.713059	5.55E-13	4.59E-12	18.62482			AA147884

225732_at	1.56165	8.686119	16.85486	2.39E-40	2.93E-38	81.13353	KLHDC5	kelch domain containing 5	AU146850
208782_at	1.56156	10.97858	13.37406	1.29E-29	5.28E-28	56.57164	FSTL1	folliculin-like 1	BC000055
212099_at	1.56124	10.96567	13.67535	1.51E-30	6.62E-29	58.70528	RHOB	ras homolog gene family, member B	AI263909
219882_at	1.55955	5.934721	12.18179	6.11E-26	1.84E-24	48.16573	TTLL7	tubulin tyrosine ligase-like family, member 7	NM_024686
207030_s_at	1.55843	9.000602	10.39787	1.51E-20	2.80E-19	35.84603	CSRP2	cysteine and glycine-rich protein 2	NM_001321
214587_at	1.55826	4.590743	10.16073	7.58E-20	1.32E-18	34.24674	COL8A1	collagen, type VIII, alpha 1	BE877796
204438_at	1.55816	8.284571	8.539543	3.28E-15	3.53E-14	23.68497	MRC1 /// MRC1L1	mannose receptor, C type 1 /// mannose receptor, C type 1-like 1	NM_002438
206071_s_at	1.55775	5.030424	13.37054	1.32E-29	5.39E-28	56.54677	EPHA3	EPH receptor A3	NM_005233
214321_at	1.55693	6.100815	10.23996	4.43E-20	7.85E-19	34.7798	NOV	nephroblastoma overexpressed gene	BF440025
1558414_at	1.55665	4.704843	16.55195	2.01E-39	2.21E-37	79.01718	C9orf4	chromosome 9 open reading frame 4	BI438189
212561_at	1.55606	8.533088	15.42958	5.63E-36	4.23E-34	71.12603	DENND5A	DENN/MADD domain containing 5A	AA349595
219179_at	1.55561	7.689385	9.947473	3.21E-19	5.21E-18	32.81861	DACT1	dapper, antagonist of beta-catenin, homolog 1 (Xenopus laevis)	NM_016651
215617_at	1.55537	5.25777	15.8357	3.16E-37	2.70E-35	73.98931	LOC26010	viral DNA polymerase-transactivated protein 6	AU145711
235210_s_at	1.55392	6.021525	6.516404	5.65E-10	3.02E-09	11.8206	C8orf84	chromosome 8 open reading frame 84	AW662373
211356_x_at	1.55343	5.741111	10.36767	1.86E-20	3.41E-19	35.6417	LEPR	leptin receptor	U66495
212188_at	1.55271	10.22729	11.99451	2.29E-25	6.57E-24	46.85413	KCTD12	potassium channel tetramerisation domain containing 12	AA551075
242934_at	1.54797	5.859926	13.13965	6.85E-29	2.61E-27	54.91339			AA780365
205501_at	1.54765	5.161258	14.28676	1.93E-32	9.96E-31	63.03847	PDE10A	phosphodiesterase 10A	AI143879
205410_s_at	1.54635	5.647065	15.17961	3.33E-35	2.31E-33	69.3602	ATP2B4	ATPase, Ca++ transporting, plasma membrane 4	NM_001684
221795_at	1.54609	5.330728	8.547752	3.11E-15	3.36E-14	23.73649	NTRK2	neurotrophic tyrosine kinase, receptor, type 2	AI346341
212817_at	1.54363	6.702403	14.74284	7.46E-34	4.49E-32	66.26982	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	AK023253
228882_at	1.54349	5.726275	14.49166	4.47E-33	2.47E-31	64.49053	TUB	tubby homolog (mouse)	AL042088
241902_at	1.54332	3.794947	13.59144	2.74E-30	1.18E-28	58.11088	MXK	mohawk homeobox	R59304
204916_at	1.54302	8.198615	11.09125	1.27E-22	2.88E-21	40.58145	RAMP1	receptor (G protein-coupled) activity modifying protein 1	NM_005855
225978_at	1.54215	6.124322	12.94821	2.67E-28	9.70E-27	53.56068	RIMKLB	ribosomal modification protein rimK-like family member B	AW409794
227945_at	1.54169	7.786327	15.93796	1.53E-37	1.35E-35	74.70892	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	BE882538
211564_s_at	1.54146	6.880979	11.70398	1.77E-24	4.73E-23	44.82609	PDLIM4	PDZ and LIM domain 4	BC003096
214012_at	1.54121	5.749539	13.35404	1.49E-29	6.05E-28	56.42996	ERAP1	endoplasmic reticulum aminopeptidase 1	BE551138
215016_x_at	1.54049	9.523615	12.46986	7.97E-27	2.57E-25	50.18888	DST	dystonin	BC004912
231130_at	1.54017	6.80815	13.60251	2.53E-30	1.09E-28	58.18927	FKBP7	FK506 binding protein 7	AA683602
242579_at	1.5401	5.140417	11.20674	5.71E-23	1.33E-21	41.37772	BMPRI1B	bone morphogenetic protein receptor, type IB	AA935461
217889_s_at	1.53991	7.37352	9.563043	4.20E-18	6.10E-17	30.2708	CYBRD1	cytochrome b reductase 1	NM_024843
230636_s_at	1.53937	5.519125	19.84454	2.74E-49	1.53E-46	101.5873	KLF9	Kruppel-like factor 9	AI458659
231579_s_at	1.539	11.33831	12.12314	9.25E-26	2.74E-24	47.75464	TIMP2	TIMP metalloproteinase inhibitor 2	BE968786
221447_s_at	1.53846	7.702179	12.98636	2.04E-28	7.47E-27	53.83013	GLT8D2	glycosyltransferase 8 domain containing 2	NM_031302
229839_at	1.53842	5.941221	7.064052	2.58E-11	1.71E-10	14.84936	SCARA5	CDNA FLJ57441 complete cds, highly similar to Homo sapiens scavenger receptor class A, member 5 (SCARA5), mRNA	AI799784
203705_s_at	1.5374	7.420444	9.92611	3.70E-19	5.99E-18	32.67611	FZD7	frizzled homolog 7 (Drosophila)	AI333651
231411_at	1.53739	6.597063	15.83877	3.09E-37	2.65E-35	74.01087	LHFP	MRNA; cDNA DKFZp434N0526 (from clone DKFZp434N0526)	BE674089
210155_at	1.53706	6.278836	14.88665	2.68E-34	1.70E-32	67.28787	MYOC	myocilin, trabecular meshwork	D88214
221900_at	1.5365	6.628925	10.78782	1.04E-21	2.15E-20	38.49914	COL8A2	inducible glucocorticoid response collagen, type VIII, alpha 2	AI806793

235213_at	1.53552	5.148507	15.73789	6.32E-37	5.22E-35	73.30044			AA348410
230030_at	1.53423	4.347665	7.427165	3.08E-12	2.31E-11	16.93837	HS6ST2	heparan sulfate 6-O-sulfotransferase 2	AI767756
228547_at	1.53392	4.137632	10.98473	2.67E-22	5.83E-21	39.8488	NRXN1	neurexin 1	BF509242
205756_s_at	1.53354	7.073158	12.35284	1.82E-26	5.70E-25	49.36623	F8	coagulation factor VIII, procoagulant component	NM_000132
215388_s_at	1.53075	9.048158	9.79452	8.96E-19	1.39E-17	31.80066	CFH /// CFHR1	complement factor H /// complement factor H-related 1	X56210
231859_at	1.53022	6.391156	18.27237	1.24E-44	2.92E-42	90.93908	C14orf132 /// LOC100132684	chromosome 14 open reading frame 132 /// hypothetical protein LOC100132684	AK025915
217763_s_at	1.52987	9.682328	11.57315	4.42E-24	1.15E-22	43.91586	RAB31	RAB31, member RAS oncogene family	NM_006868
235438_at	1.52981	6.687438	12.33182	2.12E-26	6.59E-25	49.21856			AW162011
241365_at	1.52907	5.441719	11.7292	1.48E-24	3.99E-23	45.00181			AA002140
206049_at	1.52755	7.276297	11.49875	7.44E-24	1.88E-22	43.39909	SELP	selectin P (granule membrane protein 140kDa, antigen CD62)	NM_003005
213067_at	1.5261	6.865683	9.549924	4.58E-18	6.63E-17	30.1845	MYH10	myosin, heavy chain 10, non-muscle	AI382123
219895_at	1.52479	5.030133	8.969435	2.08E-16	2.54E-15	26.41278	FAM70A	family with sequence similarity 70, member A	NM_017938
201581_at	1.52407	9.013174	13.60274	2.53E-30	1.09E-28	58.19092	TXNDC13	thioredoxin domain containing 13	BF572868
210073_at	1.52358	4.596892	14.77584	5.89E-34	3.60E-32	66.5035	ST8SIA1	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 1	L32867
203810_at	1.5232	8.003993	14.88912	2.63E-34	1.67E-32	67.30541	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	BG252490
228790_at	1.52247	6.399508	14.68222	1.15E-33	6.79E-32	65.84049	FAM110B	family with sequence similarity 110, member B	AW264082
204062_s_at	1.52155	6.039409	17.63008	1.06E-42	1.72E-40	86.51765	ULK2	unc-51-like kinase 2 (C. elegans)	BG526973
226864_at	1.52051	4.475024	11.18151	6.80E-23	1.57E-21	41.20357	PKIA	Protein kinase inhibitor [human, neuroblastoma cell line SH-SY-5Y, mRNA, 2147 nt]	BF245954
203372_s_at	1.51923	5.947042	10.88088	5.47E-22	1.16E-20	39.13623	SOC32	suppressor of cytokine signaling 2	AB004903
228088_at	1.51871	6.242694	13.37142	1.32E-29	5.37E-28	56.55295	SESTD1	SEC14 and spectrin domains 1	AI092265
201311_s_at	1.51836	9.60292	15.42759	5.71E-36	4.28E-34	71.11198	SH3BGR1	SH3 domain binding glutamic acid-rich protein like	AL515318
219777_at	1.51824	7.891756	11.35995	1.96E-23	4.75E-22	42.4369	GIMAP6	GTPase, IMAP family member 6	NM_024711
230550_at	1.51814	6.366157	11.08841	1.30E-22	2.94E-21	40.56195	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	AA045175
242137_at	1.51765	3.912546	20.79936	4.65E-52	4.04E-49	107.9206			H10545
235740_at	1.51761	5.906402	11.03943	1.82E-22	4.07E-21	40.22486			BG250585
239533_at	1.5176	6.261821	8.651322	1.61E-15	1.80E-14	24.38844	GPR155	G protein-coupled receptor 155	AI970061
226252_at	1.51689	7.605875	16.05298	6.79E-38	6.16E-36	75.51774			AA058578
241745_at	1.51606	4.281623	19.74369	5.41E-49	2.76E-46	100.9123			BF671564
220276_at	1.51578	5.164006	9.522342	5.51E-18	7.91E-17	30.00319	RERGL	RERG/RAS-like	NM_024730
207808_s_at	1.51549	8.395635	9.366987	1.54E-17	2.11E-16	28.98575	PROS1	protein S (alpha)	NM_000313
222121_at	1.51375	4.097046	14.09191	7.73E-32	3.84E-30	61.65743	SGEF	Src homology 3 domain-containing guanine nucleotide exchange factor	AU118383
221541_at	1.5135	9.557047	12.25941	3.53E-26	1.08E-24	48.71019	CRISPLD2	cysteine-rich secretory protein LCCL domain containing 2	AL136861
1552316_a_at	1.51316	6.30338	11.94081	3.34E-25	9.52E-24	46.47863	GIMAP1	GTPase, IMAP family member 1	NM_130759
212091_s_at	1.51303	8.156324	12.92578	3.14E-28	1.13E-26	53.40226	COL6A1	collagen, type VI, alpha 1	AI141603
203324_s_at	1.51193	9.385745	8.319164	1.32E-14	1.32E-13	22.3107	CAV2	caveolin 2	NM_001233
226250_at	1.51192	6.969132	15.85498	2.76E-37	2.38E-35	74.12497			AU144961
211354_s_at	1.51138	5.260435	10.35734	1.99E-20	3.65E-19	35.57186	LEPR	leptin receptor	U52913
202191_s_at	1.51136	7.46232	14.62193	1.77E-33	1.02E-31	65.41346	GAS7	growth arrest-specific 7	BE439987
209086_x_at	1.51104	8.684374	15.36531	8.89E-36	6.54E-34	70.67221	MCAM	melanoma cell adhesion molecule	BE964361
214369_s_at	1.51041	5.817155	14.76583	6.33E-34	3.84E-32	66.43258	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	AI688812

214297_at	1.50704	5.409376	14.78352	5.58E-34	3.42E-32	66.55782	CSPG4	chondroitin sulfate proteoglycan 4	BE857703
208637_x_at	1.50615	10.28557	13.24013	3.35E-29	1.32E-27	55.62399	ACTN1	actinin, alpha 1	BC003576
213103_at	1.50587	7.68979	16.33771	9.09E-39	9.24E-37	77.51656	STARD13	STAR-related lipid transfer (START) domain containing 13	AA128023
224964_s_at	1.50563	8.364081	12.0423	1.64E-25	4.76E-24	47.18852	GNG2	guanine nucleotide binding protein (G protein), gamma 2	AK026424
241703_at	1.50526	5.476418	10.87896	5.54E-22	1.18E-20	39.12306	RUNDC3B	RUN domain containing 3B	AI928037
212192_at	1.5051	10.49174	11.17077	7.33E-23	1.69E-21	41.12952	KCTD12	potassium channel tetramerisation domain containing 12	AI718937
202759_s_at	1.50505	8.9824	15.00239	1.17E-34	7.77E-33	68.10687	AKAP2 /// PALM2 /// PALM2-AKAP2	A kinase (PRKA) anchor protein 2 /// paralemmin 2 /// PALM2-AKAP2 readthrough transcript	BE879367
244008_at	1.50487	6.596798	14.65835	1.36E-33	7.96E-32	65.67144			AW874263
203151_at	1.50365	7.116871	17.78479	3.62E-43	6.54E-41	87.58604	MAP1A	microtubule-associated protein 1A	AW296788
214040_s_at	1.50318	8.011157	14.16681	4.53E-32	2.28E-30	62.18832	GSN	gelsolin (amyloidosis, Finnish type)	BE675337
202458_at	1.5016	9.992866	11.79744	9.17E-25	2.52E-23	45.47753	PRSS23	protease, serine, 23	NM_007173
225798_at	1.50119	7.659366	13.25378	3.04E-29	1.20E-27	55.72054	JAZF1	JAZF zinc finger 1	AL047908
212298_at	1.50105	8.255944	11.9215	3.83E-25	1.09E-23	46.34367	NRP1	neuropilin 1	BE620457
224901_at	1.50073	7.072714	10.74645	1.38E-21	2.83E-20	38.21638	SCD5	stearoyl-CoA desaturase 5	AL571375
217762_s_at	1.50066	10.11223	12.02519	1.85E-25	5.36E-24	47.06876	RAB31	RAB31, member RAS oncogene family	BE789881
231993_at	1.49981	6.339928	8.772751	7.39E-16	8.54E-15	25.15734	ITGBL1	Osteoblast specific cysteine-rich protein	AK026784
219670_at	1.49981	6.01688	12.04363	1.62E-25	4.72E-24	47.19783	BEND5	BEN domain containing 5	NM_024603
213122_at	1.4996	7.55084	7.877052	2.05E-13	1.79E-12	19.6078	TSPYL5	TSPY-like 5	AI096375
208609_s_at	1.49944	7.133261	13.36223	1.40E-29	5.71E-28	56.48795	TNXB	tenascin XB	NM_019105
1568658_at	1.49928	6.256636	10.48225	8.48E-21	1.62E-19	36.41773	C2orf74	chromosome 2 open reading frame 74	BU069195
203811_s_at	1.49855	6.346945	14.34649	1.26E-32	6.64E-31	63.46185	DNAJB4	DnaJ (Hsp40) homolog, subfamily B, member 4	NM_007034
221935_s_at	1.49833	7.578243	12.68816	1.70E-27	5.77E-26	51.72595	C3orf64	chromosome 3 open reading frame 64	AK023140
222668_at	1.49801	7.127547	11.30528	2.87E-23	6.86E-22	42.05854	KCTD15	potassium channel tetramerisation domain containing 15	W73820
204036_at	1.49779	7.72777	10.35546	2.02E-20	3.69E-19	35.55915	LPAR1	lysophosphatidic acid receptor 1	AW269335
219829_at	1.49772	5.863783	15.0688	7.32E-35	4.89E-33	68.57667	ITGB1BP2	integrin beta 1 binding protein (melusin) 2	NM_012278
207002_s_at	1.49748	8.006976	10.60401	3.68E-21	7.27E-20	37.24515	PLAGL1	pleiomorphic adenoma gene-like 1	NM_002656
205608_s_at	1.49726	6.746608	12.75195	1.08E-27	3.73E-26	52.17564	ANGPT1	angiopoietin 1	U83508
232458_at	1.49678	6.145487	9.639216	2.53E-18	3.75E-17	30.77277	COL3A1	MRNA 3' region for pro-alpha1(III) collagen	AU146808
214247_s_at	1.49673	10.12285	11.03347	1.90E-22	4.23E-21	40.18385	DKK3	dickkopf homolog 3 (Xenopus laevis)	AU148057
236270_at	1.49654	5.144155	19.31886	9.59E-48	3.97E-45	98.05623	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	AI806528
226607_at	1.49545	8.025992	15.90178	1.98E-37	1.73E-35	74.4544	C20orf194	chromosome 20 open reading frame 194	AI498144
209487_at	1.49483	9.60694	13.02935	1.50E-28	5.56E-27	54.13382	RBPM5	RNA binding protein with multiple splicing	D84109
228962_at	1.4945	6.008911	13.1443	6.63E-29	2.53E-27	54.94629	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	BF507941
242828_at	1.49445	5.098303	12.61784	2.79E-27	9.34E-26	51.23046	FIGN	fidgetin	BG109695
226676_at	1.49427	6.081676	11.18273	6.74E-23	1.56E-21	41.21202	ZNF521	zinc finger protein 521	AK021452
201147_s_at	1.49374	8.292863	8.957484	2.24E-16	2.74E-15	26.33616	TIMP3	TIMP metalloproteinase inhibitor 3	BF347089
222725_s_at	1.49367	5.408679	13.25128	3.10E-29	1.22E-27	55.70283	PALMD	palmdelphin	AI082747
226192_at	1.49295	5.405189	14.0528	1.02E-31	5.00E-30	61.38022			T68445
1555989_at	1.49252	6.6987	9.010824	1.59E-16	1.96E-15	26.6785			AA890373
215870_s_at	1.4918	4.809827	10.76508	1.22E-21	2.50E-20	38.34374	PLA2G5	phospholipase A2, group V	AL158172
212397_at	1.4912	9.197911	9.97135	2.73E-19	4.47E-18	32.97801	RDX	radixin	AL137751

213283_s_at	1.49061	6.958253	15.16635	3.66E-35	2.53E-33	69.26641	SALL2	sal-like 2 (Drosophila)	BG285616
209379_s_at	1.49057	7.845296	16.75392	4.85E-40	5.82E-38	80.42902	KIAA1128	KIAA1128	AF241785
212736_at	1.49032	7.522125	16.3333	9.37E-39	9.50E-37	77.4857	C16orf45	chromosome 16 open reading frame 45	BE299456
206488_s_at	1.48849	7.002153	7.403797	3.53E-12	2.64E-11	16.80211	CD36	CD36 molecule (thrombospondin receptor)	NM_000072
230479_at	1.48615	5.457177	14.47264	5.12E-33	2.79E-31	64.35578			AI872374
217437_s_at	1.48608	8.938525	12.24843	3.82E-26	1.17E-24	48.63318	TACC1	transforming, acidic coiled-coil containing protein 1	AB029026
242680_at	1.48495	6.281022	8.891596	3.44E-16	4.11E-15	25.91449			AW242409
213290_at	1.48474	7.664715	17.70305	6.38E-43	1.10E-40	87.02186	COL6A2	collagen, type VI, alpha 2	AL531750
216321_s_at	1.48467	9.238652	13.41078	9.94E-30	4.10E-28	56.83159	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	X03348
228304_at	1.48353	6.713762	14.56461	2.66E-33	1.50E-31	65.00739			BE674118
212254_s_at	1.48334	9.290638	13.28504	2.43E-29	9.74E-28	55.94169	DST	dystonin	AI798790
206481_s_at	1.48119	7.644828	10.68727	2.08E-21	4.19E-20	37.81241	LDB2	LIM domain binding 2	NM_001290
201312_s_at	1.48115	10.98967	14.67113	1.24E-33	7.29E-32	65.76198	SH3BGR1	SH3 domain binding glutamic acid-rich protein like	NM_003022
201560_at	1.48108	10.7797	14.98627	1.32E-34	8.65E-33	67.99285	CLIC4	chloride intracellular channel 4	NM_013943
235798_at	1.48066	4.91875	11.70507	1.75E-24	4.69E-23	44.83366	TMEM170B	transmembrane protein 170B	BE671123
235494_at	1.4804	5.775418	17.11323	3.90E-41	5.19E-39	82.93332			AA702209
219821_s_at	1.48018	7.492454	16.50505	2.79E-39	3.02E-37	78.689	GFOD1	glucose-fructose oxidoreductase domain containing 1	NM_018988
229367_s_at	1.47967	7.307425	11.14765	8.61E-23	1.97E-21	40.97005	GIMAP6	GTPase, IMAP family member 6	AW130536
235044_at	1.4793	6.62708	12.16745	6.76E-26	2.03E-24	48.0652	CYYR1	cysteine/tyrosine-rich 1	H06649
203231_s_at	1.47915	7.05332	13.0545	1.26E-28	4.68E-27	54.3115	ATXN1	ataxin 1	AW235612
205694_at	1.47896	6.731585	5.660124	5.15E-08	1.91E-07	7.414694	TYRP1	tyrosinase-related protein 1	NM_000550
209070_s_at	1.47812	10.41322	9.737499	1.31E-18	1.99E-17	31.42257	RGS5	regulator of G-protein signaling 5	AI183997
229114_at	1.47678	6.955717	12.82458	6.44E-28	2.27E-26	52.68796	GAB1	GRB2-associated binding protein 1	AW237741
225939_at	1.47612	5.129333	14.89943	2.44E-34	1.56E-32	67.37834	EIF4E3	eukaryotic translation initiation factor 4E family member 3	AL161983
213131_at	1.47465	7.185143	9.481729	7.21E-18	1.02E-16	29.7366	OLFM1	olfactomedin 1	R38389
204454_at	1.47429	7.456461	13.39986	1.07E-29	4.41E-28	56.75431	LDOC1	leucine zipper, down-regulated in cancer 1	NM_012317
229084_at	1.47428	6.579924	9.707773	1.60E-18	2.41E-17	31.22579	CNTN4	contactin 4	R42166
212667_at	1.47366	10.28795	10.37528	1.76E-20	3.25E-19	35.69319	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	AL575922
49452_at	1.47353	7.093288	10.73506	1.50E-21	3.05E-20	38.13862	ACACB	acetyl-Coenzyme A carboxylase beta	AI057637
225812_at	1.47351	7.142227	13.68846	1.37E-30	6.06E-29	58.79818	C6orf225	chromosome 6 open reading frame 225	N36759
212670_at	1.47335	7.599963	11.35402	2.05E-23	4.94E-22	42.39585	ELN	elastin	AA479278
226065_at	1.47285	7.540532	12.66431	2.01E-27	6.79E-26	51.55785	PRICKLE1	prickle homolog 1 (Drosophila)	N98595
242051_at	1.47077	4.969984	13.54236	3.89E-30	1.65E-28	57.76322			AI695695
227554_at	1.4707	6.58407	16.22333	2.04E-38	1.97E-36	76.71419			AU145805
204099_at	1.47066	7.227374	16.2218	2.06E-38	1.98E-36	76.70346	SMARCD3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	NM_003078
219563_at	1.46995	6.798664	11.02731	1.98E-22	4.40E-21	40.14149	C14orf139	chromosome 14 open reading frame 139	NM_024633
212494_at	1.46949	7.354864	16.40875	5.51E-39	5.73E-37	78.01453	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	AB028998
213894_at	1.46812	5.817576	11.74058	1.37E-24	3.70E-23	45.08107	THSD7A	thrombospondin, type I, domain containing 7A	BF447246
203299_s_at	1.468	7.12815	19.32726	9.06E-48	3.83E-45	98.11288	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	AF251295
1556695_a at	1.46785	4.159884	21.76893	7.99E-55	1.46E-51	114.2402	FLJ42709	hypothetical gene supported by AK124699	AK095719
227279_at	1.46761	9.042873	12.01805	1.94E-25	5.62E-24	47.01875	TCEAL3	transcription elongation factor A (SII)-like 3	AA847654
205265_s_at	1.46735	6.566696	15.89213	2.12E-37	1.85E-35	74.38645	SPEG	SPEG complex locus	NM_005876
202948_at	1.46674	9.552641	11.41112	1.37E-23	3.38E-22	42.79131	IL1R1	interleukin 1 receptor, type I	NM_000877

235432_at	1.46622	7.04913	15.10883	5.51E-35	3.71E-33	68.85975	ACAD11 /// NPHP3	acyl-Coenzyme A dehydrogenase family, member 11 /// nephronophthsis 3 (adolescent)	BE865779
202947_s_at	1.46619	8.710748	18.1274	3.37E-44	7.30E-42	89.94444	GYPC	glycophorin C (Gerbich blood group)	NM_002101
231726_at	1.46518	5.712399	10.42904	1.22E-20	2.29E-19	36.05706	PCDHB14	protocadherin beta 14	NM_018934
205902_at	1.46488	6.35275	12.09587	1.12E-25	3.31E-24	47.56358	KCNN3 /// LOC100133958	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 /// similar to small	AJ251016
								conductance calcium-activated potassium channel protein 3	#N/A
223283_s_at	1.4646	8.483059	14.69466	1.05E-33	6.23E-32	65.92863	TSHZ1	teashirt zinc finger homeobox 1	AF039698
202686_s_at	1.46445	8.641337	12.05637	1.48E-25	4.33E-24	47.28701	AXL	AXL receptor tyrosine kinase	NM_021913
202746_at	1.46426	8.75618	7.589051	1.17E-12	9.28E-12	17.88898	ITM2A	integral membrane protein 2A	AL021786
226382_at	1.46406	6.661802	11.82792	7.40E-25	2.05E-23	45.69018	LOC283070	hypothetical protein LOC283070	AA528080
201151_s_at	1.46402	8.557672	13.06211	1.19E-28	4.45E-27	54.3653	MBNL1	muscleblind-like (Drosophila)	BF512200
207173_x_at	1.46388	10.06185	9.097454	9.02E-17	1.14E-15	27.23631	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	D21254
209230_s_at	1.46342	8.733586	10.82019	8.31E-22	1.74E-20	38.72063	NUPR1	nuclear protein 1	AF135266
1557167_at	1.46307	4.502405	14.67348	1.22E-33	7.19E-32	65.77858	HCG11	HLA complex group 11	AK024111
204529_s_at	1.4621	7.435207	7.717578	5.40E-13	4.47E-12	18.65176	TOX	thymocyte selection-associated high mobility group box	AI961231
236396_at	1.46156	5.161803	12.8357	5.95E-28	2.10E-26	52.76642			AW051952
202409_at	1.46117	8.440905	5.902612	1.50E-08	6.17E-08	8.618614	IGF2 /// INS-IGF2	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	X07868
238332_at	1.46016	6.669069	8.858398	4.26E-16	5.04E-15	25.70254	ANKRD29	ankyrin repeat domain 29	AI307802
227272_at	1.45911	6.668971	11.51095	6.83E-24	1.74E-22	43.48376	C15orf52	chromosome 15 open reading frame 52	BE673226
232568_at	1.45908	4.398903	14.20997	3.33E-32	1.70E-30	62.49422	MGC24103	hypothetical protein MGC24103	AU145658
226022_at	1.45849	8.908127	14.40053	8.56E-33	4.57E-31	63.84479	SASH1	SAM and SH3 domain containing 1	AU144882
232884_s_at	1.45797	5.780365	16.87217	2.11E-40	2.63E-38	81.25432	ZNF853	zinc finger protein 853	AL133055
210078_s_at	1.45772	5.746718	10.18025	6.64E-20	1.16E-18	34.37796	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	L39833
204236_at	1.45667	7.059221	10.78611	1.05E-21	2.18E-20	38.48745	FLI1	Friend leukemia virus integration 1	NM_002017
225355_at	1.45591	8.580359	11.50802	6.98E-24	1.77E-22	43.46342	LOC54492	neuralized-2	AK026748
242286_at	1.45489	4.430843	14.67834	1.18E-33	6.95E-32	65.81303	GRIN2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	N48896
226484_at	1.45416	6.875262	15.96859	1.23E-37	1.10E-35	74.9244	ZBTB47	zinc finger and BTB domain containing 47	AA532640
241752_at	1.45274	5.249718	14.88862	2.64E-34	1.68E-32	67.30186	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	AA094434
228665_at	1.45259	7.744403	12.07448	1.30E-25	3.84E-24	47.41378	CYYR1	cysteine/tyrosine-rich 1	AI458003
212681_at	1.45235	6.281342	8.716355	1.06E-15	1.21E-14	24.79964	EPB41L3	erythrocyte membrane protein band 4.1-like 3	AI770004
213657_s_at	1.45207	6.547128	11.19014	6.41E-23	1.49E-21	41.26314			BE858194
1552318_at	1.45138	5.52779	13.67256	1.54E-30	6.75E-29	58.6855	GIMAP1	GTPase, IMAP family member 1	AK091818
213228_at	1.45093	5.879698	15.16919	3.58E-35	2.48E-33	69.28654	PDE8B	phosphodiesterase 8B	AK023913
244455_at	1.4504	4.722501	13.10633	8.68E-29	3.28E-27	54.67782	KCNT2	potassium channel, subfamily T, member 2	AI732637
238905_at	1.45033	6.593943	17.51233	2.41E-42	3.70E-40	85.70299	RHOJ	ras homolog gene family, member J	BE218803
219607_s_at	1.45027	8.189857	6.989348	3.96E-11	2.55E-10	14.42732	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	NM_024021
213541_s_at	1.4492	6.394693	12.84809	5.45E-28	1.93E-26	52.85384	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	AI351043

210375_at	1.44862	4.4296	10.83245	7.64E-22	1.60E-20	38.80453	PTGER3	prostaglandin E receptor 3 (subtype EP3)	X83858
228740_at	1.44794	4.423813	14.69616	1.04E-33	6.17E-32	65.93921			BF059276
213006_at	1.44793	5.803576	11.05557	1.63E-22	3.65E-21	40.33585	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	AV655640
227273_at	1.44785	8.053942	16.71296	6.47E-40	7.70E-38	80.14293			AI126798
229313_at	1.44719	5.566219	9.867518	5.49E-19	8.70E-18	32.28581	ANOS	anoctamin 5	AA843962
227995_at	1.44621	6.465733	12.47187	7.86E-27	2.53E-25	50.20299			AI051950
221958_s_at	1.44617	9.202841	10.66388	2.44E-21	4.90E-20	37.65295	GPR177	G protein-coupled receptor 177	AA775681
219091_s_at	1.44592	7.200316	14.02661	1.23E-31	5.98E-30	61.19454	MMRN2	multimerin 2	NM_024756
205139_s_at	1.44536	6.419916	9.258857	3.14E-17	4.16E-16	28.28146	UST	uronyl-2-sulfotransferase	NM_005715
226972_s_at	1.44531	5.59032	12.57568	3.77E-27	1.25E-25	50.93356	CCDC136	coiled-coil domain containing 136	AI678057
230418_s_at	1.44449	5.013376	15.14582	4.23E-35	2.91E-33	69.12131	GALNTL1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase-like 1	AI097463
225687_at	1.44396	9.328333	7.445658	2.76E-12	2.09E-11	17.04638	FAM83D	family with sequence similarity 83, member D	BC001068
239250_at	1.44344	6.040754	14.42498	7.19E-33	3.87E-31	64.01803	ZNF542	zinc finger protein 542	BE966038
225459_at	1.44328	6.234612	17.04178	6.44E-41	8.35E-39	82.43611	AMOTL1	angiomin like 1	AU157155
208848_at	1.44286	9.280931	15.1703	3.56E-35	2.46E-33	69.29433	ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide	M30471
228335_at	1.44226	5.834348	6.670892	2.40E-10	1.36E-09	12.65938	CLDN11	claudin 11	AW264204
229327_s_at	1.44206	5.610669	10.23389	4.61E-20	8.16E-19	34.7389			BE674528
201280_s_at	1.44153	9.23396	11.0122	2.20E-22	4.86E-21	40.03763	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	NM_001343
228390_at	1.44062	6.729026	10.70333	1.86E-21	3.77E-20	37.92198			AA489100
1553962_s_at	1.44039	7.558668	12.39514	1.35E-26	4.29E-25	49.66352	RHOB	ras homolog gene family, member B	BI668074
204134_at	1.44024	6.721912	14.0527	1.02E-31	5.00E-30	61.37952	PDE2A	phosphodiesterase 2A, cGMP-stimulated	NM_002599
230435_at	1.43937	6.915102	17.8225	2.78E-43	5.17E-41	87.84618	LOC375190	hypothetical LOC375190	BF108666
227400_at	1.43838	8.623442	14.39915	8.64E-33	4.61E-31	63.83499	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	AI355848
203542_s_at	1.43834	8.09754	12.04304	1.63E-25	4.74E-24	47.19368	KLF9	Kruppel-like factor 9	AI690205
228399_at	1.43749	5.633436	10.67088	2.33E-21	4.68E-20	37.70065	OSR1	odd-skipped related 1 (Drosophila)	AI569974
235471_at	1.43577	5.770515	17.11947	3.74E-41	4.98E-39	82.97672	C10orf72	chromosome 10 open reading frame 72	BE858464
211355_x_at	1.43465	5.67123	10.16488	7.37E-20	1.28E-18	34.27463	LEPR	leptin receptor	U52914
218380_at	1.43452	7.212586	11.53781	5.66E-24	1.45E-22	43.67029	NLRP1	NLR family, pyrin domain containing 1	NM_021730
227148_at	1.4345	5.329201	13.38682	1.18E-29	4.83E-28	56.662	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	AI913749
225878_at	1.43368	7.894959	14.83215	3.95E-34	2.46E-32	66.90211	KIF1B	kinesin family member 1B	AL135264
238636_at	1.43355	4.966143	14.04267	1.10E-31	5.36E-30	61.30839	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	BG430061
223392_s_at	1.43341	7.049477	17.52923	2.14E-42	3.35E-40	85.82001	TSHZ3	teashirt zinc finger homeobox 3	BF510588
200953_s_at	1.43291	9.558073	9.243893	3.46E-17	4.56E-16	28.18425	CCND2	cyclin D2	NM_001759
217757_at	1.43265	11.5918	12.80942	7.17E-28	2.51E-26	52.58099	A2M	alpha-2-macroglobulin	NM_000014
226066_at	1.43254	7.923851	11.6941	1.89E-24	5.05E-23	44.75725	MITF	microphthalmia-associated transcription factor	AL117653
226203_at	1.43109	7.281781	20.32689	1.08E-50	7.75E-48	104.8			AA868896
228141_at	1.43052	6.709392	9.88412	4.91E-19	7.82E-18	32.39632	GPX8	glutathione peroxidase 8 (putative)	AA173223
204115_at	1.43036	9.137159	13.13175	7.25E-29	2.75E-27	54.85755	GNG11	guanine nucleotide binding protein (G protein), gamma 11	NM_004126
206710_s_at	1.42997	6.444627	8.489051	4.52E-15	4.78E-14	23.3686	EPB41L3	erythrocyte membrane protein band 4.1-like 3	NM_012307
230715_at	1.42996	4.962712	15.10766	5.55E-35	3.74E-33	68.8515	ZNF518B	zinc finger protein 518B	AI138969
235164_at	1.42837	6.127428	18.8841	1.86E-46	5.89E-44	95.11315	ZNF25	zinc finger protein 25	BG433539
209118_s_at	1.42726	11.82382	13.38062	1.23E-29	5.04E-28	56.61809	TUBA1A	tubulin, alpha 1a	AF141347
203180_at	1.42633	8.61219	9.328437	1.98E-17	2.68E-16	28.73429	ALDH1A3	aldehyde dehydrogenase 1 family, member A3	NM_000693
224694_at	1.42612	9.856494	8.629252	1.85E-15	2.06E-14	24.24921	ANTXR1	anthrax toxin receptor 1	AF279145

230708_at	1.42592	5.850787	13.70714	1.20E-30	5.32E-29	58.93051	PRICKLE1	Prickle homolog 1 (Drosophila) (PRICKLE1), mRNA	AA206141
223340_at	1.42577	6.946264	12.96092	2.44E-28	8.90E-27	53.65043	ATL1	atlastin GTPase 1	AF131801
205593_s_at	1.42394	6.288634	10.52015	6.54E-21	1.26E-19	36.67502	PDE9A	phosphodiesterase 9A	NM_002606
219779_at	1.42393	6.505065	14.04827	1.06E-31	5.16E-30	61.34806	ZFX4	zinc finger homeobox 4	NM_024721
210832_x_at	1.42387	6.109343	13.22146	3.83E-29	1.50E-27	55.49192	PTGER3	prostaglandin E receptor 3 (subtype EP3)	D38298
226694_at	1.42367	10.12156	13.92766	2.49E-31	1.18E-29	60.49319	AKAP2 /// PALM2 /// PALM2-AKAP2	A kinase (PRKA) anchor protein.2 /// paralemmin 2 /// PALM2-AKAP2 readthrough transcript	BG540494
1556185_a_at	1.42304	4.529368	12.14197	8.10E-26	2.41E-24	47.88656			BC035072
230866_at	1.42226	5.329733	11.70137	1.80E-24	4.81E-23	44.80793	CYSLTR1	cysteinyl leukotriene receptor 1	BE549540
225045_at	1.42212	6.177627	12.11301	9.94E-26	2.94E-24	47.68362	CCDC88A	coiled-coil domain containing 88A	AB033038
205514_at	1.42206	5.029776	10.95017	3.39E-22	7.34E-21	39.6115	ZNF415	zinc finger protein 415	NM_018355
230369_at	1.42015	6.197358	13.26068	2.89E-29	1.15E-27	55.76936	GPR161	G protein-coupled receptor 161	AI743151
202742_s_at	1.42014	7.809898	9.060406	1.15E-16	1.44E-15	26.99748	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	NM_002731
201278_at	1.42006	8.411464	11.54471	5.40E-24	1.39E-22	43.71824	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	N21202
220817_at	1.41922	4.110644	12.53109	5.17E-27	1.69E-25	50.61965	TRPC4	transient receptor potential cation channel, subfamily C, member 4	NM_016179
212158_at	1.41787	9.402354	11.08017	1.38E-22	3.10E-21	40.50522	SDC2	syndecan 2	AL577322
204773_at	1.41767	6.679766	16.94857	1.24E-40	1.57E-38	81.78689	IL11RA	interleukin 11 receptor, alpha	NM_004512
225575_at	1.4176	7.721548	7.646096	8.31E-13	6.71E-12	18.22666	LIFR	leukemia inhibitory factor receptor alpha	AI680541
209120_at	1.41653	10.05977	13.50707	5.00E-30	2.11E-28	57.51334	NR2F2	nuclear receptor subfamily 2, group F, member 2	AI037401
235666_at	1.4164	7.562962	7.375707	4.17E-12	3.08E-11	16.63864			AA903473
223614_at	1.41559	5.927258	12.88747	4.12E-28	1.48E-26	53.13178	MMP16	matrix metalloproteinase 16 (membrane-inserted)	AL136588
238669_at	1.41549	7.284672	11.98636	2.43E-25	6.94E-24	46.79712	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	BE613133
211671_s_at	1.41501	9.093462	11.53285	5.86E-24	1.50E-22	43.63586	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	U01351
229779_at	1.41395	5.57242	8.016993	8.66E-14	7.95E-13	20.45519	COL4A4	collagen, type IV, alpha 4	BF476080
219106_s_at	1.41342	3.685307	11.50162	7.29E-24	1.85E-22	43.41902	KBTBD10	kelch repeat and BTB (POZ) domain containing 10	NM_006063
222101_s_at	1.41316	8.129169	13.53541	4.09E-30	1.73E-28	57.71404	DCHS1	dachsous 1 (Drosophila)	BF222893
242007_at	1.41301	4.95458	16.5565	1.94E-39	2.15E-37	79.04903			AI678258
206580_s_at	1.41285	8.381673	15.24448	2.10E-35	1.47E-33	69.81864	EFEMP2	EGF-containing fibulin-like extracellular matrix protein 2	NM_016938
234936_s_at	1.41118	6.81007	18.25335	1.41E-44	3.28E-42	90.80868	CC2D2A	coiled-coil and C2 domain containing 2A	AK023876
202047_s_at	1.41101	8.601599	14.08897	7.89E-32	3.91E-30	61.63657	CBX6	chromobox homolog 6	AI458128
201389_at	1.41084	8.475695	10.95212	3.34E-22	7.24E-21	39.62489	ITGA5	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	NM_002205
217599_s_at	1.41036	6.043812	12.17211	6.55E-26	1.97E-24	48.0978	MDFIC	MyoD family inhibitor domain containing	BE910600
37590_g_at	1.41033	6.260613	11.24332	4.42E-23	1.04E-21	41.6303			AL109698
219514_at	1.41019	6.546667	13.92018	2.63E-31	1.24E-29	60.4402	ANGPTL2	angiopoietin-like 2	NM_012098
235733_at	1.41003	5.894226	9.826272	7.24E-19	1.13E-17	32.01153			AW043921
222719_s_at	1.40841	6.276834	10.11886	1.01E-19	1.73E-18	33.96557	PDGFC	platelet derived growth factor C	AB033831
209197_at	1.408	6.947467	14.82384	4.19E-34	2.59E-32	66.84328	SYT11	synaptotagmin XI	AA626780
217506_at	1.40762	6.621993	10.70611	1.82E-21	3.70E-20	37.941	LOC400642	Hypothetical gene supported by BC041875; BX648984, mRNA (cDNA clone IMAGE:5271951)	H49382
227099_s_at	1.40762	10.95635	9.420437	1.08E-17	1.50E-16	29.33508	LOC387763	hypothetical LOC387763	AW276078
226541_at	1.40761	8.764279	15.73839	6.30E-37	5.21E-35	73.30392	FBXO30	F-box protein 30	AI808182
235355_at	1.40724	5.026911	10.82511	8.04E-22	1.68E-20	38.7543			AL037998

229228_at	1.40695	4.970987	11.57205	4.46E-24	1.16E-22	43.90816	CREB5	cAMP responsive element binding protein 5	AI819043
204045_at	1.40651	8.387656	13.14777	6.47E-29	2.47E-27	54.97081	TCEAL1	transcription elongation factor A (SII)-like 1	NM_004780
219090_at	1.40552	7.496489	9.883654	4.93E-19	7.84E-18	32.39322	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	NM_020689
213415_at	1.40514	7.282157	10.05711	1.53E-19	2.57E-18	33.55154	CLIC2	chloride intracellular channel 2	AI768628
232544_at	1.40386	4.590783	15.83113	3.26E-37	2.78E-35	73.95708			AU144916
238488_at	1.40357	5.777963	11.55959	4.86E-24	1.26E-22	43.82163	hCG_2045899	synleurin	BF511602
204063_s_at	1.40273	5.827766	18.62456	1.10E-45	3.16E-43	93.34678	ULK2	unc-51-like kinase 2 (C. elegans)	NM_014683
229072_at	1.4027	6.062139	11.44193	1.11E-23	2.75E-22	43.00491			BF968097
228325_at	1.40215	7.088197	10.62108	3.27E-21	6.50E-20	37.36132	KIAA0146	Clone C4E 5.1 (CAC)n/(GTG)n repeat-containing mRNA	AI363213
235504_at	1.40158	5.112519	10.76864	1.19E-21	2.44E-20	38.36801	GREM2	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	BE786990
229317_at	1.40118	5.848356	13.52505	4.40E-30	1.86E-28	57.64064	KPNA5	karyopherin alpha 5 (importin alpha 6)	BG231980
214434_at	1.40094	5.677212	17.47205	3.19E-42	4.78E-40	85.42407	HSPA12A	heat shock 70kDa protein 12A	AB007877
230661_at	1.40065	5.726191	9.25175	3.29E-17	4.35E-16	28.23528	RPESP	RPE-spondin (RPESP), mRNA	AW451999
210986_s_at	1.39969	12.41135	15.08118	6.70E-35	4.49E-33	68.66419	TPM1	tropomyosin 1 (alpha)	Z24727
226653_at	1.39961	5.040546	9.681478	1.91E-18	2.85E-17	31.05189	MARK1	MAP/microtubule affinity-regulating kinase 1	AB040910
226810_at	1.39883	8.350518	11.51495	6.64E-24	1.69E-22	43.51155	OGFRL1	opioid growth factor receptor-like 1	BE500942
204339_s_at	1.39786	6.246994	10.83499	7.51E-22	1.58E-20	38.82192	RGS4	regulator of G-protein signaling 4	BC000737
239218_at	1.39665	4.307941	11.86029	5.89E-25	1.65E-23	45.91611	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	AI800515
203232_s_at	1.39663	8.433395	15.59201	1.78E-36	1.41E-34	72.27213	ATXN1	ataxin 1	NM_000332
229623_at	1.39652	6.455886	9.450121	8.89E-18	1.25E-16	29.52942	FLJ12993	Hypothetical LOC441027 (FLJ12993), mRNA	BF508344
201133_s_at	1.3965	9.126352	17.84626	2.36E-43	4.45E-41	88.01004	PJA2	praja ring finger 2	AA142966
225975_at	1.39649	8.356779	11.15242	8.33E-23	1.91E-21	41.00293	PCDH18	protocadherin 18	AW189885
209525_at	1.39577	5.419983	15.81976	3.54E-37	3.00E-35	73.87705	HDGFRP3	Hepatoma-derived growth factor 2 (HDGF2)	BG285017
230175_s_at	1.39476	5.977136	10.46992	9.23E-21	1.75E-19	36.3341			AA805633
237802_at	1.394	3.869279	11.12062	1.04E-22	2.37E-21	40.78378	XKR4	XK, Kell blood group complex subunit-related family, member 4	R54212
204037_at	1.39374	6.611776	13.48529	5.84E-30	2.45E-28	57.35908	LPAR1	lysophosphatidic acid receptor 1	BF055366
224840_at	1.39306	9.711121	11.21729	5.30E-23	1.24E-21	41.45053	FKBP5	FK506 binding protein 5	AI753747
238668_at	1.39289	6.410466	9.905808	4.24E-19	6.82E-18	32.54079			AI130690
204221_x_at	1.39262	6.423773	13.70121	1.25E-30	5.55E-29	58.88846	GLIPR1	GLI pathogenesis-related 1	U16307
202796_at	1.39261	8.336355	14.28539	1.94E-32	1.00E-30	63.02882	SYNPO	synaptopodin	NM_007286
213906_at	1.39223	5.308058	8.490106	4.49E-15	4.75E-14	23.37521	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	AW592266
1557169_x_at	1.39203	4.763147	14.603	2.02E-33	1.16E-31	65.27936	HCG11	HLA complex group 11	AK024111
205100_at	1.392	6.62849	10.52517	6.32E-21	1.22E-19	36.70908	GFPT2	glutamine-fructose-6-phosphate transaminase 2	NM_005110
213069_at	1.39086	9.242794	13.7962	6.37E-31	2.90E-29	59.56154	HEG1	HEG homolog 1 (zebrafish)	AI148659
244521_at	1.39037	4.890902	16.82676	2.91E-40	3.52E-38	80.93748	TSHZ2	Cell growth-inhibiting protein 7	BG236742
230085_at	1.39031	6.592879	11.77938	1.04E-24	2.84E-23	45.3516			AW263542
231866_at	1.38997	8.268946	14.87365	2.94E-34	1.86E-32	67.19589	LNPEP	leucyl/cystinyl aminopeptidase	AA767440
229092_at	1.38992	5.654129	12.73226	1.24E-27	4.27E-26	52.03685	NR2F2	nuclear receptor subfamily 2, group F, member 2	AI420144
226977_at	1.38982	7.856841	16.89798	1.76E-40	2.21E-38	81.4343	LOC49231	similar to bovine IgA regulatory protein	N26029
230218_at	1.38981	6.179315	13.97846	1.74E-31	8.31E-30	60.8533	HIC1	hypermethylated in cancer 1	BF476403
229657_at	1.38894	7.02774	8.813369	5.69E-16	6.65E-15	25.41561	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	BF431989
225185_at	1.38834	7.718901	16.58138	1.63E-39	1.83E-37	79.22308	MRAS	muscle RAS oncogene homolog	BF343625

242332_at	1.38809	6.841297	14.21982	3.10E-32	1.59E-30	62.56407	LOC28390	4	hypothetical protein LOC283904	AI356966
204759_at	1.3879	8.190257	14.99796	1.21E-34	7.99E-33	68.07556	RCBTB2		regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	NM_001268
218031_s_at	1.38714	8.565104	14.28335	1.97E-32	1.02E-30	63.0143	FOXN3		forkhead box N3	NM_018589
225303_at	1.38676	6.975491	14.49318	4.42E-33	2.45E-31	64.5013	KIRREL		kin of IRRE like (Drosophila)	AI049973
210831_s_at	1.38641	5.65857	12.69252	1.64E-27	5.61E-26	51.75666	PTGER3		prostaglandin E receptor 3 (subtype EP3)	L27489
227395_at	1.38586	6.988745	12.42747	1.08E-26	3.44E-25	49.89073	TBCEL		Tubulin folding cofactor E-like (TBCEL), transcript variant 1, mRNA	BE672045
203758_at	1.38524	8.511091	12.37036	1.61E-26	5.08E-25	49.48931	CTSO		cathepsin O	AV729484
235831_at	1.38497	3.819972	13.8695	3.78E-31	1.75E-29	60.08103				AI590238
236473_at	1.38494	5.564679	18.10319	3.98E-44	8.50E-42	89.7782	CC2D2A		coiled-coil and C2 domain containing 2A	AI765222
218980_at	1.38463	5.202364	11.64073	2.75E-24	7.29E-23	44.38576	FHOD3		formin homology 2 domain containing 3	NM_025135
207119_at	1.38413	4.132435	21.35083	1.23E-53	1.64E-50	111.5291	PRKG1		protein kinase, cGMP-dependent, type I	NM_006258
204646_at	1.38343	8.871551	10.29923	2.96E-20	5.33E-19	35.1794	DPYD		dihydropyrimidine dehydrogenase	NM_000110
201604_s_at	1.38266	8.5334	14.65348	1.41E-33	8.21E-32	65.63691	PPP1R12A		protein phosphatase 1, regulatory (inhibitor) subunit 12A	NM_002480
227178_at	1.38244	7.048802	17.927	1.35E-43	2.62E-41	88.5663	CUGBP2		CUG triplet repeat, RNA binding protein 2	AI652861
218718_at	1.38235	9.276599	9.385083	1.37E-17	1.88E-16	29.10393	PDGFC		platelet derived growth factor C	NM_016205
201602_s_at	1.38162	8.426554	14.99127	1.27E-34	8.36E-33	68.02825	PPP1R12A		protein phosphatase 1, regulatory (inhibitor) subunit 12A	BE737620
1554474_a_at	1.3811	6.875492	10.11829	1.01E-19	1.73E-18	33.96173	MOXD1		monooxygenase, DBH-like 1	BC018756
210764_s_at	1.37901	9.85161	7.729282	5.03E-13	4.19E-12	18.72156	CYR61		cysteine-rich, angiogenic inducer, 61	AF003114
202921_s_at	1.37837	5.291714	16.5765	1.69E-39	1.88E-37	79.18897	ANK2		ankyrin 2, neuronal	NM_001148
229613_at	1.3778	5.595325	11.07418	1.43E-22	3.23E-21	40.46392				BF724178
225651_at	1.37724	8.617604	11.04662	1.74E-22	3.88E-21	40.27432	UBE2E2		ubiquitin-conjugating enzyme E2E2 (UBC4/5 homolog, yeast)	BF431962
231964_at	1.37664	4.919466	14.08797	7.95E-32	3.94E-30	61.62947				AL117598
219578_s_at	1.37591	5.188218	19.72755	6.03E-49	3.05E-46	100.8041	CPEB1		cytoplasmic polyadenylation element binding protein 1	NM_030594
205348_s_at	1.3756	6.036956	13.39269	1.13E-29	4.64E-28	56.70349	DYNC111		dynein, cytoplasmic 1, intermediate chain 1	NM_004411
206702_at	1.37511	6.755277	11.16707	7.52E-23	1.73E-21	41.10402	TEK		TEK tyrosine kinase, endothelial	NM_000459
235410_at	1.37438	6.508205	14.29795	1.78E-32	9.24E-31	63.11782	ACAD11	/// NPHP3	acyl-Coenzyme A dehydrogenase family, member 11 /// nephronophthisis 3 (adolescent)	BG034966
239336_at	1.37423	4.978311	10.54157	5.65E-21	1.10E-19	36.82049	THBS1		(clone lambda-TS-33) thrombospondin (THBS) mRNA, 5' end	BF109732
225855_at	1.37412	6.31803	15.88148	2.28E-37	1.98E-35	74.3115	EPB41L5		erythrocyte membrane protein band 4.1 like 5	AB046768
207980_s_at	1.37405	6.910154	9.787804	9.37E-19	1.45E-17	31.75609	CITED2		Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	NM_006079
205109_s_at	1.3736	5.412324	12.23471	4.21E-26	1.28E-24	48.53686	ARHGEF4		Rho guanine nucleotide exchange factor (GEF) 4	NM_015320
202008_s_at	1.37275	7.287011	14.51203	3.86E-33	2.15E-31	64.63491	NID1		nidogen 1	NM_002508
209147_s_at	1.37272	9.453946	14.08665	8.02E-32	3.97E-30	61.62014	PPAP2A		phosphatidic acid phosphatase type 2A	AB000888
212263_at	1.37242	8.851109	13.35292	1.50E-29	6.09E-28	56.42207	QKI		quaking homolog, KH domain RNA binding (mouse)	AI114716
241864_x_at	1.37219	4.821532	12.22698	4.44E-26	1.35E-24	48.48267				AW025980
205683_x_at	1.37215	8.368604	6.876581	7.54E-11	4.64E-10	13.79543	TPSAB1	///	tryptase alpha/beta 1 /// tryptase	
200982_s_at	1.37201	9.191333	14.91536	2.18E-34	1.40E-32	67.49106	TPSB2		beta 2	NM_003294
1554464_a_at	1.37173	8.593676	11.54264	5.47E-24	1.41E-22	43.70384	ANXA6		annexin A6	NM_001155
							CRTAP		cartilage associated protein	BC008745

221016_s_at	1.37163	6.685149	14.83165	3.96E-34	2.46E-32	66.89858	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)	NM_031283
226377_at	1.37127	7.426043	12.49666	6.59E-27	2.14E-25	50.37739			AI093722
202465_at	1.37018	9.045147	9.716898	1.51E-18	2.27E-17	13.28618	PCOLCE	procollagen C-endopeptidase enhancer	NM_002593
212385_at	1.36983	8.002916	12.26873	3.31E-26	1.02E-24	48.77558	TCF4	transcription factor 4	AU118026
212195_at	1.36964	10.70137	15.57615	1.99E-36	1.57E-34	72.1603	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	AL049265
203753_at	1.36962	9.640834	12.53877	4.89E-27	1.60E-25	50.67373	TCF4	transcription factor 4	NM_003199
225566_at	1.3679	6.916473	14.56772	2.60E-33	1.46E-31	65.02945	NRP2	neuropilin 2	AI819729
219872_at	1.36768	5.701457	9.986619	2.46E-19	4.06E-18	33.08001	C4orf18	chromosome 4 open reading frame 18	NM_016613
226157_at	1.36734	7.581632	13.55211	3.63E-30	1.54E-28	57.83228	TFDP2	CDNA clone IMAGE:4817695	AI569747
211323_s_at	1.36661	6.775033	15.12486	4.91E-35	3.35E-33	68.97311	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	L38019
228268_at	1.36606	6.961572	8.886192	3.56E-16	4.25E-15	25.87996	FMO2	flavin containing monooxygenase 2 (non-functional)	AI758223
201445_at	1.36569	9.400151	12.11238	9.98E-26	2.95E-24	47.6792	CNN3	calponin 3, acidic	NM_001839
241302_at	1.3656	4.810622	16.48434	3.23E-39	3.48E-37	78.54395			AI654048
215294_s_at	1.36552	6.469937	8.883157	3.63E-16	4.33E-15	25.86058	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	AK026426
213644_at	1.36537	6.246253	16.73583	5.51E-40	6.60E-38	80.3027	CCDC46	coiled-coil domain containing 46	AI979276
211675_s_at	1.36516	8.969335	11.45849	9.86E-24	2.46E-22	43.11974	MDFIC	MyoD family inhibitor domain containing	AF054589
201061_s_at	1.36434	10.72959	13.81712	5.49E-31	2.51E-29	59.70981	STOM	stomatin	M81635
211685_s_at	1.36337	7.128835	12.58058	3.64E-27	1.21E-25	50.96804	NCALD	neurocalcin delta	AF251061
221881_s_at	1.36306	7.940159	11.93353	3.52E-25	1.00E-23	46.42775	CLIC4	chloride intracellular channel 4	AI638420
209005_at	1.36285	8.047759	19.06431	5.42E-47	1.90E-44	96.3355	FBXL5	F-box and leucine-rich repeat protein 5	AF157323
209071_s_at	1.36234	11.11341	9.344886	1.78E-17	2.42E-16	28.84154	RGS5	regulator of G-protein signaling 5	AF159570
212157_at	1.36207	7.171478	14.58223	2.34E-33	1.33E-31	65.1322	SDC2	syndecan 2	BE048514
224955_at	1.36204	9.518663	13.27972	2.53E-29	1.01E-27	55.90409	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	AI590088
207761_s_at	1.36144	10.38411	7.909467	1.68E-13	1.49E-12	19.80339	METTL7A	methyltransferase like 7A	NM_014033
209357_at	1.36086	8.318107	9.45667	8.51E-18	1.20E-16	29.57232	CITED2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	AF109161
205577_at	1.36082	6.056623	15.23393	2.26E-35	1.59E-33	69.74411	PYGM	phosphorylase, glycogen, muscle	NM_005609
238512_at	1.36026	6.115541	7.779206	3.71E-13	3.15E-12	19.01997			BF961733
1557073_s_at	1.36008	5.605857	20.16314	3.23E-50	2.05E-47	103.7123	TTBK2	Tau-tubulin kinase	AK074481
214449_s_at	1.35994	8.190382	14.60011	2.06E-33	1.18E-31	65.25892	RHOQ	ras homolog gene family, member Q	NM_012249
1554126_at	1.35878	8.266954	16.03854	7.52E-38	6.78E-36	75.41622	MSRB3	methionine sulfoxide reductase B3	BC040053
208158_s_at	1.35871	8.916056	10.32912	2.41E-20	4.38E-19	35.38121	OSBP1A	oxysterol binding protein-like 1A	NM_018030
225278_at	1.35862	7.955039	11.2526	4.15E-23	9.79E-22	41.69439	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	BF593382
228409_at	1.3573	6.512761	11.05604	1.63E-22	3.64E-21	40.3391	KIAA1881	KIAA1881	T62068
225602_at	1.35678	8.003236	13.20244	4.38E-29	1.71E-27	55.35739	GLIPR2	GLI pathogenesis-related 2	H92988
225048_at	1.35642	7.717419	14.37408	1.03E-32	5.49E-31	63.65738	PHF10	PHD finger protein 10	AI818048
227769_at	1.35625	5.606201	6.859586	8.30E-11	5.08E-10	13.70075			AI703476
203874_s_at	1.35581	7.092959	8.05553	6.82E-14	6.33E-13	20.68991	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	NM_003069
211126_s_at	1.35566	8.53675	11.01754	2.12E-22	4.70E-21	40.07429	CSRP2	cysteine and glycine-rich protein 2	U46006
229531_at	1.3556	6.251837	16.68013	8.15E-40	9.53E-38	79.91355			AW182938
225163_at	1.35459	6.812074	14.21979	3.10E-32	1.59E-30	62.56383	FRMD4A	FERM domain containing 4A	BF000162
215021_s_at	1.35448	5.76125	12.26424	3.41E-26	1.05E-24	48.74409	NRXN3	neurexin 3	AF123462
228562_at	1.35433	7.057	7.456085	2.59E-12	1.97E-11	17.10735			N29918

200771_at	1.35412	10.31352	13.30294	2.14E-29	8.61E-28	56.06838	LAMC1	laminin, gamma 1 (formerly LAMB2)	NM_002293
231720_s_at	1.35394	5.931515	14.34473	1.27E-32	6.71E-31	63.44932	JAM3	junctional adhesion molecule 3	AF356518
242985_x_at	1.35371	4.39845	18.32396	8.68E-45	2.12E-42	91.29251	RNF180	ring finger protein 180	H05502
241457_at	1.35364	3.914308	12.74821	1.11E-27	3.83E-26	52.14929			AI821935
226546_at	1.35259	6.384053	13.0545	1.26E-28	4.68E-27	54.31151			BG477064
205833_s_at	1.35178	6.032429	12.00635	2.11E-25	6.07E-24	46.93689	PART1	prostate androgen-regulated transcript.1	AI770098
223629_at	1.35175	4.937952	8.541957	3.23E-15	3.48E-14	23.70012	PCDH85	protocadherin beta 5	BC001186
226210_s_at	1.35172	6.039244	9.388231	1.34E-17	1.84E-16	29.1245	MEG3	maternally expressed 3 (non-protein coding)	AI291123
225162_at	1.35127	9.623555	13.30713	2.08E-29	8.36E-28	56.09799	SH3D19	SH3 domain containing 19	BG285417
212387_at	1.35101	9.004994	12.8624	4.92E-28	1.75E-26	52.95487	TCF4	transcription factor 4	BG495771
214180_at	1.35034	7.071806	14.42095	7.40E-33	3.98E-31	63.98949	MAN1C1	mannosidase, alpha, class 1C, member 1	AW340588
206941_x_at	1.34904	4.426991	9.967607	2.80E-19	4.58E-18	32.95301	SEMA3E	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	NM_012431
216474_x_at	1.34845	8.449723	6.708549	1.94E-10	1.12E-09	12.86574	TPSB2	tryptase alpha/beta 1 /// tryptase beta 2	AF206667
241700_at	1.34744	5.096011	13.57103	3.17E-30	1.35E-28	57.96628	ZFX4	zinc finger homeobox 4	AW963185
204451_at	1.34743	7.830989	11.76442	1.16E-24	3.14E-23	45.24728	FZD1	frizzled homolog 1 (Drosophila)	NM_003505
238483_at	1.34664	3.545027	18.9807	9.59E-47	3.21E-44	95.76883			AL566553
238835_at	1.34609	5.253426	9.456152	8.54E-18	1.20E-16	29.56892			AV707318
229465_s_at	1.3459	7.170581	11.73245	1.45E-24	3.91E-23	45.02442			BF433071
229310_at	1.34568	6.939654	10.12012	9.99E-20	1.71E-18	33.97399	KLHL29	kelch-like 29 (Drosophila)	BE465475
1557553_at	1.34546	4.860638	14.77942	5.75E-34	3.51E-32	66.52882	PPP1R12B	CDNA FLJ40942 fls, clone UTERU2008516	BF438357
205824_at	1.34533	6.109111	16.30493	1.15E-38	1.14E-36	77.28674	HSPB2	heat shock 27kDa protein 2	NM_001541
218332_at	1.34477	6.864549	5.597532	7.05E-08	2.54E-07	7.109851	BEX1	brain expressed, X-linked 1	NM_018476
1556696_s_at	1.34428	4.404695	20.56126	2.26E-51	1.82E-48	106.3513	FLJ42709	hypothetical gene supported by AK124699	AK095719
211959_at	1.34389	10.34832	8.47989	4.79E-15	5.06E-14	23.3113	IGFBP5	insulin-like growth factor binding protein 5	AW007532
204201_s_at	1.34332	5.275928	12.99229	1.95E-28	7.17E-27	53.87196	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	NM_006264
228182_at	1.34324	5.625233	18.27295	1.23E-44	2.92E-42	90.94305	ADCY5	adenylate cyclase 5	AI935802
209485_s_at	1.34309	8.930913	10.12377	9.74E-20	1.67E-18	33.9985	OSBPL1A	oxysterol binding protein-like 1A	W19983
235349_at	1.34246	6.616213	11.97863	2.56E-25	7.33E-24	46.74306	FAM82A1	family with sequence similarity 82, member A1	AI261321
243984_at	1.3424	3.514493	14.44796	6.10E-33	3.31E-31	64.18089			AV725169
239942_at	1.34211	4.379913	16.50449	2.80E-39	3.03E-37	78.68505			AW052186
230466_s_at	1.34181	9.113951	11.04162	1.80E-22	4.01E-21	40.23989			AI092770
229910_at	1.34161	7.078461	13.4468	7.69E-30	3.19E-28	57.08655	SHE	Src homology 2 domain containing E	AI797276
226002_at	1.34137	6.599144	16.093	5.12E-38	4.69E-36	75.79902	GAB1	GRB2-associated binding protein 1	AK022142
1554690_a_at	1.34084	8.199293	11.39835	1.50E-23	3.68E-22	42.70283	TACC1	transforming, acidic coiled-coil containing protein 1	BC041391
228585_at	1.34081	6.400956	14.02149	1.28E-31	6.19E-30	61.15825	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	AI301948
224997_x_at	1.33991	6.90317	4.50404	1.13E-05	2.64E-05	2.206188	H19	H19, imprinted maternally expressed transcript (non-protein coding)	AL575306
232027_at	1.33961	4.29616	15.61019	1.56E-36	1.25E-34	72.40031	SYNE1	Spectrin repeat containing, nuclear envelope 1, mRNA (cDNA clone IMAGE:4830497)	AL049548
226968_at	1.33928	7.212368	16.64428	1.05E-39	1.20E-37	79.66299	KIF1B	kinesin family member 1B	AK023184
1568609_s_at	1.33811	7.922544	9.839594	6.62E-19	1.04E-17	32.10008	FAM91A2 /// FLJ39739 /// LOC72885 5 /// LOC72887 5	family with sequence similarity 91, member A2 /// hypothetical FLJ39739 ///	AL118843

								hypothetical LOC728855 /// hypothetical LOC728875	#N/A
228772_at	1.33724	6.917111	11.01476	2.16E-22	4.78E-21	40.05517	HNMT	histamine N-methyltransferase	AU157303
201667_at	1.3365	10.68462	8.708207	1.12E-15	1.27E-14	24.74804	GJA1	gap junction protein, alpha 1, 43kDa	NM_000165
211966_at	1.33582	8.851752	10.93773	3.69E-22	7.97E-21	39.5261	COL4A2	collagen, type IV, alpha 2	AA909035
201603_at	1.33573	9.909678	15.5966	1.72E-36	1.37E-34	72.30451	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	AI817061
209496_at	1.33431	9.545071	10.15943	7.65E-20	1.33E-18	34.23796	RARRES2	retinoic acid receptor responder (tazarotene induced) 2	BC000069
231747_at	1.3337	6.432383	10.51416	6.82E-21	1.31E-19	36.63435	CYSLTR1	cysteinyl leukotriene receptor 1	NM_006639
205381_at	1.33356	6.358643	7.435742	2.92E-12	2.20E-11	16.98845	LRRC17	leucine rich repeat containing 17	NM_005824
206030_at	1.33284	5.26137	9.480445	7.27E-18	1.03E-16	29.72818	ASPA	aspartoacylase (Canavan disease)	NM_000049
223842_s_at	1.3324	5.595159	15.17087	3.54E-35	2.45E-33	69.2984	SCARA3	scavenger receptor class A, member 3	AB007830
209633_at	1.33213	7.403766	11.00778	2.27E-22	5.01E-21	40.00723	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha	AL389975
213423_x_at	1.33193	7.650649	8.685582	1.29E-15	1.46E-14	24.60489	TUSC3	tumor suppressor candidate 3	AI884858
225202_at	1.33157	9.284737	7.976514	1.11E-13	1.01E-12	20.20929	RHOBTB3	Rho-related BTB domain containing 3	BE620739
211596_s_at	1.33095	8.917504	9.988721	2.43E-19	4.01E-18	33.09406	LRIG1	leucine-rich repeats and immunoglobulin-like domains 1	AB050468
201295_s_at	1.33071	5.8983	10.89141	5.08E-22	1.09E-20	39.20844	WSB1	WD repeat and SOCS box- containing 1	BF111821
209568_s_at	1.32966	8.610758	14.20996	3.33E-32	1.70E-30	62.49418	RGL1	rat guanine nucleotide dissociation stimulator-like 1	AF186779
222146_s_at	1.32767	8.319717	12.20642	5.14E-26	1.55E-24	48.33846	TCF4	transcription factor 4	AK026674
214533_at	1.32714	4.672996	9.323275	2.05E-17	2.77E-16	28.70065	CMA1	chymase 1, mast cell	NM_001836
213032_at	1.32696	7.873278	9.654205	2.29E-18	3.40E-17	30.87171	NFIB	nuclear factor I/B	AI186739
213891_s_at	1.3263	9.801957	12.51567	5.76E-27	1.88E-25	50.51114	TCF4	transcription factor 4	AI927067
227934_at	1.3259	6.998045	12.59498	3.28E-27	1.09E-25	51.0695	KPNA5	karyopherin alpha 5 (importin alpha 6)	AI769559
202760_s_at	1.32533	8.99615	13.19387	4.66E-29	1.81E-27	55.29676	PALM2- AKAP2	PALM2-AKAP2 readthrough transcript	NM_007203
212120_at	1.32527	9.520632	15.27397	1.70E-35	1.21E-33	70.02702	RHOQ	ras homolog gene family, member Q	BE897886
206042_x_at	1.32502	8.152693	11.50588	7.08E-24	1.80E-22	43.44855	SNRPN /// SNURF	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	NM_022804
214890_s_at	1.32381	6.317862	10.15441	7.92E-20	1.37E-18	34.20422	FAM149A	family with sequence similarity 149, member A	AL080065
208491_s_at	1.32364	6.136658	13.78853	6.73E-31	3.06E-29	59.50718	PGM5	phosphoglucosyltransferase 5	NM_021965
241762_at	1.32336	5.019407	9.598149	3.33E-18	4.87E-17	30.50196	FBXO32	F-box protein 32 (FBXO32), transcript variant 2, mRNA	BF244402
238066_at	1.32291	6.983516	9.034548	1.36E-16	1.69E-15	26.83103	RBP7	retinol binding protein 7, cellular	AI733027
202898_at	1.32261	8.331946	14.65401	1.40E-33	8.19E-32	65.64066	SDC3	syndecan 3	NM_014654
201110_s_at	1.32245	9.8339	8.557925	2.92E-15	3.16E-14	23.80037	THBS1	thrombospondin 1	NM_003246
214844_s_at	1.32242	6.801862	10.19775	5.90E-20	1.03E-18	34.49565	DOK5	docking protein 5	AL050069
225731_at	1.32188	8.29571	13.17052	5.50E-29	2.12E-27	55.1317	ANKRD50	ankyrin repeat domain 50	BF196876
219489_s_at	1.32155	9.912441	11.42019	1.29E-23	3.18E-22	42.85416	NXN	nucleoredoxin	NM_017821
1555579_s_at	1.32	8.411511	12.97271	2.25E-28	8.21E-27	53.73372	PTPRM	protein tyrosine phosphatase, receptor type, M	BC029442
201438_at	1.3198	11.87024	9.0605	1.15E-16	1.44E-15	26.99809	COL6A3	collagen, type VI, alpha 3	NM_004369
231361_at	1.31925	3.776214	13.87844	3.54E-31	1.65E-29	60.14436	NLGN1	Full length insert cDNA clone YW19A06	AI912122
242973_at	1.3187	5.327993	14.82421	4.18E-34	2.58E-32	66.84591	CACNA1C	calcium channel, voltage- dependent, L type, alpha 1C subunit	F11066
232676_x_at	1.31772	7.076872	7.953884	1.28E-13	1.15E-12	20.07209	MYEF2	myelin expression factor 2	AK002075
205830_at	1.31772	4.628916	6.578679	4.01E-10	2.19E-09	12.15719	CLGN	calmegin	NM_004362
209298_s_at	1.31766	6.942269	12.75947	1.02E-27	3.54E-26	52.22869	ITSN1	intersectin 1 (SH3 domain protein)	AF114488
214606_at	1.31765	4.743113	13.34952	1.54E-29	6.24E-28	56.39801	TSPAN2	tetraspanin 2	BF129969

214265_at	1.31709	6.908006	7.317526	5.88E-12	4.26E-11	16.30119	ITGA8	integrin, alpha 8	AI193623
226982_at	1.31653	7.884577	9.617218	2.93E-18	4.32E-17	30.62766	ELL2	elongation factor, RNA polymerase II, 2	AI745624
222312_s_at	1.31622	6.761877	12.96809	2.32E-28	8.46E-27	53.70103			AW969803
224856_at	1.31589	7.986029	10.34537	2.16E-20	3.94E-19	35.49096	FKBP5	FK506 binding protein 5	W86302
205591_at	1.31535	6.366821	10.02028	1.96E-19	3.27E-18	33.30504	OLFM1	olfactomedin 1	NM_006334
219993_at	1.31524	5.605121	12.36217	1.71E-26	5.36E-25	49.43181	SOX17	SRX (sex determining region Y)-box 17	NM_022454
219892_at	1.31502	6.093754	10.44769	1.07E-20	2.03E-19	36.18339	TM6SF1	transmembrane 6 superfamily member 1	NM_023003
214044_at	1.31407	4.1605	12.4147	1.18E-26	3.76E-25	49.80098	RXR2	ryanodine receptor 2 (cardiac)	BE968750
202966_at	1.31393	5.930858	8.075693	6.02E-14	5.63E-13	20.81294	CAPN6	calpain 6	NM_014289
209700_x_at	1.31309	4.057067	14.43586	6.65E-33	3.59E-31	64.09514	PDE4DIP	phosphodiesterase 4D interacting protein	AB042555
232315_at	1.31298	5.34313	7.05657	2.69E-11	1.78E-10	14.80696	LOC400713	zinc finger-like	AU149712
211458_s_at	1.31273	9.047838	10.37674	1.74E-20	3.22E-19	35.70303	GABARAPL1 /// GABARAPL3	GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3 (pseudogene)	AF180519
216044_x_at	1.31241	8.122648	12.06161	1.43E-25	4.19E-24	47.32363	FAM69A	family with sequence similarity 69, member A	AK027146
209348_s_at	1.31179	9.129316	11.90942	4.17E-25	1.18E-23	46.25928	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	AF055376
210571_s_at	1.31154	5.274123	13.75758	8.39E-31	3.76E-29	59.28791	CMAH	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminic monooxygenase) pseudogene	AF074480
								(CMP-N-acetylneuraminic monooxygenase) pseudogene	#N/A
210632_s_at	1.31102	5.529573	14.06075	9.65E-32	4.74E-30	61.43654	SGCA	sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein)	L35853
43427_at	1.31073	7.047406	10.74119	1.43E-21	2.94E-20	38.1805	ACACB	acetyl-Coenzyme A carboxylase beta	AI970898
202976_s_at	1.31054	8.170522	7.997418	9.77E-14	8.92E-13	20.3362	RHOBTB3	Rho-related BTB domain containing 3	NM_014899
204684_at	1.31053	5.72559	11.71856	1.60E-24	4.29E-23	44.92768	NPTX1	neuronal pentraxin I	NM_002522
230962_at	1.31045	4.062501	18.16503	2.60E-44	5.77E-42	90.20279	DCLK1	doublecortin-like kinase 1	BE672499
226518_at	1.30931	8.949288	17.80812	3.08E-43	5.70E-41	87.747	KCTD10	potassium channel tetramerisation domain containing 10	AW073741
229824_at	1.30907	5.058125	10.13995	8.73E-20	1.51E-18	34.1071			AL133706
242488_at	1.30827	6.714514	7.078364	2.37E-11	1.58E-10	14.93052			R55784
219049_at	1.30749	8.337251	8.432828	6.45E-15	6.71E-14	23.01737	CSGALNAC11	chondroitin sulfate N-acetylglucosaminyltransferase 1	NM_018371
224928_at	1.30595	9.519953	14.4015	8.50E-33	4.54E-31	63.85167	SETD7	SET domain containing (lysine methyltransferase) 7	AK024846
45297_at	1.30557	8.165073	14.76206	6.50E-34	3.94E-32	66.40588	EHD2	EH-domain containing 2	AI417917
225945_at	1.30554	8.13992	9.715927	1.52E-18	2.29E-17	31.27975	ZNF655	zinc finger protein 655	BF219240
207480_s_at	1.30515	8.832444	8.998531	1.72E-16	2.12E-15	26.59952	MEIS2	Meis homeobox 2	NM_020149
235721_at	1.30507	7.59413	15.11627	5.22E-35	3.53E-33	68.91233	DTX3	deltex 3 homolog (Drosophila)	N62126
213194_at	1.3045	8.71853	10.47029	9.21E-21	1.75E-19	36.33662	ROBO1	roundabout, axon guidance receptor, homolog 1 (Drosophila)	BF059159
202371_at	1.30448	9.939446	11.75049	1.27E-24	3.46E-23	45.15019	TCEAL4	transcription elongation factor A (SII)-like 4	NM_024863
227791_at	1.30421	6.961274	14.84766	3.53E-34	2.21E-32	67.01192	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	BE222668
203339_at	1.30396	6.937812	14.07584	8.67E-32	4.27E-30	61.5435	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	AI887457
212196_at	1.30348	8.904083	13.78771	6.77E-31	3.07E-29	59.50142	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	AW242916
225825_at	1.30308	7.452381	14.86482	3.13E-34	1.97E-32	67.13336	C20orf194	chromosome 20 open reading frame 194	AL110249
220032_at	1.30306	6.481386	16.94492	1.27E-40	1.60E-38	81.76145	C7orf58	chromosome 7 open reading frame 58	NM_024913
207134_x_at	1.30263	8.391208	6.638266	2.88E-10	1.61E-09	12.48119	TPSB2	tryptase beta 2	NM_024164

230943_at	1.30263	4.93914	13.22979	3.61E-29	1.42E-27	55.55088	SOX17	SRY (sex determining region Y)-box 17	AI821669
211964_at	1.3019	11.30286	11.83667	6.96E-25	1.93E-23	45.75122	COL4A2	collagen, type IV, alpha 2	X05610
207943_x_at	1.30176	7.193651	10.95285	3.32E-22	7.21E-21	39.62992	PLAGL1	pleiomorphic adenoma gene-like 1	NM_006718
209506_s_at	1.30173	7.340852	15.32888	1.15E-35	8.32E-34	70.41493	NR2F1	nuclear receptor subfamily 2, group F, member 1	BC004154
57588_at	1.30173	7.60112	9.980973	2.56E-19	4.21E-18	33.04229	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	R62432
207135_at	1.30171	5.527593	14.16293	4.66E-32	2.34E-30	62.1608	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	NM_000621
230237_at	1.30028	4.749587	9.159223	6.03E-17	7.76E-16	27.63541	ADCYAP1	adenylate cyclase activating polypeptide 1 (pituitary)	BE220888
228109_at	1.29997	6.351005	15.02543	9.97E-35	6.62E-33	68.26986	RASGRF2	CDNA clone IMAGE:5301750	AI912976
212606_at	1.29872	7.06588	14.08064	8.38E-32	4.13E-30	61.57755	WDFY3	WD repeat and FYVE domain containing 3	AL536319
212535_at	1.29859	8.704969	17.03287	6.85E-41	8.87E-39	82.37412	MEF2A	myocyte enhancer factor 2A	AA142929
211000_s_at	1.29801	8.170201	14.20181	3.53E-32	1.79E-30	62.43637	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	AB015706
235850_at	1.29769	5.766575	11.44261	1.10E-23	2.74E-22	43.00957	WDR5B	WD repeat domain 5B	BF434228
222570_at	1.29701	6.241932	14.99998	1.19E-34	7.89E-33	68.08988	FREQ	frequenin homolog (Drosophila)	AA045247
228584_at	1.29688	7.508685	12.39831	1.32E-26	4.20E-25	49.68578	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	AI089025
230351_at	1.29677	4.86795	11.92896	3.64E-25	1.03E-23	46.39579	LOC283481	hypothetical protein LOC283481	AW070248
201522_x_at	1.29632	9.374611	10.35652	2.00E-20	3.67E-19	35.56632	SNRPN /// SNURF	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	NM_003097
224937_at	1.29595	9.313427	13.04764	1.32E-28	4.91E-27	54.26305	PTGFRN	prostaglandin F2 receptor negative regulator	BF311866
206544_x_at	1.29379	7.391761	12.51157	5.93E-27	1.93E-25	50.48232	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	NM_003070
202112_at	1.29278	9.316163	10.67486	2.26E-21	4.55E-20	37.72778	VWF	von Willebrand factor	NM_000552
201792_at	1.2924	9.513324	8.817642	5.54E-16	6.48E-15	25.44281	AEBP1	AE binding protein 1	NM_001129
219451_at	1.2912	7.072863	12.88119	4.31E-28	1.54E-26	53.08752	MSRB2	methionine sulfoxide reductase B2	NM_016064
203887_s_at	1.29084	8.210441	8.97324	2.02E-16	2.48E-15	26.43719	THBD	thrombomodulin	NM_000361
226395_at	1.28956	7.770497	12.52131	5.54E-27	1.80E-25	50.55084	HOOK3	hook homolog 3 (Drosophila)	AI912618
1559277_at	1.28868	4.36866	10.28226	3.32E-20	5.96E-19	35.06487	FLJ35700	hypothetical protein FLJ35700	AK093019
223877_at	1.28857	5.054545	14.44502	6.23E-33	3.38E-31	64.16005	C1QTNF7	C1q and tumor necrosis factor related protein 7	AF329839
226186_at	1.28843	5.598043	13.52802	4.31E-30	1.83E-28	57.66171			AW207699
204497_at	1.28816	8.214862	14.176	4.24E-32	2.14E-30	62.25344	ADCY9	adenylate cyclase 9	AB011092
203724_s_at	1.28804	4.857438	15.02049	1.03E-34	6.85E-33	68.23497	RUFY3	RUN and FYVE domain containing 3	NM_014961
212599_at	1.28681	8.482094	8.784176	6.87E-16	7.96E-15	25.22994	AUTS2	autism susceptibility candidate 2	AK025298
235848_x_at	1.28601	7.254565	10.72187	1.64E-21	3.34E-20	38.04853	ATL2	ADP-ribosylation factor-like 6 interacting protein 2, mRNA (cDNA clone IMAGE:3450768)	N35250
208669_s_at	1.28476	10.23263	13.09229	9.60E-29	3.61E-27	54.57862	EID1	EP300 interacting inhibitor of differentiation 1	AF109873
209121_x_at	1.28448	10.00436	13.55591	3.53E-30	1.50E-28	57.85922	NR2F2	nuclear receptor subfamily 2, group F, member 2	M64497
220122_at	1.28372	7.274194	8.455803	5.58E-15	5.85E-14	23.16076	MCTP1	multiple C2 domains, transmembrane 1	NM_024717
240869_at	1.2831	4.379409	15.27811	1.65E-35	1.18E-33	70.05629			H12055
224911_s_at	1.28249	7.360422	8.831966	5.05E-16	5.94E-15	25.53404	DCBLD2	discoidin, CUB and LCCL domain containing 2	AA722799
203886_s_at	1.28209	7.245488	9.060751	1.15E-16	1.44E-15	26.99971	FBLN2	fibulin 2	NM_001998
204732_s_at	1.28131	5.583164	16.33914	9.00E-39	9.17E-37	77.52662	TRIM23	tripartite motif-containing 23	AI021991
215646_s_at	1.2812	8.606549	6.693171	2.12E-10	1.22E-09	12.78138	VCAN	versican	R94644
227761_at	1.28117	7.207934	12.66224	2.04E-27	6.88E-26	51.54325	MYO5A	myosin VA (heavy chain 12, myoxin)	AW235548
214077_x_at	1.28069	7.477333	8.601687	2.21E-15	2.43E-14	24.07555	MEIS3P1	Meis homeobox 3 pseudogene 1	H15129

208670_s_at	1.28043	9.283877	14.62451	1.73E-33	9.98E-32	65.43176	EID1	EP300 interacting inhibitor of differentiation 1	AF274951
204466_s_at	1.28038	6.339199	9.702294	1.66E-18	2.50E-17	31.18954	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	BG260394
221213_s_at	1.28022	6.693636	14.48467	4.70E-33	2.58E-31	64.44104	ZNF280D	zinc finger protein 280D	NM_017661
203185_at	1.27967	7.753393	10.96657	3.02E-22	6.57E-21	39.72408	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	NM_014737
216060_s_at	1.27907	8.115193	12.87241	4.58E-28	1.63E-26	53.02552	DAAM1	dishevelled associated activator of morphogenesis 1	AK021890
221901_at	1.2782	6.324867	12.22604	4.47E-26	1.36E-24	48.47607	LL22NC03-75B3.6	KIAA1644 protein	BF516072
219167_at	1.27816	7.037494	12.63902	2.40E-27	8.08E-26	51.37971	RASL12	RAS-like, family 12	NM_016563
235131_at	1.27811	6.936993	16.57906	1.66E-39	1.85E-37	79.20686	RHOJ	ras homolog gene family, member J	AA461242
212398_at	1.27648	6.961567	9.251722	3.29E-17	4.35E-16	28.2351	RDX	radixin	AI057093
212154_at	1.2762	8.211922	8.600641	2.22E-15	2.44E-14	24.06896	SDC2	syndecan 2	AI380298
225629_s_at	1.27575	8.97952	17.92748	1.34E-43	2.62E-41	88.5696	ZBTB4	zinc finger and BTB domain containing 4	AI669498
210990_s_at	1.27532	6.596086	13.77575	7.37E-31	3.32E-29	59.41665	LAMA4	laminin, alpha 4	U77706
223588_at	1.27532	4.314222	14.95853	1.60E-34	1.05E-32	67.7966	THAP2	THAP domain containing, apoptosis associated protein 2	AL136607
1560562_a_at	1.27505	5.812365	13.18783	4.86E-29	1.88E-27	55.25406	ZNF677	zinc finger protein 677	AK026366
206805_at	1.27472	6.529307	9.333009	1.93E-17	2.60E-16	28.76409	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	NM_006080
208869_s_at	1.27422	7.561952	12.10333	1.06E-25	3.15E-24	47.6158	GABARAPL1	GABA(A) receptor-associated protein like 1	AF087847
201289_at	1.27353	10.84307	7.588489	1.17E-12	9.31E-12	17.88566	CYR61	cysteine-rich, angiogenic inducer, 61	NM_001554
37512_at	1.27349	5.898638	7.184799	1.28E-11	8.82E-11	15.5372	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	U89281
227022_at	1.2734	7.103556	14.05609	9.98E-32	4.89E-30	61.40354	GNPDA2	glucosamine-6-phosphate deaminase 2	AI817388
226380_at	1.27274	7.417602	14.49594	4.33E-33	2.40E-31	64.52089	PTPN21	protein tyrosine phosphatase, non-receptor type 21	N21442
226352_at	1.27194	8.627671	14.49017	4.51E-33	2.49E-31	64.48003	JMY	junction-mediating and regulatory protein	BF447037
1552733_at	1.27149	5.667426	16.34697	8.51E-39	8.71E-37	77.58154	KLHDC1	kelch domain containing 1	NM_172193
212464_s_at	1.27092	11.81851	7.461625	2.51E-12	1.91E-11	17.13976	FN1	fibronectin 1	X02761
216100_s_at	1.27066	7.203521	10.49952	7.54E-21	1.45E-19	36.53491	TOR1AIP1	torsin A interacting protein 1	BG289527
205991_s_at	1.27057	6.369183	8.881538	3.67E-16	4.37E-15	25.85023	PRRX1	paired related homeobox 1	NM_006902
208636_at	1.27053	11.5283	14.48863	4.56E-33	2.51E-31	64.46911	ACTN1	actinin, alpha 1	AI082078
204992_s_at	1.27044	9.359324	7.289361	6.94E-12	4.98E-11	16.13839	PFN2	profilin 2	NM_002628
228731_at	1.27034	5.491127	9.275625	2.81E-17	3.74E-16	28.39046			AW236803
209576_at	1.27024	6.825871	8.40477	7.70E-15	7.93E-14	22.8425	GNAI1	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	AL049933
238461_at	1.27019	6.089447	11.30425	2.89E-23	6.90E-22	42.05147	EIF4E3	eukaryotic translation initiation factor 4E family member 3	AA228031
213922_at	1.27009	5.26031	16.68031	8.14E-40	9.53E-38	79.91485	TTBK2	tau tubulin kinase 2	AW294686
225921_at	1.26788	8.09921	13.16773	5.61E-29	2.16E-27	55.11191	NIN	ninein (GSK3B interacting protein)	AL359571
228372_at	1.26765	7.492748	10.63679	2.94E-21	5.86E-20	37.46834	C10orf128	chromosome 10 open reading frame 128	AW204712
207031_at	1.26721	5.890229	9.105495	8.56E-17	1.09E-15	27.28821	NKX3-2	NK3 homeobox 2	NM_001189
206932_at	1.2672	7.105504	7.249129	8.78E-12	6.19E-11	15.90647	CH25H	cholesterol 25-hydroxylase	NM_003956
224358_s_at	1.2671	6.352984	9.947611	3.20E-19	5.21E-18	32.81954	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	AF237916
212957_s_at	1.26709	6.17418	11.32093	2.58E-23	6.17E-22	42.16681	LOC92249	hypothetical LOC92249	AU154785
208760_at	1.26707	7.623494	16.10923	4.56E-38	4.22E-36	75.91302	UBE2I	Ubiquitin-conjugating enzyme UBC9	AL031714
233546_at	1.2667	4.006918	17.48236	2.96E-42	4.48E-40	85.49553			AK023065
201162_at	1.26532	12.45092	13.03606	1.43E-28	5.32E-27	54.18126	IGFBP7	insulin-like growth factor binding protein 7	NM_001553
212179_at	1.26463	7.931424	15.33082	1.14E-35	8.23E-34	70.42862	SFRS18	splicing factor, arginine/serine-rich 18	AW157501

219315_s_at	1.26417	8.103829	14.69873	1.02E-33	6.07E-32	65.95746	TMEM204	transmembrane protein 204	NM_024600
226344_at	1.26382	4.434083	12.85286	5.27E-28	1.87E-26	52.88754	ZMAT1	zinc finger, matrin type 1	AI741051
238429_at	1.26341	5.650226	10.20117	5.76E-20	1.01E-18	34.51861	TMEM71	transmembrane protein 71	AI342543
210716_s_at	1.26332	7.040701	11.72164	1.56E-24	4.20E-23	44.94914	CLIP1	CAP-GLY domain containing linker protein 1	M97501
205541_s_at	1.26315	7.085031	7.766812	4.00E-13	3.38E-12	18.9458	GSPT2	G1 to S phase transition 2	NM_018094
235046_at	1.2631	7.256174	9.495247	6.59E-18	9.40E-17	29.82529			AA456099
203919_at	1.2629	6.869831	12.07035	1.34E-25	3.94E-24	47.38485	TCEA2	transcription elongation factor A (SII), 2	NM_003195
221814_at	1.26248	7.810086	13.61791	2.27E-30	9.81E-29	58.29837	GPR124	G protein-coupled receptor 124	BF511315
217820_s_at	1.26237	8.796691	11.25586	4.05E-23	9.59E-22	41.71691	ENAH	enabled homolog (Drosophila)	NM_018212
235360_at	1.26232	6.081628	14.10214	7.19E-32	3.57E-30	61.72989	PLEKHM3	pleckstrin homology domain containing, family M, member 3	AW967747
221246_x_at	1.26212	8.039304	14.24111	2.67E-32	1.37E-30	62.71492	TNS1	tensin 1	NM_018274
200696_s_at	1.26177	10.93469	13.73679	9.73E-31	4.34E-29	59.14057	GSN	gelsolin (amyloidosis, Finnish type)	NM_000177
240890_at	1.26122	6.100637	13.93813	2.31E-31	1.09E-29	60.56739	LOC643733	hypothetical LOC643733	AA041298
229459_at	1.26098	5.214464	8.20823	2.64E-14	2.57E-13	21.62553	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	AV723914
208983_s_at	1.26061	8.359967	10.54917	5.36E-21	1.04E-19	36.87212	PECAM1	platelet/endothelial cell adhesion molecule	M37780
1554789_a_at	1.26039	4.286351	15.09014	6.29E-35	4.22E-33	68.72757	PDE8B	phosphodiesterase 8B	AB085825
209290_s_at	1.26032	9.805403	9.793065	9.05E-19	1.40E-17	31.791	NFIB	nuclear factor I/B	BC001283
202664_at	1.25925	8.587135	10.85939	6.34E-22	1.34E-20	38.989	WIPF1	WAS/WASL interacting protein family, member 1	AW058622
212386_at	1.2586	10.47384	11.61098	3.39E-24	8.91E-23	44.17885	TCF4	transcription factor 4	BF592782
212249_at	1.25832	6.858759	12.73064	1.25E-27	4.32E-26	52.0254	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	AI934473
213358_at	1.25782	8.038024	7.329581	5.48E-12	3.98E-11	16.37098	KIAA0802	KIAA0802	AB018345
205888_s_at	1.25735	5.511205	10.62447	3.20E-21	6.36E-20	37.3844	JAKMIP2	janus kinase and microtubule interacting protein 2	AI962693
214266_s_at	1.25677	6.056849	12.81547	6.87E-28	2.41E-26	52.62371	PDLIM7	PDZ and LIM domain 7 (enigma)	AW206786
205729_at	1.25667	6.474526	7.717575	5.40E-13	4.47E-12	18.65174	OSMR	oncostatin M receptor	NM_003999
226641_at	1.25622	7.062685	8.470836	5.07E-15	5.34E-14	23.25469			AU157224
210084_x_at	1.25568	8.008363	6.684523	2.22E-10	1.27E-09	12.73399	TPSAB1	tryptase alpha/beta 1	AF206665
209868_s_at	1.25566	9.058282	9.631183	2.67E-18	3.95E-17	30.71976	RBMS1	RNA binding motif, single stranded interacting protein 1	D28482
211160_x_at	1.25553	9.753916	13.1695	5.54E-29	2.14E-27	55.12447	ACTN1	actinin, alpha 1	M95178
205611_at	1.25549	6.264404	20.06299	6.31E-50	3.96E-47	103.0456	TNFSF12	tumor necrosis factor (ligand) superfamily, member 12	NM_003809
213479_at	1.2553	5.568905	8.291053	1.57E-14	1.57E-13	22.13665	NPTX2	neuronal pentraxin II	U26662
227839_at	1.2548	5.478929	15.29884	1.43E-35	1.02E-33	70.20274	MBD5	methyl-CpG binding domain protein 5	AI911379
204844_at	1.25452	5.642501	8.095037	5.34E-14	5.02E-13	20.93112	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	L12468
213125_at	1.25411	7.919475	8.582365	2.50E-15	2.73E-14	23.95397	OLFML2B	olfactomedin-like 2B	AW007573
224605_at	1.25393	8.941711	16.60308	1.40E-39	1.58E-37	79.37492	C4orf3	chromosome 4 open reading frame 3	AV727336
205257_s_at	1.25375	5.838417	12.5604	4.20E-27	1.38E-25	50.82599	AMPH	amphiphysin	NM_001635
201008_s_at	1.25343	10.8837	9.951102	3.13E-19	5.09E-18	32.84284	TXNIP	thioredoxin interacting protein	AA812232
214460_at	1.25298	6.215468	13.7917	6.58E-31	2.99E-29	59.52971	LSAMP	limbic system-associated membrane protein	NM_002338
230578_at	1.25291	3.953421	18.71094	6.07E-46	1.78E-43	93.93544			AL042523
202780_at	1.25274	8.469935	8.860071	4.21E-16	4.99E-15	25.71321	OXCT1	3-oxoacid CoA transferase 1	NM_000436
209646_x_at	1.25166	7.313455	11.78992	9.66E-25	2.65E-23	45.42508	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	BC001619
212504_at	1.25121	8.29672	16.04885	6.99E-38	6.33E-36	75.48869	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N31807
203408_s_at	1.25084	8.913497	9.91605	3.96E-19	6.39E-18	32.60905	SATB1	SATB homeobox 1	NM_002971
212187_x_at	1.25078	9.615328	6.221831	2.79E-09	1.32E-08	10.25714	PTGDS	prostaglandin D2 synthase 21kDa (brain)	NM_000954
219949_at	1.25028	3.980454	10.89758	4.87E-22	1.04E-20	39.25068	LRRC2	leucine rich repeat containing 2	NM_024512
228461_at	1.25018	6.946256	14.46486	5.41E-33	2.94E-31	64.30068	SH3RF3	SH3 domain containing ring finger 3	AL566989
204345_at	1.24984	8.149813	10.18913	6.25E-20	1.09E-18	34.43763	COL16A1	collagen, type XVI, alpha 1	NM_001856
235956_at	1.24961	5.673445	11.3541	2.04E-23	4.94E-22	42.39635	KIAA1377	KIAA1377	AI797063

213222_at	1.24908	8.941699	8.135319	4.16E-14	3.96E-13	21.17768	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	AL049593
213217_at	1.24867	6.748878	13.03214	1.47E-28	5.47E-27	54.15353	ADCY2 /// LOC10013 3953	adenylate cyclase 2 (brain) /// similar to adenylate cyclase 2	AU149572
228716_at	1.24847	6.650921	7.908699	1.68E-13	1.49E-12	19.79875	THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v- erb-a) oncogene homolog 2, avian)	BG494007
206742_at	1.2478	5.100945	6.932899	5.47E-11	3.44E-10	14.11021	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)	NM_004469
220187_at	1.24761	4.043374	9.754702	1.17E-18	1.79E-17	31.53656	STEAP4	STEAP family member 4	NM_024636
227108_at	1.24721	5.712337	18.88532	1.84E-46	5.88E-44	95.12143	STARD9	StAR-related lipid transfer (START) domain containing 9	AB037721
229201_at	1.24573	4.082998	11.99444	2.29E-25	6.57E-24	46.8536			AW044658
200884_at	1.24569	9.014239	7.493311	2.08E-12	1.60E-11	17.3254	CKB	creatine kinase, brain	NM_001823
227386_s_at	1.24505	6.27127	13.23213	3.55E-29	1.39E-27	55.5674	TMEM200 B	transmembrane protein 200B	N63821
220416_at	1.24453	4.494927	13.22696	3.68E-29	1.44E-27	55.53086	ATP8B4	ATPase, class I, type 8B, member 4	NM_024837
203083_at	1.24424	8.948763	5.595667	7.11E-08	2.57E-07	7.100808	THBS2	thrombospondin 2	NM_003247
36030_at	1.24413	7.28036	15.75766	5.49E-37	4.57E-35	73.43966	IFFO1	intermediate filament family orphan 1	AL080214
1556314_a_at	1.24394	5.847093	11.28894	3.22E-23	7.66E-22	41.94556			BQ002274
201279_s_at	1.24373	8.750598	9.841573	6.53E-19	1.03E-17	32.11323	DAB2	disabled homolog 2, mitogen- responsive phosphoprotein (Drosophila)	BC003064
238009_at	1.24334	5.794502	12.23553	4.18E-26	1.28E-24	48.5426			AI446064
236277_at	1.24313	5.13557	9.605822	3.16E-18	4.65E-17	30.55253			H23551
236831_at	1.24296	6.814716	11.04581	1.75E-22	3.90E-21	40.26871	CCDC50	coiled-coil domain containing 50	AV683852
221959_at	1.2429	5.774612	12.23453	4.21E-26	1.28E-24	48.5356	FAM110B	family with sequence similarity 110, member B	BE672313
236154_at	1.2428	4.293333	21.46368	5.86E-54	8.42E-51	112.263	QKI	CDNA FLJ39382 fis, clone PERIC2000473	R41907
204556_s_at	1.24279	6.675322	14.87919	2.82E-34	1.79E-32	67.23508	DZIP1	DAZ interacting protein 1	AL568422
203373_at	1.24273	9.001962	10.60001	3.78E-21	7.47E-20	37.21789	SOCS2	suppressor of cytokine signaling 2	NM_003877
213316_at	1.24187	5.795439	10.69589	1.96E-21	3.96E-20	37.87122	KIAA1462	KIAA1462	AL050154
221527_s_at	1.24153	6.887905	13.85692	4.13E-31	1.91E-29	59.99186	PARD3	par-3 partitioning defective 3 homolog (C. elegans)	AF196185
235369_at	1.24123	6.390737	15.66476	1.06E-36	8.62E-35	72.78503	C14orf28	chromosome 14 open reading frame 28	BF435952
223204_at	1.24095	10.50615	10.5336	5.97E-21	1.16E-19	36.76634	C4orf18	chromosome 4 open reading frame 18	AF260333
229947_at	1.24074	6.050271	4.945081	1.60E-06	4.42E-06	4.084455	PI15	peptidase inhibitor 15	AI088609
214889_at	1.24063	6.357928	10.0512	1.59E-19	2.68E-18	33.51196	FAM149A	family with sequence similarity 149, member A	AL080065
212936_at	1.2403	8.591869	15.75917	5.43E-37	4.52E-35	73.45029	FAM172A	family with sequence similarity 172, member A	AI927701
228635_at	1.24025	4.568474	12.55337	4.41E-27	1.45E-25	50.77653	PCDH10	protocadherin 10	AI640307
210089_s_at	1.24002	6.982548	13.46251	6.87E-30	2.86E-28	57.19782	LAMA4	laminin, alpha 4	BC004241
212390_at	1.23913	7.143063	13.39129	1.14E-29	4.68E-28	56.69364	LOC72789 3 /// PDE4DIP	similar to phosphodiesterase 4D interacting protein (myomegalin) /// phosphodiesterase 4D interacting protein	AB007923
200911_s_at	1.23875	10.60725	12.06552	1.39E-25	4.07E-24	47.35102	TACC1	transforming, acidic coiled-coil containing protein 1	NM_006283
1561180_at	1.23742	6.157982	11.75078	1.27E-24	3.45E-23	45.15221			AK021807
1555801_s_at	1.23715	4.164039	7.642525	8.49E-13	6.84E-12	18.20548	ZNF385B	zinc finger protein 385B	BC038422
218224_at	1.23714	9.284984	11.35917	1.97E-23	4.78E-22	42.43145	PNMA1	paraneoplastic antigen MA1	NM_006029
210495_x_at	1.23713	11.85548	7.565685	1.35E-12	1.06E-11	17.75106	FN1	fibronectin 1	AF130095
216442_x_at	1.23703	11.87248	7.582503	1.22E-12	9.62E-12	17.8503	FN1	fibronectin 1	AK026737
209289_at	1.23681	9.605357	10.67865	2.20E-21	4.44E-20	37.75367	NFIB	nuclear factor I/B	AI700518
205225_at	1.23614	5.05729	13.21667	3.96E-29	1.55E-27	55.45802	ESR1	estrogen receptor 1	NM_000125
228863_at	1.23587	7.200581	9.327277	2.00E-17	2.70E-16	28.72673	PCDH17	protocadherin 17	N69091
228411_at	1.23524	7.288986	14.58275	2.33E-33	1.33E-31	65.13593	PARD3B	par-3 partitioning defective 3 homolog B (C. elegans)	BF109252
204802_at	1.23505	5.910686	9.960864	2.93E-19	4.78E-18	32.908	RRAD	Ras-related associated with diabetes	NM_004165

213010_at	1.23433	8.295849	11.2758	3.53E-23	8.37E-22	41.85472	PRKCDBP	protein kinase C, delta binding protein	AI088622
218196_at	1.2342	8.106014	12.07334	1.31E-25	3.87E-24	47.40583	OSTM1	osteopetrosis associated transmembrane protein 1	NM_014028
213029_at	1.23418	9.184511	11.01464	2.17E-22	4.78E-21	40.05438	NFIB	nuclear factor I/B	BG478428
205700_at	1.23334	6.233941	7.251232	8.68E-12	6.13E-11	15.91857	HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	NM_003725
207172_s_at	1.23286	8.261868	9.202905	4.53E-17	5.90E-16	27.9183	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	NM_001797
225956_at	1.23265	8.328896	14.89397	2.54E-34	1.62E-32	67.33968	C5orf41	chromosome 5 open reading frame 41	AL565238
212382_at	1.23263	8.406508	10.87906	5.54E-22	1.18E-20	39.12377	TCF4	transcription factor 4	BF433429
208850_s_at	1.23224	9.572809	9.111585	8.23E-17	1.05E-15	27.32752	THY1	Thy-1 cell surface antigen	AL558479
202975_s_at	1.23183	8.216658	8.214673	2.54E-14	2.47E-13	21.6652	RHOBTB3	Rho-related BTB domain containing 3	N21138
218870_at	1.23128	7.950232	9.579793	3.76E-18	5.48E-17	30.38105	ARHGAP15	Rho GTPase activating protein 15	NM_018460
242206_at	1.23128	4.857724	8.9462	2.41E-16	2.93E-15	26.26385			AW590588
204736_s_at	1.22849	5.880457	12.939	2.85E-28	1.03E-26	53.49563	CSPG4	chondroitin sulfate proteoglycan 4	NM_001897
230624_at	1.22828	4.613331	13.51803	4.63E-30	1.95E-28	57.59096	SLC25A27	solute carrier family 25, member 27	AW779950
222409_at	1.22815	9.628739	12.90375	3.67E-28	1.32E-26	53.24677	CORO1C	coronin, actin binding protein, 1C	AL162070
213340_s_at	1.22809	7.0546	10.87854	5.56E-22	1.18E-20	39.12019	KIAA0495	KIAA0495	AI073551
226688_at	1.22803	6.682339	12.68387	1.75E-27	5.94E-26	51.69571	C3orf23	chromosome 3 open reading frame 23	AW003508
205404_at	1.22647	6.5755	7.393962	3.74E-12	2.78E-11	16.74484	HSD11B1	hydroxysteroid (11-beta) dehydrogenase 1	NM_005525
224604_at	1.2263	10.64456	15.88164	2.28E-37	1.98E-35	74.31268	C4orf3	chromosome 4 open reading frame 3	AL571684
201105_at	1.22591	12.07575	11.44301	1.10E-23	2.74E-22	43.01238	LGALS1	lectin, galactoside-binding, soluble, 1	NM_002305
201069_at	1.22582	10.39582	7.569311	1.32E-12	1.04E-11	17.77245	MMP2	matrix metalloproteinase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	NM_004530
205279_s_at	1.22514	4.987591	13.45883	7.06E-30	2.94E-28	57.17175	GLRB	glycine receptor, beta	AF094754
213939_s_at	1.22487	7.513665	12.05933	1.45E-25	4.25E-24	47.3077	RUFY3	RUN and FYVE domain containing 3	AI871641
210946_at	1.2248	9.809906	13.17557	5.31E-29	2.05E-27	55.16739	PPAP2A	phosphatidic acid phosphatase type 2A	AF014403
211719_x_at	1.2247	11.98431	7.634838	8.89E-13	7.14E-12	18.15991	FN1	fibronectin 1	BC005858
232481_s_at	1.22459	5.937219	6.733415	1.69E-10	9.86E-10	13.0024	SLITRK6	SLIT and NTRK-like family, member 6	AL137517
213331_s_at	1.22358	6.705777	13.2582	2.95E-29	1.17E-27	55.75184	NEK1	NIMA (never in mitosis gene a)-related kinase 1	AV700007
221272_s_at	1.22328	5.419621	14.33334	1.38E-32	7.24E-31	63.36864	C1orf21	chromosome 1 open reading frame 21	NM_030806
204730_at	1.223	5.889058	12.36432	1.68E-26	5.29E-25	49.44687	RIMS3	regulating synaptic membrane exocytosis 3	NM_014747
211698_at	1.22284	8.923047	11.57816	4.27E-24	1.11E-22	43.95068	EID1	EP300 interacting inhibitor of differentiation 1	AF349444
226895_at	1.22241	9.513202	11.63164	2.93E-24	7.75E-23	44.32256	NFIC	CAAT-box binding transcription factor CTF-1 (syn. CTF/NFI or CTF or NF-I or NF-1)	AW134798
227394_at	1.22223	6.485373	9.321887	2.07E-17	2.79E-16	28.69161	NCAM1	neural cell adhesion molecule 1	W94001
211748_x_at	1.2218	10.09119	6.080637	5.91E-09	2.64E-08	9.525063	PTGDS	prostaglandin D2 synthase 21kDa (brain)	BC005939
207574_s_at	1.22164	8.874894	10.23949	4.44E-20	7.87E-19	34.77664	GADD45B	growth arrest and DNA-damage-inducible, beta	NM_015675
202336_s_at	1.22162	10.88809	12.28931	2.86E-26	8.83E-25	48.92005	PAM	peptidylglycine alpha-amidating monooxygenase	NM_000919
210973_s_at	1.22091	7.532962	15.347	1.01E-35	7.37E-34	70.54293	FGFR1	fibroblast growth factor receptor 1	M63889
203501_at	1.2209	8.169326	9.971698	2.72E-19	4.46E-18	32.98033	PGCP	plasma glutamate carboxypeptidase	NM_006102
231879_at	1.22024	7.258435	6.269604	2.16E-09	1.04E-08	10.50742	COL12A1	collagen, type XII, alpha 1	AL096771
210148_at	1.22015	5.94394	8.718906	1.04E-15	1.19E-14	24.8158	HIPK3	homeodomain interacting protein kinase 3	AF305239

225056_at	1.21989	8.101048	10.30568	2.83E-20	5.12E-19	35.22291	SIPA1L2	signal-induced proliferation-associated 1 like 2	AB037810
241808_at	1.21968	5.904273	10.90646	4.58E-22	9.83E-21	39.31158			AW190593
228448_at	1.21933	5.259134	16.24536	1.74E-38	1.70E-36	76.86884	MAP6	microtubule-associated protein 6	AL134650
204606_at	1.21897	7.430242	6.555177	4.56E-10	2.47E-09	12.02992	CCL21	chemokine (C-C motif) ligand 21	NM_002989
230660_at	1.21895	6.596783	8.321338	1.30E-14	1.31E-13	22.32418	SERTAD4	CDNA FLJ39062 fis, clone NT2RP7013999	AU146709
204748_at	1.21891	7.668395	4.626339	6.65E-06	1.63E-05	2.712905	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	NM_000963
201867_s_at	1.21887	7.594423	8.943655	2.45E-16	2.98E-15	26.24754	TBL1X	transducin (beta)-like 1X-linked	AW968555
212239_at	1.21843	8.756938	14.19232	3.78E-32	1.91E-30	62.36912	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	AI680192
228121_at	1.21738	6.623822	9.650978	2.34E-18	3.47E-17	30.85041	TGFB2	transforming growth factor, beta 2	AU145950
231947_at	1.21696	6.572306	11.795	9.33E-25	2.56E-23	45.46047	MYCT1	myc target 1	AI242583
208788_at	1.2167	9.712842	8.848942	4.52E-16	5.35E-15	25.64223	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	AL136939
212119_at	1.2165	10.13195	15.04116	8.91E-35	5.94E-33	68.38116	RHOQ	ras homolog gene family, member Q	BF670447
204491_at	1.2163	7.895083	11.59049	3.92E-24	1.02E-22	44.03639	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	R40917
215321_at	1.21578	5.201226	10.10088	1.14E-19	1.94E-18	33.8449	RUNDC3B	RUN domain containing 3B	AI825798
216264_s_at	1.21544	8.300856	12.66164	2.05E-27	6.91E-26	51.53907	LAMB2	laminin, beta 2 (laminin S)	X79683
203548_s_at	1.2154	6.769247	5.667088	4.97E-08	1.85E-07	7.448761	LPL	lipoprotein lipase	BF672975
226207_at	1.21521	7.32999	14.81645	4.41E-34	2.72E-32	66.79099	RILPL1	Rab interacting lysosomal protein-like 1	AI358954
210815_s_at	1.21509	6.777987	9.416916	1.11E-17	1.54E-16	29.31204	CALCL	calcitonin receptor-like	U17473
209539_at	1.21489	7.682603	12.30137	2.63E-26	8.12E-25	49.00476	ARHGEF6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	D25304
202238_s_at	1.21428	9.980504	7.07432	2.43E-11	1.62E-10	14.90758	NNMT	nicotinamide N-methyltransferase	NM_006169
226137_at	1.21356	8.080939	13.25552	3.00E-29	1.19E-27	55.73284	ZFXH3	zinc finger homeobox 3	AI288759
201865_x_at	1.21356	9.642374	11.71284	1.66E-24	4.45E-23	44.88778	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	AI432196
229497_at	1.21315	5.365343	13.96511	1.91E-31	9.10E-30	60.75869	ANKDD1A	ankyrin repeat and death domain containing 1A	AI760630
219317_at	1.213	6.025801	11.92111	3.84E-25	1.09E-23	46.34096	POLI	polymerase (DNA directed) iota	NM_007195
204864_s_at	1.21123	5.797329	12.60606	3.04E-27	1.01E-25	51.14755	IL6ST	interleukin 6 signal transducer (gp130, oncostatin M receptor)	NM_002184
240317_at	1.21119	5.996783	15.58636	1.85E-36	1.46E-34	72.23225	PCDHB4	protocadherin beta 4	BE222389
213689_x_at	1.21007	8.353926	11.09979	1.20E-22	2.72E-21	40.6403	FAM69A	family with sequence similarity 69, member A	AL137958
228339_at	1.21007	7.75378	11.69706	1.86E-24	4.95E-23	44.77791	ECSM2	endothelial cell-specific molecule 2	AA181256
201185_at	1.20968	9.919279	10.10025	1.14E-19	1.95E-18	33.84069	HTRA1	HtrA serine peptidase 1	NM_002775
219506_at	1.20949	9.379628	13.01317	1.68E-28	6.22E-27	54.01946	C1orf54	chromosome 1 open reading frame 54	NM_024579
221740_x_at	1.20885	6.078552	15.96544	1.26E-37	1.12E-35	74.90224	LRRC37A2	CDNA FLJ34414 fis, clone HEART2003168, highly similar to Homo sapiens c114 SLIT-like	AI140364
								testicular protein (LOC474170), mRNA	#N/A
225957_at	1.20802	7.930775	11.89526	4.61E-25	1.30E-23	46.16031	C5orf41	chromosome 5 open reading frame 41	AI307750
227276_at	1.20746	7.445171	10.21483	5.25E-20	9.23E-19	34.61058	PLXDC2	plexin domain containing 2	AI264121
227041_at	1.20721	7.212114	12.05074	1.54E-25	4.50E-24	47.24754	SESTD1	SEC14 and spectrin domains 1	BE466145
208634_s_at	1.20698	10.07946	17.68229	7.37E-43	1.25E-40	86.8784	MACF1	microtubule-actin crosslinking factor 1	AB029290
200931_s_at	1.20686	10.57132	13.25985	2.91E-29	1.16E-27	55.76346	VCL	vinculin	NM_014000
226656_at	1.20672	8.1503	17.4654	3.34E-42	4.99E-40	85.37805	CRTAP	cartilage associated protein	AW024741
1556209_at	1.20662	4.492775	11.63518	2.86E-24	7.56E-23	44.34719	CLEC2B	C-type lectin domain family 2, member B	CA447397

219134_at	1.2059	8.404563	9.771113	1.05E-18	1.61E-17	31.64536	ELTD1	EGF, latrophilin and seven transmembrane domain containing 1	NM_022159
228452_at	1.20561	6.923666	13.50069	5.24E-30	2.20E-28	57.46816	C17orf39	chromosome 17 open reading frame 39	AA827865
224646_x_at	1.20451	8.397733	3.557204	0.0004672	0.0008239	-1.32756	H19	H19, imprinted maternally expressed transcript (non-protein coding)	BF569051
231887_s_at	1.20372	6.921269	13.29323	2.30E-29	9.21E-28	55.99967	KIAA1274	KIAA1274	AB033100
239185_at	1.20363	3.826268	14.50331	4.11E-33	2.28E-31	64.57307	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	AI284184
202825_at	1.20238	8.584076	10.73456	1.50E-21	3.06E-20	38.13522	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	NM_001151
1558397_at	1.20209	6.370884	9.9018	4.36E-19	7.00E-18	32.51408			BF976693
218236_s_at	1.20108	7.740842	9.913013	4.04E-19	6.51E-18	32.5888	PRKD3	protein kinase D3	NM_005813
211709_s_at	1.20055	7.142388	9.62207	2.84E-18	4.18E-17	30.65965	CLEC11A	C-type lectin domain family 11, member A	BC005810
58780_s_at	1.20021	7.77468	11.82457	7.58E-25	2.10E-23	45.66682	FUJ10357	hypothetical protein FUJ10357	R42449
207175_at	1.20017	4.117859	4.041867	7.54E-05	0.0001519	0.393083	ADIPOQ	adiponectin, C1Q and collagen domain containing	NM_004797
226666_at	1.20006	8.098527	13.65878	1.70E-30	7.40E-29	58.58787	DAAM1	dishevelled associated activator of morphogenesis 1	BG434703
1556364_at	1.19936	5.320133	16.51176	2.66E-39	2.89E-37	78.73591	LOC730057	Homo sapiens, clone IMAGE:5759975, mRNA	AK057923
228438_at	1.19895	5.409018	10.1676	7.24E-20	1.26E-18	34.29288	LOC100132891	PREDICTED: Homo sapiens hypothetical protein LOC100132891 (LOC100132891), mRNA	AI948599
229734_at	1.19806	5.496002	12.15235	7.53E-26	2.25E-24	47.9593	LOC283174	hypothetical LOC283174	BF507379
228959_at	1.19767	8.584494	12.33666	2.05E-26	6.37E-25	49.25256			AI676241
240214_at	1.19757	5.389858	16.43296	4.64E-39	4.88E-37	78.18415			BF059209
219432_at	1.19578	6.385088	15.55231	2.36E-36	1.84E-34	71.99214	EVC	Ellis van Creveld syndrome	NM_014556
210757_x_at	1.19522	9.046478	9.91618	3.96E-19	6.38E-18	32.60991	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	AF188298
209732_at	1.19474	9.285787	9.146993	6.53E-17	8.37E-16	27.5563	CLEC2B	C-type lectin domain family 2, member B	BC005254
215446_s_at	1.19471	7.996445	5.92232	1.35E-08	5.62E-08	8.718033	LOX	lysyl oxidase	L16895
243502_at	1.19468	5.001483	14.18912	3.86E-32	1.96E-30	62.34641	GJC1	gap junction protein, gamma 1, 45kDa	BF035598
228843_at	1.19421	6.124865	11.48163	8.39E-24	2.12E-22	43.28026			AI824171
223008_s_at	1.19343	10.08529	14.51157	3.88E-33	2.16E-31	64.63162	C9orf5	chromosome 9 open reading frame 5	AF153415
240044_x_at	1.19341	6.288083	14.57159	2.53E-33	1.43E-31	65.05685	TNRC6B	CDNA FLJ60637 complete cds, highly similar to Trinucleotide repeat-containing 6B protein	AI864078
212486_s_at	1.19329	6.451214	10.31589	2.64E-20	4.78E-19	35.29181	FYN	FYN oncogene related to SRC, FGR, YES	N20923
1555630_a_at	1.19298	9.239492	7.77017	3.92E-13	3.32E-12	18.96589	RAB34	RAB34, member RAS oncogene family	AF327350
209337_at	1.19293	9.484244	12.95266	2.59E-28	9.41E-27	53.59208	PSIP1	PC4 and SFRS1 interacting protein. 1	AF063020
208562_s_at	1.19232	4.802543	16.68009	8.15E-40	9.53E-38	79.91329	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	NM_020297
213005_s_at	1.19135	8.301386	10.87995	5.50E-22	1.17E-20	39.12983	KANK1	KN motif and ankyrin repeat domains 1	D79994
228620_at	1.19124	5.209402	12.41644	1.16E-26	3.72E-25	49.81324			AW664056
235030_at	1.1911	5.135942	11.23798	4.59E-23	1.08E-21	41.59342	FAM55C	family with sequence similarity 55, member C	BF969254
202192_s_at	1.19108	8.124363	13.3264	1.81E-29	7.32E-28	56.23437	GAS7	growth arrest-specific 7	NM_005890
225930_at	1.19099	7.100558	15.02573	9.95E-35	6.62E-33	68.27201	NKIRAS1	NFKB inhibitor interacting Ras-like 1	AI970120
211985_s_at	1.19091	9.989685	12.22529	4.50E-26	1.36E-24	48.47082	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	AI653730
									#N/A

223006_s_at	1.19082	10.26492	14.40379	8.36E-33	4.47E-31	63.86791	C9orf5	chromosome 9 open reading frame 5	AL567431
201141_at	1.19062	10.40906	6.56421	4.34E-10	2.36E-09	12.0788	GPNMB	glycoprotein (transmembrane) nmb	NM_002510
212887_at	1.19023	9.607602	10.53731	5.82E-21	1.13E-19	36.79156	SEC23A	Sec23 homolog A (S. cerevisiae)	AI753659
203645_s_at	1.19022	8.889338	7.225175	1.01E-11	7.07E-11	15.76874	CD163	CD163 molecule	NM_004244
203729_at	1.19003	8.889166	10.31743	2.61E-20	4.73E-19	35.30227	EMP3	epithelial membrane protein 3	NM_001425
223041_at	1.18989	7.372236	14.64096	1.54E-33	8.93E-32	65.54824	CD99L2	CD99 molecule-like 2	AL136580
231795_at	1.18952	4.802033	16.58083	1.64E-39	1.83E-37	79.21925	STON1	stonin 1	BG289281
236439_at	1.18938	5.959572	8.093192	5.40E-14	5.08E-13	20.91985			AI733564
203504_s_at	1.18915	8.015025	9.931217	3.58E-19	5.79E-18	32.71017	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	NM_005502
							LOC100132214 /// LOC100133005 /// LOC100134722 ///	similar to HSPC047 protein /// similar to RAS p21 protein activator 4	
212706_at	1.18866	6.361666	8.616279	2.01E-15	2.22E-14	24.16745	RASA4	/// similar to HSPC047 protein /// RAS p21 protein activator 4	AB011110
									#N/A
236046_at	1.18858	5.155939	13.42793	8.79E-30	3.64E-28	56.95301	FLJ44896	FLJ44896 protein	AA781880
219871_at	1.18835	4.654992	17.12225	3.67E-41	4.91E-39	82.99607	FLJ13197	hypothetical FLJ13197	NM_024614
								purinergic receptor P2Y, G-protein coupled, 12	AA810452
235885_at	1.18829	4.273491	8.866185	4.05E-16	4.81E-15	25.75222	P2RY12		AA810452
212489_at	1.18767	8.114744	6.785897	1.26E-10	7.48E-10	13.2919	COL5A1	collagen, type V, alpha 1	AI983428
								guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	BE670563
204762_s_at	1.18734	4.889271	12.85441	5.21E-28	1.85E-26	52.8985	GNAO1	tumor suppressor candidate 3	U42349
209228_x_at	1.18703	7.668967	8.51933	3.73E-15	3.99E-14	23.55822	TUSC3		BF509371
242907_at	1.18699	7.787384	8.473618	4.98E-15	5.25E-14	23.27208			U88870
210657_s_at	1.18616	6.173728	15.37344	8.39E-36	6.20E-34	70.72963	SEPT4	septin 4	
								cytoplasmic linker associated protein 2	AL137636
212308_at	1.18598	6.143153	13.78494	6.90E-31	3.13E-29	59.48176	CLASP2		AU158444
233825_s_at	1.1859	7.076549	15.37569	8.26E-36	6.11E-34	70.74552	CD99L2	formin binding protein 1	BE046511
230389_at	1.18507	6.280916	12.36125	1.72E-26	5.39E-25	49.42533	FNBP1		
								amyloid beta (A4) precursor protein-binding, family B, member 2	BF115739
212985_at	1.1849	7.662152	10.68551	2.10E-21	4.24E-20	37.80041	APBB2	RNA binding motif protein 9	AL049748
216215_s_at	1.18482	8.937145	19.86334	2.41E-49	1.36E-46	101.713	RBM9		
								trinucleotide repeat containing 6C	AW005818
222820_at	1.18481	6.352245	12.63826	2.42E-27	8.11E-26	51.37436	TNRC6C	cartilage associated protein	NM_006371
201380_at	1.18481	8.154292	14.55929	2.76E-33	1.55E-31	64.96975	CRTAP	keratocan	NM_007035
220504_at	1.18459	3.846383	9.211915	4.27E-17	5.58E-16	27.97672	KERA	forkhead box N3	AW051527
222494_at	1.18444	9.282511	15.10392	5.70E-35	3.83E-33	68.82505	FOXN3	FERM domain containing 3	BF110588
230645_at	1.18378	6.458885	7.367109	4.39E-12	3.23E-11	16.58868	FRMD3	glycogenin 1	NM_004130
201554_x_at	1.18346	9.866786	12.16486	6.89E-26	2.06E-24	48.047	GYG1		
								guanine nucleotide binding protein (G protein), beta polypeptide 4	AW504458
223487_x_at	1.18285	6.204661	13.81695	5.49E-31	2.51E-29	59.70861	GNB4		
								potassium channel tetramerisation domain containing 15	AI808448
222664_at	1.18266	6.886803	11.06526	1.53E-22	3.42E-21	40.40252	KCTD15	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	NM_005424
204468_s_at	1.18216	6.582139	9.535056	5.06E-18	7.29E-17	30.08674	TIE1	fidgetin	AA993515
239710_at	1.18116	3.904448	11.38083	1.70E-23	4.14E-22	42.58145	FIGN	interleukin 6 signal transducer (gp130, oncostatin M receptor)	BE856546
204863_s_at	1.17999	8.29349	12.97644	2.19E-28	8.00E-27	53.76005	IL6ST	forkhead box P2	NM_148898
1552902_a_at	1.17989	4.828799	13.98161	1.70E-31	8.15E-30	60.87562	FOXP2		
								nerve growth factor receptor (TNFRSF16) associated protein 1	NM_014380
217963_s_at	1.17937	10.98156	8.113075	4.78E-14	4.51E-13	21.04146	NGFRAP1	chromosome 6 open reading frame 168	AI630979
230447_at	1.17915	3.783922	12.72009	1.35E-27	4.64E-26	51.95102	C6orf168	chromosome 8 open reading frame 84	AW662373
235209_at	1.17895	6.316343	6.004792	8.80E-09	3.79E-08	9.136592	C8orf84	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	NM_003705
203340_s_at	1.17878	7.695013	12.54395	4.72E-27	1.55E-25	50.71017	SLC25A12		

218559_s_at	1.17771	9.486908	8.31206	1.38E-14	1.38E-13	22.26669	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	NM_005461
207034_s_at	1.1776	5.440261	12.53477	5.03E-27	1.65E-25	50.64559	GLI2	GLI-Kruppel family member GLI2 erythrocyte membrane protein band 4.1-like 3	NM_030379
211776_s_at	1.17717	6.306329	8.220534	2.45E-14	2.39E-13	21.7013	EPB41L3		BC006141
226959_at	1.17699	6.933198	12.28573	2.93E-26	9.05E-25	48.89498	LOC283070	CDNA FLJ40058 fls, clone TCOLN1000180	AI137430
208127_s_at	1.17637	7.985139	12.39206	1.38E-26	4.37E-25	49.64186	SOCS5	suppressor of cytokine signaling 5 protein kinase, cAMP-dependent, catalytic, beta	NM_014011
202741_at	1.17612	9.909454	8.836249	4.91E-16	5.78E-15	25.56132	PRKACB		AA130247
209632_at	1.17607	6.058488	10.33195	2.37E-20	4.30E-19	35.40027	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	AI760130
227780_s_at	1.17602	7.464411	11.42469	1.25E-23	3.09E-22	42.88536	ECSM2	endothelial cell-specific molecule 2	AI422211
213447_at	1.17561	6.44883	11.82251	7.69E-25	2.13E-23	45.65244	IPW	imprinted in Prader-Willi syndrome (non-protein coding)	AI672541
239146_at	1.17543	4.378365	16.93941	1.32E-40	1.66E-38	81.72306	CLDN1	claudin domain containing 1	AI634844
229844_at	1.17532	7.04207	14.00467	1.44E-31	6.95E-30	61.03903			AI699465
228745_at	1.1748	7.392315	11.75025	1.28E-24	3.46E-23	45.14846	SGTB	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	AI376997
201060_x_at	1.17431	10.29022	12.04427	1.61E-25	4.70E-24	47.2023	STOM	stomatol	AI537887
219738_s_at	1.1741	4.306764	12.57615	3.75E-27	1.24E-25	50.93687	PCDH9	protocadherin 9	NM_020403
213422_s_at	1.17389	9.067943	11.59104	3.90E-24	1.02E-22	44.04015	MXRA8	matrix-remodelling associated 8	AW888223
205122_at	1.17365	5.951048	7.425271	3.11E-12	2.34E-11	16.92732	TMEFF1	transmembrane protein with EGF-like and two follistatin-like domains 1	BF439316
212354_at	1.17359	9.763277	5.66389	5.06E-08	1.88E-07	7.433115	SULF1	sulfatase 1	BE500977
212488_at	1.17335	9.313354	7.16963	1.40E-11	9.59E-11	15.45041	COL5A1	collagen, type V, alpha 1	N30339
221905_at	1.17334	6.898585	13.30839	2.06E-29	8.30E-28	56.10689	CYLD	cylindromatosis (turban tumor syndrome)	BF516433
236208_at	1.17224	5.893122	14.50168	4.16E-33	2.31E-31	64.56152	MOCS2	molybdenum cofactor synthesis 2	BE467697
243976_at	1.1721	6.012337	13.97012	1.84E-31	8.80E-30	60.79418			AW779916
1559287_at	1.17104	3.810901	13.71285	1.15E-30	5.12E-29	58.97095			BG341640
209227_at	1.17096	4.856867	10.24022	4.42E-20	7.84E-19	34.78154	TUSC3	tumor suppressor candidate 3	AU158251
227843_at	1.17083	4.496143	11.06488	1.53E-22	3.43E-21	40.39996	NDE1	nudE nuclear distribution gene E homolog 1 (A. nidulans)	AI261455
1554012_at	1.17059	3.735618	9.227049	3.86E-17	5.08E-16	28.0749	RSPO2	R-spondin 2 homolog (Xenopus laevis)	BC027938
208070_s_at	1.17014	8.39956	12.98309	2.09E-28	7.64E-27	53.80703	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	NM_002912
238029_s_at	1.17004	6.731071	7.480511	2.24E-12	1.71E-11	17.25035	SLC16A14	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	R15072
225021_at	1.16963	7.121191	11.22561	5.00E-23	1.17E-21	41.50799	ZNF532	zinc finger protein 532	AA861416
214156_at	1.16951	5.856216	6.27045	2.15E-09	1.04E-08	10.51186	MYRIP	myosin VIIA and Rab interacting protein	AL050090
202878_s_at	1.16947	9.495298	9.046036	1.26E-16	1.58E-15	26.90496	CD93	CD93 molecule	NM_012072
204612_at	1.16885	6.216237	8.684317	1.30E-15	1.47E-14	24.59689	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	NM_006823
209285_s_at	1.16877	7.81601	14.35088	1.22E-32	6.44E-31	63.49292	C3orf63	chromosome 3 open reading frame 63	N38985
209198_s_at	1.16856	5.947417	10.1174	1.02E-19	1.74E-18	33.95577	SYT11	synaptotagmin XI	BC004291
235626_at	1.16831	7.229712	10.73234	1.52E-21	3.11E-20	38.12003	CAMK1D	calcium/calmodulin-dependent protein kinase ID	AA835485
203254_s_at	1.16707	7.388173	13.69998	1.26E-30	5.59E-29	58.87977	TLN1	talin 1	NM_006289
235737_at	1.16674	4.169973	10.41733	1.32E-20	2.47E-19	35.97777	TSLP	thymic stromal lymphopoietin	AW118681
227779_at	1.16664	7.418821	12.69914	1.57E-27	5.36E-26	51.80335	ECSM2	Endothelial cell-specific molecule 2, mRNA (cDNA clone MGC:182015 IMAGE:9056840)	AI422211
209583_s_at	1.16659	7.695263	8.471785	5.04E-15	5.31E-14	23.26062	CD200	CD200 molecule	AF063591
209355_s_at	1.16656	8.792653	9.688079	1.83E-18	2.74E-17	31.09553	PPAP2B	phosphatidic acid phosphatase type 2B	AB000889

200952_s_at	1.16613	5.237181	8.354077	1.06E-14	1.08E-13	22.52727	CCND2	cyclin D2	AI635187
213295_at	1.16565	7.348493	14.62859	1.68E-33	9.72E-32	65.46062	CYLD	cylindromatosis (turban tumor syndrome)	AA555096
206542_s_at	1.16556	8.257806	11.99458	2.29E-25	6.57E-24	46.85458	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	AV725365
1552455_at	1.16487	4.494525	9.679887	1.93E-18	2.88E-17	31.04138	PRUNE2	prune homolog 2 (Drosophila)	NM_138818
236335_at	1.16425	5.030549	9.408335	1.17E-17	1.62E-16	29.25592			AW298375
239999_at	1.16381	3.801325	14.5763	2.44E-33	1.38E-31	65.09023	C21orf34	CDNA FLJ38295 fis, clone FCBBF3012332	N66393
242541_at	1.16368	4.920003	15.36876	8.68E-36	6.39E-34	70.69661	ABCA9	ATP-binding cassette, sub-family A (ABC1), member 9	AV692159
1555154_a_at	1.16312	6.681981	13.92733	2.50E-31	1.18E-29	60.49088	QKI	quaking homolog, KH domain RNA binding (mouse)	AF142421
224772_at	1.16302	6.961193	11.25272	4.14E-23	9.79E-22	41.69525	NAV1	neuron navigator 1	AB032977
212958_x_at	1.1624	10.30617	11.99081	2.35E-25	6.73E-24	46.82822	PAM	peptidylglycine alpha-amidating monooxygenase	AI022882
221870_at	1.16198	9.059172	13.62581	2.15E-30	9.32E-29	58.35434	EHD2	EH-domain containing 2	AI417917
1558101_at	1.16144	4.7512	12.28078	3.04E-26	9.35E-25	48.86022	LOC100190890	hypothetical LOC100190890	BM546261
227289_at	1.16071	7.072674	9.551969	4.52E-18	6.55E-17	30.19795	PCDH17	protocadherin 17	AU119437
209747_at	1.15951	7.305952	13.68834	1.37E-30	6.06E-29	58.79733	TGFB3	transforming growth factor, beta 3	J03241
202177_at	1.15923	8.559077	10.96564	3.04E-22	6.61E-21	39.71773	GAS6 /// LOC100133684	growth arrest-specific 6 /// similar to growth arrest-specific 6	NM_000820
1558604_a_at	1.15919	5.386636	21.22659	2.78E-53	3.23E-50	110.7193			AL536899
32259_at	1.15913	7.73255	17.91954	1.42E-43	2.74E-41	88.51489	EZH1	enhancer of zeste homolog 1 (Drosophila)	AB002386
231925_at	1.15887	4.48862	10.47016	9.21E-21	1.75E-19	36.33577			AK026659
212117_at	1.1586	9.292395	14.38857	9.32E-33	4.96E-31	63.76005	RHOQ	ras homolog gene family, member Q	BF978689
227728_at	1.15844	8.322149	14.05694	9.92E-32	4.87E-30	61.40956	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	AA886888
217540_at	1.15809	4.893936	11.37925	1.72E-23	4.19E-22	42.57051	FAM55C	family with sequence similarity 55, member C	AA721025
215049_x_at	1.1578	9.049886	7.122572	1.84E-11	1.24E-10	15.18185	CD163	CD163 molecule	Z22969
203570_at	1.15693	8.379915	8.837361	4.88E-16	5.74E-15	25.56841	LOXL1	lysyl oxidase-like 1	NM_005576
222235_s_at	1.15561	8.017209	11.28612	3.28E-23	7.80E-22	41.92605	CSGALNAC T2	chondroitin sulfate N-acetylglucosaminyltransferase 2	AL139812
201810_s_at	1.15537	8.267185	10.81575	8.57E-22	1.79E-20	38.6902	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	AL562152
227909_at	1.15489	5.322131	9.454882	8.61E-18	1.21E-16	29.5606	CXorf48 /// NCRNA00086	chromosome X open reading frame 48 /// non-protein coding RNA 86	AI742434
214770_at	1.15476	6.816379	7.307973	6.22E-12	4.49E-11	16.24593	MSR1	macrophage scavenger receptor 1	AI299239
231841_s_at	1.15406	5.606842	8.469213	5.12E-15	5.39E-14	23.24455	KIAA1462	KIAA1462	AL553774
200762_at	1.15395	10.67649	12.48231	7.30E-27	2.36E-25	50.27643	DPYSL2	dihydropyrimidinase-like 2	NM_001386
206170_at	1.15361	6.497786	9.227022	3.87E-17	5.08E-16	28.07472	ADRB2	adrenergic, beta-2-, receptor, surface	NM_000024
213348_at	1.15353	8.046087	6.851456	8.69E-11	5.30E-10	13.6555	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	N33167
212647_at	1.1527	9.366584	11.33587	2.32E-23	5.58E-22	42.27021	RRAS	related RAS viral (r-ras) oncogene homolog	NM_006270
225265_at	1.1525	8.244831	8.543807	3.19E-15	3.45E-14	23.71173	RBMS1	RNA binding motif, single stranded interacting protein 1	AI580100
241926_s_at	1.15228	4.92497	13.7802	7.14E-31	3.22E-29	59.44821	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	AA296657
204114_at	1.15112	8.270656	7.48539	2.18E-12	1.67E-11	17.27895	NID2	nidogen 2 (osteonidogen)	NM_007361
205978_at	1.15072	4.416586	8.914519	2.96E-16	3.57E-15	26.06103	KL	klotho	NM_004795
226627_at	1.15058	5.91623	15.21349	2.62E-35	1.82E-33	69.59967	SEPT8	septin 8	AI912094
227870_at	1.15053	5.956655	7.677604	6.87E-13	5.61E-12	18.41377	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	AB046848
209101_at	1.15036	11.02047	8.071031	6.20E-14	5.79E-13	20.78448	CTGF	connective tissue growth factor	M92934
204813_at	1.15021	6.932617	16.96769	1.08E-40	1.38E-38	81.92015	MAPK10	mitogen-activated protein kinase 10	NM_002753
228948_at	1.14977	5.23533	10.3531	2.05E-20	3.75E-19	35.5432	EPHA4	EPH receptor A4	T15545

214457_at	1.14837	5.771188	14.47943	4.87E-33	2.67E-31	64.40392	HOXA2	homeobox A2	NM_006735
201506_at	1.14785	11.01991	8.947824	2.39E-16	2.90E-15	26.27425	TGFB1	transforming growth factor, beta-induced, 68kDa	NM_000358
204604_at	1.14683	8.30374	9.343336	1.80E-17	2.44E-16	28.83143	PFTK1	PFTAIRE protein kinase 1	NM_012395
243946_at	1.14661	6.175396	12.35389	1.81E-26	5.67E-25	49.3736	SMOC2	SPARC related modular calcium binding 2	AI679149
204872_at	1.14658	8.32896	11.52153	6.35E-24	1.62E-22	43.55721	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	NM_007005
228471_at	1.14644	6.415456	8.831368	5.07E-16	5.96E-15	25.53022			AA744636
209287_s_at	1.14634	6.955231	14.03269	1.18E-31	5.74E-30	61.23768	CDC42EP3	CDC42 effector protein (Rho GTPase binding) 3	AF104857
210786_s_at	1.14599	5.67123	11.64114	2.75E-24	7.27E-23	44.3886	FLI1	Friend leukemia virus integration 1	M93255
206197_at	1.14581	5.635677	10.07421	1.36E-19	2.31E-18	33.66611	NME5	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	NM_003551
215382_x_at	1.14581	8.016314	6.972596	4.36E-11	2.79E-10	14.33304	TPSAB1	trypsin alpha/beta 1	AF206666
212757_s_at	1.1454	8.375957	12.36339	1.69E-26	5.32E-25	49.44037	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	BF111268
1555594_a_at	1.14507	6.585894	11.34335	2.20E-23	5.30E-22	42.32198	MBNL1	muscleblind-like (Drosophila)	AF401998
209264_s_at	1.14446	7.542406	11.02153	2.07E-22	4.57E-21	40.10173	TSPAN4	tetraspanin 4	AF054841
212230_at	1.14411	8.871085	10.26552	3.72E-20	6.64E-19	34.952	PPAP2B	phosphatidic acid phosphatase type 2B	AV725664
225735_at	1.14393	6.719821	13.36314	1.40E-29	5.68E-28	56.4944	ANKRD50	ankyrin repeat domain 50	AL110131
201841_s_at	1.14297	11.32532	9.678243	1.95E-18	2.91E-17	31.03051	HSPB1	heat shock 27kDa protein 1	NM_001540
206289_at	1.14261	6.686013	14.98053	1.37E-34	9.00E-33	67.95225	HOXA4	homeobox A4	NM_002141
230142_s_at	1.14197	6.714672	13.77339	7.49E-31	3.37E-29	59.39996	CIRBP	cold inducible RNA binding protein	AW088030
219532_at	1.14195	4.811945	13.2314	3.57E-29	1.40E-27	55.56221	ELOVL4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	NM_022726
219922_s_at	1.14187	8.591185	9.571456	3.97E-18	5.78E-17	30.32617	LTBP3	latent transforming growth factor beta binding protein 3	NM_021070
218573_at	1.14182	8.450432	10.09222	1.21E-19	2.05E-18	33.78688	MAGEH1	melanoma antigen family H, 1	NM_014061
212566_at	1.1418	9.562163	15.99969	9.90E-38	8.87E-36	75.14313	MAP4	microtubule-associated protein 4	AL523310
226558_at	1.14146	7.560666	6.031321	7.66E-09	3.34E-08	9.272086	LOC653071	similar to CG32820-PA, Isoform A	BE856637
230433_at	1.14141	5.998048	13.7863	6.83E-31	3.10E-29	59.4914	LOC729970	hypothetical LOC729970	BE857101
227404_s_at	1.14048	11.09687	7.481889	2.22E-12	1.70E-11	17.25842	EGR1	Putative zinc finger protein mRNA, 3' flank	AI459194
210702_s_at	1.13925	4.569759	11.57852	4.26E-24	1.11E-22	43.95318	PTGIS	prostaglandin I2 (prostacyclin) synthase	D38145
214319_at	1.13884	5.293853	10.10113	1.14E-19	1.94E-18	33.84664	FRY	furry homolog (Drosophila)	W58342
201234_at	1.13828	10.24558	15.3526	9.73E-36	7.11E-34	70.58244	ILK	integrin-linked kinase	NM_004517
206339_at	1.13786	6.247315	10.97953	2.76E-22	6.04E-21	39.8131	CARTPT	CART prepropeptide	NM_004291
227370_at	1.13775	6.977005	7.990881	1.02E-13	9.26E-13	20.29649	FAM171B	family with sequence similarity 171, member B	AW043602
221805_at	1.13768	3.741628	7.283812	7.17E-12	5.13E-11	16.10635	NEFL	neurofilament, light polypeptide	AL537457
214620_x_at	1.13756	8.819905	12.60076	3.15E-27	1.05E-25	51.11018	PAM	peptidylglycine alpha-amidating monooxygenase	BF038548
203708_at	1.1374	8.131867	8.130977	4.27E-14	4.06E-13	21.15108	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	NM_002600
244419_at	1.13728	4.251253	14.82437	4.17E-34	2.58E-32	66.84705	FRZB	Fritz	BE549700
240172_at	1.13716	6.381023	15.42045	6.01E-36	4.49E-34	71.0616	ERGIC2	ERGIC and golgi 2	AA102332
229544_at	1.13659	6.241113	9.334124	1.91E-17	2.59E-16	28.77136			AI690169
204803_s_at	1.1364	6.930156	9.287506	2.60E-17	3.47E-16	28.46775	RRAD	Ras-related associated with diabetes	NM_004165
220145_at	1.13614	5.555596	8.25325	1.99E-14	1.96E-13	21.90304	MAP9	microtubule-associated protein 9	NM_024826
234192_s_at	1.13582	6.753049	9.341537	1.82E-17	2.47E-16	28.8197	GKAP1	G kinase anchoring protein 1	AK026487
204969_s_at	1.13548	5.462602	8.994019	1.77E-16	2.18E-15	26.57055	RDX	radixin	NM_002906
228045_at	1.13461	6.435158	9.341435	1.82E-17	2.47E-16	28.81903			BF438106
209946_at	1.13429	7.056061	10.62135	3.27E-21	6.49E-20	37.36319	VEGFC	vascular endothelial growth factor C	U58111
235079_at	1.13428	6.955482	7.734987	4.86E-13	4.05E-12	18.75562			AW265065
1553112_s_at	1.13386	7.033573	8.102309	5.11E-14	4.81E-13	20.97559	CDK8	cyclin-dependent kinase 8	NM_001260

224817_at	1.13351	8.909494	12.51876	5.64E-27	1.84E-25	50.53289	SH3PXD2A	SH3 and PX domains 2A	W93554
208981_at	1.13327	9.385352	10.20122	5.76E-20	1.01E-18	34.51899	PECAM1	platelet/endothelial cell adhesion molecule	AA702701
1556121_at	1.13323	6.095427	11.68512	2.02E-24	5.37E-23	44.69474			AK021751
210870_s_at	1.1332	5.264428	13.78248	7.02E-31	3.18E-29	59.46431	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	BC005286
206389_s_at	1.1331	4.853824	15.70389	8.04E-37	6.57E-35	73.06087	PDE3A	phosphodiesterase 3A, cGMP-inhibited	NM_000921
209311_at	1.13236	8.621175	14.33237	1.39E-32	7.28E-31	63.36178	BCL2L2	BCL2-like 2	D87461
213901_x_at	1.13203	7.83512	12.74228	1.15E-27	3.99E-26	52.10747	RBM9	RNA binding motif protein 9	AW149379
241897_at	1.13155	5.677815	8.322778	1.29E-14	1.30E-13	22.3331			AA491949
228365_at	1.13089	5.985753	8.524554	3.61E-15	3.86E-14	23.59096	CPNE8	copine VIII	AI765180
208454_s_at	1.13061	8.100993	12.33843	2.02E-26	6.30E-25	49.26503	PGCP	plasma glutamate carboxypeptidase	NM_016134
201811_x_at	1.13021	8.976152	11.08233	1.35E-22	3.06E-21	40.52005	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	NM_004844
224747_at	1.12999	9.492709	11.37857	1.72E-23	4.20E-22	42.56578	UBE2Q2	ubiquitin-conjugating enzyme E2Q family member 2	AK000617
213400_s_at	1.12952	8.325022	8.817008	5.56E-16	6.50E-15	25.43877	TBL1X	transducin (beta)-like 1X-linked	AV753028
204677_at	1.12934	7.179417	9.281271	2.71E-17	3.61E-16	28.42718	CDH5	cadherin 5, type 2 (vascular endothelium)	NM_001795
228819_at	1.12923	6.687781	12.35787	1.76E-26	5.51E-25	49.4016	TSPAN18	tetraspanin 18	AI161133
227087_at	1.12917	8.741703	13.3728	1.30E-29	5.32E-28	56.56273	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	AA126419
231766_s_at	1.12897	7.811094	5.442024	1.52E-07	5.16E-07	6.363258	COL12A1	collagen, type XII, alpha 1	U73778
212822_at	1.1289	8.317261	13.32693	1.81E-29	7.30E-28	56.23813	HEG1	HEG homolog 1 (zebrafish)	AA121502
218717_s_at	1.12876	7.686978	6.610914	3.35E-10	1.86E-09	12.33223	LEPREL1	leprecan-like 1	NM_018192
205961_s_at	1.12871	8.46856	10.56605	4.78E-21	9.35E-20	36.98693	PSIP1	PC4 and SFRS1 interacting protein 1	NM_004682
239277_at	1.12867	7.029135	12.35987	1.74E-26	5.44E-25	49.41561			AI559696
214632_at	1.12837	5.991483	11.46106	9.69E-24	2.42E-22	43.13759	NRP2	neuropilin 2	AA295257
212240_s_at	1.12814	9.345963	12.05744	1.47E-25	4.30E-24	47.29446	PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	AI679268
204832_s_at	1.12814	7.590098	11.15694	8.07E-23	1.85E-21	41.0341	BMPRI1A	bone morphogenetic protein receptor, type IA	NM_004329
228501_at	1.12745	5.208949	8.027999	8.09E-14	7.45E-13	20.52217	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	BF055343
235171_at	1.12699	6.087301	7.355705	4.69E-12	3.45E-11	16.52245			AI354636
212328_at	1.12674	6.98067	7.722076	5.25E-13	4.36E-12	18.67858	LIMCH1	LIM and calponin homology domains 1	AB029025
225660_at	1.12607	7.289837	6.07047	6.23E-09	2.77E-08	9.47279	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	W92748
225664_at	1.12562	10.31146	5.983695	9.82E-09	4.19E-08	9.029138	COL12A1	collagen, type XII, alpha 1	AA788946
232935_at	1.12543	4.765976	11.29185	3.16E-23	7.52E-22	41.96568			AA569225
226722_at	1.12463	8.247131	10.772	1.16E-21	2.39E-20	38.39098	FAM20C	family with sequence similarity 20, member C	BE874872
1557223_at	1.12459	4.660687	14.68206	1.15E-33	6.79E-32	65.83936	RBPMS /// SDHALP2	RNA binding protein with multiple splicing /// succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	AK057533
224893_at	1.12444	10.16374	15.98893	1.07E-37	9.55E-36	75.06745	ATL3	atlastin GTPase 3	AA775408
1554757_a_at	1.12439	6.658611	10.4222	1.28E-20	2.39E-19	36.01072	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	AF273055
211602_s_at	1.12382	3.985696	17.66053	8.58E-43	1.44E-40	86.7281	TRPC1	transient receptor potential cation channel, subfamily C, member 1	U31110
219295_s_at	1.12352	5.251517	5.938751	1.24E-08	5.20E-08	8.8011	PCOLCE2	procollagen C-endopeptidase enhancer 2	NM_013363
235867_at	1.12328	6.891174	12.32308	2.25E-26	7.00E-25	49.15717	GSTM3	glutathione S-transferase mu 3 (brain)	AI459140
219666_at	1.12273	8.7434	8.430991	6.53E-15	6.78E-14	23.00591	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	NM_022349
230008_at	1.12253	5.963795	10.35482	2.03E-20	3.71E-19	35.55482	THSD7A	thrombospondin, type I, domain containing 7A	AI740914

213381_at	1.12193	5.705786	17.6311	1.05E-42	1.72E-40	86.52468	C10orf72	chromosome 10 open reading frame 72	N91149
214318_s_at	1.12135	5.171337	12.0385	1.68E-25	4.88E-24	47.1619	FRY	furry homolog (Drosophila)	W58342
200600_at	1.11988	10.50062	11.71323	1.66E-24	4.44E-23	44.89052	MSN	moesin	NM_002444
219243_at	1.11961	7.990925	9.422544	1.07E-17	1.48E-16	29.34887	GIMAP4	GTPase, IMAP family member 4	NM_018326
219501_at	1.1184	5.754874	14.17782	4.19E-32	2.11E-30	62.26638	ENOX1	ecto-NOX disulfide-thiol exchanger 1	NM_017993
232099_at	1.11733	4.752292	8.417309	7.11E-15	7.35E-14	22.92061	PCDH16	protocadherin beta 16	AB046841
224397_s_at	1.1168	6.56216	14.28687	1.92E-32	9.96E-31	63.03927	TMTC1	transmembrane and tetra-ricopeptide repeat containing 1	AF319520
208944_at	1.11678	10.51984	10.85245	6.65E-22	1.40E-20	38.94143	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	D50683
211571_s_at	1.11636	8.204243	6.203906	3.07E-09	1.44E-08	10.16357	VCAN	versican	D32039
223126_s_at	1.11617	6.979974	11.10774	1.14E-22	2.58E-21	40.69505	C1orf21	chromosome 1 open reading frame 21	AI159874
216048_s_at	1.11595	6.133295	8.329804	1.23E-14	1.24E-13	22.37666	RHOBTB3	Rho-related BTB domain containing 3	AK023621
205259_at	1.11582	7.460596	6.788891	1.24E-10	7.37E-10	13.30846	NR3C2	nuclear receptor subfamily 3, group C, member 2	NM_000901
224505_s_at	1.1157	4.983975	11.94939	3.15E-25	8.98E-24	46.53858	PLCD4	phospholipase C, delta 4	BC006355
212991_at	1.11567	5.613693	11.07604	1.42E-22	3.19E-21	40.47673	FBXO9	F-box protein 9	AL137520
238623_at	1.11536	6.705697	4.853076	2.43E-06	6.48E-06	3.681121			AI633559
224356_x_at	1.11536	9.055415	7.712174	5.58E-13	4.61E-12	18.61954	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	AF237908
213326_at	1.11505	6.44524	11.25019	4.22E-23	9.95E-22	41.67777	VAMP1	vesicle-associated membrane protein 1 (synaptobrevin 1)	AU150319
209343_at	1.11504	6.613267	11.79198	9.53E-25	2.62E-23	45.43944	EFHD1	EF-hand domain family, member D1	BC002449
212855_at	1.1149	8.030748	11.503	7.22E-24	1.83E-22	43.42857	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	D87466
203903_s_at	1.11474	9.093864	5.447962	1.48E-07	5.02E-07	6.391484	HEPH	hephaestin	NM_014799
203140_at	1.11453	9.355094	10.70594	1.83E-21	3.71E-20	37.93982	BCL6	B-cell CLL/lymphoma 6	NM_001706
211958_at	1.1142	7.424003	9.494505	6.62E-18	9.44E-17	29.82042	IGFBP5	insulin-like growth factor binding protein 5	R73554
204358_s_at	1.11414	6.35316	13.55799	3.48E-30	1.48E-28	57.87394	FLRT2	fibronectin leucine rich transmembrane protein 2	AF169676
227138_at	1.11399	7.165997	13.44673	7.69E-30	3.19E-28	57.08607	CRTAP	cartilage associated protein	AA025858
218330_s_at	1.11336	7.977842	8.315153	1.35E-14	1.36E-13	22.28585	NAV2	neuron navigator 2	NM_018162
201348_at	1.11323	9.173099	5.611847	6.56E-08	2.39E-07	7.179352	GPX3	glutathione peroxidase 3 (plasma)	NM_002084
212353_at	1.11251	9.461389	4.877606	2.18E-06	5.86E-06	3.788074	SULF1	sulfatase 1	AI479175
240397_x_at	1.11194	5.223086	15.54579	2.47E-36	1.92E-34	71.94608			AI801626
205805_s_at	1.11187	7.126383	9.680237	1.92E-18	2.88E-17	31.04369	ROR1	receptor tyrosine kinase-like orphan receptor 1	NM_005012
211981_at	1.11183	9.508964	8.437396	6.27E-15	6.52E-14	23.04586	COL4A1	collagen, type IV, alpha 1	NM_001845
226841_at	1.11161	8.043575	7.828584	2.75E-13	2.37E-12	19.31613	MPEG1	macrophage expressed 1	BF590697
244040_at	1.11141	4.795484	11.62583	3.06E-24	8.06E-23	44.28209			N47474
229319_at	1.11122	7.613775	13.94892	2.14E-31	1.02E-29	60.64391			AA057585
207266_x_at	1.11102	9.085055	9.519855	5.60E-18	8.04E-17	29.98686	RBMS1	RNA binding motif, single stranded interacting protein 1	NM_016837
223344_s_at	1.11088	8.393451	7.81409	3.00E-13	2.57E-12	19.2291	MS4A7	membrane-spanning 4-domains, subfamily A, member 7	AB026043
213652_at	1.11066	6.773454	8.771463	7.45E-16	8.60E-15	25.14916	PCSK5	Protease PC6 isoform A (PCSK5)	AU152579
201426_s_at	1.11055	12.44709	11.34089	2.24E-23	5.39E-22	42.30492	VIM	vimentin	AI922599
204482_at	1.11044	8.233187	10.5706	4.63E-21	9.08E-20	37.01782	CLDN5	claudin 5	NM_003277
1566482_at	1.11028	4.042871	14.20676	3.41E-32	1.73E-30	62.47148			AL833114
235121_at	1.11014	5.249624	11.11076	1.11E-22	2.53E-21	40.71584	ZNF542	zinc finger protein 542	BE966943
212409_s_at	1.10998	7.631882	12.54342	4.73E-27	1.55E-25	50.70645	TOR1AIP1	torsin A interacting protein 1	AK021613
209474_s_at	1.10807	7.353728	9.360731	1.60E-17	2.19E-16	28.94492	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	U87967
225176_at	1.10752	9.23538	13.94907	2.14E-31	1.02E-29	60.64496			AA156754
233136_at	1.10731	3.298594	21.21695	2.96E-53	3.37E-50	110.6564	LOC100131622 /// PABPC5	hypothetical protein LOC100131622 /// poly(A) binding protein, cytoplasmic 5	AL122118
227339_at	1.10682	6.768249	10.52525	6.32E-21	1.22E-19	36.70965	RGM B	RGM domain family, member B	BE206621

226818_at	1.10592	8.318934	7.108144	2.00E-11	1.34E-10	15.09972	MPEG1	macrophage expressed 1	T64884
216005_at	1.10591	4.642318	8.625759	1.89E-15	2.10E-14	24.22719	TNC	Tenascin	BF434846
214078_at	1.10555	4.34594	9.635265	2.60E-18	3.84E-17	30.74669			AF070581
212094_at	1.10524	6.162818	3.77707	0.0002088	0.0003905	-0.57057	PEG10	paternally expressed 10	AL582836
213684_s_at	1.105	5.602155	11.53297	5.86E-24	1.50E-22	43.63665	PDLIM5	PDZ and LIM domain 5	BF671400
209220_at	1.10429	6.744754	5.063319	9.27E-07	2.69E-06	4.611465	GPC3	glypican 3	L47125
212791_at	1.10414	7.664202	14.00752	1.41E-31	6.82E-30	61.05927	C1orf216	chromosome 1 open reading frame 216	AL042729
211067_s_at	1.10412	6.857833	12.31596	2.37E-26	7.34E-25	49.10721	GAS7	growth arrest-specific 7	BC006454
36612_at	1.10377	7.074552	13.80851	5.83E-31	2.67E-29	59.64878	FAM168A	family with sequence similarity 168, member A	D87470
210258_at	1.10338	4.668759	5.438468	1.55E-07	5.24E-07	6.346367	RGS13	regulator of G-protein signaling 13	AF030107
1553113_s_at	1.10265	7.613301	6.877135	7.51E-11	4.63E-10	13.79851	CDK8	cyclin-dependent kinase 8	BF700678
1555997_s_at	1.10248	5.818927	10.46967	9.24E-21	1.75E-19	36.33244	IGFBP5	insulin-like growth factor binding protein 5	BM128432
227448_at	1.10173	5.462238	11.91301	4.07E-25	1.15E-23	46.28434	ARGLU1	arginine and glutamate rich 1	AL045916
225958_at	1.1015	7.010592	14.92527	2.03E-34	1.32E-32	67.56121	PHC1	polyhomeotic homolog 1 (Drosophila)	AI554106
65718_at	1.10146	7.298686	15.70947	7.73E-37	6.33E-35	73.10015	GPR124	G protein-coupled receptor 124	AI655903
222426_at	1.10129	7.593299	11.48236	8.35E-24	2.11E-22	43.28531	MAPKAP1	mitogen-activated protein kinase associated protein 1	BG499947
238081_at	1.10083	4.020379	13.67113	1.55E-30	6.81E-29	58.67535	C4orf12	chromosome 4 open reading frame 12	AI694300
227131_at	1.10065	7.587501	17.67341	7.84E-43	1.32E-40	86.81708	MAP3K3	mitogen-activated protein kinase kinase kinase 3	BG231756
1555191_a_at	1.10065	5.303971	8.38548	8.70E-15	8.91E-14	22.72244	FHL5	four and a half LIM domains 5	BC021723
225509_at	1.10049	7.846603	13.09295	9.55E-29	3.60E-27	54.58324	SAP30L	SAP30-like	AI862477
219201_s_at	1.1003	7.38023	9.47304	7.63E-18	1.08E-16	29.67961	TWSG1	twisted gastrulation homolog 1 (Drosophila)	NM_020648
223253_at	1.09957	7.979906	6.164893	3.78E-09	1.75E-08	9.960543	EPDR1	ependymin related protein 1 (zebrafish)	BC000686
228722_at	1.09916	6.046657	12.82564	6.39E-28	2.25E-26	52.69542	PRMT2	protein arginine methyltransferase 2	AI928367
207864_at	1.09878	3.526605	13.27783	2.56E-29	1.02E-27	55.89069	SCN7A	sodium channel, voltage-gated, type VII, alpha	NM_002976
55872_at	1.09871	6.852956	7.885071	1.95E-13	1.71E-12	19.65615	ZNF512B	zinc finger protein 512B	AI493119
209982_s_at	1.09821	5.394831	10.52606	6.28E-21	1.22E-19	36.71513	NRXN2	neurexin 2	AA608820
204642_at	1.09727	7.47091	11.72745	1.50E-24	4.04E-23	44.9896	S1PR1	sphingosine-1-phosphate receptor 1	NM_001400
226197_at	1.09716	5.479256	14.59477	2.14E-33	1.22E-31	65.22105			AW173504
209648_x_at	1.0968	7.942034	12.71584	1.39E-27	4.78E-26	51.92104	SOC5	suppressor of cytokine signaling 5	AL136896
229951_x_at	1.09634	4.409976	13.02152	1.59E-28	5.87E-27	54.07847			H24473
222444_at	1.09626	7.982854	8.797856	6.29E-16	7.32E-15	25.31691	ARMCX3	armadillo repeat containing, X-linked 3	AL121883
209305_s_at	1.09583	7.644347	9.945231	3.25E-19	5.29E-18	32.80365	GADD45B	growth arrest and DNA-damage-inducible, beta	AF078077
226828_s_at	1.09576	7.252068	9.967727	2.80E-19	4.58E-18	32.95382	HEYL	hairly/enhancer-of-split related with YRPW motif-like	AL040198
213139_at	1.09557	7.459985	6.394038	1.10E-09	5.60E-09	11.16532	SNAI2	snail homolog 2 (Drosophila)	AI572079
206666_at	1.09503	7.386693	5.436589	1.56E-07	5.28E-07	6.337449	GZMK	granzyme K (granzyme 3; tryptase II)	NM_002104
223119_s_at	1.09491	6.638029	14.5833	2.32E-33	1.33E-31	65.13979	USP47	ubiquitin specific peptidase 47	BC000226
240432_x_at	1.0949	6.911103	12.01641	1.96E-25	5.68E-24	47.0073			AI333006
226037_s_at	1.0941	7.836511	11.79454	9.36E-25	2.57E-23	45.45727	LOC728198 /// TAF9B	similar to transcription associated factor TAFII31L /// TAF9B RNA polymerase II, associated factor, 31kDa	AL049589
									#N/A
230003_at	1.09337	5.929654	5.913742	1.41E-08	5.86E-08	8.674731			AW779917
202237_at	1.09326	10.8594	6.823143	1.02E-10	6.15E-10	13.49821	NNMT	nicotinamide N-methyltransferase	NM_006169
205234_at	1.09319	7.127985	7.305787	6.30E-12	4.54E-11	16.23329	SLC16A4	solute carrier family 16, member 4 (monocarboxylic acid transporter: 5)	NM_004696
238647_at	1.09312	6.119273	13.26523	2.80E-29	1.12E-27	55.80156	C14orf28	chromosome 14 open reading frame 28	AA496213
231048_at	1.09311	4.535229	9.825435	7.28E-19	1.14E-17	32.00597			BF675806
212427_at	1.09232	5.271716	11.61078	3.40E-24	8.92E-23	44.17747	KIAA0368	KIAA0368	AB002366
226826_at	1.09229	7.382014	10.53771	5.80E-21	1.13E-19	36.79426			AU152993

201310_s_at	1.09222	9.447094	7.70705	5.75E-13	4.75E-12	18.58901	C5orf13	chromosome 5 open reading frame 13	NM_004772
234989_at	1.09159	8.923514	7.223838	1.02E-11	7.12E-11	15.76106	NCRNA00084	non-protein coding RNA 84	AV699657
214043_at	1.09151	5.257151	7.210861	1.10E-11	7.66E-11	15.68656	PTPRD	protein tyrosine phosphatase, receptor type, D	BF062299
203748_x_at	1.0915	9.134195	9.855108	5.97E-19	9.41E-18	32.20325	RBMS1	RNA binding motif, single stranded interacting protein 1	NM_016839
229178_at	1.09135	4.433125	11.80765	8.53E-25	2.36E-23	45.54875	LOC145786	hypothetical protein LOC145786	AV699825
1555403_a_at	1.09111	3.813318	10.36311	1.91E-20	3.51E-19	35.61086	CDH19	cadherin 19, type 2	BC015877
225406_at	1.0906	10.07219	10.78522	1.06E-21	2.19E-20	38.48136	TWSG1	twisted gastrulation homolog 1 (Drosophila)	AA195009
203325_s_at	1.09024	8.877816	7.646665	8.28E-13	6.69E-12	18.23004	COL5A1	collagen, type V, alpha 1	AI130969
209955_s_at	1.08988	7.709025	5.569606	8.10E-08	2.89E-07	6.974641	FAP	fibroblast activation protein, alpha	U76833
204671_s_at	1.08976	5.723591	8.478855	4.82E-15	5.09E-14	23.30482	ANKRD6	ankyrin repeat domain 6	BE677131
1558027_s_at	1.08895	6.976789	10.42372	1.27E-20	2.37E-19	36.02099	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	AL552001
202982_s_at	1.08875	8.016378	10.81088	8.87E-22	1.85E-20	38.6569	ACOT1 /// ACOT2	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	NM_006821
210222_s_at	1.08872	6.122617	8.503096	4.13E-15	4.40E-14	23.45652	RTN1	reticulon 1	BC000314
220146_at	1.08789	5.819849	8.276412	1.73E-14	1.71E-13	22.04611	TLR7	toll-like receptor 7	NM_016562
236635_at	1.08758	4.772494	17.07693	5.03E-41	6.62E-39	82.68081	ZNF667	zinc finger protein 667	AI332774
228456_s_at	1.08718	7.954404	13.25039	3.11E-29	1.23E-27	55.69656	LOC149832	hypothetical protein LOC149832	AU151357
205968_at	1.0861	7.682975	7.344123	5.03E-12	3.67E-11	16.45526	KCN53	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	NM_002252
230741_at	1.08609	5.951142	8.624659	1.91E-15	2.11E-14	24.22026			AI655467
214091_s_at	1.08599	8.598052	5.757237	3.15E-08	1.22E-07	7.892511	GPX3	glutathione peroxidase 3 (plasma)	AW149846
1555728_a_at	1.08598	7.270102	6.52804	5.30E-10	2.84E-09	11.88333	MS4A4A	membrane-spanning 4-domains, subfamily A, member 4	AF354928
206115_at	1.08572	7.459176	5.215949	4.52E-07	1.40E-06	5.305952	EGR3	early growth response 3	NM_004430
228973_at	1.08571	4.454331	13.29598	2.25E-29	9.03E-28	56.0191	DLG2	discs, large homolog 2 (Drosophila)	AA057445
216866_s_at	1.08564	5.571644	13.90665	2.90E-31	1.36E-29	60.34428	COL14A1	collagen, type XIV, alpha 1	M64108
229674_at	1.08536	6.506243	8.183975	3.07E-14	2.96E-13	21.47632	SERTAD4	SERTA domain containing 4	AL035414
229011_at	1.08519	6.45527	8.363687	9.98E-15	1.02E-13	22.58696			AA150501
232176_at	1.08493	5.159386	6.66247	2.52E-10	1.42E-09	12.61333	SLITRK6	SLIT and NTRK-like family, member 6	R70320
203999_at	1.08489	5.837588	5.357445	2.29E-07	7.50E-07	5.963756	SYT1	synaptotagmin I	AV731490
223005_s_at	1.08487	8.539871	9.666148	2.11E-18	3.15E-17	30.95059	C9orf5	chromosome 9 open reading frame 5	BG402553
203006_at	1.08484	9.513899	11.56033	4.84E-24	1.25E-22	43.82675	INPP5A	inositol polyphosphate-5-phosphatase, 40kDa	NM_005539
228630_at	1.08478	7.056584	11.77013	1.11E-24	3.03E-23	45.28709	ZNF84	zinc finger protein 84	W92744
209307_at	1.08474	8.207531	9.633656	2.63E-18	3.89E-17	30.73608	SWAP70	SWAP-70 protein	AB014540
244130_at	1.08468	4.140286	13.89502	3.15E-31	1.47E-29	60.2619			AI379882
236361_at	1.08446	6.097892	8.035967	7.70E-14	7.11E-13	20.57069	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase-like 2	BF432376
1555894_s_at	1.08393	5.344735	13.04508	1.34E-28	5.00E-27	54.24498	MTSS1L	metastasis suppressor 1-like	AA829283
212624_s_at	1.08388	8.269373	9.867199	5.50E-19	8.72E-18	32.28369	CHN1	chimerin (chimaerin) 1	BF339445
224710_at	1.08385	9.139244	7.706257	5.78E-13	4.77E-12	18.58429	RAB34	RAB34, member RAS oncogene family	AF322067
1553696_s_at	1.08367	4.595913	12.61181	2.91E-27	9.74E-26	51.18801	ZNF569	zinc finger protein 569	NM_152484
228582_x_at	1.0834	5.770177	9.865728	5.56E-19	8.80E-18	32.27389			AI475544
227243_s_at	1.08283	4.949043	10.83739	7.38E-22	1.55E-20	38.83834	EBF3	early B-cell factor 3	AL354950
225093_at	1.08251	9.085517	10.06498	1.45E-19	2.45E-18	33.60427	UTRN	utrophin	N66570
225098_at	1.08225	8.94079	13.16603	5.68E-29	2.18E-27	55.09989	ABI2	abl interactor 2	BF245400
227566_at	1.08209	6.886324	5.151546	6.13E-07	1.84E-06	5.010979	HNT	neurotrimin	AW085558
204619_s_at	1.08168	8.245989	7.166264	1.42E-11	9.76E-11	15.43116	VCAN	versican	BF590263
219935_at	1.08151	7.123716	6.919514	5.90E-11	3.69E-10	14.03526	ADAMTSS	ADAM metalloproteinase with thrombospondin type 1 motif, 5	NM_007038

1553678_a_at	1.08141	10.5772	8.824186	5.31E-16	6.22E-15	25.48448	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	NM_133376
205022_s_at	1.08137	9.211537	14.29192	1.86E-32	9.63E-31	63.07507	FOXP3	forkhead box N3	NM_005197
227860_at	1.08123	6.65557	6.34188	1.46E-09	7.27E-09	10.88851	CPXM1	carboxypeptidase X (M14 family), member 1	NM_019609
1558378_a_at	1.08114	5.658569	6.928776	5.60E-11	3.52E-10	14.08712	AHNAK2	AHNAK nucleoprotein 2	BC004283
214175_x_at	1.08035	7.641654	11.46387	9.50E-24	2.38E-22	43.15702	PDLM4	PDZ and LIM domain 4	AI254547
206314_at	1.0802	5.276025	10.78572	1.05E-21	2.18E-20	38.48483	ZNF167	zinc finger protein 167	NM_018651
205018_s_at	1.07983	7.086766	8.609694	2.10E-15	2.31E-14	24.12597	MBNL2	muscleblind-like 2 (Drosophila)	NM_005757
209203_s_at	1.0797	6.730235	12.64076	2.37E-27	7.99E-26	51.39191	BICD2	bicaudal D homolog 2 (Drosophila)	BC002327
206826_at	1.07969	4.213353	10.11935	1.00E-19	1.72E-18	33.96883	PMP2	peripheral myelin protein 2	NM_002677
213761_at	1.07952	6.873667	10.55558	5.13E-21	1.00E-19	36.91571	MDM1	Mdm1 nuclear protein homolog (mouse)	AW664850
212473_s_at	1.07913	10.14984	9.804874	8.36E-19	1.30E-17	31.86939	MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	BE965029
217721_at	1.07912	6.282077	15.10614	5.61E-35	3.78E-33	68.84074			BE551361
215307_at	1.07896	4.172999	19.13643	3.32E-47	1.21E-44	96.82369	ZNF529	Zinc finger protein 529 (ZNF529), mRNA	AL109722
236330_at	1.07882	5.114455	13.78207	7.04E-31	3.18E-29	59.46146			AW292996
204156_at	1.07881	6.216888	13.15563	6.11E-29	2.34E-27	55.0264	KIAA0999	KIAA0999 protein	AA044154
229027_at	1.07869	5.83391	13.32818	1.79E-29	7.24E-28	56.24698	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	AI241945
235606_at	1.07864	4.352765	14.92633	2.02E-34	1.31E-32	67.56871	LOC344595	hypothetical LOC344595	AA417117
223095_at	1.07776	8.659638	12.46839	8.05E-27	2.59E-25	50.17853	MARVELD1	MARVEL domain containing 1	BC004995
207358_x_at	1.07722	8.735195	14.77169	6.07E-34	3.70E-32	66.47408	MACF1	microtubule-actin crosslinking factor 1	NM_012090
202432_at	1.0771	9.773157	15.32166	1.21E-35	8.74E-34	70.36392	PPP3CB	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	NM_021132
207691_x_at	1.07618	7.437377	9.445619	9.15E-18	1.28E-16	29.49992	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	NM_001776
235352_at	1.07611	7.000856	10.14613	8.37E-20	1.45E-18	34.14861			AI270356
212653_s_at	1.07606	9.342323	10.95563	3.26E-22	7.07E-21	39.64898	EHBP1	EH domain binding protein 1	AB020710
231899_at	1.07551	6.710409	6.918528	5.93E-11	3.71E-10	14.02974	ZC3H12C	zinc finger CCCH-type containing 12C	AB051513
213905_x_at	1.07541	9.406476	7.055937	2.70E-11	1.79E-10	14.80338	BGN	biglycan	AA845258
213236_at	1.0745	8.369471	13.00778	1.75E-28	6.46E-27	53.98145	SASH1	SAM and SH3 domain containing 1	AK025495
201852_x_at	1.07387	12.41336	6.855442	8.50E-11	5.19E-10	13.67768	COL3A1	collagen, type III, alpha 1	AI813758
221031_s_at	1.07384	8.214942	7.640167	8.61E-13	6.93E-12	18.1915	APOLD1	apolipoprotein L domain containing 1	NM_030817
209473_at	1.07369	8.775873	12.55763	4.28E-27	1.41E-25	50.80649	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	AV717590
224686_x_at	1.07361	8.923906	12.87685	4.44E-28	1.59E-26	53.05686	LRR37A2	CDNA FLJ34414 fis, clone HEART2003168, highly similar to Homo sapiens c114	AA045233
								SLIT-like testicular protein (LOC474170), mRNA	#N/A
219689_at	1.07359	6.158849	9.018341	1.51E-16	1.87E-15	26.72681	SEMA3G	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	NM_020163
205121_at	1.07347	5.72787	11.80012	9.00E-25	2.48E-23	45.49619	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	NM_000232
244313_at	1.07345	5.794219	6.951601	4.91E-11	3.12E-10	14.2151	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	AI052659
225016_at	1.07338	7.986117	5.70798	4.05E-08	1.53E-07	7.649421	APCDD1	adenomatous polyposis coli down-regulated 1	N48299
212982_at	1.07315	8.034521	13.22591	3.71E-29	1.45E-27	55.52337	ZDHHC17	zinc finger, DHHC-type containing 17	AI621223
230560_at	1.07302	6.77094	5.459047	1.40E-07	4.77E-07	6.444228	STXBP6	syntaxin binding protein 6 (amisyn)	N21096
205150_s_at	1.07295	6.129715	8.528009	3.53E-15	3.78E-14	23.61263	KIAA0644	KIAA0644 gene product	AV724192

223730_at	1.07229	6.988024	8.813427	5.69E-16	6.64E-15	25.41598	GPC6	glypican 6	AF111178
210997_at	1.07226	4.34443	10.33807	2.27E-20	4.13E-19	35.44167	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	M77227
213170_at	1.0722	6.628971	8.148769	3.83E-14	3.65E-13	21.26015	GPX7	glutathione peroxidase 7	AA406605
210889_s_at	1.07161	6.970103	6.809872	1.10E-10	6.60E-10	13.42462	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	M31933
219400_at	1.07144	6.913689	13.10139	9.00E-29	3.39E-27	54.64294	CNTNAP1	contactin associated protein 1	NM_003632
204310_s_at	1.07097	5.857171	18.28303	1.15E-44	2.77E-42	91.01212	NPR2	natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B)	NM_003995
230250_at	1.0708	8.087544	8.205779	2.68E-14	2.60E-13	21.61044	PTPRB	protein tyrosine phosphatase, receptor type, B	AI670852
234996_at	1.0708	5.252391	10.29241	3.10E-20	5.58E-19	35.13335	CALCRL	calcitonin receptor-like	AI478743
235593_at	1.07062	5.198272	10.47097	9.16E-21	1.74E-19	36.34123	LOC100128821 /// ZEB2	hypothetical protein LOC100128821 /// zinc finger E-box binding homeobox 2	AL546529
235028_at	1.07042	6.045812	8.155209	3.68E-14	3.52E-13	21.29965			BG288330
227923_at	1.06993	6.621201	10.4714	9.14E-21	1.74E-19	36.34413	SHANK3	SH3 and multiple ankyrin repeat domains 3	BF439330
214894_x_at	1.0697	8.398412	14.77206	6.06E-34	3.70E-32	66.47667	MACF1	microtubule-actin crosslinking factor 1	AK023285
221104_s_at	1.06948	3.811534	13.09394	9.49E-29	3.57E-27	54.59024	NIPSNAP3 B	nipsnap homolog 3B (C. elegans)	NM_018376
204150_at	1.06885	7.864579	11.88658	4.90E-25	1.37E-23	46.09971	STAB1	stabilin 1	NM_015136
213489_at	1.06863	7.182233	14.53074	3.38E-33	1.89E-31	64.76748	MAPREZ	RP1 homolog mRNA, 3'UTR region	BE671156
205653_at	1.06839	6.257803	8.075603	6.03E-14	5.63E-13	20.81239	CTSG	cathepsin G	NM_001911
214701_s_at	1.068	7.109354	6.965295	4.54E-11	2.90E-10	14.29201	FN1	fibronectin 1	AJ276395
220494_s_at	1.06766	6.741655	9.508686	6.03E-18	8.63E-17	29.9135			NM_018678
239300_at	1.06754	5.177104	12.59737	3.23E-27	1.08E-25	51.08629			AI632214
206584_at	1.06739	8.377966	6.682669	2.25E-10	1.28E-09	12.72384	LY96	lymphocyte antigen 96	NM_015364
202748_at	1.0673	9.452648	9.783363	9.66E-19	1.49E-17	31.72662	GBP2	guanylate binding protein 2, interferon-inducible	NM_004120
224219_s_at	1.0671	3.708956	9.567863	4.07E-18	5.91E-17	30.30252	TRPC4	transient receptor potential cation channel, subfamily C, member 4	AF063825
205364_at	1.06706	6.952951	10.05914	1.51E-19	2.54E-18	33.56517	ACOX2	acyl-Coenzyme A oxidase 2, branched chain	NM_003500
226282_at	1.06626	8.820154	12.91472	3.39E-28	1.22E-26	53.32418			AW129783
235061_at	1.06578	7.324596	8.898269	3.29E-16	3.95E-15	25.95713	PPM1K	protein phosphatase 1K (PP2C domain containing)	AV706522
229850_at	1.06542	7.684883	8.739014	9.18E-16	1.05E-14	24.94324	KDSR	3-ketodihydrosphingosine reductase	N30152
218854_at	1.06536	8.365202	7.563003	1.37E-12	1.08E-11	17.73525	DSE	dermatan sulfate epimerase	NM_013352
204462_s_at	1.06513	6.881798	8.66661	1.46E-15	1.64E-14	24.48498	SLC16A2	solute carrier family 16, member 2 (monocarboxylic acid transporter 8)	NM_006517
201828_x_at	1.065	9.956604	10.81341	8.71E-22	1.82E-20	38.67421	FAM127A	family with sequence similarity 127, member A	NM_003928
228698_at	1.0648	7.048455	6.295007	1.89E-09	9.19E-09	10.64102	SOX7	SRY (sex determining region Y)-box 7	AI808807
204020_at	1.06473	9.21359	14.00574	1.43E-31	6.90E-30	61.04663	PURA	purine-rich element binding protein A	BF739943
218691_s_at	1.0647	4.937033	12.08235	1.23E-25	3.63E-24	47.46891	PDLIM4	PDZ and LIM domain 4	AF153882
1553530_a_at	1.0643	10.24092	9.105166	8.58E-17	1.09E-15	27.28608	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	NM_033669
204552_at	1.06371	6.222232	11.89139	4.74E-25	1.33E-23	46.13331	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	AA355179
223280_x_at	1.06294	9.085203	7.906614	1.71E-13	1.51E-12	19.78615	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	AF253977
202709_at	1.06234	9.508869	6.58201	3.93E-10	2.16E-09	12.17526	FMOD	fibromodulin	NM_002023
230146_s_at	1.06225	5.845967	11.694	1.90E-24	5.05E-23	44.75659	FREQ	frequenin homolog (Drosophila)	BF111850
202630_at	1.06127	7.925043	11.38226	1.68E-23	4.10E-22	42.59134	APPBP2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	AA046411
227312_at	1.06099	6.755185	11.43567	1.16E-23	2.88E-22	42.96151	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	AI694536

223734_at	1.0607	4.936978	12.96884	2.31E-28	8.42E-27	53.70638	C4orf49	chromosome 4 open reading frame 49	AF329088
232166_at	1.06068	4.980582	12.4055	1.26E-26	4.00E-25	49.7363	KIAA1377	KIAA1377	AL045516
212747_at	1.06065	8.925809	14.36733	1.08E-32	5.75E-31	63.60952	ANKS1A	ankyrin repeat and sterile alpha motif domain containing 1A	AI990523
230305_at	1.06052	6.016654	10.2775	3.43E-20	6.15E-19	35.0328			AW000995
240289_at	1.0598	5.659313	14.48671	4.63E-33	2.55E-31	64.45549	LOC100131683	hypothetical protein LOC100131683	W86910
229222_at	1.05961	5.180871	8.078631	5.91E-14	5.53E-13	20.83088	ACSS3	acyl-CoA synthetase short-chain family member 3	AI123815
206331_at	1.05931	7.397072	9.122043	7.68E-17	9.81E-16	27.39505	CALCRL	calcitonin receptor-like FRAS1 related extracellular matrix 1	NM_005795
228233_at	1.05927	4.891415	11.33836	2.28E-23	5.48E-22	42.28739	FREM1		AI824037
203859_s_at	1.05815	7.384474	13.77631	7.34E-31	3.31E-29	59.42059	PALM	paralemmin	NM_002579
201261_x_at	1.05807	8.712987	7.300984	6.48E-12	4.67E-11	16.20553	BGN	biglycan	BC002416
214104_at	1.05718	6.851624	9.53693	5.00E-18	7.21E-17	30.09906	GPR161	G protein-coupled receptor 161	AI703188
231202_at	1.05713	5.160537	7.277849	7.42E-12	5.30E-11	16.07195	ALDH1L2	Full length insert cDNA clone ZAO2A01	AI654224
204421_s_at	1.05712	5.58174	15.57594	1.99E-36	1.57E-34	72.15876	FGF2	fibroblast growth factor 2 (basic)	M27968
236344_at	1.05702	5.667752	10.87998	5.50E-22	1.17E-20	39.13007	PDE1C	phosphodiesterase 1C, calmodulin-dependent 70kDa	AW299452
224894_at	1.05672	10.1264	8.996209	1.74E-16	2.15E-15	26.58461	YAP1	Yes-associated protein 1, 65kDa	BF247906
219410_at	1.05661	8.388109	5.787917	2.70E-08	1.06E-07	8.044674	TMEM45A	transmembrane protein 45A	NM_018004
213388_at	1.0565	6.891577	9.776787	1.01E-18	1.56E-17	31.68299	PDE4DIP	phosphodiesterase 4D interacting protein	H15535
238115_at	1.05645	5.557196	15.79532	4.21E-37	3.54E-35	73.70492			T03492
1555793_a_at	1.05644	5.958033	9.9858	2.48E-19	4.08E-18	33.07454	ZFP82	zinc finger protein 82 homolog (mouse)	AL834267
228904_at	1.0561	8.509535	7.522012	1.75E-12	1.36E-11	17.49392	HOXB3	homeobox B3	AW510657
244289_at	1.056	4.555834	12.57888	3.68E-27	1.22E-25	50.95611	LOC134466	hypothetical protein LOC134466	AI242408
225273_at	1.05553	8.143326	10.93245	3.83E-22	8.26E-21	39.48989	WWC3	WWC family member 3	AB033106
219626_at	1.05509	6.331656	17.59027	1.40E-42	2.25E-40	86.24237	MAP7D3	MAP7 domain containing 3	NM_024597
207741_x_at	1.05488	8.148267	6.532567	5.17E-10	2.78E-09	11.90776	TPSAB1	trypsin alpha/beta 1	NM_003293
201536_at	1.05456	9.874582	13.05131	1.28E-28	4.79E-27	54.289	DUSP3	dual specificity phosphatase 3	AL048503
202616_s_at	1.05338	7.146766	16.70113	7.03E-40	8.33E-38	80.06031	MECP2	methyl CpG binding protein 2 (Rett syndrome)	AI631140
212558_at	1.05318	8.98162	10.93639	3.72E-22	8.04E-21	39.51693	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	BF508662
211467_s_at	1.05313	6.709141	11.8723	5.42E-25	1.52E-23	46.00001	NFIB	nuclear factor I/B	U70862
218648_at	1.05271	9.386506	15.62754	1.38E-36	1.12E-34	72.52267	CRTC3	CREB regulated transcription coactivator 3	NM_022769
212377_s_at	1.05241	9.047154	11.77099	1.10E-24	3.01E-23	45.29307	NOTCH2	Notch homolog 2 (Drosophila)	AU158495
223504_at	1.05224	5.54133	14.03711	1.14E-31	5.57E-30	61.26896	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	AL117490
210479_s_at	1.05219	6.15151	9.97606	2.64E-19	4.34E-18	33.00947	RORA	RAR-related orphan receptor A	L14611
212344_at	1.05171	8.527967	5.513456	1.07E-07	3.72E-07	6.704278	SULF1	sulfatase 1	AW043713
223378_at	1.05149	7.780471	9.198524	4.66E-17	6.07E-16	27.88991	GLIS2	GLIS family zinc finger 2	AA705182
232382_s_at	1.05149	8.151957	8.248472	2.06E-14	2.02E-13	21.87355	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	BE150929
37408_at	1.05131	9.426745	10.51458	6.80E-21	1.31E-19	36.63716	MRC2	mannose receptor, C type 2	AB014609
225283_at	1.05049	8.79488	7.705853	5.79E-13	4.78E-12	18.58188	ARRDC4	arrestin domain containing 4	AV701177
221731_x_at	1.05045	10.50599	6.853147	8.61E-11	5.25E-10	13.66491	VCAN	versican	BF218922
202450_s_at	1.05016	10.0547	6.306802	1.77E-09	8.67E-09	10.70318	CTSK	cathepsin K	NM_000396
242121_at	1.04977	7.429585	7.635565	8.85E-13	7.11E-12	18.16422	RNF12	Full length insert cDNA clone ZD86G12	AW973232
229464_at	1.0495	6.166403	7.641311	8.55E-13	6.89E-12	18.19828	MYEF2	myelin expression factor 2	N50034
201010_s_at	1.04901	11.75181	9.821316	7.49E-19	1.17E-17	31.9786	TXNIP	thioredoxin interacting protein	NM_006472
235302_at	1.0488	5.450411	13.68189	1.44E-30	6.34E-29	58.75159			BF968187
222433_at	1.04828	10.02497	9.231719	3.75E-17	4.93E-16	28.10521	ENAH	enabled homolog (Drosophila)	AK025108
209454_s_at	1.04818	7.357383	11.36625	1.88E-23	4.56E-22	42.48049	TEAD3	TEA domain family member 3	AF142482
212265_at	1.04818	9.737014	9.458496	8.41E-18	1.18E-16	29.58428	QKI	quaking homolog, KH domain RNA binding (mouse)	AL031781

201387_s_at	1.04809	7.260921	5.509206	1.09E-07	3.80E-07	6.6839	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	NM_004181
205582_s_at	1.04764	7.295892	13.37364	1.29E-29	5.29E-28	56.56868	GGT5	gamma-glutamyltransferase 5	NM_004121
218983_at	1.0471	7.821209	9.877143	5.15E-19	8.16E-18	32.34987	C1RL	complement component 1, r subcomponent-like	NM_016546
201655_s_at	1.04594	10.2307	11.35167	2.08E-23	5.01E-22	42.37956	HSPG2	heparan sulfate proteoglycan 2	M85289
1554767_s_at	1.04566	6.092984	10.65522	2.59E-21	5.18E-20	37.59392	CRYZL1	crystallin, zeta (quinone reductase)-like 1	BC013155
231986_at	1.04551	5.772677	6.737504	1.65E-10	9.65E-10	13.02491	RIMS1	regulating synaptic membrane exocytosis 1	AL035633
225269_s_at	1.04537	9.651356	9.94279	3.31E-19	5.37E-18	32.78737	C2orf12	chromosome 2 open reading frame 12	BE384529
225941_at	1.04492	7.621858	8.847103	4.58E-16	5.41E-15	25.63051	EIF4E3	eukaryotic translation initiation factor 4E family member 3	AI935522
212565_at	1.04484	8.140924	10.15847	7.70E-20	1.33E-18	34.23157	STK38L	serine/threonine kinase 38 like	BE302191
230849_at	1.04382	4.427443	10.78659	1.05E-21	2.17E-20	38.49075	KCNA1	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	N64750
220117_at	1.04369	5.033098	11.5288	6.03E-24	1.54E-22	43.60773	ZNF385D	zinc finger protein 385D	NM_024697
1558934_a_at	1.04366	3.59203	14.33373	1.38E-32	7.23E-31	63.3714			AL134162
228297_at	1.04324	9.488153	10.06115	1.49E-19	2.51E-18	33.57863			AI807004
230454_at	1.04256	5.904319	11.94759	3.19E-25	9.09E-24	46.52599	ICA1L	islet cell autoantigen 1,69kDa-like	AW470508
243209_at	1.04254	5.381455	11.0685	1.49E-22	3.35E-21	40.42488	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	BF725804
215271_at	1.04157	5.474963	8.450995	5.75E-15	6.02E-14	23.13074	TNN	tenascin N	BF432086
244740_at	1.04151	6.298168	13.69928	1.27E-30	5.62E-29	58.87481	MGC9913	hypothetical protein MGC9913	BE855713
239846_at	1.04131	3.874533	18.21943	1.78E-44	4.04E-42	90.57609	MTHFD1	CDNA FLJ38195 fis, clone FCBBF1000314	AW451784
228496_s_at	1.04096	8.638588	10.1146	1.04E-19	1.77E-18	33.93696	CRIM1	CDNA: FLJ22506 fis, clone HRC11695	AW243081
222016_s_at	1.04095	6.913875	8.726213	9.96E-16	1.14E-14	24.86209	ZNF323	zinc finger protein 323	AW086021
203657_s_at	1.04086	8.498544	13.1724	5.43E-29	2.09E-27	55.14497	CTSF	cathepsin F	NM_003793
204560_at	1.04085	6.239226	8.262499	1.88E-14	1.86E-13	21.96015	FKBP5	FK506 binding protein 5	NM_004117
212367_at	1.04081	8.104985	10.64677	2.74E-21	5.48E-20	37.53635	FEM1B	fem-1 homolog b (C. elegans)	AI799061
211984_at	1.0408	10.42386	13.19865	4.50E-29	1.75E-27	55.33063	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	AI653730
230319_at	1.04004	5.356419	5.599059	6.99E-08	2.53E-07	7.117256			AI222435
235240_at	1.03996	6.394263	15.50176	3.37E-36	2.60E-34	71.63548	ATXN3	ataxin 3	N51479
203888_at	1.03962	7.611921	9.090068	9.47E-17	1.20E-15	27.18867	THBD	thrombomodulin	NM_000361
208633_s_at	1.0396	7.54678	14.65317	1.41E-33	8.22E-32	65.63475	MACF1	microtubule-actin crosslinking factor 1	W61052
244294_at	1.0395	4.634978	14.68338	1.14E-33	6.74E-32	65.8487			AA461190
228618_at	1.03948	6.062365	14.36922	1.07E-32	5.68E-31	63.62293	PEAR1	platelet endothelial aggregation receptor 1	AL040178
203604_at	1.03946	5.931633	13.66689	1.60E-30	7.01E-29	58.64535	ZNF516	zinc finger protein 516	N38750
201009_s_at	1.03902	11.4536	9.295189	2.47E-17	3.30E-16	28.51774	TXNIP	thioredoxin interacting protein	AI439556
233899_x_at	1.03889	6.105363	5.596512	7.08E-08	2.56E-07	7.104905	ZBTB10	zinc finger and BTB domain containing 10	AK024296
239587_at	1.03879	6.578634	6.240542	2.53E-09	1.21E-08	10.35501			AI686890
226909_at	1.03874	6.982032	7.585218	1.20E-12	9.48E-12	17.86634	ZNF518B	zinc finger protein 518B	AW270138
218528_s_at	1.03851	8.928225	14.54181	3.12E-33	1.75E-31	64.84589	RNF38	ring finger protein 38	NM_022781
1558142_at	1.03829	7.897829	12.70258	1.53E-27	5.24E-26	51.82761	TNRC6B	trinucleotide repeat containing 6B	AL831862
201801_s_at	1.03807	7.501989	9.769256	1.06E-18	1.63E-17	31.63305	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	AF079117
242845_at	1.03783	4.50491	15.64871	1.19E-36	9.62E-35	72.67188			AI366780

210330_at	1.03768	4.323212	13.39119	1.14E-29	4.68E-28	56.69293	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	U58331
235849_at	1.03756	6.878599	5.94886	1.18E-08	4.95E-08	8.852287	SCARA5	scavenger receptor class A, member 5 (putative)	BE787752
202048_s_at	1.03747	8.651643	13.36741	1.35E-29	5.51E-28	56.5246	CBX6	chromobox homolog 6	NM_014292
221523_s_at	1.03739	6.098259	7.23214	9.70E-12	6.81E-11	15.80876	RRAGD	Ras-related GTP binding D	AL138717
1555800_at	1.03723	4.174787	6.893475	6.85E-11	4.24E-10	13.88969	ZNF385B	zinc finger protein 385B	BC038422
228528_at	1.0367	6.086832	8.208416	2.64E-14	2.56E-13	21.62667			AI927692
1565681_s_at	1.03665	6.637039	12.84977	5.38E-28	1.91E-26	52.8657	DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	N42910
1552760_at	1.03634	3.879388	9.733209	1.35E-18	2.05E-17	31.39416	HDAC9	histone deacetylase 9	BM726008
226112_at	1.03581	8.777469	13.20075	4.44E-29	1.73E-27	55.34542	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	AI678717
203549_s_at	1.03579	7.348381	5.774323	2.89E-08	1.13E-07	7.977179	LPL	lipoprotein lipase	NM_000237
225937_at	1.03537	6.193846	12.16144	7.06E-26	2.11E-24	48.02304			BF002121
227013_at	1.03532	9.3927	9.470282	7.78E-18	1.10E-16	29.66154	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	AI535735
223276_at	1.03517	8.326306	9.174424	5.46E-17	7.06E-16	27.73379	MST150	MSTP150	AF313413
1555234_a_at	1.03491	6.177408	13.59911	2.60E-30	1.12E-28	58.16519	RHJQ	ras homolog gene family, member J	BC025770
208982_at	1.034	10.31588	8.638046	1.75E-15	1.95E-14	24.30467	PECAM1	platelet/endothelial cell adhesion molecule	AW574504
224002_s_at	1.0339	6.93257	9.737556	1.31E-18	1.99E-17	31.42296	FKBP7	FK506 binding protein 7	AF100751
207233_s_at	1.03365	8.065318	10.22395	4.94E-20	8.70E-19	34.67196	MITF	microphthalmia-associated transcription factor	NM_000248
242590_at	1.03364	5.521566	15.79902	4.10E-37	3.45E-35	73.73101			BE464643
238360_s_at	1.03362	4.956471	13.05881	1.22E-28	4.55E-27	54.34197			AI885665
244163_at	1.0334	3.807497	9.106977	8.48E-17	1.08E-15	27.29777	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	BF215018
228030_at	1.0329	6.487827	8.529985	3.49E-15	3.74E-14	23.62502			AI041522
229344_x_at	1.03287	5.80215	10.25555	3.98E-20	7.08E-19	34.88489	RIMKLB	ribosomal modification protein rimK-like family member B	AW135012
238476_at	1.03279	6.616958	11.00468	2.32E-22	5.11E-21	39.98591	C5orf41	chromosome 5 open reading frame 41	AA481560
216831_s_at	1.03269	4.709275	11.8041	8.75E-25	2.41E-23	45.52398	RUNX1T1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	AF018283
235976_at	1.03231	3.629142	6.382571	1.17E-09	5.93E-09	11.10433	SLITRK6	SLIT and NTRK-like family, member 6	AI680986
225940_at	1.03191	8.105035	11.62255	3.13E-24	8.24E-23	44.2593	EIF4E3	eukaryotic translation initiation factor 4E family member 3	BE465037
213434_at	1.0319	7.504976	14.2152	3.21E-32	1.64E-30	62.53126	STX2	syntaxin 2	H95263
212549_at	1.03173	8.580946	16.28625	1.31E-38	1.29E-36	77.15571	STAT5B	signal transducer and activator of transcription 5B	BE645861
227069_at	1.03166	7.157147	13.33729	1.68E-29	6.80E-28	56.31142			AA806989
208851_s_at	1.03154	9.027534	8.49481	4.36E-15	4.62E-14	23.40465	THY1	Thy-1 cell surface antigen	AL161958
220617_s_at	1.03143	7.863931	11.75421	1.24E-24	3.37E-23	45.17607	ZNF532	zinc finger protein 532	NM_018181
229430_at	1.03127	3.828457	10.70277	1.87E-21	3.78E-20	37.91815	C8orf46	chromosome 8 open reading frame 46	AI421311
213940_s_at	1.03111	7.852945	11.46675	9.31E-24	2.34E-22	43.17706	FBNP1	formin binding protein 1	AU145053
223641_at	1.03081	5.675546	12.97093	2.28E-28	8.31E-27	53.72109			BC000885
205872_x_at	1.03081	6.767166	9.77709	1.01E-18	1.55E-17	31.68501	PDE4DIP	phosphodiesterase 4D interacting protein	NM_022359
231738_at	1.03056	5.426939	8.543766	3.19E-15	3.45E-14	23.71148	PCDH87	protocadherin beta 7	NM_018940
219767_s_at	1.03052	7.354709	11.6926	1.91E-24	5.10E-23	44.74687	CRYZL1	crystallin, zeta (quinone reductase)-like 1	NM_005111
204469_at	1.03027	5.801318	4.354438	2.12E-05	4.72E-05	1.60147	PTPRZ1	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	NM_002851
235978_at	1.03023	4.281555	6.007841	8.66E-09	3.74E-08	9.152143	FABP4	fatty acid binding protein 4, adipocyte	AI766029

[illegible]

9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B,									#N/A
5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily C, 5									#N/A
236123_at	1.02969	6.437029	6.428534	9.14E-10	4.70E-09	11.34922	ST7L	Suppression of tumorigenicity 7 like, mRNA (cDNA clone MGC:42217 IMAGE:4812133)	BE220209
235821_at	1.02953	5.78919	7.097197	2.13E-11	1.43E-10	15.03747			AI917494
201148_s_at	1.0284	8.59286	10.26009	3.86E-20	6.88E-19	34.91543	TIMP3	TIMP metalloproteinase inhibitor 3	AW338933
202401_s_at	1.02804	8.071453	14.84002	3.73E-34	2.33E-32	66.95786	SRF	serum response factor (c-fos serum response element-binding transcription factor)	NM_003131
230490_x_at	1.02719	8.086748	15.73196	6.59E-37	5.44E-35	73.2586	RSU1	Ras suppressor protein 1	AI866717
232205_at	1.02715	6.612711	8.544254	3.18E-15	3.44E-14	23.71454			AL133627
238740_at	1.02714	4.496993	11.1439	8.83E-23	2.02E-21	40.94422	AARSD1	alanyl-tRNA synthetase domain containing 1	AA180872
203329_at	1.02692	7.709273	13.33326	1.73E-29	6.99E-28	56.28293	PTPRM	protein tyrosine phosphatase, receptor type, M	NM_002845
213040_s_at	1.02667	5.688587	10.55158	5.27E-21	1.03E-19	36.88922	NPTXR	neuronal pentraxin receptor	AL008583
210374_x_at	1.0263	6.141155	12.00906	2.07E-25	5.96E-24	46.95591	PTGER3	prostaglandin E receptor 3 (subtype EP3)	D38300
210683_at	1.02606	5.107389	7.993677	1.00E-13	9.11E-13	20.31347	NRTN	neurturin	AL161995
233543_s_at	1.02602	5.97722	9.869808	5.41E-19	8.57E-18	32.30105	FAM175A	family with sequence similarity 175, member A	AK021582
226331_at	1.02601	8.442	12.34123	1.98E-26	6.18E-25	49.28466	BBX	bobby sox homolog (Drosophila)	BF508813
211986_at	1.02563	10.59087	11.3122	2.74E-23	6.54E-22	42.10642	AHNAK	AHNAK nucleoprotein	BG287862
229019_at	1.02519	5.414221	6.924223	5.75E-11	3.60E-10	14.06162	ZNF385B	zinc finger protein 385B	AI694320
242172_at	1.02511	4.817228	15.44363	5.10E-36	3.87E-34	71.22519	MEIS1	Leukemogenic homolog protein (MEIS1)	N50406
220182_at	1.02455	5.934696	11.37513	1.77E-23	4.29E-22	42.54199	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	NM_024103
209278_s_at	1.02437	5.965305	4.264539	3.08E-05	6.65E-05	1.246215	TFPI2	tissue factor pathway inhibitor 2	L27624

213135_at	1.02368	6.743659	7.778976	3.72E-13	3.15E-12	19.0186	TIAM1	T-cell lymphoma invasion and metastasis 1	U90902
229809_at	1.02352	4.593043	17.47506	3.12E-42	4.69E-40	85.44491			AW445212
212327_at	1.02351	7.088024	8.154199	3.70E-14	3.54E-13	21.29346	UMCH1	LIM and calponin homology domains 1	AK026815
215222_x_at	1.02347	8.473163	15.33016	1.14E-35	8.26E-34	70.42398	MACF1	microtubule-actin crosslinking factor 1	AK023406
221249_s_at	1.02307	7.725906	10.82721	7.92E-22	1.66E-20	38.76862	FAM117A	family with sequence similarity 117, member A	NM_030802
203571_s_at	1.02299	9.009715	4.806345	3.00E-06	7.86E-06	3.478555	C10orf116	chromosome 10 open reading frame 116	NM_006829
225763_at	1.02295	6.57266	7.46459	2.46E-12	1.87E-11	17.15711	RCSD1	RCSD domain containing 1	AI659418
219469_at	1.02267	6.039358	11.90412	4.33E-25	1.22E-23	46.22219	DYNC2H1	dynein, cytoplasmic 2, heavy chain 1	NM_024606
222156_x_at	1.02265	7.252729	8.933207	2.62E-16	3.18E-15	26.18063	CCPG1	cell cycle progression 1	AK022459
239848_at	1.0225	5.201701	11.41416	1.34E-23	3.31E-22	42.81237			BF939569
228194_s_at	1.02179	4.568947	9.899758	4.42E-19	7.08E-18	32.50048	SORCS1	sortilin-related VPS10 domain containing receptor 1	AI675836
1552347_at	1.02145	6.894818	13.19898	4.49E-29	1.75E-27	55.33296	CRYZL1	crystallin, zeta (quinone reductase)-like 1	NM_145311
238868_at	1.02135	5.181238	9.788028	9.36E-19	1.45E-17	31.75757	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	AW264269
225999_at	1.02085	5.237472	9.065839	1.11E-16	1.40E-15	27.03248	RIMKLB	ribosomal modification protein rimK-like family member B	AI743612
214279_s_at	1.02076	7.036295	7.797426	3.32E-13	2.83E-12	19.12914	NDRG2	NDRG family member 2	W74452
227559_at	1.02053	6.362401	11.15607	8.12E-23	1.86E-21	41.02811			AL521129
244043_at	1.02043	5.835592	10.44191	1.12E-20	2.10E-19	36.14426			AI049624
214829_at	1.01912	5.419865	10.57685	4.44E-21	8.73E-20	37.06035	AASS	amino adipate-semialdehyde synthase	AK023446
218589_at	1.01894	8.509165	10.07927	1.32E-19	2.23E-18	33.70007	P2RY5	purinergic receptor P2Y, G-protein coupled, 5	NM_005767
217943_s_at	1.01858	8.581948	13.50073	5.24E-30	2.20E-28	57.4684	MAP7D1	MAP7 domain containing 1	NM_018057
227401_at	1.01845	5.517823	11.51132	6.82E-24	1.73E-22	43.48632	IL17D	interleukin 17D	BE856748
214725_at	1.0175	3.806016	9.149283	6.43E-17	8.25E-16	27.57111	C8orf84	chromosome 8 open reading frame 84	BE968773
204620_s_at	1.01729	10.21205	6.630981	3.00E-10	1.68E-09	12.44148	VCAN	versican	NM_004385
221139_s_at	1.01713	6.355909	12.20567	5.16E-26	1.56E-24	48.33314	CSAD	cysteine sulfinic acid decarboxylase	NM_015989
1558279_a_at	1.01683	6.522838	8.524912	3.60E-15	3.86E-14	23.59321	KDSR	3-ketodihydrosphingosine reductase	BF666293
212104_s_at	1.01671	9.251105	14.3439	1.28E-32	6.75E-31	63.44348	RBM9	RNA binding motif protein 9	N95026
229716_at	1.0167	6.062656	10.70428	1.85E-21	3.75E-20	37.92847			AI288607
235320_at	1.01664	5.791729	10.51254	6.89E-21	1.33E-19	36.62329	ARL6	ADP-ribosylation factor-like 6	AL138043
236153_at	1.0165	4.62993	13.78758	6.77E-31	3.07E-29	59.50046			BF447323
235311_at	1.0164	5.107439	10.42953	1.22E-20	2.29E-19	36.06036	FKBP14	FK506 binding protein 14, 22 kDa, mRNA (cDNA clone MGC:12218 IMAGE:4042173)	BG110260
205003_at	1.01603	7.67241	9.302121	2.36E-17	3.16E-16	28.56286	DOCK4	dedicator of cytokinesis 4	NM_014705
202663_at	1.01575	6.000233	9.043423	1.28E-16	1.60E-15	26.88814	WIPF1	WAS/WASL interacting protein family, member 1	AI005043
204787_at	1.01532	7.804486	6.9946	3.84E-11	2.48E-10	14.4569	VSIG4	V-set and immunoglobulin domain containing 4	NM_007268
204829_s_at	1.01529	7.491573	10.44496	1.09E-20	2.06E-19	36.16491	FOLR2	folate receptor 2 (fetal)	NM_000803
215813_s_at	1.01472	7.482126	7.301399	6.46E-12	4.65E-11	16.20793	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	S36219
226793_at	1.01454	7.576175	11.91074	4.13E-25	1.17E-23	46.26849	LOC283267	hypothetical LOC283267	AI913533
212848_s_at	1.01332	9.43245	10.56562	4.79E-21	9.38E-20	36.98396	C9orf3	chromosome 9 open reading frame 3	BG036668
224941_at	1.01225	5.723377	6.538097	5.01E-10	2.70E-09	11.93762	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	BF107618
214602_at	1.01223	5.162949	7.158122	1.49E-11	1.02E-10	15.38463	COL4A4	collagen, type IV, alpha 4	D17391
213908_at	1.01208	5.299212	16.00302	9.67E-38	8.68E-36	75.16656	WHDC1L1	similar to junction-mediating and regulatory protein /// WAS protein homology region 2 domain containing 1-like 1	AI824078
204176_at	1.01165	7.06247	11.56872	4.56E-24	1.19E-22	43.88501	KLHL20	kelch-like 20 (Drosophila)	AA808694
225725_at	1.01161	8.284403	10.94196	3.58E-22	7.75E-21	39.55513			AL533234
211161_s_at	1.01144	11.90531	7.128596	1.77E-11	1.20E-10	15.21617	COL3A1	collagen, type III, alpha 1	AF130082

57715_at	1.01113	7.362529	11.91179	4.10E-25	1.16E-23	46.27582	CALHM2	calcium homeostasis modulator 2	W72694
218486_at	1.01072	7.854152	9.830237	7.05E-19	1.10E-17	32.03788	KLF11	Kruppel-like factor 11	AA149594
211302_s_at	1.01071	6.547389	7.673838	7.03E-13	5.74E-12	18.39138	PDE4B	phosphodiesterase 4B, CAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila)	L20966
200808_s_at	1.01048	8.643414	10.8884	5.19E-22	1.11E-20	39.18777	ZYX	zyxin	NM_003461
227300_at	1.00951	6.74285	6.536962	5.04E-10	2.72E-09	11.93149	TMEM119	transmembrane protein 119	AL521682
211929_at	1.00922	9.35946	12.93968	2.84E-28	1.03E-26	53.50042	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	AA527502
205992_s_at	1.00896	7.216916	8.597035	2.28E-15	2.49E-14	24.04627	IL15	Interleukin 15	NM_000585
205453_at	1.00894	8.312589	9.865219	5.58E-19	8.82E-18	32.27051	HOXB2	homeobox B2	NM_002145
1552754_a_at	1.00878	3.612754	7.829812	2.73E-13	2.35E-12	19.3235	CADM2	cell adhesion molecule 2	AA640422
203875_at	1.00873	8.21868	7.840772	2.55E-13	2.21E-12	19.38938	SMARCA1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	NM_003069
213012_at	1.00871	6.897519	11.21406	5.42E-23	1.26E-21	41.42825	NEDD4	neural precursor cell expressed, developmentally down-regulated 4	D42055
207496_at	1.00757	4.14977	8.577257	2.58E-15	2.81E-14	23.92185	MS4A2	membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide)	NM_000139
235388_at	1.0074	5.890944	12.43631	1.01E-26	3.24E-25	49.95292	CHD9	chromodomain helicase DNA binding protein 9	BG538482
242470_at	1.00596	4.760782	10.65778	2.54E-21	5.10E-20	37.61134	EID2B	EP300 interacting inhibitor of differentiation 2B	AI093963
203264_s_at	1.00564	6.731546	11.0984	1.21E-22	2.75E-21	40.6307	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	NM_015185
227847_at	1.0053	7.820342	9.75015	1.21E-18	1.84E-17	31.50639	EPM2AIP1	EPM2A (laforin) interacting protein 1	BF432224
222291_at	1.00528	4.7427	9.278633	2.75E-17	3.67E-16	28.41002	FAM149A	family with sequence similarity 149, member A	AI478795
213578_at	1.0051	8.841875	10.50428	7.29E-21	1.40E-19	36.56723	BMPRI1A	bone morphogenetic protein receptor, type IA	AI678679
218128_at	1.00465	7.49736	11.43549	1.16E-23	2.88E-22	42.96022	NFYB	nuclear transcription factor Y, beta	AU151875
228006_at	1.00437	8.039411	12.48554	7.13E-27	2.31E-25	50.2992			BG403361
211275_s_at	1.00418	10.54466	12.56119	4.17E-27	1.38E-25	50.83153	GYG1	glycogenin 1	AF087942
1556047_s_at	1.0041	5.4463	12.37842	1.52E-26	4.80E-25	49.54601	MAGEE1	melanoma antigen family E, 1	AI298393
219855_at	1.00375	5.795956	11.41271	1.36E-23	3.35E-22	42.80234	NUDT11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	NM_018159
215127_s_at	1.00372	10.2265	9.376744	1.44E-17	1.98E-16	29.04946	RBMS1	RNA binding motif, single stranded interacting protein 1	AI517946
210075_at	1.0036	7.506829	13.32078	1.89E-29	7.62E-28	56.19457	MARCH2	membrane-associated ring finger (C3HC4) 2	AF151074
1569566_at	1.00334	4.080408	11.83601	6.99E-25	1.94E-23	45.74666	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	BC028196
236383_at	1.00308	4.800388	8.929073	2.70E-16	3.26E-15	26.15417			R07502
222454_s_at	1.00273	8.530721	12.2197	4.68E-26	1.42E-24	48.43158	PARVA	parvin, alpha	BG107577
231969_at	1.00257	5.20522	6.889373	7.01E-11	4.34E-10	13.86679	STOX2	storkhead box 2	AB037813
226440_at	1.00253	8.083595	14.85999	3.24E-34	2.03E-32	67.09917	DUSP22 LOC100134371	dual specificity phosphatase 22 similar to dual specificity phosphatase 22	BE222746
211380_s_at	1.00241	5.451174	14.68599	1.12E-33	6.62E-32	65.86718	PRKG1	protein kinase, cGMP-dependent, type I	D45864
224797_at	1.00214	8.511545	9.511987	5.90E-18	8.46E-17	29.93518	ARRDC3	arrestin domain containing 3	AB037797
228532_at	1.00163	7.576747	7.494189	2.06E-12	1.59E-11	17.33055	C1orf162	chromosome 1 open reading frame 162	AW662189
204273_at	1.0014	6.917754	5.569405	8.11E-08	2.89E-07	6.973669	EDNRB	endothelin receptor type B	NM_000115
236488_s_at	1.00108	6.330278	9.036608	1.34E-16	1.67E-15	26.84429			AI683805
203845_at	1.00101	7.991432	8.743855	8.90E-16	1.02E-14	24.97393	KAT2B	K(lysine) acetyltransferase 2B	AV727449
230147_at	1.00088	7.191384	5.587119	7.42E-08	2.67E-07	7.059376	F2RL2	coagulation factor II (thrombin) receptor-like 2	AI378647
222073_at	1.00068	4.602017	5.399955	1.87E-07	6.21E-07	6.163964	COL4A3	collagen, type IV, alpha 3 (Goodpasture antigen)	AI694562

							PCDHA1 /// PCDHA10 /// PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 ///		
210674_s_at	1.00044	5.071611	5.649366	5.44E-08	2.01E-07	7.362121	///	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11	AF152308
								/// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 ///	#N/A
								protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 ///	#N/A
								protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 ///	#N/A
								protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	#N/A
222129_at	1.00036	6.636132	12.01703	1.95E-25	5.65E-24	47.01166	FAM134A	family with sequence similarity 134, member A	AK026155
219390_at	0.9999	7.032344	8.706761	1.13E-15	1.28E-14	24.73889	FKBP14	FK506 binding protein 14, 22 kDa	NM_017946
209815_at	0.99986	8.12143	5.955804	1.14E-08	4.79E-08	8.887479	PTCH1	patched homolog 1 (Drosophila)	BG054916
235764_at	0.99925	3.946439	13.40978	1.00E-29	4.13E-28	56.82453			AA029888
212819_at	0.99917	4.352301	15.44206	5.15E-36	3.90E-34	71.21413	ASB1	ankyrin repeat and SOCS box- containing 1	AF055024
235007_at	0.99904	6.517906	11.02713	1.99E-22	4.41E-21	40.14026	BBS7	Bardet-Biedl syndrome 7	AI683802
208328_s_at	0.99888	6.753318	12.80744	7.27E-28	2.55E-26	52.56707	MEF2A	myocyte enhancer factor 2A	NM_005587
223316_at	0.99855	8.608735	10.87075	5.86E-22	1.24E-20	39.0668	CCDC3	coiled-coil domain containing 3	AL136562
219204_s_at	0.99827	6.022789	12.47503	7.68E-27	2.48E-25	50.2252	SRR	serine racemase	NM_021947
206363_at	0.99812	7.169377	8.330723	1.23E-14	1.24E-13	22.38236	MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	NM_005360
212912_at	0.99792	7.962634	8.960867	2.19E-16	2.68E-15	26.35784	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	AI992251
236565_s_at	0.99766	7.334591	5.844426	2.02E-08	8.11E-08	8.326448	LARP6	La ribonucleoprotein domain family, member 6	BF792126
227167_s_at	0.99746	9.924873	11.18234	6.76E-23	1.56E-21	41.2093			AW511319
242471_at	0.99729	5.006789	9.713796	1.54E-18	2.32E-17	31.26564			AI916641
218266_s_at	0.99728	5.900797	11.4269	1.23E-23	3.04E-22	42.9007	FREQ	frequenin homolog (Drosophila)	NM_014286
227325_at	0.99689	8.047021	14.59634	2.12E-33	1.21E-31	65.23222	LOC25578	hypothetical protein LOC255783	AW172584
207968_s_at	0.99635	5.72143	14.84662	3.56E-34	2.22E-32	67.00457	MEF2C	myocyte enhancer factor 2C	NM_002397
218675_at	0.99631	6.41303	12.53455	5.04E-27	1.65E-25	50.64405	SLC22A17	solute carrier family 22, member 17	NM_020372
217795_s_at	0.99604	9.182765	11.89064	4.76E-25	1.34E-23	46.12809	TMEM43	transmembrane protein 43	W74580

223422_s_at	0.99602	8.051144	9.819094	7.60E-19	1.19E-17	31.96384	ARHGAP24	Rho GTPase activating protein 24	AI743534
221564_at	0.99571	8.270527	15.41971	6.04E-36	4.51E-34	71.05634	PRMT2	protein arginine methyltransferase 2	AL570294
207749_s_at	0.99427	7.116883	10.33896	2.26E-20	4.11E-19	35.44765	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha	NM_002718
225558_at	0.99425	8.630089	15.81735	3.60E-37	3.05E-35	73.8601	GIT2	G protein-coupled receptor kinase interacting ArfGAP 2	R38084
232431_at	0.99413	4.782605	7.389589	3.84E-12	2.85E-11	16.71938			AI934556
235443_at	0.99341	5.907921	14.27238	2.13E-32	1.10E-30	62.93656	LOC100131067	hypothetical protein LOC100131067	BG284827
207557_s_at	0.99329	5.237994	9.789003	9.30E-19	1.44E-17	31.76405	RYR2	ryanodine receptor 2 (cardiac)	NM_001035
225516_at	0.99327	7.233443	6.283156	2.01E-09	9.76E-09	10.57865	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	AA876372
222111_at	0.99273	7.591626	9.952417	3.10E-19	5.05E-18	32.85161			AU145293
203771_s_at	0.99235	7.077755	8.408901	7.50E-15	7.73E-14	22.86823	BLVRA	biliverdin reductase A	AA740186
239548_at	0.99198	3.387389	15.12245	5.00E-35	3.40E-33	68.95606	NEGR1	neuronal growth regulator 1	AW001754
210305_at	0.99166	4.935331	8.814048	5.67E-16	6.62E-15	25.41993	PDE4DIP	phosphodiesterase 4D interacting protein	AB042557
232064_at	0.99153	5.255095	13.84551	4.48E-31	2.07E-29	59.91103			AK021888
226692_at	0.99063	8.326015	12.72267	1.33E-27	4.56E-26	51.96922	SERF2	small EDRK-rich factor 2	AI092931
228255_at	0.9905	5.443389	10.76046	1.26E-21	2.58E-20	38.3121	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	AU150140
218127_at	0.99047	8.385135	12.01245	2.02E-25	5.83E-24	46.9796	NFYB	nuclear transcription factor Y, beta	AI804118
230174_at	0.99036	7.414069	10.08077	1.30E-19	2.21E-18	33.71007	LYPLAL1	lysophospholipase-like 1	AI953360
209795_at	0.99019	6.944126	5.103166	7.70E-07	2.27E-06	4.791247	CD69	CD69 molecule	L07555
224860_at	0.99008	5.972502	10.57582	4.47E-21	8.78E-20	37.05332	C9orf123	chromosome 9 open reading frame 123	AL137489
214743_at	0.99001	8.427293	10.85656	6.47E-22	1.37E-20	38.96959	CUX1	cut-like homeobox 1	BE046521
212739_s_at	0.98994	8.619823	10.37582	1.76E-20	3.24E-19	35.69682	NME4	non-metastatic cells 4, protein expressed in	AL523860
243495_s_at	0.98987	6.708082	6.08743	5.70E-09	2.55E-08	9.56002			AL036450
203424_s_at	0.98946	7.677875	7.163137	1.45E-11	9.93E-11	15.41329	IGFBP5	insulin-like growth factor binding protein 5	AW157548
226581_at	0.98936	8.237848	13.94289	2.24E-31	1.06E-29	60.60117	ZFYVE20	zinc finger, FYVE domain containing 20	AA524034
226612_at	0.98895	5.535948	5.833084	2.14E-08	8.55E-08	8.269737	FLJ25076	similar to CG4502-PA	H17038
229159_at	0.98886	4.0844	10.4863	8.25E-21	1.57E-19	36.44523	THSD7A	CDNA clone IMAGE:4791783	AW612111
205419_at	0.98816	8.069995	7.635366	8.86E-13	7.12E-12	18.16304	GPR183	G protein-coupled receptor 183	NM_004951
209119_x_at	0.98814	6.819755	8.140517	4.03E-14	3.84E-13	21.20954	NR2F2	nuclear receptor subfamily 2, group F, member 2	AV703465

							PCDHGA1 /// PCDHGA1 0 /// PCDHGA1 1 /// PCDHGA1 2 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 ///		
215836_s_at	0.98768	8.569865	12.3795	1.51E-26	4.77E-25	49.55356	///	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 ///	AK026188
								protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 ///	#N/A
								protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 ///	#N/A
								protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 ///	#N/A
								protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 ///	#N/A
								protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 ///	#N/A
								protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 ///	#N/A
								protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 ///	#N/A
								protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 ///	#N/A
								protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 ///	#N/A
								protocadherin gamma subfamily C, 4 /// protocadherin gamma subfamily C, 5 ///	#N/A
235427_at	0.9875	6.405111	10.64223	2.83E-21	5.65E-20	37.50539			AA418074
224793_s_at	0.98717	9.764975	9.860383	5.76E-19	9.10E-18	32.23833	TGFB1	transforming growth factor, beta receptor 1	AA604375
215199_at	0.98713	4.395963	13.27087	2.69E-29	1.07E-27	55.84145	CALD1	caldesmon 1	AU147402

218665_at	0.98662	7.817307	12.56551	4.05E-27	1.34E-25	50.86196	FZD4	frizzled homolog 4 (Drosophila)	NM_012193
201866_s_at	0.98645	7.680004	9.755027	1.17E-18	1.79E-17	31.53871	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	NM_000176
211616_s_at	0.9862	5.128252	12.5686	3.96E-27	1.31E-25	50.88375	HTR2A	5-hydroxytryptamine (serotonin) receptor 2A	M86841
213016_at	0.98607	9.106282	11.67332	2.19E-24	5.83E-23	44.61259	BBX	bobby sox homolog (Drosophila)	AA573805
204831_at	0.98604	8.882357	7.019284	3.33E-11	2.18E-10	14.59611	CDK8	cyclin-dependent kinase 8	R59697
203104_at	0.98571	8.367647	10.05049	1.60E-19	2.69E-18	33.50725	CSF1R	colony stimulating factor 1 receptor	NM_005211
203812_at	0.98566	6.513632	12.00507	2.13E-25	6.12E-24	46.92796			AB011538
226571_s_at	0.98561	6.898564	10.78934	1.03E-21	2.13E-20	38.50955	PTPR5	protein tyrosine phosphatase, receptor type, 5	N38920
242321_at	0.98552	4.827211	11.88579	4.93E-25	1.38E-23	46.09419			AI628689
202747_s_at	0.98548	8.930636	6.599038	3.58E-10	1.98E-09	12.26768	ITM2A	Integral membrane protein 2A	NM_004867
227193_at	0.98543	7.356409	10.52444	6.35E-21	1.23E-19	36.70414			AI955713
236656_s_at	0.98539	6.549971	9.140501	6.81E-17	8.72E-16	27.51433	LOC100130506	hypothetical protein LOC100130506	AW014647
1554726_at	0.98538	4.798534	8.94416	2.44E-16	2.97E-15	26.25077	ZNF655	zinc finger protein 655	AY099353
224995_at	0.98534	7.870818	8.276707	1.72E-14	1.71E-13	22.04794	SPIRE1	spire homolog 1 (Drosophila)	AJ277587
210273_at	0.98533	6.574595	10.22418	4.93E-20	8.69E-19	34.67352	PCDH7	protocadherin 7	AB006757
217838_s_at	0.98523	7.992707	8.887379	3.53E-16	4.22E-15	25.88755	EVL	Enah/Vasp-like	NM_016337
227717_at	0.98501	7.568822	7.807002	3.14E-13	2.68E-12	19.18656	FLJ41603	FLJ41603 protein	BF939317
1553960_at	0.98493	7.128982	12.82355	6.48E-28	2.28E-26	52.68072	SNX21	sorting nexin family member 21	CA447177
205425_at	0.98475	6.50236	8.279571	1.69E-14	1.68E-13	22.06564	HIP1	huntingtin interacting protein 1	NM_005338
225673_at	0.98429	11.06115	10.02842	1.85E-19	3.10E-18	33.35954	MYADM	myeloid-associated differentiation marker	BE908995
241484_x_at	0.98418	5.329038	12.09804	1.10E-25	3.26E-24	47.57875			AI668696
212878_s_at	0.98407	8.146936	11.55826	4.91E-24	1.27E-22	43.81233	KLC1	kinesin light chain 1	AA284075
225157_at	0.98365	8.601646	12.01177	2.03E-25	5.86E-24	46.97487	MLXIP	MLX interacting protein, mRNA (cDNA clone IMAGE:4995872)	AW245631
228457_at	0.98357	6.305494	9.694799	1.75E-18	2.62E-17	31.13997			AI590190
212472_at	0.98347	8.355994	8.784022	6.87E-16	7.97E-15	25.22896	MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2	BE965029
238569_at	0.98344	5.862216	14.04547	1.08E-31	5.26E-30	61.32821	GABBR1	GABA-BR1a (hGB1a) receptor	N45228
235391_at	0.98329	7.783559	6.649591	2.70E-10	1.52E-09	12.54298	FAM92A1	family with sequence similarity 92, member A1	AW960748
228709_at	0.98286	5.546936	13.50859	4.95E-30	2.09E-28	57.52412	TPR	translocated promoter region (to activated MET oncogene)	BF109993
209829_at	0.98274	5.736953	6.071706	6.19E-09	2.75E-08	9.479143	FAM65B	family with sequence similarity 65, member B	AB002384
1556329_a_at	0.98247	3.295337	10.06904	1.41E-19	2.38E-18	33.63146			BC042378
236079_at	0.98236	5.398498	13.26487	2.81E-29	1.12E-27	55.799	DKFZp667E0512	hypothetical protein DKFZp667E0512	AA649070
227579_at	0.9822	7.035034	13.59199	2.73E-30	1.17E-28	58.11474			BF740245
225613_at	0.98217	7.58528	9.695498	1.74E-18	2.61E-17	31.14459	LOC100128443 /// 8443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	AI096389
228967_at	0.98206	7.398901	9.717466	1.50E-18	2.27E-17	31.28993	EIF1	Eukaryotic translation initiation factor 1, mRNA (cDNA clone MGC:15684 IMAGE:3350981)	BE964053
201152_s_at	0.98184	10.81248	16.6469	1.03E-39	1.18E-37	79.68127	MBNL1	muscleblind-like (Drosophila)	N31913
236331_at	0.98177	4.737626	11.00383	2.34E-22	5.13E-21	39.98005	CDKL2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	AW299729
225935_at	0.98159	8.044661	12.40508	1.26E-26	4.01E-25	49.73338			AI350995
213656_s_at	0.98135	9.210656	16.95758	1.16E-40	1.48E-38	81.84973	KLC1	kinesin light chain 1	BF593594
208763_s_at	0.98047	10.28933	7.635756	8.84E-13	7.11E-12	18.16535	TSC22D3	TSC22 domain family, member 3	AL110191
41644_at	0.97988	8.412225	12.35629	1.78E-26	5.57E-25	49.39048	SASH1	SAM and SH3 domain containing 1	AB018333
231137_at	0.97915	5.940126	15.8599	2.66E-37	2.30E-35	74.15961			AI686126
218259_at	0.97897	9.236458	12.4478	9.32E-27	2.99E-25	50.03373	MKL2	MKL/myocardin-like 2	NM_014048
203868_s_at	0.97857	8.705669	6.049785	6.95E-09	3.06E-08	9.366634	VCAM1	vascular cell adhesion molecule 1	NM_001078
225219_at	0.97832	9.018049	11.48729	8.06E-24	2.04E-22	43.31954	SMAD5	SMAD family member 5	BF526175

229890_at	0.9783	5.559855	13.13127	7.27E-29	2.76E-27	54.85413	PRRT1	proline-rich transmembrane protein 1	AI799702
200810_s_at	0.97817	10.30968	13.29271	2.30E-29	9.23E-28	55.99597	CIRBP	cold inducible RNA binding protein	NM_001280
212253_x_at	0.97811	7.205352	11.66125	2.38E-24	6.33E-23	44.52855	DST	dystonin	BG253119
1557261_at	0.97799	4.739055	14.77036	6.13E-34	3.73E-32	66.46468	LOC652637 /// WHDC1L1 /// WHDC1L2	similar to junction-mediating and regulatory protein /// WAS protein homology region 2	AK091254
201744_s_at	0.97798	11.59166	7.526307	1.70E-12	1.33E-11	17.51918	LUM	domain containing 1-like 1 /// WAS protein homology region 2 domain containing 1-like 2	NM_002345
202973_x_at	0.97758	8.869638	7.435238	2.93E-12	2.21E-11	16.9855	FAM13A1	lumican	NM_014883
225914_s_at	0.97749	6.852441	9.484606	7.07E-18	1.01E-16	29.75547	CAB39L	family with sequence similarity 13, member A1	AW242839
223672_at	0.97736	4.81015	12.83686	5.90E-28	2.09E-26	52.7746	SGIP1	calcium binding protein 39-like	AL136561
218338_at	0.97731	7.227393	14.28725	1.92E-32	9.94E-31	63.04198	PHG1 /// PHC1B	SH3-domain GRB2-like (endophilin) interacting protein 1	NM_004426
202386_s_at	0.97707	8.132143	11.07921	1.38E-22	3.12E-21	40.49857	KIAA0430	polyhomeotic homolog 1 (Drosophila) /// polyhomeotic homolog 1B (Drosophila)	NM_019081
225623_at	0.97662	7.229537	9.895941	4.53E-19	7.26E-18	32.47505	KIAA1737	KIAA0430	AI621225
210278_s_at	0.97649	5.425146	10.89158	5.08E-22	1.09E-20	39.20956	AP451	adaptor-related protein complex 4, sigma 1 subunit	AF155159
217707_x_at	0.9759	8.539938	10.97488	2.85E-22	6.22E-21	39.78118	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	AI535683
209304_x_at	0.97581	8.673646	9.552498	4.51E-18	6.53E-17	30.20143	GADD45B	growth arrest and DNA-damage-inducible, beta	AF087853
219534_x_at	0.9756	6.680574	6.348149	1.42E-09	7.05E-09	10.92169	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	NM_000076
226773_at	0.97558	7.795262	10.20454	5.63E-20	9.88E-19	34.54128			AW290940
229357_at	0.97534	5.976925	6.805874	1.12E-10	6.74E-10	13.40246	ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif, 5	BF060767
202125_s_at	0.97526	8.85732	14.53817	3.21E-33	1.80E-31	64.82009	TRAK2	trafficking protein, kinesin binding 2	NM_015049
214596_at	0.97494	7.029487	5.754249	3.20E-08	1.24E-07	7.877719	CHRM3	cholinergic receptor, muscarinic 3	T15991
210407_at	0.97437	6.26448	12.53125	5.16E-27	1.69E-25	50.62083	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	AF070670
212361_s_at	0.97428	9.603904	12.49936	5.47E-27	2.10E-25	50.39639	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	AW190070
212012_at	0.97422	9.078529	7.692174	6.29E-13	5.16E-12	18.50044	PXDN	peroxidasin homolog (Drosophila)	BF342851
212937_s_at	0.97403	7.021977	10.28963	3.16E-20	5.69E-19	35.11461	COL6A1	collagen, type VI, alpha 1	M20776
236192_at	0.97387	6.861579	9.930237	3.60E-19	5.83E-18	32.70363	HOOK3	hook homolog 3 (Drosophila)	BF447112
213566_at	0.97372	8.198987	6.591001	3.74E-10	2.06E-09	12.22404	RNASE6	ribonuclease, RNase A family, k6	NM_005615
222911_s_at	0.97355	6.018911	11.37664	1.75E-23	4.25E-22	42.55245	CXorf36	chromosome X open reading frame 36	AI796127
223366_at	0.97343	7.513333	7.37139	4.28E-12	3.16E-11	16.61355			BC004287
232197_x_at	0.97322	5.433855	11.73145	1.46E-24	3.93E-23	45.01743	ARSB	arylsulfatase B	AW168942
215046_at	0.97298	5.190886	10.27157	3.57E-20	6.38E-19	34.9928	C2orf67	chromosome 2 open reading frame 67	AL133053
202443_x_at	0.97298	9.551391	12.08332	1.22E-25	3.61E-24	47.4757	NOTCH2	Notch homolog 2 (Drosophila)	AA291203
202311_s_at	0.97254	8.670426	4.181484	4.32E-05	9.07E-05	0.923505	COL1A1	collagen, type I, alpha 1	AI743621
214913_at	0.97234	4.308709	10.27601	3.47E-20	6.20E-19	35.02273	ADAMTS3	ADAM metalloproteinase with thrombospondin type 1 motif, 3	AB002364
233587_s_at	0.97232	7.54321	8.585791	2.44E-15	2.67E-14	23.97552	SIPA1L2	signal-induced proliferation-associated 1 like 2	AK022852
242789_at	0.97206	4.502286	13.53611	4.07E-30	1.73E-28	57.71899	PDE1A	phosphodiesterase 1A, calmodulin-dependent	H17817
203998_s_at	0.9718	4.445565	4.576012	8.28E-06	1.99E-05	2.503051	SYT1	synaptotagmin I	AV723167
209183_s_at	0.97147	9.36327	6.7259	1.76E-10	1.02E-09	12.96107	C10orf10	chromosome 10 open reading frame 10	AL136653

211663_x_at	0.97147	8.112682	5.77861	2.83E-08	1.10E-07	7.998451	PTGDS	prostaglandin D2 synthase 21kDa (brain)	M61900
228718_at	0.97104	5.261997	13.65918	1.69E-30	7.38E-29	58.59074	ZNF44	zinc finger protein 44	A1379070
226621_at	0.97059	8.583273	7.113733	1.93E-11	1.30E-10	15.13152			A1133452
213805_at	0.97017	6.213764	8.69282	1.23E-15	1.39E-14	24.65067	ABHD5	abhydrolase domain containing 5	A1692428
209959_at	0.96986	7.941131	5.398447	1.88E-07	6.25E-07	6.156843	NR4A3	nuclear receptor subfamily 4, group A, member 3	U12767
239741_at	0.96942	3.83418	13.61945	2.25E-30	9.71E-29	58.30928	LOC28365	hypothetical protein LOC283658	AA233912
226873_at	0.96832	7.04833	10.02731	1.87E-19	3.12E-18	33.35207			A1631210
229713_at	0.96831	7.876085	9.796397	8.85E-19	1.37E-17	31.81312			AW665227
235385_at	0.96826	5.88645	6.554446	4.58E-10	2.48E-09	12.02597			A1935334
225755_at	0.96802	8.031156	12.01921	1.92E-25	5.58E-24	47.02692	KLHDC8B	kelch domain containing 8B	A1160540
227722_at	0.96522	7.847486	11.01572	2.15E-22	4.75E-21	40.06179	RPS23	ribosomal protein S23	AW043594
238992_at	0.96595	4.198032	13.12512	7.60E-29	2.88E-27	54.81069	POL1	polymerase (DNA directed) iota	AW129145
228091_at	0.96577	6.740857	13.5942	2.69E-30	1.15E-28	58.13042	STX17	syntaxin 17	A1800609
203249_at	0.96567	7.471983	16.40243	5.76E-39	5.98E-37	77.97024	EZH1	enhancer of zeste homolog 1 (Drosophila)	AB002386
219574_at	0.96557	6.321887	6.302362	1.81E-09	8.86E-09	10.67978	MARCH1	membrane-associated ring finger (C3HC4) 1	NM_017923
202440_s_at	0.9651	8.590349	12.34133	1.98E-26	6.17E-25	49.28538	ST5	suppression of tumorigenicity 5	NM_005418
219304_s_at	0.96472	7.27214	5.079709	8.59E-07	2.51E-06	4.685282	PDGFD	platelet derived growth factor D	NM_025208
244680_at	0.96471	3.794242	14.95045	1.70E-34	1.10E-32	67.7394	GLRB	glycine receptor, beta	A1701428
228523_at	0.96452	4.905169	6.187319	3.36E-09	1.57E-08	10.07714	NANOS1	nanos homolog 1 (Drosophila)	AW970089
202052_s_at	0.96416	9.098427	8.795344	6.39E-16	7.43E-15	25.30093	RAI14	retinoic acid induced 14	NM_015577
225913_at	0.96402	9.238544	15.15862	3.86E-35	2.66E-33	69.21178	SGK269	NKF3 kinase family member	AK025943
227169_at	0.96377	5.526818	13.99587	1.53E-31	7.37E-30	60.97668	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	AA729502
229705_at	0.96362	5.274795	11.06455	1.53E-22	3.44E-21	40.39764			A1927212
215972_at	0.9636	4.490344	8.477725	4.86E-15	5.12E-14	23.29776			AF070547
230779_at	0.96351	7.310209	9.881692	4.99E-19	7.94E-18	32.38015	TNRC6B	trinucleotide repeat containing 6B	BF594371
235803_at	0.9633	4.722009	10.1309	9.28E-20	1.60E-18	34.0464			AA843122
243591_at	0.96318	4.993451	9.816602	7.73E-19	1.20E-17	31.94729			A1887749
235344_at	0.96292	6.121853	12.99901	1.86E-28	6.85E-27	53.91944	PPM1A	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	BG288054
211844_s_at	0.96267	5.272857	10.55157	5.28E-21	1.03E-19	36.88845	NRP2	neuropilin 2	AF022859
205923_at	0.96265	5.54361	8.677006	1.37E-15	1.54E-14	24.55067	RELN	reelin	NM_005045
205559_s_at	0.96249	7.664379	5.897125	1.54E-08	6.33E-08	8.590973	PCSK5	proprotein convertase subtilisin/kexin type 5	NM_006200
201309_x_at	0.96247	7.501163	7.11102	1.96E-11	1.32E-10	15.11608	C5orf13	chromosome 5 open reading frame 13	U36189
204584_at	0.96242	5.709411	4.608898	7.18E-06	1.74E-05	2.639972	L1CAM	L1 cell adhesion molecule	A1653981
204040_at	0.96237	7.06643	9.361373	1.50E-17	2.18E-16	28.94911	RNF144A	ring finger protein 144A	NM_014746
225055_at	0.96229	7.440173	11.51353	6.71E-24	1.71E-22	43.50172			AV735241
202124_s_at	0.96217	8.496373	12.93168	3.01E-28	1.08E-26	53.44395	TRAK2	trafficking protein, kinesin binding 2	AV705253
200788_s_at	0.96193	10.547	15.27388	1.70E-35	1.21E-33	70.0264	PEA15	phosphoprotein enriched in astrocytes 15	NM_003768
242277_at	0.96187	6.604795	6.826032	1.00E-10	6.06E-10	13.51424			AW880875
213218_at	0.96182	6.798822	13.48732	5.76E-30	2.41E-28	57.37345	ZNF187	zinc finger protein 187	AV705032
226040_at	0.96171	6.932843	11.14868	8.55E-23	1.96E-21	40.97714			BE856302
212851_at	0.96083	7.340217	10.90238	4.71E-22	1.01E-20	39.28364	DCUN1D4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	AA194584
224819_at	0.96051	8.728737	7.103306	2.05E-11	1.38E-10	15.0722	TCEAL8	transcription elongation factor A (SII)-like 8	A1743979
202273_at	0.96038	8.304667	8.893942	3.38E-16	4.05E-15	25.92948	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	NM_002609
204344_s_at	0.96029	7.396374	10.53798	5.79E-21	1.12E-19	36.79611	SEC23A	Sec23 homolog A (S. cerevisiae)	NM_006364
212408_at	0.95995	10.24249	14.64263	1.52E-33	8.85E-32	65.56007	TOR1AIP1	torsin A interacting protein 1	AK023204
228751_at	0.95971	6.575969	10.15678	7.79E-20	1.35E-18	34.22018	CLK4	CDC-like kinase 4	AW975057
1562139_a at	0.95895	3.761706	12.47057	7.93E-27	2.56E-25	50.19386	FOXP2	forkhead box P2	AF467254
1569150_x at	0.95891	5.503924	12.8271	6.32E-28	2.23E-26	52.70573	PDUM7	CDNA clone IMAGE:4763486	BC023629
221911_at	0.95862	6.285211	5.635426	5.83E-08	2.14E-07	7.294113	ETV1	ets variant 1	BE881590
226575_at	0.95859	7.549147	7.84774	2.45E-13	2.12E-12	19.43129	ZNF462	zinc finger protein 462	T89120

215606_s_at	0.95858	7.378257	10.7754	1.13E-21	2.34E-20	38.41425	ERC1	ELKS/RAB6-interacting/CAST family member 1	AB029004
243225_at	0.95845	4.716553	10.56309	4.88E-21	9.53E-20	36.96676	LOC283481	hypothetical protein LOC283481	AI042341
226959_at	0.95761	7.380364	12.79163	8.13E-28	2.84E-26	52.45555	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	AV706396
235534_at	0.95758	6.275331	11.22047	5.19E-23	1.21E-21	41.47252			AI624156
205610_at	0.95728	5.76982	11.06418	1.54E-22	3.45E-21	40.39513	MYOM1	myomesin 1, 185kDa	NM_003803
244453_at	0.95724	4.179058	13.50907	4.93E-30	2.08E-28	57.52746	ADAM23	ADAM metalloproteinase domain 23	AI879064
223443_s_at	0.95708	6.772674	10.82879	7.83E-22	1.64E-20	38.77949	FLJ32065	hypothetical protein FLJ32065	BC003669
226164_x_at	0.95648	4.630247	9.504262	6.21E-18	8.87E-17	29.88446	RIMKLB	Homo sapiens, clone IMAGE:4722056, mRNA	AI760919
204672_s_at	0.95635	4.920153	9.21285	4.24E-17	5.55E-16	27.98279	ANKRD6	ankyrin repeat domain 6	NM_014942
212646_at	0.95624	9.430527	8.886224	3.56E-16	4.25E-15	25.88017	RFTN1	raftlin, lipid raft linker 1	D42043
237719_x_at	0.95622	4.072142	9.965687	2.84E-19	4.64E-18	32.9402	RGS7BP	regulator of G-protein signaling 7 binding protein	H05023
228342_s_at	0.95597	5.40811	9.35	1.72E-17	2.34E-16	28.8749	ALPK3	alpha-kinase 3	AA843297
204249_s_at	0.95591	7.916708	9.119424	7.82E-17	9.97E-16	27.37813	LMO2	LIM domain only 2 (rhombotin-like 1)	NM_005574
221760_at	0.95546	9.963235	7.885262	1.94E-13	1.71E-12	19.65729	MAN1A1	CDNA: FLJ21946 fis, clone HEP04860, highly similar to HSHUMM9 Homo sapiens HUMM9 mRNA	BG287153
206326_at	0.95516	4.623977	6.386992	1.15E-09	5.80E-09	11.12784	GRP	gastrin-releasing peptide	NM_002091
1552658_a_at	0.95483	4.364111	10.6318	3.04E-21	6.05E-20	37.43432	NAV3	neuron navigator 3	NM_014903
214293_at	0.95482	6.767348	11.19365	6.25E-23	1.45E-21	41.28733	SEPT11	CDNA FLJ37154 fis, clone BRACE2026054, highly similar to SEPTIN 2	AI539361
212690_at	0.95465	7.868954	10.18171	6.58E-20	1.15E-18	34.38771	DDHD2	DDHD domain containing 2	AB018268
228416_at	0.95428	6.806712	9.203531	4.51E-17	5.88E-16	27.92236	ACVR2A	activin A receptor, type IIA	AI149508
1555420_a_at	0.95401	6.585215	8.098401	5.23E-14	4.92E-13	20.95169	KLF7	Kruppel-like factor 7 (ubiquitous)	BC012919
206726_at	0.95386	5.720727	8.483065	4.69E-15	4.96E-14	23.33116	PGDS	prostaglandin D2 synthase, hematopoietic	NM_014485
38487_at	0.95359	8.173426	10.86221	6.22E-22	1.32E-20	39.0083	STAB1	stabilin 1	D87433
219700_at	0.95345	6.773711	9.130512	7.27E-17	9.30E-16	27.44976	PLXDC1	plexin domain containing 1	NM_020405
213737_x_at	0.95343	9.033974	10.83208	7.66E-22	1.61E-20	38.802	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	AI620911
229265_at	0.95298	9.228742	12.24001	4.05E-26	1.24E-24	48.57407	SKI	v-ski sarcoma viral oncogene homolog (avian)	AA927480
201427_s_at	0.95247	11.89554	5.918579	1.38E-08	5.72E-08	8.699145	SEPP1	selenoprotein P, plasma, 1	NM_005410
231789_at	0.9522	4.407152	12.14355	8.01E-26	2.39E-24	47.89762	PCDH815	protocadherin beta 15	AV722990
229549_at	0.9521	7.421136	9.244726	3.44E-17	4.54E-16	28.18966			AA868461
231991_at	0.95174	6.752573	11.91074	4.13E-25	1.17E-23	46.2685	C20orf160	chromosome 20 open reading frame 160	BF970287
217783_s_at	0.95166	10.39014	13.98031	1.71E-31	8.21E-30	60.86636	YPEL5	yippee-like 5 (Drosophila)	NM_016061
228011_at	0.95158	7.654767	9.55028	4.57E-18	6.62E-17	30.18684	FAM92A1	family with sequence similarity 92, member A1	BF338870
227918_s_at	0.95146	6.076148	10.05487	1.55E-19	2.61E-18	33.53655	ZYG11B	zyg-11 homolog B (C. elegans)	N21008
226056_at	0.951	6.210012	12.10326	1.06E-25	3.15E-24	47.61536	CDGAP	Cdc42 GTPase-activating protein	AB033030
204633_s_at	0.95088	7.817245	8.903988	3.17E-16	3.81E-15	25.99369	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	AF074393
222846_at	0.95074	6.513442	6.715024	1.88E-10	1.08E-09	12.90129	RAB8B	RAB8B, member RAS oncogene family	AB038995
225112_at	0.94979	8.650339	13.71815	1.11E-30	4.94E-29	59.00852	ABI2	abl interactor 2	AA058571
231950_at	0.94948	4.888738	9.190468	4.91E-17	6.38E-16	27.8377	ZNF658	zinc finger protein 658	AW874634
1560271_at	0.94911	4.334083	13.38702	1.18E-29	4.82E-28	56.66341			BC030757
228875_at	0.94846	6.500748	7.527373	1.69E-12	1.32E-11	17.52545	FAM162B	family with sequence similarity 162, member B	AI540210
231292_at	0.94838	4.310601	12.70757	1.48E-27	5.06E-26	51.86274	EID3	EP300 interacting inhibitor of differentiation 3	AI964053
225998_at	0.94805	7.09431	14.07341	8.82E-32	4.34E-30	61.52626	GAB1	GRB2-associated binding protein 1	AK022142
238688_at	0.9478	7.083936	10.88633	5.27E-22	1.12E-20	39.17362	TPM1	Alpha-tropomyosin	AI521618
225018_at	0.9478	6.723254	7.034076	3.06E-11	2.01E-10	14.67968	SPIRE1	spire homolog 1 (Drosophila)	BF512188
219576_at	0.94676	6.244829	13.47155	6.44E-30	2.59E-28	57.26182	MAP7D3	MAP7 domain containing 3	NM_024765
230081_at	0.94673	4.081977	6.969994	4.42E-11	2.83E-10	14.31842	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	AI694325

205249_at	0.94619	7.682806	6.592182	3.72E-10	2.05E-09	12.23045	EGR2	early growth response 2 (Krox-20 homolog, Drosophila)	NM_000399
213568_at	0.94584	6.422758	5.034687	1.06E-06	3.04E-06	4.48296	OSR2	odd-skipped related 2 (Drosophila)	AI811298
215561_s_at	0.94572	4.85077	10.69427	1.98E-21	4.00E-20	37.86019	IL1R1	interleukin 1 receptor, type I	AK026803
201975_at	0.94544	9.049555	13.18887	4.83E-29	1.87E-27	55.2614	CLIP1	CAP-GLY domain containing linker protein 1	NM_002956
232020_at	0.9452	5.200671	11.83927	6.83E-25	1.90E-23	45.76941	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	AU157259
212950_at	0.94508	7.837657	7.402363	3.56E-12	2.66E-11	16.79376	GPR116	G protein-coupled receptor 116	BF941499
214030_at	0.94504	8.053558	11.99611	2.27E-25	6.51E-24	46.8653	CRYBG3	beta-gamma crystallin domain containing 3	BE501352
229881_at	0.94502	5.405547	12.87047	4.65E-28	1.65E-26	53.01182	KLF12	Kruppel-like factor 12	R41200
236016_at	0.94483	5.659869	8.057979	6.72E-14	6.24E-13	20.70484			AI702962
213293_s_at	0.94457	9.791258	6.789265	1.24E-10	7.36E-10	13.31053	TRIM22	tripartite motif-containing 22	AA083478
213313_at	0.94403	8.9795	11.5352	5.77E-24	1.48E-22	43.65216	RABGAP1	RAB GTPase activating protein 1	AI922519
202468_s_at	0.94397	9.176154	9.366736	1.54E-17	2.11E-16	28.98412	CTNNAL1	catenin (cadherin-associated protein), alpha-like 1	NM_003798
224927_at	0.94365	8.765194	10.26551	3.72E-20	6.64E-19	34.95193	KIAA1949	KIAA1949	BG251556
212468_at	0.94315	7.439727	10.04741	1.63E-19	2.74E-18	33.48663	SPAG9	sperm associated antigen 9	AK023512
201236_s_at	0.94281	10.1176	8.19572	2.86E-14	2.76E-13	21.54854	BTG2	BTG family, member 2	NM_006763
208868_s_at	0.94119	7.333815	11.2411	4.49E-23	1.06E-21	41.61499	1	GABARAPL GABA(A) receptor-associated protein like 1	BF125756
226763_at	0.9405	9.278159	9.815614	7.78E-19	1.21E-17	31.94072	SESTD1	SEC14 and spectrin domains 1	AW409611
235198_at	0.93994	7.333015	9.091929	9.35E-17	1.18E-15	27.20067	OSTM1	osteopetrosis associated transmembrane protein 1	AV713913
1569129_s_at	0.93968	5.874121	9.44337	9.29E-18	1.30E-16	29.48519	C3orf38	chromosome 3 open reading frame 38	BC016013
214038_at	0.93964	7.627343	4.248043	3.29E-05	7.07E-05	1.1817	CCL8	chemokine (C-C motif) ligand 8	AI984980
236561_at	0.93963	5.664321	7.761002	4.15E-13	3.49E-12	18.91105	TGFBR1	Homo sapiens, clone IMAGE:4750477, mRNA	AV700621
204334_at	0.93954	7.789099	10.01485	2.03E-19	3.39E-18	33.26875	KLF7	Kruppel-like factor 7 (ubiquitous)	AA488672
224229_s_at	0.93945	4.570568	12.94678	2.70E-28	9.78E-27	53.55057	AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AL117525
238468_at	0.9394	7.492639	12.54365	4.73E-27	1.55E-25	50.70806	TNRC6B	trinucleotide repeat containing 6B	AA214704
212977_at	0.93924	8.5194	6.011877	8.48E-09	3.67E-08	9.172736	CXCR7	chemokine (C-X-C motif) receptor 7	AI817041
213688_at	0.93907	6.899928	11.76833	1.12E-24	3.06E-23	45.27449	CALM1 /// CALM2 /// CALM3	calmodulin 1 (phosphorylase kinase, delta) /// calmodulin 2 (phosphorylase kinase, delta) /// calmodulin 3 (phosphorylase kinase, delta)	N25325
								/// calmodulin 3 (phosphorylase kinase, delta)	#N/A
219165_at	0.93903	7.872572	9.036462	1.34E-16	1.67E-15	26.84335	PDLIM2	PDZ and LIM domain 2 (mystique)	NM_021630
203884_s_at	0.93896	7.731913	8.620241	1.96E-15	2.17E-14	24.19241	RAB11FIP2	RAB11 family interacting protein 2 (class I)	NM_014904
231240_at	0.93885	7.210365	4.599441	7.48E-06	1.81E-05	2.600517	DIO2	deiodinase, iodothyronine, type II	AI038059
217608_at	0.93882	6.474353	10.88596	5.28E-22	1.12E-20	39.17103	SFRS12IP1	SFRS12-interacting protein 1	AW408767
201124_at	0.9385	6.643774	10.00403	2.19E-19	3.63E-18	33.19638	ITGB5	integrin, beta 5	AL048423
227038_at	0.93806	9.210501	6.248971	2.42E-09	1.16E-08	10.39916	SGMS2	sphingomyelin synthase 2	AI963083
228494_at	0.93759	6.697526	4.142601	5.05E-05	0.0001048	0.774259	PPP1R9A	protein phosphatase 1, regulatory (inhibitor) subunit 9A	AI888150
1553974_at	0.93754	7.711297	10.55259	5.24E-21	1.02E-19	36.89538	C22orf39	chromosome 22 open reading frame 39	BC030758
209543_s_at	0.9375	7.633927	11.14457	8.79E-23	2.01E-21	40.94885	CD34	CD34 molecule	MB1104
210426_x_at	0.93638	6.137401	8.718017	1.05E-15	1.20E-14	24.81016	RORA	RAR-related orphan receptor A	U04897
224763_at	0.93591	7.069529	10.00279	2.21E-19	3.66E-18	33.18807	RPL37	Ribosomal protein L37, mRNA (cDNA clone IMAGE:6671394)	BF724210
233249_at	0.93564	4.988435	13.96541	1.91E-31	9.10E-30	60.76079	LOC73020	PREDICTED: Homo sapiens hypothetical LOC730200 (LOC730200), mRNA	AU155297

225553_at	0.93558	8.847283	10.01674	2.01E-19	3.34E-18	33.28135			AL042817
221565_s_at	0.93543	7.631361	11.32642	2.48E-23	5.94E-22	42.20477	CALHM2	calcium homeostasis modulator 2	BC000039
203791_at	0.93442	8.060734	10.47936	8.65E-21	1.65E-19	36.39812	DMXL1	Dmrx-like 1	NM_005509
209967_s_at	0.93432	8.612944	8.841724	4.74E-16	5.59E-15	25.59622	CREM	cAMP responsive element modulator	D14826
207120_at	0.93404	4.134669	15.36942	8.64E-36	6.37E-34	70.70125	ZNF667	zinc finger protein 667	NM_022103
39582_at	0.93387	6.947289	13.40152	1.06E-29	4.37E-28	56.76605	CYLD	cylindromatosis (turban tumor syndrome)	AL050166
231215_at	0.93384	5.005545	13.47097	6.47E-30	2.70E-28	57.25773			AI733145
213298_at	0.93333	6.408982	11.07326	1.44E-22	3.25E-21	40.4576	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	X12492
213154_s_at	0.9333	8.378584	11.67272	2.20E-24	5.85E-23	44.60843	BICD2	bicaudal D homolog 2 (Drosophila)	AI934125
214240_at	0.93317	6.291588	3.538972	0.0004987	0.000875	-1.38854	GAL	galanin prepropeptide	AL556409
237071_at	0.93317	4.252509	14.60812	1.95E-33	1.12E-31	65.31567			AI342132
218181_s_at	0.9331	7.761398	8.854508	4.37E-16	5.17E-15	25.67773	MAP4K4	mitogen-activated protein kinase kinase kinase 4	NM_017792
219520_s_at	0.93286	7.883835	10.34689	2.14E-20	3.90E-19	35.50123	WWC3	WWC family member 3	NM_018458
227859_at	0.93264	5.822669	14.87454	2.92E-34	1.85E-32	67.20221	DNAJC27	DnaJ (Hsp40) homolog, subfamily C, member 27	AV706343
1556194_a_at	0.93252	5.513399	5.514394	1.06E-07	3.71E-07	6.708778			BC042959
231980_at	0.93241	3.839792	15.92083	1.73E-37	1.51E-35	74.58846			AL120332
208671_at	0.93206	10.70081	13.16783	5.61E-29	2.16E-27	55.11261	SERINC1	serine incorporator 1	AF164794
213817_at	0.93159	5.657018	5.444196	1.50E-07	5.10E-07	6.373579	IRAK3	interleukin-1 receptor-associated kinase 3	AL049435
205262_at	0.93155	6.101922	9.210423	4.31E-17	5.63E-16	27.96705	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	NM_000238
219478_at	0.93151	8.331591	5.160383	5.88E-07	1.77E-06	5.051288	WFDC1	WAP four-disulfide core domain 1	NM_021197
212669_at	0.93147	7.486138	10.7374	1.47E-21	3.01E-20	38.15458	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	AI093569
204983_s_at	0.93138	6.936791	7.247477	8.87E-12	6.25E-11	15.89696	GPC4	glypican 4	AF064826
206272_at	0.93114	8.048576	8.610946	2.08E-15	2.30E-14	24.13385	RAB4A /// SPHAR	RAB4A, member RAS oncogene family /// S-phase response (cyclin-related)	NM_006542
213375_s_at	0.93099	7.796246	7.688054	6.45E-13	5.29E-12	18.47592	N4BP2L1	NEDD4 binding protein 2-like 1	N80918
226795_at	0.93097	8.060446	11.01521	2.16E-22	4.77E-21	40.05829			AW007739
202551_s_at	0.93072	9.269529	10.67761	2.22E-21	4.47E-20	37.74652	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	BG546884
222772_at	0.93068	4.598636	8.608108	2.12E-15	2.33E-14	24.11598	MYEF2	myelin expression factor 2	BG179854
242366_at	0.93025	7.295677	10.92181	4.12E-22	8.88E-21	39.41691			AI921844
240041_at	0.93011	3.614529	11.36556	1.89E-23	4.57E-22	42.4757	PTCHD1	patched domain containing 1	AA148535
232734_at	0.92986	4.437147	9.952235	3.10E-19	5.05E-18	32.8504	TTC23	tetratricopeptide repeat domain 23	AK023230
207053_at	0.92984	3.831646	13.2474	3.18E-29	1.25E-27	55.6754	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	NM_021097
207978_s_at	0.92969	5.710548	6.165214	3.78E-09	1.75E-08	9.962211	NR4A3	nuclear receptor subfamily 4, group A, member 3	NM_006981
226528_at	0.92934	7.308571	9.986021	2.47E-19	4.08E-18	33.07602	MTX3	metaxin 3	AI743044
226756_at	0.92926	8.17642	8.075035	6.05E-14	5.65E-13	20.80892			AA191741
201107_s_at	0.92872	5.605623	8.46729	5.19E-15	5.45E-14	23.23253	THBS1	thrombospondin 1	AI812030
235782_at	0.92871	5.141753	12.64735	2.27E-27	7.64E-26	51.4384			BF432875
217781_s_at	0.92866	8.568376	16.23866	1.83E-38	1.78E-36	76.82182	ZFP106	zinc finger protein 106 homolog (mouse)	NM_022473
235368_at	0.92859	7.401292	6.830319	9.80E-11	5.92E-10	13.53804	ADAMTS5	ADAM metalloproteinase with thrombospondin type 1 motif, 5	AI123555
221872_at	0.9284	8.689663	4.061307	6.99E-05	0.0001415	0.456025	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	AI669229
209834_at	0.92821	6.738088	10.6587	2.53E-21	5.07E-20	37.61761	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	AB017915
202362_at	0.92804	11.09048	12.49202	6.81E-27	2.21E-25	50.34472	RAP1A	RAP1A, member of RAS oncogene family	NM_002884
208927_at	0.92803	9.27551	10.54208	5.63E-21	1.09E-19	36.82398	SPOP	speckle-type POZ protein	BF673888
227251_at	0.928	5.565398	15.66384	1.07E-36	8.67E-35	72.77856	WDR22	WD repeat domain 22	AI431597
203505_at	0.92781	8.332451	10.22476	4.91E-20	8.66E-19	34.6774	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	AF285167

209090_s_at	0.9278	9.300411	12.8323	6.09E-28	2.15E-26	52.74244	SH3GLB1	SH3-domain GRB2-like endophilin B1	AL049597
217627_at	0.92721	5.746178	9.354406	1.67E-17	2.28E-16	28.90365	ZNF573	zinc finger protein 573	BE515346
222614_at	0.92721	6.102029	7.29163	6.85E-12	4.92E-11	16.15149	RWDD2B	RWDD domain containing 2B	AF212232
1559776_at	0.92706	7.842934	9.916253	3.96E-19	6.38E-18	32.6104			H41167
205726_at	0.92704	8.080772	9.798992	8.70E-19	1.35E-17	31.83035	DIAPH2	diaphanous homolog 2 (Drosophila)	NM_006729
217047_s_at	0.92682	8.310756	7.348904	4.89E-12	3.58E-11	16.48299	FAM13A1	family with sequence similarity 13, member A1	AK027138
209702_at	0.92667	9.064845	15.99136	1.05E-37	9.40E-36	75.08452	FTO	fat mass and obesity associated	U79260
211592_s_at	0.92656	4.949227	11.3926	1.56E-23	3.83E-22	42.66296	CACNA1C	calcium channel, voltage-dependent, L type, alpha 1C subunit	L29536
217367_s_at	0.92643	6.067498	16.50855	2.73E-39	2.95E-37	78.7135	ZHX3	zinc fingers and homeoboxes 3	AB007855
242766_at	0.92629	4.48091	10.56607	4.78E-21	9.35E-20	36.987			AI360832
228793_at	0.92614	5.828251	7.573588	1.28E-12	1.01E-11	17.79768	JMJD1C	jumonji domain containing 1C	BF002296
212257_s_at	0.92607	6.947009	10.61875	3.33E-21	6.60E-20	37.3455	SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	AW131754
221773_at	0.92596	9.398528	8.97624	1.99E-16	2.44E-15	26.45643	ELK3	ELK3, ETS-domain protein (SRF accessory protein 2), mRNA (cDNA clone MGC:13551 IMAGE:4287696)	AW575374
208965_s_at	0.92582	9.262403	7.033236	3.08E-11	2.02E-10	14.67493	IFI16	interferon, gamma-inducible protein 16	BG256677
222891_s_at	0.92532	6.922889	4.517877	1.06E-05	2.51E-05	2.262964	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	AI912275
202364_at	0.9252	9.99159	10.42186	1.28E-20	2.40E-19	36.00845	MXI1	MAX interactor 1	NM_005962
201408_at	0.92502	9.10354	11.75732	1.22E-24	3.30E-23	45.19778	PPP1CB	protein phosphatase 1, catalytic subunit, beta isoform	W67887
232098_at	0.92465	5.325627	7.280639	7.30E-12	5.22E-11	16.08804	DST	dystonin	AK025142
228174_at	0.92448	5.652808	10.17908	6.70E-20	1.17E-18	34.37006			AI832363
226905_at	0.92395	8.610011	8.123367	4.48E-14	4.25E-13	21.10446	FAM101B	family with sequence similarity 101, member B	BG036514
229687_s_at	0.92389	4.641104	12.58709	3.47E-27	1.15E-25	51.01396			AA621763
1563466_at	0.92378	4.090515	10.77576	1.13E-21	2.33E-20	38.41668	MYLK	myosin light chain kinase	AL832211
206874_s_at	0.92376	8.720376	9.137953	6.93E-17	8.87E-16	27.49785			AL138761
1559584_a_at	0.92373	6.379839	4.599371	7.48E-06	1.81E-05	2.600222	C16orf54 /// hCG_1644 884	chromosome 16 open reading frame 54 /// similar to chromosome 16 open reading frame 54	BC025741
1559901_s_at	0.92353	4.00526	16.44387	4.30E-39	4.55E-37	78.26058	C21orf34	chromosome 21 open reading frame 34	BM194465
1559965_at	0.92352	3.579939	7.964824	1.19E-13	1.08E-12	20.13838	LOC100192378	hypothetical LOC100192378	BC037827
230519_at	0.92346	6.38891	13.9159	2.71E-31	1.28E-29	60.40984	FAM124A	family with sequence similarity 124A	D59502
208370_s_at	0.92343	9.602483	7.975938	1.11E-13	1.01E-12	20.20579	RCAN1	regulator of calcineurin 1	NM_004414
204640_s_at	0.92313	9.692307	12.54541	4.67E-27	1.53E-25	50.7205	SPOP	speckle-type POZ protein	NM_003563
231842_at	0.92303	5.367659	8.530468	3.48E-15	3.73E-14	23.62805	KIAA1462	KIAA1462	AL553774
218871_x_at	0.92296	8.944261	11.33174	2.39E-23	5.73E-22	42.24159	CSGALNAC T2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	NM_018590
227976_at	0.92292	5.053652	13.41201	9.85E-30	4.07E-28	56.84028	LOC644538	hypothetical protein LOC644538	AW242009

							PCDHGA1 1 /// PCDHGA1 0 /// PCDHGA1 1 /// PCDHGA1 2 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 ///	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 ///	
205717_x_at	0.92286	8.367687	11.569	4.55E-24	1.18E-22	43.88697	///		NM_002588
1598_g_at	0.92282	9.927947	10.49415	7.82E-21	1.50E-19	36.49846	GAS6 /// LOC10013 3684	growth arrest-specific 6 /// similar to growth arrest-specific 6	L13720
208498_s_at	0.92247	4.855108	7.861034	2.26E-13	1.96E-12	19.5113	AMY1A /// AMY1B /// AMY1C /// AMY2A /// AMY2B	amylase, alpha 1A (salivary) /// amylase, alpha 1B (salivary) /// amylase, alpha 1C (salivary) /// amylase, alpha 2A (pancreatic) /// amylase, alpha 2B (pancreatic)	NM_004038
205253_at	0.92216	6.593122	9.833134	6.92E-19	1.08E-17	32.05713	PBX1	pre-B-cell leukemia homeobox 1	NM_002585
200811_at	0.92215	9.249134	12.29069	2.83E-26	8.75E-25	48.92979	CIRBP	cold inducible RNA binding protein	NM_001280
227699_at	0.92188	5.594198	12.39617	1.34E-26	4.26E-25	49.67073	C14orf149	chromosome 14 open reading frame 149	BF511003
243606_at	0.92188	5.62904	10.2865	3.23E-20	5.80E-19	35.09352	FAM55C	family with sequence similarity 55, member C	BE883167
206767_at	0.9215	6.149667	11.05412	1.65E-22	3.69E-21	40.32588	RBMS3	RNA binding motif, single stranded interacting protein	NM_014483
219867_at	0.92105	5.183006	7.837013	2.61E-13	2.26E-12	19.36678	CHODL	chondrolectin	NM_024944
241681_at	0.92049	6.288465	6.601709	3.53E-10	1.95E-09	12.28219			AW296451
225092_at	0.92019	8.562411	10.60521	3.65E-21	7.22E-20	37.25329	RABEP1	rabaptin, RAB GTPase binding effector protein 1	AL550977
201021_s_at	0.9201	12.06402	11.78478	1.00E-24	2.74E-23	45.38923	DSTN	destrin (actin depolymerizing factor)	BF697964
223922_x_at	0.91997	9.038576	7.541647	1.56E-12	1.22E-11	17.60943	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	AB013104
206114_at	0.91955	6.645623	9.173333	5.50E-17	7.10E-16	27.72672	EPHA4	EPH receptor A4	NM_004438
225239_at	0.91954	9.03528	5.542769	9.25E-08	3.26E-07	6.845169			AI355441
219487_at	0.91936	6.461889	7.813486	3.01E-13	2.58E-12	19.22547	BBS10	Bardet-Biedl syndrome 10	NM_024685
244533_at	0.91881	6.783601	9.677549	1.96E-18	2.93E-17	31.02593			BE617483
226113_at	0.9187	7.546493	14.6696	1.26E-33	7.36E-32	65.7511	ZNF436	zinc finger protein 436	AB051497
202172_at	0.91868	8.90862	13.60315	2.52E-30	1.09E-28	58.19382	VEZF1	vascular endothelial zinc finger 1	BG035116
202403_s_at	0.91848	12.84843	6.935259	5.39E-11	3.40E-10	14.12344	COL1A2	collagen, type I, alpha 2	AA788711
211892_s_at	0.91828	4.730888	9.726806	1.41E-18	2.13E-17	31.35177	PTGIS	prostaglandin I2 (prostacyclin) synthase	AF297052
225144_at	0.91813	9.227784	11.7913	9.57E-25	2.62E-23	45.43468	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	AI457436
226114_at	0.91764	6.917834	13.62291	2.19E-30	9.49E-29	58.33381	ZNF436	zinc finger protein 436	AI829509

204442_x_at	0.91746	7.851207	9.823947	7.36E-19	1.15E-17	31.99608	LTBP4	latent transforming growth factor beta binding protein 4	NM_003573
219312_s_at	0.9173	6.013725	4.709686	4.61E-05	1.16E-05	3.064508	ZBTB10	zinc finger and BTB domain containing 10	NM_023929
202806_at	0.91699	7.815045	7.386487	3.91E-12	2.90E-11	16.70134	DBN1	drebrin 1	NM_004395
230903_s_at	0.91665	5.724522	10.52197	6.46E-21	1.25E-19	36.68735	C8orf42	chromosome 8 open reading frame 42	H11634
221834_at	0.91663	6.84468	12.39399	1.36E-26	4.32E-25	49.65541	LONP2	Lon peptidase 2, peroxisomal (LONP2), mRNA	AV700132
1556306_at	0.91638	4.147141	11.63104	2.95E-24	7.78E-23	44.31837			AA082707
209106_at	0.91611	8.398221	12.3067	2.53E-26	7.83E-25	49.04215	NCOA1	nuclear receptor coactivator 1	BF576458
228837_at	0.91546	5.798822	11.5377	5.67E-24	1.45E-22	43.66954	TCF4	transcription factor 4	BE857360
204993_at	0.9154	6.578021	10.58854	4.09E-21	8.07E-20	37.13988	GNAZ	guanine nucleotide binding protein (G protein), alpha z polypeptide	NM_002073
206332_s_at	0.91532	9.458162	7.405828	3.49E-12	2.61E-11	16.81394	IFI16	interferon, gamma-inducible protein 16	NM_005531
244111_at	0.91521	3.93514	9.089474	9.51E-17	1.20E-15	27.18484	KRT222P	keratin 222 pseudogene	AA699598
1560296_at	0.91512	7.081173	13.06533	1.16E-28	4.35E-27	54.38807			AV702787
211772_x_at	0.91488	5.529921	11.16734	7.51E-23	1.73E-21	41.10583	CHRNA3	cholinergic receptor, nicotinic, alpha 3	BC006114
202877_s_at	0.91482	8.320099	8.366332	9.81E-15	1.00E-13	22.60339	CD93	CD93 molecule	W72082
225776_at	0.9147	7.471133	10.98837	2.60E-22	5.69E-21	39.87381	RBMS2	RNA binding motif, single stranded interacting protein 2	AW205585
223075_s_at	0.91459	6.651784	5.851646	1.95E-08	7.84E-08	8.36259	AIF1L	allograft inflammatory factor 1-like	AL136566
201591_s_at	0.91459	9.249308	14.88212	2.77E-34	1.75E-32	67.25582	NISCH	nischarin	NM_007184
225342_at	0.91402	8.47766	4.960757	1.49E-06	4.14E-06	4.15377	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	AK026966
227058_at	0.9138	7.945022	5.15692	5.98E-07	1.80E-06	5.035486	C13orf33	chromosome 13 open reading frame 33	AW084730
203153_at	0.91372	8.446747	4.746417	3.92E-06	1.00E-05	3.221058	IFIT1	interferon-induced protein with tetratricopeptide repeats 1	NM_001548
1554997_a_at	0.91339	6.22756	4.00345	8.77E-05	0.0001747	0.249814	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	AY151286
230728_at	0.91284	7.806741	10.8981	4.85E-22	1.04E-20	39.2543			BF516305
225167_at	0.91248	7.435037	9.473811	7.60E-18	1.08E-16	29.68467	FRMD4A	FERM domain containing 4A	AW515645
205878_at	0.91222	5.323666	12.95696	2.51E-28	9.14E-27	53.62245	POU6F1	POU class 6 homeobox 1	NM_002702
244433_at	0.91202	5.123072	8.298371	1.50E-14	1.50E-13	22.18193			AI950023
223499_at	0.9117	8.713676	8.26099	1.90E-14	1.87E-13	21.95083	C1QTNF5 /// MFRP	C1q and tumor necrosis factor related protein 5 /// membrane frizzled-related protein	AF329841
220173_at	0.91165	6.180933	11.54495	5.39E-24	1.39E-22	43.71985	C14orf45	chromosome 14 open reading frame 45	NM_025057
219025_at	0.91154	8.531048	8.787747	6.71E-16	7.78E-15	25.25263	CD248	CD248 molecule, endosialin	NM_020404
217023_x_at	0.91152	8.250197	6.520263	5.53E-10	2.96E-09	11.8414	TPSAB1 /// TPSB2	tryptase alpha/beta 1 /// tryptase beta 2	AF099143
211965_at	0.91109	7.309671	7.147832	1.59E-11	1.08E-10	15.32587	ZFP36L1	zinc finger protein 36, C3H type-like 1	BE620915
201877_s_at	0.91108	9.502982	12.19241	5.67E-26	1.71E-24	48.24019	PPP2R5C	protein phosphatase 2, regulatory subunit B', gamma isoform	NM_002719
231823_s_at	0.91104	8.360373	9.694083	1.75E-18	2.63E-17	31.13523	SH3PXD2B	SH3 and PX domains 2B	BG054798
209582_s_at	0.91072	6.105867	8.43767	6.26E-15	6.52E-14	23.04757	CD200	CD200 molecule	H23979
222582_at	0.91068	7.39104	9.764567	1.10E-18	1.68E-17	31.60196	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	AF087875
229281_at	0.91053	4.29308	8.917456	2.91E-16	3.51E-15	26.07982	NPAS3	neuronal PAS domain protein 3	N51682
238990_x_at	0.91036	4.940474	14.99307	1.25E-34	8.27E-33	68.04098	TRIM61	CDNA FLJ60274 complete cds, moderately similar to Homo sapiens tripartite motif-containing 60 (TRIM60), mRNA	AI763262
217904_s_at	0.91018	7.340143	11.8375	6.92E-25	1.92E-23	45.75705	BACE1	beta-site APP-cleaving enzyme 1	NM_012104
230913_at	0.90994	5.804133	8.754397	8.32E-16	9.57E-15	25.04081			BE674309
218175_at	0.90953	8.58668	10.90931	4.49E-22	9.65E-21	39.33116	CCDC92	coiled-coil domain containing 92	NM_025140

209004_s_at	0.90927	10.48334	12.90487	3.64E-28	1.31E-26	53.25467	FBXL5	F-box and leucine-rich repeat protein 5	AF142481
216247_at	0.90918	4.7855	9.528856	5.27E-18	7.59E-17	30.04599	RPS20	ribosomal protein S20	AF113008
211421_s_at	0.9084	4.448627	8.608801	2.11E-15	2.32E-14	24.12034	RET	ret proto-oncogene	M31213
226964_at	0.90836	5.392923	17.24979	1.50E-41	2.08E-39	83.88249			BG289838
228723_at	0.90826	5.034507	10.61558	3.40E-21	6.74E-20	37.32389			AL360198
218634_at	0.9081	7.689148	10.27307	3.54E-20	6.32E-19	35.00292	PHLDA3	pleckstrin homology-like domain, family A, member 3	NM_012396
238463_at	0.90791	4.836237	15.36617	8.84E-36	6.50E-34	70.67832			AA448328
211864_s_at	0.90753	8.9104	6.06492	6.42E-09	2.84E-08	9.444283	MYOF	myoferlin	AF207990
202137_s_at	0.90744	7.744761	9.311974	2.21E-17	2.97E-16	28.62703	ZMYND11	zinc finger, MYND domain containing 11	NM_006624
202310_s_at	0.90736	11.09172	4.769994	3.53E-06	9.12E-06	3.322057	COL1A1	collagen, type I, alpha 1	K01228
214720_x_at	0.90718	7.683042	8.889875	3.47E-16	4.16E-15	25.90349	SEPT10	septin 10	BF981543
203973_s_at	0.90663	10.99949	11.95369	3.05E-25	8.72E-24	46.56868	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	NM_005195
233442_at	0.90652	5.095705	11.61388	3.32E-24	8.74E-23	44.19899			AU147500
1556402_at	0.90645	4.306294	11.08188	1.36E-22	3.07E-21	40.51697			CA425190
219338_s_at	0.9064	6.159304	10.59799	3.84E-21	7.57E-20	37.20414	LRRC49	leucine rich repeat containing 49	NM_017691
230644_at	0.90598	4.861874	10.83876	7.31E-22	1.54E-20	38.84774	LRFN5	leucine rich repeat and fibronectin type III domain containing 5	AI375083
225050_at	0.90595	8.076122	11.5608	4.82E-24	1.25E-22	43.82998	ZNF512	zinc finger protein 512	N22677
226683_at	0.90595	9.546722	11.51203	6.78E-24	1.73E-22	43.49124	SNX18	sorting nexin 18	AU146771
221928_at	0.90581	7.357258	9.189127	4.96E-17	6.43E-16	27.82901	ACACB	acetyl-Coenzyme A carboxylase beta	AI057637
226397_s_at	0.9053	6.238094	9.445653	9.15E-18	1.28E-16	29.50015			BG502771
213808_at	0.90517	3.94771	13.75594	8.49E-31	3.80E-29	59.27627			BE674466
217865_at	0.90514	9.254874	9.467371	7.93E-18	1.12E-16	29.64245	RNF130	ring finger protein 130	NM_018434
1555889_a_at	0.90509	10.56127	12.68673	1.71E-27	5.83E-26	51.71586	CRTAP	cartilage associated protein	BQ876971
202619_s_at	0.905	8.321547	6.513072	5.75E-10	3.07E-09	11.80265	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	AI754404
229315_at	0.9048	4.56151	11.09673	1.23E-22	2.78E-21	40.6192			AI912175
217862_at	0.9047	8.103155	11.4618	9.64E-24	2.41E-22	43.1427	PIAS1	protein inhibitor of activated STAT, 1	N24868
223474_at	0.90467	10.28252	13.13181	7.24E-29	2.75E-27	54.85797	C14orf4	chromosome 14 open reading frame 4	AI932310
1554018_at	0.90452	6.359916	4.679108	5.28E-06	1.32E-05	2.934929	GPNMB	glycoprotein (transmembrane) nmb	BC011595
201153_s_at	0.90436	10.73505	16.14847	3.46E-38	3.24E-36	76.18867	MBNL1	muscleblind-like (Drosophila)	NM_021038
212940_at	0.90435	6.811188	9.841608	6.53E-19	1.03E-17	32.11347	COL6A1	collagen, type VI, alpha 1	BE350145
204577_s_at	0.90427	5.297973	12.77415	9.21E-28	3.20E-26	52.33224	CLUAP1	clusterin associated protein 1	NM_024793
202908_at	0.9037	8.294822	10.79752	9.72E-22	2.02E-20	38.56548	WFS1	Wolfram syndrome 1 (wolframin)	NM_006005
213227_at	0.90363	8.716606	10.45449	1.03E-20	1.94E-19	36.22949	PGRMC2	progesterone receptor membrane component 2	BE879873
217911_s_at	0.90358	9.479791	8.774678	7.30E-16	8.44E-15	25.16959	BAG3	BCL2-associated athanogene 3	NM_004281
235151_at	0.90338	5.994649	9.426205	1.04E-17	1.45E-16	29.37282	LOC28335	hypothetical protein LOC283357	AA807060
228642_at	0.90316	7.610269	7.827932	2.76E-13	2.38E-12	19.31221			BF593636
214177_s_at	0.90289	9.337778	11.36131	1.94E-23	4.71E-22	42.44628	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	AI935162
202123_s_at	0.9028	8.889047	14.48027	4.85E-33	2.66E-31	64.40982	ABL1	c-abl oncogene 1, receptor tyrosine kinase	NM_005157
213278_at	0.90277	7.286555	11.1925	6.30E-23	1.46E-21	41.27944	MTMR9	myotubularin related protein 9	AW014788
223741_s_at	0.90199	7.036293	9.232905	3.72E-17	4.90E-16	28.11291	TTYH2	tweety homolog 2 (Drosophila)	BC004233
224614_at	0.90191	7.635891	11.23803	4.59E-23	1.08E-21	41.59376	DYNC1L2	dynein, cytoplasmic 1, light intermediate chain 2	AK024863
244572_at	0.90178	4.755159	10.3979	1.51E-20	2.80E-19	35.84621	KY	kyphoscoliosis peptidase	AI147310
227188_at	0.9013	6.82331	6.682747	2.25E-10	1.28E-09	12.72427	C21orf63	chromosome 21 open reading frame 63	AI744591
213182_x_at	0.90127	6.612868	5.992004	9.41E-09	4.03E-08	9.071428	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	R78668
221045_s_at	0.90026	6.933398	6.830071	9.81E-11	5.93E-10	13.53666	PER3	period homolog 3 (Drosophila)	NM_016831
214722_at	0.90018	8.416061	10.51684	6.69E-21	1.29E-19	36.65254	NOTCH2N	Notch homolog 2 (Drosophila) N-terminal like	AW516297
1569149_at	0.89999	5.349392	12.19951	5.39E-26	1.63E-24	48.28998	PDLIM7	CDNA clone IMAGE:4763486	BC023629
229670_at	0.89966	6.859054	7.745039	4.57E-13	3.83E-12	18.81564			BF056369

203414_at	0.89936	9.041998	7.675618	6.95E-13	5.68E-12	18.40197	MMD	monocyte to macrophage differentiation-associated	NM_012329
217066_s_at	0.89897	6.593385	12.64593	2.29E-27	7.71E-26	51.42837	DMPK	dystrophin myotonia-protein kinase	M87313
235787_at	0.89843	5.672108	12.77397	9.22E-28	3.21E-26	52.33095			T65394
229506_at	0.89838	6.098551	9.057353	1.17E-16	1.47E-15	26.97782			BF114646
227410_at	0.89798	8.135306	7.256217	8.43E-12	5.96E-11	15.94727	FAM43A	family with sequence similarity 43, member A	AW264102
204851_s_at	0.89788	3.890676	7.211946	1.09E-11	7.61E-11	15.69279	DCX	doublecortin	AF040254
202909_at	0.89787	8.691063	7.908501	1.69E-13	1.49E-12	19.79755	EPM2AIP1	EPM2A (laforin) interacting protein 1	NM_014805
224341_x_at	0.89787	6.123745	7.371167	4.29E-12	3.16E-11	16.61225	TLR4	toll-like receptor 4	U93091
205082_s_at	0.89785	5.941999	8.482204	4.72E-15	4.99E-14	23.32577	AOX1	aldehyde oxidase 1	AB046692
212190_at	0.89726	9.425648	5.100399	7.80E-07	2.30E-06	4.778725	SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	AL541302
1555564_a_at	0.89664	7.326033	4.62673	6.64E-06	1.63E-05	2.714541	CFI	complement factor I	BC020718
235036_at	0.8966	4.658049	14.08614	8.05E-32	3.98E-30	61.6165	LIX1L	Lix1 homolog (mouse)-like	AA923372
202075_s_at	0.89623	8.500648	5.69831	4.25E-08	1.60E-07	7.601877	PLTP	phospholipid transfer protein	NM_006227
1558692_at	0.89565	6.637559	8.028588	8.06E-14	7.43E-13	20.52576	C1orf85	chromosome 1 open reading frame 85	AW090182
225338_at	0.89535	8.89501	12.38733	1.43E-26	4.52E-25	49.60859	ZYG11B	zyg-11 homolog B (C. elegans)	AI767447
235856_at	0.89508	5.817462	11.04886	1.71E-22	3.82E-21	40.28972			AI660245
226155_at	0.89501	8.448145	12.7803	8.82E-28	3.07E-26	52.37563	FAM160B1	family with sequence similarity 160, member B1	AB046820
203801_at	0.89487	6.861241	9.977437	2.62E-19	4.30E-18	33.01867	MRPS14	mitochondrial ribosomal protein S14	AA013164
211980_at	0.89423	11.3013	7.860787	2.26E-13	1.97E-12	19.50981	COL4A1	collagen, type IV, alpha 1	AI922605
203518_at	0.894	7.517288	8.694495	1.22E-15	1.38E-14	24.66127	LYST	lysosomal trafficking regulator	NM_000081
228128_x_at	0.89385	6.875483	5.14782	6.24E-07	1.87E-06	4.994001	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	AI110886
228540_at	0.89379	5.719524	16.48302	3.26E-39	3.50E-37	78.53471	QKI	quaking homolog, KH domain RNA binding (mouse)	BE218313
228855_at	0.8937	6.854292	6.843746	9.08E-11	5.52E-10	13.61263	NUDT7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	AI927964
241780_at	0.89367	4.822445	9.052324	1.21E-16	1.52E-15	26.94544			AI040305
204530_s_at	0.89352	4.790011	9.882177	4.97E-19	7.92E-18	32.38339	TOX	thymocyte selection-associated high mobility group box	NM_014729
1558964_at	0.89297	3.674034	10.10223	1.13E-19	1.92E-18	33.85397	FAT3	FAT tumor suppressor homolog 3 (Drosophila)	AA334950
203278_s_at	0.89294	8.061179	13.58759	2.82E-30	1.21E-28	58.0836	PHF21A	PHD finger protein 21A	NM_016621
212373_at	0.8926	7.350164	9.046303	1.26E-16	1.57E-15	26.90668	FEM1B	fem-1 homolog b (C. elegans)	AW139179
226757_at	0.89254	8.033077	5.34589	2.43E-07	7.89E-07	5.909541	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	AA131041
235411_at	0.89249	4.686153	9.42436	1.05E-17	1.47E-16	29.36075	PGBD1	piggyBac transposable element derived 1	BE883300
227239_at	0.89243	8.384403	7.607718	1.05E-12	8.35E-12	17.99933	FAM126A	family with sequence similarity 126, member A	AV734839
229891_x_at	0.89225	7.08552	8.329743	1.23E-14	1.24E-13	22.37628	KIAA1704	KIAA1704	AI630799
241835_at	0.89222	4.652777	7.312897	6.04E-12	4.37E-11	16.27441			AI733297
201041_s_at	0.89218	11.45824	6.473629	7.15E-10	3.75E-09	11.59061	DUSP1	dual specificity phosphatase 1	NM_004417
219342_at	0.89206	7.173531	9.299423	2.40E-17	3.21E-16	28.5453	CASD1	CAS1 domain containing 1	NM_022900
238520_at	0.89121	6.326318	8.246238	2.08E-14	2.05E-13	21.85977	TRERF1	transcriptional regulating factor 1	BF724270
235457_at	0.89115	8.116582	8.710576	1.10E-15	1.25E-14	24.76304	MAML2	mastermind-like 2 (Drosophila)	AI769569
227930_at	0.89077	7.7197	8.513594	3.87E-15	4.13E-14	23.52227	EIF2C4	MRNA; cDNA DKFZp547H229 (from clone DKFZp547H229)	AI669957
226685_at	0.89044	8.666686	13.44732	7.66E-30	3.18E-28	57.09027	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	AI695684
236698_at	0.89028	4.825617	10.00349	2.20E-19	3.64E-18	33.1928			AI823600
226638_at	0.88999	7.595061	9.458827	8.39E-18	1.18E-16	29.58645	ARHGAP23	Rho GTPase activating protein 23	AV701292
228826_at	0.88977	4.485675	10.2358	4.56E-20	8.06E-19	34.75178			AK000271
226889_at	0.88935	6.781977	11.2992	3.00E-23	7.15E-22	42.01654	WDR35	WD repeat domain 35	AU151732

232071_at	0.88933	4.736521	11.39986	1.49E-23	3.65E-22	42.71328	MRPL19	CDNA FLJ57115 complete cds, highly similar to 39S ribosomal protein L19, mitochondrial precursor	BF670827
41577_at	0.88887	6.85229	6.670741	2.40E-10	1.37E-09	12.65855	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	AB020630
237413_at	0.88868	4.339558	15.73926	6.26E-37	5.19E-35	73.31007			AI568447
218805_at	0.88842	8.104795	8.562513	2.84E-15	3.07E-14	23.82918	GIMAP5	GTPase, IMAP family member 5	NM_018384
37022_at	0.88835	7.717967	12.8809	4.31E-28	1.54E-26	53.08544	PRELP	proline/arginine-rich end leucine-rich repeat protein	U41344
200951_s_at	0.88831	6.773081	5.821362	2.27E-08	9.04E-08	8.211206	CCND2	cyclin D2	AW026491
203487_s_at	0.88817	7.478177	11.12944	9.77E-23	2.23E-21	40.84458	ARMC8	armadillo repeat containing 8	NM_015396
244546_at	0.88741	5.908236	7.145558	1.61E-11	1.10E-10	15.3129	CYCS	cytochrome c, somatic	AI760495
215198_s_at	0.88726	6.321544	11.2398	4.53E-23	1.07E-21	41.60595	CALD1	caldesmon 1	AU147402
223261_at	0.88721	8.120005	10.42702	1.24E-20	2.32E-19	36.04336	POLK	polymerase (DNA directed) kappa	AF194973
229984_at	0.88692	7.399763	12.80878	7.20E-28	2.52E-26	52.57648			AI971519
228216_at	0.88562	5.447817	9.862674	5.67E-19	8.97E-18	32.25358			AI953914
230383_x_at	0.88556	7.537215	9.900677	4.39E-19	7.04E-18	32.5066			AA133285
238477_at	0.88545	7.110838	10.20304	5.69E-20	9.98E-19	34.53121			BF674236
1557051_s_at	0.88524	6.403905	8.625993	1.89E-15	2.09E-14	24.22867			CA448125
239952_at	0.88488	5.298647	13.89537	3.14E-31	1.47E-29	60.26439	ZEB1	zinc finger E-box binding homeobox 1	AI743662
226736_at	0.88478	8.528725	7.108697	1.99E-11	1.34E-10	15.10287	CHURC1	churchill domain containing 1	BE568660
225704_at	0.88434	7.246328	11.0216	2.06E-22	4.57E-21	40.10223	KIAA1545	HBV X-transactivated gene 9 protein	AA527531
205656_at	0.8842	8.209061	8.010495	9.01E-14	8.26E-13	20.41568	PCDH17	protocadherin 17	NM_014459
218194_at	0.88414	10.51084	10.36064	1.95E-20	3.57E-19	35.59419	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	NM_015523
204845_s_at	0.88383	4.679801	7.047903	2.83E-11	1.86E-10	14.75789	ENPEP	glutamyl aminopeptidase (aminopeptidase A)	NM_001977
209909_s_at	0.88374	4.391894	6.686076	2.20E-10	1.26E-09	12.7425	TGFB2	transforming growth factor, beta 2	M19154
224280_s_at	0.88364	7.874378	12.04052	1.66E-25	4.81E-24	47.17604	FAM54B	family with sequence similarity 54, member B	AL512766
230178_s_at	0.88339	6.662702	9.68274	1.89E-18	2.83E-17	31.06024			BE672676
209031_at	0.8833	7.636384	5.019851	1.13E-06	3.23E-06	4.416595	CADM1	cell adhesion molecule 1	AL519710
235334_at	0.8832	5.27781	8.17168	3.32E-14	3.19E-13	21.40078	ST6GALNA C3	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 3	AW963951
1555881_s_at	0.88286	8.29606	12.30668	2.53E-26	7.83E-25	49.04206	LZTS2	leucine zipper, putative tumor suppressor 2	AK097997
230538_at	0.8828	4.235419	11.63763	2.81E-24	7.44E-23	44.36421	SHC4	SHC (Src homology 2 domain containing) family, member 4	AI027957
205326_at	0.8821	7.917758	9.447185	9.06E-18	1.27E-16	29.51018	RAMP3	receptor (G protein-coupled) activity modifying protein 3	NM_005856
212226_s_at	0.88189	10.10269	9.057623	1.17E-16	1.47E-15	26.97956	PPAP2B	phosphatidic acid phosphatase type 2B	AA628586
228788_at	0.88185	4.415539	9.819035	7.60E-19	1.19E-17	31.96345	YPEL1	yippee-like 1 (Drosophila)	AA425358
224698_at	0.88179	9.523859	10.77614	1.13E-21	2.33E-20	38.41929	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	AB033054
201681_s_at	0.88138	8.668207	8.709728	1.11E-15	1.26E-14	24.75767	DLG5	discs, large homolog 5 (Drosophila)	AB011155
213895_at	0.88122	5.599692	6.181826	3.46E-09	1.61E-08	10.04855	EMP1	epithelial membrane protein 1	BF445047
225223_at	0.88106	8.707212	10.20033	5.80E-20	1.01E-18	34.51299	SMAD5	SMAD family member 5	AI478523
201809_s_at	0.88094	8.211333	8.895099	3.36E-16	4.02E-15	25.93687	ENG	endoglin	NM_000118
227373_at	0.8808	8.464388	10.70428	1.85E-21	3.75E-20	37.92847	ATXN1L	ataxin 1-like	AW299653
227917_at	0.88071	8.351542	9.429738	1.02E-17	1.42E-16	29.39594	FAM85A	family with sequence similarity 85, member A	AW192692
203482_at	0.8806	6.813583	10.97623	2.83E-22	6.17E-21	39.79041	FAM178A	family with sequence similarity 178, member A	AL133215
226151_x_at	0.88037	8.327886	11.94248	3.31E-25	9.42E-24	46.49028	CRYZL1	crystallin, zeta (quinone reductase)-like 1	AK001293
227562_at	0.87951	7.235043	10.46498	9.55E-21	1.81E-19	36.30064	LOC100132990 /// MAPKSP1	PRO0633 /// MAPK scaffold protein 1	AI335267

214121_x_at	0.87949	7.181191	10.7363	1.48E-21	3.03E-20	38.14711	PDLIM7	PDZ and LIM domain 7 (enigma)	AA086229
223690_at	0.87904	7.99477	7.711003	5.62E-13	4.64E-12	18.61257	LTBP2	latent transforming growth factor beta binding protein 2	AF113211
213869_x_at	0.87798	8.752429	7.841601	2.54E-13	2.20E-12	19.39437	THY1	Thy-1 cell surface antigen	AA218868
225469_at	0.87754	9.381556	7.168946	1.40E-11	9.62E-11	15.44649	LYRM5	LYR motif containing 5	AA015609
209297_at	0.87744	7.876725	13.02185	1.58E-28	5.86E-27	54.08084	ITSN1	intersectin 1 (SH3 domain protein)	AF114488
202861_at	0.87741	7.566968	9.135711	7.03E-17	9.00E-16	27.48336	PER1	period homolog 1 (Drosophila)	NM_002616
207971_s_at	0.87707	6.691257	12.74094	1.17E-27	4.02E-26	52.09805	CEP68	centrosomal protein 68kDa	NM_015147
227246_at	0.87655	6.561129	9.915525	3.97E-19	6.41E-18	32.60554	PLRG1	Pleiotropic regulator 1 (PLRG1)	BF438014
1554029_a_at	0.87653	5.316892	8.105018	5.02E-14	4.73E-13	20.99216	TTC37	tetratricopeptide repeat domain 37	BC030966
214736_s_at	0.87608	9.395133	16.53472	2.27E-39	2.48E-37	78.89663	ADD1	adducin 1 (alpha)	BE898639
229679_at	0.87599	6.511344	12.24452	3.93E-26	1.20E-24	48.60569	FLJ40142	FLJ40142 protein	AI870880
224579_at	0.87582	10.15857	6.050498	6.93E-09	3.05E-08	9.370287	SLC38A1	solute carrier family 38, member 1	BF247552
228007_at	0.87567	7.658846	7.5589	1.40E-12	1.10E-11	17.71105	C6orf204	CDNA clone IMAGE:5265665	AL133101
211998_at	0.87555	8.481166	9.260446	3.10E-17	4.12E-16	28.29178	H3F3A /// H3F3B /// LOC440926	H3 histone, family 3A /// H3 histone, family 3B (H3.3B) /// H3 histone, family 3A pseudogene	AW138159
212518_at	0.87507	7.643444	14.21361	3.24E-32	1.66E-30	62.52006	PIP5K1C	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	AB011161
205127_at	0.87463	6.064152	11.17152	7.29E-23	1.68E-21	41.13466	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_000962
208925_at	0.87444	8.719304	9.565567	4.13E-18	6.00E-17	30.28741	CLDN1	claudin domain containing 1	AF161522
230158_at	0.87442	3.859055	10.91449	4.33E-22	9.33E-21	39.36665	DPY19L2	dpy-19-like 2 (C. elegans)	AA758751
222498_at	0.87417	8.034032	11.03819	1.84E-22	4.10E-21	40.21629	AZI2	5-azacytidine induced 2	AI809206
206762_at	0.87401	5.287619	11.3493	2.11E-23	5.09E-22	42.36317	KCNA5	potassium voltage-gated channel, shaker-related subfamily, member 5	NM_002234
209308_s_at	0.87384	8.021905	9.469302	7.83E-18	1.11E-16	29.65511	BNIP2	BCL2/adenovirus E1B 19kDa interacting protein 2	BC002461
229278_at	0.87379	5.657845	11.76953	1.12E-24	3.03E-23	45.28291			AW474916
244007_at	0.87349	6.376494	9.691397	1.79E-18	2.68E-17	31.11747	ZNF462	zinc finger protein 462	BE889301
209079_x_at	0.87345	8.432712	11.10763	1.14E-22	2.58E-21	40.69431	PCDHGA1 PCDHGA1 PCDHGA1 PCDHGA1 PCDHGA1 PCDHGA2 PCDHGA3 PCDHGA4 PCDHGA5 PCDHGA6 PCDHGA7 PCDHGA8 PCDHGA9 PCDHGB1 PCDHGB2	protocadherin gamma subfamily A, 1 /// protocadherin gamma subfamily A, 10 /// protocadherin gamma subfamily A, 11 /// protocadherin gamma subfamily A, 12 /// protocadherin gamma subfamily A, 2 /// protocadherin gamma subfamily A, 3 /// protocadherin gamma subfamily A, 4 /// protocadherin gamma subfamily A, 5 /// protocadherin gamma subfamily A, 6 /// protocadherin gamma subfamily A, 7 /// protocadherin gamma subfamily A, 8 /// protocadherin gamma subfamily A, 9 /// protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// protocadherin gamma subfamily B, 3 /// protocadherin gamma subfamily B, 4 /// protocadherin gamma subfamily B, 5 /// protocadherin gamma subfamily B, 6 /// protocadherin gamma subfamily B, 7 /// protocadherin gamma subfamily C, 3 /// protocadherin gamma subfamily C, 4 ///	AF152318
204521_at	0.87339	6.832948	6.510091	5.85E-10	3.11E-09	11.78659	C12orf24	chromosome 12 open reading frame 24	NM_013300
212702_s_at	0.87319	7.70474	12.20356	5.24E-26	1.58E-24	48.31839	BICD2	bicaudal D homolog 2 (Drosophila)	N45111
203607_at	0.87304	7.370611	9.371901	1.49E-17	2.04E-16	29.01784	INPP5F	inositol polyphosphate-5-phosphatase F	NM_014937

201693_s_at	0.87301	8.577151	5.021173	1.13E-06	3.21E-06	4.422503	EGR1	early growth response 1	AV733950
204912_at	0.87299	7.851255	6.983395	4.10E-11	2.64E-10	14.3938	IL10RA	interleukin 10 receptor, alpha	NM_001558
241986_at	0.87269	3.672581	10.50926	7.05E-21	1.36E-19	36.60104	BMPER	BMP binding endothelial regulator	AI423201
205379_at	0.87266	7.681498	9.789167	9.29E-19	1.44E-17	31.76513	CBR3	carbonyl reductase 3	NM_001236
233230_s_at	0.87261	5.660431	11.48718	8.07E-24	2.04E-22	43.3188	SLAIN2	SLAIN motif family, member 2	AV723459
206929_s_at	0.87195	7.681859	10.08167	1.30E-19	2.20E-18	33.71616	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	NM_005597
204527_at	0.87186	6.349864	8.170555	3.34E-14	3.21E-13	21.39387	MYO5A	myosin VA (heavy chain 12, myosin)	NM_000259
201161_s_at	0.87173	10.67382	9.595473	3.39E-18	4.96E-17	30.48433	CSDA	cold shock domain protein A	NM_003651
235072_s_at	0.87165	9.012144	9.878712	5.09E-19	8.09E-18	32.36032			BF594695
232327_at	0.87164	4.335478	7.519364	1.78E-12	1.38E-11	17.47836	THSD7B	thrombospondin, type I, domain containing 7B	AB051466
212289_at	0.87154	7.344949	12.70668	1.49E-27	5.09E-26	51.85651	ANKRD12	ankyrin repeat domain 12	AB020681
220244_at	0.87129	5.82558	8.914235	2.97E-16	3.58E-15	26.05922	LOH3CR2A	loss of heterozygosity, 3, chromosomal region 2, gene A	NM_013343
225225_at	0.87073	9.529007	13.25116	3.10E-29	1.22E-27	55.70204	LOC72908	CDNA clone IMAGE:4813218	BF791544
91703_at	0.87066	7.43111	11.23544	4.67E-23	1.10E-21	41.57589	EHBPL1	EH domain binding protein 1-like 1	AA149545
223130_s_at	0.87045	8.703727	11.78876	9.74E-25	2.67E-23	45.41696	MYLIP	myosin regulatory light chain interacting protein	AF212221
227210_at	0.8703	6.419328	8.360115	1.02E-14	1.04E-13	22.56477			T65020
219431_at	0.87017	7.306346	14.4281	7.03E-33	3.79E-31	64.0402	ARHGAP10	Rho GTPase activating protein 10	NM_024605
242523_at	0.8701	4.674378	10.1397	8.75E-20	1.51E-18	34.10546			AW770320
237247_at	0.86999	4.898885	10.25136	4.10E-20	7.28E-19	34.85661	USP51	ubiquitin specific peptidase 51	AI341140
219637_at	0.86987	6.167136	9.034352	1.36E-16	1.69E-15	26.82977	ARMC9	armadillo repeat containing 9	NM_025139
235337_at	0.86979	4.187829	8.328898	1.24E-14	1.25E-13	22.37104			AI276403
201849_at	0.86979	8.163814	4.347941	2.18E-05	4.84E-05	1.575588	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	NM_004052
210976_s_at	0.86977	8.766187	10.3579	1.98E-20	3.64E-19	35.57563	PFKM	phosphofructokinase, muscle	U24183
222670_s_at	0.86975	8.696706	8.19394	2.89E-14	2.79E-13	21.53759	MAFB	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	AW135013
212163_at	0.86957	8.855679	9.351298	1.71E-17	2.32E-16	28.88337	KIDINS220	kinase D-interacting substrate, 220kDa	AB033076
219519_s_at	0.86957	6.205537	6.686514	2.20E-10	1.26E-09	12.74489	SIGLEC1	sialic acid binding ig-like lectin 1, sialoadhesin	NM_023068
223167_s_at	0.86937	6.738612	11.42714	1.23E-23	3.04E-22	42.90234	USP25	ubiquitin specific peptidase 25	AF170562
227584_at	0.86931	6.773779	13.22541	3.72E-29	1.46E-27	55.51984	NAV1	neuron navigator 1	BF339566
224875_at	0.86927	7.520232	8.45482	5.61E-15	5.89E-14	23.15462	C5orf24	chromosome 5 open reading frame 24	BG492488
1553275_s_at	0.86892	3.94598	12.31809	2.33E-26	7.24E-25	49.12215			NM_173594
238964_at	0.86873	4.344618	9.312269	2.21E-17	2.97E-16	28.62895	FIGN	fidgetin	BE960968
224861_at	0.8682	8.68268	9.817567	7.68E-19	1.20E-17	31.95369	GNAQ	GTP-binding protein alpha q (GQ)	AA628423
243009_at	0.86784	5.181125	10.97034	2.94E-22	6.41E-21	39.75001	LOC44124	CDNA FLJ36432 fis, clone THYMU2011875	AW513654
230228_at	0.8678	5.949861	12.99112	1.97E-28	7.23E-27	53.86375	LOC28429	hypothetical LOC284297	W94546
206243_at	0.86775	5.470145	5.709009	4.03E-08	1.53E-07	7.654486	TIMP4	TIMP metalloproteinase inhibitor 4	NM_003256
206574_s_at	0.86773	7.369737	7.016853	3.38E-11	2.21E-10	14.58239	LOC100131062	similar to protein tyrosine phosphatase type IVA, member 3	NM_007079
225624_at	0.86771	7.217887	13.8264	5.13E-31	2.36E-29	59.77557	PTP4A3	protein tyrosine phosphatase type IVA, member 3	AL044019
213243_at	0.86769	8.055613	10.20595	5.58E-20	9.79E-19	34.55079	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	AI052003
204984_at	0.86766	7.753463	6.530846	5.22E-10	2.80E-09	11.89848	GPC4	glypican 4	NM_001448
209392_at	0.86745	9.363284	4.865486	2.30E-06	6.16E-06	3.735177	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	L35594
1557353_at	0.86736	6.240711	13.19962	4.47E-29	1.74E-27	55.33746			BM985423
235775_at	0.8673	7.224144	7.176549	1.34E-11	9.23E-11	15.48998	TMT2	transmembrane and tetrapeptide repeat containing 2	AI765006
229297_at	0.86729	6.456748	13.40823	1.01E-29	4.17E-28	56.81355			AA031303
242273_at	0.86728	6.380203	7.967107	1.18E-13	1.06E-12	20.15223			AA747287

201022_s_at	0.86719	12.7461	13.66055	1.68E-30	7.31E-29	58.60042	DSTN	destrin (actin depolymerizing factor)	NM_006870
226119_at	0.86679	9.819645	12.88175	4.29E-28	1.54E-26	53.09143	PCMTD1	protein-L-isopartate (D-aspartate) O-methyltransferase domain containing 1	AA453163
232124_at	0.8667	4.463861	9.880913	5.02E-19	7.98E-18	32.37497	LOC72908	hypothetical protein LOC729085	AL117530
230141_at	0.86658	6.821902	11.44623	1.07E-23	2.68E-22	43.03473	ARID4A	AT rich interactive domain 4A (RBP1-like)	AI640594
209721_s_at	0.86649	7.234103	17.50828	2.47E-42	3.80E-40	85.67499	IFFO1	intermediate filament family orphan 1	BC002857
221727_at	0.86636	8.90727	9.093746	9.24E-17	1.17E-15	27.21239	SUB1	SUB1 homolog (S. cerevisiae)	AA456973
224645_at	0.86604	7.458637	10.12431	9.71E-20	1.67E-18	34.0021	EIF4EBP2	eukaryotic translation initiation factor 4E binding protein 2	BG106477
213725_x_at	0.86592	7.410335	6.991745	3.90E-11	2.52E-10	14.44081	XYLT1	xylosyltransferase I	AI693140
215000_s_at	0.86585	9.803111	10.19247	6.11E-20	1.07E-18	34.46009	FEZ2	fasciculation and elongation protein zeta 2 (zyglin II)	AL117593
225302_at	0.86562	7.856211	9.453756	8.67E-18	1.22E-16	29.55323	TXNDC10	thioredoxin domain containing 10	BE503286
201294_s_at	0.86548	7.3977	8.504056	4.11E-15	4.37E-14	23.46253	WSB1	WD repeat and SOCS box-containing 1	N24643
207001_x_at	0.86536	7.620816	9.011662	1.58E-16	1.95E-15	26.68388	TSC22D3	TSC22 domain family, member 3	NM_004089
211756_at	0.86501	4.321703	6.292669	1.91E-09	9.30E-09	10.62871	PTH1H	parathyroid hormone-like hormone	BC005961
202073_at	0.86495	8.666911	10.26054	3.85E-20	6.86E-19	34.91848	OPTN	optineurin	AV757675
236035_at	0.86479	3.976807	11.13658	9.30E-23	2.12E-21	40.89379			AW190406
225332_at	0.86456	7.529486	9.454776	8.62E-18	1.21E-16	29.55991	LOC72908	CDNA clone IMAGE:4813218	BF674064
209866_s_at	0.86441	5.247458	5.087375	8.29E-07	2.43E-06	4.719869	LPHN3	latrophilin 3	RS0822
204270_at	0.86425	6.25731	13.02041	1.60E-28	5.91E-27	54.07065	SKI	v-ski sarcoma viral oncogene homolog (avian)	AI568728
232024_at	0.86423	7.983509	5.7829	2.77E-08	1.08E-07	8.019752	GIMAP2	GTPase, IMAP family member 2	AI431931
223449_at	0.86412	7.417846	6.577432	4.03E-10	2.21E-09	12.15044	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	AF225425
1552275_s_at	0.86399	6.459061	9.729045	1.39E-18	2.10E-17	31.36659	PXK	PX domain containing serine/threonine kinase	BG573647
242605_at	0.86381	4.320134	10.99725	2.44E-22	5.36E-21	39.93488			AI453137
226370_at	0.86319	7.388863	9.286058	2.62E-17	3.50E-16	28.45833	KLHL15	kelch-like 15 (Drosophila)	BG149487
201505_at	0.86313	9.498414	7.329868	5.47E-12	3.97E-11	16.37265	LAMB1	laminin, beta 1	NM_002291
201743_at	0.86285	9.217777	6.194508	3.23E-09	1.51E-08	10.11458	CD14	CD14 molecule	NM_000591
244428_at	0.86271	5.582523	12.79714	7.82E-28	2.73E-26	52.4944	DNMT3A	DNA (cytosine-5)-methyltransferase 3 alpha	AW572279
211009_s_at	0.86253	7.538951	8.837696	4.87E-16	5.73E-15	25.57055	ZNF271	zinc finger protein 271	AF159567
43511_s_at	0.86244	7.462041	11.37602	1.75E-23	4.27E-22	42.54816			AI201594
221030_s_at	0.86243	5.714125	10.08742	1.25E-19	2.12E-18	33.75469	ARHGAP24	Rho GTPase activating protein 24	NM_031305
204783_at	0.86241	5.813825	4.518104	1.06E-05	2.50E-05	2.263893	MLF1	myeloid leukemia factor 1	AI911434
1569512_at	0.86235	4.349545	9.727188	1.41E-18	2.13E-17	31.35429			BC022883
208966_x_at	0.86223	9.456041	7.133176	1.73E-11	1.17E-10	15.24228	IFI16	Interferon, gamma-inducible protein 16	AF208043
225339_at	0.862	8.449849	11.7764	1.06E-24	2.90E-23	45.33077	SPAG9	sperm associated antigen 9	BG290577
244506_at	0.86172	4.479014	14.12228	6.22E-32	3.10E-30	61.87269	TMTC1	transmembrane and tetrapeptide repeat containing 1	BE297946
207057_at	0.86155	7.033549	5.058109	9.50E-07	2.75E-06	4.58804	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	NM_004731
208030_s_at	0.86137	9.729131	17.02404	7.29E-41	9.41E-39	82.31263	ADD1	adducin 1 (alpha)	NM_001119
203910_at	0.86106	8.801746	7.004026	3.64E-11	2.36E-10	14.51003	ARHGAP29	Rho GTPase activating protein 29	NM_004815
218456_at	0.86076	7.682169	10.40769	1.41E-20	2.63E-19	35.91246	CAPRIN2	caprin family member 2	NM_023925
235735_at	0.86051	6.466627	6.386724	1.15E-09	5.81E-09	11.12641			AI936516
236583_at	0.86038	5.67357	10.27075	3.59E-20	6.42E-19	34.98727			AA286867
226508_at	0.86014	9.039231	10.75556	1.30E-21	2.67E-20	38.27867	PHC3	polyhomeotic homolog 3 (Drosophila)	AI042019
228104_at	0.86008	5.888426	10.49849	7.59E-21	1.45E-19	36.52795	PLXNA4	plexin A4	AL117427
223886_s_at	0.8596	9.122584	10.70757	1.81E-21	3.67E-20	37.95092	RNF146	ring finger protein 146	AL136829

210133_at	0.85952	8.503881	3.762366	0.0002206	0.0004111	-0.62243	CCL11	chemokine (C-C motif) ligand 11	D49372
211105_s_at	0.85934	7.384967	8.878633	3.74E-16	4.45E-15	25.83168	NFATC1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	U80918
203835_at	0.85917	8.285532	8.864495	4.09E-16	4.86E-15	25.74144	LRRC32	leucine rich repeat containing 32	NM_005512
205128_x_at	0.85885	7.794822	7.376726	4.15E-12	3.07E-11	16.64456	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	NM_000962
225809_at	0.85795	7.393514	4.439739	1.48E-05	3.40E-05	1.944213	DKFZP564O0823	DKFZP564O0823 protein	AI659927
229969_at	0.85794	6.956481	9.353469	1.68E-17	2.29E-16	28.89753	SEC63	SEC63 homolog (S. cerevisiae)	AV723931
235980_at	0.85776	5.808742	15.44067	5.21E-36	3.94E-34	71.20432	PIK3CA	HBV preS1-transactivated protein 3 binding protein 1 (PS1TP3BP1)	AA767763
226521_s_at	0.85758	6.924008	9.023336	1.46E-16	1.81E-15	26.75892	FAM175A	family with sequence similarity 175, member A	AK023676
229529_at	0.85746	6.242416	10.54891	5.37E-21	1.05E-19	36.87036	TCF21	transcription factor 21	AI827830
203238_s_at	0.85733	7.835226	7.741468	4.67E-13	3.91E-12	18.79431	NOTCH3	Notch homolog 3 (Drosophila)	NM_000435
1569472_s_at	0.85713	5.353182	8.130801	4.28E-14	4.06E-13	21.15	ITC3	tetratricopeptide repeat domain 3	BC026260
231873_at	0.85704	8.125894	9.486123	7.00E-18	9.96E-17	29.76542	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	AL046696
206701_x_at	0.85672	6.253725	6.047539	7.03E-09	3.09E-08	9.355124	EDNRB	endothelin receptor type B	NM_003991
205755_at	0.85663	4.983115	7.513573	1.84E-12	1.42E-11	17.44434	TIH3	inter-alpha (globulin) inhibitor H3	NM_002217
227613_at	0.85662	6.920698	5.955935	1.14E-08	4.79E-08	8.888146	ZNF331	zinc finger protein 331	AW450874
221003_s_at	0.85658	6.470212	11.3217	2.56E-23	6.14E-22	42.17213	CAB39L	calcium binding protein 39-like	NM_030925
210995_s_at	0.85648	5.098765	11.06118	1.57E-22	3.52E-21	40.37446	TRIM23	tripartite motif-containing 23	AF230399
231262_at	0.85643	4.125089	11.59782	3.72E-24	9.73E-23	44.08734			AI356003
204860_s_at	0.85612	6.41437	7.691761	6.31E-13	5.17E-12	18.49798	NAIP	NLR family, apoptosis inhibitory protein	AI817801
223435_s_at	0.85603	5.678094	4.216526	3.75E-05	7.96E-05	1.059015	PCDHA10 PCDHA11 PCDHA12 PCDHA13 PCDHA2 PCDHA3 PCDHA4 PCDHA5 PCDHA6 PCDHA7 PCDHA8 PCDHA9 PCDHAC1	protocadherin alpha 1 /// protocadherin alpha 10 /// protocadherin alpha 11 /// protocadherin alpha 12 /// protocadherin alpha 13 /// protocadherin alpha 2 /// protocadherin alpha 3 /// protocadherin alpha 4 /// protocadherin alpha 5 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protocadherin alpha 8 /// protocadherin alpha 9 /// protocadherin alpha subfamily C, 1 /// protocadherin alpha subfamily C, 2	AI268404
227288_at	0.85554	7.728847	9.966836	2.81E-19	4.60E-18	32.94787	SFRS12IP1	SFRS12-interacting protein 1	BE645776
209263_x_at	0.85553	8.636204	11.44622	1.07E-23	2.68E-22	43.03465	TSPAN4	tetraspanin 4	BC000389
212614_at	0.85505	9.763327	7.510121	1.88E-12	1.45E-11	17.42406	ARID5B	AT rich interactive domain 5B (MRF1-like)	BG285011
202620_s_at	0.85505	9.426594	5.686346	4.51E-08	1.69E-07	7.543132	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	NM_000935
231867_at	0.85388	5.105803	6.961126	4.65E-11	2.96E-10	14.26858	ODZ2	odz, odd Oz/ten-m homolog 2 (Drosophila)	AB032953

216620_s_at	0.85387	8.076674	10.41429	1.35E-20	2.52E-19	35.95714	ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	AF009205
213183_s_at	0.85386	5.597582	6.399593	1.07E-09	5.44E-09	11.19489	CDKN1C	Cyclin-dependent kinase inhibitor 1C transcript variant 3 (CDKN1C) mRNA, complete cds, alternatively spliced	N95363
211874_s_at	0.85373	7.264576	11.87373	5.36E-25	1.50E-23	46.00997	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	AF119230
227204_at	0.85344	6.878442	10.08321	1.28E-19	2.18E-18	33.72643	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	AI817448
204369_at	0.85297	7.589603	8.940759	2.50E-16	3.04E-15	26.22899	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	NM_006218
208860_s_at	0.85291	8.188929	10.00477	2.18E-19	3.61E-18	33.2013	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	U09820
212586_at	0.85288	10.3979	11.16142	7.82E-23	1.80E-21	41.06503	CAST	calpastatin	AA195244
219228_at	0.85263	8.073397	5.830236	2.17E-08	8.67E-08	8.255509	ZNF331	zinc finger protein 331	NM_018555
206943_at	0.8522	5.600783	7.276436	7.48E-12	5.34E-11	16.0638	TGFB1	transforming growth factor, beta receptor 1	NM_004612
226985_at	0.85213	7.607114	9.798856	8.70E-19	1.35E-17	31.82944	FGD5	FYVE, RhoGEF and PH domain containing 5	AW269340
205858_at	0.85202	5.080697	10.5219	6.47E-21	1.25E-19	36.68687	NGFR	nerve growth factor receptor (TNFR superfamily, member 16)	NM_002507
204439_at	0.85166	7.36917	4.047496	7.38E-05	0.0001488	0.414173	IFI44L	interferon-induced protein 44-like	NM_006820
218237_s_at	0.85151	9.247569	6.241796	2.51E-09	1.20E-08	10.36158	SLC38A1	solute carrier family 38, member 1	NM_030674
214961_at	0.85117	4.128353	6.31018	1.74E-09	8.52E-09	10.721	KIAA0774	KIAA0774	AI818409
223652_at	0.85111	5.507058	8.233193	2.26E-14	2.21E-13	21.77931	AS3MT	arsenic (+3 oxidation state) methyltransferase	AF226730
212508_at	0.85074	9.434376	10.27883	3.40E-20	6.10E-19	35.04179	MOAP1	modulator of apoptosis 1	AK024029
1558924_s_at	0.85064	7.641025	8.793118	6.48E-16	7.53E-15	25.28678	CLIP1	CAP-GLY domain containing linker protein 1	BF673049
228249_at	0.85021	7.164757	10.2283	4.79E-20	8.47E-19	34.70126	C11orf74	chromosome 11 open reading frame 74	AA535128
219992_at	0.85011	6.991463	7.47653	2.29E-12	1.75E-11	17.22702	TAC3	tachykinin 3	NM_013251
209993_at	0.85005	5.716255	5.942995	1.21E-08	5.09E-08	8.822582	ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	AF016535
226244_at	0.84997	7.517079	10.57896	4.37E-21	8.60E-20	37.07471	CLEC14A	C-type lectin domain family 14, member A	BF059395
235111_at	0.84992	4.477107	13.9802	1.71E-31	8.21E-30	60.86558			AW953150
219929_s_at	0.84987	7.194227	8.428095	6.65E-15	6.90E-14	22.98785	ZFYVE21	zinc finger, FYVE domain containing 21	NM_024071
223176_at	0.84958	8.571684	8.702989	1.16E-15	1.31E-14	24.71501	KCTD20	potassium channel tetramerisation domain containing 20	BC003697
236042_at	0.84939	4.854256	12.50337	6.29E-27	2.04E-25	50.42463	LOC100130219	similar to hCG2041987	AI700506
238902_at	0.84928	6.144252	11.54285	5.47E-24	1.41E-22	43.70529	PCMTD1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 (PCMTD1), mRNA	T85248
228919_at	0.84913	7.206966	5.75747	3.15E-08	1.22E-07	7.893663			AA601031
235834_at	0.84909	6.276492	10.97357	2.88E-22	6.28E-21	39.77218	CALD1	Caldesmon, 3' UTR	BF063186
219291_at	0.84834	7.538729	10.32169	2.54E-20	4.60E-19	35.33103	DTWD1	DTW domain containing 1	NM_020234
210872_x_at	0.84781	5.984952	12.36762	1.64E-26	5.18E-25	49.47012	GAS7	growth arrest-specific 7	BC001152
209012_at	0.84759	7.054063	10.30062	2.93E-20	5.29E-19	35.18875	TRIO	triple functional domain (PTPRF interacting)	AV718192
228771_at	0.84731	6.509942	6.751736	1.53E-10	8.96E-10	13.10331	ADRBK2	adrenergic, beta, receptor kinase 2	AI651212
201990_s_at	0.8473	8.532728	9.194738	4.78E-17	6.22E-16	27.86537	CREBL2	cAMP responsive element binding protein-like 2	NM_001310
209657_s_at	0.84701	7.44162	7.606534	1.05E-12	8.40E-12	17.99232	HSF2	heat shock transcription factor 2	M65217
203628_at	0.84685	7.708763	6.835507	9.51E-11	5.76E-10	13.56685	IGF1R	insulin-like growth factor 1 receptor	H05812
48031_r_at	0.84618	6.59624	13.18216	5.06E-29	1.96E-27	55.21396	C5orf4	chromosome 5 open reading frame 4	H93077

214663_at	0.84602	6.51833	13.19428	4.64E-29	1.80E-27	55.29968	DSTYK	dual serine/threonine and tyrosine protein kinase	AB007941
212462_at	0.84601	9.130726	11.26086	3.92E-23	9.27E-22	41.7515	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	AU144267
205277_at	0.84587	6.354158	15.27141	1.73E-35	1.23E-33	70.00897	PRDM2	PR domain containing 2, with ZNF domain	NM_012231
227771_at	0.84562	6.327569	6.25142	2.38E-09	1.14E-08	10.412	LIFR	leukemia inhibitory factor receptor alpha	AW592684
202743_at	0.84541	8.171022	9.172225	5.54E-17	7.15E-16	27.71955	PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	BE622627
204774_at	0.84484	7.879648	5.481434	1.25E-07	4.31E-07	6.550995	EV12A /// EV12B	ecotropic viral integration site 2A /// ecotropic viral integration site 2B	NM_014210
200675_at	0.84478	11.75503	12.67952	1.80E-27	6.12E-26	51.66503	CD81	CD81 molecule	NM_004356
211473_s_at	0.84438	4.629102	10.65523	2.59E-21	5.18E-20	37.59399	COL4A6	collagen, type IV, alpha 6	U04845
213238_at	0.84415	7.629571	8.297304	1.51E-14	1.51E-13	22.17533	ATP10D	ATPase, class V, type 10D	AI478147
220917_s_at	0.84409	7.039565	11.79118	9.58E-25	2.62E-23	45.43389	WDR19	WD repeat domain 19	NM_025132
204368_at	0.84393	8.050223	5.99642	9.19E-09	3.95E-08	9.093916	SLC02A1	solute carrier organic anion transporter family, member 2A1	NM_005630
202646_s_at	0.84366	10.32072	13.25206	3.08E-29	1.22E-27	55.70838	CSDE1	cold shock domain containing E1, RNA-binding	AA167775
223380_s_at	0.84356	9.296248	8.877028	3.77E-16	4.49E-15	25.82144	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	AF207547
1563498_s_at	0.84347	3.654716	11.52633	6.14E-24	1.57E-22	43.59057	SLC25A45	solute carrier family 25, member 45	AK090434
203803_at	0.84329	8.196202	7.485481	2.17E-12	1.67E-11	17.27948	PCYOX1	prenylcysteine oxidase 1	N45309
238178_at	0.8423	4.163056	9.19357	4.81E-17	6.26E-16	27.8578			BF110268
206978_at	0.84223	5.702956	5.295423	3.09E-07	9.86E-07	5.673784	CCR2 /// FU78302	chemokine (C-C motif) receptor 2 /// chemokine (C-C motif) receptor 2-like	NM_000647
220319_s_at	0.84213	8.085915	10.81786	8.45E-22	1.77E-20	38.70462	MYLIP	myosin regulatory light chain interacting protein	NM_013262
209481_at	0.84205	9.361076	12.68585	1.72E-27	5.86E-26	51.70964	SNRK	SNF related kinase	AF226044
223287_s_at	0.842	10.16555	10.47544	8.89E-21	1.69E-19	36.37153	FOXP1	forkhead box P1	AF146696
228314_at	0.84183	7.376955	7.969898	1.16E-13	1.05E-12	20.16915	LRRCBC	leucine rich repeat containing 8 family, member C	BE877357
225611_at	0.84173	7.862221	10.07153	1.39E-19	2.35E-18	33.64817	LOC100128443 /// MAST4	hypothetical protein LOC100128443 /// microtubule associated serine/threonine kinase family member 4	AI922968
225972_at	0.84124	6.469585	8.386473	8.64E-15	8.86E-14	22.72861	TMEM64	transmembrane protein 64	AA524005
228097_at	0.84123	5.299257	8.627928	1.87E-15	2.07E-14	24.24087	MYLIP	myosin regulatory light chain interacting protein	AW292746
227809_at	0.841	6.972781	11.58363	4.11E-24	1.07E-22	43.98867	ZC3H6	zinc finger CCCH-type containing 6	AI703114
205207_at	0.84094	7.082347	3.557817	0.0004662	0.0008222	-1.3255	IL6	interleukin 6 (interferon, beta 2)	NM_000600
212615_at	0.84061	7.977558	10.25345	4.04E-20	7.18E-19	34.87067	CHD9	chromodomain helicase DNA binding protein 9	AI742305
223488_s_at	0.8406	6.956319	10.81	8.92E-22	1.86E-20	38.65086	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	BC000873
208116_s_at	0.84054	7.009202	5.724422	3.72E-08	1.42E-07	7.730399	MAN1A1	mannosidase, alpha, class 1A, member 1	NM_005907
220260_at	0.84045	6.076115	10.28868	3.18E-20	5.72E-19	35.10823	TBC1D19	TBC1 domain family, member 19	NM_018317
1554241_at	0.84009	8.889495	8.116051	4.69E-14	4.43E-13	21.05967	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	BC007230
231862_at	0.83995	6.66916	8.302853	1.46E-14	1.46E-13	22.20968	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	AK023520
229828_at	0.83988	7.157379	12.00486	2.13E-25	6.13E-24	46.92651			AL044007
37384_at	0.83982	7.662555	16.30177	1.17E-38	1.17E-36	77.26457	PPM1F	protein phosphatase 1F (PP2C domain containing)	D86995
242100_at	0.83973	5.630243	8.503215	4.13E-15	4.39E-14	23.45726	CHSY3	chondroitin sulfate synthase 3	AI076484
224365_s_at	0.83969	5.350128	7.545156	1.52E-12	1.19E-11	17.63009	TIGD7	tigger transposable element derived 7	AF251050
227567_at	0.83967	7.748451	8.650569	1.62E-15	1.80E-14	24.38369	AMZ2	Archaealysin family metalloproteinase 2 (AMZ2), transcript variant 2, mRNA	AL524467
221730_at	0.83965	9.218818	4.865233	2.30E-06	6.17E-06	3.734072	COL5A2	collagen, type V, alpha 2	NM_000393
212928_at	0.83951	8.914972	8.273006	1.76E-14	1.75E-13	22.02506	TSPYL4	TSPY-like 4	AL050331

206453_s_at	0.83928	8.813213	7.521264	1.76E-12	1.36E-11	17.48953	NDRG2	NDRG family member 2	NM_016250
224162_s_at	0.83927	7.947355	12.85338	5.25E-28	1.86E-26	52.8912	FBXO31	F-box protein 31	BC002985
203068_at	0.83919	6.85886	9.463093	8.15E-18	1.15E-16	29.61441	KLHL21	kelch-like 21 (Drosophila)	NM_014851
202404_s_at	0.8391	12.50029	5.054955	9.64E-07	2.79E-06	4.573869	COL1A2	collagen, type I, alpha 2	NM_000089
200816_s_at	0.83904	9.526347	11.37372	1.78E-23	4.33E-22	42.53219	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit 45kDa	NM_000430
204308_s_at	0.83878	7.562048	15.38921	7.50E-36	5.57E-34	70.84099	KIAA0329		NM_014844
227191_at	0.83845	5.904539	10.59188	4.00E-21	7.89E-20	37.16257			AI743744
221768_at	0.83832	6.558684	9.033239	1.37E-16	1.71E-15	26.82261	SFPQ	Myoblast cell surface antigen 24.1D5	AV705803
212829_at	0.83826	8.947512	10.89632	4.91E-22	1.05E-20	39.24206	PIP4K2A	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	BE878277
230643_at	0.83789	5.460814	13.03009	1.49E-28	5.54E-27	54.13905	WNT9A	wingless-type MMTV Integration site family, member 9A	BE220265
1556658_a_at	0.83787	4.778287	8.13674	4.12E-14	3.93E-13	21.18639			AA744622
224705_s_at	0.83777	7.874562	9.44252	9.34E-18	1.31E-16	29.47963	TNRC6A	trinucleotide repeat containing 6A	AI684626
225820_at	0.83764	6.540731	7.367626	4.38E-12	3.22E-11	16.59168	PHF17	PHD finger protein 17	AV646599
228334_x_at	0.83759	7.094571	9.112167	8.20E-17	1.04E-15	27.33127	KIAA1712	KIAA1712	AI633734
206392_s_at	0.8375	8.370264	3.517187	0.0005389	0.0009402	-1.46104	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	NM_002888
204298_s_at	0.83743	6.140828	4.567089	8.60E-06	2.06E-05	2.46604	LOX	lysyl oxidase	NM_002317
45714_at	0.83712	8.500354	11.57583	4.34E-24	1.13E-22	43.93449	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	AA436930
222605_at	0.83685	8.133866	9.721676	1.46E-18	2.21E-17	31.3178	RCOR3	REST corepressor 3	AI807073
212567_s_at	0.83682	7.284961	15.21493	2.59E-35	1.81E-33	69.60978	MAP4	microtubule-associated protein 4	AL523310
236311_at	0.83678	4.774764	11.15581	8.13E-23	1.87E-21	41.02634	LOH12CR2	loss of heterozygosity, 12, chromosomal region 2	BE645784
219631_at	0.83676	5.667323	7.876112	2.06E-13	1.80E-12	19.60213	LRP12	low density lipoprotein-related protein 12	NM_024937
210839_s_at	0.83661	7.88009	5.006682	1.21E-06	3.42E-06	4.357813	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	D45421
215990_s_at	0.83616	6.686087	9.536555	5.01E-18	7.23E-17	30.0966	BCL6	B-cell CLL/lymphoma 6	S67779
213034_at	0.83612	8.137295	14.5752	2.46E-33	1.39E-31	65.08242	KIAA0999	KIAA0999 protein	AB023216
229512_at	0.83576	6.227562	10.26261	3.80E-20	6.77E-19	34.93239	FAM120C	family with sequence similarity 120C	BE464337
1553175_s_at	0.83576	5.026045	10.99192	2.54E-22	5.56E-21	39.89823	PDE5A	phosphodiesterase 5A, cGMP-specific	AB015656
213033_s_at	0.83478	6.234515	9.158969	6.04E-17	7.77E-16	27.63376	NFIB	nuclear factor I/B	AI186739
239415_at	0.83478	6.679463	9.393644	1.29E-17	1.78E-16	29.15988	MAP9	microtubule-associated protein 9	AW117322
213925_at	0.83461	5.893469	8.842712	4.71E-16	5.56E-15	25.60251	C1orf95	Clone 23798 and 23825 mRNA sequence	AL134612
212765_at	0.83452	8.793629	10.28338	3.30E-20	5.92E-19	35.07246	CAMSAP1L	calmodulin regulated spectrin-associated protein 1-like 1	AB029001
229034_at	0.83426	5.35223	9.9758	2.65E-19	4.35E-18	33.00773	SOBP	sine oculis binding protein homolog (Drosophila)	BF511724
235629_at	0.83392	4.264487	8.067762	6.33E-14	5.90E-13	20.76452			AI333596
214862_x_at	0.83377	4.154017	9.371813	1.49E-17	2.04E-16	29.01725			AL080082
235199_at	0.83357	7.211374	6.110821	5.04E-09	2.28E-08	9.680598	RNF125	ring finger protein 125	AI969697
224920_x_at	0.83351	8.453992	8.425097	6.77E-15	7.02E-14	22.96916	MYADM	myeloid-associated differentiation marker	AA909044
216033_s_at	0.83309	7.756861	7.847045	2.46E-13	2.13E-12	19.42711	FYN	FYN oncogene related to SRC, FGR, YES	S74774
239154_at	0.83308	5.859076	8.935869	2.58E-16	3.13E-15	26.19768			AW962705
221645_s_at	0.83297	7.058692	7.981884	1.07E-13	9.75E-13	20.24187	ZNF83	zinc finger protein 83	M27877
204686_at	0.83252	8.105666	7.080044	2.35E-11	1.57E-10	14.94005	IRS1	insulin receptor substrate 1	NM_005544
223063_at	0.83231	9.725408	10.50888	7.07E-21	1.36E-19	36.59846	C1orf198	chromosome 1 open reading frame 198	BC004870
210994_x_at	0.83229	5.271765	11.2813	3.40E-23	8.07E-22	41.89273	TRIM23	tripartite motif-containing 23	AF230398
236666_s_at	0.832	5.846056	8.153855	3.71E-14	3.54E-13	21.29135			AA923289
235108_at	0.83186	5.570788	10.08661	1.25E-19	2.13E-18	33.74924			BG105700
239286_at	0.83061	5.854494	8.740231	9.11E-16	1.04E-14	24.95095	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)	AI038737
228042_at	0.83057	5.737841	10.37292	1.79E-20	3.30E-19	35.6772	ADPRH	ADP-ribosylarginine hydrolase	N54957
226701_at	0.83037	5.874819	6.802638	1.15E-10	6.85E-10	13.38454	GJA5	gap junction protein, alpha 5, 40kDa	AI692880

217886_at	0.83019	8.438762	12.69784	1.58E-27	5.40E-26	51.79418	EPS15	epidermal growth factor receptor pathway substrate 15	BF213575
203586_s_at	0.83015	6.615672	12.43551	1.02E-26	3.26E-25	49.94728	ARL4D	ADP-ribosylation factor-like 4D	NM_001661
226071_at	0.82994	5.734347	6.892622	6.88E-11	4.26E-10	13.88493	ADAMTSL4	ADAMTS-like 4	AF217974
241722_x_at	0.82967	6.553369	7.218108	1.05E-11	7.36E-11	15.72816			BF724558
236764_at	0.82937	4.973121	14.07939	8.45E-32	4.17E-30	61.56868			H49911
227126_at	0.8293	7.653442	7.048322	2.82E-11	1.86E-10	14.76026			AI857788
219552_at	0.82921	3.617079	13.76326	8.06E-31	3.61E-29	59.32815	SVEP1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	NM_024500
239270_at	0.82899	4.954673	6.812802	1.08E-10	6.50E-10	13.44086	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	AL133721
244286_at	0.82893	3.917334	13.24167	3.31E-29	1.30E-27	55.63487			AI017983
1563947_a_at	0.82823	6.03156	10.79547	9.86E-22	2.05E-20	38.55146	ERC1	ELKS/RAB6-interacting/CAST family member 1	AK097177
243438_at	0.8282	4.880876	12.71704	1.38E-27	4.74E-26	51.92954	PDE7B	phosphodiesterase 7B	BE968570
201719_s_at	0.8281	9.179795	6.970612	4.41E-11	2.82E-10	14.32189	EPB41L2	erythrocyte membrane protein band 4.1-like 2	NM_001431
226169_at	0.82806	8.398952	10.46261	9.70E-21	1.84E-19	36.28452	SBF2	SET binding factor 2	AW276572
209574_s_at	0.82766	6.237711	9.774942	1.02E-18	1.57E-17	31.67076	C18orf1	chromosome 18 open reading frame 1	AI349506
218641_at	0.82742	8.124995	8.296578	1.52E-14	1.52E-13	22.17084	MGC3032	hypothetical protein MGC3032	NM_023941
203774_at	0.82692	8.397624	11.10895	1.13E-22	2.56E-21	40.7034	MTR	5-methyltetrahydrofolate-homocysteine methyltransferase	NM_000254
228240_at	0.82665	7.084563	10.79251	1.01E-21	2.09E-20	38.53123			AW952320
229580_at	0.82664	5.075187	6.387299	1.14E-09	5.79E-09	11.12947			R71596
210176_at	0.82633	5.902259	5.993749	9.32E-09	4.00E-08	9.080314	TLR1	toll-like receptor 1	AL050262
219743_at	0.82624	5.794095	9.588474	3.55E-18	5.18E-17	30.43822	HEY2	hairly/enhancer-of-split related with YRPW motif 2	NM_012259
224582_s_at	0.82576	8.630306	7.521544	1.75E-12	1.36E-11	17.49117	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	H09085
240467_at	0.82534	4.062333	11.39657	1.52E-23	3.72E-22	42.69047			AA947873
212775_at	0.82523	7.315277	4.899491	1.97E-06	5.35E-06	3.883854	OBSL1	obscurin-like 1	AI978623
229244_at	0.82521	5.463046	11.73154	1.46E-24	3.93E-23	45.01811			AI400057
211086_x_at	0.82498	5.715508	13.62441	2.17E-30	9.40E-29	58.34438	NEK1	NIMA (never in mitosis gene a)-related kinase 1	Z25431
33850_at	0.82494	7.416009	14.90981	2.27E-34	1.46E-32	67.45183	MAP4	microtubule-associated protein 4	W28892
209560_s_at	0.82419	4.124758	4.949649	1.57E-06	4.34E-06	4.104635	DLK1	delta-like 1 homolog (Drosophila)	U15979
220952_s_at	0.82403	9.283341	8.380918	8.95E-15	9.16E-14	22.69406	PLEKHA5	pleckstrin homology domain containing, family A member 5	NM_019012
220005_at	0.82384	5.469174	5.756131	3.17E-08	1.23E-07	7.887032	P2RY13	purinergic receptor P2Y, G-protein coupled, 13	NM_023914
243023_at	0.82369	5.046897	7.892718	1.86E-13	1.64E-12	19.70227			N34402
216184_s_at	0.82349	5.006819	6.059344	6.61E-09	2.92E-08	9.415663	RIMS1	regulating synaptic membrane exocytosis 1	AF263310
209015_s_at	0.82335	8.568276	8.000212	9.60E-14	8.78E-13	20.35317	DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	BC002446
229585_at	0.82307	5.893369	8.639682	1.73E-15	1.93E-14	24.31499	ADAMTSL1	ADAMTS-like 1	AI803088
228695_at	0.82295	3.397692	9.857996	5.85E-19	9.24E-18	32.22246	C3orf46	chromosome 8 open reading frame 46	H17349
203561_at	0.82292	7.41494	5.289635	3.18E-07	1.01E-06	5.64685	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	NM_021642
235747_at	0.82275	7.662386	7.998113	9.73E-14	8.88E-13	20.34042	SLC25A16	CDNA FLJ59258 complete cds, highly similar to Grave disease carrier protein	AI305170
227979_at	0.82273	7.241232	8.819967	5.45E-16	6.39E-15	25.45761			AU152162
226028_at	0.82233	7.599264	8.420662	6.97E-15	7.21E-14	22.94151	ROBO4	roundabout homolog 4, magic roundabout (Drosophila)	AA156022
218373_at	0.82203	8.234974	11.50045	7.35E-24	1.86E-22	43.41089	AKTIP	AKT interacting protein	NM_022476
226939_at	0.82203	8.362274	8.193267	2.90E-14	2.80E-13	21.53346	CPEB2	cytoplasmic polyadenylation element binding protein 2	AI202327
226820_at	0.8216	9.121533	11.47531	8.77E-24	2.21E-22	43.23644	ZNF362	zinc finger protein 362	W72455
226933_s_at	0.8215	5.370102	6.969048	4.45E-11	2.84E-10	14.3131	ID4	Id-related helix-loop-helix protein Id4	AV646610
204513_s_at	0.82138	6.702137	7.849775	2.42E-13	2.10E-12	19.44353	ELMO1	engulfment and cell motility 1	NM_014800

221729_at	0.82116	10.15401	4.807	2.99E-06	7.84E-06	3.481381	COL5A2	collagen, type V, alpha 2	AL575735
							HLA-DQA1 HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2	
212671_s_at	0.82108	10.27521	4.024783	8.07E-05	0.0001616	0.329229			BG397856
1558605_at	0.82079	5.740316	7.453622	2.63E-12	2.00E-11	17.09294			BC040287
203156_at	0.82059	9.302464	11.19784	6.07E-23	1.41E-21	41.3163	AKAP11	A kinase (PRKA) anchor protein 11	NM_016248
235698_at	0.82043	7.714806	9.944494	3.27E-19	5.31E-18	32.79874	ZFP90	zinc finger protein 90 homolog (mouse)	AA771779
223894_s_at	0.82031	7.78131	9.78758	9.39E-19	1.45E-17	31.7546	AKTIP	AKT interacting protein	BC001134
228098_s_at	0.82011	9.359513	10.97342	2.88E-22	6.28E-21	39.77114	MYLIP	myosin regulatory light chain interacting protein	AW292746
205440_s_at	0.81995	3.949159	4.474094	1.28E-05	2.98E-05	2.083797	NPY1R	neuropeptide Y receptor Y1	NM_000909
219834_at	0.81994	4.389245	12.2127	4.91E-26	1.49E-24	48.38251	ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	NM_024744
230061_at	0.81984	6.035314	6.651253	2.68E-10	1.51E-09	12.55205	TM4SF18	MRNA; cDNA DKFZp313N1532 (from clone DKFZp313N1532)	AW338625
212299_at	0.81966	8.772256	16.33634	9.18E-39	9.31E-37	77.50699	NEK9	NIMA (never in mitosis gene a)-related kinase 9	AL117502
235879_at	0.81959	6.718294	5.880338	1.68E-08	6.85E-08	8.506529	MBNL1	MBNL protein	AI697540
210432_s_at	0.81946	4.62683	5.21818	4.48E-07	1.38E-06	5.316218	SCN3A	sodium channel, voltage-gated, type III, alpha subunit	AF225986
235179_at	0.81899	5.894759	12.87925	4.37E-28	1.56E-26	53.07376	ZNF641	zinc finger protein 641	BF541598
213061_s_at	0.81887	8.534701	9.690919	1.79E-18	2.69E-17	31.11431	NTAN1	N-terminal asparagine amidase	AA643304
228293_at	0.81884	5.658252	3.776058	0.0002096	0.0003919	-0.57414	DEPDC7	DEP domain containing 7	AJ245600
241685_x_at	0.81851	4.004202	12.23074	4.33E-26	1.32E-24	48.50903			AI806169
201824_at	0.81843	8.301904	8.84254	4.72E-16	5.56E-15	25.60142	RNF14	ring finger protein 14	AB022663
235639_at	0.81829	4.892543	10.29976	2.95E-20	5.32E-19	35.183			AL137939
201462_at	0.8182	8.908267	5.359571	2.27E-07	7.43E-07	5.97374	SCRNI	secernin 1	NM_014766
213910_at	0.81818	4.099174	14.48553	4.67E-33	2.56E-31	64.44711	IGFBP7	insulin-like growth factor binding protein 7	AW770896
222418_s_at	0.81807	8.457248	10.001	2.23E-19	3.70E-18	33.1761	TMEM43	transmembrane protein 43	AA115485
229007_at	0.81791	5.80401	6.362249	1.31E-09	6.57E-09	10.99643	LOC28378	hypothetical protein LOC283788	N50864
238454_at	0.81788	4.120725	12.75713	1.04E-27	3.60E-26	52.21217	ZNF540	zinc finger protein 540	AA013398
221039_s_at	0.81779	7.371408	7.441425	2.83E-12	2.13E-11	17.02165	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	NM_018482
241138_at	0.81771	6.724634	10.3936	1.55E-20	2.88E-19	35.81713			AI082569
228946_at	0.81765	4.980681	9.430818	1.01E-17	1.41E-16	29.40302	INTU	inturned planar cell polarity effector homolog (Drosophila)	AW150229
230836_at	0.81761	6.665958	6.167992	3.72E-09	1.73E-08	9.976637	ST8SIA4	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 4	AI422986
225796_at	0.81749	6.795612	9.194427	4.79E-17	6.23E-16	27.86336	PXK	PX domain containing serine/threonine kinase	AI684747
203640_at	0.81738	9.85763	8.9235	2.79E-16	3.38E-15	26.1185	MBNL2	muscleblind-like 2 (Drosophila)	BE328496
228667_at	0.81734	5.344476	11.0485	1.71E-22	3.83E-21	40.2872	AGPAT4	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	AI733330
214492_at	0.81682	6.296383	13.6811	1.45E-30	6.37E-29	58.74599	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	NM_000337
244026_at	0.81674	5.236463	5.419263	1.70E-07	5.70E-07	6.25529			BF063657
202519_at	0.81655	9.104035	10.38822	1.61E-20	2.98E-19	35.78068	MLXIP	MLX interacting protein	NM_014938
231042_s_at	0.81653	5.027103	7.023938	3.25E-11	2.12E-10	14.6224			AA809487
230511_at	0.81624	6.410988	8.520851	3.69E-15	3.95E-14	23.56775	CREM	cAMP responsive element modulator	AI800640
227628_at	0.81624	8.221781	5.350422	2.37E-07	7.73E-07	5.930793	GPX8	glutathione peroxidase 8 (putative)	AL571557
208206_s_at	0.81623	6.800693	9.816278	7.74E-19	1.21E-17	31.94513	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	NM_005825
215775_at	0.81587	4.997488	8.411314	7.39E-15	7.62E-14	22.88326	THBS1	(clone lambda-TS-33) thrombospondin (THBS) mRNA, 5' end	BF084105
213269_at	0.81573	6.262571	12.28429	2.96E-26	9.13E-25	48.88486	ZNF248	zinc finger protein 248	N21541
1569167_at	0.81569	4.18729	14.64189	1.53E-33	8.88E-32	65.55483			BC013250

202552_s_at	0.81541	7.994653	10.30394	2.87E-20	5.18E-19	35.21116	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	NM_016441
240310_at	0.81541	5.421332	14.72572	8.42E-34	5.06E-32	66.14856	TOR1AIP1	torsin A interacting protein 1	AI807835
1554806_a_at	0.81522	8.216778	9.369476	1.51E-17	2.07E-16	29.002	FBXO8	F-box protein 8	BC040456
223208_at	0.81515	8.21383	11.74134	1.36E-24	3.68E-23	45.0864	KCTD10	potassium channel tetramerisation domain containing 10	AF113208
203002_at	0.81497	8.788658	7.588152	1.18E-12	9.33E-12	17.88366	AMOTL2	angiomin like 2	NM_016201
213027_at	0.81495	8.629303	10.39047	1.59E-20	2.94E-19	35.7959	TROVE2	SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit	AU146655
215785_s_at	0.81489	8.01315	6.218752	2.84E-09	1.34E-08	10.24105	CYFIP2	cytoplasmic FMR1 interacting protein 2	AI161999
225350_s_at	0.81486	9.111372	13.22113	3.84E-29	1.50E-27	55.48958	ZYG11B	zyg-11 homolog B (C. elegans)	AV701229
226085_at	0.81458	8.389755	6.805118	1.13E-10	6.76E-10	13.39828	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	AA181060
244677_at	0.81449	5.247944	9.312557	2.20E-17	2.96E-16	28.63083			AA416756
224518_s_at	0.81435	6.980152	7.394201	3.74E-12	2.78E-11	16.74623	ZNF559	zinc finger protein 559	BC006436
204742_s_at	0.81369	6.700819	9.657032	2.25E-18	3.34E-17	30.89038	PDS5B	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	NM_015032
1552315_at	0.81358	6.609086	10.15545	7.86E-20	1.36E-18	34.21123	GIMAP1	GTPase, IMAP family member 1	NM_130759
1557749_at	0.81324	5.105586	12.35012	1.86E-26	5.81E-25	49.34711	EHBP1L1	EH domain binding protein 1-like 1	AK092750
241827_at	0.81314	7.007953	9.442316	9.36E-18	1.31E-16	29.47829	ZNF615	zinc finger protein 615	AL577866
210260_s_at	0.81297	9.133244	7.122765	1.83E-11	1.24E-10	15.18295	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	BC005352
221127_s_at	0.81201	5.502444	11.28713	3.26E-23	7.75E-22	41.93307	RIG	regulated in glioma	NM_006394
204303_s_at	0.81186	6.630703	11.83208	7.19E-25	2.00E-23	45.71919	KIAA0427	KIAA0427	NM_014772
227107_at	0.81181	8.179458	8.095624	5.32E-14	5.01E-13	20.93471			AI807404
204635_at	0.81161	6.949623	9.052085	1.21E-16	1.52E-15	26.9439	RPS6KAS	ribosomal protein S6 kinase, 90kDa, polypeptide 5	NM_004755
212326_at	0.81147	6.932579	12.48751	7.03E-27	2.28E-25	50.313	VP513D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	AB007922
217196_s_at	0.81139	7.360136	7.650792	8.08E-13	6.53E-12	18.25452	CAMSAP1L	calmodulin regulated spectrin-associated protein 1-like 1	AL110158
208460_at	0.81136	5.337181	9.754773	1.17E-18	1.79E-17	31.53703	GJC1	gap junction protein, gamma 1, 45kDa	NM_005497
207630_s_at	0.81135	8.044811	7.374212	4.21E-12	3.11E-11	16.62995	CREM	cAMP responsive element modulator	NM_001881
202393_s_at	0.81101	10.30054	9.901244	4.38E-19	7.02E-18	32.51037	KLF10	Kruppel-like factor 10	NM_005655
235197_s_at	0.81099	6.0964	9.799982	8.64E-19	1.34E-17	31.83692	OSTM1	osteopetrosis associated transmembrane protein 1	AV713913
213982_s_at	0.81099	8.199613	8.600754	2.22E-15	2.44E-14	24.06968	RABGAP1L	RAB GTPase activating protein 1-like	BG107203
205903_s_at	0.81084	5.382964	7.39766	3.66E-12	2.73E-11	16.76637	KCNN3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	NM_002249
214684_at	0.81057	8.352221	9.879064	5.08E-19	8.07E-18	32.36266	MEF2A	myocyte enhancer factor 2A	X63381
200665_s_at	0.81048	11.94423	6.002765	8.89E-09	3.83E-08	9.126256	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	NM_003118
224838_at	0.81037	10.44499	9.957605	2.99E-19	4.88E-18	32.88624	FOXP1	forkhead box P1	AK026898
201044_x_at	0.80988	7.399349	6.206931	3.02E-09	1.42E-08	10.17934	DUSP1	dual specificity phosphatase 1	AA530892
221752_at	0.8097	7.346024	10.42904	1.22E-20	2.29E-19	36.05705	SSH1	CDNA FLJ38102 fis, clone D3OST2000618, moderately similar to Drosophila melanogaster slingshot mRNA	AL041728
215076_s_at	0.80954	13.15522	6.402052	1.06E-09	5.37E-09	11.20799	COL3A1	collagen, type III, alpha 1	AU144167
214578_s_at	0.80954	7.343181	10.45819	1.00E-20	1.89E-19	36.25459	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	AV683882
229172_at	0.80934	6.637026	10.47375	8.99E-21	1.71E-19	36.36006	HSPA12B	heat shock 70kD protein 12B	AI150641
225191_at	0.80903	7.062859	9.004953	1.65E-16	2.03E-15	26.64077	CIRBP	cold inducible RNA binding protein	AL565767
206132_at	0.80897	6.748546	12.12468	9.15E-26	2.71E-24	47.76544	MCC	mutated in colorectal cancers	NM_002387
203638_s_at	0.80849	8.437678	4.050575	7.29E-05	0.0001472	0.42572	FGFR2	fibroblast growth factor receptor 2	NM_022969
221833_at	0.80831	6.090435	10.01275	2.06E-19	3.43E-18	33.25466	LONP2	Lon peptidase 2, peroxisomal (LONP2), mRNA	AI971258
224473_x_at	0.80815	7.743823	12.46434	8.29E-27	2.67E-25	50.15005	LZT52	leucine zipper, putative tumor suppressor 2	BC006212

205027_s_at	0.8081	6.585284	6.143185	4.25E-09	1.95E-08	9.84795	MAP3K8	mitogen-activated protein kinase kinase kinase 8	NM_005204
205131_x_at	0.80787	6.066019	8.515735	3.82E-15	4.07E-14	23.53569	CLEC11A	C-type lectin domain family 11, member A	NM_002975
206624_at	0.80754	4.194016	5.158979	5.92E-07	1.79E-06	5.04488	LOC100130216 /// USP9Y	hypothetical protein LOC100130216 /// ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	NM_004654
236197_at	0.80751	4.075897	14.35247	1.21E-32	6.37E-31	63.50418			AA905353
221430_s_at	0.80718	6.485936	10.09916	1.15E-19	1.96E-18	33.8334	RNF146	ring finger protein 146	NM_030963
234563_at	0.80698	4.713917	10.83239	7.64E-22	1.60E-20	38.80411			AK000795
222533_at	0.8069	9.631376	12.13263	8.65E-26	2.57E-24	47.82111	CRBN	cereblon	AI676103
218490_s_at	0.80676	7.699383	7.827558	2.77E-13	2.38E-12	19.30996	ZNF302	zinc finger protein 302	NM_018443
244149_at	0.80674	6.2562	9.233645	3.70E-17	4.87E-16	28.11771			AA864758
210613_s_at	0.80631	6.881694	8.970001	2.07E-16	2.53E-15	26.41641	SYNGR1	synaptogyrin 1	BC000731
235996_at	0.80516	4.417036	13.08184	1.03E-28	3.88E-27	54.50472	RASSF8	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	BF979984
204431_at	0.80486	6.795657	8.641192	1.72E-15	1.91E-14	24.32451	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	NM_003260
225341_at	0.80465	6.32692	9.17881	5.30E-17	6.86E-16	27.76219	MTERFD3	MTERF domain containing 3	BF697312
225997_at	0.80439	7.896115	9.334917	1.90E-17	2.57E-16	28.77653	MOBK1A	MOB1, Mps One Binder kinase activator-like 1A (yeast)	AL162039
212259_s_at	0.80435	8.119976	11.37608	1.75E-23	4.27E-22	42.54853	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	BF344265
224835_at	0.80428	7.52554	9.25653	3.18E-17	4.22E-16	28.26634	RP5-1022P6.2	hypothetical protein KIAA1434	AL109935
1558111_at	0.80421	5.715746	7.807947	3.12E-13	2.66E-12	19.19223	MBNL1	muscleblind-like (Drosophila)	AL562860
241874_at	0.80384	5.848912	13.43878	8.14E-30	3.38E-28	57.0298	LOC49231	similar to bovine IgA regulatory protein	H05025
223557_s_at	0.80347	4.071236	6.644371	2.78E-10	1.56E-09	12.51449	TMEFF2	transmembrane protein with EGF-like and two follistatin-like domains 2	AB017269
214691_x_at	0.80319	6.274931	7.824728	2.81E-13	2.42E-12	19.29297	FAM63B	family with sequence similarity 63, member B	AU121431
201924_at	0.803	9.904555	13.08174	1.03E-28	3.88E-27	54.50402	AFF1	AF4/FMR2 family, member 1	NM_005935
210105_s_at	0.80281	9.414666	8.33874	1.17E-14	1.18E-13	22.43208	FYN	FYN oncogene related to SRC, FGR, YES	M14333
206391_at	0.80268	7.591762	3.804652	0.0001883	0.0003545	-0.47282	RARRES1	retinoic acid receptor responder (tazarotene induced) 1	NM_002888
223453_s_at	0.80249	4.83296	8.652249	1.60E-15	1.79E-14	24.39429	ATL3	atlastin GTPase 3	BC005096
239082_at	0.80214	7.190363	5.602514	6.88E-08	2.49E-07	7.134024			BF437161
203890_s_at	0.80186	6.663301	9.73028	1.38E-18	2.09E-17	31.37477	DAPK3	death-associated protein kinase 3	BF686824
217220_at	0.80172	3.509064	15.26416	1.82E-35	1.29E-33	69.95769			AL050153
226364_at	0.8017	6.680577	7.908728	1.68E-13	1.49E-12	19.79893	HIP1	Huntingtin interacting protein (HIP1)	AU145049
1558739_at	0.80147	4.120502	12.03629	1.71E-25	4.96E-24	47.14642			R30807
209561_at	0.80083	7.648833	11.22792	4.93E-23	1.15E-21	41.52392	THBS3	thrombospondin 3	L38969
228046_at	0.80077	7.662882	6.436875	8.74E-10	4.51E-09	11.39379	ZNF827	CDNA clone IMAGE:5440683	AA741243
227873_at	0.80073	8.805396	12.97838	2.16E-28	7.89E-27	53.77372	TXNDC15	thioredoxin domain containing 15	BE547587
228932_at	0.80021	5.305335	13.21632	3.97E-29	1.55E-27	55.4556			BE467383
235225_at	0.80015	3.984072	13.94688	2.17E-31	1.03E-29	60.62946	SCN2B	sodium channel, voltage-gated, type II, beta	AA447729
242856_at	0.79999	4.110177	9.499115	6.42E-18	9.17E-17	29.85067			AI291804
232156_at	0.79971	4.825762	11.2783	3.47E-23	8.23E-22	41.87204			AK024921
205005_s_at	0.7997	7.382472	7.368497	4.35E-12	3.21E-11	16.59674	NMT2	N-myrystoyltransferase 2	AW293531
203525_s_at	0.79949	7.493795	9.404395	1.20E-17	1.66E-16	29.23016	APC	adenomatous polyposis coli	AI375486
227047_x_at	0.79924	8.168157	13.89095	3.24E-31	1.51E-29	60.23303	ZBTB4	zinc finger and BTB domain containing 4	N63748
221918_at	0.79912	8.996282	9.730201	1.38E-18	2.09E-17	31.37425	PCTK2	PCTAIRE protein kinase 2	AI742210
219109_at	0.79877	7.651373	4.429464	1.55E-05	3.54E-05	1.902637	SPAG16	sperm associated antigen 16	NM_024532
212605_s_at	0.79866	8.221727	9.157768	6.08E-17	7.83E-16	27.62599			AK025759
212357_at	0.79843	7.137452	13.72608	1.05E-30	4.68E-29	59.06473	FAM168A	family with sequence similarity 168, member A	AI096888
1557113_at	0.79792	3.915432	11.99493	2.28E-25	6.56E-24	46.85703	LOC28358	hypothetical protein LOC28358	AK095276

227866_at	0.79792	6.081356	8.187232	3.01E-14	2.91E-13	21.49634	LOC729436	PREDICTED: Homo sapiens hypothetical LOC729436 (LOC729436), mRNA	AI743557
212063_at	0.79768	11.10765	7.404525	3.52E-12	2.63E-11	16.80635	CD44	CD44 molecule (Indian blood group)	BE903880
221755_at	0.79732	7.772815	10.66276	2.46E-21	4.93E-20	37.64529	EHBP1L1	EH domain binding protein 1-like 1	BG334196
203699_s_at	0.79728	7.607221	4.093497	6.15E-05	0.0001258	0.587459	DIO2	deiodinase, iodothyronine, type II	U53506
233814_at	0.79677	5.898056	5.68369	4.58E-08	1.71E-07	7.530105	EFNA5	Receptor tyrosine kinase ligand LERK-7 precursor (EPLG7)	AK025909
1554132_a_at	0.7962	6.435619	9.630043	2.69E-18	3.97E-17	30.71224	KIAA1128	KIAA1128	BC030528
218142_s_at	0.79618	8.719446	12.62564	2.64E-27	8.85E-26	51.28541	CRBN	cereblon	NM_016302
207702_s_at	0.79602	4.943663	10.02701	1.87E-19	3.13E-18	33.35009	MAGI2	membrane associated guanylate kinase, WW and PDZ domain containing 2	NM_012301
212588_at	0.79588	8.730031	4.786827	3.27E-06	8.51E-06	3.394409	PTPRC	protein tyrosine phosphatase, receptor type, C	Y00062
243179_at	0.79567	5.368615	8.895524	3.35E-16	4.01E-15	25.93959	LOC100130360	CDNA FLJ33993 fis, clone DFNES2007757	BG231554
226093_at	0.79556	7.846173	10.02479	1.90E-19	3.17E-18	33.33523	DCP1B	DCP1 decapping enzyme homolog B (S. cerevisiae)	AW204088
235132_at	0.7952	6.519126	9.96096	2.93E-19	4.78E-18	32.90864	LOC254128	hypothetical protein LOC254128	BF939830
228492_at	0.79506	4.995014	3.819003	0.0001784	0.0003373	-0.42171	LOC100130216 /// USP9Y	hypothetical protein LOC100130216 /// ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)	AV681765
218471_s_at	0.79434	7.878643	12.12865	8.90E-26	2.64E-24	47.79326	BBS1	Bardet-Biedl syndrome 1	NM_024649
219288_at	0.79431	7.663019	4.388699	1.84E-05	4.14E-05	1.738475	C3orf14	chromosome 3 open reading frame 14	NM_020685
213474_at	0.79426	6.695868	13.76112	8.18E-31	3.67E-29	59.31298	KCTD7	potassium channel tetramerisation domain containing 7	AI890903
220088_at	0.79418	7.456695	4.99133	1.29E-06	3.64E-06	4.289442	CSAR1	complement component 5a receptor 1	NM_001736
203862_s_at	0.79407	3.748094	7.446925	2.74E-12	2.07E-11	17.05379	ACTN2	actinin, alpha 2	H16245
212990_at	0.79407	6.876047	9.031235	1.39E-16	1.73E-15	26.80972	SYNJ1	synaptojanin 1	AB020717
225331_at	0.79391	9.47801	9.465101	8.05E-18	1.14E-16	29.62757	CCDC50	coiled-coil domain containing 50	BF941088
230986_at	0.7939	4.497473	11.73557	1.42E-24	3.82E-23	45.04617	KLF8	CDNA selection clone ADS40	AI821447
223464_at	0.79388	6.588532	10.68806	2.07E-21	4.17E-20	37.81784	OSBPL5	oxysterol binding protein-like 5	AL136918
218764_at	0.79354	8.327517	7.701843	5.94E-13	4.89E-12	18.558	PRKCH	protein kinase C, eta	NM_024064
204021_s_at	0.79348	8.071937	9.028386	1.41E-16	1.76E-15	26.7914	PURA	purine-rich element binding protein A	NM_005859
232226_at	0.79317	4.830708	8.923415	2.80E-16	3.38E-15	26.11796	LRRRC4C	leucine rich repeat containing 4C	AW118214
212698_s_at	0.79313	10.37656	9.578241	3.80E-18	5.54E-17	30.37083	SEPT10	septin 10	BF966021
204392_at	0.79234	6.63312	10.39893	1.50E-20	2.79E-19	35.8532	CAMK1	calcium/calmodulin-dependent protein kinase I	NM_003656
204028_s_at	0.79227	9.272208	11.99518	2.28E-25	6.55E-24	46.85877	RABGAP1	RAB GTPase activating protein 1	NM_012197
202260_s_at	0.79206	8.031297	5.545098	9.15E-08	3.23E-07	6.856386	STXBP1	syntaxin binding protein 1	NM_003165
210852_s_at	0.79157	4.896004	9.975148	2.66E-19	4.37E-18	33.00338	AASS	aminoadipate-semialdehyde synthase	AF229180
204784_s_at	0.79141	6.722124	3.810158	0.0001844	0.0003479	-0.45323	MLF1	myeloid leukemia factor 1	NM_022443
47550_at	0.79133	5.782421	8.919611	2.87E-16	3.46E-15	26.09361	LZTS1	leucine zipper, putative tumor suppressor 1	N21184
1554153_a_at	0.79132	6.708038	13.31271	2.00E-29	8.06E-28	56.13746	PHF21A	PHD finger protein 21A	BC015714
217371_s_at	0.79127	5.140749	8.388446	8.54E-15	8.76E-14	22.74089	IL15	interleukin 15	Y09908
207124_s_at	0.79118	7.2944	7.187581	1.26E-11	8.69E-11	15.55313	GNB5	guanine nucleotide binding protein (G protein), beta 5	NM_006578
226415_at	0.79113	6.154546	6.55035	4.69E-10	2.54E-09	12.00382	VAT1L	vesicle amine transport protein 1 homolog (T. californica)-like	AA156723
227420_at	0.79108	7.941351	9.4268	1.04E-17	1.44E-16	29.37672	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	BF338045
238356_at	0.79091	4.503825	11.49757	7.50E-24	1.90E-22	43.39086	DOCK11	dedicator of cytokinesis 11	AW968823
206067_s_at	0.79089	4.610289	4.23515	3.47E-05	7.42E-05	1.131417	WT1	Wilms tumor 1	NM_024426
238076_at	0.79051	6.310001	10.01268	2.07E-19	3.43E-18	33.25419	GATAD2B	GATA zinc finger domain containing 2B	AI818098

236081_at	0.79051	4.065943	9.773385	1.03E-18	1.59E-17	31.66043			AI929792
1558686_at	0.78978	4.642383	6.60557	3.45E-10	1.91E-09	12.30318			BM983749
226181_at	0.78975	7.444129	8.13459	4.18E-14	3.97E-13	21.17321	TUBE1	tubulin, epsilon 1	AI613127
213093_at	0.78972	8.697585	6.84929	8.80E-11	5.36E-10	13.64346	PRKCA	protein kinase C, alpha	AI471375
242738_s_at	0.78966	7.100959	11.0266	1.99E-22	4.42E-21	40.13661	ZFH3	zinc finger homeobox 3	BG402859
								colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	
205159_at	0.78966	7.880685	4.876969	2.18E-06	5.87E-06	3.785293	CSF2RB		AV756141
207753_at	0.78955	6.42427	6.288868	1.95E-09	9.48E-09	10.60871	ZNF304	zinc finger protein 304	NM_020657
225147_at	0.78915	8.350197	9.994727	2.33E-19	3.85E-18	33.13419	CYTH3	cytohesin 3	AL521959
								transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	
40837_at	0.78911	7.9684	8.477438	4.86E-15	5.13E-14	23.29597	TLE2		M99436
								sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	
233882_s_at	0.78903	4.37887	7.725604	5.14E-13	4.28E-12	18.69962	SEMA6D		AK022831
								family with sequence similarity 85, member A	
238716_at	0.78897	5.96541	9.007908	1.62E-16	2.00E-15	26.65976	FAM85A		AL527331
								transforming growth factor, beta receptor II (70/80kDa)	
207334_s_at	0.78872	6.190336	9.034474	1.36E-16	1.69E-15	26.83056	TGFBR2		NM_003242
								chromosome 5 open reading frame 24	
1553106_at	0.78868	6.463611	6.494825	6.36E-10	3.36E-09	11.70445	C5orf24		NM_152409
								spondin 2, extracellular matrix protein	
218638_s_at	0.78844	8.848743	5.984965	9.76E-09	4.17E-08	9.035599	SPON2		NM_012445
227663_at	0.78816	5.884955	8.358983	1.03E-14	1.05E-13	22.55774			BE674006
							LOC72997	CDNA FLJ37477 fis, clone	
235691_at	0.78799	4.246858	11.21969	5.22E-23	1.22E-21	41.46712	0	BRAWH2013047	AW269338
228914_at	0.78748	6.362448	9.178903	5.30E-17	6.86E-16	27.76279			AI769673
203423_at	0.78735	7.629346	5.025973	1.10E-06	3.15E-06	4.443964	RBP1	retinol binding protein 1, cellular	NM_002899
							LOC439994 /// LOC642361	hypothetical gene supported by AF064843; AK025716 /// hypothetical LOC642361	
228839_s_at	0.787	7.966439	9.962948	2.89E-19	4.72E-18	32.92191	1		AA810864
								GTPase activating Rap/RanGAP domain-like 1	
214855_s_at	0.78682	7.148353	8.446609	5.91E-15	6.18E-14	23.10336	GARNL1		AL050050
								metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	
224568_x_at	0.78662	10.47273	5.923224	1.35E-08	5.59E-08	8.722599	MALAT1		AW005982
								Mdm1 nuclear protein homolog (mouse)	
220397_at	0.78628	5.164691	6.956248	4.78E-11	3.04E-10	14.24119	MDM1		NM_020128
219484_at	0.78609	6.622158	10.5485	5.39E-21	1.05E-19	36.86763	HCFC2	host cell factor C2	NM_013320
203130_s_at	0.78603	5.966345	6.206852	3.03E-09	1.42E-08	10.17893	KIF5C	kinesin family member 5C	NM_004522
								3-hydroxybutyrate dehydrogenase, type 2	
235155_at	0.78595	4.252332	9.301886	2.36E-17	3.17E-16	28.56133	BDH2		AW136198
201028_s_at	0.7858	9.928173	8.415367	7.20E-15	7.44E-14	22.90851	CD99	CD99 molecule	U82164
								SHC (Src homology 2 domain containing) family, member 4	
235238_at	0.78529	4.793207	11.296	3.07E-23	7.30E-22	41.99436	SHC4		BF676462
								phosphatidylinositol binding clathrin assembly protein	
212511_at	0.78509	8.392639	9.345899	1.77E-17	2.40E-16	28.84815	PICALM		AI766247
								splicing factor, arginine/serine-rich 18	
212177_at	0.78497	6.810272	7.034874	3.05E-11	2.00E-10	14.68419	SFRS18		AW081113
								tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	
225308_s_at	0.78491	8.995772	9.122791	7.65E-17	9.76E-16	27.39988	TANC1		AB051515
								chromosome 21 open reading frame 91	
226109_at	0.78476	8.408812	9.106257	8.52E-17	1.08E-15	27.29312	C21orf91		AK023825
203620_s_at	0.78455	8.034314	9.195469	4.75E-17	6.19E-16	27.87011	FCHSD2	FCH and double SH3 domains 2	NM_014824
								quaking homolog, KH domain RNA binding (mouse)	
214543_x_at	0.78454	7.56454	11.00758	2.28E-22	5.01E-21	40.00582	QKI		AF142421
227576_at	0.78437	6.264582	7.512968	1.85E-12	1.43E-11	17.44078			AW003140
223606_x_at	0.78434	7.427014	8.149825	3.80E-14	3.63E-13	21.26663	KIAA1704	KIAA1704	AF245045
								family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	
237094_at	0.78432	4.67685	7.148112	1.58E-11	1.08E-10	15.32747	FAM19A5		AI953086
								chromosome 9 open reading frame 150	
227443_at	0.78421	8.123817	7.056051	2.70E-11	1.78E-10	14.80402	C9orf150		AI972386
226297_at	0.78411	10.87673	12.01013	2.05E-25	5.92E-24	46.96336			AV693403
241925_x_at	0.78409	4.636748	5.785199	2.73E-08	1.07E-07	8.03117			BF207870
								zinc finger protein 36, C3H type-like 1	
211962_s_at	0.78395	10.83306	10.37964	1.71E-20	3.16E-19	35.72266	ZFP36L1		BG250310
								unc-51-like kinase 2 (C. elegans)	
1554112_a_at	0.78391	4.579431	11.88752	4.87E-25	1.37E-23	46.10626	ULK2		BC034988

202319_at	0.78386	6.703937	10.21456	5.26E-20	9.24E-19	34.60876	SENP6	SUMO1/sentrin specific peptidase 6	NM_015571
209695_at	0.78382	7.61015	6.61318	3.31E-10	1.84E-09	12.34456	LOC100131062 /// PTP4A3	similar to protein tyrosine phosphatase type IVA, member 3 /// protein tyrosine phosphatase type IVA, member 3	BC003105
215706_x_at	0.78366	8.888785	10.00783	2.13E-19	3.54E-18	33.22179	ZYX	zyxin	BC002323
220253_s_at	0.78359	4.823153	7.424877	3.12E-12	2.34E-11	16.92502	LRP12	low density lipoprotein-related protein 12	NM_013437
208924_at	0.78319	10.22204	11.54352	5.44E-24	1.40E-22	43.70993	RNF11	ring finger protein 11	AB024703
239294_at	0.78314	6.978597	5.433331	1.59E-07	5.36E-07	6.321983			AA810265
227115_at	0.78307	6.262598	10.85062	6.74E-22	1.42E-20	38.92891			AW291331
206423_at	0.78307	4.738431	9.262062	3.07E-17	4.07E-16	28.30229	ANGPTL7	angiotensin-like 7	NM_021146
225706_at	0.78297	8.085229	5.94183	1.22E-08	5.12E-08	8.816685	GLCC1	glucocorticoid induced transcript 1	AI761989
235657_at	0.78294	6.085985	10.32488	2.48E-20	4.51E-19	35.35257			BF061389
225530_at	0.7829	8.40799	11.54029	5.57E-24	1.43E-22	43.68752	MOBK2A	MOB1, Mps One Binder kinase activator-like 2A (yeast)	BE396735
212013_at	0.78273	7.645657	5.845028	2.01E-08	8.08E-08	8.329461	PXDN	peroxidasin homolog (Drosophila)	D86983
208228_s_at	0.7827	7.534068	3.712739	0.0002653	0.0004874	-0.79616	FGFR2	fibroblast growth factor receptor 2	M87771
1558512_at	0.7826	4.663923	12.72316	1.32E-27	4.55E-26	51.9727			CA336272
229017_s_at	0.78195	5.910096	12.57083	3.90E-27	1.29E-25	50.89942	DSTYK	dual serine/threonine and tyrosine protein kinase	N31717
225811_at	0.78108	9.214169	10.34501	2.17E-20	3.95E-19	35.48853			AI652868
226102_at	0.78107	7.279838	9.740716	1.28E-18	1.95E-17	31.44389			AI920953
203563_at	0.78098	5.279311	12.87669	4.45E-28	1.59E-26	53.05571	AFAP1	actin filament associated protein 1	NM_021638
228623_at	0.78091	5.600194	8.087192	5.61E-14	5.26E-13	20.88317			AI224133
227242_s_at	0.78085	3.488883	7.911944	1.65E-13	1.47E-12	19.81835	EBF3	early B-cell factor 3	BF592034
242981_at	0.78072	6.657658	9.280692	2.72E-17	3.62E-16	28.42342			N79601
217863_at	0.78071	7.951164	11.53677	5.70E-24	1.46E-22	43.66305	PIAS1	protein inhibitor of activated STAT, 1	AI348378
202328_s_at	0.78049	6.897022	16.19963	2.41E-38	2.30E-36	76.54784	PKD1	polycystic kidney disease 1 (autosomal dominant)	NM_000296
242979_at	0.78036	5.810426	7.318864	5.83E-12	4.23E-11	16.30893	IRS1	insulin receptor substrate 1	AI474666
222407_s_at	0.78021	8.453172	13.71456	1.14E-30	5.06E-29	58.9831	ZFP106	zinc finger protein 106 homolog (mouse)	AI493587
220770_s_at	0.77998	5.566752	6.945356	5.09E-11	3.22E-10	14.18005	LOC63920	transposon-derived Buster3 transposase-like	NM_022090
232049_at	0.77984	3.728018	12.73947	1.18E-27	4.06E-26	52.08767			AK026718
216894_x_at	0.7797	6.580211	5.755851	3.18E-08	1.23E-07	7.885651	CDKN1C	cyclin-dependent kinase inhibitor 1C (p57, Kip2)	D64137
200835_s_at	0.77919	7.584948	10.88684	5.25E-22	1.12E-20	39.17706	MAP4	microtubule-associated protein 4	AI553791
204627_s_at	0.77917	4.60805	9.604382	3.19E-18	4.68E-17	30.54303	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	M35999
229411_at	0.77892	5.901602	10.72928	1.56E-21	3.18E-20	38.09912	PNCK	pregnancy up-regulated non-ubiquitously expressed CaM kinase	AI986390
238784_at	0.77885	4.238048	9.193197	4.83E-17	6.27E-16	27.85538	DPY19L2	dpy-19-like 2 (C. elegans)	AI039361
229312_s_at	0.77862	6.8225	7.247339	8.88E-12	6.26E-11	15.89616	GKAP1	G kinase anchoring protein 1	BF434321
213118_at	0.7785	7.400941	7.911937	1.65E-13	1.47E-12	19.81831	UHRF1BP1	UHRF1 binding protein 1-like	AL136821
239425_at	0.77822	4.521836	10.03764	1.74E-19	2.92E-18	33.4212			N52773
214510_at	0.77805	6.196283	9.907275	4.20E-19	6.76E-18	32.55056	GPR20	G protein-coupled receptor 20	NM_005293
228608_at	0.77801	4.964831	6.663647	2.50E-10	1.42E-09	12.61976	NALCN	sodium leak channel, non-selective	N49852
212294_at	0.77786	10.52621	9.027509	1.42E-16	1.77E-15	26.78576	GNG12	guanine nucleotide binding protein (G protein), gamma 12	BG111761
32625_at	0.7778	6.107297	10.06314	1.47E-19	2.48E-18	33.59197	NPR1	natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	X15357
1558487_a_at	0.77768	8.30689	10.22139	5.02E-20	8.85E-19	34.65471	TMED4	transmembrane emp24 protein transport domain containing 4	AK074557
204850_s_at	0.77759	4.057695	6.368235	1.27E-09	6.38E-09	11.02819	DCX	doublecortin	NM_000555
230781_at	0.77752	3.803984	8.580048	2.54E-15	2.77E-14	23.9394			AI143988

204929_s_at	0.77742	7.575714	8.35751	1.04E-14	1.05E-13	22.54859	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	NM_006634
219761_at	0.77705	6.325856	11.02431	2.03E-22	4.49E-21	40.12083	CLEC1A	C-type lectin domain family 1, member A	NM_016511
219569_s_at	0.77672	6.832078	5.158144	5.95E-07	1.79E-06	5.041069	TMEM22	transmembrane protein 22	NM_025246
227162_at	0.77669	7.016295	8.891966	3.43E-16	4.10E-15	25.91685	ZBTB26	zinc finger and BTB domain containing 26	BF214688
217813_s_at	0.77623	8.016486	8.955816	2.27E-16	2.76E-15	26.32547	SPIN1	spindlin 1	NM_006717
218748_s_at	0.7762	6.411599	5.90672	1.47E-08	6.05E-08	8.639316	EXOC5	exocyst complex component 5	NM_006544
203695_s_at	0.77619	8.136438	4.798975	3.10E-06	8.10E-06	3.446748	DFNA5	deafness, autosomal dominant 5	NM_004403
240557_at	0.77618	5.652257	10.48415	8.37E-21	1.60E-19	36.43063			N34514
1557286_at	0.77597	4.457323	14.57308	2.50E-33	1.41E-31	65.06738			AK001007
227557_at	0.77595	6.231132	9.03027	1.40E-16	1.74E-15	26.80351	SCARF2	scavenger receptor class F, member 2	AI127800
200899_s_at	0.77582	8.963602	11.03018	1.95E-22	4.32E-21	40.16119	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	NM_012215
213930_at	0.7757	6.56967	10.755	1.30E-21	2.68E-20	38.2748			N51708
229285_at	0.7757	7.358632	7.074706	2.42E-11	1.61E-10	14.90977	RNASEL	ribonuclease L (2',5'-oligoadenylate synthetase-dependent)	AI669749
229723_at	0.77566	7.195184	4.303236	2.62E-05	5.75E-05	1.398381	TAGAP	T-cell activation RhoGTPase activating protein	BF591040
230421_at	0.77556	5.816696	9.215863	4.16E-17	5.45E-16	28.00233	DKFZp686E2433	similar to hypothetical protein 9630041N07	AI340241
213418_at	0.77553	6.797649	5.346094	2.42E-07	7.89E-07	5.910497	HSPA6	heat shock 70kDa protein 6 (HSP70B)	NM_002155
235094_at	0.77546	7.101157	6.397648	1.08E-09	5.50E-09	11.18453			AI972661
215933_s_at	0.77501	6.930629	4.797531	3.12E-06	8.15E-06	3.440522	HHEX	hematopoietically expressed homeobox	Z21533
201580_s_at	0.77492	9.212918	7.374404	4.20E-12	3.11E-11	16.63107	TXNDC13	thioredoxin domain containing 13	AL544094
226807_at	0.77475	6.773597	9.711081	1.57E-18	2.36E-17	31.24767	ZFP1	zinc finger protein 1 homolog (mouse)	AL038511
202617_s_at	0.77449	6.530926	14.14729	5.21E-32	2.60E-30	62.04995	MECP2	methyl CpG binding protein 2 (Rett syndrome)	NM_004992
235746_s_at	0.77418	4.77805	7.520651	1.75E-12	1.37E-11	17.48593	PLA2R1	phospholipase A2 receptor 1, 180kDa	BE048919
200940_s_at	0.77413	8.631725	10.78431	1.06E-21	2.20E-20	38.47519	RERE	arginine-glutamic acid dipeptide (RE) repeats	AB036737
204075_s_at	0.77412	5.914904	9.834289	6.86E-19	1.08E-17	32.06481	KIAA0562	KIAA0562	NM_014704
224325_at	0.77408	5.871323	6.396549	1.09E-09	5.53E-09	11.17868	FZD8	frizzled homolog 8 (Drosophila)	AB043703
204959_at	0.77392	7.3411	4.614516	7.00E-06	1.71E-05	2.663437	MNDA	myeloid cell nuclear differentiation antigen	NM_002432
212779_at	0.77391	9.090496	10.01853	1.99E-19	3.31E-18	33.29335	KIAA1109	KIAA1109	AB029032
220818_s_at	0.77375	4.998921	8.900896	3.23E-16	3.88E-15	25.97392	TRPC4	transient receptor potential cation channel, subfamily C, member 4	NM_016179
214508_x_at	0.77341	7.808349	8.306003	1.43E-14	1.43E-13	22.22918	CREM	cAMP responsive element modulator	U44836
213328_at	0.77324	7.72103	10.47054	9.19E-21	1.75E-19	36.33834	NEK1	NIMA (never in mitosis gene a)-related kinase 1	AI936517
233536_at	0.77282	4.351863	8.460257	5.42E-15	5.69E-14	23.18859	ASXL3	additional sex combs like 3 (Drosophila)	AI202664
232051_at	0.77277	6.062016	11.70859	1.71E-24	4.58E-23	44.85823	CCDC102A	coiled-coil domain containing 102A	BC004307
231919_at	0.77261	5.53412	8.247475	2.07E-14	2.03E-13	21.8674	DBT	dihydrolipoamide branched chain transacylase E2	AK024946
223210_at	0.77256	8.441839	9.051399	1.22E-16	1.52E-15	26.93948	CHURC1	churchill domain containing 1	AF060510
224844_at	0.77253	8.513396	10.94726	3.45E-22	7.48E-21	39.59152	SLAIN2	SLAIN motif family, member 2	BE551691
207118_s_at	0.77244	5.497623	8.286391	1.62E-14	1.61E-13	22.10781	MMP23A /// MMP23B	matrix metalloproteinase 23A (pseudogene) /// matrix metalloproteinase 23B	NM_004559
241996_at	0.77218	6.125792	10.55457	5.17E-21	1.01E-19	36.90888			AI669591
225573_at	0.77215	6.127644	11.46871	9.18E-24	2.31E-22	43.19065	ACAD11 /// NPHP3	acyl-Coenzyme A dehydrogenase family, member 11 /// nephronophthisis 3 (adolescent)	AL518293
220007_at	0.7721	6.935526	8.88846	3.50E-16	4.18E-15	25.89691	METTL8	methyltransferase like 8	NM_024770
207703_at	0.77209	4.061341	6.894377	6.81E-11	4.23E-10	13.89473	NLGN4Y	neuroligin 4, Y-linked	NM_014893

226759_at	0.77188	6.207886	9.909012	4.15E-19	6.68E-18	32.56213	IKZF4	IKAROS family zinc finger 4 (Eos)	AI261467
227481_at	0.77185	7.677643	6.027481	7.81E-09	3.40E-08	9.25245	CNKSRR3	CNKSRR family member 3	BG165333
228162_at	0.77168	6.040891	9.772593	1.04E-18	1.60E-17	31.65518	ESD	esterase D/formylglutathione hydrolase	AA193515
212650_at	0.77167	8.199919	7.750443	4.42E-13	3.71E-12	18.84792	EHBP1	EH domain binding protein 1	BF116032
203700_s_at	0.77153	7.447948	4.172594	4.48E-05	9.37E-05	0.88928	DIO2	deiodinase, iodothyronine, type II	NM_013989
224906_at	0.77147	9.681151	10.14147	8.64E-20	1.49E-18	34.11737	ANO6	anoctamin 6	AL041280
219628_at	0.77146	8.069963	8.07977	5.87E-14	5.50E-13	20.83784	ZMAT3	zinc finger, matrin type 3	NM_022470
213304_at	0.7713	7.726785	8.743544	8.92E-16	1.02E-14	24.97196	FAM179B	family with sequence similarity 179, member B	AI823592
203574_at	0.77103	8.890101	6.70154	2.02E-10	1.16E-09	12.82727	NFIL3	nuclear factor, interleukin 3 regulated	NM_005384
52651_at	0.77073	6.744641	9.665625	2.12E-18	3.16E-17	30.94714	COL8A2	collagen, type VIII, alpha 2	AI806793
227388_at	0.77071	8.919185	6.980569	4.16E-11	2.68E-10	14.37789	TUSC1	tumor suppressor candidate 1	AA479016
218449_at	0.77058	8.066428	12.04172	1.64E-25	4.78E-24	47.18444	UFSP2	UFM1-specific peptidase 2	NM_018359
228770_at	0.77046	5.229002	9.77447	1.02E-18	1.58E-17	31.66763	GPR146	G protein-coupled receptor 146	BE645027
209598_at	0.77021	6.890968	3.724415	0.0002541	0.0004684	-0.75547	PNMA2	paraneoplastic antigen MA2	AB020690
213661_at	0.77019	7.273989	8.760275	8.01E-16	9.22E-15	25.07812	DKFZP586H2123	regeneration associated muscle protease	AI671186
230640_at	0.77002	6.135552	11.38886	1.60E-23	3.92E-22	42.63709			AW027431
238418_at	0.76972	6.127955	10.27734	3.43E-20	6.15E-19	35.03174	SLC35B4	solute carrier family 35, member B4	AI590926
219205_at	0.76972	7.092438	11.47077	9.05E-24	2.28E-22	43.20492	SRR	serine racemase	NM_021947
225128_at	0.76961	7.99432	9.432946	9.96E-18	1.39E-16	29.41695	KDELC2	KDEL (Lys-Asp-Glu-Leu) containing 2	AL548941
226383_at	0.76949	7.863263	10.78114	1.09E-21	2.25E-20	38.45351	C11orf46	chromosome 11 open reading frame 46	AI652452
205560_at	0.76941	6.235032	5.67827	4.70E-08	1.76E-07	7.503528	PCSK5	proprotein convertase subtilisin/kexin type 5	NM_006200
238923_at	0.7694	6.141074	9.983158	2.52E-19	4.15E-18	33.05689	SPOP	speckle-type POZ protein	AW449169
202527_s_at	0.76923	8.572673	7.053359	2.74E-11	1.81E-10	14.78878	SMAD4	SMAD family member 4	NM_005359
225028_at	0.76913	5.622706	7.832523	2.68E-13	2.32E-12	19.33983	LOC550643	hypothetical LOC550643	AI417268
229323_at	0.76896	6.409276	7.634315	8.92E-13	7.16E-12	18.15681	LOC387723	similar to hCG1648656	AI991561
230561_s_at	0.76889	6.298373	8.906139	3.13E-16	3.76E-15	26.00744	C2orf67	chromosome 2 open reading frame 67	AA252512
226981_at	0.7688	8.003589	10.99631	2.46E-22	5.40E-21	39.92838	MLL	Homo sapiens, clone IMAGE:6062880, mRNA	AW002079
205201_at	0.76878	7.095035	11.46495	9.43E-24	2.37E-22	43.16456	GLI3	GLI-Kruppel family member GLI3	NM_000168
221511_x_at	0.7687	8.294405	8.013562	8.84E-14	8.11E-13	20.43433	CCPG1	cell cycle progression 1	AB033080
238050_at	0.76864	3.730038	11.12156	1.03E-22	2.35E-21	40.79027			R94785
212450_at	0.76808	8.295861	9.260749	3.10E-17	4.11E-16	28.29375	KIAA0256	KIAA0256 gene product	D87445
202250_s_at	0.76796	7.314591	9.287205	2.60E-17	3.47E-16	28.46579	WDR42A	WD repeat domain 42A	NM_015726
211651_s_at	0.76784	8.993881	7.319965	5.80E-12	4.20E-11	16.3153	LAMB1	laminin, beta 1	M20206
202434_s_at	0.7677	5.118204	8.170891	3.34E-14	3.21E-13	21.39593	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	N21019
221014_s_at	0.76751	6.697361	9.88712	4.81E-19	7.68E-18	32.4163	RAB33B	RAB33B, member RAS oncogene family	NM_031296
243296_at	0.7675	8.049108	4.37778	1.92E-05	4.32E-05	1.694716	NAMPT	G0S9 mRNA, instability elements	AA873350
237515_at	0.76722	5.152435	5.58972	7.33E-08	2.64E-07	7.071975	TMEM56	transmembrane protein 56	AA054642
206756_at	0.76707	6.179339	9.155125	6.19E-17	7.96E-16	27.60889	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	NM_019886
228943_at	0.76703	6.505016	14.5786	2.40E-33	1.36E-31	65.10651	MAP6	microtubule-associated protein 6	AW003666
238558_at	0.76657	6.187871	6.775116	1.34E-10	7.92E-10	13.23232			AI445833
229141_at	0.76641	4.690856	11.7439	1.34E-24	3.61E-23	45.10421	WDR33	WD repeat domain 33	AW275379
214591_at	0.76626	3.697774	8.563206	2.82E-15	3.06E-14	23.83354	KLHL4	kelch-like 4 (Drosophila)	BF215673
209537_at	0.76623	7.792741	8.248387	2.06E-14	2.02E-13	21.87303	EXTL2	exostosins (multiple)-like 2	AF000416
228024_at	0.76615	6.874559	8.035644	7.72E-14	7.12E-13	20.56872	VPS37A	Vacuolar protein sorting 37 homolog A (S. cerevisiae) (VPS37A), mRNA	AW028100
201694_s_at	0.76606	10.78557	6.062465	6.50E-09	2.88E-08	9.431681	EGR1	early growth response 1	NM_001964
1556051_a at	0.76597	5.60895	9.901431	4.37E-19	7.01E-18	32.51162	BICD1	bicaudal D homolog 1 (Drosophila)	CA777994
212616_at	0.76575	9.2388	10.11226	1.05E-19	1.80E-18	33.9213	CHD9	chromodomain helicase DNA binding protein 9	BF668950

201262_s_at	0.76564	7.586064	6.004073	8.83E-09	3.81E-08	9.132925	BGN	biglycan	NM_001711
220326_s_at	0.76562	7.515693	10.5641	4.84E-21	9.47E-20	36.97367	FUJ10357	hypothetical protein FUJ10357	NM_018071
244334_at	0.76542	4.953485	8.440391	6.15E-15	6.41E-14	23.06455	TRAM1L1	translocation associated membrane protein 1-like 1	AA169554
212660_at	0.76536	8.53473	8.81167	5.75E-16	6.72E-15	25.4048	PHF15	PHD finger protein 15	AI735639
227064_at	0.76504	8.553396	11.51686	6.56E-24	1.67E-22	43.52482	ANKRD40	ankyrin repeat domain 40	AV712687
228367_at	0.76493	4.858201	6.417724	9.70E-10	4.97E-09	11.29152	ALPK2	alpha-kinase 2	BE551416
226464_at	0.76483	9.133233	9.73542	1.33E-18	2.02E-17	31.40881	C3orf58	chromosome 3 open reading frame 58	BE348597
203756_at	0.76482	7.588339	16.69007	7.60E-40	8.94E-38	79.98303	ARHGEF17	Rho guanine nucleotide exchange factor (GEF) 17	NM_014786
228841_at	0.76471	7.979029	8.87731	3.77E-16	4.49E-15	25.82324	LYRM7	Lyrm7 homolog (mouse)	AW299250
232094_at	0.76465	5.123524	8.024265	8.28E-14	7.62E-13	20.49944	C15orf29	chromosome 15 open reading frame 29	AU144048
201325_s_at	0.76453	9.31195	5.140993	6.45E-07	1.93E-06	4.962913	EMP1	epithelial membrane protein 1	NM_001423
222520_s_at	0.76423	4.731328	9.521218	5.55E-18	7.97E-17	29.99581	IFT57	Intraflagellar transport 57 homolog (Chlamydomonas)	AF139576
226030_at	0.76414	6.741178	8.869718	3.96E-16	4.70E-15	25.77477	ACADSB	acyl-Coenzyme A dehydrogenase, short/branched chain	BE897866
212715_s_at	0.76406	6.176386	9.402727	1.22E-17	1.68E-16	29.21925	MICAL3	microtubule associated monooxygenase, calponin and LIM domain containing 3	AB020626
210968_s_at	0.76396	11.64468	9.239672	3.56E-17	4.69E-16	28.15683	RTN4	reticulon 4	AF333336
205540_s_at	0.76377	5.642831	10.49812	7.61E-21	1.46E-19	36.52546	RRAGB	Ras-related GTP binding B	NM_016656
210833_at	0.76351	3.606364	10.07154	1.39E-19	2.35E-18	33.64823	PTGER3	prostaglandin E receptor 3 (subtype EP3)	AL031429
230713_at	0.76341	4.636138	9.474412	7.57E-18	1.07E-16	29.68861			BF115786
36553_at	0.7631	8.746795	8.721023	1.03E-15	1.18E-14	24.8292	ASMTL	acetylserotonin O- methyltransferase-like	AA669799
222975_s_at	0.76289	10.61792	9.812449	7.94E-19	1.24E-17	31.9197	CSDE1	cold shock domain containing E1, RNA-binding	AI423180
201989_s_at	0.76288	9.819542	11.24867	4.26E-23	1.01E-21	41.66728	CREBL2	cAMP responsive element binding protein-like 2	AL529409
209293_x_at	0.76261	7.139963	8.256868	1.95E-14	1.92E-13	21.92538	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	U16153
203773_x_at	0.76212	9.315306	7.83012	2.72E-13	2.35E-12	19.32536	BLVRA	biliverdin reductase A	NM_000712
206375_s_at	0.76175	4.770494	6.072393	6.17E-09	2.74E-08	9.482676	HSPB3	heat shock 27kDa protein 3	NM_006308
214787_at	0.76138	5.977585	8.418619	7.06E-15	7.30E-14	22.92877	DENND4A	DENN/MADD domain containing 4A	BE268538
224657_at	0.76125	9.817619	5.707091	4.07E-08	1.54E-07	7.645051	ERRF1	ERBB receptor feedback inhibitor 1	AL034417
201798_s_at	0.76112	10.36993	5.883433	1.65E-08	6.75E-08	8.522084	MYOF	myoferlin	NM_013451
235228_at	0.7611	4.116402	7.196072	1.20E-11	8.31E-11	15.60176	CCDC85A	coiled-coil domain containing 85A	AI376433
204352_at	0.76108	7.980766	7.557027	1.42E-12	1.11E-11	17.70002	TRAF5	TNF receptor-associated factor 5	NM_004619
203538_at	0.76102	9.773804	12.80196	7.56E-28	2.64E-26	52.5284	CAMLG	calcium modulating ligand	NM_001745
215719_x_at	0.76097	6.862326	4.569736	8.50E-06	2.04E-05	2.477015	FAS	Fas (TNF receptor superfamily, member 6)	X83493
204396_s_at	0.76078	9.243974	6.150412	4.09E-09	1.88E-08	9.885405	GRK5	G protein-coupled receptor kinase 5	NM_005308
205931_s_at	0.76045	4.658504	8.363034	1.00E-14	1.02E-13	22.5829	CREB5	cAMP responsive element binding protein 5	NM_004904
218892_at	0.76023	5.856443	11.61103	3.39E-24	8.91E-23	44.1792	DCHS1	dachsous 1 (Drosophila)	NM_024542
204589_at	0.76013	8.147194	7.199464	1.17E-11	8.16E-11	15.62121	NUAK1	NUAK family, SNF1-like kinase, 1	NM_014840
1555270_a_at	0.76008	6.941711	9.337437	1.87E-17	2.53E-16	28.79296	WFS1	Wolfram syndrome 1 (wolframin)	BC030130
212550_at	0.76005	7.571401	11.53477	5.78E-24	1.48E-22	43.64917	STAT5B	signal transducer and activator of transcription 5B	AI149535
223809_at	0.76005	5.231889	6.245903	2.46E-09	1.17E-08	10.38309	RGS18	regulator of G-protein signaling 18	AF076642
244187_at	0.75974	6.619158	5.846059	2.00E-08	8.05E-08	8.334619			AA053853
218292_s_at	0.7593	7.30052	9.438193	9.62E-18	1.34E-16	29.45129	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	NM_016203
205964_at	0.75916	6.043859	9.621627	2.84E-18	4.19E-17	30.65673	ZNF426	zinc finger protein 426	NM_024106
205752_s_at	0.75913	6.790096	11.85319	6.20E-25	1.73E-23	45.86655	GSTM5	glutathione S-transferase mu 5	NM_000851
230773_at	0.75892	5.004914	10.57191	4.59E-21	9.00E-20	37.02677			AA628511

228149_at	0.75883	7.145431	9.034094	1.36E-16	1.70E-15	26.82811	C7orf60	chromosome 7 open reading frame 60	BF432926
226846_at	0.75877	6.495756	9.889682	4.73E-19	7.56E-18	32.43336	PHYHD1	phytanoyl-CoA dioxygenase domain containing 1	AL545998
209840_s_at	0.75868	5.13924	8.006006	9.26E-14	8.48E-13	20.38839	LRRN3	leucine rich repeat neuronal 3	AI221950
210203_at	0.75864	4.24608	12.69869	1.57E-27	5.37E-26	51.80019	CNOT4	CCR4-NOT transcription complex, subunit 4	R64001
222108_at	0.75857	8.968694	3.882989	0.0001398	0.0002693	-0.19184	AMIGO2	adhesion molecule with Ig-like domain 2	ACC04010
201836_s_at	0.75821	6.526851	9.78258	9.71E-19	1.50E-17	31.72143	SUPT7L	suppressor of Ty 7 (<i>S. cerevisiae</i>)-like	AU154740
226633_at	0.75807	9.008656	8.519538	3.73E-15	3.98E-14	23.55952	RAB8B	RAB8B, member RAS oncogene family	AI807023
238736_at	0.75713	4.966895	8.560864	2.86E-15	3.10E-14	23.81883	REV3L	DNA polymerase zeta (REV3)	AA805939
221216_s_at	0.75698	7.767536	11.2314	4.81E-23	1.12E-21	41.54794	SCMH1	sex comb on midleg homolog 1 (<i>Drosophila</i>)	NM_012236
227856_at	0.75685	8.691158	5.881651	1.67E-08	6.81E-08	8.513128	C4orf32	chromosome 4 open reading frame 32	AI110850
201718_s_at	0.75672	7.630813	6.069159	6.28E-09	2.79E-08	9.466056	EPB41L2	erythrocyte membrane protein band 4.1-like 2	BF511685
241966_at	0.75661	5.027582	10.91047	4.46E-22	9.58E-21	39.33908	MYO5A	myosin VA (heavy chain 12, myoxin)	N67810
212206_s_at	0.75647	8.41977	9.97664	2.63E-19	4.33E-18	33.01334	H2AFV	H2A histone family, member V	BF343852
226126_at	0.75619	8.319233	8.081318	5.82E-14	5.45E-13	20.84729	MGC1616	hypothetical protein MGC16169	AA702160
225346_at	0.7561	7.158633	8.402786	7.80E-15	8.03E-14	22.83014	MTERFD3	MTERF domain containing 3	NM_025198
218306_s_at	0.75588	8.224567	12.87273	4.57E-28	1.63E-26	53.02775	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	NM_003922
218700_s_at	0.75584	7.406583	6.097709	5.40E-09	2.43E-08	9.61297	RAB7L1	RAB7, member RAS oncogene family-like 1	BC002585
201538_s_at	0.75582	6.948215	7.01531	3.41E-11	2.22E-10	14.57368	DUSP3	dual specificity phosphatase 3	NM_004090
203049_s_at	0.75522	9.172064	7.964922	1.19E-13	1.08E-12	20.13898	TTC37	tetratricopeptide repeat domain 37	NM_014639
218212_s_at	0.75521	8.061378	8.375701	9.25E-15	9.46E-14	22.66162	MOCS2	molybdenum cofactor synthesis 2	NM_004531
223349_s_at	0.75475	8.118652	7.506462	1.92E-12	1.48E-11	17.40257	BOK	BCL2-related ovarian killer	BE614255
205728_at	0.75449	3.826981	5.840316	2.06E-08	8.27E-08	8.305891			AL022718
219884_at	0.75448	6.432233	9.409495	1.16E-17	1.61E-16	29.2635	LHX6	UM homeobox 6	NM_014368
209765_at	0.75431	7.139943	8.659722	1.53E-15	1.71E-14	24.44148	ADAM19	ADAM metalloproteinase domain 19 (meltrin beta)	Y13786
226534_at	0.75409	9.809489	6.638622	2.87E-10	1.61E-09	12.48313	KITLG	KIT ligand	AI446414
224559_at	0.75397	7.250361	7.34413	5.03E-12	3.67E-11	16.4553	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AF001540
213480_at	0.75378	8.099301	11.52586	6.16E-24	1.57E-22	43.5873	VAMP4	vesicle-associated membrane protein 4	AF052100
226393_at	0.75363	6.967652	12.39934	1.31E-26	4.17E-25	49.69304	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	AW055161
226657_at	0.75351	6.650983	9.710636	1.57E-18	2.37E-17	31.24473	MGC3389	transcript expressed during hematopoiesis 2	H27948
224916_at	0.75345	7.027554	7.888348	1.91E-13	1.68E-12	19.6759	TMEM173	transmembrane protein 173	BG110811
1559266_s_at	0.75342	3.854186	9.343291	1.80E-17	2.44E-16	28.83114	C10orf140	chromosome 10 open reading frame 140	AI363206
1564308_a_at	0.75339	6.082583	6.938743	5.29E-11	3.34E-10	14.14297	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	AK057360
1568900_a_at	0.75266	3.819097	13.13045	7.31E-29	2.77E-27	54.84837	ZNF568	zinc finger protein 568	BC031218
209741_x_at	0.75259	7.084339	8.871398	3.91E-16	4.66E-15	25.78549	SCAPER	S phase cyclin A-associated protein in the ER	AF119814
212641_at	0.75248	6.43541	9.717932	1.50E-18	2.26E-17	31.29302	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	AL023584
235767_x_at	0.75246	7.566983	8.947219	2.40E-16	2.91E-15	26.27037			AI338514
219174_at	0.75245	6.342267	7.547145	1.51E-12	1.18E-11	17.6418	IFT74	intraflagellar transport 74 homolog (<i>Chlamydomonas</i>)	NM_025103
203883_s_at	0.75216	8.038161	6.872251	7.72E-11	4.75E-10	13.77129	RAB11FIP2	RAB11 family interacting protein 2 (class I)	BG249608
209034_at	0.75186	10.23475	11.84886	6.39E-25	1.78E-23	45.8363	PNRC1	proline-rich nuclear receptor coactivator 1	AF279899
201313_at	0.75173	6.703883	5.590227	7.31E-08	2.63E-07	7.074435	ENO2	enolase 2 (gamma, neuronal)	NM_001975

213044_at	0.75169	10.22452	10.73681	1.48E-21	3.02E-20	38.15055	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	N22548
243999_at	0.75168	6.528562	6.375699	1.22E-09	6.14E-09	11.06782	SLFN5	schlafen family member 5	AW962850
213352_at	0.75146	6.597178	6.875578	7.58E-11	4.67E-10	13.78983	TMCC1	transmembrane and coiled-coil domain family 1	AB018322
207277_at	0.75141	6.848379	7.080946	2.34E-11	1.56E-10	14.94517	CD209	CD209 molecule	AF290886
233868_x_at	0.75141	7.841378	9.498627	6.44E-18	9.20E-17	29.84747	ADAM33	ADAM metalloproteinase domain 33	AL117415
218232_at	0.75084	9.190427	5.153665	6.07E-07	1.83E-06	5.02064	C1QA	complement component 1, q subcomponent, A chain	NM_015991
230630_at	0.75053	7.03027	5.277781	3.37E-07	1.07E-06	5.591768	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	AI566130
206283_s_at	0.75045	5.198171	8.563236	2.82E-15	3.06E-14	23.83373	TAL1	T-cell acute lymphocytic leukemia 1	NM_003189
205009_at	0.75026	6.107	11.16749	7.50E-23	1.73E-21	41.1069	ITGA9	integrin, alpha 9	NM_002207
224719_s_at	0.75022	10.56852	8.772284	7.41E-16	8.56E-15	25.15438	C12orf57	chromosome 12 open reading frame 57	BG339653
228795_at	0.75008	5.806617	9.354546	1.67E-17	2.27E-16	28.90456	PRKCB	protein kinase C, beta	AI523569
1554807_a_at	0.75006	6.118444	6.252143	2.37E-09	1.14E-08	10.41579	SPIRE1	spire homolog 1 (Drosophila)	BC016825
221725_at	0.74987	8.747221	12.82246	6.53E-28	2.30E-26	52.67302			AI962978
213258_at	0.74952	9.419715	4.48824	1.21E-05	2.81E-05	2.141529	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	BF511231
212818_s_at	0.74931	6.989974	14.00297	1.46E-31	7.03E-30	61.02701	ASB1	ankyrin repeat and SOCS box-containing 1	AF055024
203627_at	0.74898	7.210587	5.812461	2.38E-08	9.42E-08	8.166822	IGF1R	insulin-like growth factor 1 receptor	AI830698
231869_at	0.74889	4.974703	8.420649	6.97E-15	7.21E-14	22.94143	KIAA1586	KIAA1586	BF339845
223940_x_at	0.74886	10.8368	6.380855	1.19E-09	5.98E-09	11.09521	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AF132202
230791_at	0.74882	5.124517	5.952976	1.15E-08	4.86E-08	8.873145			AU146924
231798_at	0.74881	4.160948	9.401504	1.23E-17	1.69E-16	29.21126	NOG	noggin	AL575177
222431_at	0.74861	10.01936	10.70076	1.89E-21	3.83E-20	37.9045	SPIN1	spindlin 1	AL136719
235647_at	0.74846	6.737157	12.35047	1.86E-26	5.80E-25	49.3496	AP4S1	CDNA FLJ50952 complete cds, highly similar to Adapter-related protein complex 4 sigma-1 subunit	AI298279
226955_at	0.74845	5.716269	6.856674	8.44E-11	5.16E-10	13.68454	AFAP1L1	actin filament associated protein 1-like 1	H28999
228243_at	0.74838	6.441246	9.463961	8.11E-18	1.14E-16	29.6201			AI949772
217858_s_at	0.74827	9.639527	6.538286	5.01E-10	2.70E-09	11.93864	ARMCX3	armadillo repeat containing, X-linked 3	NM_016607
236401_at	0.74817	5.07696	10.49298	7.88E-21	1.51E-19	36.49055			AA514370
227610_at	0.74762	6.546423	9.141594	6.76E-17	8.66E-16	27.52139	TSPAN11	tetraspanin 11	BE858239
222844_s_at	0.74761	4.957782	9.577337	3.82E-18	5.57E-17	30.36488	SRR	serine racemase	AF169974
212580_at	0.7474	4.374091	11.16927	7.41E-23	1.71E-21	41.11916	ERAP1	KIAA0525 protein	BG111635
224952_at	0.74739	6.299785	6.110719	5.04E-09	2.28E-08	9.68007	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	BF115054
224804_s_at	0.74738	7.810998	14.37392	1.03E-32	5.49E-31	63.65625	C15orf17	chromosome 15 open reading frame 17	AU152410
218674_at	0.74717	6.456395	7.314282	5.99E-12	4.33E-11	16.28242	C5orf44	chromosome 5 open reading frame 44	NM_024941
212350_at	0.74672	8.713392	10.36585	1.88E-20	3.45E-19	35.62939	TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	AB029031
228278_at	0.74652	7.231217	12.45409	8.91E-27	2.86E-25	50.07798	NFIX	nuclear factor I/X (CCAAT-binding transcription factor)	AI817698
208296_x_at	0.74646	8.8723	6.736316	1.66E-10	9.71E-10	13.01837	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	NM_014350
214600_at	0.74645	6.486631	8.561312	2.86E-15	3.09E-14	23.82164	TEAD1	TEA domain family member 1 (SV40 transcriptional enhancer factor)	AW771935
201324_at	0.74639	10.41356	4.933294	1.69E-06	4.65E-06	4.032451	EMP1	epithelial membrane protein 1	NM_001423
210471_s_at	0.74627	5.221148	8.39549	8.16E-15	8.39E-14	22.78473	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	U33428
236977_at	0.74617	4.848268	8.478181	4.84E-15	5.11E-14	23.30061	LOC64658	hypothetical protein LOC646588	AW026465

223374_s_at	0.74585	6.383039	4.837453	2.61E-06	6.91E-06	3.613227	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	AF154848
203173_s_at	0.74569	8.17298	8.027493	8.11E-14	7.48E-13	20.51909	C16orf62	chromosome 16 open reading frame 62	AW080196
233233_at	0.74569	5.402545	8.664274	1.48E-15	1.66E-14	24.47022			BE540060
202017_at	0.74564	8.526772	6.775847	1.33E-10	7.90E-10	13.23636	EPHX1	epoxide hydrolase 1, microsomal (xenobiotic)	NM_000120
203855_at	0.74561	7.706791	9.314867	2.17E-17	2.92E-16	28.64587	WDR47	WD repeat domain 47	NM_014969
202957_at	0.74556	8.389325	5.285594	3.24E-07	1.03E-06	5.628061	HCLS1	hematopoietic cell-specific Lyn substrate 1	NM_005335
225130_at	0.74554	5.952885	11.18124	6.81E-23	1.57E-21	41.20173	ZRANB1	zinc finger, RAN-binding domain containing 1	AW003734
222558_at	0.74528	6.644814	6.729951	1.72E-10	1.00E-09	12.98335	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	T79568
228968_at	0.74515	6.715563	10.23394	4.61E-20	8.16E-19	34.73925	ZNF449	zinc finger protein 449	AI888786
223618_at	0.74505	4.139712	5.774411	2.89E-08	1.13E-07	7.977615	FMN2	formin 2	AF225426
209842_at	0.74485	5.169691	9.225729	3.90E-17	5.12E-16	28.06634	SOX10	SRY (sex determining region Y)-box 10	AI367319
222421_at	0.74477	9.162346	9.120102	7.78E-17	9.93E-16	27.38251	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	BF435617
224616_at	0.7446	11.17209	12.337	2.04E-26	6.36E-25	49.25496	DYNC1U2	dynein, cytoplasmic 1, light intermediate chain 2	BG110975
227911_at	0.74456	5.294992	6.458206	7.78E-10	4.05E-09	11.50793	ARHGAP28	Rho GTPase activating protein 28	AI935647
242638_at	0.74436	4.205291	8.325878	1.27E-14	1.27E-13	22.35231			AA045088
1557374_at	0.74428	4.094196	11.50386	7.18E-24	1.82E-22	43.43456	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	AK056519
221234_s_at	0.74366	4.866336	6.150784	4.08E-09	1.88E-08	9.887335	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	NM_021813
211729_x_at	0.74354	9.361952	7.799421	3.28E-13	2.80E-12	19.1411	BLVRA	biliverdin reductase A	BC005902
228057_at	0.74308	4.926931	10.38921	1.60E-20	2.96E-19	35.78737	DDIT4L	DNA-damage-inducible transcript 4-like	AA528140
227480_at	0.74294	6.506976	7.399506	3.62E-12	2.70E-11	16.77711	SUSD2	sushi domain containing 2	Z92546
228172_at	0.74293	6.26845	12.22598	4.47E-26	1.36E-24	48.4756			BE549909
230424_at	0.74268	5.584719	9.116954	7.94E-17	1.01E-15	27.36218	CSorf13	chromosome 5 open reading frame 13	AU144860
223989_s_at	0.74262	7.853337	9.194264	4.79E-17	6.23E-16	27.8623	REXO2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	BC003502
212530_at	0.74256	10.21803	10.08135	1.30E-19	2.20E-18	33.71399	NEK7	NIMA (never in mitosis gene a)-related kinase 7	AL080111
213327_s_at	0.74233	7.575927	9.117988	7.89E-17	1.01E-15	27.36886	USP12	ubiquitin specific peptidase 12	AI820101
1553603_s_at	0.74229	5.955511	6.227121	2.72E-09	1.29E-08	10.28479	ATL2	atlastin GTPase 2	NM_022374
201537_s_at	0.74219	8.088418	7.718946	5.35E-13	4.44E-12	18.65991	DUSP3	dual specificity phosphatase 3	BC002682
203063_at	0.74211	7.498242	14.31718	1.55E-32	8.08E-31	63.25412	PPM1F	protein phosphatase 1F (PP2C domain containing)	NM_014634
202815_s_at	0.74123	7.540188	11.01571	2.15E-22	4.75E-21	40.06173	HEXIM1	hexamethylene bis-acetamide inducible 1	NM_006460
239329_at	0.74105	6.547606	9.614912	2.97E-18	4.38E-17	30.61245			AI308862
219497_s_at	0.74099	6.573772	3.976771	9.74E-05	0.0001924	0.151004	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	NM_022893
243115_at	0.73993	4.439771	10.99609	2.46E-22	5.40E-21	39.92691			AI633618
205421_at	0.73963	4.705674	4.70355	4.74E-06	1.19E-05	3.038454	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3	NM_021977
202974_at	0.7395	7.691898	6.968045	4.47E-11	2.86E-10	14.30746	MPP1	membrane protein, palmitoylated 1, 55kDa	NM_002436
219343_at	0.73941	7.36998	8.342432	1.14E-14	1.15E-13	22.45499	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	NM_017913
227095_at	0.7393	8.874024	8.226271	2.36E-14	2.31E-13	21.73664			AU151151
202990_at	0.73893	6.938515	5.607416	6.71E-08	2.43E-07	7.157823	PYGL	phosphorylase, glycogen, liver	NM_002863
227346_at	0.73884	6.89276	4.692599	4.97E-06	1.25E-05	2.992015	IKZF1	IKAROS family zinc finger 1 (Ikaros)	AI741188
209826_at	0.73867	6.336845	10.66315	2.45E-21	4.92E-20	37.64794	PPT2	palmitoyl-protein thioesterase 2	AF020544
213508_at	0.73855	8.738984	7.590589	1.16E-12	9.21E-12	17.89806	C14orf147	chromosome 14 open reading frame 147	AA142942
211547_s_at	0.73852	6.663817	6.762153	1.44E-10	8.48E-10	13.16075	PAFAH1B1	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit 45kDa	L13387
228734_at	0.73843	5.280846	8.260872	1.90E-14	1.88E-13	21.9501			BF447286

								KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// RP11-	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// hypothetical protein LOC200030	
227926_s_at	0.73827	7.584642	6.348839	1.41E-09	7.02E-09	10.92535	9412.2			AI498207
214376_at	0.73824	4.26398	12.51838	5.65E-27	1.84E-25	50.5302				AI263044
207785_s_at	0.73818	9.045004	8.569247	2.72E-15	2.95E-14	23.8715	RBPJ	recombination signal binding protein for immunoglobulin kappa J region		NM_015874
219939_s_at	0.7379	11.09235	13.72833	1.03E-30	4.61E-29	59.08064	CSDE1	cold shock domain containing E1, RNA-binding		NM_007158
212635_at	0.73771	8.751195	9.968466	2.78E-19	4.56E-18	32.95876	TNPO1	transportin 1		AW161626
225330_at	0.73766	8.254483	5.761357	3.09E-08	1.20E-07	7.91291	IGF1R	insulin-like growth factor 1 receptor		AL044092
238204_at	0.73719	4.271821	8.952329	2.32E-16	2.82E-15	26.30312				AI242160
237006_at	0.73706	4.118268	10.17338	6.96E-20	1.21E-18	34.33175				AA703523
220199_s_at	0.73705	9.012616	7.88914	1.90E-13	1.67E-12	19.68068	AIDA	axin interactor, dorsalization associated		NM_022831
206142_at	0.73704	3.941963	14.71035	9.40E-34	5.60E-32	66.03972	ZNF135	zinc finger protein 135		NM_003436
222559_s_at	0.73696	7.966901	6.453717	7.97E-10	4.14E-09	11.48389	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A		T79568
203894_at	0.73671	5.356416	12.39742	1.33E-26	4.22E-25	49.6795	TUBG2	tubulin, gamma 2		NM_016437
238430_x_at	0.7366	9.202503	7.6492	8.16E-13	6.59E-12	18.24508	SLFN5	schlafen family member 5		AI923675
201823_s_at	0.73653	7.759062	6.974404	4.31E-11	2.76E-10	14.34322	RNF14	ring finger protein 14		NM_004290
238165_at	0.73644	5.233545	9.36418	1.57E-17	2.14E-16	28.96743	LOC10012 9282	PREDICTED: Homo sapiens hypothetical protein LOC100129282 (LOC100129282), mRNA		AW665629
225949_at	0.73642	7.20353	10.78694	1.05E-21	2.17E-20	38.49312	NRBP2	nuclear receptor binding protein 2		N21030
1556190_s_at	0.73639	4.103729	6.469977	7.29E-10	3.81E-09	11.57102	PRNP	prion protein		AK056897
241763_s_at	0.73633	5.43364	8.078284	5.93E-14	5.54E-13	20.82876	FBXO32	F-box protein 32 (FBXO32), transcript variant 2, mRNA		BF244402
226778_at	0.73623	5.006643	8.403321	7.77E-15	8.00E-14	22.83348	C8orf42	chromosome 8 open reading frame 42		AI632224
207547_s_at	0.73609	6.883622	8.806408	5.95E-16	6.94E-15	25.37131	FAM107A	family with sequence similarity 107, member A		NM_007177
1554479_a_at	0.73597	7.660299	7.645793	8.32E-13	6.72E-12	18.22487	CARD8	caspase recruitment domain family, member 8		AF511652
212796_s_at	0.7358	8.560414	11.23531	4.68E-23	1.10E-21	41.57496	TBC1D28	TBC1 domain family, member 28		BF195608
219387_at	0.73448	6.131044	6.726985	1.75E-10	1.02E-09	12.96703	CCDC88A	coiled-coil domain containing 88A		NM_017571
235893_at	0.73422	5.165924	10.40419	1.45E-20	2.69E-19	35.88876				BE646451
228811_at	0.73391	5.791902	11.1505	8.44E-23	1.93E-21	40.98974				AI493276
219279_at	0.7338	6.219003	5.871911	1.75E-08	7.12E-08	8.464203	DOCK10	dedicator of cytokinesis 10		NM_017718
227531_at	0.73373	8.424573	7.918271	1.59E-13	1.41E-12	19.85658				AI816849
1559633_a_at	0.73366	5.060431	4.572636	8.40E-06	2.02E-05	2.489042	CHRM3	cholinergic receptor, muscarinic 3		AK056349
232068_s_at	0.73356	4.580352	6.438674	8.65E-10	4.47E-09	11.40341	TLR4	toll-like receptor 4		AF177755
212672_at	0.73281	7.382366	10.0378	1.74E-19	2.92E-18	33.42231	ATM	ataxia telangiectasia mutated		U82828
227708_at	0.73267	9.060598	7.143207	1.63E-11	1.11E-10	15.29948	EEF1A1	eukaryotic translation elongation factor 1 alpha 1		AW469790
234299_s_at	0.73244	5.083759	9.636965	2.57E-18	3.81E-17	30.75792	NIN	ninein (GSK3B interacting protein)		AK027054
201194_at	0.7323	11.45072	10.46344	9.65E-21	1.83E-19	36.29019	SEPW1	selenoprotein W, 1		NM_003009
201163_s_at	0.7323	12.25121	10.37301	1.79E-20	3.30E-19	35.67783	IGFBP7	Insulin-like growth factor binding protein 7		NM_001553

214436_at	0.73219	6.344241	8.185969	3.04E-14	2.93E-13	21.48858	FBXL2	F-box and leucine-rich repeat protein 2	AF176518
227426_at	0.73216	8.793281	11.79265	9.48E-25	2.60E-23	45.44413	SOS1	son of sevenless homolog 1 (Drosophila)	AV702692
219568_x_at	0.73216	5.070769	7.113917	1.93E-11	1.30E-10	15.13257	SOX18	SRY (sex determining region Y)-box 18	NM_018419
235086_at	0.73209	6.232804	4.502862	1.13E-05	2.66E-05	2.201358	THBS1	(clone lambda-TS-33) thrombospondin (THBS) mRNA, 5' end	AW956580
211022_s_at	0.73188	5.465217	8.909691	3.06E-16	3.68E-15	26.03016	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	BC002521
227351_at	0.73169	7.133305	9.972218	2.71E-19	4.45E-18	32.98381	C16orf52	chromosome 16 open reading frame 52	H06491
205006_s_at	0.7315	7.081443	7.354134	4.74E-12	3.48E-11	16.51333	NMT2	N-myristoyltransferase 2	NM_004808
209901_x_at	0.73106	9.17656	6.517671	5.61E-10	3.00E-09	11.82743	AIF1	allograft inflammatory factor 1	U19713
235513_at	0.73082	4.932133	10.41374	1.35E-20	2.53E-19	35.95341			AW131450
202438_x_at	0.73051	5.169749	8.3198	1.31E-14	1.32E-13	22.31464	IDS	iduronate 2-sulfatase	BF346014
228988_at	0.73045	5.411407	4.670927	5.47E-06	1.36E-05	2.900372	ZNF711	zinc finger protein 711	AU157017
225885_at	0.73041	9.172005	8.293982	1.55E-14	1.54E-13	22.15477	EEA1	early endosome antigen 1	AI336848
228096_at	0.7304	6.311403	10.40038	1.48E-20	2.76E-19	35.86302	C1orf151	chromosome 1 open reading frame 151	R44979
213715_s_at	0.73036	6.359202	9.855454	5.95E-19	9.39E-18	32.20554	KANK3	KN motif and ankyrin repeat domains 3	AF070591
235567_at	0.73011	5.247624	10.36716	1.86E-20	3.42E-19	35.63824	RORA	Hypothetical protein LOC283666, mRNA (cDNA clone IMAGE:4750925)	AA034012
235658_at	0.72965	4.580739	14.58042	2.37E-33	1.35E-31	65.11941			AW058580
232095_at	0.72963	7.015672	7.892708	1.86E-13	1.64E-12	19.70221			BG109134
226348_at	0.7296	7.44568	9.579538	3.76E-18	5.49E-17	30.37937			AK026764
220027_s_at	0.72949	7.161087	8.961552	2.18E-16	2.67E-15	26.36223	RASIP1	Ras interacting protein 1	NM_017805
232412_at	0.72948	5.601127	5.889556	1.60E-08	6.56E-08	8.552876			AK024690
212905_at	0.72947	7.727991	7.555807	1.43E-12	1.12E-11	17.69283	CSTF2T	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	AI872408
223118_s_at	0.72947	7.245431	9.620087	2.87E-18	4.24E-17	30.64657	USP47	ubiquitin specific peptidase 47	AI123715
1555363_s_at	0.72937	4.878092	8.18718	3.01E-14	2.91E-13	21.49602			BC034236
229393_at	0.7293	6.117392	8.532973	3.42E-15	3.67E-14	23.64376	L3MBTL3	l(3)mbt-like 3 (Drosophila)	AA088346
232008_s_at	0.72884	8.552043	10.39423	1.55E-20	2.87E-19	35.8214	BBX	bobby sox homolog (Drosophila)	AF283775
225923_at	0.72881	7.67987	7.802682	3.22E-13	2.75E-12	19.16065			AW291083
211502_s_at	0.72881	5.835414	7.467123	2.43E-12	1.85E-11	17.17193	PFTK1	PFTAIKE protein kinase 1	AF119833
229073_at	0.72881	4.137044	11.26583	3.78E-23	8.95E-22	41.78583	LOC14578	CDNA FU13221 fis, clone NT2RP4002075	AA912476
203526_s_at	0.72865	5.440712	10.89189	5.07E-22	1.08E-20	39.2117	APC	adenomatous polyposis coli	M74088
208754_s_at	0.72843	9.244128	6.983019	4.10E-11	2.64E-10	14.39169	NAP1L1	nucleosome assembly protein 1-like 1	AL162068
206545_at	0.72839	4.85206	6.543212	4.87E-10	2.63E-09	11.96524	CD28	CD28 molecule	NM_006139
235801_at	0.72817	4.164396	6.858913	8.33E-11	5.10E-10	13.697			AI760262
210794_s_at	0.72794	6.270924	8.865247	4.07E-16	4.84E-15	25.74623	MEG3	maternally expressed 3 (non-protein coding)	AF119863
227428_at	0.72757	6.361805	8.839911	4.80E-16	5.65E-15	25.58466	GABPA	GA binding protein transcription factor, alpha subunit 60kDa	BE876628
223269_at	0.72752	8.760735	8.454083	5.64E-15	5.91E-14	23.15002	POLR3GL	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	BC004355
225800_at	0.7275	6.64046	7.057504	2.67E-11	1.77E-10	14.81226	JAZF1	JAZF zinc finger 1	AI990891
230298_at	0.72736	7.086958	9.786666	9.44E-19	1.46E-17	31.74854	LOC15336	similar to metallo-beta-lactamase superfamily protein	AI692906
238091_at	0.72736	4.555045	10.86494	6.10E-22	1.29E-20	39.02699			AW026243
204347_at	0.72733	7.429697	4.937897	1.65E-06	4.56E-06	4.052747	AK3L1 ///	adenylate kinase 3-like 1 ///	AI653169
224843_at	0.72731	6.097223	10.67702	2.23E-21	4.49E-20	37.74256	AK3L2	adenylate kinase 3-like 2	AB040891
225180_at	0.72728	8.281213	6.407047	1.03E-09	5.24E-09	11.23459	SLAIN2	SLAIN motif family, member 2	AL040341
200878_at	0.72722	11.07371	7.977545	1.10E-13	1.00E-12	20.21554	TTC14	tetratricopeptide repeat domain 14	AF052094
213221_s_at	0.72718	6.988775	7.997236	9.78E-14	8.93E-13	20.33509	EPAS1	endothelial PAS domain protein 1	AF052094
213934_s_at	0.72661	5.929801	9.603051	3.22E-18	4.72E-17	30.53426	SIK2	salt-inducible kinase 2	AB018324
225504_at	0.72632	7.469258	12.36731	1.65E-26	5.19E-25	49.4679	ZNF23	zinc finger protein 23 (KOX 16)	AL567808
1554574_a at	0.72623	8.610975	9.901244	4.38E-19	7.02E-18	32.51037			AW294031
							CYB5R3	cytochrome b5 reductase 3	AF361370

204682_at	0.72615	8.503055	6.036474	7.45E-09	3.26E-08	9.298453	LTBP2	latent transforming growth factor beta binding protein 2	NM_000428
218692_at	0.72613	8.069867	4.716991	4.47E-06	1.13E-05	3.095567	GOLSYN	Golgi-localized protein	NM_017786
238932_at	0.72606	4.671486	9.883359	4.94E-19	7.86E-18	32.39125			AA810263
1558445_at	0.72601	5.227314	8.53306	3.42E-15	3.67E-14	23.6443			AW827204
223712_at	0.72586	6.429453	9.90267	4.33E-19	6.96E-18	32.51988	PCBD2	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	AL136721
209647_s_at	0.72563	8.134239	7.14015	1.66E-11	1.13E-10	15.28204	SOCS5	suppressor of cytokine signaling 5	AW664421
220095_at	0.72509	4.594007	13.88626	3.35E-31	1.56E-29	60.19977	CNTLN	centlein, centrosomal protein	NM_017738
211339_s_at	0.7249	6.22782	4.360214	2.07E-05	4.62E-05	1.624505	ITK	IL2-inducible T-cell kinase	D13720
238723_at	0.72487	5.265006	10.49402	7.83E-21	1.50E-19	36.4976	ATXN3	ataxin 3	AW083849
224897_at	0.7247	8.242409	9.342609	1.81E-17	2.45E-16	28.82669	WDR26	WD repeat domain 26	BF510490
215233_at	0.72459	5.086874	11.00981	2.24E-22	4.94E-21	40.02115	JMJD6	jumonji domain containing 6	AA351360
220637_at	0.72446	5.0642	11.70335	1.77E-24	4.75E-23	44.8217	FAM124B	family with sequence similarity 124B	NM_024785
211930_at	0.72442	8.180837	12.05427	1.50E-25	4.39E-24	47.27225	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	AW080932
202305_s_at	0.7244	8.940607	10.06633	1.44E-19	2.43E-18	33.61335	FEZ2	fasciculation and elongation protein zeta 2 (zyglin II)	AI685892
206554_x_at	0.72427	6.46834	8.43465	6.38E-15	6.63E-14	23.02873	SETMAR	SET domain and mariner transposase fusion gene	NM_006515
214823_at	0.72375	5.539221	6.132898	4.48E-09	2.05E-08	9.794692	ZNF204	zinc finger protein 204 pseudogene	AF033199
203048_s_at	0.72368	8.127815	8.281034	1.68E-14	1.66E-13	22.07469	TTC37	tetratricopeptide repeat domain 37	BE566023
227824_at	0.72364	4.474114	8.993478	1.78E-16	2.19E-15	26.56707	PRKCB	protein kinase C, beta	H14703
236045_x_at	0.72357	6.488662	5.898833	1.53E-08	6.28E-08	8.599574			AW451197
206667_s_at	0.72301	6.34952	5.043995	1.01E-06	2.92E-06	4.524674	SCAMP1	secretory carrier membrane protein 1	AF005037
228315_at	0.72298	9.042493	7.873611	2.09E-13	1.83E-12	19.58706			AI632728
225477_s_at	0.72289	8.37672	9.572499	3.95E-18	5.74E-17	30.33303	NR2C2	nuclear receptor subfamily 2, group C, member 2	AL138444
201466_s_at	0.7228	9.235889	5.759407	3.12E-08	1.21E-07	7.903253	JUN	jun oncogene	NM_002228
229905_at	0.72279	7.061971	7.723017	5.22E-13	4.34E-12	18.68419	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	N92500
232752_at	0.72241	5.496004	5.029463	1.09E-06	3.10E-06	4.459577			AK001164
201235_s_at	0.7222	8.106882	6.982943	4.11E-11	2.64E-10	14.39125	BTG2	BTG family, member 2	BG339064
202136_at	0.72214	10.74212	11.62247	3.13E-24	8.24E-23	44.25876	ZMYND11	zinc finger, MYND domain containing 11	BE250417
205945_at	0.72213	6.375257	5.144196	6.35E-07	1.90E-06	4.977493	IL6R	interleukin 6 receptor	NM_000565
229342_at	0.72189	6.686706	8.696834	1.20E-15	1.36E-14	24.67606			AI708256
240383_at	0.72187	5.406035	6.346221	1.43E-09	7.12E-09	10.91149	UBE2D3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	AI239832
227489_at	0.72182	7.873091	11.42085	1.28E-23	3.17E-22	42.85872	SMURF2	CDNA clone IMAGE:4825278	BE962027
222700_at	0.72169	9.718904	7.150582	1.56E-11	1.07E-10	15.34157	ATL2	atlastin GTPase 2	AV700003
224940_s_at	0.72151	6.765262	4.944031	1.61E-06	4.44E-06	4.079819	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	BF107618
228239_at	0.72145	6.059111	7.891045	1.88E-13	1.65E-12	19.69218	FAM165B	family with sequence similarity 165, member B	AA148789
225926_at	0.72143	7.592079	8.411301	7.39E-15	7.62E-14	22.88318	VTI1B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	AI307763
208753_s_at	0.72126	9.406168	7.692992	6.26E-13	5.14E-12	18.50531	NAP1L1	nucleosome assembly protein 1-like 1	BC002387
201030_x_at	0.72116	11.359	5.296428	3.08E-07	9.82E-07	5.67846	LDHB	lactate dehydrogenase B	NM_002300
228821_at	0.7211	3.653777	6.595742	3.65E-10	2.01E-09	12.24978	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	AW004016
225200_at	0.7211	8.626478	6.727935	1.74E-10	1.01E-09	12.97226	DPH3	DPH3, KTI11 homolog (S. cerevisiae)	AU151106
1552329_at	0.72095	6.350405	6.936525	5.36E-11	3.38E-10	14.13054	RBBP6	retinoblastoma binding protein 6	BC029352
227536_at	0.72083	8.222104	10.18115	6.60E-20	1.15E-18	34.384	ZC3H13	zinc finger CCH-type containing 13	AI472196
219221_at	0.72081	9.251689	8.620187	1.96E-15	2.17E-14	24.19207	ZBTB38	zinc finger and BTB domain containing 38	NM_024724
204456_s_at	0.72069	4.98799	7.139482	1.66E-11	1.13E-10	15.27823	GAS1	growth arrest-specific 1	AW611727
218437_s_at	0.72046	7.615695	7.584515	1.20E-12	9.52E-12	17.86219	LZTFL1	leucine zipper transcription factor-like 1	NM_020347
227009_at	0.72026	6.22261	12.45726	8.71E-27	2.80E-25	50.10023			AK025253

206796_at	0.72019	5.982917	6.058152	6.65E-09	2.94E-08	9.409546	WISP1	WNT1 inducible signaling pathway protein 1	NM_003882
243813_at	0.72012	3.91217	7.556442	1.42E-12	1.12E-11	17.69657			AA418028
224720_at	0.71973	8.691481	7.001856	3.68E-11	2.39E-10	14.49779	MIB1	mindbomb homolog 1 (Drosophila)	AW243097
205862_at	0.71963	3.853784	7.063759	2.58E-11	1.71E-10	14.8477	GREB1	GREB1 protein	NM_014668
216399_s_at	0.71922	6.353663	8.582625	2.49E-15	2.73E-14	23.9556	SCAPER	S phase cyclin A-associated protein in the ER	AK025663
230163_at	0.71895	5.340274	9.01125	1.58E-16	1.96E-15	26.68123	LOC143381	CDNA FLJ31546 fis, clone NT2RI2000974	AW263087
222760_at	0.71871	8.972527	6.081727	5.88E-09	2.62E-08	9.530669	ZNF703	zinc finger protein 703	BG290193
223315_at	0.7187	8.033858	4.433418	1.52E-05	3.48E-05	1.918627	NTN4	netrin 4	AF278532
238823_at	0.71869	4.889131	11.43487	1.16E-23	2.89E-22	42.95593	FMNL3	formin-like 3	AA481044
214808_at	0.71847	6.970082	9.409295	1.16E-17	1.61E-16	29.2622			AU147851
225460_at	0.71844	8.91599	10.56787	4.72E-21	9.24E-20	36.99925	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	BG432489
229435_at	0.71826	6.2217	4.403794	1.73E-05	3.91E-05	1.799116	GLIS3	GLIS family zinc finger 3	AW025602
202351_at	0.71819	11.0859	8.26794	1.82E-14	1.80E-13	21.99376	ITGAV	Integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	AI093579
209760_at	0.71811	7.15303	8.065157	6.43E-14	5.99E-13	20.74863	KIAA0922		AL136932
1559883_s_at	0.71802	5.783362	4.790384	3.22E-06	8.39E-06	3.409724	SAMHD1	SAM domain and HD domain 1	AF147427
201858_s_at	0.71801	10.42897	4.679199	5.28E-06	1.32E-05	2.935311	SRGN	serglycin	J03223
221763_at	0.71753	9.071612	9.42866	1.02E-17	1.43E-16	29.38889	JMJD1C	jumonji domain containing 1C	AI694023
235635_at	0.71736	6.180421	5.641922	5.64E-08	2.08E-07	7.325792	ARHGAP5	Rho GTPase activating protein 5	N50119
210284_s_at	0.71732	8.226417	8.068857	6.28E-14	5.86E-13	20.77121	MAP3K7IP2	mitogen-activated protein kinase kinase 7 interacting protein 2	AF241230
226049_at	0.71728	7.522044	14.43583	6.65E-33	3.59E-31	64.09492	ERC1	ELKS/RAB6-interacting/CAST family member 1	AI271420
229912_at	0.71723	5.186878	5.550302	8.91E-08	3.15E-07	6.881466	SDK1	slk1c homolog 1, cell adhesion molecule (chicken)	AL042166
203590_at	0.71677	10.01854	11.4705	9.07E-24	2.28E-22	43.20303	DYNC1L2	dynein, cytoplasmic 1, light intermediate chain 2	NM_006141
209075_s_at	0.7166	11.21754	14.02002	1.29E-31	6.24E-30	61.14788	ISCU	iron-sulfur cluster scaffold homolog (E. coli)	AY009128
204489_s_at	0.7165	9.478813	5.8055	2.47E-08	9.74E-08	8.132139	CD44	CD44 molecule (Indian blood group)	NM_000610
242607_at	0.71647	4.422509	9.479342	7.32E-18	1.04E-16	29.72094			AW975512
241689_at	0.71627	5.483544	10.48111	8.55E-21	1.63E-19	36.41004			AA866199
228927_at	0.71627	7.119942	8.427962	6.65E-15	6.90E-14	22.98702	ZNF397	zinc finger protein 397	AW291411
1560741_at	0.71618	5.25022	9.733041	1.35E-18	2.05E-17	31.39305	SNRPN	small nuclear ribonucleoprotein polypeptide N	AL832250
1558795_at	0.71584	3.550651	8.713604	1.08E-15	1.23E-14	24.78222	LOC728052	similar to hCG2031213	AL833240
231234_at	0.71581	6.488235	9.530755	5.21E-18	7.49E-17	30.05848	CTSC	cathepsin C	AV699565
231781_s_at	0.71571	4.570411	9.538146	4.96E-18	7.15E-17	30.10705	LRRC2	leucine rich repeat containing 2	AK021919
205696_s_at	0.71548	4.109989	9.439701	9.52E-18	1.33E-16	29.46117	GFRA1	GDNF family receptor alpha 1	NM_005264
204271_s_at	0.71536	7.913795	5.390806	1.95E-07	6.46E-07	6.120775	EDNRB	endothelin receptor type B	M74921
1556657_at	0.71495	4.579286	9.096185	9.10E-17	1.15E-15	27.22813			AA744622
207838_x_at	0.7149	7.110862	10.8933	5.02E-22	1.07E-20	39.22138	PBXIP1	pre-B-cell leukemia homeobox interacting protein 1	NM_020524
228971_at	0.71485	7.356718	9.447076	9.07E-18	1.27E-16	29.50946			AI357655
213411_at	0.71481	3.996039	8.982379	1.91E-15	2.34E-15	26.49582			AW242701
224581_s_at	0.71443	10.11169	9.209067	4.35E-17	5.68E-16	27.95825	NUCKS1	nuclear casein kinase and cyclin-dependent kinase substrate 1	AI707721
212970_at	0.71433	7.191842	9.666213	2.11E-18	3.15E-17	30.95102	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	AI694303
202098_s_at	0.7142	8.26677	10.49069	8.01E-21	1.53E-19	36.47501	PRMT2	protein arginine methyltransferase 2	NM_001535
225658_at	0.7141	8.927849	8.493786	4.39E-15	4.65E-14	23.39823	SPOPL	speckle-type POZ protein-like	BF034206
228831_s_at	0.71404	5.989226	8.422985	6.86E-15	7.11E-14	22.95599	GNG7	guanine nucleotide binding protein (G protein), gamma 7	AL039870
203683_s_at	0.71376	7.312982	9.008725	1.61E-16	1.99E-15	26.66501	VEGFB	vascular endothelial growth factor B	NM_003377

225572_at	0.71371	8.570186	12.01386	2.00E-25	5.78E-24	46.98944	CREB1	cAMP responsive element binding protein 1	AI652633
227086_at	0.71343	6.398478	12.93458	2.95E-28	1.06E-26	53.4644	C22orf39	chromosome 22 open reading frame 39	AA194312
234300_s_at	0.7134	4.758093	10.42029	1.30E-20	2.42E-19	35.99782	ZFP28	zinc finger protein 28 homolog (mouse)	AF226995
226120_at	0.713	7.586935	8.093943	5.38E-14	5.06E-13	20.92444	TTC8	tetratricopeptide repeat domain 8	AW293939
49111_at	0.71281	6.875527	10.46853	9.32E-21	1.77E-19	36.32467			N80935
							LOC28514		
236166_at	0.71267	4.441426	10.89927	4.81E-22	1.03E-20	39.2623	7	hypothetical protein LOC285147	AW195071
225256_at	0.71258	8.179314	7.567478	1.33E-12	1.05E-11	17.76164			AI457965
213564_x_at	0.71242	11.83024	5.434876	1.57E-07	5.32E-07	6.329316	LDHB	lactate dehydrogenase B	BE042354
							KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF3 /// NBPF8 /// NBPF9 /// RP11-	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 15 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 3 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// hypothetical protein LOC200030	
230712_at	0.71239	6.685195	8.102986	5.09E-14	4.79E-13	20.97973	94I2.2		AI634549
221530_s_at	0.71202	8.669295	4.316504	2.48E-05	5.46E-05	1.450815	BHLHE41	basic helix-loop-helix family, member e41	BE857425
224950_at	0.712	8.49767	8.450644	5.76E-15	6.03E-14	23.12855	PTGFRN	prostaglandin F2 receptor negative regulator	BF476250
202173_s_at	0.71198	8.567211	9.007751	1.62E-16	2.00E-15	26.65875	VEZF1	vascular endothelial zinc finger 1	NM_007146
218472_s_at	0.71183	7.783711	9.088349	9.57E-17	1.21E-15	27.17758	PELO	pelota homolog (Drosophila)	NM_015946
204361_s_at	0.71183	7.248852	6.145809	4.19E-09	1.92E-08	9.861545	SKAP2	src kinase associated phosphoprotein 2	AB014486
202808_at	0.71175	9.457264	10.26464	3.74E-20	6.68E-19	34.9461	C10orf26	chromosome 10 open reading frame 26	AK000161
225856_at	0.71174	7.812711	9.208726	4.36E-17	5.69E-16	27.95604			BF512028
242268_at	0.71149	4.079511	7.410512	3.40E-12	2.54E-11	16.84124	CUGBP2	Full length insert cDNA clone ZD81F07	BE157991
209002_s_at	0.71144	8.049567	14.18735	3.91E-32	1.98E-30	62.33393	CALCOCO1	calcium binding and coiled-coil domain 1	BC003177
218298_s_at	0.71135	8.07976	8.577062	2.58E-15	2.82E-14	23.92062	C14orf159	chromosome 14 open reading frame 159	NM_024952
							LOC39094		
213556_at	0.71133	6.257462	8.880586	3.69E-16	4.40E-15	25.84415	0	similar to R28379_1	BE673445
230276_at	0.71124	5.61955	12.17028	6.63E-26	1.99E-24	48.08502	FAM49A	family with sequence similarity 49, member A	AI934342
239024_at	0.71108	7.063321	10.57931	4.36E-21	8.59E-20	37.07705	ZNF148	zinc finger protein 148	AI478771
219416_at	0.71098	6.890763	11.3557	2.02E-23	4.89E-22	42.40748	SCARA3	scavenger receptor class A, member 3	NM_016240
226211_at	0.71094	4.990126	6.418768	9.64E-10	4.94E-09	11.29709	MEG3	maternally expressed 3 (non-protein coding)	AI291123
235067_at	0.71084	7.596098	7.894593	1.84E-13	1.62E-12	19.71359	MKLN1	muskelin 1, intracellular mediator containing kelch motifs	D81987
223227_at	0.71081	7.465325	8.186773	3.02E-14	2.91E-13	21.49353	BBS2	Bardet-Biedl syndrome 2	AF342736
240344_x_at	0.71075	7.012936	9.04447	1.27E-16	1.59E-15	26.89488	LYRM7	Lyrm7 homolog (mouse)	AA424065
1552327_at	0.71073	3.984218	13.91492	2.73E-31	1.28E-29	60.40293	ARMCX4	armadillo repeat containing, X-linked 4	NM_152583
201988_s_at	0.71067	7.987674	9.467102	7.94E-18	1.12E-16	29.64069	CREBL2	cAMP responsive element binding protein-like 2	BF438056
229129_at	0.71047	6.493565	7.318747	5.84E-12	4.23E-11	16.30825			AI948456

1552789_at	0.71044	6.225183	5.876366	1.71E-08	6.98E-08	8.486573	SEC62	SEC62 homolog (S. cerevisiae)	NM_153039
230180_at	0.7104	8.585682	5.759652	3.11E-08	1.21E-07	7.904465			AA521056
218304_s_at	0.7102	7.989928	7.26251	8.12E-12	5.76E-11	15.98352	OSBPL11	oxysterol binding protein-like 11	NM_022776
225138_at	0.7102	8.001437	9.463567	8.13E-18	1.15E-16	29.61752	ZRANB1	zinc finger, RAN-binding domain containing 1	N52625
212741_at	0.71015	9.273355	3.907168	0.0001275	0.0002469	-0.10412	MAOA	monoamine oxidase A	AA923354
235766_x_at	0.71013	8.10378	5.663326	5.07E-08	1.88E-07	7.430355			AA743462
238536_at	0.71	6.175774	7.917577	1.60E-13	1.42E-12	19.85239			AW968465
210605_s_at	0.70963	7.96112	8.354297	1.06E-14	1.07E-13	22.52863	MFGE8	milk fat globule-EGF factor 8 protein	BC003610
238431_at	0.70954	7.413715	8.746277	8.76E-16	1.01E-14	24.9893			W68845
226343_at	0.70954	8.593374	12.16594	6.84E-26	2.05E-24	48.05458			W74486
1556138_a_at	0.70954	5.041404	11.90615	4.27E-25	1.20E-23	46.23642			CA430162
228188_at	0.70948	8.890913	6.912967	6.13E-11	3.83E-10	13.99862	FOSL2	FOS-like antigen 2	AI860150
227256_at	0.70945	6.513961	7.270727	7.74E-12	5.50E-11	16.03088	USP31	ubiquitin specific peptidase 31	BG289456
221310_at	0.7092	4.264541	5.545844	9.11E-08	3.22E-07	6.859982	FGF14	fibroblast growth factor 14	NM_004115
64064_at	0.70901	8.214946	9.086239	9.71E-17	1.23E-15	27.16398	GIMAP5	GTPase, IMAP family member 5	AI435089
218285_s_at	0.70899	9.039452	6.269973	2.16E-09	1.04E-08	10.50935	BDH2	3-hydroxybutyrate dehydrogenase, type 2	NM_020139
239466_at	0.70891	4.94628	11.53849	5.64E-24	1.45E-22	43.67499	LOC344595	hypothetical LOC344595	AA463827
1555240_s_at	0.70868	7.059076	7.168928	1.40E-11	9.62E-11	15.44639	GNG12	guanine nucleotide binding protein (G protein), gamma 12	AF493879
228195_at	0.70854	5.835687	5.263465	3.61E-07	1.14E-06	5.525364	MGC13057	hypothetical protein MGC13057	BE645119
228466_at	0.70784	6.68438	9.63641	2.58E-18	3.82E-17	30.75425			AI150690
224929_at	0.70782	7.713641	8.476787	4.88E-15	5.15E-14	23.29189	TMEM173	transmembrane protein 173	AA100891
238191_at	0.70752	5.667812	6.352075	1.39E-09	6.91E-09	10.94249			AW771908
236577_at	0.7075	4.121425	8.53187	3.44E-15	3.70E-14	23.63684			AI860775
222161_at	0.70743	3.50977	8.934177	2.61E-16	3.16E-15	26.18684	NAALAD2	N-acetylated alpha-linked acidic dipeptidase 2	AJ012370
1553218_a_at	0.70742	7.739207	11.80289	8.82E-25	2.43E-23	45.51555	ZNF512	zinc finger protein 512	NM_032434
210277_at	0.70739	6.308524	9.778588	9.97E-19	1.54E-17	31.69494	AP4S1	adaptor-related protein complex 4, sigma 1 subunit	AF155159
1556069_s_at	0.70739	5.236663	6.009394	8.59E-09	3.71E-08	9.160066	HIF3A	hypoxia inducible factor 3, alpha subunit	AK021881
238472_at	0.70738	6.191037	7.796621	3.34E-13	2.84E-12	19.12431	FBXO9	F-box protein 9	R73399
226268_at	0.70721	6.269613	8.398673	8.00E-15	8.23E-14	22.80454	RAB21	RAB21, member RAS oncogene family, mRNA (cDNA clone MGC:16965 IMAGE:4342334)	AI309554
244406_at	0.70702	5.79565	8.921246	2.84E-16	3.42E-15	26.10407	ZNF20 /// ZNF625	zinc finger protein 20 /// zinc finger protein 625	AI352507
202915_s_at	0.70699	8.139471	8.223114	2.41E-14	2.35E-13	21.71719	FAM20B	family with sequence similarity 20, member B	BF115776
207431_s_at	0.70664	9.285044	7.670123	7.19E-13	5.86E-12	18.36931	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	NM_003676
229699_at	0.70649	6.82062	8.769048	7.57E-16	8.74E-15	25.13382	LOC100129550	Hypothetical protein LOC100129550 (LOC100129550), mRNA	AW237752
244655_at	0.70648	3.955757	9.439254	9.55E-18	1.34E-16	29.45824	LOC100132798	Full length insert cDNA clone ZD42A11	W68045
203637_s_at	0.70643	8.194102	6.103214	5.25E-09	2.37E-08	9.641352	MID1	midline 1 (Opitz/BBB syndrome) chromosome 17 open reading frame 91	NM_000381
214696_at	0.70638	8.552047	6.222636	2.78E-09	1.32E-08	10.26135	C17orf91		AF070569
222344_at	0.70635	4.528765	6.471068	7.25E-10	3.79E-09	11.57687			AW972765
227031_at	0.70613	8.231831	7.70657	5.77E-13	4.76E-12	18.58615	SNX13	sorting nexin 13	AV681975
242476_at	0.70607	5.253119	6.509014	5.88E-10	3.13E-09	11.7808			AI436356
221047_s_at	0.70586	5.87624	5.580527	7.67E-08	2.75E-07	7.027456	MARK1	MAP/microtubule affinity-regulating kinase 1	NM_018650
217317_s_at	0.70567	7.993753	10.00926	2.11E-19	3.51E-18	33.23138	HERC2P2 /// HERC2P3 /// LOC44024	hect domain and RLD 2 pseudogene 2 /// hect domain and RLD 2 pseudogene 3 /// hect domain and RLD 2 pseudogene	AB002391
1559425_at	0.70562	5.779599	7.729223	5.03E-13	4.19E-12	18.72122			AL512701
213592_at	0.70559	8.203547	5.815759	2.34E-08	9.28E-08	8.183261	APLNR	apelin receptor	X89271
209535_s_at	0.70536	5.804164	9.575156	3.88E-18	5.64E-17	30.35053			AF127481

225674_at	0.70532	9.068001	8.982997	1.90E-16	2.33E-15	26.49979	BCAP29	B-cell receptor-associated protein 29	AW873330
208086_s_at	0.70525	5.012654	9.715042	1.53E-18	2.30E-17	31.27389	DMD	dystrophin	M92650
1565577_s_at	0.7051	4.643656	10.22812	4.80E-20	8.47E-19	34.70001			AA524123
222565_s_at	0.70507	7.241447	8.099973	5.18E-14	4.88E-13	20.9613	PRKD3	protein kinase D3	BF978541
1556935_at	0.70502	4.31424	8.548333	3.10E-15	3.35E-14	23.74014			AF085839
238653_at	0.70493	6.604959	8.46674	5.21E-15	5.47E-14	23.22909	LRIG2	Leucine-rich repeats and immunoglobulin-like domains 2, mRNA (cDNA clone IMAGE:4608480)	BF967997
32094_at	0.70461	6.785898	9.865211	5.58E-19	8.82E-18	32.27046	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3	AB017915
224733_at	0.70445	8.508135	6.776202	1.33E-10	7.88E-10	13.23831	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	AL574900
211587_x_at	0.70414	6.48451	9.482573	7.17E-18	1.02E-16	29.74213	CHRNA3	cholinergic receptor, nicotinic, alpha 3	M37981
224984_at	0.70412	8.943777	9.344108	1.79E-17	2.43E-16	28.83647	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	W61007
208384_s_at	0.70409	6.592958	10.00436	2.18E-19	3.62E-18	33.19858	MID2	midline 2	NM_012216
44702_at	0.70404	8.269186	13.00526	1.78E-28	6.56E-27	53.96362	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	R77097
216205_s_at	0.7039	7.002769	7.749131	4.46E-13	3.74E-12	18.84008	MFN2	mitofusin 2	AK021947
227630_at	0.70367	8.278609	8.948478	2.38E-16	2.89E-15	26.27844			AW274445
227266_s_at	0.70366	7.098812	4.303773	2.62E-05	5.74E-05	1.4005	FYB	FYN binding protein (FYB-120/130)	BF679849
206718_at	0.70359	4.973213	8.774773	7.30E-16	8.43E-15	25.17019	LMO1	LIM domain only 1 (rhombotin 1)	NM_002315
226665_at	0.70338	6.321581	7.53831	1.59E-12	1.24E-11	17.58979	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	AI986239
236202_at	0.70333	4.42014	10.7078	1.80E-21	3.66E-20	37.95251			AW467480
230360_at	0.70326	6.061319	4.952598	1.55E-06	4.29E-06	4.117671	GLDN	gliomedin	AW006648
218432_at	0.70304	8.503333	6.726911	1.75E-10	1.02E-09	12.96663	FBXO3	F-box protein 3	NM_012175
232129_s_at	0.70297	6.578441	10.90676	4.57E-22	9.81E-21	39.31365	LZTS2	leucine zipper, putative tumor suppressor 2	BF032717
205584_at	0.70295	6.235723	10.68334	2.13E-21	4.30E-20	37.78561	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	NM_024810
208859_s_at	0.7027	8.417995	7.671956	7.11E-13	5.80E-12	18.3802	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	AI650257
203651_at	0.70252	7.997195	9.257881	3.16E-17	4.18E-16	28.27511	ZFYVE16	zinc finger, FYVE domain containing 16	NM_014733
243_g_at	0.70236	9.26531	12.92594	3.13E-28	1.13E-26	53.40343	MAP4	microtubule-associated protein 4	M64571
213530_at	0.70215	7.075903	9.170756	5.59E-17	7.22E-16	27.71004	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	AI040009
230350_at	0.70204	7.530546	9.307906	2.27E-17	3.05E-16	28.60053			AA503360
214845_s_at	0.70204	8.421977	5.225547	4.32E-07	1.34E-06	5.35015	CALU	calumenin	AF257659
225627_s_at	0.70197	6.933077	4.970577	1.42E-06	3.97E-06	4.197274	CACHD1	cache domain containing 1	AK024256
218935_at	0.70194	6.611001	8.499225	4.24E-15	4.50E-14	23.43228	EHD3	EH-domain containing 3	NM_014600
38892_at	0.70191	7.74119	8.695354	1.21E-15	1.37E-14	24.6667	KIAA0240	KIAA0240	D87077
209274_s_at	0.70161	9.724896	7.975829	1.12E-13	1.01E-12	20.20512	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	BC002675
1553961_s_at	0.70147	7.25646	12.41081	1.21E-26	3.86E-25	49.77367	SNX21	sorting nexin family member 21	CA447177
46665_at	0.70139	9.03208	9.329565	1.97E-17	2.66E-16	28.74164	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	AI949392
234998_at	0.70117	7.391528	6.365898	1.29E-09	6.45E-09	11.01578			N57510
213224_s_at	0.70111	7.490342	9.367725	1.53E-17	2.10E-16	28.99057	NCRNA00081	non-protein coding RNA 81	AK025724
227045_at	0.70088	6.595602	5.119233	7.14E-07	2.12E-06	4.864044	ZNF614	zinc finger protein 614	AI087872
203243_s_at	0.70078	10.16711	6.549319	4.71E-10	2.55E-09	11.99824	PDLIM5	PDZ and LIM domain 5	NM_006457

							GTF2A1L /// STON1 /// STON1- GTF2A1L	general transcription factor IIA, 1- like /// stonin 1 /// STON1- GTF2A1L readthrough transcript	NM_006873
220190_s_at	0.70073	3.537394	8.680754	1.33E-15	1.50E-14	24.57436			
219801_at	0.70058	5.967762	10.88385	5.36E-22	1.14E-20	39.15566	ZNF34	zinc finger protein 34	NM_030580
235365_at	0.70054	5.017394	13.72222	1.08E-30	4.80E-29	59.03736	DFNB59	deafness, autosomal recessive 59	AA744520
243993_at	0.70021	5.03794	6.740928	1.62E-10	9.48E-10	13.04376			AA436887
205854_at	0.70019	7.968133	9.511516	5.92E-18	8.48E-17	29.93209	TULP3	tubby like protein 3	AK024246
216865_at	0.69998	4.727597	11.26895	3.70E-23	8.77E-22	41.80746	COL14A1	collagen, type XIV, alpha 1	M64108
233036_at	0.69974	5.239471	6.979693	4.18E-11	2.69E-10	14.37297			AU146418
226776_at	0.69961	5.796721	6.757215	1.48E-10	8.70E-10	13.13352	ENY2	enhancer of yellow 2 homolog (Drosophila)	BF433516
205151_s_at	0.6992	6.455703	7.012296	3.47E-11	2.26E-10	14.55667	KIAA0644	KIAA0644 gene product	NM_014817
239762_at	0.69898	6.369025	10.5427	5.61E-21	1.09E-19	36.82818	LOC28643 7	hypothetical protein LOC286437	AI080505
222984_at	0.6989	10.26087	11.00292	2.35E-22	5.16E-21	39.97384	PAIP2	poly(A) binding protein interacting protein 2	AF151052
1554161_at	0.69887	3.715575	13.21451	4.02E-29	1.57E-27	55.44279	SLC25A27	solute carrier family 25, member 27	BC033091
235118_at	0.69881	3.086517	7.194271	1.21E-11	8.39E-11	15.59145			AV724769
1555897_at	0.6987	4.995508	12.94759	2.69E-28	9.73E-27	53.55628	AOF2	amine oxidase (flavin containing) domain 2	CA306222
220392_at	0.69864	4.4394	7.9909	1.02E-13	9.26E-13	20.2966	EBF2	early B-cell factor 2	NM_022659
240095_at	0.69854	6.090074	12.60793	3.00E-27	1.00E-25	51.16069			AI287817
226413_at	0.69846	7.593898	6.471174	7.24E-10	3.79E-09	11.57744	LOC40002 7	hypothetical gene supported by BC047417	AA044705
225677_at	0.6984	8.553151	10.04543	1.66E-19	2.78E-18	33.47333	BCAP29	B-cell receptor-associated protein 29	AW152589
226183_at	0.69834	6.719464	7.998881	9.68E-14	8.84E-13	20.34508			AW139538
223616_at	0.69832	5.477109	6.843771	9.08E-11	5.52E-10	13.61277	ZNF649	zinc finger protein 649	BC005368
227295_at	0.69814	6.678966	6.07546	6.07E-09	2.70E-08	9.498439	IKIP	IKK interacting protein	AW182575
212987_at	0.69802	9.903955	8.933604	2.62E-16	3.17E-15	26.18317	FBXO9	F-box protein 9	AL031178
238752_at	0.69788	3.876964	9.747238	1.23E-18	1.87E-17	31.48709			AA780295
234937_x_at	0.6977	5.359323	10.28356	3.29E-20	5.92E-19	35.0737	ZFP28	zinc finger protein 28 homolog (mouse)	AC007228
207974_s_at	0.6976	10.93875	9.423954	1.06E-17	1.47E-16	29.35809	SKP1	S-phase kinase-associated protein 1	NM_006930
202986_at	0.69719	5.934404	5.28189	3.30E-07	1.05E-06	5.610848	ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	NM_014862
230502_s_at	0.69718	5.910838	10.78984	1.03E-21	2.13E-20	38.51297	LOC14983 2	CDNA clone IMAGE:4403164	BE501966
213241_at	0.69716	7.995935	5.039482	1.04E-06	2.98E-06	4.504443	PLXNC1	plexin C1	AF035307
221606_s_at	0.69683	6.713082	4.5255	1.03E-05	2.43E-05	2.294302	NSBP1	nucleosomal binding protein 1	BC005342
227074_at	0.69594	7.429891	9.887569	4.80E-19	7.65E-18	32.41928	LOC10013 1564	hypothetical protein LOC100131564	AA524669
205786_s_at	0.69589	6.927935	5.543836	9.21E-08	3.25E-07	6.850309	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	NM_000632
201908_at	0.69542	8.460075	9.005176	1.65E-16	2.03E-15	26.64221	DVL3	dishevelled, dsh homolog 3 (Drosophila)	NM_004423
203636_at	0.69542	8.245057	6.347675	1.42E-09	7.07E-09	10.91918	MID1	midline 1 (Opitz/BBB syndrome)	BE967532
240665_at	0.69539	4.146878	8.219786	2.46E-14	2.40E-13	21.69669			R40515
211062_s_at	0.6953	6.818537	6.671508	2.39E-10	1.36E-09	12.66275	CPZ	carboxypeptidase Z	BC006393
235122_at	0.69521	5.567417	7.846419	2.47E-13	2.14E-12	19.42335	HIVEP3	human immunodeficiency virus type 1 enhancer binding protein 3	AI800713
204568_at	0.69498	7.447687	10.52006	6.55E-21	1.26E-19	36.67438	KIAA0831	KIAA0831	NM_014924
222682_s_at	0.69496	7.289099	7.931542	1.46E-13	1.31E-12	19.93683	FAM114A2	family with sequence similarity 114, member A2	AI307615
225910_at	0.69483	7.557005	10.4716	9.12E-21	1.74E-19	36.34551	HELZ	helicase with zinc finger	BF514723
209789_at	0.69466	4.221363	9.163405	5.86E-17	7.56E-16	27.66246	CORO2B	coronin, actin binding protein, 2B	BF939649
210645_s_at	0.69454	10.12721	8.618226	1.99E-15	2.20E-14	24.17972	TTC3	tetratricopeptide repeat domain 3	D83077
204900_x_at	0.6941	8.812555	5.999318	9.05E-09	3.89E-08	9.108686	SAP30	Sin3A-associated protein, 30kDa	NM_003864
219583_s_at	0.69383	6.544168	8.115701	4.70E-14	4.44E-13	21.05753	SPATA7	spermatogenesis associated 7	NM_018418
222791_at	0.69371	8.601375	8.041882	7.42E-14	6.86E-13	20.60672	RSBN1	round spermatid basic protein 1	AK022166

224977_at	0.69369	8.472662	11.24746	4.30E-23	1.01E-21	41.65887	C6orf89	chromosome 6 open reading frame 89	AL119182
235891_at	0.69343	4.687276	12.40917	1.22E-26	3.90E-25	49.76209			AI961147
40687_at	0.69334	6.718071	8.859325	4.23E-16	5.01E-15	25.70845	GJA4	gap junction protein, alpha 4, 37kDa	M96789
202410_x_at	0.69333	6.554971	3.546887	0.0004848	0.0008526	-1.3621	IGF2 /// INS-IGF2	insulin-like growth factor 2 (somatomedin A) /// INS-IGF2 readthrough transcript	NM_000612
226096_at	0.69308	5.869073	6.565409	4.31E-10	2.35E-09	12.08529	FNDC5	fibronectin type III domain containing 5	AI760132
210276_s_at	0.69306	9.279602	9.21153	4.28E-17	5.59E-16	27.97422	TRIOBP	TRIO and F-actin binding protein	AF281030
235470_at	0.69289	6.400357	7.64852	8.19E-13	6.62E-12	18.24104			AI766279
209994_s_at	0.6928	5.815119	5.36285	2.23E-07	7.32E-07	5.989148	ABCB1 /// ABCB4	ATP-binding cassette, sub-family B (MDR/TAP), member 1 /// ATP-binding cassette, sub-family B (MDR/TAP), member 4	AF016535
214846_s_at	0.69259	5.537351	8.279494	1.69E-14	1.68E-13	22.06516	ALPK3	alpha-kinase 3	A8037751
208990_s_at	0.69251	9.828699	10.36787	1.85E-20	3.41E-19	35.64304	HNRNP3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	AF132362
204563_at	0.69251	7.464536	3.667745	0.0003131	0.0005684	-0.95193	SELL	selectin L	NM_000655
225178_at	0.69233	6.611272	6.500279	6.17E-10	3.27E-09	11.73378	TTC14	tetratricopeptide repeat domain 14	W73788
219353_at	0.69229	7.348359	7.86832	2.16E-13	1.88E-12	19.55518	NHLRC2	NHL repeat containing 2	NM_017687
223250_at	0.69207	8.713885	7.745561	4.55E-13	3.82E-12	18.81876	KLHL7	kelch-like 7 (Drosophila)	AL136597
226632_at	0.69207	8.090552	6.226434	2.73E-09	1.29E-08	10.2812	CYGB	cytoglobin	AL513673
212732_at	0.69207	4.11305	7.622697	9.57E-13	7.66E-12	18.08798	MEG3	maternally expressed 3 (non-protein coding)	AI950273
204428_s_at	0.69199	5.420358	12.42088	1.13E-26	3.60E-25	49.84446	LCAT	lecithin-cholesterol acyltransferase	NM_000229
230161_at	0.69192	6.646268	10.53023	6.11E-21	1.18E-19	36.74346			BF513346
223129_x_at	0.69187	8.285013	10.86194	6.23E-22	1.32E-20	39.00644	MYLIP	myosin regulatory light chain interacting protein	T63512
221898_at	0.69148	7.442782	4.804323	3.03E-06	7.92E-06	3.469825	PDPN	podoplanin	AU154455
230815_at	0.69131	5.557909	8.343437	1.13E-14	1.15E-13	22.46122	LOC38976 5	similar to KIF27C	AI684760
201335_s_at	0.69124	5.298796	11.40018	1.48E-23	3.64E-22	42.71548	ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	NM_015313
207231_at	0.6912	4.650333	8.316054	1.35E-14	1.35E-13	22.29143	DZIP3	DAZ interacting protein 3, zinc finger	NM_014648
226347_at	0.69119	8.987733	8.847332	4.57E-16	5.40E-15	25.63196			AI754928
206412_at	0.69113	6.82629	10.15561	7.85E-20	1.36E-18	34.21233	FER	fer (fps/fes related) tyrosine kinase	NM_005246
1555259_at	0.69109	4.572755	8.496717	4.31E-15	4.57E-14	23.41658	ZAK	sterile alpha motif and leucine zipper containing kinase AZK	AF465843
215175_at	0.69104	4.221792	9.429181	1.02E-17	1.42E-16	29.3923	PCNX	pecanex homolog (Drosophila)	AB023212
220116_at	0.69103	4.608855	6.348379	1.41E-09	7.04E-09	10.92291	KCNN2	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2	NM_021614
221011_s_at	0.69076	8.516557	5.831063	2.16E-08	8.63E-08	8.259642	LBH	limb bud and heart development homolog (mouse)	NM_030915
232317_at	0.69028	4.745482	8.573153	2.65E-15	2.88E-14	23.89605	PLXNA4	plexin A4	AB046770
209250_at	0.69028	9.965205	9.478023	7.39E-18	1.05E-16	29.71229	DEGS1	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	BC000961
205308_at	0.69016	7.904922	8.30152	1.47E-14	1.47E-13	22.20142	FAM164A	family with sequence similarity 164, member A	NM_016010
206682_at	0.68983	6.288004	5.84015	2.06E-08	8.27E-08	8.305061	CLEC10A	C-type lectin domain family 10, member A	NM_006344
233748_x_at	0.68977	7.941955	9.152704	6.29E-17	8.08E-16	27.59323	PRKAG2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	AI249976
212306_at	0.68961	8.099197	8.715363	1.07E-15	1.22E-14	24.79336	CLASP2	cytoplasmic linker associated protein 2	AI741784
226673_at	0.68948	7.190397	9.692017	1.78E-18	2.67E-17	31.12157	SH2D3C	SH2 domain containing 3C	AW665063
228055_at	0.68937	6.571328	4.357273	2.10E-05	4.67E-05	1.612773	NAPSB	napsin B aspartic peptidase pseudogene	AI763426
222423_at	0.68931	9.169044	9.470779	7.75E-18	1.10E-16	29.66479	NDFIP1	Nedd4 family interacting protein 1	H05010

224704_at	0.68916	7.926593	9.835101	6.82E-19	1.07E-17	32.07021	TNRC6A	trinucleotide repeat containing 6A	N21600
227466_at	0.689	8.466075	10.47304	9.03E-21	1.72E-19	36.35527	LOC285550	hypothetical protein LOC285550	BF108695
35776_at	0.68898	7.627824	11.42561	1.24E-23	3.07E-22	42.89176	ITSN1	intersectin 1 (SH3 domain protein)	AF064243
225562_at	0.68885	7.722748	8.617553	2.00E-15	2.20E-14	24.17547	RASA3	RAS p21 protein activator 3	AI684746
218370_s_at	0.68874	7.255051	8.751927	8.45E-16	9.72E-15	25.02514	S100PBP	S100P binding protein	NM_022753
223510_at	0.68848	5.251639	10.1181	1.01E-19	1.73E-18	33.96048	NRP2	neuropilin 2	AF280545
229384_at	0.68782	7.055363	10.60286	3.71E-21	7.33E-20	37.23728			BE044193
226542_at	0.68747	7.216641	8.277906	1.71E-14	1.69E-13	22.05535			AI300571
218537_at	0.68728	8.120892	12.36558	1.67E-26	5.25E-25	49.45577	HCFC1R1	host cell factor C1 regulator 1 (XPO1 dependent)	NM_017885
235195_at	0.68712	4.946539	8.579843	2.54E-15	2.77E-14	23.93811	FBXW2	F-box and WD repeat domain containing 2	BG109988
228375_at	0.6871	4.09878	7.207356	1.12E-11	7.81E-11	15.66646	IGSF11	immunoglobulin superfamily, member 11	BE221674
240433_x_at	0.68665	3.342138	7.076021	2.40E-11	1.60E-10	14.91723			H39185
211124_s_at	0.68657	4.56198	5.505648	1.11E-07	3.86E-07	6.666845	KITLG	KIT ligand	AF119835
244534_at	0.6865	5.777173	7.419514	3.22E-12	2.41E-11	16.89373			AI695743
212830_at	0.68648	7.315837	8.01701	8.66E-14	7.95E-13	20.4553	MEGF9	multiple EGF-like-domains 9	W68084
209814_at	0.68642	8.605363	8.580642	2.53E-15	2.76E-14	23.94313	ZNF330	zinc finger protein 330	BC004421
223125_s_at	0.68624	8.864653	5.630339	5.98E-08	2.19E-07	7.269323	C1orf21	chromosome 1 open reading frame 21	AL563236
229300_at	0.6862	5.040945	8.351752	1.08E-14	1.09E-13	22.51283			AW590679
210561_s_at	0.68619	10.0614	7.885032	1.95E-13	1.71E-12	19.6559	WSB1	WD repeat and SOCS box-containing 1	AL110243
1554333_at	0.68618	4.861651	4.219331	3.70E-05	7.88E-05	1.069901	DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	BC031044
1553027_a_at	0.68609	4.295238	8.207454	2.66E-14	2.58E-13	21.62075	KLHL4	kelch-like 4 (Drosophila)	NM_057162
232429_at	0.68598	3.52349	12.94082	2.82E-28	1.02E-26	53.50845			AL122040
214474_at	0.68594	6.489042	8.08098	5.83E-14	5.46E-13	20.84523	PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	NM_005399
206271_at	0.68593	6.771663	4.520941	1.05E-05	2.47E-05	2.275554	TLR3	toll-like receptor 3	NM_003265
229560_at	0.6858	6.239506	3.802765	0.0001896	0.0008569	-0.47952	TLR8	toll-like receptor 8	AW872374
1558702_at	0.6856	5.085457	11.17686	7.03E-23	1.62E-21	41.17152	TEX10	CDNA FLJ57815 complete cds	BG622833
230893_at	0.68556	6.674844	6.977679	4.23E-11	2.71E-10	14.36164	DNAJC21	DnaJ (Hsp40) homolog, subfamily C, member 21	AI223870
235962_at	0.68551	5.123667	12.16385	6.94E-26	2.08E-24	48.03996			AI336192
207326_at	0.6854	5.052798	7.955407	1.26E-13	1.14E-12	20.08131	BTC	betacellulin	NM_001729
229406_at	0.68497	4.642847	5.912206	1.42E-08	5.90E-08	8.66698	hCG_1776007	hexaribonucleotide binding protein 3	AI674243
211952_at	0.68468	6.602476	7.248222	8.83E-12	6.23E-11	15.90124	IPO5	importin 5	AF339834
217617_at	0.68424	4.756813	6.936303	5.36E-11	3.38E-10	14.12929			AW451711
202254_at	0.6839	6.223206	8.365371	9.87E-15	1.01E-13	22.59742	SIPA1L1	KIAA0440	AB007900
221883_at	0.68388	6.731704	10.08248	1.29E-19	2.19E-18	33.72156	PKNOX1	PBX/knotted 1 homeobox 1	AA133342
216997_x_at	0.68374	4.057928	10.64518	2.77E-21	5.54E-20	37.5255	TLE4	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	AL358975
212750_at	0.68373	7.313264	5.824178	2.24E-08	8.92E-08	8.225259	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	AB020630
225159_s_at	0.68364	8.646281	8.809743	5.83E-16	6.79E-15	25.39254			AW614072
221211_s_at	0.68357	5.732037	7.45493	2.61E-12	1.98E-11	17.10059	C21orf7	chromosome 21 open reading frame 7	NM_020152
203420_at	0.68351	9.699048	8.80638	5.95E-16	6.94E-15	25.37113	FAM8A1	family with sequence similarity 8, member A1	NM_016255
239058_at	0.68305	6.048068	7.985696	1.05E-13	9.54E-13	20.26501			BF446723
60471_at	0.68296	7.662275	10.06274	1.47E-19	2.48E-18	33.58931	RIN3	Ras and Rab interactor 3	AA625133
217359_s_at	0.68295	3.927187	11.20724	5.69E-23	1.32E-21	41.38115	NCAM1	neural cell adhesion molecule 1	M22094
212205_at	0.68288	10.33095	10.04125	1.70E-19	2.85E-18	33.44537	H2AFV	H2A histone family, member V	AA534860
228857_at	0.68211	6.011612	9.731318	1.37E-18	2.07E-17	31.38164	GNL1 /// LOC285831	guanine nucleotide binding protein-like 1 /// hypothetical protein LOC285831	AA775731
226785_at	0.68194	8.236	8.228458	2.33E-14	2.28E-13	21.75012	ATP11C	ATPase, class VI, type 11C	BF475862
239849_at	0.68187	3.55967	9.216287	4.15E-17	5.43E-16	28.00507			AI417595
204496_at	0.68186	8.284915	7.410216	3.40E-12	2.54E-11	16.83952	STRN3	striatin, calmodulin binding protein 3	NM_014574
218425_at	0.68176	7.099266	10.00846	2.12E-19	3.53E-18	33.226	RNF216	ring finger protein 216	BC000787

228299_at	0.68124	9.506091	10.53584	5.88E-21	1.14E-19	36.78156	KCTD20	potassium channel tetramerisation domain containing 20	AV707142
210756_s_at	0.68118	7.622082	9.754045	1.17E-18	1.80E-17	31.53221	NOTCH2	Notch homolog 2 (Drosophila)	AF308601
239629_at	0.68114	6.826173	5.158744	5.93E-07	1.79E-06	5.043808	CFLAR	I-FLICE isoform 5	AI634046
1555929_s_at	0.68102	3.492701	8.586044	2.44E-15	2.67E-14	23.97711			BM873997
212742_at	0.68095	8.225768	8.023911	8.30E-14	7.64E-13	20.49729	RNF115	ring finger protein 115	AL530462
212746_s_at	0.68063	8.211985	7.32674	5.57E-12	4.05E-11	16.35453	CEP170	centrosomal protein 170kDa	AA126789
205112_at	0.68058	6.621751	6.161228	3.86E-09	1.78E-08	9.941515	PLCE1	phospholipase C, epsilon 1	NM_016341
225064_at	0.68053	7.801021	10.09426	1.19E-19	2.02E-18	33.80056	RABEP1	rabaptin, RAB GTPase binding effector protein 1	R60018
214683_s_at	0.5805	8.572848	8.031465	7.92E-14	7.30E-13	20.54327	CLK1	CDC-like kinase 1	AI251890
238658_at	0.68021	4.349381	10.79429	9.94E-22	2.07E-20	38.54342			AA832474
227499_at	0.68012	4.604018	5.553857	8.76E-08	3.10E-07	6.898605			AA001400
224820_at	0.68006	9.346287	7.402515	3.56E-12	2.65E-11	16.79464	FAM36A	family with sequence similarity 36, member A	AA831192
203861_s_at	0.67997	6.385266	6.058357	6.64E-09	2.94E-08	9.410598	ACTN2	actinin, alpha 2	AU146889
232628_at	0.67971	5.093944	5.819683	2.29E-08	9.11E-08	8.202829			AI740529
227065_at	0.67955	7.391015	11.87001	5.50E-25	1.54E-23	45.98397	RNF216	ring finger protein 216	AA523105
44790_s_at	0.67941	5.956973	4.203135	3.96E-05	8.37E-05	1.007119	C13orf18 LOC72897	chromosome 13 open reading frame 18 /// hypothetical LOC728970	AI129310
219714_s_at	0.6793	4.497845	7.471613	2.36E-12	1.80E-11	17.19823	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3	NM_018398
235142_at	0.67912	7.917438	7.028432	3.16E-11	2.07E-10	14.64778	RP1-2705.1 /// ZBTB8	zinc finger and BTB domain containing 8-like /// zinc finger and BTB domain containing 8	AW006067
224837_at	0.6791	10.45672	10.13028	9.32E-20	1.60E-18	34.04223	FOXP1	forkhead box P1	AW080845
226399_at	0.67897	8.359712	8.323969	1.28E-14	1.29E-13	22.34048			AL121021
204122_at	0.67889	8.770954	4.53137	1.00E-05	2.37E-05	2.318463	TYROBP	TYRO protein tyrosine kinase binding protein	NM_003332
225641_at	0.67876	7.266187	12.24432	3.93E-26	1.20E-24	48.60428	MEF2D	myocyte enhancer factor 2D	AI829724
228737_at	0.6787	5.796458	5.212027	4.61E-07	1.42E-06	5.287908	TOX2	TOX high mobility group box family member 2	AA211909
1553055_a_at	0.67854	5.608498	6.135456	4.42E-09	2.02E-08	9.807929	SLFN5	schlafen family member 5	NM_144975
228346_at	0.67848	6.818558	7.996916	9.80E-14	8.94E-13	20.33315	ZNF844	zinc finger protein 844	H47630
215051_x_at	0.67845	9.511283	5.816384	1.06E-10	6.38E-10	13.46072	AIF1	allograft inflammatory factor 1	BF213829
235722_at	0.6783	7.020384	5.853726	1.83E-08	7.40E-08	8.423132	SYNJ2BP	synaptojanin 2 binding protein	AI671431
213482_at	0.67805	4.273624	8.74332	8.93E-16	1.02E-14	24.97054	DOCK3	dedicator of cytokinesis 3	BF593175
235295_at	0.67804	6.691382	6.943292	5.15E-11	3.26E-10	14.16848			BG401950
227485_at	0.67794	5.644476	7.071049	2.47E-11	1.65E-10	14.88903	DDX26B	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B	AI828015
235938_at	0.67764	5.861181	10.13816	8.84E-20	1.52E-18	34.09509			AI018174
204159_at	0.6776	8.206818	5.286654	3.23E-07	1.03E-06	5.632992	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	NM_001262
215784_at	0.6774	4.351838	4.7183	4.44E-06	1.12E-05	3.101136	CD1E	CD1e molecule	AA309511
1553955_at	0.67728	8.215052	8.17275	3.30E-14	3.17E-13	21.40735	KLRAQ1	KLRAQ motif containing 1	AY134855
226648_at	0.67728	7.282944	7.245185	8.99E-12	6.33E-11	15.88377	HIF1AN	hypoxia inducible factor 1, alpha subunit inhibitor	AI769745
226876_at	0.6771	8.258427	7.143249	1.63E-11	1.11E-10	15.29972	FAM101B	family with sequence similarity 101, member B	AI961778
201029_s_at	0.67692	11.70416	8.954345	2.29E-16	2.79E-15	26.31603	CD99	CD99 molecule	NM_002414
219747_at	0.67674	6.118646	4.630441	6.53E-06	1.60E-05	2.730091	C4orf31	chromosome 4 open reading frame 31	NM_024574
212573_at	0.67668	7.956946	6.49654	6.30E-10	3.33E-09	11.71367	ENDOD1	endonuclease domain containing 1	AF131747
210172_at	0.67633	6.136361	6.324381	1.61E-09	7.94E-09	10.79597	SF1	splicing factor 1	D26121
226800_at	0.67626	6.002298	6.640428	2.84E-10	1.59E-09	12.49298	EFCAB7	EF-hand calcium binding domain 7	AL109925
239744_at	0.67605	7.860925	8.859508	4.23E-16	5.01E-15	25.70962			AW151660
238819_at	0.67583	5.116412	5.658459	5.19E-08	1.93E-07	7.406553	ZNF347	zinc finger protein 347	AA776564
227525_at	0.6756	8.328611	5.393986	1.92E-07	6.37E-07	6.135783	GLCC1	glucocorticoid induced transcript 1	AA058770
218729_at	0.67515	8.656555	4.70588	4.69E-06	1.18E-05	3.048343	LXN	latexin	NM_020169
213049_at	0.67503	8.290659	8.542849	3.21E-15	3.47E-14	23.70572	GARNL1	GTPase activating Rap/RanGAP domain-like 1	BG436400
238937_at	0.67495	6.299617	5.525231	1.01E-07	3.53E-07	6.760808	ZNF420	zinc finger protein 420	AI339586

214322_at	0.67477	5.231078	9.750725	1.20E-18	1.83E-17	31.5102	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	AA284757
212345_s_at	0.67448	9.393815	9.177102	5.36E-17	6.94E-16	27.75113	CREB3L2	cAMP responsive element binding protein 3-like 2	BE675139
220760_x_at	0.67428	8.335722	9.699132	1.70E-18	2.55E-17	31.16862	ZNF665	zinc finger protein 665	NM_024733
220076_at	0.67425	5.021656	7.175826	1.35E-11	9.27E-11	15.48585	ANKH	ankylosis, progressive homolog (mouse)	NM_019847
225962_at	0.67424	5.517264	8.933299	2.62E-16	3.18E-15	26.18122	ZNRF1	zinc and ring finger 1	AI199541
232352_at	0.67406	5.699422	7.553076	1.45E-12	1.14E-11	17.67674	ISL2	ISL LIM homeobox 2	AK001022
201143_s_at	0.67401	8.106316	5.931589	1.29E-08	5.38E-08	8.764871	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	BC002513
229083_at	0.67366	7.667663	7.885429	1.94E-13	1.71E-12	19.6583	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	AI672356
32541_at	0.67353	6.31526	7.598504	1.11E-12	8.80E-12	17.94484	PPP3CC	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform	S46622
223089_at	0.67351	6.965283	5.687148	4.50E-08	1.69E-07	7.54707	VEZT	vezatin, adherens junctions transmembrane protein	AI805297
207417_s_at	0.67333	5.111026	7.993035	1.00E-13	9.14E-13	20.30957	ZNF177	zinc finger protein 177	NM_003451
232182_at	0.67329	3.902793	10.94439	3.52E-22	7.62E-21	39.57184	LOC286272	hypothetical protein LOC286272	AI142853
224703_at	0.67311	8.212068	13.26695	2.77E-29	1.10E-27	55.81372	WDR22	WD repeat domain 22	AI814644
1558820_a_at	0.67297	5.167446	7.327489	5.54E-12	4.03E-11	16.35887	C18orf34	chromosome 18 open reading frame 34	AK000027
223444_at	0.67297	6.31146	8.931753	2.65E-16	3.21E-15	26.17132	SEN7	SUMO1/sentrin specific peptidase 7	AL136599
205511_at	0.67297	4.784537	7.958815	1.24E-13	1.12E-12	20.10196	FLJ10038	hypothetical protein FLJ10038	NM_017976
212572_at	0.67266	9.455348	7.410516	3.40E-12	2.54E-11	16.84127	STK38L	serine/threonine kinase 38 like	AW779556
1562275_at	0.6725	4.455907	5.65377	5.32E-08	1.97E-07	7.383634			AL832835
214496_x_at	0.67247	7.348587	10.37814	1.73E-20	3.19E-19	35.71252	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	NM_012330
222571_at	0.67241	6.956903	12.19405	5.61E-26	1.69E-24	48.25167	ST6GALNA C6	ST6 (alpha-N-acetyl-neuraminyl-2,3 beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6	AK023900
235589_s_at	0.67239	7.306319	5.807213	2.44E-08	9.66E-08	8.140674	MDM4	CDNA FLJ39869 fis, clone SPLEN2015433	AW379042
203085_s_at	0.67209	7.894194	6.215405	2.89E-09	1.37E-08	10.22358	TGFB1	transforming growth factor, beta 1	BC000125
203197_s_at	0.67196	8.866957	14.42049	7.42E-33	3.99E-31	63.98623	C1orf123	chromosome 1 open reading frame 123	AW157077
205771_s_at	0.6719	7.350115	4.51333	1.08E-05	2.55E-05	2.244291	AKAP7	A kinase (PRKA) anchor protein 7	AL137063
238007_at	0.67179	5.536363	8.983258	1.90E-16	2.33E-15	26.50146	ZNF271	zinc finger protein 271	AA464945
238516_at	0.67169	5.945541	8.982324	1.91E-16	2.34E-15	26.49547	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	BF247383
203355_s_at	0.67165	7.490636	4.335842	2.29E-05	5.07E-05	1.52748	PSD3	pleckstrin and Sec7 domain containing 3	NM_015310
227049_at	0.67133	7.641238	7.613079	1.01E-12	8.09E-12	18.03104	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	N21127
1553977_a_at	0.67131	6.384511	7.266335	7.94E-12	5.63E-11	16.00556	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1	BC010358
227418_at	0.67101	8.173815	6.178837	3.51E-09	1.64E-08	10.03301	KIAA1826	KIAA1826	AI808746
223604_at	0.67099	5.928183	11.50321	7.21E-24	1.83E-22	43.43004	GARNL3	GTPase activating Rap/RanGAP domain-like 3	AL136573
225576_at	0.67097	9.726963	10.78987	1.02E-21	2.13E-20	38.51316	C6orf72	chromosome 6 open reading frame 72	AI948460
238940_at	0.67079	4.286555	13.16874	5.57E-29	2.14E-27	55.1191	KLF12	Kruppel-like factor 12	BE328128
202522_at	0.67055	10.38219	11.84817	6.42E-25	1.79E-23	45.83151	PITPNB	phosphatidylinositol transfer protein, beta	AL031591
238719_at	0.67053	7.409378	8.849947	4.50E-16	5.31E-15	25.64864			BF060712
212452_x_at	0.67052	7.750402	11.24486	4.38E-23	1.03E-21	41.64095	MYST4	MYST histone acetyltransferase (monocytic leukemia) 4	AF113514

210807_s_at	0.67048	5.690473	5.674334	4.80E-08	1.79E-07	7.484242	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	AF049608
244774_at	0.67038	6.310624	4.848744	2.48E-06	6.60E-06	3.662279	PHACTR2	phosphatase and actin regulator 2	R81072
202289_s_at	0.67021	9.23914	6.300128	1.83E-09	8.96E-09	10.568	TACC2	transforming, acidic coiled-coil containing protein 2	NM_006997
213015_at	0.67007	8.507296	9.095653	9.13E-17	1.16E-15	27.22469	BBX	bobby sox homolog (Drosophila)	BF448315
222857_s_at	0.66995	6.629234	5.703806	4.13E-08	1.56E-07	7.628892	KCNMB4	potassium large conductance calcium-activated channel, subfamily M, beta member 4	AF160967
227889_at	0.66972	7.245414	4.776491	3.43E-06	8.88E-06	3.349956	LPCAT2	lysophosphatidylcholine acyltransferase 2	AI765437
228222_at	0.66946	11.27735	6.491683	6.47E-10	3.41E-09	11.68756			AI700962
235077_at	0.6693	4.889427	7.648999	8.17E-13	6.60E-12	18.24388	MEG3	maternally expressed 3 (non-protein coding)	BF956762
227840_at	0.66929	7.208633	7.848987	2.43E-13	2.11E-12	19.43879	C2orf76	chromosome 2 open reading frame 76	AA738440
63305_at	0.66926	5.644086	14.18174	4.07E-32	2.06E-30	62.29412	PKNOX2	PBX/knotted 1 homeobox 2	D81792
229710_at	0.66913	7.426424	9.154503	6.22E-17	7.99E-16	27.60487			AA843541
1559296_at	0.66855	3.513047	15.41152	6.40E-36	4.77E-34	70.99853	LOC730057	Homo sapiens, clone IMAGE:5759975, mRNA	BC040632
239791_at	0.66853	5.211299	6.210889	2.96E-09	1.40E-08	10.2	LOC100130740	similar to hCG2042068	AI125255
242086_at	0.66851	5.760453	5.883982	1.65E-08	6.74E-08	8.524845			AI824719
222669_s_at	0.66827	9.984966	6.944464	5.12E-11	3.24E-10	14.17506	SBD5 /// SBDSP	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	AK001779
212309_at	0.66823	7.324864	11.81935	7.86E-25	2.18E-23	45.63039	CLASP2	cytoplasmic linker associated protein 2	AV725315
206432_at	0.66819	5.600385	3.668197	0.0003126	0.0005676	-0.95037	HAS2	hyaluronan synthase 2	NM_005328
227112_at	0.66809	8.177067	8.107963	4.93E-14	4.65E-13	21.01017	TMCC1	transmembrane and coiled-coil domain family 1	AW270037
227844_at	0.66797	4.851487	10.61352	3.45E-21	6.84E-20	37.30984	FMNL3	formin-like 3	AI089932
217552_x_at	0.66781	4.727504	5.835382	2.12E-08	8.46E-08	8.281219	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	AI432713
235611_at	0.66769	4.941437	8.478799	4.82E-15	5.09E-14	23.30448			AA026666
228714_at	0.66748	5.416811	9.254242	3.23E-17	4.28E-16	28.25147			AI681888
236649_at	0.66717	5.359948	8.008916	9.10E-14	8.33E-13	20.40608	DTWD1	DTW domain containing 1	AA907927
211621_at	0.66694	4.371557	11.54555	5.36E-24	1.39E-22	43.72405	AR	androgen receptor	M73069
212223_at	0.6668	8.351833	7.268442	7.84E-12	5.57E-11	16.01771	IDS	iduronate 2-sulfatase	AI926544
205583_s_at	0.66676	7.868813	6.530146	5.24E-10	2.81E-09	11.8947	ALG13	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	NM_024810
201012_at	0.66675	10.85933	5.083088	8.46E-07	2.48E-06	4.700522	ANXA1	annexin A1	NM_000700
223790_at	0.66663	4.609859	10.45812	1.00E-20	1.89E-19	36.25412	KATNAL1	katanin p60 subunit A-like 1	BC000612
223135_s_at	0.66655	8.574746	11.2586	3.98E-23	9.41E-22	41.73588	BBX	bobby sox homolog (Drosophila)	AL136769
212956_at	0.66654	8.513511	4.591726	7.73E-06	1.87E-05	2.568379	TBC1D9	TBC1 domain family, member 9 (with GRAM domain)	AI348094
232501_at	0.66653	4.512693	13.00349	1.80E-28	6.64E-27	53.95108			AU144956
201494_at	0.66633	9.933723	7.590872	1.16E-12	9.19E-12	17.89974	PRCP	prolylcarboxypeptidase (angiotensinase C)	NM_005040
227505_at	0.66558	5.939496	11.35178	2.08E-23	5.01E-22	42.38031			N64630
237351_at	0.66531	3.901946	6.59939	3.57E-10	1.97E-09	12.26959			AI732190
213186_at	0.66527	7.100539	6.626108	3.08E-10	1.72E-09	12.41493	DZIP3	DAZ interacting protein 3, zinc finger	BG502305
231101_at	0.66527	6.794485	7.195597	1.20E-11	8.33E-11	15.59904			AI689803
225871_at	0.66526	8.309277	4.77797	3.41E-06	8.82E-06	3.356312	STEAP2	six transmembrane epithelial antigen of the prostate 2	BF680588
225902_at	0.66523	7.480674	10.20731	5.53E-20	9.70E-19	34.55995			AW194716
225512_at	0.66521	9.745448	9.808298	8.17E-19	1.27E-17	31.89213	ZBTB38	zinc finger and BTB domain containing 38	AI005245
228493_at	0.66519	4.374014	11.22764	4.93E-23	1.15E-21	41.52201	NKAP	CDNA clone IMAGE:3445361	T87628
224791_at	0.66512	9.137673	7.88178	1.99E-13	1.74E-12	19.6363	ASAP1	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	AW513835
1553719_s_at	0.66465	5.443314	6.848346	8.85E-11	5.39E-10	13.6382	ZNF548	zinc finger protein 548	NM_152909
239409_at	0.66455	5.334953	6.561731	4.40E-10	2.39E-09	12.06539			AA828280

209236_at	0.66438	6.773432	8.852111	4.43E-16	5.25E-15	25.66244	SLC23A2	solute carrier family 23 (nucleobase transporters), member 2	AL389886
228446_at	0.66438	8.007801	8.84563	4.62E-16	5.46E-15	25.62112	KIAA2026	KIAA2026	BF062203
201910_at	0.66417	8.075699	9.014613	1.55E-16	1.92E-15	26.70284	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	BF213279
235957_at	0.66414	5.382372	4.91919	1.80E-06	4.93E-06	3.970351			BE672408
209859_at	0.66405	4.214193	7.342857	5.06E-12	3.70E-11	16.44792	TRIM9	tripartite motif-containing 9	AF220036
230353_at	0.66401	5.85067	10.98942	2.58E-22	5.65E-21	39.88104	LOC284112	hypothetical protein LOC284112	AA627075
213022_s_at	0.66392	6.451733	7.867599	2.17E-13	1.89E-12	19.55083	UTRN	utrophin	NM_007124
201860_s_at	0.66367	8.764719	4.451338	1.41E-05	3.25E-05	1.991243	PLAT	plasminogen activator, tissue	NM_000930
216899_s_at	0.66348	7.771785	5.95868	1.12E-08	4.73E-08	8.902069	SKAP2	src kinase associated phosphoprotein 2	AC003999
242191_at	0.6632	6.123806	7.024149	3.24E-11	2.12E-10	14.62359	NBPF10 /// RP11-94I2.2	neuroblastoma breakpoint family, member 10 /// hypothetical protein LOC200030	AI701905
213853_at	0.66314	7.553565	9.885283	4.87E-19	7.76E-18	32.40406	DNAJC24	DnaJ (Hsp40) homolog, subfamily C, member 24	AL050199
227166_at	0.66301	6.29147	9.162777	5.89E-17	7.59E-16	27.6584	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	AI017750
239866_at	0.66271	5.664119	9.65436	2.29E-18	3.40E-17	30.87273			AA705933
235664_at	0.66255	5.599831	10.41404	1.35E-20	2.52E-19	35.95544			AI393695
238073_at	0.66246	3.804595	5.1433	6.38E-07	1.91E-06	4.973416	ELAVL4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	R55745
205113_at	0.66204	3.969838	7.393191	3.76E-12	2.80E-11	16.74035	NEFM	neurofilament, medium polypeptide	NM_005382
228184_at	0.66176	6.491887	6.620988	3.17E-10	1.76E-09	12.38705	DISP1	dispatched homolog 1 (Drosophila)	AK023679
221994_at	0.6617	5.096293	11.43001	1.20E-23	2.98E-22	42.92225	PDLIM5	PDZ and LIM domain 5	AA196325
1557078_at	0.66161	6.0906	5.625202	6.14E-08	2.24E-07	7.24431	SLFN5	schlafen family member 5	AK054668
201980_s_at	0.66145	9.588178	8.126644	4.39E-14	4.16E-13	21.12454	RSU1	Ras suppressor protein 1	NM_012425
221569_at	0.6612	7.363217	8.06526	6.42E-14	5.98E-13	20.74926	AHI1	Abelson helper integration site 1	AL136797
229893_at	0.6612	6.557892	5.806928	2.45E-08	9.67E-08	8.139251	FRMD3	FERM domain containing 3	BF589413
244579_at	0.66118	5.047418	7.94172	1.38E-13	1.23E-12	19.99842			AI086336
243084_at	0.66111	4.933288	12.77203	9.35E-28	3.25E-26	52.31726	CALD1	caldesmon 1	AA705063
225026_at	0.66111	6.256429	7.792711	3.42E-13	2.91E-12	19.10087	CHD6	chromodomain helicase DNA binding protein 6	BF572029
237521_x_at	0.66105	3.443362	4.436673	1.50E-05	3.44E-05	1.931802			R55749
221381_s_at	0.66088	10.35232	6.536364	5.06E-10	2.72E-09	11.92826	MORF4 MORF4L1	mortality factor 4 /// mortality factor 4 like 1	NM_006792
222171_s_at	0.66077	4.872114	12.3962	1.34E-26	4.26E-25	49.6709	PKNOX2	PBX/knotted 1 homeobox 2	AK023792
226198_at	0.66075	7.036828	10.46596	9.48E-21	1.80E-19	36.30726	TOM1L2	target of myb1-like 2 (chicken)	AV751731
226829_at	0.66068	6.000663	5.749145	3.29E-08	1.27E-07	7.852471	AFAP1L2	actin filament associated protein 1-like 2	AW138743
205857_at	0.66067	4.98287	6.304371	1.79E-09	8.77E-09	10.69037	SLC18A2	solute carrier family 18 (vesicular monoamine), member 2	AI269290
220591_s_at	0.66036	5.662232	4.866964	2.28E-06	6.12E-06	3.741624	EFHC2	EF-hand domain (C-terminal) containing 2	NM_025184
209009_at	0.66033	10.98416	8.579188	2.55E-15	2.78E-14	23.93399	ESD	esterase D/formylglutathione hydrolase	BC001169
235215_at	0.66024	5.787087	7.867935	2.16E-13	1.89E-12	19.55286	ERCC4	excision repair cross-complementing rodent repair deficiency, complementation group 4	AI694544
203923_s_at	0.66019	8.321927	4.385732	1.86E-05	4.19E-05	1.726576	CYBB	cytochrome b-245, beta polypeptide	NM_000397
200787_s_at	0.66007	9.074557	8.435519	6.34E-15	6.60E-14	23.03415	PEA15	phosphoprotein enriched in astrocytes 15	BC002426
235309_at	0.66007	7.063279	6.835623	9.51E-11	5.76E-10	13.56749	RPS15A	Ribosomal protein S15a	AA126311
244414_at	0.65998	5.194218	6.937041	5.34E-11	3.37E-10	14.13343			AI148006
209341_s_at	0.65974	7.973977	8.540986	3.25E-15	3.50E-14	23.69403	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	AU153366
211990_at	0.65937	11.7799	4.669608	5.50E-06	1.37E-05	2.894809	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	M27487
229841_at	0.65916	6.905947	6.725364	1.77E-10	1.03E-09	12.95812			BF223464

218545_at	0.65907	7.897501	6.334192	1.53E-09	7.56E-09	10.84783	CCDC91	coiled-coil domain containing 91	NM_018318
223853_at	0.65863	3.964425	8.6969	1.20E-15	1.36E-14	24.67648	BVES	blood vessel epicardial substance	AF204172
201654_s_at	0.65861	6.558327	8.272708	1.77E-14	1.75E-13	22.02322	HSPG2	heparan sulfate proteoglycan 2	AI991033
1552790_a_at	0.65838	8.243381	5.730523	3.51E-08	1.38E-07	7.760487	SEC62	SEC62 homolog (S. cerevisiae)	NM_153039
231171_at	0.65787	4.878486	10.91053	4.45E-22	9.58E-21	39.3395			AI948581
226902_at	0.65781	6.340517	8.767455	7.65E-16	8.82E-15	25.12371	USP13	isopeptidase T-3 (ISOT-3)	BF109140
212065_s_at	0.6578	6.714172	7.915144	1.62E-13	1.44E-12	19.83769	USP34	ubiquitin specific peptidase 34	AW502434
213341_at	0.65779	7.845142	6.431818	8.98E-10	4.63E-09	11.36677	FEM1C	fem-1 homolog c (C. elegans)	AI862658
223494_at	0.65776	7.426099	7.050352	2.79E-11	1.84E-10	14.77175	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	AF307332
213864_s_at	0.65771	11.06089	7.561493	1.38E-12	1.09E-11	17.72634	NAP1L1	nucleosome assembly protein 1-like 1	AI985751
1570523_s_at	0.65755	5.297158	7.045652	2.86E-11	1.89E-10	14.74515	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	AF318326
213455_at	0.65754	10.00764	8.226832	2.35E-14	2.30E-13	21.7401	FAM114A1	family with sequence similarity 114, member A1	W87466
212215_at	0.65752	8.67215	8.546428	3.14E-15	3.39E-14	23.72818	PREPL	prolyl endopeptidase-like	AB007896
204467_s_at	0.6574	5.718873	7.652073	8.02E-13	6.49E-12	18.26212	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	NM_000345
229822_at	0.65733	5.711476	10.06732	1.43E-19	2.41E-18	33.61993			AA564926
226429_at	0.65731	6.67704	7.096521	2.14E-11	1.43E-10	15.03363	KIAA1704	KIAA1704	BE218238
228153_at	0.65725	8.111093	5.567601	8.18E-08	2.91E-07	6.964954	RNF144B	ring finger protein 144B	AI953847
224953_at	0.65681	7.991206	6.808056	1.11E-10	6.66E-10	13.41456	YIPF5	Yip1 domain family, member 5	AW001618
232004_at	0.65674	6.622491	8.576107	2.60E-15	2.83E-14	23.91462	HNRNPR	heterogeneous nuclear ribonucleoprotein R	AK001846
230865_at	0.65661	3.239081	7.320419	5.78E-12	4.19E-11	16.31793	LIX1	Lix1 homolog (chicken)	N29837
53991_at	0.65655	6.553727	8.513581	3.87E-15	4.13E-14	23.5222	DENND2A	DENN/MADD domain containing 2A	AA127623
219837_s_at	0.65651	5.370505	6.223673	2.77E-09	1.31E-08	10.26677	CYTL1	cytokine-like 1	NM_018659
235012_at	0.65651	6.687682	8.363447	9.99E-15	1.02E-13	22.58547	LRCH1	leucine-rich repeats and calponin homology (CH) domain containing 1	D81713
229757_at	0.65631	7.661462	7.676414	6.92E-13	5.65E-12	18.4067	NAF1	CDNA FLJ40033 fis, clone STOMA2009289	AI741365
203337_x_at	0.65619	7.045398	5.516086	1.06E-07	3.68E-07	6.716899	ITGB1BP1	integrin beta 1 binding protein 1	NM_004763
214110_s_at	0.6561	7.598279	4.787283	3.27E-06	8.50E-06	3.39637	LOC65434	similar to lymphocyte-specific protein 1	BF195104
224895_at	0.65596	9.374184	5.587741	7.40E-08	2.66E-07	7.062387	YAP1	Yes-associated protein 1, 65kDa	AA557632
202259_s_at	0.65581	7.771255	6.462526	7.59E-10	3.96E-09	11.53108	N4BP2L2	NEDD4 binding protein 2-like 2	NM_014887
207704_s_at	0.65541	5.79697	8.859603	4.22E-16	5.01E-15	25.71022	GAS7	growth arrest-specific 7	NM_003644
233799_at	0.6554	3.646948	11.00598	2.30E-22	5.06E-21	39.99483			AU144136
226993_at	0.65535	9.331971	9.536449	5.01E-18	7.23E-17	30.0959			AA973551
234987_at	0.65526	9.47485	5.702697	4.16E-08	1.57E-07	7.623442			AV715309
204501_at	0.65501	5.844083	8.157631	3.62E-14	3.47E-13	21.31452	NOV	nephroblastoma overexpressed gene	NM_002514
229394_s_at	0.65436	9.189058	8.165534	3.45E-14	3.31E-13	21.36303	GRLF1	glucocorticoid receptor DNA binding factor 1	AI275597
203906_at	0.6543	7.583498	11.42309	1.26E-23	3.12E-22	42.8743	IQSEC1	IQ motif and Sec7 domain 1	AI652645
225816_at	0.65428	7.890654	6.78602	1.26E-10	7.48E-10	13.29258	PHF17	PHD finger protein 17	AW138134
202561_at	0.65417	7.59907	7.2926	6.81E-12	4.89E-11	16.15709	TNKS	tankyrase, TRF1-interacting ankyrin related ADP-ribose polymerase	AF070613
205188_s_at	0.6539	7.687022	7.250591	8.71E-12	6.15E-11	15.91488	SMAD5	SMAD family member 5	NM_005903
208033_s_at	0.65388	5.474287	9.788555	9.33E-19	1.44E-17	31.76107	ZFXH3	zinc finger homeobox 3	NM_006885
203146_s_at	0.65366	6.346635	8.952939	2.31E-16	2.81E-15	26.30703	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	NM_001470
225546_at	0.65366	7.849302	8.530227	3.48E-15	3.73E-14	23.62654	EEF2K	eukaryotic elongation factor-2 kinase	W68180
238782_at	0.65362	5.018412	9.17643	5.39E-17	6.97E-16	27.74678			BE877955
1557079_at	0.65346	3.530595	7.51812	1.79E-12	1.39E-11	17.47105	ITGBL1	Osteoblast specific cysteine-rich protein	AI753143
203599_s_at	0.65341	7.437123	8.753384	8.37E-16	9.63E-15	25.03439	WBP4	WW domain binding protein 4 (formin binding protein 21)	NM_007187
203939_at	0.65333	8.374919	3.984149	9.46E-05	0.0001874	0.178274	NT5E	5'-nucleotidase, ecto (CD73)	NM_002526
234405_s_at	0.65317	7.62892	7.462164	2.50E-12	1.90E-11	17.14291	PHAX	phosphorylated adaptor for RNA export	AK024065
202724_s_at	0.65313	7.829823	7.264915	8.01E-12	5.68E-11	15.99738	FOXO1	forkhead box O1	NM_002015

218699_at	0.65309	8.435555	6.263087	2.24E-09	1.08E-08	10.4732	RAB7L1	RAB7, member RAS oncogene family-like 1	BG338251
205846_at	0.65304	6.589876	8.419117	7.03E-15	7.28E-14	22.93188	PTPRB	protein tyrosine phosphatase, receptor type, B	NM_002837
221060_s_at	0.65298	6.093136	6.180902	3.47E-09	1.62E-08	10.04375	TLR4	toll-like receptor 4	NM_003266
223189_x_at	0.6529	9.006703	10.16014	7.61E-20	1.32E-18	34.24275	MLL5	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	AW082219
220936_s_at	0.65269	5.183604	8.330965	1.23E-14	1.24E-13	22.38386	H2AFJ	H2A histone family, member J	NM_018267
227122_at	0.6526	6.578135	9.533916	5.10E-18	7.34E-17	30.07925	ZNF791	Zinc finger protein 791 (ZNF791), mRNA	AI807498
244404_at	0.65253	5.243243	10.42228	1.28E-20	2.39E-19	36.01125	STXBPA	syntaxis binding protein 4	AI376134
202499_s_at	0.65234	8.17442	3.712757	0.0002653	0.0004874	-0.79609	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	NM_006931
213075_at	0.65233	7.718312	6.790205	1.23E-10	7.32E-10	13.31573	OLFML2A	olfactomedin-like 2A	AL050002
229884_s_at	0.65228	7.476919	6.991195	3.92E-11	2.53E-10	14.43772	MRPL2	mitochondrial ribosomal protein L2	AA187325
221897_at	0.65208	6.41861	8.151937	3.75E-14	3.58E-13	21.27958	TRIM52	tripartite motif-containing 52	AA205660
239984_at	0.65198	3.399429	9.888349	4.77E-19	7.62E-18	32.42448			AI333640
232088_x_at	0.65193	4.027345	9.189343	4.95E-17	6.42E-16	27.83041			AL137569
1553646_at	0.65164	3.655266	11.91603	3.98E-25	1.13E-23	46.30544	HDX	highly divergent homeobox	NM_144657
204904_at	0.65157	7.299202	8.609455	2.10E-15	2.32E-14	24.12446	GJA4	gap junction protein, alpha 4, 37kDa	NM_002060
204436_at	0.65157	8.440614	9.889025	4.75E-19	7.59E-18	32.42898	PLEKHO2	pleckstrin homology domain containing, family O member 2	NM_025201
227319_at	0.65153	9.065245	10.5766	4.44E-21	8.74E-20	37.05866			AI693862
232898_at	0.65149	4.977372	8.171076	3.33E-14	3.20E-13	21.39706	DAB2	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	R79120
220467_at	0.65137	4.534144	8.811367	5.76E-16	6.73E-15	25.40287	FUJ1272	hypothetical protein FUJ1272	NM_025032
235301_at	0.65131	6.336444	5.14391	6.36E-07	1.91E-06	4.976191	KIAA1324L	KIAA1324-like	AI797353
230292_at	0.65124	5.999419	6.792676	1.21E-10	7.23E-10	13.3294	LOC100131993	similar to hCG2020760	AA868809
212967_x_at	0.65111	11.17058	8.447213	5.89E-15	6.16E-14	23.10713	NAP1L1	nucleosome assembly protein 1-like 1	AW148801
230821_at	0.65109	6.950423	8.532635	3.43E-15	3.68E-14	23.64164	ZNF148	zinc finger protein 148	AW594167
221264_s_at	0.651	7.281174	9.006386	1.63E-16	2.02E-15	26.64998	LOC100128223 /// TARDBP	hypothetical protein LOC100128223 /// TAR DNA binding protein	NM_031214
204763_s_at	0.65093	6.271989	7.195648	1.20E-11	8.33E-11	15.59934	GNAO1	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	NM_020988
208102_s_at	0.65088	5.499255	10.11715	1.02E-19	1.74E-18	33.95409	PSD	pleckstrin and Sec7 domain containing	NM_002779
1555968_a_at	0.65082	6.221315	7.305329	6.32E-12	4.55E-11	16.23064			AA362254
222868_s_at	0.65074	7.421964	5.102553	7.72E-07	2.28E-06	4.788474	IL18BP	interleukin 18 binding protein	AI521549
235129_at	0.65069	4.766277	6.977773	4.23E-11	2.71E-10	14.36216	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A	BF510098
226441_at	0.65064	7.323524	8.792246	6.52E-16	7.57E-15	25.28123			AA045204
213998_s_at	0.65042	7.937817	6.165509	3.77E-09	1.75E-08	9.963741	DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	AW188131
239571_at	0.65034	4.84506	6.467878	7.37E-10	3.86E-09	11.55977			AI123399
201160_s_at	0.65007	11.64382	9.014545	1.55E-16	1.92E-15	26.70241	CSDA	cold shock domain protein A	AL556190
202953_at	0.64979	9.286072	3.781312	0.0002055	0.0003847	-0.55557	C1QB	complement component 1, q subcomponent, B chain	NM_000491
218221_at	0.64979	7.237414	9.218349	4.09E-17	5.37E-16	28.01845	ARNT	aryl hydrocarbon receptor nuclear translocator	AL042842
221478_at	0.64974	10.22521	7.435023	2.94E-12	2.21E-11	16.98425	BNIP3L	BCL2/adenovirus E1B 19kDa interacting protein 3-like	AL132665
219156_at	0.64957	7.889723	7.419232	3.22E-12	2.42E-11	16.89209	SYNU2BP	synaptotagmin 2 binding protein	NM_018373
205499_at	0.64956	6.81823	4.466471	1.32E-05	3.06E-05	2.052752	SRPX2	sushi-repeat-containing protein, X-linked 2	NM_014467
236358_at	0.64955	4.808822	9.838788	6.66E-19	1.05E-17	32.09472			BF445865
228506_at	0.6491	5.936165	6.446118	8.31E-10	4.30E-09	11.44321	NSMCE4A	non-SMC element 4 homolog A (S. cerevisiae)	AA009947
232701_at	0.64905	4.289813	9.704072	1.64E-18	2.47E-17	31.20131			AU159344
223134_at	0.64903	8.919465	8.69645	1.21E-15	1.36E-14	24.67363	BBX	bobby sox homolog (Drosophila)	AI795970

226880_at	0.64873	10.48203	7.120917	1.85E-11	1.25E-10	15.17242	NUCKS1	Unknown mRNA	AL035851
204192_at	0.64873	6.653416	3.769543	0.0002148	0.0004009	-0.59714	CD37	CD37 molecule	NM_001774
234982_at	0.64871	8.338908	8.469265	5.12E-15	5.38E-14	23.24487	UBR3	ubiquitin protein ligase E3 component n-recognin 3 (putative)	BF577193
229009_at	0.64846	7.468063	9.032437	1.38E-16	1.71E-15	26.81745	SIX5	SIX homeobox 5	AA527770
230311_s_at	0.64842	6.70983	8.189548	2.97E-14	2.87E-13	21.51058	PRDM6	PR domain containing 6	AF272898
228537_at	0.64817	6.692197	11.4344	1.17E-23	2.90E-22	42.9527	GLI2	GLI-Kruppel family member GLI2	AI797248
226715_at	0.64802	7.953631	7.380238	4.06E-12	3.00E-11	16.66499	FOXK1	forkhead box K1	AW007319
219479_at	0.64796	6.570642	5.226923	4.29E-07	1.33E-06	5.35649	KDELC1	KDEL (Lys-Asp-Glu-Leu) containing 1	NM_024089
224724_at	0.6475	9.775265	5.046472	1.00E-06	2.89E-06	4.535785	SULF2	sulfatase 2	AL133001
212870_at	0.64735	8.726496	8.239452	2.17E-14	2.13E-13	21.81791	SOS2	son of sevenless homolog 2 (Drosophila)	AI628605
1554667_s_at	0.64726	7.492543	7.214351	1.08E-11	7.52E-11	15.70659	METTL8	methyltransferase like 8	BC025250
208178_x_at	0.64714	7.283531	8.680798	1.33E-15	1.50E-14	24.57464	TRIO	triple functional domain (PTPRF interacting)	NM_007118
238489_at	0.64709	5.071417	12.0578	1.47E-25	4.29E-24	47.29702	PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	BF575153
1556579_s_at	0.64707	4.220051	6.361673	1.32E-09	6.59E-09	10.99337	IGSF10	immunoglobulin superfamily, member 10	AF087980
1558220_at	0.6467	5.228945	7.140887	1.65E-11	1.12E-10	15.28625	MUC20	Mucin 20, cell surface associated (MUC20), transcript variant L, mRNA	BM914560
226326_at	0.64665	8.579525	7.951554	1.30E-13	1.16E-12	20.05797	PCGF5	polycomb group ring finger 5	AI798098
212480_at	0.64661	7.966868	10.73616	1.48E-21	3.03E-20	38.14609	CYTSA	cytoslin A	AB002374
228749_at	0.6464	5.042621	7.19949	1.17E-11	8.16E-11	15.62135	ZDBF2	zinc finger, DBF-type containing 2	AV734793
205792_at	0.64636	5.746893	5.074033	8.82E-07	2.57E-06	4.659699	WISP2	WNT1 inducible signaling pathway protein 2	NM_003881
207764_s_at	0.64613	5.204199	7.190067	1.24E-11	8.58E-11	15.56736	HIPK3	homeodomain interacting protein kinase 3	NM_005734
201869_s_at	0.646	6.856385	7.495058	2.05E-12	1.58E-11	17.33564	TBL1X	transducin (beta)-like 1X-linked	BF593932
1568594_s_at	0.64592	6.719467	8.541893	3.23E-15	3.48E-14	23.69972	TRIM52	tripartite motif-containing 52	AW965171
208656_s_at	0.64589	11.66877	13.52008	4.56E-30	1.93E-28	57.60544	CCNI	cyclin I	AF135162
241401_at	0.64588	3.617657	10.83793	7.36E-22	1.55E-20	38.842	C4orf12	chromosome 4 open reading frame 12	BG496631
242363_at	0.64585	7.403249	6.574019	4.11E-10	2.25E-09	12.13194			BF592008
210329_s_at	0.64572	6.020978	12.4274	1.08E-26	3.44E-25	49.8903	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	U58331
1558881_at	0.64562	4.34071	10.31314	2.69E-20	4.87E-19	35.27328	LOC145820	hypothetical protein LOC145820	AK057337
206001_at	0.64546	5.377228	4.286085	2.82E-05	6.13E-05	1.330798	NPY	neuropeptide Y	NM_000905
1554089_s_at	0.64542	10.12805	7.260242	8.23E-12	5.83E-11	15.97045	SBDS /// SBDSP	Shwachman-Bodian-Diamond syndrome /// Shwachman-Bodian-Diamond syndrome pseudogene	BC010183
231840_x_at	0.64536	6.585055	8.045947	7.24E-14	6.70E-13	20.63149	LYRM7	Lyrm7 homolog (mouse)	AK000803
208655_at	0.64528	11.31189	13.12129	7.81E-29	2.96E-27	54.78356			BG530368
215028_at	0.64462	4.120668	5.352611	2.35E-07	7.66E-07	5.941063	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	AB002438
221501_x_at	0.64445	10.30023	9.10087	8.82E-17	1.12E-15	27.25836	LOC100132540 /// LOC100132620 /// LOC339047	similar to LOC339047 protein /// similar to LOC339047 protein /// hypothetical protein LOC339047 /// nuclear pore complex interacting protein	AF229069
215096_s_at	0.64432	10.79114	7.963565	1.20E-13	1.09E-12	20.13075	ESD	esterase D/formylglutathione hydrolase	AU145746
230800_at	0.64412	7.395965	8.442741	6.06E-15	6.32E-14	23.07922	ADCY4	adenylate cyclase 4	AV699353
235009_at	0.6437	7.052507	6.679653	2.29E-10	1.30E-09	12.70732	FAM44A	family with sequence similarity 44, member A	AI049791
200605_s_at	0.6437	11.24131	10.48751	8.18E-21	1.56E-19	36.45345	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	NM_002734

229063_s_at	0.64335	7.664145	9.789212	9.28E-19	1.44E-17	31.76543	CCDC107	coiled-coil domain containing 107	AI912238
237025_at	0.64334	5.090981	12.23462	4.21E-26	1.28E-24	48.53623			AI127738
240418_at	0.64332	4.494662	12.94338	2.77E-28	1.00E-26	53.52654			AW015426
229968_at	0.6432	6.388408	7.22604	1.01E-11	7.04E-11	15.77371			AA504245
203552_at	0.64297	8.026846	7.011363	3.49E-11	2.27E-10	14.55141	MAP4K5	mitogen-activated protein kinase kinase kinase 5	AW298170
208873_s_at	0.64293	10.21165	7.669801	7.20E-13	5.87E-12	18.36739	REEP5	receptor accessory protein 5	BC000232
210778_s_at	0.64269	7.437081	10.03006	1.84E-19	3.07E-18	33.37047	MXD4	MAX dimerization protein 4	BC002713
222983_s_at	0.64249	9.728764	8.691749	1.24E-15	1.40E-14	24.64389	PAIP2	poly(A) binding protein interacting protein 2	BC001716
217100_s_at	0.64247	7.016481	6.730756	1.72E-10	9.99E-10	12.98777	UBXN7	UBX domain protein 7	AK026451
231854_at	0.64236	4.673158	14.02079	1.28E-31	6.21E-30	61.15329	PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide	W63579
229974_at	0.64234	4.293874	9.227228	3.86E-17	5.08E-16	28.07606	EVC2	Ellis van Creveld syndrome 2	AA234305
212124_at	0.64223	9.944763	9.135562	7.04E-17	9.00E-16	27.4824	ZMI21	zinc finger, MIZ-type containing 1	AF070622
211825_s_at	0.64223	6.112505	7.446542	2.74E-12	2.08E-11	17.05155	EWSR1 /// FLI1	Ewing sarcoma breakpoint region 1 /// Friend leukemia virus Integration 1	AF327066
214693_x_at	0.6419	9.419356	8.313387	1.37E-14	1.37E-13	22.27491	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// RP11-94I2.2	KIAA1245 /// neuroblastoma breakpoint family, member 1 /// neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family, member 11 /// neuroblastoma breakpoint family, member 14 /// neuroblastoma breakpoint family, member 16 /// neuroblastoma breakpoint family, member 20 /// neuroblastoma breakpoint family, member 8 /// neuroblastoma breakpoint family, member 9 /// hypothetical protein LOC200030	BE732345
208861_s_at	0.64162	8.998659	8.52131	3.68E-15	3.94E-14	23.57063	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevisiae</i>)	U72937
218613_at	0.64146	7.168288	5.882587	1.66E-08	6.78E-08	8.517831	PSD3	pleckstrin and Sec7 domain containing 3	NM_018422
200785_s_at	0.64129	7.539111	8.83729	4.88E-16	5.74E-15	25.56796	LRP1	similar to low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) /// low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	NM_002332
209818_s_at	0.64122	6.496593	11.81739	7.97E-25	2.20E-23	45.61667	HABP4	hyaluronan binding protein 4	AF241831
210146_x_at	0.64115	5.063968	5.311621	2.86E-07	9.18E-07	5.749268	LILRB2	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2	AF004231
206356_s_at	0.64108	4.64992	8.167555	3.41E-14	3.27E-13	21.37544	GNAL	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type	NM_002071
210510_s_at	0.64094	6.644501	6.746527	1.57E-10	9.20E-10	13.0746	NRP1	neuropilin 1	AF145712
238523_at	0.64087	7.360777	8.810928	5.78E-16	6.74E-15	25.40008	KLHL36	kelch-like 36 (<i>Drosophila</i>)	BF941204
210916_s_at	0.64065	8.333682	5.045069	1.01E-06	2.91E-06	4.529493	CD44	CD44 molecule (Indian blood group)	AF098641
222726_s_at	0.64058	7.271751	7.275262	7.54E-12	5.37E-11	16.05703	EXOC5	exocyst complex component 5	BF696912
209019_s_at	0.64033	8.464431	10.49836	7.60E-21	1.46E-19	36.52708	PINK1	PTEN induced putative kinase 1	AF316873
237860_at	0.64031	3.558835	11.4705	9.07E-24	2.28E-22	43.20305			AI821998
227260_at	0.64027	6.578331	4.702759	4.76E-06	1.20E-05	3.035095	ANKRD10	Ankyrin repeat domain 10, mRNA (cDNA clone IMAGE:5752308)	AV724266

204538_x_at	0.64019	10.04864	9.528658	5.28E-18	7.59E-17	30.04469	NPIP	nuclear pore complex interacting protein	NM_006985
212209_at	0.64014	8.274199	10.85837	6.39E-22	1.35E-20	38.98203	MED13L	mediator complex subunit 13-like	AL133033
215287_at	0.6401	5.623318	6.893216	6.86E-11	4.25E-10	13.88824			AA975427
1559954_s_at	0.64	7.405926	7.418284	3.24E-12	2.43E-11	16.88656	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	AF147429
223093_at	0.63989	7.131679	5.822728	2.26E-08	8.98E-08	8.218026	ANKH	ankylosis, progressive homolog (mouse)	T99215
239432_at	0.63972	4.796246	9.204242	4.49E-17	5.85E-16	27.92697	FLJ31306	hypothetical protein FLJ31306	AV729086
219234_x_at	0.63967	5.64287	5.911131	1.43E-08	5.93E-08	8.661559	SCRN3	secernin 3	NM_024583
233599_at	0.63962	5.524593	6.23391	2.62E-09	1.25E-08	10.3203	hCG_2003663	hCG2003663	AK025151
205845_at	0.63955	6.449781	10.13905	8.78E-20	1.51E-18	34.10111	CACNA1H	calcium channel, voltage-dependent, T type, alpha 1H subunit	NM_021098
225953_at	0.63954	9.100233	5.921464	1.36E-08	5.64E-08	8.713708	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	AI684281
226075_at	0.63945	7.09686	6.766098	1.41E-10	8.30E-10	13.18252	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	AF131840
221792_at	0.63908	7.034583	8.569348	2.71E-15	2.95E-14	23.87213	RAB6B	RAB6B, member RAS oncogene family	AW118072
235082_at	0.63901	4.103298	10.72276	1.63E-21	3.32E-20	38.05461	PCNX	pecanex homolog (Drosophila)	BG024649
223387_at	0.639	8.040896	10.82128	8.25E-22	1.73E-20	38.72809	ZFYVE1	zinc finger, FYVE domain containing 1	AB046809
230803_s_at	0.63899	5.652206	8.848144	4.55E-16	5.37E-15	25.63714	ARHGAP24	Rho GTPase activating protein 24	AI761947
222357_at	0.6386	5.665358	6.075015	6.09E-09	2.71E-08	9.496153	ZBTB20	zinc finger and BTB domain containing 20	AW974823
1552274_at	0.63838	7.039224	8.065687	6.41E-14	5.97E-13	20.75186	PXK	PX domain containing serine/threonine kinase	BC014479
205551_at	0.63804	5.28955	7.169358	1.40E-11	9.60E-11	15.44885	SV2B	synaptic vesicle glycoprotein 2B	NM_014848
227119_at	0.63804	6.983322	7.503597	1.95E-12	1.51E-11	17.38575	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	BF103856
206061_s_at	0.63793	7.403994	6.488816	6.57E-10	3.46E-09	11.67216	DICER1	dicer 1, ribonuclease type III	NM_030621
230226_s_at	0.63773	6.094446	9.117011	7.94E-17	1.01E-15	27.36255	JARID1A	Jumonji, AT rich interactive domain 1A	AW612682
1557081_at	0.6377	6.382697	7.325448	5.61E-12	4.07E-11	16.34705	RBM25	RNA binding motif protein 25	AA580691
234947_s_at	0.63726	7.83915	7.653027	7.97E-13	6.45E-12	18.26778	C10orf84	chromosome 10 open reading frame 84	AK026630
222826_at	0.63706	9.114717	7.519983	1.77E-12	1.37E-11	17.482	PLDN	pallidin homolog (mouse)	BC004819
209750_at	0.63698	7.598795	5.332744	2.59E-07	8.36E-07	5.847968	NR102	nuclear receptor subfamily 1, group D, member 2	N32859
205917_at	0.63688	7.414688	6.812076	1.09E-10	6.53E-10	13.43683	ZNF264	zinc finger protein 264	NM_003417
202321_at	0.63647	7.076275	6.499409	6.20E-10	3.28E-09	11.7291	GGPS1	geranylgeranyl diphosphate synthase 1	AW299507
218032_at	0.63645	8.164319	6.501165	6.14E-10	3.25E-09	11.73855	SNN	stannin	AF070673
243521_at	0.63633	5.989045	7.569192	1.32E-12	1.04E-11	17.77175			AW590862
227405_s_at	0.63624	7.836389	6.36832	1.27E-09	6.37E-09	11.02864	FZD8	frizzled homolog 8 (Drosophila)	AW340311
205237_at	0.63624	5.76813	4.848636	2.48E-06	6.60E-06	3.661808	FCN1	ficolin (collagen/fibrinogen domain containing) 1	NM_002003
230211_at	0.63607	4.283661	9.383281	1.38E-17	1.90E-16	29.09217			R32893
213252_at	0.63584	6.700815	8.431085	6.52E-15	6.78E-14	23.0065	SH3PXD2A	SH3 and PX domains 2A	AI739005
225199_at	0.6358	8.840177	8.805372	5.99E-16	6.98E-15	25.36472			AA526970
210635_s_at	0.63564	6.19297	8.47408	4.97E-15	5.24E-14	23.27497	KLHL20	kelch-like 20 (Drosophila)	BC005253
235424_at	0.63553	6.913433	10.0337	1.79E-19	2.99E-18	33.39487			N66727
203186_s_at	0.63537	11.06728	4.36277	2.05E-05	4.57E-05	1.634705	S100A4	S100 calcium binding protein A4 family with sequence similarity 65, member C	NM_002961
227654_at	0.63518	6.233992	4.382509	1.89E-05	4.24E-05	1.713657	FAM65C		AI056877
227092_at	0.63495	7.07661	6.926302	5.68E-11	3.56E-10	14.07326			AI341383
218450_at	0.63448	9.645749	6.725357	1.77E-10	1.03E-09	12.95808	HEBP1	heme binding protein 1	NM_015987
1559412_at	0.6344	4.110075	16.30976	1.11E-38	1.11E-36	77.32057	C21orf34	chromosome 21 open reading frame 34	H04858
219137_s_at	0.63429	9.047101	7.747314	4.51E-13	3.78E-12	18.82923	MF	mitochondrial fission factor	NM_020194
205091_x_at	0.63419	8.363352	6.674513	2.35E-10	1.34E-09	12.67919	RECQL	RecQ protein-like (DNA helicase Q1 like)	NM_002907
242467_at	0.63417	6.189123	5.390321	1.96E-07	6.48E-07	6.118488			BF433200

225928_at	0.634	7.596569	8.229294	2.32E-14	2.26E-13	21.75528	VT11B	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	AI984620
201963_at	0.63395	8.995332	4.66099	5.72E-06	1.42E-05	2.858468	ACSL1	acyl-CoA synthetase long-chain family member 1	NM_021122
212582_at	0.63394	10.00924	6.321245	1.64E-09	8.06E-09	10.7794	OSBPL8	oxysterol binding protein-like 8	AL049923
233329_s_at	0.63385	8.490285	5.722767	3.76E-08	1.43E-07	7.722241	KRCC1	lysine-rich coiled-coil 1	AK025986
200760_s_at	0.63371	10.69038	8.768289	7.61E-16	8.78E-15	25.129	ARL6IP5	ADP-ribosylation-like factor 6 interacting protein 5	N92494
1556989_at	0.6336	5.015886	6.416839	9.75E-10	4.99E-09	11.2868			AF086069
226872_at	0.63347	6.175533	7.12353	1.83E-11	1.24E-10	15.18731	RFX2	regulatory factor X, 2 (influences HLA class II expression)	AK024288
224999_at	0.63346	7.778927	4.747241	3.91E-06	1.00E-05	3.224582			BE878463
212441_at	0.63346	9.085688	8.728985	9.79E-16	1.12E-14	24.87966	KIAA0232	KIAA0232	D86985
224989_at	0.63339	9.08761	4.8495	2.47E-06	6.58E-06	3.665565			AI824013
235390_at	0.63332	7.052599	7.332967	5.37E-12	3.91E-11	16.3906	SFRS12IP1	SFRS12-interacting protein 1	AA398321
223667_at	0.63317	4.05976	10.55339	5.21E-21	1.02E-19	36.90082	FKBP7	FK506 binding protein 7	AF092137
229352_at	0.63279	4.467774	5.426091	1.64E-07	5.53E-07	6.287642	NOX5 /// SPESP1	NADPH oxidase, EF-hand calcium binding domain 5 /// sperm equatorial segment protein 1	AA885360
223495_at	0.63262	6.24411	8.370798	9.54E-15	9.75E-14	22.63115	CCDC8	coiled-coil domain containing 8	AI970823
1560101_at	0.63238	4.025181	9.983808	2.51E-19	4.13E-18	33.06123	SYDE2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	AL834286
222793_at	0.63237	7.205866	5.830265	2.17E-08	8.67E-08	8.255653	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	AK023651
223634_at	0.63228	5.001372	9.227579	3.85E-17	5.06E-16	28.07834	RASD2	RASD family, member 2	AF279143
201054_at	0.63213	10.31659	9.986866	2.46E-19	4.06E-18	33.08166	HNRNPA0	heterogeneous nuclear ribonucleoprotein A0	BE966599
235305_s_at	0.63203	6.782493	9.509906	5.98E-18	8.57E-17	29.92151	ECHDC2	enoyl Coenzyme A hydratase domain containing 2	AI903313
207238_s_at	0.63199	8.086923	3.845242	0.0001615	0.0003076	-0.32784	PTPRC	protein tyrosine phosphatase, receptor type, C	NM_002838
236922_at	0.63196	6.230846	8.149291	3.81E-14	3.64E-13	21.26335			AA772352
212538_at	0.63196	8.526516	7.91883	1.58E-13	1.41E-12	19.85997	DOCK9	dedicator of cytokinesis 9	AL576253
239272_at	0.63183	6.589056	3.610212	0.0003861	0.0006903	-1.14869	MMP28	matrix metalloproteinase 28	AI927208
225971_at	0.63159	7.05964	7.909795	1.67E-13	1.48E-12	19.80537	DDHD1	DDHD domain containing 1	AI741411
209084_s_at	0.63135	6.591865	8.107316	4.95E-14	4.67E-13	21.00621	RAB28	RAB28, member RAS oncogene family	BE504689
226690_at	0.63112	5.430421	7.237652	9.39E-12	6.60E-11	15.84045	ADCYAP1R1	CDNA FLJ39226 fis, clone OCBFF2007232	AW451961
222967_at	0.63107	3.611437	8.286423	1.62E-14	1.61E-13	22.10801	SLC5A7	solute carrier family 5 (choline transporter), member 7	AB043997
1562235_s_at	0.63097	3.849947	6.354756	1.37E-09	6.82E-09	10.9567			AL832146
212463_at	0.63095	9.487497	7.492994	2.08E-12	1.60E-11	17.32353	CD59	CD59 molecule, complement regulatory protein	BE379006
208741_at	0.63082	7.930815	7.50881	1.89E-12	1.46E-11	17.41636	SAP18	Sin3A-associated protein, 18kDa	AW274856
228835_at	0.63079	7.385662	8.512859	3.89E-15	4.14E-14	23.51767			AV700050
230068_s_at	0.63056	4.318784	10.42281	1.27E-20	2.39E-19	36.01483	PEG3	KIAA0287 gene	W93046
227978_s_at	0.63038	6.808655	6.207964	3.01E-09	1.42E-08	10.18474	ZADH2	zinc binding alcohol dehydrogenase domain containing 2	BF591611
1558199_at	0.63025	4.636644	5.720646	3.80E-08	1.45E-07	7.711786	FN1	fibronectin 1	W73431
227471_at	0.63019	7.240772	7.572452	1.29E-12	1.02E-11	17.79098	HACE1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	AB037741
204140_at	0.63016	6.844818	5.852578	1.94E-08	7.80E-08	8.367258	TPST1	tyrosylprotein sulfotransferase 1	NM_003596
236862_at	0.62989	4.387863	8.366494	9.80E-15	1.00E-13	22.6044	GOPC	CFTR-associated ligand (CAL)	AA279958
219278_at	0.62974	7.032836	9.242645	3.49E-17	4.60E-16	28.17614	MAP3K6	mitogen-activated protein kinase kinase kinase 6	NM_004672
223524_s_at	0.62956	5.689558	7.5192	1.78E-12	1.38E-11	17.4774	TMEM108	transmembrane protein 108	BC000568
232181_at	0.62954	6.715242	5.16842	5.67E-07	1.71E-06	5.087992	LOC15334	hypothetical protein LOC153346	AU157049
218678_at	0.62941	7.989854	6.205406	3.05E-09	1.43E-08	10.17139	NES	nestin	NM_024609
220055_at	0.62941	4.127976	10.63	3.08E-21	6.13E-20	37.42208	ZNF287	zinc finger protein 287	NM_020653
229803_s_at	0.62923	8.557176	9.305277	2.31E-17	3.10E-16	28.58341			AI347000

213709_at	0.62904	5.365394	6.823983	1.02E-10	6.13E-10	13.50287	BHLHB9	basic helix-loop-helix domain containing, class B, 9	H11725
238062_at	0.62891	5.622877	7.701655	5.94E-13	4.89E-12	18.55688	GPIHBP1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1	W72062
229586_at	0.62891	7.462358	6.518798	5.58E-10	2.98E-09	11.8335	CHD9	chromodomain helicase DNA binding protein 9	AW300405
226580_at	0.62887	7.63725	7.993533	1.00E-13	9.12E-13	20.31259	BRMS1L	breast cancer metastasis-suppressor 1-like	AA779684
244112_x_at	0.62882	4.121866	7.027396	3.18E-11	2.08E-10	14.64193			N73550
228180_at	0.62882	5.418828	8.331039	1.22E-14	1.24E-13	22.38431			AA805653
241859_at	0.62882	4.13795	12.67503	1.86E-27	6.30E-26	51.63344	PLCL1	phospholipase C-like 1	BF593050
206163_at	0.62881	3.859668	8.07585	6.02E-14	5.62E-13	20.8139	MAB21L1	mab-21-like 1 (C. elegans)	NM_005584
226831_at	0.62864	8.885714	6.481188	6.86E-10	3.60E-09	11.63118	SLC25A46	CDNA FLJ56268 complete cds	AA928542
242587_at	0.62861	6.049274	9.281539	2.70E-17	3.60E-16	28.42893	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	AA029791
65472_at	0.62856	5.382696	8.879719	3.71E-16	4.42E-15	25.83862	C2orf68	chromosome 2 open reading frame 68	AI161338
221858_at	0.62851	7.420797	7.790907	3.46E-13	2.94E-12	19.09006	TBC1D12	TBC1 domain family, member 12	N34407
222088_s_at	0.62845	7.422077	3.871274	0.0001462	0.0002806	-0.23417	SLC2A14 /// SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 14 /// solute carrier family 2 (facilitated glucose transporter), member 3	AA778684
208933_s_at	0.6284	8.116564	6.719206	1.83E-10	1.06E-09	12.92427	LGALS8	lectin, galactoside-binding, soluble, 8	AI659005
221916_at	0.62836	4.21518	5.875707	1.72E-08	7.00E-08	8.483262	NEFL	neurofilament, light polypeptide	BF055311
237444_at	0.62834	6.145339	7.485305	2.18E-12	1.67E-11	17.27845			AI801902
216252_x_at	0.62812	6.280989	4.108653	5.79E-05	0.0001188	0.644914	FAS	Fas (TNF receptor superfamily, member 6)	Z70519
204849_at	0.62803	8.017082	5.188274	5.16E-07	1.57E-06	5.178854	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	NM_006602
235267_at	0.62798	3.445252	12.62441	2.67E-27	8.92E-26	51.27674			AV732165
225875_s_at	0.62793	7.378118	8.629643	1.85E-15	2.05E-14	24.25168	NPAL3	NIPA-like domain containing 3	T84558
205088_at	0.62752	5.839348	7.205811	1.13E-11	7.87E-11	15.6576	MAMLD1	mastermind-like domain containing 1	NM_005491
229603_at	0.62751	5.640703	6.569995	4.20E-10	2.29E-09	12.11013	BBS12	Bardet-Biedl syndrome 12	AA971753
202011_at	0.62745	10.52327	8.475323	4.93E-15	5.20E-14	23.28274	TJP1	tight junction protein 1 (zona occludens 1)	NM_003257
212184_s_at	0.62739	9.16909	9.065246	1.14E-16	1.40E-15	27.02866	MAP3K7IP2	mitogen-activated protein kinase kinase 7 interacting protein 2	AL117407
1555536_at	0.62727	6.980885	10.60409	3.68E-21	7.27E-20	37.24567	ANTXR2	anthrax toxin receptor 2	AY040326
211395_x_at	0.62725	7.594635	4.8897	2.06E-06	5.57E-06	3.840959	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	U90940
228686_at	0.62724	6.242724	6.121087	4.77E-09	2.17E-08	9.733619	FLJ33630	hypothetical LOC644873	BE217923
228569_at	0.62711	7.484172	5.970085	1.05E-08	4.48E-08	8.959957	PAPOLA	poly(A) polymerase alpha	AV683473
227730_at	0.62702	6.315488	9.848336	6.24E-19	9.84E-18	32.1582			AI052390
221771_s_at	0.62696	8.266436	8.377066	9.17E-15	9.38E-14	22.67011	MPHOSPH8	M-phase phosphoprotein 8	BC003542
226158_at	0.62691	8.064726	5.59111	7.28E-08	2.62E-07	7.078713	KLHL24	kelch-like 24 (Drosophila)	AL120021
226447_at	0.62684	8.49556	7.814306	3.00E-13	2.57E-12	19.23039	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	BG290742
212585_at	0.62682	9.60334	8.651768	1.60E-15	1.79E-14	24.39125	OSBPL8	oxysterol binding protein-like 8	BF970829
221634_at	0.62672	7.155946	7.426504	3.09E-12	2.32E-11	16.93452	RPL23AP7	ribosomal protein L23a pseudogene 7	BC000596
209475_at	0.62672	7.813605	8.820122	5.45E-16	6.38E-15	25.4586	USP15	ubiquitin specific peptidase 15	AF106069
222863_at	0.62671	4.668832	6.05592	6.73E-09	2.97E-08	9.398096	ZBTB10	zinc finger and BTB domain containing 10	BG483802
201685_s_at	0.62671	7.616258	9.252473	3.27E-17	4.33E-16	28.23998	TOX4	TOX high mobility group box family member 4	NM_014828
227274_at	0.62643	8.729551	7.526993	1.70E-12	1.32E-11	17.52321	SYNJ2BP	synaptotagmin 2 binding protein	AI709389
230104_s_at	0.62637	7.533788	5.228594	4.26E-07	1.32E-06	5.364193	TPPP	tubulin polymerization promoting protein	BG055052
226124_at	0.62637	7.528263	9.842427	6.50E-19	1.02E-17	32.11891	ZFP90	zinc finger protein 90 homolog (mouse)	AA747309
203872_at	0.62636	4.147512	6.913989	6.09E-11	3.80E-10	14.00434	ACTA1	actin, alpha 1, skeletal muscle	NM_001100
225274_at	0.62632	9.529928	7.53764	1.59E-12	1.24E-11	17.58585	PCYOX1	prenylcysteine oxidase 1	BF247054

226219_at	0.62608	7.267968	4.811206	2.94E-06	7.70E-06	3.499551	ARRHGAP30	Rho GTPase activating protein 30	AW575123
214467_at	0.6256	6.996436	4.905812	1.91E-06	5.21E-06	3.911579	GPR65	G protein-coupled receptor 65	NM_003608
1553192_at	0.62557	3.837727	13.5091	4.93E-30	2.08E-28	57.52771	ZNF441	zinc finger protein 441	NM_152355
227665_at	0.62552	7.171683	8.706511	1.13E-15	1.28E-14	24.7373			BE968576
225881_at	0.62547	7.5373	8.079876	5.87E-14	5.49E-13	20.83848	SLC35B4	solute carrier family 35, member B4	AL513639
205510_s_at	0.62547	6.38212	8.928292	2.71E-16	3.28E-15	26.14917	FLJ10038	hypothetical protein FLJ10038	NM_017976
209042_s_at	0.62532	9.012947	8.651133	1.61E-15	1.80E-14	24.38725	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	BC001738
225507_at	0.62523	9.1722	7.709862	5.65E-13	4.67E-12	18.60577	SFRS18	splicing factor, arginine/serine-rich 18	BF591408
1552386_at	0.62514	4.114305	5.989962	9.51E-09	4.07E-08	9.06103	GAPT	GRB2-binding adaptor protein, transmembrane	NM_152687
218909_at	0.62504	7.613794	6.316067	1.68E-09	8.28E-09	10.75207	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	NM_012424
212752_at	0.62501	8.432186	10.45322	1.03E-20	1.95E-19	36.22092	CLASP1	cytoplasmic linker associated protein 1	AA176798
235381_at	0.62496	8.474188	9.351995	1.70E-17	2.31E-16	28.88791			BF033855
201885_s_at	0.6248	11.15293	13.06075	1.20E-28	4.49E-27	54.35566	CYB5R3	cytochrome b5 reductase 3	NM_000398
203735_x_at	0.62458	7.793569	7.447099	2.73E-12	2.07E-11	17.0548	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	N35896
228758_at	0.62454	6.016251	6.509604	5.86E-10	3.12E-09	11.78397	BCL6	Zinc finger protein	AW264036
232615_at	0.62454	7.259886	5.50401	1.12E-07	3.89E-07	6.658997			AA632758
226305_at	0.62453	6.484924	9.701263	1.67E-18	2.51E-17	31.18272	LYNX1	Ly6/neurotoxin 1	AV696976
214850_at	0.62442	5.505847	6.983436	4.10E-11	2.64E-10	14.39403	LOC100170939	glucuronidase, beta pseudogene	X75940
235444_at	0.62411	6.342915	7.111622	1.96E-11	1.32E-10	15.11951	FOXP1	forkhead box P1	AI417897
204575_s_at	0.62405	7.304952	4.9854	1.33E-06	3.73E-06	4.263078	MMP19	matrix metalloproteinase 19	U38321
204452_s_at	0.62403	5.372348	7.890396	1.88E-13	1.66E-12	19.68826	FZD1	frizzled homolog 1 (Drosophila)	AF072872
201628_s_at	0.62399	10.08763	9.784611	9.57E-19	1.48E-17	31.7349	RRAGA	Ras-related GTP binding A	NM_006570
209838_at	0.62398	6.863523	8.160987	3.55E-14	3.40E-13	21.33512	COPS2	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	AA496247
224787_s_at	0.62381	9.800843	6.658227	2.58E-10	1.46E-09	12.59014	RAB18	RAB18, member RAS oncogene family	AI333232
228044_at	0.62381	5.84209	6.121558	4.76E-09	2.16E-08	9.736051	SERP2	stress-associated endoplasmic reticulum protein family member 2	AI420319
236268_at	0.6234	6.827475	6.742984	1.60E-10	9.38E-10	13.05509	SEC22C	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	BF732413
227697_at	0.62339	9.168259	3.767653	0.0002163	0.0004035	-0.6038	SOCS3	suppressor of cytokine signaling 3	AI244908
209006_s_at	0.62323	7.146721	5.629329	6.01E-08	2.20E-07	7.264404	C1orf63	chromosome 1 open reading frame 63	AF247168
218344_s_at	0.62302	6.838967	6.885704	7.15E-11	4.42E-10	13.84632	RCOR3	REST corepressor 3	NM_018254
213151_s_at	0.62291	11.29737	12.70067	1.55E-27	5.31E-26	51.81414	SEPT7	septin 7	AU157515
235421_at	0.62289	5.04765	7.009494	3.53E-11	2.29E-10	14.54086	MAP3K8	CDNA FLJ78064 complete cds, highly similar to Human mRNA for proto-oncogene protein	AV713062
219505_at	0.62282	8.668575	4.259952	3.14E-05	6.77E-05	1.228256	CECR1	cat eye syndrome chromosome region, candidate 1	NM_017424
202949_s_at	0.6225	10.63932	4.604165	7.33E-06	1.78E-05	2.620216	FHL2	four and a half LIM domains 2	NM_001450
223824_at	0.62232	6.242819	6.976038	4.27E-11	2.74E-10	14.35241	C10orf59	chromosome 10 open reading frame 59	BC005364
224769_at	0.62222	9.947096	8.712067	1.09E-15	1.24E-14	24.77248			AL110163
220246_at	0.62191	5.166044	7.321263	5.75E-12	4.17E-11	16.32282	CAMK1D	calcium/calmodulin-dependent protein kinase ID	NM_020397
235953_at	0.62183	4.28959	7.937011	1.42E-13	1.27E-12	19.96992	ZNF610	zinc finger protein 610	AA776810
220999_s_at	0.6217	6.235285	5.014292	1.16E-06	3.31E-06	4.391767	CYFIP2	cytoplasmic FMR1 interacting protein 2	NM_030778
206631_at	0.62146	6.606744	4.767726	3.57E-06	9.20E-06	3.312323	PTGER2	prostaglandin E receptor 2 (subtype EP2), 53kDa	NM_000956
212017_at	0.62131	8.747771	9.258853	3.14E-17	4.16E-16	28.28143	FAM168B	family with sequence similarity 168, member B	BF677404
209185_s_at	0.62125	9.516813	4.485664	1.22E-05	2.84E-05	2.131006	IRS2	insulin receptor substrate 2	AF073310
207510_at	0.6211	5.719886	5.995365	9.24E-09	3.97E-08	9.088545	BDKRB1	bradykinin receptor B1	NM_000710
241470_x_at	0.62082	5.449805	5.247131	3.90E-07	1.22E-06	5.449767			R97781

212923_s_at	0.62072	8.735231	6.269077	2.17E-09	1.05E-08	10.50465	C6orf145	chromosome 6 open reading frame 145	AK024828
221824_s_at	0.62072	7.913964	6.942055	5.19E-11	3.28E-10	14.16154	MARCH8	membrane-associated ring finger (C3HC4) 8	AA770170
213351_s_at	0.62071	7.342101	6.563751	4.35E-10	2.36E-09	12.07632	TMCC1	transmembrane and coiled-coil domain family 1	AB018322
214629_x_at	0.62035	12.01047	9.212959	4.24E-17	5.54E-16	27.98349	RTN4	reticulin 4	AF320999
202087_s_at	0.62015	10.06273	5.546163	5.53E-08	2.04E-07	7.346487	CTSL1	cathepsin L1	NM_001912
212776_s_at	0.6201	6.933977	4.319583	2.45E-05	5.40E-05	1.463003	OBSL1	obscurin-like 1	AI978623
203080_s_at	0.62006	8.689643	8.482761	4.70E-15	4.97E-14	23.32925	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	NM_013450
219599_at	0.62004	6.510835	7.463588	2.48E-12	1.89E-11	17.15125	EIF4B	eukaryotic translation initiation factor 4B	NM_018507
228791_at	0.62	7.525017	8.285877	1.63E-14	1.62E-13	22.10463	LOC100129502	hypothetical protein LOC100129502	BF434655
225074_at	0.61978	8.459826	9.850702	6.15E-19	9.69E-18	32.17394	RAB2B	RAB2B, member RAS oncogene family	AA531016
200799_at	0.61963	11.72258	4.517482	1.06E-05	2.51E-05	2.26134	HSPA1A HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	NM_005345
228604_at	0.61962	6.261566	7.675116	6.98E-13	5.70E-12	18.39898	FAM76A	family with sequence similarity 76, member A	AI805069
33767_at	0.6196	4.029263	7.527593	1.69E-12	1.32E-11	17.52674	NEFH	neurofilament, heavy polypeptide	X15306
230063_at	0.61954	6.501783	7.775976	3.79E-13	3.21E-12	19.00063	ZNF264	zinc finger protein 264	BF063192
222553_x_at	0.61929	9.05163	6.634861	2.93E-10	1.64E-09	12.46262	OXR1	oxidation resistance 1	AL541048
204780_s_at	0.61928	8.209584	4.132834	5.25E-05	0.0001086	0.736954	FAS	Fas (TNF receptor superfamily, member 6)	AA164751
212026_s_at	0.61926	7.069789	10.50253	7.38E-21	1.42E-19	36.55537	EXOC7	exocyst complex component 7	BE646386
213062_at	0.61899	8.318464	9.744844	1.25E-18	1.90E-17	31.47124	NTAN1	N-terminal asparagine amidase	AA643304
202134_s_at	0.61896	6.834266	5.580523	7.67E-08	2.75E-07	7.027438	WWTR1	WW domain containing transcription regulator 1	NM_015472
220014_at	0.61894	5.586111	4.128643	5.34E-05	0.0001103	0.72097	PRR16	proline rich 16	NM_016644
224649_x_at	0.61883	6.903017	7.902049	1.75E-13	1.55E-12	19.75859	CCNY	cyclin Y	AI765014
227026_at	0.61882	8.547213	9.300847	2.38E-17	3.19E-16	28.55458	MPHOSPH8	M-phase phosphoprotein 8	AI016714
227572_at	0.61873	7.502788	7.809608	3.09E-13	2.64E-12	19.2022	USP30	ubiquitin specific peptidase 30	AA528138
1552705_at	0.6187	4.621053	6.823458	1.02E-10	6.14E-10	13.49996	DUSP19	dual specificity phosphatase 19	BC035000
232681_at	0.6187	6.105493	8.28273	1.66E-14	1.65E-13	22.08517			AI252087
215418_at	0.61865	5.579202	9.181062	5.22E-17	6.77E-16	27.77677	PARVA	parvin, alpha	AK022316
224488_s_at	0.61865	4.885397	6.995923	3.81E-11	2.47E-10	14.46435	SPON1	spodin 1, extracellular matrix protein	BC006262
224566_at	0.61847	9.990249	4.589513	7.81E-06	1.88E-05	2.559165	NCRNA00084	non-protein coding RNA 84	AI042152
235123_at	0.61847	6.425322	6.307996	1.76E-09	8.62E-09	10.70948			AI951144
213173_at	0.61847	5.274154	10.42661	1.24E-20	2.33E-19	36.04057	PCNX	pecanex homolog (Drosophila)	AI815033
204348_s_at	0.61831	8.672435	3.502765	0.0005671	0.0009858	-1.50882	AK3L1 /// AK3L2	adenylate kinase 3-like 1 /// adenylate kinase 3-like 2	NM_013410
202498_s_at	0.61828	7.06298	3.913408	0.0001244	0.0002416	-0.0814	SLC2A3	solute carrier family 2 (facilitated glucose transporter), member 3	BE550486
1557260_a_at	0.61817	3.686209	11.74426	1.33E-24	3.61E-23	45.10671	ZNF382	zinc finger protein 382	BM973530
226074_at	0.61812	6.84977	10.04541	1.66E-19	2.78E-18	33.47321	PPM1M	protein phosphatase 1M (PP2C domain containing)	N22918
204314_s_at	0.61808	8.449772	9.828343	7.14E-19	1.12E-17	32.02529	CREB1	cAMP responsive element binding protein 1	NM_004379
212980_at	0.61806	6.18806	6.859448	8.31E-11	5.08E-10	13.69998	USP34	ubiquitin specific peptidase 34	AL050376
213463_s_at	0.61781	7.414503	7.513061	1.85E-12	1.43E-11	17.44133	FAM149B1	family with sequence similarity 149, member B1	AW300504
225231_at	0.61759	8.060622	9.450111	8.89E-18	1.25E-16	29.52935	CBL	Cas-BR-M (murine) ecotropic retroviral transforming sequence	AI828967
233300_at	0.61757	5.123286	6.177417	3.54E-09	1.65E-08	10.02562			AU144781
223353_at	0.61712	8.153111	11.31644	2.66E-23	6.35E-22	42.13577	HCCA2	HCCA2 protein	AB028173
220330_s_at	0.61702	8.111992	3.931865	0.0001159	0.0002261	-0.01404	SAMS1	SAM domain, SH3 domain and nuclear localization signals 1	NM_022136
243745_at	0.61682	4.215642	8.723259	1.02E-15	1.16E-14	24.84337			N74507
207012_at	0.61671	3.940127	9.700698	1.68E-18	2.52E-17	31.17898	MMP16	matrix metalloproteinase 16 (membrane-inserted)	U79292
206813_at	0.61652	6.312986	10.21392	5.29E-20	9.28E-19	34.60447	CTF1	cardiotrophin 1	NM_001330

230508_at	0.61652	5.562287	6.494902	6.36E-10	3.36E-09	11.70487	DKK3	dickkopf homolog 3 (Xenopus laevis)	AL569501
229537_at	0.61645	5.701592	5.553823	8.76E-08	3.10E-07	6.898445	LMO4	LIM domain only 4	AI694521
204362_at	0.61645	9.578946	6.601162	3.54E-10	1.95E-09	12.27922	SKAP2	src kinase associated phosphoprotein 2	NM_003930
1556583_a at	0.61644	3.399962	10.50231	7.39E-21	1.42E-19	36.55391	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1	H23209
229121_at	0.6163	6.650829	8.021265	8.43E-14	7.75E-13	20.48119	CMKLR1	Orphan G-protein coupled receptor Dez isoform b	BE857553
242868_at	0.61628	5.076965	5.936657	1.25E-08	5.25E-08	8.790507			T70087
203879_at	0.61627	7.417733	6.207222	3.02E-09	1.42E-08	10.18086	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	U86453
218574_s at	0.61625	8.331333	5.35775	2.29E-07	7.49E-07	5.965187	LMCD1	LIM and cysteine-rich domains 1	NM_014583
230154_at	0.61623	5.706458	10.2157	5.22E-20	9.18E-19	34.6164			AW003119
240259_at	0.61614	3.824542	9.072007	1.07E-16	1.34E-15	27.07223	FLRT2	CDNA FLJ51243 complete cds, highly similar to Leucine-rich repeat transmembrane protein FLRT2 precursor	AI188161
1569785_at	0.61598	4.098614	10.35083	2.08E-20	3.80E-19	35.52784			BC031271
236310_at	0.61572	4.37772	8.518503	3.75E-15	4.01E-14	23.55304			BE645334
201308_s at	0.61563	6.322598	4.831889	2.68E-06	7.08E-06	3.589089	SEPT11	septin 11	NM_018243
212951_at	0.61538	7.694124	6.12502	4.67E-09	2.13E-08	9.753943	GPR116	G protein-coupled receptor 116	N95226
244669_at	0.61485	6.659251	6.672705	2.38E-10	1.35E-09	12.6693	SNHG5 /// SNORD50 A /// SNORD50B	small nucleolar RNA host gene 5 (non-protein coding) /// small nucleolar RNA, C/D box 50A /// small nucleolar RNA, C/D box 50B	T16443
212938_at	0.61434	5.810585	7.834369	2.65E-13	2.29E-12	19.35089	COL6A1	collagen, type VI, alpha 1	M20776
214753_at	0.61406	6.765736	6.261233	2.26E-09	1.09E-08	10.46347	N4BP2L2	BRCA2 region, mRNA sequence CG006	AW084068
222116_s at	0.61381	7.239363	7.809091	3.10E-13	2.65E-12	19.1991	TBC1D16	TBC1 domain family, member 16	AI157485
214151_s at	0.61378	8.143502	6.595954	3.64E-10	2.01E-09	12.25093	CCPG1	cell cycle progression 1	AU144243
208073_x at	0.61373	10.25046	8.471721	5.04E-15	5.31E-14	23.26022	TTC3	tetratricopeptide repeat domain 3	NM_003316
227510_x at	0.61359	6.651763	6.06604	6.38E-09	2.83E-08	9.450038	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AL037917
220092_s at	0.61344	5.106919	5.674691	4.79E-08	1.79E-07	7.485992	ANTXR1	anthrax toxin receptor 1	NM_018153
212451_at	0.61339	8.745849	7.59279	1.14E-12	9.09E-12	17.91107	KIAA0256	KIAA0256 gene product	N52532
236647_at	0.61316	5.579764	10.28931	3.17E-20	5.70E-19	35.11245			BF437470
205913_at	0.61298	6.177786	3.60823	0.0003889	0.0006948	-1.15542	PLIN	perilipin	NM_002666
244552_at	0.61292	5.212131	7.172323	1.38E-11	9.45E-11	15.4658	ZNF788	zinc finger family member 788	AI190287
229532_at	0.6129	5.747968	7.506005	1.92E-12	1.49E-11	17.39989	ZNF502	zinc finger protein 502	AI056364
208740_at	0.61282	8.464813	6.992062	3.90E-11	2.52E-10	14.4426	SAP18	Sin3A-associated protein, 18kDa	BF593650
229731_at	0.61279	5.56459	7.3326	5.38E-12	3.92E-11	16.38847	FOX51	forkhead box S1	AL160175
212457_at	0.61267	9.566109	10.34293	2.20E-20	4.01E-19	35.47448	TFE3	transcription factor binding to IGHM enhancer 3	AL161985
222391_at	0.61259	10.05295	9.503333	6.25E-18	8.92E-17	29.87836	TMEM30A	transmembrane protein 30A	AL080250
201365_at	0.61236	8.375369	12.02206	1.89E-25	5.47E-24	47.04681	OAZ2	ornithine decarboxylase antizyme 2	NM_002537
236328_at	0.61221	4.933032	6.205654	3.05E-09	1.43E-08	10.17268	ZNF285A	zinc finger protein 285A	AW513227
244704_at	0.61208	4.70989	9.594881	1.75E-18	2.62E-17	31.14051	NFYB	nuclear transcription factor Y, beta	AW083948
224445_s at	0.61207	9.282997	8.294067	1.54E-14	1.54E-13	22.1553	ZFYVE21	zinc finger, FYVE domain containing 21	BC005999
219457_s at	0.61203	6.594625	9.78613	9.48E-19	1.47E-17	31.74498	RIN3	Ras and Rab interactor 3	NM_024832
225579_at	0.61183	9.229331	6.18982	3.31E-09	1.55E-08	10.09016	PQLC3	PQ loop repeat containing 3	AL516202
230391_at	0.61154	7.623683	4.861052	2.35E-06	6.27E-06	3.715849			BF439449
225698_at	0.61153	8.990974	7.001731	3.69E-11	2.39E-10	14.49709	C5orf26	chromosome 5 open reading frame 26	BF314746
212481_s at	0.61153	9.201936	6.843383	9.10E-11	5.53E-10	13.61061	TPM4	tropomyosin 4	AI214061
206583_at	0.61142	6.783886	7.490119	2.12E-12	1.63E-11	17.30667	ZNF673	zinc finger family member 673	NM_017776
235378_at	0.61141	4.824307	11.07774	1.40E-22	3.16E-21	40.48847			AI082216
1553705_a at	0.61137	6.755372	4.90318	1.94E-06	5.27E-06	3.900031	CHRM3	cholinergic receptor, muscarinic 3	NM_000740

202056_at	0.61123	8.125668	8.211245	2.59E-14	2.52E-13	21.64409	KPNA1	karyopherin alpha 1 (importin alpha 5)	AW051311
213620_s_at	0.61119	9.187491	5.102099	7.74E-07	2.28E-06	4.786419	ICAM2	intercellular adhesion molecule 2	AA126728
238700_at	0.61115	6.165554	7.338826	5.19E-12	3.78E-11	16.42455			AI825302
235725_at	0.61106	7.203342	7.886285	1.93E-13	1.70E-12	19.66347	SMAD4	SMAD family member 4	AW055351
224945_at	0.61104	7.983956	8.08217	5.79E-14	5.42E-13	20.8525	BTBD7	BTB (POZ) domain containing 7	AI935657
205187_at	0.6108	7.473325	7.430041	3.02E-12	2.28E-11	16.95516	SMAD5	SMAD family member 5	AF010601
218029_at	0.61076	7.50995	9.636223	2.58E-18	3.82E-17	30.75302	FAM65A	family with sequence similarity 65, member A	NM_024519
210751_s_at	0.61063	6.608385	3.695668	0.0002826	0.0005168	-0.85546	RGN	regucalcin (senescence marker protein-30)	D31815
228292_at	0.61059	7.086407	7.810216	3.07E-13	2.63E-12	19.20584			AI291989
227731_at	0.61055	7.729191	9.412914	1.14E-17	1.58E-16	29.28587	CNBP	CCHC-type zinc finger, nucleic acid binding protein	BF063728
208663_s_at	0.61018	9.345245	8.032142	7.88E-14	7.27E-13	20.54739	TTC3	tetratricopeptide repeat domain 3	AI652848
244687_at	0.60967	6.152958	7.548446	1.49E-12	1.17E-11	17.64947	DBT	dihydrolipoamide branched chain transacylase E2	AI632010
226975_at	0.60963	7.220442	7.588586	1.17E-12	9.31E-12	17.88623	RNPC3	RNA-binding region (RNP1, RRM) containing 3	BF116157
211382_s_at	0.60962	7.868519	5.834202	2.13E-08	8.50E-08	8.275324	TACC2	transforming, acidic coiled-coil containing protein 2	AF220152
222663_at	0.60948	6.406168	7.462895	2.49E-12	1.89E-11	17.14719	RIOK2	RIO kinase 2 (yeast)	AK001697
227020_at	0.6094	8.170517	7.258436	8.32E-12	5.89E-11	15.96005	YPEL2	yippee-like 2 (Drosophila)	BE502982
243013_at	0.60931	4.154335	10.41724	1.32E-20	2.47E-19	35.97715			AW439817
244170_at	0.6093	3.822969	7.445232	2.76E-12	2.09E-11	17.04389			H05254
222665_at	0.60928	7.36907	8.689695	1.26E-15	1.42E-14	24.6309	FAM82B	family with sequence similarity 82, member B	AK000672
201230_s_at	0.6091	7.448143	9.263279	3.05E-17	4.04E-16	28.3102	ARIH2	ariadne homolog 2 (Drosophila)	NM_006321
219973_at	0.60901	6.316795	5.305992	2.94E-07	9.41E-07	5.723018	ARSJ	arylsulfatase family, member J	NM_024590
1558515_at	0.60894	6.389512	5.49796	1.15E-07	4.00E-07	6.630021			AK057701
204953_at	0.60879	4.045171	9.378688	1.42E-17	1.96E-16	29.06216	SNAP91	synaptosomal-associated protein, 91kDa homolog (mouse)	NM_014841
211789_s_at	0.60854	4.321913	9.68405	1.88E-18	2.81E-17	31.0689	MLXIP	MLX interacting protein	AF312918
224876_at	0.60854	10.16455	8.976425	1.98E-16	2.43E-15	26.45762	C5orf24	chromosome 5 open reading frame 24	AV707506
204085_s_at	0.60852	7.45958	5.562491	8.39E-08	2.99E-07	6.940272	CLN5	ceroid-lipofuscinosis, neuronal 5	NM_006493
214607_at	0.60843	6.085896	6.918351	5.94E-11	3.72E-10	14.02875	PAK3	p21 protein (Cdc42/Rac)-activated kinase 3	AW085556
228561_at	0.60798	6.237812	7.45143	2.66E-12	2.02E-11	17.08012	CDC37L1	cell division cycle 37 homolog (S. cerevisiae)-like 1	BF510563
207112_s_at	0.60794	5.518871	11.13856	9.17E-23	2.10E-21	40.90742	GAB1	GRB2-associated binding protein 1	NM_002039
205062_x_at	0.60777	7.153574	9.714626	1.53E-18	2.31E-17	31.27114	ARID4A	AT rich interactive domain 4A (RBP1-like)	NM_002892
1558093_s_at	0.60753	7.85968	5.921696	1.36E-08	5.63E-08	8.714879	MATR3	matrin 3	BI832461
238320_at	0.60747	5.883313	6.16683	3.74E-09	1.74E-08	9.970604	NCRNA00084	non-protein coding RNA 84	AV659198
228937_at	0.60746	7.169683	5.624515	6.16E-08	2.25E-07	7.240962	C13orf31	chromosome 13 open reading frame 31	AI659800
229673_at	0.60741	5.519823	12.43146	1.05E-26	3.35E-25	49.91882			AI950390
211084_x_at	0.60723	6.834916	6.917231	5.98E-11	3.74E-10	14.02248	PRKD3	protein kinase D3	Z25429
206972_s_at	0.6071	6.001646	8.742579	8.97E-16	1.03E-14	24.96584	GPR161	G protein-coupled receptor 161	NM_007369
203037_s_at	0.60707	9.126939	4.192955	4.12E-05	8.59E-05	0.967761	MTSS1	metastasis suppressor 1	NM_014751
226398_s_at	0.60688	8.492411	9.257343	3.17E-17	4.20E-16	28.27162	C10orf4	chromosome 10 open reading frame 4	AI804930
224898_at	0.60677	6.369777	7.281274	7.28E-12	5.20E-11	16.09171	WDR26	WD repeat domain 26	BG177759
224506_s_at	0.60668	6.373372	11.32762	2.46E-23	5.89E-22	42.21313	PPAPDC3	phosphatidic acid phosphatase type 2 domain containing 3	BC006362
219765_at	0.60661	6.659685	5.533885	9.67E-08	3.40E-07	6.802411	ZNF329	zinc finger protein 329	NM_024620
223708_at	0.60644	4.105422	11.94378	3.27E-25	9.33E-24	46.49939	C1QTNF4	C1q and tumor necrosis factor related protein 4	AF329838
201868_s_at	0.60606	5.875116	6.628554	3.04E-10	1.70E-09	12.42825	TBL1X	transducin (beta)-like 1X-linked	AI082187

239461_at	0.60593	4.016471	6.97685	4.25E-11	2.73E-10	14.35697	GALNTL2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase-like 2	AW205686
227329_at	0.60584	5.224339	7.336919	5.24E-12	3.82E-11	16.4135	ZBTB46	zinc finger and BTB domain containing 46	AU156821
242865_at	0.6058	5.111647	6.264309	2.22E-09	1.07E-08	10.47962			AI332638
239568_at	0.60572	4.030988	10.79275	1.00E-21	2.09E-20	38.53289	PLEKH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	AW451832
229898_at	0.60571	7.131791	12.05594	1.49E-25	4.34E-24	47.28398			AI141426
205672_at	0.60554	7.991018	9.625511	2.77E-18	4.10E-17	30.68234	XPA	xeroderma pigmentosum, complementation group A	NM_000380
209726_at	0.60527	6.737893	7.35415	4.74E-12	3.48E-11	16.51343	CA11	carbonic anhydrase XI	AB018195
235492_at	0.60526	4.676515	9.075653	1.04E-16	1.31E-15	27.09573	RNF217	ring finger protein 217	AI888256
212244_at	0.60524	8.667929	9.650571	2.35E-18	3.48E-17	30.84772	GCOM1 GRINL1A	GRINL1A complex locus /// glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	AL050091
223214_s_at	0.60502	8.003601	6.073101	6.15E-09	2.73E-08	9.486311	ZHX1	zinc fingers and homeoboxes 1	AF195766
206668_s_at	0.60499	7.076429	6.213093	2.93E-09	1.38E-08	10.2115	SCAMP1	secretory carrier membrane protein 1	NM_004866
208935_s_at	0.60499	7.343818	6.584876	3.87E-10	2.13E-09	12.1908	LGALS8	lectin, galactoside-binding, soluble, 8	L78132
223796_at	0.60486	5.214417	4.4428	1.46E-05	3.36E-05	1.956615	CNTNAP3 CNTNAP3B LOC64382 7 LOC65335 5 RP11-138L21.1	contactin associated protein-like 3 /// contactin associated protein-like 3B /// similar to cell recognition molecule CASPR3 /// hypothetical LOC653355 /// similar to cell recognition molecule CASPR3	AF333769
229880_at	0.60485	5.773115	9.394791	1.28E-17	1.77E-16	29.16738	LOC64351	hypothetical LOC643517	H28731
213161_at	0.60471	7.914679	8.566886	2.76E-15	2.99E-14	23.85666	C9orf97	chromosome 9 open reading frame 97	AI583393
228120_at	0.60467	6.249164	6.357373	1.35E-09	6.73E-09	10.97057			AW136032
212917_x_at	0.60464	9.442077	6.651823	2.67E-10	1.50E-09	12.55516	RECQL	RecQ protein-like (DNA helicase Q1-like)	AI814728
224642_at	0.60464	8.116738	6.849799	8.77E-11	5.34E-10	13.64629	FYTTD1	forty-two-three domain containing 1	BG291550
227880_s_at	0.60456	7.104806	6.813397	1.08E-10	6.48E-10	13.44415	LOC100132969 TMEM185A	hypothetical protein LOC100132969 /// transmembrane protein 185A	AW300965
244422_at	0.60455	3.949862	9.26326	3.05E-17	4.04E-16	28.31007			AI494573
211991_s_at	0.60451	10.70051	3.791475	0.0001978	0.0003714	-0.51959	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	M27487
209906_at	0.60436	8.182033	5.748511	3.30E-08	1.27E-07	7.849339	C3AR1	complement component 3a receptor 1	U62027
230177_at	0.60426	6.753154	7.233392	9.63E-12	6.76E-11	15.81596			AI884495
228890_at	0.60425	5.615658	8.593071	2.33E-15	2.56E-14	24.02132	ATOX8	atonal homolog 8 (Drosophila)	BF434995
239960_x_at	0.60411	4.532527	8.24889	2.05E-14	2.02E-13	21.87614	LYRM7	Lyrm7 homolog (mouse), mRNA (cDNA clone MGC:44056 IMAGE:5284728)	AW303539
231016_s_at	0.60405	6.549652	9.70137	1.67E-18	2.51E-17	31.18343			BE465380
206695_x_at	0.60398	6.42426	7.475049	2.31E-12	1.77E-11	17.21835	ZNF43	zinc finger protein 43	NM_003423
236962_at	0.60397	4.495071	8.024215	8.28E-14	7.62E-13	20.49914			AA521018
228598_at	0.60382	3.353692	5.506782	1.11E-07	3.84E-07	6.672277	DPP10	dipeptidyl-peptidase 10	AL538781
225886_at	0.60369	8.362731	7.34334	5.05E-12	3.69E-11	16.45072	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	AA156797
217430_x_at	0.60352	8.589133	4.082711	6.42E-05	0.0001309	0.546679	COL1A1	collagen, type I, alpha 1	Y15916
229032_at	0.60338	6.413988	6.217733	2.85E-09	1.35E-08	10.23573	WSCD2	WSC domain containing 2	BE962770
207826_s_at	0.60334	9.307276	5.082041	8.50E-07	2.49E-06	4.695799	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	NM_002167
203556_at	0.60327	8.580172	6.265912	2.21E-09	1.06E-08	10.48803	ZHX2	zinc fingers and homeoboxes 2	NM_014943

230261_at	0.60302	6.131413	4.915622	1.83E-06	5.00E-06	3.954664	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	AA552969
211317_s_at	0.60287	7.846265	6.214284	2.91E-09	1.37E-08	10.21772	CFLAR	CASP8 and FADD-like apoptosis regulator	AF041461
238469_at	0.60272	4.717676	6.789673	1.23E-10	7.34E-10	13.31279	OGFRL1	opioid growth factor receptor-like 1	BE620374
207719_x_at	0.60264	9.252456	6.865807	8.01E-11	4.91E-10	13.73539	CEP170	centrosomal protein 170kDa	NM_014812
223152_at	0.60244	7.483904	10.4502	1.06E-20	1.99E-19	36.20042	PPP1R12C	protein phosphatase 1, regulatory (inhibitor) subunit 12C	AF312028
219645_at	0.60236	3.936005	8.60181	2.21E-15	2.43E-14	24.07632	CASQ1	calsequestrin 1 (fast-twitch, skeletal muscle)	NM_001231
204155_s_at	0.60233	6.89061	11.74463	1.33E-24	3.60E-23	45.10932	KIAA0999	KIAA0999 protein	AA044154
225229_at	0.60224	9.163111	7.775035	3.81E-13	3.22E-12	18.995	AFF4	AF4/FMR2 family, member 4	AL044396
201848_s_at	0.60215	6.667486	3.753067	0.0002284	0.0004245	-0.65513	BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	U15174
230692_at	0.60215	3.425012	8.272314	1.77E-14	1.75E-13	22.02078	LOC157503	hypothetical protein LOC157503	C14047
209068_at	0.60201	8.286867	7.918766	1.58E-13	1.41E-12	19.85958	HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	D89678
228817_at	0.60188	6.845792	7.646092	8.31E-13	6.71E-12	18.22664	ALG9	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)	AI085361
239043_at	0.60169	3.863787	6.35751	1.35E-09	6.73E-09	10.9713	ZNF404	zinc finger protein 404	AA084273
225745_at	0.60159	8.328099	6.104349	5.21E-09	2.35E-08	9.647206	LRP6	low density lipoprotein receptor-related protein 6	AV725248
230183_at	0.60143	6.41243	6.538015	5.02E-10	2.70E-09	11.93717	EXT1	exostoses (multiple) 1	AW189467
229431_at	0.60143	6.859679	5.530104	9.85E-08	3.46E-07	6.784229	RFXAP	regulatory factor X-associated protein	AI742868
224780_at	0.60136	7.713296	7.210575	1.10E-11	7.67E-11	15.68492	RBM17	RNA binding motif protein 17	N48353
210347_s_at	0.60132	7.462994	4.287178	2.80E-05	6.10E-05	1.335096	BCL11A	B-cell CLL/lymphoma 11A (zinc finger protein)	AF080216
209112_at	0.60131	10.3073	8.522044	3.67E-15	3.92E-14	23.57523	CDKN1B	cyclin-dependent kinase inhibitor 1B (p27, Kip1)	BC001971
234103_at	0.60126	3.369465	7.970636	1.15E-13	1.04E-12	20.17363	KCNT2	Sodium activated potassium channel (KCNT2)	AU145191
229111_at	0.60123	6.281306	8.123301	4.48E-14	4.25E-13	21.10406			AA033699
222835_at	0.6008	7.325304	4.591213	7.75E-06	1.87E-05	2.566242	THSD4	thrombospondin, type I, domain containing 4	BG163478
218263_s_at	0.60056	9.116511	8.315387	1.35E-14	1.35E-13	22.2873	ZBED5	zinc finger, BED-type containing 5	NM_021211
235109_at	0.60054	7.231871	6.313188	1.71E-09	8.40E-09	10.73687			AI887983
221571_at	0.60047	7.644438	8.615607	2.02E-15	2.23E-14	24.16321	TRAF3	TNF receptor-associated factor 3	AI721219
238792_at	0.60046	4.84756	12.80252	7.53E-28	2.63E-26	52.53233	PCNX	pecanex homolog (Drosophila)	BF209668
212875_s_at	0.60043	8.388164	8.707907	1.12E-15	1.27E-14	24.74614	C2CD2	C2 calcium-dependent domain containing 2	AP001745
237252_at	0.60041	5.452013	6.540436	4.95E-10	2.67E-09	11.95025	THBD	thrombomodulin	AW119113
1553704_x_at	0.6004	8.481209	8.88181	3.66E-16	4.37E-15	25.85197	ZNF791	zinc finger protein 791	NM_153358
224580_at	0.60034	6.726769	6.13986	4.32E-09	1.98E-08	9.830732	SLC38A1	solute carrier family 38, member 1	BF515894
222667_s_at	0.60032	9.244023	7.102794	2.06E-11	1.38E-10	15.06929	ASH1L	ash1 (absent, small, or homeotic)-like (Drosophila)	AI806500
233866_at	0.6003	4.171657	9.6691	2.07E-18	3.09E-17	30.9701	KLHL5	kelch-like 5 (Drosophila)	AK001836
202972_s_at	0.60023	7.341781	6.099584	5.35E-09	2.41E-08	9.62263	FAM13A1	family with sequence similarity 13, member A1	AW450403
211203_s_at	0.60019	5.142028	8.417313	7.11E-15	7.35E-14	22.92064	CNTN1	contactin 1	U07820
219636_s_at	0.60019	6.084518	7.598137	1.11E-12	8.82E-12	17.94267	ARMC9	armadillo repeat containing 9	NM_025139
1559942_at	0.60013	4.932175	7.582094	1.22E-12	9.65E-12	17.84789	MDFIC	MyoD family inhibitor domain containing	BC040713
226493_at	0.6001	8.169432	7.269623	7.79E-12	5.54E-11	16.02451	KCTD18	potassium channel tetramerisation domain containing 18	AI627249
202916_s_at	0.60004	8.133516	8.135049	4.17E-14	3.96E-13	21.17603	FAM20B	family with sequence similarity 20, member B	NM_014864
209755_at	0.59987	5.383562	5.335623	2.55E-07	8.26E-07	5.861439	NMNAT2	hypothetical protein LOC100131795 /// nicotinamide nucleotide adenylyltransferase 2	AF288395
1552667_a_at	0.59971	6.103769	7.85609	2.32E-13	2.02E-12	19.48154	SH2D3C	SH2 domain containing 3C	NM_005489

227899_at	0.59966	5.399223	5.559452	8.52E-08	3.03E-07	6.9256	VIT	vitrin	AI817458
234975_at	0.59961	6.071091	6.16213	3.84E-09	1.78E-08	9.9462	GSPT1	G1 to S phase transition 1	BE544748
219683_at	0.59951	5.689342	4.379805	1.91E-05	4.29E-05	1.702825	FZD3	frizzled homolog 3 (Drosophila)	NM_017412
223213_s_at	0.59951	7.742879	6.881182	7.34E-11	4.53E-10	13.82108	ZHX1	zinc fingers and homeoboxes 1	AI123518
219979_s_at	0.59947	7.201809	5.16722	5.70E-07	1.72E-06	5.082511	C11orf73	chromosome 11 open reading frame 73	NM_016401
236223_s_at	0.5994	5.147604	5.513207	1.07E-07	3.73E-07	6.703086	RIT1	Small G protein RIBB	AL037450
1558972_s_at	0.59928	4.926275	4.06625	6.85E-05	0.000139	0.484621	C6orf190	chromosome 6 open reading frame 190	BC043608
227929_at	0.59902	5.344561	4.387978	1.84E-05	4.15E-05	1.735582			AU151342
206349_at	0.59901	3.51888	8.708198	1.12E-15	1.27E-14	24.74799	LGI1	leucine-rich, glioma inactivated 1	NM_005097
204214_s_at	0.59889	8.59438	6.303048	1.81E-09	8.82E-09	10.68339	RAB32	RAB32, member RAS oncogene family	NM_006834
225198_at	0.59879	9.202646	7.049789	2.80E-11	1.85E-10	14.76857	VAPA	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	AL571942
233020_at	0.59878	5.198513	6.531161	5.21E-10	2.80E-09	11.90017			AU154125
214202_at	0.59874	6.524049	7.186581	1.27E-11	8.74E-11	15.5474			N21364
218043_s_at	0.59869	8.033332	9.599107	3.31E-18	4.84E-17	30.50827	AZI2	5-azacytidine induced 2	NM_022461
220301_at	0.59859	4.738058	4.62513	6.69E-06	1.64E-05	2.707842	CCDC102B	coiled-coil domain containing 102B	NM_024781
226468_at	0.59856	8.457391	9.366254	1.55E-17	2.11E-16	28.98097			AA778521
206833_s_at	0.59853	7.349492	6.778381	1.31E-10	7.79E-10	13.25035	ACYP2	acylphosphatase 2, muscle type	NM_001108
204546_at	0.59853	7.032382	7.498542	2.01E-12	1.55E-11	17.35609	KIAA0513	KIAA0513	NM_014732
227397_at	0.5985	6.104183	9.888563	4.77E-19	7.61E-18	32.4259	TPM2	tropomyosin 2 (beta)	AA531086
219477_s_at	0.59844	7.278179	6.758064	1.47E-10	8.66E-10	13.13819	THSD1P	thrombospondin, type I, domain containing 1 /// thrombospondin, type I, domain containing 1 pseudogene	NM_018676
235016_at	0.59841	5.933197	3.625119	0.0003658	0.0006566	-1.09797	REEP3	receptor accessory protein 3	AL118571
228131_at	0.59839	6.904549	8.540678	3.26E-15	3.51E-14	23.69209	ERCC1	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	BG111047
230288_at	0.59829	5.502886	4.90681	1.91E-06	5.19E-06	3.915961	FGF14	fibroblast growth factor 14	AW418619
213019_at	0.59786	8.301021	7.460812	2.52E-12	1.91E-11	17.135	RANBP6	RAN binding protein 6	AI123233
206464_at	0.59785	5.311576	6.760047	1.46E-10	8.57E-10	13.14914	BMX	BMX non-receptor tyrosine kinase	NM_001721
231972_at	0.59784	5.703712	7.871895	2.11E-13	1.84E-12	19.57672			AK024681
228259_s_at	0.59783	4.152322	10.62954	3.09E-21	6.15E-20	37.41895	EPB41L4A	erythrocyte membrane protein band 4.1 like 4A	AW590155
229383_at	0.59754	7.378659	5.641605	5.65E-08	2.08E-07	7.324242			AI707896
205796_at	0.59738	5.390946	5.952987	1.15E-08	4.86E-08	8.873198	TCP11L1	t-complex 11 (mouse)-like 1	NM_018393
226333_at	0.59718	7.511622	5.25097	3.83E-07	1.20E-06	5.467519	IL6R	interleukin 6 receptor	AV700030
207294_at	0.59704	3.35642	8.330205	1.23E-14	1.24E-13	22.37914	AGTR2	angiotensin II receptor, type 2	NM_000686
238317_x_at	0.59687	4.338356	6.016203	8.29E-09	3.59E-08	9.194819			BF439728
235683_at	0.59685	4.81242	5.427678	1.63E-07	5.50E-07	6.295169	SESN3	sestrin 3	BF685808
225950_at	0.59681	7.015993	6.556522	4.53E-10	2.46E-09	12.0372			AV703731
228418_at	0.5967	7.173777	5.954983	1.14E-08	4.81E-08	8.883319	EXOC5	exocyst complex component 5	BF509391
211742_s_at	0.59654	7.970637	3.84387	0.0001623	0.0003091	-0.33277	EVI2B	ecotropic viral integration site 2B	BC005926
206090_s_at	0.59643	5.830478	8.084789	5.69E-14	5.34E-13	20.86849	DISC1	disrupted in schizophrenia 1	NM_018662
38241_at	0.59636	7.154708	4.449494	1.42E-05	3.27E-05	1.983757	BTN3A3	butyrophilin, subfamily 3, member A3	U90548
203940_s_at	0.59634	6.693675	7.076771	2.39E-11	1.60E-10	14.92148	VASH1	vasohibin 1	NM_014909
241936_x_at	0.5962	4.603107	9.063151	1.13E-16	1.42E-15	27.01517			AI654130
226010_at	0.59599	8.119094	6.203053	3.09E-09	1.45E-08	10.15912	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	BG290819
36554_at	0.59591	7.429338	6.963244	4.60E-11	2.93E-10	14.28048	ASMTL	acetylserotonin O-methyltransferase-like	Y15521
203426_s_at	0.59545	6.405748	8.620426	1.96E-15	2.17E-14	24.19358	IGFBP5	insulin-like growth factor binding protein 5	M65062
212642_s_at	0.59541	7.686716	9.777911	1.00E-18	1.54E-17	31.69045	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	AL023584

1558517_s_at	0.59516	6.142987	7.334218	5.33E-12	3.88E-11	16.39785	LRR8C8	leucine rich repeat containing 8 family, member C	CA773938
241395_at	0.59513	5.037341	8.905577	3.14E-16	3.78E-15	26.00385	NIT1	nitrilase 1	AL572553
228208_x_at	0.59496	5.83963	10.86769	5.99E-22	1.27E-20	39.04587	ZNF354C	zinc finger protein 354C	AL134573
208092_s_at	0.59487	6.401661	5.970053	1.05E-08	4.48E-08	8.959792	FAM49A	family with sequence similarity 49, member A	NM_030797
201370_s_at	0.59484	7.228803	6.714374	1.88E-10	1.09E-09	12.89772	CUL3	cullin 3	AU145232
241091_at	0.5947	5.748018	8.987343	1.85E-16	2.27E-15	26.52769			BE551142
238656_at	0.59454	6.308207	8.592942	2.34E-15	2.56E-14	24.02051			AA877043
223263_s_at	0.59402	6.814503	5.814398	2.36E-08	9.34E-08	8.176474	FGFR1OP2	FGFR1 oncogene partner 2	AF161472
219054_at	0.594	5.95717	6.540893	4.94E-10	2.66E-09	11.95271	C5orf23	chromosome 5 open reading frame 23	NM_024563
220150_s_at	0.59379	5.782836	7.088211	2.24E-11	1.50E-10	14.98642	FAM184A	family with sequence similarity 184, member A	NM_024581
202228_s_at	0.59376	11.68276	8.972645	2.03E-16	2.49E-15	26.43337	NPTN	neuroplastin	NM_017455
200757_s_at	0.59371	10.13194	8.011491	8.96E-14	8.21E-13	20.42173	CALU	calumenin	NM_001219
222834_s_at	0.59326	9.034769	6.594511	3.67E-10	2.02E-09	12.24309	GNG12	guanine nucleotide binding protein (G protein), gamma 12	N32508
228234_at	0.59323	7.978134	7.612737	1.02E-12	8.11E-12	18.02902	TICAM2 /// TMED7	toll-like receptor adaptor molecule 2 /// transmembrane emp24 protein transport domain containing 7	AI423165
218646_at	0.59316	8.430657	7.761282	4.14E-13	3.49E-12	18.91272	C4orf27	chromosome 4 open reading frame 27	NM_017867
239833_at	0.59313	5.483241	10.27872	3.40E-20	6.10E-19	35.04105			H15900
224943_at	0.59304	7.342125	8.639551	1.74E-15	1.93E-14	24.3416	BTBD7	BTB (POZ) domain containing 7	AI580162
244420_at	0.59294	4.186659	10.36858	1.84E-20	3.39E-19	35.64787			AI128130
227367_at	0.59293	6.820987	5.445942	1.49E-07	5.06E-07	6.381876			AW976431
208442_s_at	0.59285	6.068304	6.528085	5.30E-10	2.84E-09	11.88358	ATM	ataxia telangiectasia mutated	NM_000051
214870_x_at	0.59277	9.63272	8.261293	1.90E-14	1.87E-13	21.9527	LOC33904 7	hypothetical protein LOC339047	AC002045
235060_at	0.59248	5.899161	6.29854	1.85E-09	9.03E-09	10.65964	LOC10019 0986	hypothetical LOC100190986	AL047052
226449_at	0.59244	8.061659	9.504301	6.21E-18	8.87E-17	29.88471	CEP120	centrosomal protein 120kDa	AI392933
230970_at	0.59233	4.545231	5.614105	6.49E-08	2.36E-07	7.190326			AA975530
230449_x_at	0.59227	6.242458	6.978795	4.21E-11	2.70E-10	14.36792			AI253196
231940_at	0.59227	7.475389	4.789633	3.23E-06	8.41E-06	3.406489	ZNF529	zinc finger protein 529	AI369933
212454_x_at	0.59221	8.802306	8.850143	4.49E-16	5.31E-15	25.64989	HNRPD	HnRNP JKTBP	AI762552
202051_s_at	0.59215	8.332503	9.331831	1.94E-17	2.62E-16	28.75641	ZMYM4	zinc finger, MYM-type 4	NM_005095
207275_s_at	0.59211	7.94252	4.832179	2.67E-06	7.07E-06	3.590346	ACSL1	acyl-CoA synthetase long-chain family member 1	NM_001995
228763_at	0.59186	7.190088	6.696293	2.08E-10	1.20E-09	12.79849	MDP-1	magnesium-dependent phosphatase 1	AI813313
214285_at	0.59186	5.007044	3.852786	0.0001569	0.0002995	-0.30076	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	AI041520
212235_at	0.59182	7.397883	6.851856	8.67E-11	5.29E-10	13.65773	PLXND1	plexin D1	AL575403
212126_at	0.59181	7.837864	7.633436	8.97E-13	7.20E-12	18.1516	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	BG391282
210166_at	0.59168	6.934645	6.423323	9.41E-10	4.83E-09	11.3214	TLR5	toll-like receptor 5	AF051151
224558_s_at	0.59168	8.81209	6.013522	8.41E-09	3.64E-08	9.181134	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	AI446756
203336_s_at	0.59168	9.123965	6.836783	9.44E-11	5.73E-10	13.57393	ITGB1BP1	integrin beta 1 binding protein 1	AL548363
203935_at	0.59158	9.028174	6.699639	2.04E-10	1.18E-09	12.81684	ACVR1	activin A receptor, type I	NM_001105
208752_x_at	0.59144	11.13746	7.209895	1.10E-11	7.70E-11	15.68102	NAP1L1	nucleosome assembly protein 1-like 1	AI888672
216920_s_at	0.59143	6.404359	4.081053	6.46E-05	0.0001317	0.540419	TARP TRGC2	TCR gamma alternate reading frame protein /// T cell receptor gamma constant 2	M27331
209781_s_at	0.59134	7.546814	4.649538	6.01E-06	1.48E-05	2.810262	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3	AF069681
227282_at	0.59116	5.199595	8.122351	4.51E-14	4.27E-13	21.09824	PCDH19	protocadherin 19	AB037734
219372_at	0.59088	7.4421	6.128879	4.58E-09	2.09E-08	9.773899	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	NM_014055
227113_at	0.59012	6.993822	9.836969	6.74E-19	1.06E-17	32.08263	ADHFE1	alcohol dehydrogenase, iron containing, 1	BE048349

214739_at	0.59005	7.017523	10.32382	2.50E-20	4.54E-19	35.34536	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	AI357539
218706_s_at	0.59	7.667756	5.201785	4.84E-07	1.48E-06	5.24084	GRAMD3	GRAM domain containing 3	AW575493
223805_at	0.58994	5.49595	6.49752	6.27E-10	3.31E-09	11.71895	OSBPL6	oxysterol binding protein-like 6	AF323728
203445_s_at	0.58981	9.941385	10.36493	1.89E-20	3.47E-19	35.62321	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	NM_005730
241710_at	0.58971	4.439481	5.388827	1.97E-07	6.52E-07	6.111443	hCG_1645220	hCG1645220	AI436290
222463_s_at	0.58951	7.239256	7.84462	2.49E-13	2.16E-12	19.41253	BACE1	beta-site APP-cleaving enzyme 1	AF190725
238154_at	0.58941	4.781549	8.749973	8.56E-16	9.84E-15	25.01275	CEP70	Centrosomal protein 70kDa, mRNA (cDNA clone MGC:26763 IMAGE:4829481)	AI285884
204177_s_at	0.58935	7.756947	12.21043	4.99E-26	1.51E-24	48.36656	KLHL20	kelch-like 20 (Drosophila)	NM_014458
204610_s_at	0.58907	8.575264	9.554905	4.43E-18	6.43E-17	30.21726	CCDC85B	coiled-coil domain containing 85B	NM_006848
200685_at	0.58906	8.144372	7.327263	5.55E-12	4.03E-11	16.35755	SFRS11	splicing factor, arginine/serine-rich 11	AU146237
243046_at	0.58903	4.300137	6.581871	3.94E-10	2.16E-09	12.1745			BF679700
212880_at	0.5888	7.489119	9.400296	1.24E-17	1.71E-16	29.20336	WDR7	WD repeat domain 7	AB011113
221480_at	0.58878	7.140966	6.769969	1.38E-10	8.14E-10	13.20389	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	BG180941
212726_at	0.58864	8.081891	9.885461	4.87E-19	7.76E-18	32.40525	PHF2	PHD finger protein 2	AB014562
225977_at	0.58857	6.451206	8.933681	2.62E-16	3.17E-15	26.18367	PCDH18	protocadherin 18	BF062943
224567_x_at	0.58836	11.53568	5.396112	1.90E-07	6.31E-07	6.145816	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	BG534952
232600_at	0.5882	3.700007	7.159355	1.48E-11	1.01E-10	15.39168			AL137429
244058_at	0.58805	5.029221	12.94481	2.74E-28	9.91E-27	53.53668	C10orf72	chromosome 10 open reading frame 72	AI127432
230337_at	0.58784	5.621097	6.166253	3.76E-09	1.74E-08	9.967606	SOS1	son of sevenless homolog 1 (Drosophila)	AW241962
216339_s_at	0.58734	4.963089	7.147764	1.59E-11	1.08E-10	15.32549	TNXA ///	tenascin XA pseudogene ///	AF086641
224600_at	0.58726	8.528032	8.10339	5.07E-14	4.78E-13	20.9822	TNXB	tenascin XB	BE501318
222876_s_at	0.58719	7.354981	7.919081	1.58E-13	1.41E-12	19.86148	CGGBP1	CGG triplet repeat binding protein 1	BE501318
242818_x_at	0.58719	4.889926	9.449323	8.93E-18	1.25E-16	29.52419	ADAP2	ArfGAP with dual PH domains 2	AI761520
212579_at	0.58714	8.017247	6.480524	6.88E-10	3.61E-09	11.62762		structural maintenance of chromosomes flexible hinge domain containing 1	R63578
223236_at	0.58705	7.781944	9.673456	2.01E-18	3.00E-17	30.99888	SMCHD1		AB014550
235405_at	0.58693	5.786499	6.516333	5.65E-10	3.02E-09	11.82022	CCDC55	coiled-coil domain containing 55	AL136806
218396_at	0.58687	9.556555	7.966111	1.18E-13	1.07E-12	20.14619	GSTA4	glutathione S-transferase alpha 4	N79662
203929_s_at	0.58679	4.75616	8.815254	5.62E-16	6.57E-15	25.42761	VPS13C	vacuolar protein sorting 13 homolog C (S. cerevisiae)	NM_017684
213273_at	0.58672	5.255852	6.563199	4.36E-10	2.37E-09	12.07333	MAPT	microtubule-associated protein tau	AI056359
224968_at	0.58669	8.176502	7.11536	1.91E-11	1.29E-10	15.14079	ODZ4	odx, odd Oz/ten-m homolog 4 (Drosophila)	BF112171
212854_x_at	0.58646	10.25074	10.23187	4.68E-20	8.27E-19	34.7253	CCDC104	coiled-coil domain containing 104	AL518311
217122_s_at	0.58633	9.038631	8.472463	5.02E-15	5.29E-14	23.26486	NBP10	neuroblastoma breakpoint family, member 10	AB051480
211704_s_at	0.58621	6.76417	7.238218	9.36E-12	6.58E-11	15.8437	SPIN2A ///	spindlin family, member 2A ///	AF356353
1568713_a_at	0.58616	4.387029	9.910054	4.12E-19	6.64E-18	32.56908	SPIN2B	spindlin family, member 2B	AF356353
							TBC1D1	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	AI872403

232217_at	0.58616	5.494933	7.977684	1.10E-13	1.00E-12	20.21638	FAM26E	family with sequence similarity 26, member E	AI292175
1553703_at	0.58608	8.964221	8.875197	3.82E-16	4.55E-15	25.80975	ZNF791	zinc finger protein 791	NM_153358
227062_at	0.58544	8.724091	3.620223	0.0003723	0.0006674	-1.11465	NCRNA00084	non-protein coding RNA 84	AU155361
238601_at	0.58541	7.148589	5.907088	1.46E-08	6.04E-08	8.641171	PHKB	phosphorylase kinase, beta	AI798207
223679_at	0.58533	6.826732	6.53254	5.17E-10	2.78E-09	11.90761	CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	AF130085
220512_at	0.58519	4.363106	5.858613	1.88E-08	7.58E-08	8.397495	DLC1	deleted in liver cancer 1	NM_024767
208920_at	0.58516	7.494253	4.877156	2.18E-06	5.87E-06	3.786107	SRI	sorcin	AV752215
214295_at	0.58514	4.785341	5.518743	1.04E-07	3.64E-07	6.729648	KIAA0485	hypothetical LOC57235	AW129056
208978_at	0.58513	8.331156	5.273745	3.43E-07	1.08E-06	5.573034	CRIP2	cysteine-rich protein 2	U36190
235281_x_at	0.58511	5.312398	7.709812	5.66E-13	4.67E-12	18.60547	AHNAK	AHNAK nucleoprotein	AA523289

Figure 12

Proliferative-subtype up-regulated genes

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	Gene Symb	Gene Title	GeneBank_ACC
204580_at	2.81696	8.7327089	10.21749	5.17E-20	2.12E-18	34.80553	MMP12	matrix metalloproteinase 12	NM_002426
209942_x_at	2.53412	6.013717	6.313394	1.71E-09	1.19E-08	11.01575	MAGEA3	melanoma antigen family A, 3	BC000340
214612_x_at	2.5263	5.4548481	6.286398	1.98E-09	1.36E-08	10.87402	MAGEA2	melanoma antigen family A, 2b /// melanoma antigen family A, 3 ///	U10691
209642_at	2.27024	6.8563223	16.77744	4.14E-40	5.66E-36	80.49433	BUB1	budding uninhibited by	AF043294
203820_s_at	2.23679	6.8004274	9.209221	4.35E-17	1.09E-15	28.16694	IGF2BP3	insulin-like growth factor 2 mRNA	NM_006547
203967_at	2.15264	6.2821027	14.97733	1.41E-34	2.41E-31	67.91957	CDC6	cell division cycle 6 homolog (S.	U77949
203819_s_at	2.11325	6.7988647	8.365774	9.86E-15	1.63E-13	22.83076	IGF2BP3	insulin-like growth factor 2 mRNA	AU160004
204822_at	2.10707	7.2763017	13.59549	2.68E-30	9.68E-28	58.19101	TTK	TTK protein kinase	NM_003318
223381_at	2.07416	7.0490039	13.9827	1.69E-31	8.97E-29	60.91819	NUF2	NUF2, NDC80 kinetochore complex	AF326731
211506_s_at	2.06742	7.3818622	8.445952	5.94E-15	1.03E-13	23.32799	IL8	interleukin 8	AF043337
204641_at	2.05786	7.9090934	12.81439	6.95E-28	1.32E-25	52.69978	NEK2	NIMA (never in mitosis gene a)-	NM_002497
219148_at	2.03114	8.0423973	12.4408	9.83E-27	1.44E-24	50.08286	PBK	PDZ binding kinase	NM_018492
203214_x_at	2.0112	7.8418676	15.5781	1.97E-36	5.99E-33	72.13541	CDC2	cell division cycle 2, G1 to S and G2	NM_001786
210559_s_at	2.0036	8.2402795	15.10563	5.67E-35	1.19E-31	68.82108	CDC2	cell division cycle 2, G1 to S and G2	D88357
201292_at	1.99053	6.6891525	13.53623	4.08E-30	1.37E-27	57.77384	TOP2A	topoisomerase (DNA) II alpha	AL561834
222608_s_at	1.98566	8.0965293	13.24837	3.17E-29	8.13E-27	55.74831	ANLN	anillin, actin binding protein	AK023208
208079_s_at	1.97998	8.3419729	14.32047	1.52E-32	1.14E-29	63.29734	AURKA	aurora kinase A	NM_003158
203968_s_at	1.96986	6.2905783	15.59807	1.71E-36	5.50E-33	72.27529	CDC6	cell division cycle 6 homolog (S.	NM_001254
202954_at	1.96892	9.3628322	14.52385	3.57E-33	3.42E-30	64.72943	UBE2C	ubiquitin-conjugating enzyme E2C	NM_007019
203764_at	1.95586	7.4833782	13.64576	1.87E-30	6.95E-28	58.54501	DLGAP5	discs, large (Drosophila) homolog-	NM_014750
220651_s_at	1.94512	6.3143956	15.10071	5.87E-35	1.19E-31	68.78653	MCM10	minichromosome maintenance	NM_018518
209891_at	1.94244	6.2858383	15.94679	1.45E-37	6.08E-34	74.71439	SPC25	SPC25, NDC80 kinetochore	AF225416
201291_s_at	1.93807	9.4325774	12.48794	7.04E-27	1.07E-24	50.41264	TOP2A	topoisomerase (DNA) II alpha	AU159942
204092_s_at	1.93038	8.044273	15.1202	5.11E-35	1.12E-31	68.92344	AURKA	aurora kinase A	NM_003600
218542_at	1.9251	7.9078112	12.37521	1.56E-26	2.19E-24	49.62439	CEP55	centrosomal protein 55kDa	NM_018131
205476_at	1.91914	8.7415291	6.764958	1.42E-10	1.18E-09	13.44482	CCL20	chemokine (C-C motif) ligand 20	NM_004591
210052_s_at	1.90808	8.650024	14.83521	3.88E-34	5.30E-31	66.92031	TPX2	TPX2, microtubule-associated,	AF098158
1554768_a_at	1.89969	7.4506426	16.13022	3.96E-38	1.97E-34	75.99462	MAD2L1	MAD2 mitotic arrest deficient-like	AF394735
232278_s_at	1.89447	5.7856413	16.34663	8.59E-39	7.39E-35	77.50238	DEPDC1	DEP domain containing 1	AJ278112
213599_at	1.89055	7.2207207	14.35633	1.18E-32	9.33E-30	63.54987	OIP5	Opa interacting protein 5	BE045993
203213_at	1.87645	9.094314	13.81195	5.72E-31	2.58E-28	59.71543	CDC2	cell division cycle 2, G1 to S and G2	AL524035
236641_at	1.86896	5.4827652	16.33273	9.48E-39	7.39E-35	77.40562	KIF14	kinesin family member 14	AW183154
204709_s_at	1.86542	6.0292449	16.26271	1.55E-38	1.06E-34	76.91805	KIF23	kinesin family member 23	NM_004856
204962_s_at	1.86326	7.521786	13.57706	3.05E-30	1.08E-27	58.06127	CENPA	centromere protein A	NM_001809
228033_at	1.86195	5.7189117	15.12166	5.05E-35	1.12E-31	68.93366	E2F7	E2F transcription factor 7	AI341146
228729_at	1.86029	7.3211564	13.37045	1.33E-29	3.95E-27	56.60708	CCNB1	cyclin B1	N90191
210467_x_at	1.86015	4.8521861	5.617278	6.39E-08	3.44E-07	7.496459	MAGEA12	melanoma antigen family A, 12	BC003408
37892_at	1.84132	6.5833043	6.210193	2.97E-09	2.00E-08	10.47616	COL11A1	collagen, type XI, alpha 1	J04177
219918_s_at	1.84122	7.8553843	12.87344	4.57E-28	9.04E-26	53.11406	ASPM	asp (abnormal spindle) homolog,	NM_018123
1552619_a_at	1.83272	6.948843	15.04108	8.97E-35	1.63E-31	68.36757	ANLN	anillin, actin binding protein	NM_018685
203418_at	1.83173	6.9410611	15.04721	8.58E-35	1.62E-31	68.41062	CCNA2	cyclin A2	NM_001237
206224_at	1.82925	6.9770117	6.906639	6.35E-11	5.60E-10	14.22882	CST1	cystatin SN	NM_001898
202859_x_at	1.82606	9.7103312	7.305758	6.30E-12	6.56E-11	16.48986	IL8	interleukin 8	NM_000584
202870_s_at	1.82507	8.224689	14.07264	8.91E-32	5.41E-29	61.55169	CDC20	cell division cycle 20 homolog (S. cerevisiae)	NM_001255
211080_s_at	1.81423	5.821804	17.28545	1.18E-41	3.22E-37	84.0044	NEK2	NIMA (never in mitosis gene a)-related kinase 2	Z25425
206102_at	1.80419	8.4166122	13.41464	9.71E-30	3.01E-27	56.91799	GINS1	GINS complex subunit 1 (Psf1 homolog)	NM_021067
225834_at	1.79931	8.0902646	13.86829	3.83E-31	1.85E-28	60.11222	FAM72A	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// gastric cancer up-regulated-2	AL135396
218009_s_at	1.797	8.5885095	14.85165	3.45E-34	4.84E-31	67.03593	PRC1	protein regulator of cytokinesis 1	NM_003981
205828_at	1.79054	7.3642388	5.727637	3.67E-08	2.05E-07	8.035008	MMP3	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	NM_002422
218663_at	1.78782	6.7341695	13.87777	3.58E-31	1.75E-28	60.17901	NCAPG	non-SMC condensin I complex, subunit G	NM_022346
214710_s_at	1.76906	8.6870492	13.25445	3.04E-29	7.87E-27	55.79107	CCNB1	cyclin B1	BE407516
228069_at	1.74203	7.0408854	11.92108	3.85E-25	4.14E-23	46.45886	FAM54A	family with sequence similarity 54, member A	AL138828
207165_at	1.73957	8.4364214	12.24274	3.99E-26	5.16E-24	48.69927	HMMR	hyaluronan-mediated motility receptor (RHAMM)	NM_012485
218355_at	1.73584	7.0658353	13.91376	2.77E-31	1.40E-28	60.43251	KIF4A	kinesin family member 4A	NM_012310
201650_at	1.73156	11.461697	6.863038	8.14E-11	7.04E-10	13.98648	JUP	junction plakoglobin /// keratin 19	NM_002276

225792_at	1.72759	7.6683472	10.80709	9.12E-22	5.08E-20	38.7887	HOOK1	hook homolog 1 (Drosophila)	AA618420
202705_at	1.70812	8.5942333	13.14738	6.51E-29	1.57E-26	55.03826	CCNB2	cyclin B2	NM_004701
235165_at	1.70346	7.6568092	10.68473	2.12E-21	1.10E-19	37.95698	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	AW151704
227196_at	1.70105	9.2965323	7.966151	1.19E-13	1.63E-12	20.38744	RHPN2	rhophilin, Rho GTPase binding protein 2	BG054987
227174_at	1.69408	7.4425647	4.992925	1.28E-06	5.63E-06	4.597529	WDR72	WD repeat domain 72	Z98443
218782_s_at	1.69346	7.7734096	15.91828	1.77E-37	6.91E-34	74.51526	ATAD2	ATPase family, AAA domain containing 2	NM_014109
213562_s_at	1.69253	5.1164974	14.32147	1.51E-32	1.14E-29	63.30442	SQLE	squalene epoxidase	BF979497
209408_at	1.68731	8.0957903	16.14448	3.58E-38	1.95E-34	76.09409	KIF2C	kinesin family member 2C	U63743
1555731_a_at	1.68674	5.4124723	10.65537	2.59E-21	1.32E-19	37.75777	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	AF393369
222958_s_at	1.68653	6.4708594	13.77854	7.26E-31	3.14E-28	59.4801	DEPDC1	DEP domain containing 1	AK000490
201428_at	1.68607	8.5547748	8.878445	3.74E-16	7.94E-15	26.04751	CLDN4	claudin 4	NM_001305
209709_s_at	1.68197	7.4958194	13.54254	3.90E-30	1.32E-27	57.81826	HMMR	hyaluronan-mediated motility receptor (RHAMM)	U29343
202095_s_at	1.67817	8.2197556	12.4274	1.08E-26	1.57E-24	49.98917	BIRC5	baculoviral IAP repeat-containing 5	NM_001168
203560_at	1.65943	8.8117692	10.25491	4.01E-20	1.69E-18	35.05639	GGH	gamma-glutamyl hydrolase (conjugase, folylpolyglutamate hydrolase)	NM_003878
226980_at	1.65909	6.4865372	12.77461	9.21E-28	1.69E-25	52.42071	DEPDC1B	DEP domain containing 1B	AK001166
204146_at	1.65173	8.0957425	14.71579	9.09E-34	1.15E-30	66.08027	RAD51AP1	RAD51 associated protein 1	BE966146
221258_s_at	1.65156	5.9080444	15.28824	1.55E-35	3.84E-32	70.10318	KIF18A	kinesin family member 18A	NM_031217
209218_at	1.65147	8.2750934	11.38499	1.65E-23	1.29E-21	42.74798	SQLE	squalene epoxidase	AF098865
204825_at	1.65129	8.3551428	13.54369	3.87E-30	1.32E-27	57.82633	MELK	maternal embryonic leucine zipper kinase	NM_014791
203755_at	1.64448	7.9047181	12.9118	3.48E-28	7.01E-26	53.38336	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	NM_001211
204444_at	1.63596	7.4263035	12.85512	5.20E-28	1.02E-25	52.98552	KIF11	kinesin family member 11	NM_004523
244056_at	1.63302	6.5832291	6.339583	1.48E-09	1.04E-08	11.15362	SFTA2	surfactant associated 2	AW293443
202580_x_at	1.6241	7.2672713	13.7845	6.95E-31	3.06E-28	59.52205	FOXM1	forkhead box M1	NM_021953
203362_s_at	1.61997	9.0113524	13.41019	1.00E-29	3.09E-27	56.88672	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	NM_002358
206199_at	1.6195	6.8338799	5.080267	8.57E-07	3.88E-06	4.987427	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	NM_006890
201890_at	1.6154	9.8849989	10.81952	8.37E-22	4.70E-20	38.87334	RRM2	ribonucleotide reductase M2 polypeptide	BE966236
223229_at	1.61415	8.1298345	14.68569	1.13E-33	1.37E-30	65.8685	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	AB032931
202790_at	1.61319	9.8075157	9.475917	7.50E-18	2.12E-16	29.89839	CLDN7	claudin 7	NM_001307
203691_at	1.61237	8.2720806	5.674834	4.79E-08	2.63E-07	7.776384	PI3	peptidase inhibitor 3, skin-derived	NM_002638
206364_at	1.60856	6.8603975	15.07299	7.15E-35	1.39E-31	68.59177	KIF14	kinesin family member 14	NM_014875
211519_s_at	1.60396	6.423963	16.96815	1.09E-40	1.98E-36	81.81445	KIF2C	kinesin family member 2C	AY026505
222740_at	1.60141	7.2645125	14.9142	2.21E-34	3.55E-31	67.47577	ATAD2	ATPase family, AAA domain containing 2	AI925583
224650_at	1.59972	10.680606	7.086168	2.27E-11	2.15E-10	15.23649	MAL2	mal, T-cell differentiation protein 2	AL117612
41469_at	1.59795	8.5873606	5.536812	9.53E-08	5.00E-07	7.10859	PI3	peptidase inhibitor 3, skin-derived	L10343
204033_at	1.59663	7.6129813	13.54127	3.94E-30	1.33E-27	57.80933	TRIP13	thyroid hormone receptor interactor 13	NM_004237
214603_at	1.59485	4.3362058	6.026454	7.86E-09	4.91E-08	9.530493	MAGEA2	melanoma antigen family A, 2 /// melanoma antigen family A, 2B	U82671
209925_at	1.58653	7.0072906	9.601851	3.25E-18	9.83E-17	30.72251	OCLN	occludin	U53823
230951_at	1.58627	5.7759764	12.66863	1.95E-27	3.33E-25	51.67781	0	0	AW242920
209773_s_at	1.58217	9.5758272	10.73059	1.55E-21	8.28E-20	38.26836	RRM2	ribonucleotide reductase M2 polypeptide	BC001886
222037_at	1.57815	7.1175254	15.69071	8.88E-37	3.16E-33	72.92387	MCM4	mitochondrial chromosome maintenance complex component 4	AI859865
208025_s_at	1.5739	6.0452755	7.577378	1.26E-12	1.47E-11	18.07049	HMGA2	high mobility group AT-hook 2	NM_003483
205394_at	1.56738	6.5582666	13.1945	4.66E-29	1.13E-26	55.36951	CHEK1	CHK1 checkpoint homolog (S. pombe)	NM_001274
218755_at	1.56675	7.1801341	14.44449	6.28E-33	5.28E-30	64.17072	KIF20A	kinesin family member 20A	NM_005733
204128_s_at	1.5642	6.5486278	15.39928	7.03E-36	2.02E-32	70.88211	RFC3	replication factor C (activator 1) 3, 38kDa	NM_002915

209464_at	1.56321	6.6185816	14.2702	2.18E-32	1.61E-29	62.94331	AURKB	aurora kinase B	AB011446
204286_s_at	1.55812	6.3586054	11.5605	4.84E-24	4.21E-22	43.95932	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	NM_021127
203304_at	1.55528	7.6797725	7.597639	1.11E-12	1.31E-11	18.18969	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	NM_012342
213226_at	1.55109	7.6575113	13.26645	2.79E-29	7.43E-27	55.87543	CCNA2	cyclin A2	AI346350
219121_s_at	1.54783	8.6809923	8.864186	4.11E-16	8.65E-15	25.95689	RBM35A	RNA binding motif protein 35A	NM_017697
1552477_a_at	1.54718	7.0949706	9.7719	1.04E-18	3.45E-17	31.84159	IRF6	interferon regulatory factor 6	BC014852
223307_at	1.53968	8.5255071	14.16741	4.53E-32	3.00E-29	62.21927	CDC43	cell division cycle associated 3	BC002551
1555758_a_at	1.53968	8.1345908	12.51271	5.90E-27	9.11E-25	50.58591	CDKN3	cyclin-dependent kinase inhibitor 3	AF213040
214642_x_at	1.53959	4.7296783	6.799697	1.17E-10	9.82E-10	13.63612	MAGEA5	melanoma antigen family A, 5	AI200443
218963_s_at	1.53942	5.9196599	6.026954	7.84E-09	4.90E-08	9.533041	KRT23	keratin 23 (histone deacetylase inducible)	NM_015515
222680_s_at	1.53771	7.05289	13.66194	1.67E-30	6.32E-28	58.65892	DTL	denticless homolog (Drosophila)	AK001261
								similar to Ubiquitin-conjugating enzyme E25 (Ubiquitin-conjugating enzyme E2-24 kDa) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-EPF5) /// ubiquitin-conjugating enzyme E25	
202779_s_at	1.53704	9.3598724	15.37258	8.49E-36	2.32E-32	70.69483	LOC731049	claudin 3	NM_014501
203953_s_at	1.53506	7.6889885	4.933908	1.68E-06	7.22E-06	4.337059	CLDN3	selenoprotein I	BE791251
1555274_a_at	1.535	7.2914879	13.68402	1.42E-30	5.47E-28	58.81443	SEL1	cyclin E2	BC021229
205034_at	1.53203	6.9545463	11.37051	1.83E-23	1.42E-21	42.64817	CCNE2	kinesin family member 15	NM_004702
219306_at	1.5292	6.3526277	13.36305	1.40E-29	4.07E-27	56.55499	KIF15	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	NM_020242
206632_s_at	1.52498	6.6267278	7.672727	7.08E-13	8.58E-12	18.63295	APOBEC3B	KIAA0101	NM_004900
202503_s_at	1.52176	10.284072	10.77707	1.12E-21	6.19E-20	38.5844	KIAA0101	KIAA0101	NM_014736
219493_at	1.51998	6.8396345	13.83624	4.81E-31	2.23E-28	59.88651	SHCBP1	SHC SH2-domain binding protein 1	NM_024745
207039_at	1.51719	6.0480078	8.179701	3.16E-14	4.79E-13	21.68569	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	NM_000077
206858_s_at	1.50642	7.2370884	8.269475	1.80E-14	2.85E-13	22.23657	HOXC4 ///	homeobox C4 /// homeobox C6	NM_004503
215101_s_at	1.50615	6.7978066	4.333162	2.32E-05	8.16E-05	1.827377	CXCL5	chemokine (C-X-C motif) ligand 5	BG166705
212531_at	1.49947	10.725976	4.392566	1.81E-05	6.49E-05	2.063726	LCN2	lipocalin 2	NM_005564
222646_s_at	1.49549	9.1272048	12.0105	2.05E-25	2.32E-23	47.0808	ERO1L	ERO1-like (S. cerevisiae)	AW268365
205393_s_at	1.49452	5.4866335	13.72525	1.06E-30	4.34E-28	59.10475	CHEK1	CHK1 checkpoint homolog (S. pombe)	NM_001274
219787_s_at	1.49187	9.0160753	12.78583	8.51E-28	1.58E-25	52.49941	ECT2	epithelial cell transforming sequence 2 oncogene	NM_018098
1554696_s_at	1.49151	7.91476	13.55969	3.45E-30	1.19E-27	57.93902	TYMS	thymidylate synthetase	AB077208
213007_at	1.49067	7.5543217	13.87721	3.59E-31	1.75E-28	60.17509	FANCI	Fanconi anemia, complementation group I	W74442
218039_at	1.48818	8.8367201	12.35077	1.86E-26	2.57E-24	49.45357	NUSAP1	nucleolar and spindle associated protein 1	NM_016359
228273_at	1.4837	8.7405403	12.12331	9.27E-26	1.12E-23	47.86639	0	0	BG165011
223556_at	1.4809	6.4027279	13.11364	8.28E-29	1.94E-26	54.80105	HELLS	helicase, lymphoid-specific	AF155827
238542_at	1.47188	6.1034173	9.18949	4.95E-17	1.22E-15	28.03962	ULBP2	UL16 binding protein 2	AA831769
218662_s_at	1.47098	6.4766665	13.09437	9.49E-29	2.22E-26	54.66566	NCAPG	non-SMC condensin I complex, subunit G	NM_022346
1553830_s_at	1.4667	4.1853975	6.186162	3.38E-09	2.25E-08	10.35138	MAGEA2 ///	melanoma antigen family A, 2 /// melanoma antigen family A, 2B	NM_005361
230361_at	1.46523	5.9551065	12.72137	1.34E-27	2.37E-25	52.04742	HEATR7A	HEAT repeat containing 7A	AW664013
204285_s_at	1.46354	8.1251879	10.33511	2.32E-20	1.01E-18	35.59494	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	AI857639
1555772_a_at	1.45999	4.8218467	13.08261	1.03E-28	2.36E-26	54.58303	CDC25A	cell division cycle 25 homolog A (S. pombe)	AY137580
205506_at	1.45897	8.0167076	7.188161	1.25E-11	1.24E-10	15.81584	VIL1	villin 1	NM_007127
219978_s_at	1.45857	7.8645417	12.56052	4.21E-27	6.68E-25	50.92056	NUSAP1	nucleolar and spindle associated protein 1	NM_018454
223700_at	1.45844	5.2162518	14.2013	3.56E-32	2.56E-29	62.45802	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	AY028916

204162_at	1.45759	7.381303	13.22982	3.62E-29	9.15E-27	55.61786	NDC80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	NM_006101
218073_s_at	1.45689	7.421966	14.53436	3.31E-33	3.23E-30	64.80339	TMEM48	transmembrane protein 48	NM_018087
220295_x_at	1.45659	5.4257337	14.18188	4.09E-32	2.83E-29	62.32119	DEPDC1	DEP domain containing 1	NM_017779
1553764_a_at	1.45538	6.5500254	10.85321	6.63E-22	3.78E-20	39.1028	JUB	jub, ajuba homolog (Xenopus laevis)	NM_032876
222036_s_at	1.45499	7.5774819	14.57863	2.42E-33	2.44E-30	65.11504	MCM4	minichromosome maintenance complex component 4	AI859865
229610_at	1.45385	6.8530838	17.3803	6.09E-42	3.22E-37	84.65738	CKAP2L	cytoskeleton associated protein 2-like	AW088063
210387_at	1.45238	6.1265548	8.573486	2.65E-15	4.86E-14	24.12348	HIST1H2BC	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	BC001131
230323_s_at	1.45045	8.9729525	5.876985	1.71E-08	1.01E-07	8.775745	TMEM458	transmembrane protein 458	AW242836
229292_at	1.44997	7.3698011	10.82605	8.00E-22	4.51E-20	38.91777	EPB41L5	erythrocyte membrane protein band 4.1 like 5	AI652872
204602_at	1.44994	6.5660374	4.276744	2.93E-05	0.0001012	1.605375	DKK1	dickkopf homolog 1 (Xenopus laevis)	NM_012242
204320_at	1.44919	6.4875122	5.656097	5.26E-08	2.87E-07	7.685031	COL11A1	collagen, type XI, alpha 1	NM_001854
223062_s_at	1.44716	8.7019715	8.570511	2.70E-15	4.95E-14	24.10486	PSAT1	phosphoserine aminotransferase 1	BC004863
225806_at	1.44126	7.5612621	9.818284	7.65E-19	2.58E-17	32.14805	JUB	jub, ajuba homolog (Xenopus laevis)	AI289311
207178_s_at	1.44117	5.1455853	12.52198	5.53E-27	8.60E-25	50.6508	FRK	fyn-related kinase	NM_002031
204470_at	1.435	8.3022984	6.076599	6.04E-09	3.86E-08	9.78665	CXCL1	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	NM_001511
203145_at	1.43275	7.3589276	14.38233	9.79E-33	7.98E-30	63.73297	SPAG5	sperm associated antigen 5	NM_006461
221648_s_at	1.43228	8.2257711	8.106543	4.98E-14	7.29E-13	21.23898	0	0	AK025651
204733_at	1.43202	6.2658483	5.557202	8.62E-08	4.55E-07	7.206489	KLK6	kallikrein-related peptidase 6	NM_002774
204026_s_at	1.43186	9.4248662	11.10172	1.19E-22	7.89E-21	40.80123	ZWINT	ZW10 interactor	NM_007057
219990_at	1.42827	6.6557783	9.727086	1.41E-18	4.54E-17	31.54599	E2F8	E2F transcription factor 8	NM_024680
214079_at	1.42716	5.0361102	4.467788	1.32E-05	4.84E-05	2.366813	DHRS2	dehydrogenase/reductase (SDR family) member 2	AK000345
206683_at	1.4257	6.1977079	10.17002	7.13E-20	2.86E-18	34.48778	ZNF165	zinc finger protein 165	NM_003447
202107_s_at	1.42383	8.8092696	14.48345	4.76E-33	4.33E-30	64.44498	MCM2	minichromosome maintenance complex component 2	NM_004526
210715_s_at	1.41421	10.682839	9.751222	1.20E-18	3.92E-17	31.70514	SPINT2	serine peptidase inhibitor, Kunitz type, 2	AF027205
1553105_s_at	1.41005	8.7326213	7.4418	2.82E-12	3.12E-11	17.27745	DSG2	desmoglein 2	NM_001943
201130_s_at	1.40765	6.4384729	8.833248	5.01E-16	1.04E-14	25.76048	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	L08599
205339_at	1.40754	7.6316246	13.27907	2.55E-29	6.86E-27	55.96423	STIL	SCL/TAL1 interrupting locus	NM_003035
230831_at	1.40158	5.5017226	9.604812	3.19E-18	9.65E-17	30.74193	FRMD5	FERM domain containing 5	AW294986
201897_s_at	1.39978	10.023349	16.06367	6.34E-38	2.88E-34	75.5304	CKS1B	CDC28 protein kinase regulatory subunit 1B	NM_001826
205909_at	1.39858	7.0283381	13.709	1.19E-30	4.78E-28	58.99035	POLE2	polymerase (DNA directed), epsilon 2 (p59 subunit)	NM_002692
212949_at	1.39814	6.7747843	14.66678	1.29E-33	1.45E-30	65.73545	NCAPH	non-SMC condensin I complex, subunit H	D38553
210074_at	1.39684	7.7299478	12.31535	2.39E-26	3.24E-24	49.20615	CTSL2	cathepsin L2	AF070448
205046_at	1.3963	6.5445649	14.87309	2.96E-34	4.38E-31	67.18674	CENPE	centromere protein E, 312kDa	NM_001813
228323_at	1.39617	6.9584119	11.52109	6.38E-24	5.46E-22	43.68702	CASC5	cancer susceptibility candidate 5	BF248364
210334_x_at	1.3959	6.685285	14.8174	4.41E-34	5.87E-31	66.79505	BIRC5	baculoviral IAP repeat-containing 5	AB028869
235545_at	1.39422	5.9422988	13.72468	1.07E-30	4.34E-28	59.10078	DEPDC1	DEP domain containing 1	AI810054
230165_at	1.39375	6.7139075	14.48995	4.54E-33	4.21E-30	64.49077	SGOL2	shugoshin-like 2 (S. pombe)	N31731
211814_s_at	1.38952	4.6733076	12.92534	3.16E-28	6.46E-26	53.4784	CCNE2	cyclin E2	AF112857
223949_at	1.38934	7.3014864	6.008515	8.63E-09	5.36E-08	9.439215	TMPS3	transmembrane protease, serine 3	AB038160
219763_at	1.38879	6.6586579	11.27037	3.67E-23	2.67E-21	41.95897	DENND1A	DENN/MADD domain containing 1A	NM_024820
225846_at	1.38442	9.6476845	6.27975	2.05E-09	1.41E-08	10.83918	RBM35A	RNA binding motif protein 35A	BF001941
218186_at	1.3799	9.8627086	6.706431	1.97E-10	1.60E-09	13.12394	RAB25	RAB25, member RAS oncogene family	NM_020387
204379_s_at	1.37964	7.6340785	8.176259	3.23E-14	4.89E-13	21.66463	FGFR3	fibroblast growth factor receptor 3	NM_000142

239155_at	1.37793	6.7624333	8.35987	1.02E-14	1.69E-13	22.79423	CXADRP1	coxsackie virus and adenovirus receptor pseudogene 1	N34895
224753_at	1.37779	7.5615089	14.14693	5.25E-32	3.33E-29	62.07501	CDC45	cell division cycle associated 5	BE614410
222830_at	1.37632	6.8356244	10.56956	4.67E-21	2.26E-19	37.17642	GRHL1	grainyhead-like 1 (Drosophila)	BE566136
213523_at	1.37419	7.9573891	9.755999	1.16E-18	3.81E-17	31.73665	CCNE1	cyclin E1	AI671049
208170_s_at	1.37288	6.9909881	5.398082	1.88E-07	9.45E-07	6.449575	TRIM31	tripartite motif-containing 31	NM_007028
215509_s_at	1.37249	5.3916544	15.03068	9.66E-35	1.70E-31	68.29451	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	AL137654
219494_at	1.36951	6.4815437	12.93488	2.95E-28	6.08E-26	53.54533	RAD54B	RAD54 homolog B (S. cerevisiae)	NM_012415
202094_at	1.36918	6.4875513	13.09181	9.67E-29	2.23E-26	54.64769	BIRC5	baculoviral IAP repeat-containing 5	AA648913
215425_at	1.3685	6.2146767	9.098346	8.98E-17	2.13E-15	27.45293	BTG3	BTG family, member 3	AL049332
204318_s_at	1.36801	6.5014355	10.6685	2.37E-21	1.22E-19	37.84679	GTSE1	G-2 and S-phase expressed 1	NM_016426
202286_s_at	1.36541	10.937922	6.084686	5.79E-09	3.71E-08	9.828097	TACSTD2	tumor-associated calcium signal transducer 2	J04152
218145_at	1.36264	7.4378445	8.776423	7.23E-16	1.45E-14	25.40051	TRIB3	tribbles homolog 3 (Drosophila)	NM_021158
207828_s_at	1.35739	7.8405705	11.67541	2.17E-24	2.03E-22	44.75435	CENPF	centromere protein F, 350/400ka (mitosin)	NM_005196
219555_s_at	1.35567	7.8514629	13.0345	1.45E-28	3.27E-26	54.24496	CENPN	centromere protein N	NM_018455
227804_at	1.35446	7.2983999	10.80875	9.02E-22	5.04E-20	38.79996	TLCD1	TLC domain containing 1	BE328850
203358_s_at	1.35319	7.1388688	11.64965	2.59E-24	2.38E-22	44.57599	EZH2	enhancer of zeste homolog 2 (Drosophila)	NM_004456
218726_at	1.35189	6.8260601	12.9372	2.90E-28	6.01E-26	53.56165	HJURP	Holliday junction recognition protein	NM_018410
221520_s_at	1.35093	7.6729615	14.37646	1.02E-32	8.20E-30	63.69164	CDC48	cell division cycle associated 8	BC001651
202489_s_at	1.34996	11.102771	5.91796	1.38E-08	8.31E-08	8.981328	FXSD3	FXSD domain containing ion transport regulator 3	BC005238
204170_s_at	1.34986	10.391875	10.86569	6.09E-22	3.50E-20	39.1879	CKS2	CDC28 protein kinase regulatory subunit 2	NM_001827
219255_x_at	1.34733	7.6445139	8.904012	3.17E-16	6.82E-15	26.21016	IL17RB	interleukin 17 receptor B	NM_018725
213150_at	1.34132	6.8569907	5.26075	3.65E-07	1.76E-06	5.809516	HOXA10	homeobox A10	BF792917
209714_s_at	1.34114	8.1572985	11.21711	5.32E-23	3.75E-21	41.5929	CDKN3	cyclin-dependent kinase inhibitor 3	AF213033
222962_s_at	1.33993	5.9274465	13.56956	3.22E-30	1.12E-27	58.00848	MCM10	minichromosome maintenance complex component 10	AB042719
226803_at	1.3395	8.9500543	7.34366	5.04E-12	5.34E-11	16.70845	CHMP4C	chromatin modifying protein 4C	AK000049
219630_at	1.33704	9.1149237	4.994886	1.27E-06	5.58E-06	4.606229	PDZK1IP1	PDZK1 interacting protein 1	NM_005764
202934_at	1.33561	8.4575926	9.129712	7.32E-17	1.75E-15	27.65456	HK2	hexokinase 2	AI761561
228956_at	1.32957	7.2768284	5.466347	1.35E-07	6.91E-07	6.772313	UGT8	Ceramide UDPgalactosyltransferase	N22272
207463_x_at	1.32928	9.1660764	6.878698	7.45E-11	6.49E-10	14.07341	PRSS3	protease, serine, 3	NM_002771
204579_at	1.32663	7.5155332	10.22065	5.06E-20	2.08E-18	34.82677	FGFR4	fibroblast growth factor receptor 4	NM_002011
212141_at	1.32659	8.0165446	14.66594	1.30E-33	1.45E-30	65.72952	MCM4	minichromosome maintenance complex component 4	AA604621
206134_at	1.32189	7.6258263	6.115097	4.93E-09	3.20E-08	9.984297	ADAMDEC1	ADAM-like, decysin 1	NM_014479
1566764_at	1.32104	5.1762632	7.743779	4.61E-13	5.77E-12	19.05457	MACC1	metastasis associated in colon cancer 1	AL359055
237215_s_at	1.32099	6.5696861	11.97888	2.57E-25	2.84E-23	46.86081	TFRC	transferrin receptor (p90, CD71)	N76327
205822_s_at	1.32099	6.0132146	10.645	2.78E-21	1.41E-19	37.68745	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	NM_002130
212022_s_at	1.32041	7.4812824	10.77096	1.17E-21	6.43E-20	38.54283	MKI67	antigen identified by monoclonal antibody Ki-67	BF001806
204988_at	1.31991	4.8699269	5.704681	4.12E-08	2.29E-07	7.922363	FGF	fibrinogen beta chain	NM_005141
209875_s_at	1.31835	9.7935176	5.050671	9.84E-07	4.40E-06	4.854723	SPP1	secreted phosphoprotein 1	M83248
227928_at	1.31749	5.3213718	13.48762	5.77E-30	1.84E-27	57.43161	C12orf48	chromosome 12 open reading frame 48	AI224977
204240_s_at	1.31696	7.3618496	13.19486	4.64E-29	1.13E-26	55.372	SMC2	structural maintenance of chromosomes 2	NM_006444
204126_s_at	1.31612	6.8609504	14.1825	4.07E-32	2.83E-29	62.32561	CDC45L	CDC45 cell division cycle 45-like (S. cerevisiae)	NM_003504
220840_s_at	1.31581	5.6617404	14.62158	1.78E-33	1.90E-30	65.41737	C1orf112	chromosome 1 open reading frame 112	NM_018186

209172_s_at	1.31173	5.2031479	13.6541	1.76E-30	6.64E-28	58.6037	CENPF	centromere protein F, 350/400ka (mitosin)	U30872
220239_at	1.30828	6.9500493	13.49373	5.53E-30	1.79E-27	57.47462	KLHL7	kelch-like 7 (Drosophila)	NM_018846
203554_x_at	1.30121	9.8960814	12.0878	1.19E-25	1.40E-23	47.61898	PTTG1	pituitary tumor-transforming 1	NM_004219
202936_s_at	1.29957	9.4019103	7.12655	1.80E-11	1.73E-10	15.46528	SOX9	SRX (sex determining region Y)-box 9	NM_000346
211122_s_at	1.29913	6.4998206	4.916542	1.82E-06	7.78E-06	4.260879	CXCL11	chemokine (C-X-C motif) ligand 11	AF002985
220520_s_at	1.2952	5.1015396	8.428331	6.64E-15	1.13E-13	23.21852	NUP62CL	nucleoporin 62kDa C-terminal like	NM_017681
210059_s_at	1.29508	8.2944996	8.860012	4.22E-16	8.86E-15	25.93037	MAPK13	mitogen-activated protein kinase 13	BC000433
205890_s_at	1.29503	10.441285	5.791255	2.65E-08	1.52E-07	8.348881	GABBR1 ///	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D	NM_006398
223883_s_at	1.2946	5.8508055	7.125621	1.81E-11	1.74E-10	15.46001	STK31	serine/threonine kinase 31	AF332194
228281_at	1.29353	6.6803948	14.49415	4.41E-33	4.15E-30	64.52037	C11orf82	chromosome 11 open reading frame 82	BF343258
208190_s_at	1.29308	9.7626553	8.853689	4.39E-16	9.21E-15	25.89022	LSR	lipolysis stimulated lipoprotein receptor	NM_015925
210567_s_at	1.29212	5.7679997	12.94314	2.78E-28	5.80E-26	53.60337	SKP2	S-phase kinase-associated protein 2 (p45)	BC001441
226129_at	1.29176	8.9318081	8.185373	3.05E-14	4.64E-13	21.7204	FAM83H	family with sequence similarity 83, member H	AI949095
201131_s_at	1.29166	10.834747	5.164395	5.78E-07	2.68E-06	5.367896	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	NM_004360
37117_at	1.28818	7.4502035	9.495913	6.57E-18	1.89E-16	30.02897	ARHGAP8 /	Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion /// proline rich 5 (renal)	Z83838
242881_x_at	1.288	5.8973664	6.06871	6.29E-09	4.01E-08	9.746252	0	0	BG285837
207850_at	1.28733	8.0900898	5.706358	4.08E-08	2.27E-07	7.930631	CXCL3	chemokine (C-X-C motif) ligand 3	NM_002090
217551_at	1.28624	6.3148302	7.982033	1.07E-13	1.49E-12	20.48339	LOC441453	similar to olfactory receptor, family 7, subfamily A, member 17	AA719797
218883_s_at	1.28544	8.4206602	10.00777	2.14E-19	7.97E-18	33.40512	MLF1IP	MLF1 interacting protein	NM_024629
1553589_a_at	1.28509	8.9197457	5.020102	1.13E-06	5.01E-06	4.718288	PDZK1IP1	PDZK1 interacting protein 1	NM_005764
202589_at	1.28489	9.5863544	11.51109	6.85E-24	5.80E-22	43.61789	TYMS	thymidylate synthetase	NM_001071
234992_x_at	1.28441	6.7507411	13.23255	3.55E-29	9.02E-27	55.63707	ECT2	epithelial cell transforming sequence 2 oncogene	BG170335
226661_at	1.28315	7.2185517	11.01379	2.18E-22	1.37E-20	40.19923	CDCA2	cell division cycle associated 2	T90295
220060_s_at	1.28126	4.9766189	14.03959	1.13E-31	6.55E-29	61.3189	C12orf48	chromosome 12 open reading frame 48	NM_017915
212142_at	1.28011	5.8855424	13.78555	6.90E-31	3.06E-28	59.52949	MCM4	minichromosome maintenance complex component 4	AI936566
1558508_a_at	1.27572	6.401834	11.49763	7.52E-24	6.33E-22	43.52499	C1orf53	chromosome 1 open reading frame 53	BI832220
225655_at	1.27522	8.194736	10.20667	5.56E-20	2.27E-18	34.73306	UHRF1	ubiquitin-like with PHD and ring finger domains 1	AK025578
205167_s_at	1.27389	6.1344438	13.61121	2.39E-30	8.71E-28	58.3017	CDC25C	cell division cycle 25 homolog C (S. pombe)	NM_001790
209644_x_at	1.27288	7.6587368	8.374329	9.34E-15	1.55E-13	22.8837	CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	U38945
224361_s_at	1.27206	7.5094424	9.516005	5.75E-18	1.66E-16	30.16029	IL17RB	interleukin 17 receptor B	AF250309
224156_x_at	1.27151	7.6563895	8.553976	3.00E-15	5.47E-14	24.00143	IL17RB	interleukin 17 receptor B	AF208111
219588_s_at	1.27048	7.2661447	15.14265	4.35E-35	1.03E-31	69.08111	NCAPG2	non-SMC condensin II complex, subunit G2	NM_017760
218585_s_at	1.26922	7.5792764	11.66159	2.39E-24	2.21E-22	44.65871	DTL	denticleless homolog (Drosophila)	NM_016448
224097_s_at	1.26847	8.4295528	11.63076	2.96E-24	2.68E-22	44.44525	F11R	F11 receptor	AF191495
203744_at	1.26452	8.1941649	13.02645	1.54E-28	3.42E-26	54.18843	HMGB3	high-mobility group box 3	NM_005342
204887_s_at	1.26258	6.6236578	14.16543	4.60E-32	3.00E-29	62.20535	PLK4	polo-like kinase 4 (Drosophila)	NM_014264
201014_s_at	1.26167	8.551472	14.07046	9.05E-32	5.43E-29	61.53636	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	NM_006452
227452_at	1.26161	7.3438564	7.471424	2.37E-12	2.65E-11	17.45004	0	0	AI832118
205980_s_at	1.26097	7.1037791	10.33506	2.32E-20	1.01E-18	35.5946	ARHGAP8 /	Rho GTPase activating protein 8 /// PRR5-ARHGAP8 fusion /// proline rich 5 (renal)	NM_015366

213008_at	1.25941	7.5734198	11.8587	5.98E-25	6.21E-23	46.02552	FANCI	Fanconi anemia, complementation group I	BG403615
204315_s_at	1.25802	6.7023841	12.40959	1.23E-26	1.76E-24	49.86466	GTSE1	G-2 and S-phase expressed 1	AI340239
205194_at	1.25708	6.9618357	11.39413	1.55E-23	1.22E-21	42.81096	PSPH	phosphoserine phosphatase	NM_004577
228468_at	1.25559	6.113329	14.08839	7.96E-32	4.89E-29	61.66268	MASTL	microtubule associated serine/threonine kinase-like	BF108964
242787_at	1.25268	6.0606268	12.98476	2.07E-28	4.43E-26	53.8956	0	0	AI924134
229396_at	1.25204	7.584534	10.20121	5.77E-20	2.35E-18	34.69652	OVOL1	ovo-like 1 (Drosophila)	AA588400
214697_s_at	1.24998	7.804937	13.21833	3.93E-29	9.71E-27	55.53705	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	AW190873
205157_s_at	1.24972	6.5207571	5.832979	2.14E-08	1.25E-07	8.556079	KRT17	keratin 17	NM_000422
218349_s_at	1.24856	7.6780474	14.60437	2.01E-33	2.11E-30	65.29625	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	NM_017975
200832_s_at	1.24852	9.4792063	7.865099	2.20E-13	2.92E-12	19.77929	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	AB032261
200862_at	1.2472	9.1848442	8.917793	2.90E-16	6.27E-15	26.29792	DHCR24	24-dehydrocholesterol reductase	NM_014762
209270_at	1.24548	8.9759384	7.589221	1.17E-12	1.37E-11	18.14014	LAMB3	laminin, beta 3	L25541
201896_s_at	1.24485	6.6566383	12.55067	4.51E-27	7.12E-25	50.85164	PSRC1	proline/serine-rich coiled-coil 1	BC001425
225645_at	1.24451	10.182675	5.008341	1.20E-06	5.27E-06	4.665968	EHF	Ets homologous factor, mRNA (cDNA clone MGC:47678 IMAGE:6055934)	AI763378
223278_at	1.24323	8.4267468	6.454812	7.92E-10	5.83E-09	11.76473	GJB2	gap junction protein, beta 2, 26kDa	M86849
205768_s_at	1.24141	6.7817917	6.867013	7.96E-11	6.90E-10	14.00853	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	NM_003645
216238_s_at	1.24032	4.03113	6.009254	8.60E-09	5.34E-08	9.442969	FGB	fibrinogen beta chain	BG545288
213421_x_at	1.23632	9.4651054	6.482387	6.81E-10	5.09E-09	11.91204	PRSS3	protease, serine, 3	AW007273
205024_s_at	1.23378	7.202138	13.39811	1.09E-29	3.30E-27	56.80166	RAD51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	NM_002875
227372_s_at	1.23308	8.8865428	6.940172	5.25E-11	4.69E-10	14.41584	BAIAP2L1	BAI1-associated protein 2-like 1 /// hypothetical protein LOC100128461	AA496034
1559258_a_at	1.23177	5.5129825	4.094042	6.13E-05	0.0001998	0.903183	CXorf61	chromosome X open reading frame 61	AK026566
217640_x_at	1.23103	4.6582087	14.66652	1.29E-33	1.45E-30	65.73359	C18orf24	chromosome 18 open reading frame 24	BF038461
220892_s_at	1.23023	7.1108141	10.44254	1.12E-20	5.08E-19	36.31835	PSAT1	phosphoserine aminotransferase 1	NM_021154
202833_s_at	1.23005	9.4370571	4.552423	9.17E-06	3.46E-05	2.71285	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 1	NM_000295
212281_s_at	1.22975	9.6984362	8.61678	2.01E-15	3.76E-14	24.39478	TMEM97	transmembrane protein 97	BF038366
210058_at	1.22874	8.9381816	8.708967	1.11E-15	2.17E-14	24.97453	MAPK13	mitogen-activated protein kinase 13	BC000433
204855_at	1.22833	8.4495617	4.240844	3.39E-05	0.0001159	1.465372	SERPINB5	serpin peptidase inhibitor, clade B (ovalbumin), member 5	NM_002639
205220_at	1.22756	5.7341388	5.762536	3.07E-08	1.74E-07	8.206885	GPR109B	G protein-coupled receptor 109B	NM_006018
1554679_a_at	1.22715	9.3913827	8.077106	5.98E-14	8.62E-13	21.05981	LAPTM4B	lysosomal protein transmembrane 4 beta	AF317417
204127_at	1.22579	8.4343067	13.5126	4.83E-30	1.58E-27	57.60745	RFC3	replication factor C (activator 1) 3, 38kDa	BC000149
223471_at	1.2256	7.5527588	10.31749	2.62E-20	1.13E-18	35.47651	RAB3IP	RAB3A interacting protein (rabin3)	BC002556
214804_at	1.22534	5.4023544	14.17159	4.40E-32	3.00E-29	62.24874	CENPI	centromere protein I	BF793446
1555905_a_at	1.22445	6.501704	10.28938	3.17E-20	1.35E-18	35.28772	C3orf23	chromosome 3 open reading frame 23	AI147556
204768_s_at	1.22403	7.8783578	14.87666	2.89E-34	4.38E-31	67.2118	FEN1	flap structure-specific endonuclease 1	NM_004111
209498_at	1.2208	8.5677144	6.600083	3.56E-10	2.78E-09	12.54539	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	X16354
204702_s_at	1.22055	7.8577515	9.488738	6.89E-18	1.97E-16	29.9821	NFE2L3	nuclear factor (erythroid-derived 2) like 3	NM_004289
231772_x_at	1.21818	6.7254977	12.59708	3.25E-27	5.34E-25	51.17659	CENPH	centromere protein H	AL572471

232271_at	1.2164	7.0839523	6.030946	7.68E-09	4.81E-08	9.553382	HNF4G	hepatocyte nuclear factor 4, gamma	AI916600
219512_at	1.2158	6.9345849	15.68469	9.27E-37	3.16E-33	72.88172	DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	NM_024918
1555225_at	1.21544	5.2943008	12.00429	2.14E-25	2.40E-23	47.03759	C1orf43	chromosome 1 open reading frame 43	BC008306
228565_at	1.21529	7.2088302	8.185102	3.06E-14	4.65E-13	21.71874	KIAA1804	mixed lineage kinase 4	AI809005
211708_s_at	1.21481	6.5923502	8.369529	9.63E-15	1.59E-13	22.85399	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	BC005807
223038_s_at	1.21251	8.1845137	12.77551	9.15E-28	1.68E-25	52.42705	FAM60A	family with sequence similarity 60, member A	BG479856
227350_at	1.21245	6.8274623	11.57844	4.27E-24	3.74E-22	44.08337	HELLS	helicase, lymphoid-specific	AI889959
220865_s_at	1.2117	7.4734874	11.28907	3.23E-23	2.38E-21	42.08759	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	NM_014317
225847_at	1.21126	8.0273817	8.353101	1.07E-14	1.76E-13	22.75237	AADACL1	arylacetamide deacetylase-like 1	AB037784
218677_at	1.21082	8.6669952	5.879224	1.69E-08	1.00E-07	8.786955	S100A14	S100 calcium binding protein A14	NM_020672
220011_at	1.20823	6.2437986	14.41081	7.99E-33	6.61E-30	63.93354	C1orf135	chromosome 1 open reading frame 135	NM_024037
222930_s_at	1.20803	6.5716811	11.34149	2.24E-23	1.70E-21	42.44833	AGMAT	agmatine ureohydrolase (agmatinase)	BC005090
213787_s_at	1.20798	9.0677251	12.31778	2.35E-26	3.20E-24	49.22311	EBP	emopamil binding protein (sterol isomerase)	AV702405
211762_s_at	1.20798	10.395969	16.15701	3.28E-38	1.95E-34	76.18145	KPNA2 ///	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /// karyopherin alpha-2 subunit like	BC005978
215629_s_at	1.2078	5.1156985	10.1631	7.48E-20	2.98E-18	34.44145	DLEU2 ///	deleted in lymphocytic leukemia 2 (non-protein coding) /// deleted in lymphocytic leukemia 2-like	AA905286
202935_s_at	1.20757	9.7810661	6.017566	8.23E-09	5.13E-08	9.485242	SOX9	SRY (sex determining region Y)-box 9	AI382146
208358_s_at	1.20743	6.9751247	7.284911	7.13E-12	7.35E-11	16.36991	UGT8	UDP glycosyltransferase 8	NM_003360
242560_at	1.20682	7.1026318	12.38595	1.45E-26	2.04E-24	49.69939	FANCD2	Fanconi anemia, complementation group D2	AA579890
224453_s_at	1.20603	5.396711	9.261682	3.08E-17	7.91E-16	28.50599	ETNK1	ethanolamine kinase 1	BC006111
222848_at	1.20559	6.5669983	9.380133	1.41E-17	3.84E-16	29.27433	CENPK	centromere protein K	BC005400
222039_at	1.20472	7.2193294	12.77115	9.44E-28	1.72E-25	52.39648	KIF18B	kinesin family member 18B	AA292789
217901_at	1.20282	10.836954	6.541922	4.91E-10	3.75E-09	12.23149	DSG2	desmoglein 2	BF031829
201250_s_at	1.20187	7.9114382	8.882508	3.65E-16	7.74E-15	26.07335	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	NM_006516
222906_at	1.19923	6.8494722	9.019093	1.51E-16	3.41E-15	26.94474	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	AK001419
218350_s_at	1.19872	9.1351338	11.58751	4.01E-24	3.55E-22	44.14604	GMNN	geminin, DNA replication inhibitor	NM_015895
212021_s_at	1.19863	7.4103956	11.41826	1.31E-23	1.04E-21	42.97727	MKI67	antigen identified by monoclonal antibody Ki-67	AU132185
219215_s_at	1.19536	9.0839284	8.778841	7.12E-16	1.44E-14	25.41581	SLC39A4	solute carrier family 39 (zinc transporter), member 4	NM_017767
226226_at	1.19365	9.2300291	6.585189	3.87E-10	3.00E-09	12.46483	TMEM45B	transmembrane protein 45B	AI282982
1554408_a_at	1.19333	8.7435987	11.65181	2.56E-24	2.35E-22	44.59097	TK1	thymidine kinase 1, soluble	BC007986
204767_s_at	1.1896	9.1708362	14.46656	5.37E-33	4.65E-30	64.32606	FEN1	flap structure-specific endonuclease 1	BC000323
221436_s_at	1.18814	7.4186794	13.77745	7.31E-31	3.14E-28	59.47238	CDCA3	cell division cycle associated 3	NM_031299
204603_at	1.18767	6.4307279	12.69161	1.66E-27	2.90E-25	51.83883	EXO1	exonuclease 1	NM_003686
218959_at	1.18765	6.560682	6.136516	4.40E-09	2.87E-08	10.09463	HOXC10	homeobox C10	NM_017409
205597_at	1.18598	9.0490652	4.538269	9.74E-06	3.66E-05	2.65461	SLC44A4	solute carrier family 44, member 4	NM_025257
203228_at	1.18456	8.2283596	13.38137	1.23E-29	3.67E-27	56.6839	PAFAH1B3	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit 29kDa	NM_002573
212023_s_at	1.18422	6.4830462	12.48198	7.34E-27	1.11E-24	50.37094	MKI67	antigen identified by monoclonal antibody Ki-67	AU147044
201111_at	1.18376	8.8568944	12.48654	7.11E-27	1.08E-24	50.4028	CSE1L	CSE1 chromosome segregation 1-like (yeast)	AF053641
243018_at	1.18293	6.1298441	7.162607	1.46E-11	1.43E-10	15.67023	0	0	AI128388
219976_at	1.18292	6.2796578	9.622074	2.84E-18	8.69E-17	30.85522	HOOK1	hook homolog 1 (Drosophila)	NM_015888
217428_s_at	1.182	7.1155072	3.858648	0.0001535	0.0004633	0.036888	COL10A1	collagen, type X, alpha 1	X98568

232151_at	1.18004	7.0608151	6.466611	7.43E-10	5.50E-09	11.82771	MACC1	metastasis associated in colon cancer 1	AL359055
1552680_a at	1.17987	5.4961956	11.26299	3.87E-23	2.80E-21	41.90823	CASC5	cancer susceptibility candidate 5	NM_020380
1554271_a at	1.17941	6.4928375	14.46353	5.49E-33	4.68E-30	64.30477	CENPL	centromere protein L	BC019022
229490_s at	1.17665	6.404546	9.092247	9.35E-17	2.21E-15	27.41375	0	0	AW271106
209008_x at	1.17649	11.672783	7.37371	4.22E-12	4.55E-11	16.88222	KRT8	keratin 8	U76549
220638_s at	1.17637	6.8664907	8.306552	1.43E-14	2.30E-13	22.46495	CBLC	Cas-Br-M (murine) ecotropic retroviral transforming sequence c	NM_012116
214254_at	1.17586	3.9711275	5.433195	1.59E-07	8.05E-07	6.615204	MAGEA4	melanoma antigen family A, 4	AW438674
201790_s at	1.17525	7.4895161	11.83356	7.13E-25	7.29E-23	45.85097	DHCR7	7-dehydrocholesterol reductase	AW150953
230914_at	1.17357	6.4996165	9.533489	5.12E-18	1.50E-16	30.27464	HNF4A	hepatocyte nuclear factor 4, alpha	AI032108
214157_at	1.17327	7.0916814	7.853478	2.36E-13	3.12E-12	19.70961	GNAS	GNAS complex locus	AA401492
221577_x at	1.17247	8.4205068	5.381697	2.04E-07	1.02E-06	6.372563	GDF15	growth differentiation factor 15	AF003934
238513_at	1.17245	7.8749427	8.380417	8.99E-15	1.50E-13	22.9214	PRRG4	Proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane), mRNA (cDNA clone MGC:19793 IMAGE:3841745)	BF905445
234944_s at	1.17239	5.7958221	13.25532	3.02E-29	7.87E-27	55.79717	FAM54A	family with sequence similarity 54, member A	AL138828
205190_at	1.17118	10.087705	4.933464	1.69E-06	7.24E-06	4.335111	PLS1	plastin 1 (l isoform)	NM_002670
222712_s at	1.16967	8.8811886	5.071275	8.94E-07	4.03E-06	4.947045	MUC13	mucin 13, cell surface associated	AW451240
206110_at	1.16927	5.5577631	8.60954	2.10E-15	3.93E-14	24.34937	0	0	NM_003536
203276_at	1.1679	7.8560267	11.24006	4.54E-23	3.24E-21	41.75057	LMNB1	lamin B1	NM_005573
203021_at	1.16764	10.126089	4.829945	2.70E-06	1.12E-05	3.884138	SLPI	secretory leukocyte peptidase inhibitor	NM_003064
221521_s at	1.16763	7.5731973	10.31417	2.68E-20	1.15E-18	35.45423	GIN52	GIN5 complex subunit 2 (Psf2 homolog)	BC003186
216905_s at	1.16359	8.2466575	6.957156	4.76E-11	4.29E-10	14.51077	ST14	suppression of tumorigenicity 14 (colon carcinoma)	U20428
219544_at	1.16318	7.3839758	11.64335	2.71E-24	2.47E-22	44.53237	C13orf34	chromosome 13 open reading frame 34	NM_024808
227801_at	1.16208	6.4771235	11.61944	3.21E-24	2.89E-22	44.36694	TRIM59	tripartite motif-containing 59	N90779
217294_s at	1.16174	10.629378	12.85621	5.16E-28	1.01E-25	52.99319	ENO1	enolase 1, (alpha)	U88968
201791_s at	1.16108	7.4892355	11.71072	1.69E-24	1.62E-22	44.999	DHCR7	7-dehydrocholesterol reductase	NM_001360
231849_at	1.15884	5.8722515	7.937227	1.42E-13	1.93E-12	20.21296	KRT80	keratin 80	AL162069
228597_at	1.15866	7.4069901	12.41016	1.22E-26	1.76E-24	49.86864	C21orf45	chromosome 21 open reading frame 45	AW151538
209016_s at	1.15792	8.4293544	4.356538	2.10E-05	7.44E-05	1.920063	KRT7	keratin 7	BC002700
218252_at	1.1572	8.0110056	12.17948	6.23E-26	7.79E-24	48.25796	CKAP2	cytoskeleton associated protein 2	NM_018204
210394_x at	1.15678	5.3812197	5.767122	3.00E-08	1.70E-07	8.229527	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint	BC005325
223233_s at	1.15545	7.9190501	7.555814	1.43E-12	1.66E-11	17.94382	CGN	cingulin	AF263462
205769_at	1.15545	7.0246435	6.756763	1.48E-10	1.23E-09	13.39979	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	NM_003645
223225_s at	1.15512	6.9741336	12.55192	4.47E-27	7.08E-25	50.86034	SEH1L	SEH1-like (S. cerevisiae)	AI201534
222118_at	1.15434	5.4027844	16.43145	4.72E-39	5.16E-35	78.09252	CENPN	centromere protein N	AK023669
227492_at	1.15416	9.4923839	6.550649	4.58E-10	3.59E-09	12.27847	0	0	AI829721
216493_s at	1.15355	4.5718033	8.916067	2.94E-16	6.33E-15	26.28692	IGF2BP3 ///	insulin-like growth factor 2 mRNA binding protein 3 /// similar to putative RNA binding protein KOC	AL023775
227919_at	1.15112	6.097755	5.373173	2.13E-07	1.06E-06	6.332564	UCA1	urothelial cancer associated 1	AA702248
203878_s at	1.15036	8.0773894	7.118402	1.88E-11	1.81E-10	15.41906	MMP11	matrix metalloproteinase 11 (stromelysin 3)	NM_005940
209326_at	1.14949	8.8036787	12.47082	7.94E-27	1.19E-24	50.29288	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	D84454
239148_at	1.14904	6.7668757	8.812334	5.74E-16	1.18E-14	25.62788	MARVELD3	CDNA FLJ77508 complete cds, highly similar to Homo sapiens MARVEL domain containing 3 (MARVELD3), transcript variant 1, mRNA	AI493046

228401_at	1.14833	7.2543257	12.47604	7.66E-27	1.15E-24	50.32938	ATAD2	ATPase family, AAA domain containing 2	AI656807
1554020_at	1.14795	6.1071413	12.52341	5.47E-27	8.54E-25	50.66082	BICD1	bicaudal D homolog 1 (Drosophila)	BC010091
203917_at	1.14533	9.7828923	6.480968	6.87E-10	5.12E-09	11.90445	CXADR	coxsackie virus and adenovirus receptor	NM_001338
217755_at	1.14456	10.228429	9.201968	4.56E-17	1.14E-15	28.12013	HN1	hematological and neurological expressed 1	NM_016185
231784_s_at	1.14447	7.9992757	11.95806	2.97E-25	3.27E-23	46.71598	WDSOF1	WD repeats and SOF1 domain containing	AK001874
								cancer/testis antigen CT45-4 /// cancer/testis antigen CT45-6 /// hypothetical protein LOC100133581 /// cancer/testis antigen CT45 /// cancer/testis antigen CT45-3 /// cancer/testis antigen CT45-5 /// cancer/testis antigen CT45-1	U31738
1567912_s_at	1.14443	3.9019235	4.493971	1.18E-05	4.37E-05	2.473298	CT45-4 ///	antigen CT45-1	U31738
228912_at	1.14358	8.9814401	6.031185	7.67E-09	4.80E-08	9.554601	VIL1	villin 1	AI436136
209792_s_at	1.14337	7.5793614	3.746968	0.0002337	0.0006812	-0.35867	KLK10	kallikrein-related peptidase 10	BC002710
205780_at	1.14083	9.169608	6.238966	2.55E-09	1.73E-08	10.626	BIK	BCL2-interacting killer (apoptosis-inducing)	NM_001197
211725_s_at	1.13983	8.5362098	13.94854	2.16E-31	1.10E-28	60.67753	BID	BH3 interacting domain death agonist	BC005884
1555733_s_at	1.13843	5.2205415	8.604632	2.17E-15	4.05E-14	24.31859	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	AF393369
235088_at	1.13784	5.639281	11.44104	1.12E-23	9.00E-22	43.1344	C4orf46	chromosome 4 open reading frame 46	AI276663
201015_s_at	1.13715	9.842522	8.295892	1.53E-14	2.45E-13	22.39924	JUP	junction plakoglobin	NM_021991
203046_s_at	1.13694	7.6892848	13.79763	6.33E-31	2.83E-28	59.61458	TIMELESS	timeless homolog (Drosophila)	NM_003920
226912_at	1.13503	6.2730697	11.01232	2.21E-22	1.38E-20	40.18913	ZDHHC23	zinc finger, DHHC-type containing 23	AW003367
232202_at	1.13468	7.3642118	6.438404	8.67E-10	6.33E-09	11.67727	0	0	AK024927
1560916_a_at	1.13425	6.6069623	12.57371	3.83E-27	6.17E-25	51.01295	DPY19L1	dpy-19-like 1 (C. elegans)	BI461155
235456_at	1.13334	5.8245234	6.971104	4.40E-11	3.98E-10	14.58884	0	0	AI810266
204259_at	1.13324	8.8219059	3.655446	0.0003275	0.0009292	-0.6753	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	NM_002423
201839_s_at	1.13158	12.126024	5.084779	8.39E-07	3.80E-06	5.007708	EPCAM	epithelial cell adhesion molecule	NM_002354
202855_s_at	1.13042	7.1104629	9.710594	1.57E-18	5.01E-17	31.43733	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	AL513917
212282_at	1.13015	9.7484512	8.58789	2.41E-15	4.47E-14	24.21367	TMEM97	transmembrane protein 97	BF038366
229644_at	1.12998	6.217813	9.813126	7.92E-19	2.66E-17	32.11394	PREP	PEP mRNA for prolyl endopeptidase	AA534420
229332_at	1.12871	6.1461	8.867812	4.01E-16	8.46E-15	25.97993	HPDL	4-hydroxyphenylpyruvate dioxygenase-like	AI653050
1552921_a_at	1.12855	5.7072043	13.45842	7.11E-30	2.26E-27	57.22612	FIGNL1	figletin-like 1	NM_022116
235229_at	1.12844	7.901526	5.024933	1.11E-06	4.92E-06	4.739808	0	0	AI694413
203022_at	1.12809	8.4426549	12.6774	1.84E-27	3.15E-25	51.73921	RNASEH2A	ribonuclease H2, subunit A	NM_006397
201596_x_at	1.12808	12.283175	6.571808	4.16E-10	3.21E-09	12.39256	KRT18	keratin 18	NM_000224
216470_x_at	1.12764	7.3084902	6.047393	7.04E-09	4.44E-08	9.637278	PRSS1	protease, serine, 1 (trypsin 1)	AF009664
236741_at	1.1268	6.158336	6.129164	4.58E-09	2.98E-08	10.05673	WDR72	WD repeat domain 72	AW299463
214455_at	1.12664	5.1857068	7.630279	9.15E-13	1.09E-11	18.38207	HIST1H2BC	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg	NM_003526
241453_at	1.12498	4.9291844	10.83887	7.32E-22	4.15E-20	39.00512	PTK2	PTK2 protein tyrosine kinase 2	AA912743
1555716_a_at	1.1247	5.33367	9.8777	5.14E-19	1.80E-17	32.54134	CXADR	coxsackie virus and adenovirus receptor	AY072911
203256_at	1.12406	8.0834328	7.041385	2.94E-11	2.74E-10	14.98366	CDH3	cadherin 3, type 1, P-cadherin (placental)	NM_001793
219648_at	1.12294	6.8886465	10.07042	1.40E-19	5.36E-18	33.82246	MREG	melanoregulin	NM_018000
211712_s_at	1.12286	5.7474546	7.301705	6.46E-12	6.71E-11	16.46653	ANXA9	annexin A9	BC005830
219508_at	1.12181	9.5117299	4.257151	3.17E-05	0.000109	1.528845	GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type	NM_004751
202826_at	1.12167	9.0670303	7.139832	1.66E-11	1.61E-10	15.5407	SPINT1	serine peptidase inhibitor, Kunitz type 1	NM_003710
221677_s_at	1.12078	6.9843006	13.29407	2.29E-29	6.29E-27	56.0697	DONSON	downstream neighbor of SON	AF232674

222904_s_at	1.12028	8.6326593	5.220823	4.42E-07	2.09E-06	5.625768	TMC5	transmembrane channel-like 5	AW469181
205552_s_at	1.1189	8.5067528	8.07822	5.93E-14	8.57E-13	21.06658	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	NM_002534
210761_s_at	1.11851	7.1990124	8.400785	7.90E-15	1.33E-13	23.0476	GRB7	growth factor receptor-bound protein 7	AB008790
237159_x_at	1.11849	5.3824329	8.805397	6.00E-16	1.23E-14	25.58393	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	AI474433
203432_at	1.11842	8.8096888	11.79474	9.37E-25	9.38E-23	45.58157	TMPO	thymopoietin	AW272611
201663_s_at	1.11801	8.3847565	14.22755	2.95E-32	2.15E-29	62.6429	SMC4	structural maintenance of chromosomes 4	NM_005496
204751_x_at	1.11707	7.1779698	6.29518	1.88E-09	1.30E-08	10.92008	DSC2	desmocollin 2	NM_004949
225300_at	1.11665	7.5521766	13.97682	1.76E-31	9.27E-29	60.87674	C15orf23	chromosome 15 open reading frame 23	BF792864
225601_at	1.11665	7.5777415	10.6583	2.54E-21	1.30E-19	37.77759	HMGB3	high-mobility group box 3	AI806853
1559361_at	1.1164	6.1266267	8.861976	4.16E-16	8.76E-15	25.94285	MACC1	metastasis associated in colon cancer 1	AF086401
223530_at	1.11599	6.1115986	10.15136	8.10E-20	3.22E-18	34.36297	TDRKH	tudor and KH domain containing	AF227192
213647_at	1.11565	6.2063338	11.60332	3.59E-24	3.20E-22	44.25541	DNA2	DNA replication helicase 2 homolog (yeast)	D42046
219127_at	1.11467	9.1547382	4.985338	1.33E-06	5.81E-06	4.56391	ATAD4	ATPase family, AAA domain containing 4	NM_024320
218498_s_at	1.11449	8.3750565	10.42299	1.27E-20	5.76E-19	36.18654	ERO1L	ERO1-like (S. cerevisiae)	NM_014584
221586_s_at	1.11246	7.20055	11.04727	1.73E-22	1.11E-20	40.42831	E2F5	E2F transcription factor 5, p130-binding	U15642
238898_at	1.11182	5.9044061	8.373522	9.39E-15	1.56E-13	22.8787	0	0	BG028463
238567_at	1.11095	7.3755031	6.625667	3.09E-10	2.44E-09	12.68403	SGPP2	sphingosine-1-phosphate phosphatase 2	AW779536
229777_at	1.11079	8.5358079	3.905106	0.0001285	0.0003937	0.204386	CLRN3	clarin 3	AA863031
223490_s_at	1.11078	7.4310073	13.33542	1.71E-29	4.88E-27	55.36057	EXOSC3	exosome component 3	AF281132
232238_at	1.11068	5.3325603	9.852998	6.06E-19	2.08E-17	32.37773	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	AK001380
201563_at	1.11053	9.3045181	8.520313	3.71E-15	6.68E-14	23.79113	SORD	sorbitol dehydrogenase	L29008
213085_s_at	1.1102	7.4456531	8.679963	1.34E-15	2.58E-14	24.79183	WWC1	WW and C2 domain containing 1	AB020676
214895_s_at	1.11003	7.1474717	10.98493	2.67E-22	1.64E-20	40.00187	ADAM10	ADAM metalloproteinase domain 10	AU135154
212020_s_at	1.10996	6.8783928	11.92306	3.80E-25	4.09E-23	46.47269	MKI67	antigen identified by monoclonal antibody Ki-67	AU152107
225150_s_at	1.10873	7.6092816	12.46104	8.51E-27	1.26E-24	50.22443	RTKN	rhotekin	BC004558
212279_at	1.10842	9.4567491	8.777028	7.20E-16	1.45E-14	25.40434	TMEM97	transmembrane protein 97	BE779865
229372_at	1.10757	6.8635159	7.207608	1.12E-11	1.12E-10	15.92686	GOLT1A	golgi transport 1 homolog A (S. cerevisiae)	AW299924
219403_s_at	1.10748	7.0124219	8.342586	1.14E-14	1.87E-13	22.68738	HPSE	heparanase	NM_006665
210691_s_at	1.10673	9.0621579	14.32185	1.51E-32	1.14E-29	63.30706	CACYBP	calcyclin binding protein	AF275803
1555203_s_at	1.10538	7.5906091	5.168713	5.66E-07	2.63E-06	5.387555	SLC44A4	solute carrier family 44, member 4	AF466766
239002_at	1.10535	5.7484855	9.307132	2.29E-17	6.01E-16	28.80035	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	AA748494
205282_at	1.10531	5.4525785	11.7142	1.65E-24	1.58E-22	45.02307	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	NM_004631
229538_s_at	1.10442	6.6186711	9.350514	1.72E-17	4.61E-16	29.08184	IQGAP3	IQ motif containing GTPase activating protein 3	AW271106
222642_s_at	1.10422	8.2221656	13.51865	4.63E-30	1.53E-27	57.65008	TMEM33	transmembrane protein 33	BC000948
215708_s_at	1.10396	5.4524946	11.68842	1.98E-24	1.87E-22	44.84445	PRIM2	primase, DNA, polypeptide 2 (58kDa)	AL121975
214727_at	1.10343	4.6619607	14.00963	1.40E-31	7.70E-29	61.10783	BRCA2	breast cancer 2, early onset	X95152
208103_s_at	1.10187	8.1880478	13.63166	2.07E-30	7.58E-28	58.44572	ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	NM_030920
201577_at	1.10163	10.829513	14.62251	1.77E-33	1.90E-30	65.4239	NME1	non-metastatic cells 1, protein (NM23A) expressed in /// non-metastatic cells 2, protein (NM23B) expressed in	NM_000269
238075_at	1.10141	6.5051754	11.83896	6.87E-25	7.06E-23	45.88846	CHEK1	Checkpoint kinase Chk1 [CHK1]	AA224205
219010_at	1.10071	9.5768635	5.49858	1.15E-07	5.96E-07	6.925742	C1orf106	chromosome 1 open reading frame 106	NM_018265
227103_s_at	1.10004	7.2326789	13.99314	1.57E-31	8.41E-29	50.99171	ECE2	endothelin converting enzyme 2	BE646208

225185_at	1.09969	8.2782157	5.729182	3.64E-08	2.04E-07	8.042604	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1	AK026697
210827_s_at	1.09936	9.9961144	5.707034	4.07E-08	2.26E-07	7.933892	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	U73844
204653_at	1.09911	7.2478507	6.221965	2.79E-09	1.88E-08	10.53741	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	BF343007
215779_s_at	1.09855	5.7247551	9.903458	4.32E-19	1.53E-17	32.71209	HIST1H2BC	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	BE271470
209035_at	1.09846	9.124401	9.859311	5.81E-19	2.01E-17	32.41953	MDK	midkine (neurite growth-promoting factor 2)	M69148
203209_at	1.09825	7.7779139	13.28827	2.39E-29	6.49E-27	56.0289	RFC5	replication factor C (activator 1) 5, 36.5kDa	BC001866
222155_s_at	1.09727	8.1200535	11.781	1.03E-24	1.02E-22	45.48625	GPR172A	G protein-coupled receptor 172A	AK021918
235148_at	1.09582	8.6872229	7.176542	1.34E-11	1.32E-10	15.75016	KRTCAP3	keratinocyte associated protein 3	BF680458
226132_s_at	1.0901	7.0288113	7.213332	1.08E-11	1.08E-10	15.95957	MANEAL	mannosidase, endo-alpha-like	AW272422
211425_x_at	1.08915	5.0897677	5.649433	5.44E-08	2.96E-07	7.652592	SSX4 /// SSX4B	synovial sarcoma, X breakpoint 4 /// synovial sarcoma, X breakpoint 4B	AF257500
211429_s_at	1.08817	10.156232	4.389443	1.83E-05	6.56E-05	2.051237	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	AF119873
229842_at	1.0878	8.3288681	5.480863	1.26E-07	6.46E-07	6.841325	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	AA527180
215037_s_at	1.08618	6.3902624	11.02897	1.97E-22	1.24E-20	40.30306	BCL2L1	BCL2-like 1	U72398
1552478_a_at	1.08542	5.1499425	10.12279	9.83E-20	3.83E-18	34.17201	IRF6	interferon regulatory factor 6	NM_006147
208546_x_at	1.08535	7.0852837	10.12287	9.82E-20	3.83E-18	34.17255	HIST1H2BH	histone cluster 1, H2bh	NM_003524
205016_at	1.08501	7.731737	6.653689	2.64E-10	2.11E-09	12.83627	TGFA	transforming growth factor, alpha	NM_003236
205239_at	1.08474	8.1456119	4.418099	1.62E-05	5.88E-05	2.166129	AREG /// AREG	amphiregulin /// amphiregulin B	NM_001657
202016_at	1.08446	9.6429628	6.7823	1.29E-10	1.08E-09	13.54024	MEST	mesoderm specific transcript homolog (mouse)	NM_002402
218875_s_at	1.08212	7.2024528	12.50934	6.05E-27	9.30E-25	50.56235	FBXO5	F-box protein 5	NM_012177
219388_at	1.08118	7.7193516	8.187199	3.02E-14	4.59E-13	21.73158	GRHL2	grainyhead-like 2 (Drosophila)	NM_024915
209825_s_at	1.081	8.4143818	14.33353	1.39E-32	1.08E-29	63.38933	UCK2	uridine-cytidine kinase 2	BC002906
220289_s_at	1.07998	6.4016215	8.709669	1.11E-15	2.17E-14	24.97896	AIM1L	absent in melanoma 1-like	NM_017977
218115_at	1.07946	7.7032677	11.21739	5.31E-23	3.75E-21	41.59483	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	NM_018154
210983_s_at	1.07895	9.146319	12.1371	8.41E-26	1.02E-23	47.96247	MCM7	minichromosome maintenance complex component 7	AF279900
225716_at	1.07859	9.391193	9.233938	3.70E-17	9.34E-16	28.32659	0	0	AI357639
210959_s_at	1.07722	6.4253774	10.04373	1.68E-19	6.35E-18	33.64456	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	AF113128
227753_at	1.07694	7.2525752	6.407882	1.02E-09	7.38E-09	11.51496	TMEM139	transmembrane protein 139	R26843
207387_s_at	1.07644	5.626254	9.117714	7.92E-17	1.89E-15	27.5774	GK	glycerol kinase	NM_000167
209260_at	1.07589	8.46762	6.202014	3.11E-09	2.08E-08	10.43366	SFN	stratifin	BC000329
229551_x_at	1.07528	7.1203774	9.75077	1.20E-18	3.93E-17	31.70216	ZNF367	zinc finger protein 367	N62196
227133_at	1.07443	8.1676929	9.871765	5.34E-19	1.85E-17	32.50202	CXorf39	chromosome X open reading frame 39	BE856541
215444_s_at	1.07405	7.4772795	5.013915	1.17E-06	5.14E-06	4.690751	TRIM31	tripartite motif-containing 31	X81006
205053_at	1.07396	7.6925704	13.2592	2.94E-29	7.79E-27	55.82447	PRIM1	primase, DNA, polypeptide 1 (49kDa)	NM_000946
224799_at	1.07389	8.494324	10.56842	4.71E-21	2.27E-19	37.16872	NDFIP2	Nedd4 family interacting protein 2	AW290956
219474_at	1.07346	7.0477559	7.513646	1.84E-12	2.10E-11	17.6967	C3orf52	chromosome 3 open reading frame 52	NM_024616
202338_at	1.07315	8.0221081	11.05621	1.63E-22	1.05E-20	40.48951	TK1	thymidine kinase 1, soluble	NM_003258
214751_at	1.0728	8.1843073	10.91314	4.38E-22	2.59E-20	39.51151	ZNF468	zinc finger protein 468	BE541042

232079_s_at	1.07235	7.1764347	9.667218	2.10E-18	6.57E-17	31.15185	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	BE867789
231855_at	1.0721	4.9576184	11.31851	2.63E-23	1.97E-21	42.29011	KIAA1524	KIAA1524	AB040957
207223_s_at	1.0714	6.4473284	12.80967	7.18E-28	1.35E-25	52.66665	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	NM_005156
227614_at	1.07132	7.4038111	5.564732	8.30E-08	4.40E-07	7.242712	HKDC1	hexokinase domain containing 1	W81116
214290_s_at	1.07077	10.621066	9.665286	2.13E-18	6.64E-17	31.13914	HIST2H2AA	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	AI313324
224428_s_at	1.06993	9.4596321	6.775841	1.33E-10	1.11E-09	13.50469	CDC47	cell division cycle associated 7	AY029179
225777_at	1.0699	8.0837689	11.2297	4.88E-23	3.46E-21	41.67942	C9orf140	chromosome 9 open reading frame 140	AW250904
230793_at	1.0697	7.9530656	8.484969	4.64E-15	8.24E-14	23.57076	LRRC16A	leucine rich repeat containing 16A overexpressed in colon carcinoma-1	BE671038
225105_at	1.06921	9.8497391	7.549479	1.49E-12	1.72E-11	17.90664	OCC-1		BF969397
202581_at	1.06868	9.5810755	8.720568	1.03E-15	2.03E-14	25.04769	HSPA1A ///	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	NM_005346
226936_at	1.06845	9.0648633	11.27905	3.46E-23	2.54E-21	42.01862	C6orf173	chromosome 6 open reading frame 173	BG492359
222746_s_at	1.06838	7.1960762	8.482874	4.71E-15	8.34E-14	23.55771	BSPRY	B-box and SPRY domain containing	AJ276691
214469_at	1.06693	5.2834354	8.587301	2.42E-15	4.48E-14	24.20998	HIST1H2AB	histone cluster 1, H2ab /// histone cluster 1, H2ae	NM_021052
206198_s_at	1.06567	4.2548523	4.731242	4.19E-06	1.69E-05	3.461207	CEACAM7	cardnoembryonic antigen-related cell adhesion molecule 7	L31792
220658_s_at	1.06511	7.1876617	9.574136	3.91E-18	1.16E-16	30.54079	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	NM_020183
202267_at	1.06352	7.890541	6.185551	3.39E-09	2.25E-08	10.34821	LAMC2	laminin, gamma 2	NM_005562
205709_s_at	1.06231	8.9534528	5.599093	7.00E-08	3.75E-07	7.408445	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1	NM_001263
218451_at	1.06199	8.1315783	8.307193	1.42E-14	2.29E-13	22.46891	CDCP1	CUB domain containing protein 1	NM_022842
33322_l_at	1.06175	11.244944	5.531913	9.77E-08	5.12E-07	7.085111	SFN	stratifin	X57348
225702_at	1.06168	7.2218484	14.03123	1.20E-31	6.88E-29	61.25999	C8orf76	chromosome 8 open reading frame 76	AA973041
221685_s_at	1.06029	7.2510993	14.02509	1.25E-31	7.11E-29	61.21674	CCDC99	coiled-coil domain containing 99	AF269167
203625_x_at	1.06009	8.5172119	10.73159	1.53E-21	8.23E-20	38.2752	SKP2	CDNA: FLJ22571 fis, clone HSI02239	BG105365
222843_at	1.05867	8.0836836	11.3885	1.61E-23	1.27E-21	42.77212	FIGNL1	figletin-like 1	AK023411
203876_s_at	1.05852	5.877111	6.992	3.90E-11	3.57E-10	14.70598	MMP11	matrix metalloproteinase 11 (stromelysin 3)	AI761713
202145_at	1.05781	9.1193949	9.598493	3.32E-18	1.00E-16	30.70048	LY6E	lymphocyte antigen 6 complex, locus E	NM_002346
202890_at	1.05724	8.9505556	6.936516	5.36E-11	4.78E-10	14.39542	MAP7	microtubule-associated protein 7	AW242297
200606_at	1.05712	10.549137	6.479375	6.93E-10	5.16E-09	11.89593	DSP	desmoplakin	NM_004415
223785_at	1.05703	5.8795817	11.59455	1.89E-24	1.80E-22	44.88695	FANCI	Fanconi anemia, complementation group I	BC004277
204005_s_at	1.0569	7.0315522	10.69687	1.95E-21	1.02E-19	38.03933	PAWR	PRKC, apoptosis, WT1, regulator	NM_002583
231311_at	1.05689	5.2961901	7.889425	1.90E-13	2.54E-12	19.92532	0		AA725246
223984_s_at	1.05642	6.98154	10.98404	2.68E-22	1.65E-20	39.9958	NUPL1	nucleoporin like 1	BC001104
212686_at	1.05555	6.9954864	7.429524	3.04E-12	3.34E-11	17.20604	PPM1H	protein phosphatase 1H (PP2C domain containing)	AB032983
235700_at	1.05501	4.0794915	4.314504	2.51E-05	8.77E-05	1.753692	RP13-36C9	cancer/testis antigen CT45-5	AI581344
60474_at	1.05499	8.7444302	6.440721	8.56E-10	6.26E-09	11.68961	FERMT1	fermitin family homolog 1 (Drosophila)	AA469071
222077_s_at	1.0544	9.127519	11.74089	1.37E-24	1.32E-22	45.20807	RACGAP1	Rac GTPase activating protein 1	AU153848
204886_at	1.05424	4.7756064	13.65184	1.79E-30	6.70E-28	58.58783	PLK4	polo-like kinase 4 (Drosophila)	AL043646
218687_s_at	1.05423	8.9059317	4.537963	9.75E-06	3.67E-05	2.653355	MUC13	mucin 13, cell surface associated	NM_017648
203210_s_at	1.05337	6.5588415	13.31147	2.02E-29	5.70E-27	56.19212	RFC5	replication factor C (activator 1) 5, 36.5kDa	NM_007370
216985_s_at	1.05316	6.1123309	10.57016	4.65E-21	2.25E-19	37.18048	STX3	syntaxin 3	AJ002077
222496_s_at	1.0531	9.0428854	7.528504	1.68E-12	1.93E-11	17.78369	RBM47	RNA binding motif protein 47	AW241742
242890_at	1.05295	5.2901255	10.77667	1.13E-21	6.20E-20	38.58165	0		AI650364

213506_at	1.05291	10.255298	4.623783	6.73E-06	2.60E-05	3.008705	F2RL1	coagulation factor II (thrombin) receptor-like 1	BE965369
201510_at	1.05286	8.7602515	5.047467	9.98E-07	4.46E-06	4.840392	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	AF017307
210793_s_at	1.05164	7.8835789	12.10616	1.05E-25	1.25E-23	47.74691	NUP98	nucleoporin 98kDa	U41815
203713_s_at	1.05131	7.5018311	8.122416	4.51E-14	6.66E-13	21.33573	LLGL2	lethal giant larvae homolog 2 (Drosophila)	NM_004524
211899_s_at	1.05128	6.4576657	12.09884	1.10E-25	1.30E-23	47.69588	TRAF4	TNF receptor-associated factor 4	AF082185
218182_s_at	1.05111	6.46776	6.569099	4.23E-10	3.26E-09	12.37794	CLDN1	claudin 1	NM_021101
206023_at	1.04851	8.0257359	4.212165	3.81E-05	0.0001289	1.354239	NMU	neuromedin U	NM_006681
202872_at	1.04819	8.002649	12.00414	2.15E-25	2.40E-23	47.03656	ATP6V1C1	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	AW024925
215942_s_at	1.04728	5.8163291	11.8268	7.48E-25	7.61E-23	45.80403	GTSE1	G-2 and S-phase expressed 1	BF973178
232596_at	1.04644	5.6746091	11.60064	3.66E-24	3.26E-22	44.23691	DIAPH3	diaphanous homolog 3 (Drosophila)	AL354829
204675_at	1.04507	8.159673	7.747752	4.50E-13	5.65E-12	19.07821	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	NM_001047
201629_s_at	1.04441	8.6506594	13.91022	2.84E-31	1.42E-28	60.40757	ACPI	acid phosphatase 1, soluble	BE872974
235425_at	1.04344	7.3695724	10.4112	1.38E-20	6.21E-19	36.10707	SGOL2	shugoshin-like 2 (S. pombe)	AW965339
221909_at	1.04336	5.5570702	9.989889	2.41E-19	8.93E-18	33.28614	RNFT2	ring finger protein, transmembrane 2	AW299700
217234_s_at	1.04212	9.361672	8.608222	2.12E-15	3.96E-14	24.34111	EZR	ezrin	AF199015
52285_f_at	1.04145	7.0542714	9.781793	9.77E-19	3.24E-17	31.90691	CEP76	centrosomal protein 76kDa	AW002970
204331_s_at	1.04133	9.6378613	13.74651	9.12E-31	3.83E-28	59.25452	MRPS12	mitochondrial ribosomal protein S12	NM_021107
204614_at	1.04065	4.9717073	5.252216	3.81E-07	1.82E-06	5.770152	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	NM_002575
235609_at	1.04047	5.9497953	9.91241	4.07E-19	1.45E-17	32.77147	0	0	BF056791
214437_s_at	1.03932	8.5844998	12.75384	1.07E-27	1.91E-25	52.27511	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	NM_005412
235266_at	1.03927	6.768141	11.39905	1.50E-23	1.18E-21	42.84488	ATAD2	ATPase family, AAA domain containing 2	AI139629
202543_s_at	1.03841	8.3612264	10.56811	4.72E-21	2.27E-19	37.16658	GMFB	glia maturation factor, beta	BC005359
210732_s_at	1.038	5.9051217	8.693834	1.23E-15	2.37E-14	24.87917	LGALS8	lectin, galactoside-binding, soluble, 8	AF342816
209421_at	1.0379	7.5864302	11.10945	1.13E-22	7.50E-21	40.85417	MSH2	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	U04045
204533_at	1.03783	8.672231	4.975753	1.39E-06	6.05E-06	4.521494	CXCL10	chemokine (C-X-C motif) ligand 10	NM_001565
216228_s_at	1.0369	4.6546887	12.7326	1.24E-27	2.19E-25	52.12619	WDHD1	WD repeat and HMGB-box DNA binding protein 1	AK001538
216870_x_at	1.03675	5.6325234	10.146	8.40E-20	3.32E-18	34.3271	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	AF264787
218960_at	1.03595	8.7071096	5.349098	2.39E-07	1.18E-06	6.219854	TMPPSS4	transmembrane protease, serine 4	NM_016425
236957_at	1.03582	6.3333189	10.41268	1.37E-20	6.17E-19	36.11709	CDCA2	cell division cycle associated 2	AI248208
1555383_a_at	1.0352	6.4807165	5.453164	1.44E-07	7.34E-07	6.709753	POF1B	premature ovarian failure, 1B	BC017500
211778_s_at	1.03519	7.6957392	6.684483	2.23E-10	1.80E-09	13.00405	OVOL2	ovo-like 2 (Drosophila)	BC006148
210041_s_at	1.03472	7.5915089	11.48184	8.40E-24	6.97E-22	43.41599	PGM3	phosphoglucomutase 3	BC001258
223452_s_at	1.0346	7.9292245	10.01959	1.97E-19	7.39E-18	33.4838	ATL3	atlastin GTPase 3	AL117600
238021_s_at	1.03428	7.5432549	5.065535	9.18E-07	4.13E-06	4.921294	hCG_18154	hCG1815491	AA954994
217744_s_at	1.03297	10.490936	8.201091	2.77E-14	4.23E-13	21.81667	PERP	PERP, TP53 apoptosis effector	NM_022121
219454_at	1.03271	6.5778915	5.318611	2.77E-07	1.35E-06	6.077676	EGFL6	EGF-like-domain, multiple 6	NM_015507
201710_at	1.03254	7.4055752	12.07135	1.34E-25	1.56E-23	47.50443	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	NM_002466
200806_s_at	1.0317	11.320068	14.00987	1.39E-31	7.70E-29	61.10954	HSPD1	heat shock 60kDa protein 1 (chaperonin)	BE256479
235911_at	1.03149	7.7149977	7.34884	4.89E-12	5.19E-11	16.73837	0	0	AI885815
202831_at	1.03072	11.195457	4.130308	5.31E-05	0.0001751	1.040519	GPX2	glutathione peroxidase 2 (gastrointestinal)	NM_002083
242939_at	1.03005	6.8018821	9.541694	4.85E-18	1.42E-16	30.32833	TFDP1	transcription factor Dp-1	AI950069
206499_s_at	1.02999	8.2304614	13.529	4.30E-30	1.43E-27	57.7229	RCC1 /// SN	regulator of chromosome condensation 1 /// SNHG3-RCC1 readthrough transcript	NM_001269

220445_s_at	1.02941	5.9659645	5.191412	5.08E-07	2.38E-06	5.491092	CSAG2 /// CSAG	CSAG family, member 2 /// CSAG family, member 3	NM_004909
202871_at	1.02912	7.8609088	10.32933	2.41E-20	1.05E-18	35.55614	TRAF4	TNF receptor-associated factor 4	NM_004295
224320_s_at	1.02843	6.4860058	11.41646	1.33E-23	1.05E-21	42.96487	MCM8	minichromosome maintenance complex component 8	BC005170
207439_s_at	1.02775	6.367123	14.5454	3.06E-33	3.04E-30	64.88116	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	NM_005660
202735_at	1.02749	8.576586	11.26537	3.80E-23	2.76E-21	41.92454	EBP	ernopamil binding protein (sterol isomerase)	NM_006579
219000_s_at	1.02676	7.4323383	11.75589	1.23E-24	1.20E-22	45.31208	DSCC1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	NM_024094
202240_at	1.02504	6.9033664	13.30658	2.10E-29	5.84E-27	56.1577	PLK1	polo-like kinase 1 (Drosophila)	NM_005030
210652_s_at	1.02466	7.6070386	5.238775	4.06E-07	1.93E-06	5.708251	TTC39A	tetratricopeptide repeat domain 39A	BC004399
226537_at	1.02463	6.1688471	8.852028	4.44E-16	9.30E-15	25.87967	HINT3	histidine triad nucleotide binding protein 3	AW418666
222946_s_at	1.02361	5.6991032	14.85719	3.32E-34	4.77E-31	67.07494	C1orf135	chromosome 1 open reading frame 135	BC000209
219105_x_at	1.02281	7.795735	12.07347	1.32E-25	1.54E-23	47.51917	ORC6L	origin recognition complex, subunit 6 like (yeast)	NM_014321
218238_at	1.02025	8.3914458	12.97401	2.23E-28	4.75E-26	53.82013	GTPBP4	GTP binding protein 4	NM_012341
218741_at	1.02019	7.5967527	11.49868	7.47E-24	6.29E-22	43.53221	CENPM	centromere protein M	NM_024053
218772_x_at	1.01974	7.4903269	9.874679	5.24E-19	1.83E-17	32.52132	TMEM388	transmembrane protein 388	NM_018112
205654_at	1.01898	6.5574979	4.840112	2.58E-06	1.07E-05	3.928097	C4BPA	complement component 4 binding protein, alpha	NM_000715
201202_at	1.01897	10.814042	12.06281	1.42E-25	1.65E-23	47.44496	PCNA	proliferating cell nuclear antigen	NM_002592
1554878_a_at	1.01862	6.9237452	8.942335	2.48E-16	5.41E-15	26.45434	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	BC009712
209803_s_at	1.01794	9.6778991	6.518083	5.60E-10	4.24E-09	12.10335	PHLDA2	pleckstrin homology-like domain, family A, member 2	AF001294
220238_s_at	1.0167	5.5117922	10.50962	7.05E-21	3.31E-19	36.77116	KLHL7	kelch-like 7 (Drosophila)	NM_018846
214005_at	1.01656	7.7848534	13.63669	1.99E-30	7.36E-28	58.4811	GGCX	gamma-glutamyl carboxylase	BE326952
231121_at	1.01621	4.6974683	11.64445	2.69E-24	2.45E-22	44.54003	HPS3	Hermansky-Pudlak syndrome 3	N72151
209529_at	1.01597	8.2913726	6.461045	7.66E-10	5.66E-09	11.79799	PPAP2C	phosphatidic acid phosphatase type 2C	AF047760
203108_at	1.01568	10.228717	4.661572	5.70E-06	2.24E-05	3.166877	GPRC5A	G protein-coupled receptor, family C, group 5, member A	NM_003979
200737_at	1.01513	9.7921577	13.69531	1.31E-30	5.16E-28	58.89393	PGK1	phosphoglycerate kinase 1	NM_000291
223423_at	1.01408	9.5148212	5.218627	4.47E-07	2.11E-06	5.615689	GPR160	G protein-coupled receptor 160	BC000181
200894_s_at	1.01402	7.9958474	12.631	2.55E-27	4.26E-25	51.41413	FKBP4	FK506 binding protein 4, 59kDa	AA894574
231810_at	1.01376	8.7003842	8.295484	1.53E-14	2.45E-13	22.39673	BRI3BP	Cervical cancer oncogene binding protein	BG106919
234219_at	1.01357	5.5700527	6.155256	3.98E-09	2.62E-08	10.19138	0	0	AK024998
221664_s_at	1.01302	9.2174622	9.700715	1.68E-18	5.33E-17	31.37227	F11R	F11 receptor	AF154005
207620_s_at	1.01248	7.6789284	11.21061	5.57E-23	3.91E-21	41.54825	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	NM_003688
209754_s_at	1.01214	7.4713469	11.19513	6.20E-23	4.33E-21	41.44196	TMPO	thymopoietin	AF113682
223484_at	1.01211	10.247225	4.086331	6.33E-05	0.0002055	0.874114	C15orf48	chromosome 15 open reading frame 48	AF228422
219756_s_at	1.01102	7.4299472	5.411565	1.76E-07	8.88E-07	6.513078	POF1B	premature ovarian failure, 1B	NM_024921
226374_at	1.01053	9.2935018	5.650717	5.40E-08	2.94E-07	7.658837	0	0	BG260087
200903_s_at	1.00996	10.289785	13.39868	1.09E-29	3.30E-27	56.80572	AHCY	S-adenosylhomocysteine hydrolase	NM_000587
219650_at	1.00994	5.9824712	13.71276	1.16E-30	4.69E-28	59.01678	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	NM_017669
202454_s_at	1.00965	9.2740362	6.091706	5.58E-09	3.58E-08	9.864103	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	NM_001982
223839_s_at	1.00941	6.7154913	7.678973	6.82E-13	8.28E-12	18.66993	SCD /// SCD	stearoyl-CoA desaturase (delta-9-desaturase) /// stearoyl-CoA desaturase opposite strand	AF132203

202604_x_at	1.00908	7.3700243	13.48777	5.77E-30	1.84E-27	57.43272	ADAM10	ADAM metalloproteinase domain 10	NM_001110
223631_s_at	1.0089	10.043418	4.099019	6.01E-05	0.0001964	0.921972	C19orf33	chromosome 19 open reading frame 33	AF213678
223772_s_at	1.00883	4.1651703	12.17316	6.52E-26	8.13E-24	48.21385	TMEM87A	transmembrane protein 87A	BC005335
208821_at	1.00731	10.383001	13.72506	1.06E-30	4.34E-28	59.10347	SNRNPB	small nuclear ribonucleoprotein polypeptides B and B1	J04564
210163_at	1.00712	6.213906	4.024278	8.08E-05	0.0002576	0.641883	CXCL11	chemokine (C-X-C motif) ligand 11	AF030514
222606_at	1.0061	8.188295	12.91392	3.42E-28	6.93E-26	53.39819	ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila)	AA824298
204244_s_at	1.00587	8.4484039	10.0078	2.14E-19	7.97E-18	33.40531	DBF4	DBF4 homolog (S. cerevisiae)	NM_006716
219253_at	1.00548	7.7332953	11.51237	6.78E-24	5.77E-22	43.62674	TMEM185B	transmembrane protein 185B (pseudogene)	NM_024121
222309_at	1.00513	5.1945758	10.46649	9.47E-21	4.36E-19	36.47989	C6orf62	Chromosome 6 open reading frame 62, mRNA (cDNA clone IMAGE:5198625)	AW972292
221591_s_at	1.00486	6.6165056	11.94921	3.16E-25	3.45E-23	46.65443	FAM64A	family with sequence similarity 64, member A	BC005004
236769_at	1.00447	6.6265033	8.14169	4.00E-14	5.98E-13	21.45334	LOC158402	hypothetical protein LOC158402	BE504242
207590_s_at	1.00387	4.970223	13.29236	2.32E-29	6.33E-27	56.05768	CENPI	centromere protein I	NM_006733
202856_s_at	1.00383	8.3903769	8.071754	6.18E-14	8.90E-13	21.02727	SLC16A3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	NM_004207
244519_at	1.00382	7.443579	11.51103	6.85E-24	5.80E-22	43.61753	ASXL1	additional sex combs like 1 (Drosophila)	AI829840
205085_at	1.00362	5.0602919	13.67751	1.49E-30	5.69E-28	58.76855	ORC1L	origin recognition complex, subunit 1-like (yeast)	NM_004153
226287_at	1.00236	8.4631171	9.416174	1.11E-17	3.07E-16	29.50886	CCDC34	coiled-coil domain containing 34	AI458313
202874_s_at	1.00227	8.6791198	12.09599	1.12E-25	1.33E-23	47.67605	ATP6V1C1	ATPase, H ⁺ transporting, lysosomal 42kDa, V1 subunit C1	NM_001695
207291_at	1.00226	7.2066764	9.907749	4.20E-19	1.49E-17	32.74055	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	NM_024081
214061_at	1.00213	6.6615065	12.66992	1.94E-27	3.31E-25	51.68685	WDR67	WD repeat domain 67	AI017564
1554572_a_at	1.00121	7.5928776	11.11545	1.08E-22	7.21E-21	40.89531	SUV39H2	suppressor of variegation 3-9 homolog 2 (Drosophila)	BC029360
222549_at	1.00116	8.9480093	4.588928	7.83E-06	3.00E-05	2.863732	CLDN1	claudin 1	AF101051
228955_at	1.0009	5.4970971	8.325635	1.27E-14	2.06E-13	22.58269	0	0	AL041761
206074_s_at	1.00087	9.9808921	9.078015	1.03E-16	2.40E-15	27.32239	HMG1	high mobility group AT-hook 1	NM_002131
202533_s_at	0.99931	6.8146273	11.09254	1.27E-22	8.38E-21	40.73829	DHFR	dihydrofolate reductase	BC003584
201088_at	0.99925	10.444042	13.99894	1.51E-31	8.15E-29	61.03255	KPNA2 ///	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) /// karyopherin alpha-2 subunit like	NM_002266
217127_at	0.99919	6.4776126	7.188535	1.25E-11	1.24E-10	15.81797	CTH	cystathionase (cystathionine gamma-lyase)	AL354872
217678_at	0.99863	6.2518934	5.345119	2.44E-07	1.20E-06	6.201263	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AA488687
227371_at	0.99805	7.7578084	6.505516	6.00E-10	4.51E-09	12.03592	BAIAP2L1	BAI1-associated protein 2-like 1	AA496034
209398_at	0.99736	8.5609747	7.234789	9.56E-12	9.64E-11	16.08233	HIST1H1C	histone cluster 1, H1c	BC002649
205302_at	0.99704	4.0761626	5.261832	3.64E-07	1.75E-06	5.814508	IGFBP1	insulin-like growth factor binding protein 1	NM_000596
211689_s_at	0.99675	7.3972288	4.47248	1.29E-05	4.75E-05	2.385859	TMPS2	transmembrane protease, serine 2	AF270487
225676_s_at	0.99671	9.5419182	13.75361	8.67E-31	3.67E-28	59.30451	WDSOF1	WD repeats and SOF1 domain containing	BE409290
223232_s_at	0.99627	8.0066563	5.920296	1.37E-08	8.22E-08	8.993079	CGN	cingulin	AI768894
219856_at	0.99614	6.9751092	6.048767	6.99E-09	4.41E-08	9.644291	C1orf116	chromosome 1 open reading frame 116	NM_023938
210397_at	0.99554	6.6333954	4.13154	5.28E-05	0.0001743	1.045199	DEFB1	defensin, beta 1	U73945
221085_at	0.99502	5.1879196	8.398542	8.02E-15	1.35E-13	23.0337	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	NM_005118

232078_at	0.99461	7.0163277	9.116286	7.99E-17	1.90E-15	27.56822	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	BE867789
235089_at	0.99375	6.2289438	8.858701	4.25E-16	8.93E-15	25.92204	FBXL20	F-box and leucine-rich repeat protein 20	AI122770
1554576_a_at	0.99362	6.9290506	8.699785	1.18E-15	2.30E-14	24.91667	ETV4	ets variant 4	BC007242
218156_s_at	0.993	7.6020901	11.82781	7.43E-25	7.57E-23	45.81101	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	NM_018128
209832_s_at	0.9921	5.801682	12.68424	1.75E-27	3.02E-25	51.78719	CDT1	chromatin licensing and DNA replication factor 1	AF321125
212009_s_at	0.99155	8.2858831	12.32113	2.29E-26	3.13E-24	49.24656	STIP1	stress-induced-phosphoprotein 1	AL553320
206550_s_at	0.99142	7.439615	12.76733	9.70E-28	1.75E-25	52.36969	NUP155	nucleoporin 155kDa	NM_004298
225301_s_at	0.99122	9.8745577	5.662154	5.10E-08	2.79E-07	7.714538	MYO5B	myosin VB	AI991160
235783_at	0.99108	6.7086576	13.84894	4.39E-31	2.07E-28	59.97594	MRT04	mRNA turnover 4 homolog (S. cerevisiae)	BG107419
214774_x_at	0.99104	8.6911898	4.16938	4.54E-05	0.0001513	1.189617	TOX3	TOX high mobility group box family member 3	AK027006
219850_s_at	0.99088	7.0030083	5.072928	8.87E-07	4.00E-06	4.954464	EHF	ets homologous factor	NM_012153
209772_s_at	0.9907	10.753331	5.085506	8.36E-07	3.79E-06	5.01098	CD24	CD24 molecule	X69397
235092_at	0.99005	5.0841027	8.779518	7.08E-16	1.43E-14	25.42009	0	0	AI919519
229377_at	0.98986	8.108303	6.391712	1.12E-09	8.00E-09	11.42918	GRTP1	growth hormone regulated TBC protein 1	BF001483
223454_at	0.98937	9.198748	8.799113	6.25E-16	1.28E-14	25.54412	CXCL16	chemokine (C-X-C motif) ligand 16	AF275260
208622_s_at	0.98901	9.4521376	8.220646	2.45E-14	3.78E-13	21.93657	EZR	eZRin	AA670344
209433_s_at	0.9866	7.5703399	10.8704	5.89E-22	3.40E-20	39.22001	PPAT	phosphoribosyl pyrophosphate amidotransferase	AI457120
206336_at	0.98481	5.0165083	3.81249	0.0001828	0.000544	-0.12781	CXCL6	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	NM_002993
223666_at	0.98451	6.7728417	11.47164	9.02E-24	7.44E-22	43.34553	SNX5	sorting nexin 5	BC002724
201688_s_at	0.98428	9.6178639	7.315314	5.96E-12	6.23E-11	16.54491	TPD52	tumor protein D52	BG389015
235924_at	0.98412	7.7085481	6.741239	1.62E-10	1.34E-09	13.31457	0	0	N73742
244780_at	0.98352	7.5247145	4.889989	2.06E-06	8.70E-06	4.144798	SGPP2	sphingosine-1-phosphate phosphatase 2	AI800110
216088_s_at	0.98321	9.0666183	13.43446	8.43E-30	2.66E-27	57.05751	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	AL078633
213175_s_at	0.98312	11.412099	13.57433	3.11E-30	1.10E-27	58.04203	SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	AL049650
232682_at	0.98277	5.7584407	12.47649	7.63E-27	1.15E-24	50.33255	MREG	melanoregulin	BG167210
209424_s_at	0.98264	7.187005	6.846383	8.95E-11	7.68E-10	13.89416	AMACR	alpha-methylacyl-CoA racemase	AI796120
242727_at	0.98116	5.6411318	9.685937	1.86E-18	5.84E-17	31.27499	ARL5B	ADP-ribosylation factor-like 5B	BG032269
218701_at	0.98093	8.841332	8.050745	7.03E-14	1.00E-12	20.89964	LACTB2	lactamase, beta 2	NM_016027
235177_at	0.97951	7.117372	11.13931	9.14E-23	6.18E-21	41.05891	FAM119A	family with sequence similarity 119, member A	AI625022
222701_s_at	0.97825	9.1648922	13.3631	1.40E-29	4.07E-27	56.55535	CHCHD7	coiled-coil-helix-coiled-coil-helix domain containing 7	AA570393
222262_s_at	0.97819	7.5794066	6.959915	4.69E-11	4.22E-10	15.42621	ETNK1	ethanolamine kinase 1	AL137750
1554557_at	0.97734	5.5558356	10.25757	3.94E-20	1.66E-18	35.07425	ATP11B	ATPase, class VI, type 11B	BC033880
235509_at	0.97668	8.0494526	11.98252	2.50E-25	2.78E-23	46.88612	C8orf38	chromosome 8 open reading frame 38	AV662196
226961_at	0.97551	8.1332489	5.162787	5.82E-07	2.70E-06	5.360578	PRR15	proline rich 15	AI347918
33323_r_at	0.97452	11.001069	4.151834	4.87E-05	0.0001616	1.122514	SFN	stratifin	X57348
209629_s_at	0.97424	6.6929209	12.04577	1.60E-25	1.83E-23	47.32631	NXT2	nuclear transport factor 2-like export factor 2	AF201942
203925_at	0.97345	8.2629703	11.93789	3.42E-25	3.70E-23	46.57573	GCLM	glutamate-cysteine ligase, modifier subunit	NM_002061
219263_at	0.97327	9.4848863	3.776836	0.000209	0.0006152	-0.25387	RNF128	ring finger protein 128	NM_024539
222714_s_at	0.97323	9.2053677	8.399089	7.99E-15	1.34E-13	23.03708	LACTB2	lactamase, beta 2	BC000878
219502_at	0.97209	5.002213	13.01146	1.71E-28	3.75E-26	54.08316	NEIL3	nei endonuclease VIII-like 3 (E. coli)	NM_018248
227936_at	0.97154	7.4316237	11.77416	1.08E-24	1.07E-22	45.43877	TMEM68	transmembrane protein 68	AI671172
202525_at	0.97132	8.6331241	4.409946	1.68E-05	6.06E-05	2.133379	PRSS8	protease, serine, 8	NM_002773
204728_s_at	0.97106	5.2603751	12.9493	2.66E-28	5.59E-26	53.64657	WDHD1	WD repeat and HMG-box DNA binding protein 1	NM_007086
230875_s_at	0.97033	8.7764471	9.814095	7.87E-19	2.64E-17	32.12035	ATP11A	ATPase, class VI, type 11A	AW068936
209753_s_at	0.97019	6.8595179	11.59121	3.91E-24	3.46E-22	44.17168	TMPO	thymopoietin	BG391171

223811_s_at	0.96993	6.9598177	12.56085	4.20E-27	6.68E-25	50.92291	C7orf20	chromosome 7 open reading frame 20	BC003550
225822_at	0.96974	8.4656893	5.835961	2.11E-08	1.23E-07	8.570925	TMEM125	transmembrane protein 125	AV709406
205048_s_at	0.96957	8.5667543	4.341772	2.24E-05	7.89E-05	1.861467	PSPH	phosphoserine phosphatase	NM_003832
235463_s_at	0.96954	7.3807036	8.732578	9.58E-16	1.89E-14	25.12347	LASS6	LAG1 homolog, ceramide synthase 6	AI081356
218280_x_at	0.96908	9.1764436	9.222339	3.99E-17	1.00E-15	28.25165	HIST2H2AA	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	NM_003516
219258_at	0.96853	6.8897422	11.33653	2.32E-23	1.76E-21	42.41416	TIPIN	TIMELESS interacting protein	NM_017858
204006_s_at	0.96823	6.7369072	4.87899	2.16E-06	9.11E-06	4.096862	FCGR3A ///	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) /// Fc fragment of IgG, low affinity IIIb, receptor (CD16b)	NM_000570
226118_at	0.96812	6.1472657	13.21886	3.91E-29	9.71E-27	55.54078	CENPO	centromere protein O	BE326728
229500_at	0.96765	6.5166342	8.698198	1.19E-15	2.32E-14	24.90667	SLC30A9	solute carrier family 30 (zinc transporter), member 9	AI609256
205246_at	0.96739	6.7876767	12.81106	7.11E-28	1.34E-25	52.67641	PEX13	peroxisomal biogenesis factor 13	NM_002618
206482_at	0.96724	7.6557812	5.191477	5.08E-07	2.38E-06	5.491392	PTK6	PTK6 protein tyrosine kinase 6	NM_005975
201388_at	0.96647	9.0384113	10.7519	1.33E-21	7.27E-20	38.4132	PSMD3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	NM_002809
223427_s_at	0.96638	6.2233179	5.75451	3.20E-08	1.81E-07	8.167289	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	AB032179
211767_at	0.96626	5.6081047	12.51448	5.83E-27	9.02E-25	50.59834	GIN5	GIN5 complex subunit 4 (Sld5 homolog)	BC005995
1554918_a_at	0.966	5.8086146	7.904411	1.73E-13	2.34E-12	20.01539	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	BC041560
235244_at	0.96541	7.0248046	8.87556	3.82E-16	8.07E-15	26.02917	CCDC58	coiled-coil domain containing 58	BF001285
209628_at	0.9653	8.3769769	10.84148	7.19E-22	4.08E-20	39.02289	NXT2	nuclear transport factor 2-like export factor 2	AK023289
208875_s_at	0.96468	7.9356025	13.36935	1.34E-29	3.96E-27	56.59932	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	BF796470
38158_at	0.9646	7.3827151	11.76312	1.17E-24	1.15E-22	45.36224	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	D79987
208579_x_at	0.9641	9.1506502	7.655666	7.85E-13	9.45E-12	18.53203	H2BFS	H2B histone family, member S	NM_017445
207332_s_at	0.96353	11.103335	10.96681	3.02E-22	1.84E-20	39.87803	TFRC	transferrin receptor (p90, CD71)	NM_003234
208650_s_at	0.96328	10.934962	4.38723	1.85E-05	6.62E-05	2.042388	CD24	CD24 molecule	BG327863
209873_s_at	0.96296	8.7572301	7.964942	1.19E-13	1.64E-12	20.38014	PKP3	plakophilin 3	AF053719
216074_x_at	0.96272	6.3410478	10.23905	4.46E-20	1.86E-18	34.95003	WWC1	WW and C2 domain containing 1	AK001727
227451_s_at	0.96228	7.5402886	8.945597	2.43E-16	5.30E-15	26.47515	CCDC90A	Coiled-coil domain containing 90A, mRNA (cDNA clone MGC:16830 IMAGE:3886144)	BF507383
211977_at	0.96226	6.5013379	12.75065	1.09E-27	1.94E-25	52.25273	GPR107	G protein-coupled receptor 107	AK024651
218888_s_at	0.96224	6.5655831	6.412759	9.97E-10	7.20E-09	11.54086	NETO2	neuropilin (NRP) and toll-like 2	NM_018092
219143_s_at	0.9621	7.7035764	10.81291	8.76E-22	4.90E-20	38.82833	RPP25	ribonuclease P/MRP 25kDa subunit	NM_017793
230556_at	0.96199	6.4134309	10.57846	4.40E-21	2.14E-19	37.23666	IMMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	AA977197
217785_s_at	0.96172	7.3869148	12.19137	5.73E-26	7.21E-24	48.3409	YKT6	YKT6 v-SNARE homolog (S. cerevisiae)	NM_006555
219450_at	0.96162	7.3510254	5.031996	1.07E-06	4.77E-06	4.771299	C4orf19	chromosome 4 open reading frame 19	NM_018302
218261_at	0.96103	8.2424374	6.960922	4.66E-11	4.20E-10	14.53184	AP1M2	adaptor-related protein complex 1, mu 2 subunit	NM_005498
212942_s_at	0.96093	7.3043298	4.130043	5.31E-05	0.0001753	1.039508	KIAA1199	KIAA1199	AB033025
205676_at	0.96076	5.6144846	9.660106	2.20E-18	6.85E-17	31.10508	CYP27B1	cytochrome P450, family 27, subfamily B, polypeptide 1	NM_000785
227747_at	0.95922	6.7738923	8.867628	4.02E-16	8.47E-15	25.97876	MPZL3	myelin protein zero-like 3	AA772172
219681_s_at	0.95881	9.8354627	7.16977	1.40E-11	1.37E-10	15.71101	RAB11FIP1	RAB11 family interacting protein 1 (class I)	NM_025151
224467_s_at	0.9585	7.9536895	11.95319	3.07E-25	3.37E-23	46.68215	PDCD2L	programmed cell death 2-like	BC006146
211075_s_at	0.95837	10.732724	10.7344	1.51E-21	8.10E-20	38.29431	CD47	CD47 molecule	Z25521
227163_at	0.95818	7.9776242	5.552751	8.81E-08	4.65E-07	7.185095	GSTO2	glutathione S-transferase omega 2	AL162742
227650_at	0.95681	7.2923787	11.18672	6.58E-23	4.56E-21	41.38424	HSPA14	heat shock 70kDa protein 14	AV757332

218796_at	0.95677	9.6789976	5.654701	5.30E-08	2.89E-07	7.678234	FERMT1	fermitin family homolog 1 (Drosophila)	NM_017671
216623_x_at	0.95603	8.7384804	4.09226	6.18E-05	0.0002011	0.896462	TOX3	TOX high mobility group box family member 3	AK025084
203207_s_at	0.95572	8.0165022	11.4641	9.51E-24	7.81E-22	43.29355	MTFR1	mitochondrial fission regulator 1	BF214329
234488_s_at	0.95546	6.8490134	11.28541	3.31E-23	2.43E-21	42.06239	GMCL1 ///	germ cell-less homolog 1 (Drosophila) /// germ cell-less homolog 1 (Drosophila)-like	AF198534
201562_s_at	0.95537	7.8710782	9.37662	1.45E-17	3.92E-16	29.25148	SORD	sorbitol dehydrogenase	NM_003104
211883_x_at	0.95533	7.7126742	6.579924	3.98E-10	3.08E-09	12.43638	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	M76742
209969_s_at	0.95527	8.5252489	6.859208	8.32E-11	7.18E-10	13.96524	STAT1	signal transducer and activator of transcription 1, 91kDa	BC002704
229865_at	0.95432	5.9118006	9.911453	4.09E-19	1.46E-17	32.76512	FNDC3B	fibronectin type III domain containing 3B	AW058617
214769_at	0.95404	6.0845575	7.368211	4.36E-12	4.68E-11	16.85039	CLCN4	chloride channel 4	AF052117
202721_s_at	0.95334	9.0303924	10.32479	2.49E-20	1.08E-18	35.52562	GFPT1	glutamine-fructose-6-phosphate transaminase 1	BE645771
210319_x_at	0.95298	6.3569019	6.264533	2.22E-09	1.52E-08	10.75953	MSX2	msh homeobox 2	D89377
224623_at	0.95276	9.5577475	13.24999	3.14E-29	8.08E-27	55.7597	LOC728554	similar to THO complex 3 /// THO complex 3	BE614567
210004_at	0.9527	5.1529327	5.014225	1.16E-06	5.14E-06	4.692129	OLR1	oxidized low density lipoprotein (lectin-like) receptor 1	AF035776
202712_s_at	0.95247	9.0998684	5.147377	6.26E-07	2.88E-06	5.290542	CKMT1A ///	creatine kinase, mitochondrial 1A /// creatine kinase, mitochondrial 1B /// similar to Creatine kinase, ubiquitous mitochondrial precursor (U-MtCK) (Mia-CK) (Acidic-type mitochondrial creatine kinase)	NM_020990
204407_at	0.95213	6.8040272	11.86149	5.86E-25	6.10E-23	46.04487	TTF2	transcription termination factor, RNA polymerase II	AF080255
218644_at	0.95191	9.052592	6.515494	5.68E-10	4.29E-09	12.08945	PLEK2	pleckstrin 2	NM_016445
220147_s_at	0.95174	9.8614383	11.49069	7.90E-24	6.60E-22	43.47702	FAM6CA	family with sequence similarity 60, member A	NM_021238
201761_at	0.95141	10.417771	12.19069	5.76E-26	7.23E-24	48.33612	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	NM_006636
236312_at	0.95113	5.5775896	12.57096	3.91E-27	6.28E-25	50.99368	0	0	AA938184
208621_s_at	0.95106	9.2119083	7.664275	7.45E-13	9.00E-12	18.58294	EZR	ezrin	BF663141
219311_at	0.95102	7.1962257	11.32718	2.47E-23	1.87E-21	42.34981	CEP76	centrosomal protein 76kDa	NM_024899
230051_at	0.95075	5.7483654	6.879416	7.42E-11	6.46E-10	14.0774	C10orf47	chromosome 10 open reading frame 47	BF589207
217356_s_at	0.95068	10.900541	12.7595	1.03E-27	1.84E-25	52.3148	PGK1	phosphoglycerate kinase 1	S81916
206173_x_at	0.95028	6.4594812	14.95052	1.71E-34	2.83E-31	67.73114	GABPB1	GA binding protein transcription factor, beta subunit 1	NM_002041
234986_at	0.95012	6.4153981	9.897168	4.51E-19	1.59E-17	32.67038	0	0	AA630626
208083_s_at	0.94994	5.4025539	5.453353	1.44E-07	7.34E-07	6.710648	ITGB6	integrin, beta 6	NM_000888
211833_s_at	0.9499	7.7916975	11.27125	3.65E-23	2.66E-21	41.96503	BAX	BCL2-associated X protein	U19599
209921_at	0.94939	7.2101205	4.963284	1.47E-06	6.39E-06	4.466409	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	AB040875
1553984_s_at	0.94912	8.8414136	12.63769	2.43E-27	4.10E-25	51.461	DTYMK ///	deoxythymidylate kinase (thymidylate kinase) /// similar to Deoxythymidylate kinase (thymidylate kinase)	AF258562
209677_at	0.94907	5.0846143	9.631302	2.67E-18	8.22E-17	30.91581	PRKCI	protein kinase C, iota	L18964
203664_s_at	0.94854	7.3437991	15.345	1.03E-35	2.69E-32	70.5014	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	NM_004805
236471_at	0.94838	6.4899358	7.256641	8.41E-12	8.56E-11	16.20757	NFE2L3	nuclear factor (erythroid-derived 2) like 3	AI949827
203510_at	0.94832	10.088592	7.288854	6.96E-12	7.19E-11	16.39258	MET	met proto-oncogene (hepatocyte growth factor receptor)	BG170541

201013_s_at	0.94761	9.6916078	12.69107	1.67E-27	2.90E-25	51.83504	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	AA902652
204867_at	0.94717	7.5505995	9.82317	7.41E-19	2.51E-17	32.18036	GCHFR	GTP cyclohydrolase I feedback regulator	NM_005258
226483_at	0.94692	7.1631242	11.3004	2.98E-23	2.20E-21	42.16549	TMEM68	transmembrane protein 68	AI890761
204023_at	0.94621	8.6172575	12.66991	1.94E-27	3.31E-25	51.68678	RFC4	replication factor C (activator 1) 4, 37kDa	NM_002916
210117_at	0.94445	7.6157353	7.030118	3.13E-11	2.91E-10	14.9202	SPAG1	sperm associated antigen 1	AF311312
220123_at	0.94374	4.5877164	11.24612	4.35E-23	3.12E-21	41.79225	SLC35F5	solute carrier family 35, member F5	NM_025181
210213_s_at	0.94325	10.705317	13.28306	2.48E-29	6.70E-27	55.99227	EIF6	eukaryotic translation initiation factor 6	AF022229
229305_at	0.94307	4.7167589	9.300875	2.38E-17	6.24E-16	28.75979	MLF1IP	MLF1 interacting protein	AA460299
238022_at	0.9428	5.959014	5.783177	2.76E-08	1.58E-07	8.30889	hCG_18154	hCG1815491	AA954994
218458_at	0.94237	7.9066861	11.85037	6.34E-25	6.55E-23	45.96764	GMCL1	germ cell-less homolog 1 (Drosophila)	NM_022471
203397_s_at	0.94226	9.8741753	4.409581	1.68E-05	6.07E-05	2.131914	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	BF063271
200637_s_at	0.94202	7.9200627	9.965459	2.84E-19	1.04E-17	33.12371	PTPRF	protein tyrosine phosphatase, receptor type, F	AI762627
201467_s_at	0.94159	9.1083708	4.97432	1.40E-06	6.09E-06	4.515159	NQO1	NAD(P)H dehydrogenase, quinone 1	AI039874
204510_at	0.94155	6.7568673	9.067743	1.10E-16	2.55E-15	27.25648	CDC7	cell division cycle 7 homolog (S. cerevisiae)	NM_003503
208478_s_at	0.94143	7.2950651	10.77864	1.11E-21	6.13E-20	38.5951	BAX	BCL2-associated X protein	NM_004324
204507_s_at	0.94103	6.4323334	11.5543	5.06E-24	4.38E-22	43.91649	PPP3R1 ///	protein phosphatase 3 (formerly 2B), regulatory subunit B, alpha isoform /// WD repeat domain 92	NM_000945
203270_at	0.94079	7.2019794	13.03218	1.48E-28	3.31E-26	54.2287	DTYMK ///	deoxythymidylate kinase (thymidylate kinase) /// similar to Deoxythymidylate kinase (thymidylate kinase)	NM_012145
216568_x_at	0.94033	5.9475796	8.085802	5.66E-14	8.20E-13	21.1127	0	0	0283821
211048_s_at	0.94014	9.8039521	12.28877	2.88E-26	3.84E-24	49.02054	PDIA4	protein disulfide isomerase family A, member 4	BC006344
222705_s_at	0.94005	5.4299796	11.1937	6.27E-23	4.37E-21	41.43212	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	BC002702
215223_s_at	0.93944	9.1731364	7.034074	3.06E-11	2.85E-10	14.94248	SOD2	superoxide dismutase 2, mitochondrial	W46388
1556009_at	0.93922	5.796105	11.23849	4.59E-23	3.27E-21	41.7398	PEX13	peroxisomal biogenesis factor 13	AW117765
1557094_at	0.93902	4.5512966	7.110246	1.97E-11	1.89E-10	15.37281	LOC653110	hypothetical LOC653110	BC029890
202190_at	0.93891	7.318057	14.77558	5.94E-34	7.72E-31	66.50092	CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	NM_001324
224189_x_at	0.93886	6.8386168	5.657302	5.23E-08	2.86E-07	7.690898	EHF	ets homologous factor	AF124438
205195_at	0.93884	6.9183402	12.16236	7.04E-26	8.65E-24	48.13859	AP1S1	adaptor-related protein complex 1, sigma 1 subunit	NM_001283
211237_s_at	0.93867	6.7280474	10.19139	6.17E-20	2.51E-18	34.63074	FGFR4	fibroblast growth factor receptor 4	AF202063
205538_at	0.93866	7.1480172	6.591907	3.73E-10	2.90E-09	12.50115	CORO2A	coronin, actin binding protein, 2A	NM_003389
201118_at	0.93802	9.095445	10.86948	5.93E-22	3.42E-20	39.21372	PGD	phosphogluconate dehydrogenase	NM_002631
224376_s_at	0.93772	11.303413	12.40168	1.30E-26	1.85E-24	49.80938	C20orf24	chromosome 20 open reading frame 24	AF274948
215108_x_at	0.93652	8.3589292	4.273274	2.97E-05	0.0001025	1.591802	TOX3	TOX high mobility group box family member 3	U80736
219529_at	0.93637	6.3196584	5.709669	4.01E-08	2.23E-07	7.946812	CLIC3	chloride intracellular channel 3	NM_004669
202023_at	0.93623	9.1708479	8.584581	2.47E-15	4.56E-14	24.19295	EFNA1	ephrin-A1	NM_004428
227475_at	0.93544	11.108946	3.649151	0.0003352	0.0009486	-0.69682	FOXQ1	forkhead box Q1	AI676059
225830_at	0.93535	6.832263	8.31249	1.38E-14	2.22E-13	22.50157	PDZD8	PDZ domain containing 8	AI052247

211889_x_at	0.93529	7.2444656	6.989097	3.97E-11	3.62E-10	14.6897	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	D12502
204493_at	0.93501	7.7986348	11.3868	1.63E-23	1.28E-21	42.76044	BID	BH3 interacting domain death agonist	NM_001196
221178_at	0.93464	4.7973678	8.923661	2.80E-16	6.06E-15	26.3353	BAIAP2L2	BAI1-associated protein 2-like 2	NM_025045
224802_at	0.93445	9.5607231	9.702976	1.66E-18	5.26E-17	31.38716	NDFIP2	Nedd4 family interacting protein 2	AA019338
232361_s_at	0.93424	6.674032	6.848777	8.83E-11	7.59E-10	13.90742	EHF	ets homologous factor	AA565141
213695_at	0.93365	6.6877998	4.369134	2.00E-05	7.10E-05	1.970182	PON3	paraoxonase 3	L48516
209872_s_at	0.93348	6.6385919	8.469039	5.14E-15	9.04E-14	23.47157	PKP3	plakophilin 3	BF001503
209211_at	0.93347	9.4118477	4.867309	2.28E-06	9.57E-06	4.046043	KLF5	Kruppel-like factor 5 (intestinal)	AF132818
225767_at	0.93333	8.2434001	5.514125	1.07E-07	5.55E-07	6.999977	LOC284801	hypothetical protein LOC284801	AI825833
221194_s_at	0.9333	6.3766667	10.95153	3.36E-22	2.03E-20	39.77368	RNFT1	ring finger protein, transmembrane 1	NM_016125
225439_at	0.9325	9.0112699	13.23691	3.44E-29	8.78E-27	55.66771	NUDCD1	NudC domain containing 1	AI802955
205196_s_at	0.93236	7.0944007	12.27881	3.09E-26	4.10E-24	48.95105	AP151	adaptor-related protein complex 1, sigma 1 subunit	NM_001283
222067_x_at	0.93226	8.835379	8.657065	1.55E-15	2.95E-14	24.64779	HIST1H2BD	histone cluster 1, H2bd	AI353759
211318_s_at	0.93159	8.7602316	14.16478	4.62E-32	3.00E-29	62.20078	RAE1	RAE1 RNA export 1 homolog (S. pombe)	U85943
233177_s_at	0.93106	8.4834421	8.107198	4.96E-14	7.27E-13	21.24297	PNKD	paroxysmal nonkinesigenic dyskinesia	AB033010
1553132_a_at	0.93025	7.7007837	5.923144	1.35E-08	8.11E-08	9.007409	TC2N	tandem C2 domains, nuclear	NM_152332
242283_at	0.9279	5.3119961	7.778466	3.73E-13	4.76E-12	19.26117	C1orf67 ///	chromosome 1 open reading frame 67 /// dynein, axonemal, heavy chain 14	AI076810
226437_at	0.92768	7.6089235	13.32614	1.82E-29	5.19E-27	56.29534	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	AI079540
233110_s_at	0.9262	7.1344922	14.0599	9.76E-32	5.79E-29	61.46196	BCL2L12	BCL2-like 12 (proline rich)	AF289220
201583_s_at	0.92474	9.0316915	11.08004	1.38E-22	9.01E-21	40.65268	SEC23B	Sec23 homolog B (S. cerevisiae)	NM_006363
218049_s_at	0.92467	9.9096975	13.29457	2.28E-29	6.29E-27	56.07323	MRPL13	mitochondrial ribosomal protein L13	NM_014078
210437_at	0.92453	4.9482278	5.628784	6.03E-08	3.26E-07	7.552255	MAGEA9 ///	melanoma antigen family A, 9 /// melanoma antigen family A, 9B	BC002351
216641_s_at	0.92436	7.8356073	7.79231	3.43E-13	4.40E-12	19.34376	LAD1	ladinin 1	U58994
1566766_a_at	0.92431	7.1161577	6.083267	5.83E-09	3.73E-08	9.820821	MACC1	metastasis associated in colon cancer 1	AL359055
221215_s_at	0.92429	8.2963276	7.322646	5.71E-12	5.99E-11	16.58718	RIPK4	receptor-interacting serine-threonine kinase 4	NM_020639
203832_at	0.92402	10.159634	14.89112	2.61E-34	4.07E-31	67.31351	SNRPF	small nuclear ribonucleoprotein polypeptide F	NM_003095
221582_at	0.9239	7.8448849	8.534129	3.40E-15	6.16E-14	23.8774	HIST3H2A	histone cluster 3, H2a	BC001193
204817_at	0.92383	7.2727208	11.29034	3.20E-23	2.36E-21	42.09628	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	NM_012291
223274_at	0.92371	7.0107588	11.17148	7.31E-23	5.04E-21	41.27959	TCF19	transcription factor 19 (SC1)	BC002493
226213_at	0.92363	10.410928	5.643398	5.60E-08	3.05E-07	7.62324	ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	AV681807
219004_s_at	0.92361	7.2529585	11.9485	3.18E-25	3.46E-23	46.64954	C21orf45	chromosome 21 open reading frame 45	NM_018944
215931_s_at	0.92353	5.9660895	13.85722	4.14E-31	1.97E-28	60.0343	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	AV657604
210159_s_at	0.92262	7.2220685	5.107528	7.55E-07	3.44E-06	5.110188	TRIM31	tripartite motif-containing 31	AF230386
219819_s_at	0.92248	9.2470454	12.00047	2.20E-25	2.46E-23	47.01097	MRPS28	mitochondrial ribosomal protein S28	NM_014018
222752_s_at	0.92229	7.6906934	11.78397	1.01E-24	1.00E-22	45.5068	TMEM206	transmembrane protein 206	AK024066
210766_s_at	0.92174	9.6354938	13.42479	9.03E-30	2.82E-27	56.98943	CSE1L	CSE1 chromosome segregation 1-like (yeast)	AF053640
210480_s_at	0.9216	7.5602247	10.67281	2.30E-21	1.18E-19	37.87603	MYO6	myosin VI	U90236
1553810_a_at	0.92152	4.0942675	11.67164	2.22E-24	2.08E-22	44.7283	KIAA1524	KIAA1524	NM_020890
225362_at	0.92094	7.2289978	10.62978	3.09E-21	1.56E-19	37.58428	FAM122B	family with sequence similarity 122B	AI341165

227812_at	0.92015	6.3429779	4.637567	6.33E-06	2.47E-05	3.06628	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	BF432648
205891_at	0.91961	6.5952015	6.560928	4.42E-10	3.40E-09	12.33387	ADORA2B	adenosine A2b receptor	NM_000676
214866_at	0.91884	7.3212523	7.717848	5.39E-13	6.66E-12	18.90046	PLAUR	plasminogen activator, urokinase receptor	X74039
208490_x_at	0.91882	7.4310389	9.001011	1.69E-16	3.80E-15	26.82906	HIST1H2BC	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	NM_003522
206429_at	0.91871	7.4599156	5.650203	5.42E-08	2.95E-07	7.65634	F2RL1	coagulation factor II (thrombin) receptor-like 1	NM_005242
234915_s_at	0.91829	7.2130675	10.5404	5.71E-21	2.71E-19	36.97914	DENR	density-regulated protein	BC000925
235144_at	0.91819	7.9252781	4.002545	8.80E-05	0.0002781	0.561261	0	0	AA826324
218360_at	0.91807	8.6179797	12.81515	6.91E-28	1.32E-25	52.70508	RAB22A	RAB22A, member RAS oncogene family	NM_020673
212563_at	0.91747	7.550247	10.84471	7.04E-22	3.99E-20	39.04489	BOP1	block of proliferation 1	BG491842
227068_at	0.91708	9.6493071	12.43094	1.05E-26	1.54E-24	50.01392	PGK1	phosphoglycerate kinase 1	AA069778
201490_s_at	0.91686	8.4007692	10.34028	2.24E-20	9.77E-19	35.62971	PPIF	peptidylprolyl isomerase F	NM_005729
230399_at	0.91625	5.8133144	8.925563	2.76E-16	5.99E-15	26.34742	0	0	AI361034
204268_at	0.91597	6.6351453	6.201637	3.11E-09	2.08E-08	10.4317	S100A2	S100 calcium binding protein A2	NM_005978
243252_at	0.91571	6.2419928	7.221985	1.03E-11	1.03E-10	16.00905	0	0	AA173465
208450_at	0.91552	7.7131374	4.310408	2.55E-05	8.90E-05	1.737551	LGALS2	lectin, galactoside-binding, soluble, 2	NM_006498
235147_at	0.91527	4.441255	6.494387	6.38E-10	4.78E-09	11.97628	0	0	R56118
238531_x_at	0.91512	5.661868	6.237649	2.57E-09	1.74E-08	10.61913	0	0	AI912965
1554830_a_at	0.915	5.0227808	10.66836	2.37E-21	1.22E-19	37.84589	STEAP3	STEAP family member 3	AF262322
200783_s_at	0.91495	8.428305	11.84999	6.36E-25	6.55E-23	45.965	STMN1	stathmin 1/oncoprotein 18	NM_005563
213147_at	0.9148	6.9597178	6.890866	6.95E-11	6.09E-10	14.14104	HOXA10	homeobox A10	AI375919
219466_s_at	0.91428	4.1932845	4.528568	1.02E-05	3.81E-05	2.61478	APOA2	apolipoprotein A-II	NM_001643
227165_at	0.91367	7.1021695	12.12468	9.18E-26	1.11E-23	47.87595	C13orf3	chromosome 13 open reading frame 3	AI829603
201797_s_at	0.91308	7.6080518	12.94493	2.75E-28	5.75E-26	53.61596	VAR5	valyl-tRNA synthetase	NM_006295
205894_at	0.91249	6.8779078	5.256401	3.73E-07	1.79E-06	5.789449	ARSE	arylsulfatase E (chondrodysplasia punctata 1)	NM_000047
203997_at	0.91229	7.521711	8.221472	2.44E-14	3.76E-13	21.94164	PTPN3	protein tyrosine phosphatase, non-receptor type 3	NM_002829
223748_at	0.91219	6.7044937	5.719073	3.83E-08	2.14E-07	7.992948	SLC4A11	solute carrier family 4, sodium borate transporter, member 11	AF336127
201112_s_at	0.9121	10.635601	13.96612	1.90E-31	9.81E-29	60.80135	CSE1L	CSE1 chromosome segregation 1-like (yeast)	NM_001316
226421_at	0.91149	7.5774816	8.873816	3.86E-16	8.15E-15	26.01809	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	AA707320
228559_at	0.9114	7.5452054	10.34329	2.20E-20	9.61E-19	35.64995	CENPN	centromere protein N	BF111626
228931_at	0.91138	7.8146254	11.78497	1.00E-24	9.98E-23	45.51375	COQ4	coenzyme Q4 homolog (S. cerevisiae)	AW628685
228865_at	0.91116	8.2972529	4.463027	1.34E-05	4.93E-05	2.347506	C1orf116	chromosome 1 open reading frame 116	AA622392
236514_at	0.9105	6.0067326	7.533549	1.63E-12	1.88E-11	17.81324	ACOT8	HIV-Nef associated acyl CoA thioesterase (hNACTE)	AI885067
226003_at	0.91003	7.9668742	8.603562	2.19E-15	4.07E-14	24.31188	KIF21A	kinesin family member 21A	AB051495
205588_s_at	0.90969	6.9424254	12.16333	6.99E-26	8.63E-24	48.14532	FGFR1OP	FGFR1 oncogene partner	NM_007045
225869_s_at	0.90959	7.2958695	9.196102	4.74E-17	1.17E-15	28.08227	UNC93B1	unc-93 homolog B1 (C. elegans)	AW001274
231941_s_at	0.90908	6.5953408	3.702726	0.0002753	0.000791	-0.51258	MUC20	mucin 20, cell surface associated	AB037780
1554885_a_at	0.9085	4.51006	12.06009	1.45E-25	1.67E-23	47.42597	PRIM2	primase, DNA, polypeptide 2 (58kDa)	BC017833
219300_s_at	0.90837	5.5404075	5.836284	2.11E-08	1.23E-07	8.572532	CNTNAP2	contactin associated protein-like 2	AB020675
226145_s_at	0.90799	6.7471845	4.543258	9.53E-06	3.59E-05	2.675123	FRAS1	Fraser syndrome 1	AL157471
233970_s_at	0.90761	7.8763749	10.79124	1.02E-21	5.64E-20	38.68083	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	AB032979
201850_at	0.90729	9.3646171	7.750906	4.41E-13	5.55E-12	19.09698	CAPG	capping protein (actin filament), gelsolin-like	NM_001747
239834_at	0.90708	5.3057548	7.809273	3.10E-13	4.00E-12	19.44506	0	0	AW874669
214583_at	0.90556	5.5224135	12.91964	3.29E-28	6.70E-26	53.43834	RSC1A1	regulatory solute carrier protein, family 1, member 1	AI268381

212479_s_at	0.90518	7.690985	12.53194	5.15E-27	8.06E-25	50.72054	RMND5A	required for meiotic nuclear division 5 homolog A (<i>S. cerevisiae</i>)	AK022815
1552306_at	0.90472	5.1470414	11.30364	2.91E-23	2.16E-21	42.18777	ALG10	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (<i>S. pombe</i>)	BC033730
209387_s_at	0.90452	10.065879	5.737274	3.49E-08	1.96E-07	8.082397	TM4SF1	transmembrane 4 L six family member 1	M90657
200052_s_at	0.90326	10.346491	14.48103	4.84E-33	4.34E-30	64.42798	ILF2	interleukin enhancer binding factor 2, 45kDa	NM_004515
202647_s_at	0.9032	8.1450978	9.565441	4.14E-18	1.23E-16	30.48382	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	NM_002524
218500_at	0.90315	7.8280807	8.956683	2.26E-16	4.98E-15	26.54587	C8orf55	chromosome 8 open reading frame 55	NM_016647
222989_s_at	0.90315	7.8557034	12.63561	2.47E-27	4.14E-25	51.44645	UBQLN1	ubiquilin 1	NM_013438
211668_s_at	0.90277	7.1751747	6.818122	1.05E-10	8.90E-10	13.73782	PLAU	plasminogen activator, urokinase	K03226
210007_s_at	0.9024	6.1923303	11.10564	1.16E-22	7.69E-21	40.8281	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	U36310
239350_at	0.90202	7.2391024	8.204359	2.71E-14	4.15E-13	21.8367	MARVELD3	MARVEL domain containing 3	AI420156
227055_at	0.90153	7.9833918	5.267234	3.54E-07	1.70E-06	5.839457	METTL7B	methyltransferase like 7B	AI827972
219612_s_at	0.90117	4.5347217	3.700355	0.0002778	0.0007975	-0.52078	FGG	fibrinogen gamma chain	NM_000509
203775_at	0.90084	7.9128354	8.786756	6.76E-16	1.37E-14	25.46589	SLC25A13	solute carrier family 25, member 13 (citrin)	NM_014251
230122_at	0.89989	5.8378935	10.43505	1.17E-20	5.34E-19	36.26786	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>); translocated to, 10	BE219716
227314_at	0.89989	8.5418562	5.976004	1.02E-08	6.28E-08	9.274264	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	N95414
236058_at	0.89928	6.559422	9.738511	1.31E-18	4.23E-17	31.62131	C1orf172	chromosome 1 open reading frame 172	AA573775
225402_at	0.89913	8.5362524	11.72505	1.53E-24	1.47E-22	45.09829	TP53RK	TP53 regulating kinase	BG339450
205661_s_at	0.89883	7.554098	13.86356	3.96E-31	1.90E-28	60.07893	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (<i>S. cerevisiae</i>)	NM_025207
220607_x_at	0.89851	9.8617476	12.91036	3.51E-28	7.05E-26	53.37323	TH1L	TH1-like (<i>Drosophila</i>)	NM_016397
205286_at	0.89846	6.1803366	5.944673	1.20E-08	7.31E-08	9.115899	TFAP2C	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	U85658
222713_s_at	0.89823	7.2626117	12.25721	3.60E-26	4.68E-24	48.80023	FANCF	Fanconi anemia, complementation group F	AF181995
209911_x_at	0.89809	9.2606773	6.449065	8.18E-10	6.00E-09	11.73408	HIST1H2BD	histone cluster 1, H2bd	BC002842
209904_at	0.89802	5.3760428	5.709757	4.01E-08	2.23E-07	7.947243	TNNC1	troponin C type 1 (slow)	AF020769
216977_x_at	0.89787	8.9062603	14.09439	7.63E-32	4.73E-29	61.70494	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	AJ130972
218653_at	0.89725	8.0155058	10.09303	1.20E-19	4.63E-18	33.97335	SLC25A15	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	NM_014252
204667_at	0.89712	6.0928136	6.098054	5.39E-09	3.47E-08	9.896694	FOXA1	forkhead box A1	NM_004496
227177_at	0.8969	8.0044572	5.117651	7.20E-07	3.29E-06	5.155902	CORO2A	coronin, actin binding protein, 2A	AL515381
1552470_a_at	0.89669	4.9116478	9.23961	3.56E-17	9.02E-16	28.36324	ABHD11	abhydrolase domain containing 11	NM_148914
209109_s_at	0.89625	9.0988511	6.680996	2.27E-10	1.83E-09	12.98503	TSPAN6	tetraspanin 6	U84895
206665_s_at	0.89612	6.8122833	10.21901	5.12E-20	2.10E-18	34.81575	BCL2L1	BCL2-like 1	NM_001191
225737_s_at	0.89569	6.3322857	11.93078	3.60E-25	3.88E-23	46.52634	FBXO22	F-box protein 22	BE966247
224200_s_at	0.89565	5.3436825	11.07968	1.38E-22	9.03E-21	40.6502	RAD18	RAD18 homolog (<i>S. cerevisiae</i>)	AB035274
218481_at	0.89517	8.0352671	14.67856	1.19E-33	1.41E-30	65.81834	EXOSC5	exosome component 5	NM_020158
218911_at	0.89516	7.0132807	9.391	1.32E-17	3.58E-16	29.34501	YEATS4	YEATS domain containing 4	NM_006530
243661_at	0.89473	5.0128477	10.22943	4.77E-20	1.97E-18	34.88559	ZNF273	zinc finger protein 273	AW172914
202357_s_at	0.89442	9.5848188	5.202977	4.81E-07	2.26E-06	5.54398	C2 /// CFB	complement component 2 /// complement factor B	NM_001710
222611_s_at	0.89431	5.8639676	8.683604	1.31E-15	2.52E-14	24.81476	PSPC1	paraspeckle component 1	AA969958
208795_s_at	0.8939	8.6518264	10.96455	3.07E-22	1.86E-20	39.86259	MCM7	minichromosome maintenance complex component 7	D55716
211924_s_at	0.89321	9.0204113	6.572831	4.14E-10	3.20E-09	12.39808	PLAUR	plasminogen activator, urokinase receptor	AY029180

206626_x_at	0.89302	5.1426796	6.0345	7.53E-09	4.73E-08	9.571497	SSX1	synovial sarcoma, X breakpoint 1	BC001003
1558943_x_at	0.89284	7.9730771	11.08019	1.38E-22	9.01E-21	40.65368	ZNF765	zinc finger protein 765	BU686397
209520_s_at	0.89283	7.8203579	12.67979	1.81E-27	3.11E-25	51.75597	NCBP1	nuclear cap binding protein subunit 1, 80kDa	BC001450
201478_s_at	0.89229	9.4645074	13.43083	8.65E-30	2.72E-27	57.03193	DKC1	dyskeratosis congenita 1, dyskerin	U59151
237563_s_at	0.89221	7.6446855	9.346038	1.77E-17	4.74E-16	29.05278	LOC440731	similar to hCG1817424	AI286239
209212_s_at	0.89214	10.092096	4.908304	1.89E-06	8.05E-06	4.224811	KLF5	Kruppel-like factor 5 (intestinal)	AB030824
218564_at	0.89151	6.6513706	12.35483	1.81E-26	2.51E-24	49.48197	RFWD3	ring finger and WD repeat domain 3	BC002574
231894_at	0.89113	5.9953863	9.27994	2.73E-17	7.10E-16	28.62417	0	0	AU147785
213518_at	0.89089	9.2571135	8.450774	5.76E-15	9.99E-14	23.35796	PRKCI	protein kinase C, iota	AI689429
227268_at	0.89055	7.6206987	8.606788	2.14E-15	3.99E-14	24.33211	RNFT1	ring finger protein, transmembrane 1	N51514
1558152_at	0.89045	7.5354692	7.718615	5.37E-13	6.64E-12	18.90501	LOC100131	hypothetical LOC100131262	BE092211
232065_x_at	0.89027	6.6356379	11.4574	9.96E-24	8.12E-22	43.24729	CENPL	centromere protein L	N29457
206247_at	0.89007	7.586938	6.997669	3.78E-11	3.46E-10	14.73779	MICB	MHC class I polypeptide-related sequence B	NM_005931
215145_s_at	0.88962	5.8521244	6.140422	4.31E-09	2.82E-08	10.11478	CNTNAP2	contactin associated protein-like 2	AC005378
205107_s_at	0.88957	7.2717778	9.149729	6.42E-17	1.55E-15	27.78339	EFNA4	ephrin-A4	NM_005227
212236_x_at	0.88929	7.8302008	4.908806	1.89E-06	8.04E-06	4.227006	KRT17	keratin 17	Z19574
201195_s_at	0.88884	7.8887242	7.052976	2.75E-11	2.57E-10	15.04901	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	AB018009
210092_at	0.88874	8.4312559	12.04222	1.64E-25	1.87E-23	47.30156	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	AF067173
219294_at	0.88791	5.4598645	11.77512	1.08E-24	1.06E-22	45.44542	CENPQ	centromere protein Q	NM_018132
201714_at	0.88785	8.5864547	12.09036	1.17E-25	1.37E-23	47.63684	TUBG1	tubulin, gamma 1	NM_001070
231819_at	0.88725	6.2936713	10.6175	3.36E-21	1.67E-19	37.50104	0	0	BG505096
209627_s_at	0.88688	7.4512596	8.022848	8.36E-14	1.18E-12	20.73042	OSBPL3	oxysterol binding protein-like 3	AY008372
226456_at	0.88681	7.8449267	8.12764	4.37E-14	6.48E-13	21.3676	C16orf75	chromosome 16 open reading frame 75	AW138157
203216_s_at	0.88641	9.2585048	8.830248	5.11E-16	1.06E-14	25.74145	MYO6	myosin VI	NM_004999
1555278_a_at	0.88622	8.4298928	12.2558	3.64E-26	4.72E-24	48.79039	CKAP5	cytoskeleton associated protein 5	BC035554
206400_at	0.88568	5.2339907	6.181927	3.46E-09	2.29E-08	10.32943	LGALS7	lectin, galactoside-binding, soluble, 7 /// lectin, galactoside-binding, soluble, 7B	NM_002307
204695_at	0.8854	6.7840641	9.066933	1.10E-16	2.56E-15	27.25128	CDC25A	cell division cycle 25 homolog A (S. pombe)	AI343459
211527_x_at	0.88538	7.4332446	8.439002	6.21E-15	1.07E-13	23.2848	VEGFA	vascular endothelial growth factor A	M27281
209434_s_at	0.88536	6.9635228	13.89779	3.10E-31	1.54E-28	60.32006	PPAT	phosphoribosyl pyrophosphate amidotransferase	U00238
201614_s_at	0.88527	8.4711521	13.82075	5.37E-31	2.44E-28	59.7774	RUVBL1	RuvB-like 1 (E. coli)	NM_003707
204086_at	0.88507	5.1652364	5.497249	1.16E-07	5.99E-07	6.919394	PRAME	preferentially expressed antigen in melanoma	NM_006115
1552364_s_at	0.88491	5.518855	11.14727	8.65E-23	5.86E-21	41.11348	MSI2	musashi homolog 2 (Drosophila)	BC001526
202195_s_at	0.88479	7.4599589	9.319511	2.11E-17	5.59E-16	28.88062	TMED5	transmembrane emp24 protein transport domain containing 5	NM_016040
215729_s_at	0.88412	3.9734239	4.461325	1.35E-05	4.97E-05	2.340605	VGLL1	vestigial like 1 (Drosophila)	BE542323
238699_s_at	0.88405	5.5996318	9.579459	3.77E-18	1.13E-16	30.57568	CASK	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	AI659225
213577_at	0.88405	8.3247072	8.171997	3.32E-14	5.01E-13	21.63855	SQLE	squalene epoxidase	AA639705
202666_s_at	0.88392	9.2960261	11.59183	3.89E-24	3.45E-22	44.17595	ACTL6A	actin-like 6A	NM_004301
208653_s_at	0.88352	9.772572	8.700542	1.18E-15	2.28E-14	24.92144	CD164	CD164 molecule, sialomucin	AF263279
206125_s_at	0.88293	5.8736639	4.655857	5.85E-06	2.29E-05	3.142893	KLK8	kallikrein-related peptidase 8	NM_007196
203954_x_at	0.88261	8.6406908	4.454141	1.40E-05	5.11E-05	2.311513	CLDN3	claudin 3	NM_001306
212800_at	0.88238	6.4200737	11.38342	1.67E-23	1.30E-21	42.73715	STX6	syntaxin 6	AI740832
201123_s_at	0.88168	9.6405806	4.939485	1.64E-06	7.05E-06	4.361569	EIF5A	eukaryotic translation initiation factor 5A	NM_001970

1555501_s_at	0.88154	6.5153822	11.94562	3.24E-25	3.52E-23	46.62947	RSRC1	arginine/serine-rich coiled-coil 1	BC010357
206576_s_at	0.88142	7.1474792	5.836223	2.11E-08	1.23E-07	8.572229	CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	NM_001712
242546_at	0.8813	5.6581416	6.29154	1.92E-09	1.33E-08	10.90099	FLJ39632	hypothetical LOC642477	BE738279
207156_at	0.88124	5.2391942	7.82015	2.90E-13	3.76E-12	19.51008	HIST1H2AG	histone cluster 1, H2ag /// histone cluster 1, H2ah /// histone cluster 1, H2al /// histone cluster 1, H2aj /// histone cluster 1, H2ak /// histone cluster 1, H2al /// histone cluster 1, H2am	NM_021064
206108_s_at	0.88117	6.8798614	4.785806	3.29E-06	1.35E-05	3.694148	SFRS6	splicing factor, arginine/serine-rich 6	NM_006275
202690_s_at	0.88095	10.155261	11.32247	2.56E-23	1.92E-21	42.31739	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	BC001721
36830_at	0.88084	7.5023883	10.03988	1.72E-19	6.49E-18	33.61892	MIPEP	mitochondrial intermediate peptidase	U80034
229671_s_at	0.88072	4.7393722	11.67692	2.14E-24	2.01E-22	44.76482	C21orf45	CDNA FLJ90800 fis, clone Y79AA1000127	N93774
220085_at	0.88066	5.8493676	8.174231	3.27E-14	4.94E-13	21.65222	HELLS	helicase, lymphoid-specific	NM_018063
208910_s_at	0.88063	10.478061	11.58567	4.06E-24	3.57E-22	44.13335	C1QBP	complement component 1, q subcomponent binding protein	U04636
207724_s_at	0.88057	5.7135056	10.06037	1.50E-19	5.70E-18	33.75549	SPAST	spastin	NM_014946
223241_at	0.8805	6.6409095	11.38454	1.66E-23	1.29E-21	42.74485	SNX8	sorting nexin 8	AF121858
236840_at	0.88046	4.4495127	5.826884	2.21E-08	1.28E-07	8.525745	C12orf56	chromosome 12 open reading frame 56	AI522132
1053_at	0.88011	7.7452	12.45144	9.11E-27	1.34E-24	50.15732	RFC2	replication factor C (activator 1) 2, 40kDa	M87338
223880_x_at	0.87972	11.899357	12.2102	5.02E-26	6.42E-24	48.47221	C20orf24	chromosome 20 open reading frame 24	BC004446
210008_s_at	0.8793	6.3407493	13.72559	1.06E-30	4.34E-28	59.10717	MRPS12	mitochondrial ribosomal protein S12	AA513737
215471_s_at	0.87926	6.9785451	7.738326	4.76E-13	5.95E-12	19.02214	MAP7	microtubule-associated protein 7	AJ242502
205133_s_at	0.87909	10.306831	12.95174	2.62E-28	5.54E-26	53.66376	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	NM_002157
229271_x_at	0.87907	3.53484	6.141921	4.28E-09	2.80E-08	10.12252	COL11A1	collagen, type XI, alpha 1	BG028597
1553997_a_at	0.87898	8.1191102	5.308551	2.91E-07	1.41E-06	6.030894	ASPHD1	aspartate beta-hydroxylase domain containing 1	BC034275
1552486_s_at	0.87887	6.7028441	9.170845	5.59E-17	1.37E-15	27.91941	LACTB	lactamase, beta	NM_171846
243786_at	0.87811	5.6191598	10.8046	9.28E-22	5.17E-20	38.77173	ZDHHC20	zinc finger, DHHC-type containing 20	AA454190
217777_s_at	0.87757	9.025209	10.28195	3.33E-20	1.42E-18	35.23787	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	NM_016395
218239_s_at	0.87745	9.2422574	11.35024	2.11E-23	1.61E-21	42.50854	GTPBP4	GTP binding protein 4	NM_012341
205680_at	0.87724	5.3595763	4.515382	1.07E-05	4.01E-05	2.560754	MMP10	matrix metalloproteinase 10 (stromelysin 2)	NM_002425
223078_s_at	0.87716	6.2293925	10.87184	5.83E-22	3.37E-20	39.22979	TMOD3	tropomodulin 3 (ubiquitous)	AF177171
210416_s_at	0.87617	7.054675	13.77773	7.30E-31	3.14E-28	59.47438	CHEK2	CHK2 checkpoint homolog (S. pombe)	BC004207
229479_at	0.87553	4.6300887	5.101154	7.77E-07	3.53E-06	5.081438	0	0	AI739132
226560_at	0.87548	8.593398	4.355003	2.12E-05	7.49E-05	1.913965	0	0	AA576959
1569190_at	0.87536	4.9584921	10.97093	2.94E-22	1.79E-20	39.90618	SCLT1	sodium channel and clathrin linker 1	BC014677
204492_at	0.87485	4.3621396	12.78474	8.57E-28	1.59E-25	52.49179	ARHGAP11	Rho GTPase activating protein 11A	NM_014783
218984_at	0.8746	8.5597367	10.16532	7.36E-20	2.95E-18	34.45634	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	NM_019042
242053_at	0.87453	5.6199186	9.163196	5.88E-17	1.43E-15	27.87012	0	0	AW665279
202330_s_at	0.87441	8.1336655	11.74517	1.33E-24	1.29E-22	45.23773	UNG	uracil-DNA glycosylase	NM_003362
201422_at	0.87439	10.99207	7.903394	1.74E-13	2.35E-12	20.00928	IFI30	interferon, gamma-inducible protein 30	NM_006332
226350_at	0.8741	7.9442651	8.759222	8.07E-16	1.61E-14	25.29175	CHML	choroideremia-like (Rab escort protein 2)	AU155565
218308_at	0.87398	7.4486234	11.34586	2.17E-23	1.65E-21	42.4784	TACC3	transforming, acidic coiled-coil containing protein 3	NM_006342
204638_at	0.87379	8.4065428	7.119105	1.87E-11	1.80E-10	15.42304	ACP5	acid phosphatase 5, tartrate resistant	NM_001611

225903_at	0.87342	8.0451512	13.4012	1.07E-29	3.26E-27	56.8234	PIGU	phosphatidylinositol glycan anchor biosynthesis, class U	AL118520
217851_s_at	0.87259	9.1005212	10.74003	1.45E-21	7.84E-20	38.33251	SLMO2	slowmo homolog 2 (Drosophila)	NM_016045
91816_f_at	0.8725	7.1895388	8.657332	1.55E-15	2.95E-14	24.64946	MEX3D	mex-3 homolog D (C. elegans)	C18318
225807_at	0.87213	5.1248829	9.690365	1.80E-18	5.69E-17	31.30414	JUB	jub, ajuba homolog (Xenopus laevis)	AK025567
223723_at	0.87209	4.8210805	7.123262	1.83E-11	1.76E-10	15.44662	MF12	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	BC001875
222774_s_at	0.8719	5.223623	6.183327	3.43E-09	2.28E-08	10.33668	NETO2	neuroligin (NRP) and toll-like 2	AI335263
204766_s_at	0.87165	7.2837612	14.16662	4.56E-32	3.00E-29	62.2137	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	NM_002452
220688_s_at	0.87148	8.6005728	13.30955	2.05E-29	5.75E-27	56.17863	MRT04	mRNA turnover 4 homolog (S. cerevisiae)	NM_016183
219026_s_at	0.87091	5.7567092	10.92761	3.97E-22	2.37E-20	39.61033	RASAL2	RAS protein activator like 2	NM_004841
216841_s_at	0.87068	8.6308905	7.210561	1.10E-11	1.10E-10	15.94374	SOD2	superoxide dismutase 2, mitochondrial	X15132
212322_at	0.87053	8.8627373	11.65091	2.57E-24	2.36E-22	44.58477	SGPL1	sphingosine-1-phosphate lyase 1	BE999972
222441_x_at	0.87005	9.3460148	13.32208	1.88E-29	5.31E-27	56.26678	SLMO2	slowmo homolog 2 (Drosophila)	BF032213
208433_s_at	0.86979	7.0762899	8.861995	4.16E-16	8.76E-15	25.94297	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein E receptor	NM_017522
218894_s_at	0.86967	6.8655951	11.05271	1.67E-22	1.07E-20	40.46556	MAGOHB	mago-nashi homolog B (Drosophila)	NM_018048
225295_at	0.86962	8.0890773	7.982583	1.07E-13	1.48E-12	20.48671	SLC39A10	solute carrier family 39 (zinc transporter), member 10	AB033091
223461_at	0.86955	7.7563095	11.85162	6.28E-25	6.51E-23	45.97635	TBC1D7	TBC1 domain family, member 7	AF151073
1564053_a_at	0.8695	7.304673	7.000224	3.72E-11	3.41E-10	14.75214	YTHDF3	YTH domain family, member 3	AK093081
32128_at	0.86914	8.5146181	3.87872	0.0001421	0.0004321	0.109043	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	Y13710
91684_g_at	0.8691	7.79634	13.70073	1.26E-30	5.04E-28	58.93207	EXOSC4	exosome component 4	AI571298
242224_at	0.86816	5.9373824	9.961142	2.93E-19	1.07E-17	33.09502	GPATCH2	G patch domain containing 2	R40111
205114_s_at	0.86772	7.0859518	4.891338	2.04E-06	8.65E-06	4.150685	CCL3 /// CC	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3 /// similar to C-C motif chemokine 3-like 1 precursor (Small-inducible cytokine A3-like 1) (Tonsillar lymphocyte LD78 beta protein) (LD78-beta[1-70]) (G0/G1 switch regulatory protein 19-2) (G0S19-2 protein) (PAT 464.2)	NM_002983
227985_at	0.86765	6.9773842	6.057736	6.67E-09	4.23E-08	9.690116	0	0	AI928513
234863_x_at	0.86758	7.2201607	11.77797	1.05E-24	1.04E-22	45.46523	FBXO5	F-box protein 5	AK026197
208689_s_at	0.86725	11.599513	14.47115	5.20E-33	4.58E-30	64.3584	RPN2	ribophorin II	BC003560
218400_at	0.86717	8.5488223	8.236931	2.21E-14	3.44E-13	22.03653	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	NM_006187
220800_s_at	0.86712	6.4571756	8.925826	2.76E-16	5.99E-15	26.34909	TMOD3	tropomodulin 3 (ubiquitous)	NM_014547
203971_at	0.86669	8.360752	10.61188	3.50E-21	1.73E-19	37.46296	SLC31A1	solute carrier family 31 (copper transporters), member 1	NM_001859
1554101_a_at	0.86667	5.6260796	8.953489	2.30E-16	5.07E-15	26.52549	TMTC4	transmembrane and tetratricopeptide repeat containing 4	BC018707
219347_at	0.86631	8.4836119	11.14921	8.54E-23	5.79E-21	41.12679	NUDT15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	NM_018283
225890_at	0.86615	8.6013266	12.07106	1.34E-25	1.56E-23	47.5024	C20orf72	chromosome 20 open reading frame 72	AI678096
206295_at	0.86614	7.2028315	5.822278	2.26E-08	1.31E-07	8.502839	IL18	interleukin 18 (interferon-gamma-inducing factor)	NM_001562
212623_at	0.86612	8.8606477	10.58469	4.21E-21	2.06E-19	37.27884	TMEM41B	transmembrane protein 41B	AU153138
201476_s_at	0.86606	7.4312556	11.20333	5.86E-23	4.10E-21	41.4983	RRM1	ribonucleotide reductase M1	AI692974

219395_at	0.86502	7.986144	5.711364	3.98E-08	2.22E-07	7.955124	RBM35B	RNA binding motif protein 35B	NM_024939
1552485_at	0.86491	5.9373474	8.969727	2.07E-16	4.60E-15	26.62914	LACTB	lactamase, beta	NM_171846
214651_s_at	0.86438	4.7843574	4.339607	2.26E-05	7.95E-05	1.852891	HOXA9	homeobox A9	U41813
202889_x_at	0.86435	6.974846	7.946886	1.33E-13	1.82E-12	20.27119	MAP7	microtubule-associated protein 7	T62571
242069_at	0.86429	5.5216718	11.01419	2.18E-22	1.36E-20	40.20197	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	BE568225
220441_at	0.86403	6.8856685	5.651332	5.39E-08	2.94E-07	7.661833	DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	NM_024902
208767_s_at	0.86336	10.657286	7.773838	3.84E-13	4.88E-12	19.23357	LAPTM4B	lysosomal protein transmembrane 4 beta	AW149681
216952_s_at	0.86323	7.5166184	11.50262	7.26E-24	6.13E-22	43.55945	LMNB2	lamin B2	M94363
219987_at	0.86311	4.8766283	5.14696	4.16E-09	2.73E-08	10.14853	0	0	NM_024534
1568877_a_at	0.86302	6.56478	9.906488	4.23E-19	1.50E-17	32.73218	ACBD5	acyl-Coenzyme A binding domain containing 5	BC025309
210675_s_at	0.86277	5.7460281	5.04318	1.02E-06	4.54E-06	4.821229	PTPRR	protein tyrosine phosphatase, receptor type, R	U77917
225291_at	0.86252	9.3902452	14.14849	5.19E-32	3.33E-29	62.08599	PNPT1	polynucleotide nucleotidyltransferase 1	A1967971
223403_s_at	0.86212	8.1547964	11.27346	3.60E-23	2.62E-21	41.98019	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	BC004882
216202_s_at	0.86204	7.2831393	9.905615	4.26E-19	1.51E-17	32.7264	SPTLC2	serine palmitoyltransferase, long chain base subunit 2	U15555
222703_s_at	0.86194	7.8717393	13.09199	9.66E-29	2.23E-26	54.64893	YRDC	yrdC domain containing (E. coli)	BE464161
211184_s_at	0.86144	7.804755	5.036803	1.05E-06	4.67E-06	4.792746	USH1C	Usher syndrome 1C (autosomal recessive, severe)	AB006955
204531_s_at	0.86113	7.1947707	11.05452	1.65E-22	1.06E-20	40.47794	BRCA1	breast cancer 1, early onset	NM_007295
217919_s_at	0.86107	9.478242	12.46155	8.48E-27	1.26E-24	50.22801	MRPL42	mitochondrial ribosomal protein L42	BE782148
213816_s_at	0.86082	5.4376276	6.028007	7.79E-09	4.87E-08	9.538404	MET	met proto-oncogene (hepatocyte growth factor receptor)	AA005141
201582_at	0.8607	7.9929675	8.702421	1.16E-15	2.26E-14	24.93328	SEC23B	Sec23 homolog B (S. cerevisiae)	AL121900
232277_at	0.86044	5.6132935	4.392578	1.81E-05	6.49E-05	2.063776	0	0	AA643687
221923_s_at	0.85992	10.958327	10.67709	2.23E-21	1.15E-19	37.90507	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	AA191576
206055_s_at	0.85991	9.9616969	13.83071	5.00E-31	2.30E-28	59.84754	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	NM_003090
214472_at	0.85954	4.5963372	10.10127	1.14E-19	4.41E-18	34.02833	HIST1H2AD	histone cluster 1, H2ad /// histone cluster 1, H3a /// histone cluster 1, H3b /// histone cluster 1, H3c /// histone cluster 1, H3d /// histone cluster 1, H3e /// histone cluster 1, H3f /// histone cluster 1, H3g /// histone cluster 1, H3h /// histone cluster 1, H3i /// histone cluster 1, H3j	NM_003530
227921_at	0.85949	5.6623051	7.820212	2.90E-13	3.76E-12	19.51045	0	0	A1797678
209053_s_at	0.85912	7.2868445	11.58654	4.04E-24	3.56E-22	44.13938	WHSC1	Wolf-Hirschhorn syndrome candidate 1	BE793789
213253_at	0.85869	6.4037478	10.59492	3.93E-21	1.94E-19	37.34808	SMC2	structural maintenance of chromosomes 2	AU154486
219211_at	0.85866	6.9508608	7.498635	2.01E-12	2.28E-11	17.60892	USP18	ubiquitin specific peptidase 18	NM_017414
206994_at	0.85848	8.0529311	6.775232	1.34E-10	1.12E-09	13.50134	CST4	cystatin S	NM_001899
210320_s_at	0.85837	6.8772571	10.92658	4.00E-22	2.38E-20	39.6033	DDX52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	AF077033
222922_at	0.85775	7.1968297	4.745741	3.93E-06	1.59E-05	3.522897	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	AF302494
210830_s_at	0.85701	9.3566042	7.01298	3.46E-11	3.19E-10	14.8238	PON2	paraoxonase 2	AF001602
218982_s_at	0.85667	8.921884	13.22148	3.84E-29	9.58E-27	55.55919	MRPS17	mitochondrial ribosomal protein S17	NM_015969
212471_at	0.8566	6.4478445	12.26203	3.48E-26	4.54E-24	48.83389	AVL9	AVL9 homolog (S. cerevisiae)	BE503381
229097_at	0.85616	7.6404625	8.691385	1.25E-15	2.41E-14	24.86375	DIAPH3	diaphanous homolog 3 (Drosophila)	A1813331
218586_at	0.85616	6.5146761	11.50844	6.97E-24	5.90E-22	43.5996	C20orf20	chromosome 20 open reading frame 20	NM_018270

203696_s_at	0.85589	7.8035421	13.14196	6.77E-29	1.61E-26	55.00012	RFC2	replication factor C (activator 1) 2, 40kDa	NM_002914
214155_s_at	0.85559	6.8845438	9.054722	1.19E-16	2.76E-15	27.17297	LARP4	La ribonucleoprotein domain family, member 4	AI743740
203347_s_at	0.85518	6.2468665	11.66717	2.29E-24	2.13E-22	44.69733	MTF2	metal response element binding transcription factor 2	NM_007358
231022_at	0.85465	7.7121962	6.934674	5.42E-11	4.83E-10	14.38514	0	0	AI139990
203287_at	0.85445	8.2272216	6.475582	7.07E-10	5.26E-09	11.87565	LAD1	ladinin 1	NM_005558
225195_at	0.85396	8.1879955	9.569333	4.04E-18	1.20E-16	30.50932	DPH3	DPH3, KTI11 homolog (S. cerevisiae)	AI825858
230763_at	0.85391	4.5162695	7.235295	9.53E-12	9.62E-11	16.08523	SPATA17	spermatogenesis associated 17	AA905508
205148_s_at	0.85385	5.3547586	7.968478	1.17E-13	1.61E-12	20.40149	CLCN4	chloride channel 4	AA071195
222603_at	0.85375	8.167893	8.258523	1.93E-14	3.03E-13	22.16921	ERMP1	endoplasmic reticulum metalloproteinase 1	AL136980
221987_s_at	0.85344	6.9652051	12.09044	1.17E-25	1.37E-23	47.63734	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	AI803633
218465_at	0.85291	8.3496963	11.38402	1.66E-23	1.30E-21	42.74125	TMEM33	transmembrane protein 33	NM_018126
202722_s_at	0.85286	9.8548545	7.855117	2.34E-13	3.09E-12	19.71943	GFPT1	glutamine-fructose-6-phosphate transaminase 1	NM_002056
1555326_a_at	0.85252	7.6416177	6.284089	2.00E-09	1.38E-08	10.86192	ADAM9	ADAM metalloproteinase domain 9 (meltrin gamma)	AF495383
203177_x_at	0.85239	8.4177643	9.797727	8.78E-19	2.93E-17	32.01217	TFAM	transcription factor A, mitochondrial	NM_003201
1568678_s_at	0.85213	7.456702	11.45742	9.96E-24	8.12E-22	43.2474	FGFR1OP	FGFR1 oncogene partner	BC037785
205436_s_at	0.85205	9.612253	10.34149	2.22E-20	9.70E-19	35.63788	H2AFX	H2A histone family, member X	NM_002105
215034_s_at	0.8518	10.410439	5.280232	3.33E-07	1.61E-06	5.899558	TM4SF1	transmembrane 4 L six family member 1	AI189753
211042_x_at	0.85171	8.4433797	10.25463	4.02E-20	1.69E-18	35.05452	MCAM	melanoma cell adhesion molecule	BC006329
208381_s_at	0.85166	5.1692075	12.00327	2.16E-25	2.41E-23	47.03045	SGPL1	sphingosine-1-phosphate lyase 1	NM_003901
213927_at	0.85114	5.3982787	9.934496	3.50E-19	1.26E-17	32.91804	MAP3K9	mitogen-activated protein kinase kinase 9	AV753204
1555679_a_at	0.8509	6.5536048	10.66775	2.38E-21	1.22E-19	37.84174	RTN4IP1	reticulon 4 interacting protein 1	AF439711
212194_s_at	0.85049	8.2372284	11.58555	4.07E-24	3.57E-22	44.13248	TM9SF4	transmembrane 9 superfamily protein member 4	AI418892
201870_at	0.85044	8.7271843	12.90647	3.61E-28	7.22E-26	53.34593	TOMM34	translocase of outer mitochondrial membrane 34	NM_006809
229105_at	0.85038	6.7093598	6.059148	6.62E-09	4.20E-08	9.697339	GPR39	G protein-coupled receptor 39	AV717094
217835_x_at	0.85027	11.93486	12.03238	1.76E-25	2.00E-23	47.23305	C20orf24	chromosome 20 open reading frame 24	NM_018840
36936_at	0.85027	10.17651	7.319201	5.83E-12	6.11E-11	16.56732	TSTA3	tissue specific transplantation antigen P35B	U58766
202868_s_at	0.85025	9.9849152	9.635128	2.60E-18	8.03E-17	30.94094	POP4	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	NM_006627
216548_x_at	0.84979	6.7928025	11.64868	2.61E-24	2.39E-22	44.56931	HMG4L	high-mobility group (nonhistone chromosomal) protein 4-like	AL049709
223000_s_at	0.84918	11.420815	8.039321	7.55E-14	1.07E-12	20.8303	F11R	F11 receptor	AF172398
41037_at	0.84911	6.7200495	9.040818	1.31E-16	3.00E-15	27.08386	TEAD4	TEA domain family member 4	U63824
218728_s_at	0.84905	9.2003214	10.65707	2.56E-21	1.31E-19	37.76925	CNIH4	cornichon homolog 4 (Drosophila)	NM_014184
206084_at	0.84878	5.6509753	4.71333	4.54E-06	1.81E-05	3.385202	PTPRR	protein tyrosine phosphatase, receptor type, R	NM_002849
219275_at	0.84867	8.0654171	10.58177	4.30E-21	2.10E-19	37.25906	PDCD5	programmed cell death 5	NM_004708
206075_s_at	0.84827	7.7524523	12.15255	7.54E-26	9.23E-24	48.07017	CSNK2A1	casein kinase 2, alpha 1 polypeptide	NM_001895
236122_at	0.84825	6.2370451	8.190701	2.95E-14	4.50E-13	21.75303	0	0	H40696
227212_s_at	0.8482	7.7245235	10.22109	5.04E-20	2.08E-18	34.82971	PHF19	PHD finger protein 19	BES44837
203360_s_at	0.84789	8.7063597	13.30537	2.11E-29	5.86E-27	56.14918	MYCBP	c-myc binding protein	D50692
218302_at	0.84773	8.7368818	11.95084	3.13E-25	3.42E-23	46.66577	PSENEN	presenilin enhancer 2 homolog (C. elegans)	NM_018468
214975_s_at	0.84763	5.5839492	8.746624	8.75E-16	1.74E-14	25.21216	MTMR1	myotubularin related protein 1	AK001816
216640_s_at	0.84761	10.878265	12.63592	2.47E-27	4.14E-25	51.44862	PDIA6	protein disulfide isomerase family A, member 6	AK026926
219411_at	0.84744	7.3975278	6.490241	6.53E-10	4.88E-09	11.95408	ELMO3	engulfment and cell motility 3	NM_024712

200641_s_at	0.84694	11.12767	11.08139	1.37E-22	8.96E-21	40.66191	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	U28964
203499_at	0.84681	8.1197671	5.769513	2.96E-08	1.68E-07	8.241336	EPHA2	EPH receptor A2	NM_004431
225436_at	0.84679	9.4080413	6.019098	8.17E-09	5.09E-08	9.49304	FAM108C1	family with sequence similarity 108, member C1	AI339710
213092_x_at	0.84675	7.7096687	9.771214	1.05E-18	3.46E-17	31.83706	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	AW241779
219739_at	0.8466	6.6414544	4.623736	6.73E-06	2.60E-05	3.008506	RNF186	ring finger protein 186	NM_019062
203936_s_at	0.84645	8.3352525	4.528428	1.02E-05	3.81E-05	2.614205	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	NM_004994
1554246_at	0.84603	6.8019599	6.111458	5.02E-09	3.25E-08	9.965576	C1orf210	chromosome 1 open reading frame 210	BC041633
222837_s_at	0.84567	5.9883688	10.49438	7.82E-21	3.64E-19	36.66821	NARG1	NMDA receptor regulated 1	AF327722
225841_at	0.84534	8.2265382	7.694499	6.21E-13	7.59E-12	18.76192	C1orf59	chromosome 1 open reading frame 59	BE502436
205063_at	0.84523	6.1417116	8.96273	2.17E-16	4.80E-15	26.58447	SIP1	survival of motor neuron protein interacting protein 1	NM_003616
202925_s_at	0.8452	7.3324493	9.396359	1.27E-17	3.47E-16	29.37987	PLAGL2	pleiomorphic adenoma gene-like 2	NM_002657
218847_at	0.84519	8.759146	6.01035	8.55E-09	5.31E-08	9.448544	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	NM_006548
224523_s_at	0.84499	8.4964392	11.66629	2.31E-24	2.14E-22	44.69124	C3orf26	chromosome 3 open reading frame 26	BC006475
218816_at	0.84474	8.7879482	9.129164	7.35E-17	1.76E-15	27.65103	LRR1	leucine rich repeat containing 1	NM_018214
206670_s_at	0.84361	4.4283751	6.511505	5.81E-10	4.38E-09	12.06804	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	NM_013445
204798_at	0.84356	7.6470512	4.86855	2.27E-06	9.52E-06	4.051438	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	NM_005375
201634_s_at	0.8424	8.4154814	9.274172	2.84E-17	7.34E-16	28.58683	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	NM_030579
227211_at	0.84229	7.2827926	10.50029	7.51E-21	3.50E-19	36.7081	PHF19	PHD finger protein 19	BE544837
201946_s_at	0.84219	10.135873	10.31028	2.75E-20	1.18E-18	35.42808	CCT2	chaperonin containing TCP1, subunit 2 (beta)	AL545982
234976_x_at	0.84208	5.0182869	11.80392	8.78E-25	8.87E-23	45.64525	SLC4A5	Solute carrier family 4, sodium bicarbonate cotransporter, member 5 (SLC4A5), transcript variant c, mRNA	BG324504
223296_at	0.84208	8.4628336	9.724844	1.43E-18	4.60E-17	31.53121	SLC25A33	solute carrier family 25, member 33	BC004991
223948_s_at	0.8416	7.441456	5.857817	1.89E-08	1.11E-07	8.679921	TMPRSS3	transmembrane protease, serine 3	AB038160
219510_at	0.84151	6.6741528	11.79419	9.41E-25	9.39E-23	45.57774	POLQ	polymerase (DNA directed), theta	NM_006596
212662_at	0.84144	7.3740419	9.919334	3.88E-19	1.39E-17	32.81741	PVR	poliovirus receptor	BE615277
219911_s_at	0.84092	7.8080126	5.189798	5.12E-07	2.40E-06	5.483722	LOC100134	similar to Solute carrier organic anion transporter family, member 4A1 /// solute carrier organic anion transporter family, member 4A1	NM_016354
218512_at	0.84078	9.0853709	12.3888	1.42E-26	2.01E-24	49.71932	WDR12	WD repeat domain 12	NM_018256
210236_at	0.84065	4.8661809	11.05395	1.65E-22	1.06E-20	40.474	PPFIA1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (Iiprin), alpha 1	U22815
65517_at	0.84061	7.8543952	6.811025	1.09E-10	9.24E-10	13.69863	AP1M2	adaptor-related protein complex 1, mu 2 subunit	AA910946
234932_s_at	0.83994	5.3792516	9.317905	2.13E-17	5.64E-16	28.87021	CDCP1	CUB domain containing protein 1	AK026028
204853_at	0.83915	7.285515	12.50067	6.43E-27	9.86E-25	50.50166	ORC2L	origin recognition complex, subunit 2-like (yeast)	NM_006190
214435_x_at	0.83913	9.4078498	10.4293	1.22E-20	5.53E-19	36.2291	RALA	v-rat simian leukemia viral oncogene homolog A (ras related)	NM_005402
1559052_s_at	0.83909	6.8008646	12.60486	3.07E-27	5.08E-25	51.23105	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	U25975
210845_s_at	0.83903	9.3123087	6.038834	7.36E-09	4.63E-08	9.5936	PLAUR	plasminogen activator, urokinase receptor	U08839

225762_x_at	0.83875	7.4472444	6.65899	2.57E-10	2.05E-09	12.86512	LOC284801	hypothetical protein LOC284801	AL531683
201774_s_at	0.83822	7.4425553	12.54403	4.73E-27	7.44E-25	50.80514	NCAPD2	non-SMC condensin I complex, subunit D2	AK022511
218399_s_at	0.83816	7.8425939	12.81379	6.98E-28	1.32E-25	52.69557	CDC44	cell division cycle associated 4	NM_017955
224618_at	0.83762	8.252638	11.42453	1.25E-23	1.01E-21	43.02056	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	BF059136
208029_s_at	0.83668	10.87476	7.528017	1.69E-12	1.94E-11	17.78083	LAPTM4B	lysosomal protein transmembrane 4 beta	NM_018407
235141_at	0.83657	8.7998719	5.295541	3.09E-07	1.50E-06	5.970492	MARVELD2	MARVEL domain containing 2	AW009562
1554006_a_at	0.83653	7.5156057	8.59122	2.36E-15	4.38E-14	24.23453	LLGL2	lethal giant larvae homolog 2 (Drosophila)	BC006503
1559051_s_at	0.83635	6.2141812	8.531696	3.45E-15	6.24E-14	23.8622	C6orf150	chromosome 6 open reading frame 150	AK097148
203465_at	0.83564	8.2633378	10.66563	2.42E-21	1.24E-19	37.82733	MRPL19	mitochondrial ribosomal protein L19	NM_014763
228191_at	0.83561	8.7566933	7.006455	3.59E-11	3.30E-10	14.78714	0	0	AA206016
225711_at	0.83506	6.4142601	10.81886	8.41E-22	4.72E-20	38.86883	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	AA654338
204827_s_at	0.83451	5.0618985	12.93277	3.00E-28	6.15E-26	53.53052	CCNF	cyclin F	U17105
218295_s_at	0.83421	7.3341304	10.8387	7.33E-22	4.15E-20	39.00398	NUP50	nucleoporin 50kDa	NM_007172
204779_s_at	0.83418	8.640541	5.415972	1.73E-07	8.71E-07	6.533864	HOXB7	homeobox B7	NM_004502
215722_s_at	0.83408	7.8046525	13.35864	1.45E-29	4.18E-27	56.52398	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	AJ130971
216973_s_at	0.83354	8.3893334	5.879562	1.69E-08	1.00E-07	8.788645	HOXB7	homeobox B7	S49765
226606_s_at	0.83341	7.8038375	9.942014	3.33E-19	1.21E-17	32.96796	GTPBP5	GTP binding protein 5 (putative)	AI860690
210608_s_at	0.8334	8.306716	4.851286	2.45E-06	1.02E-05	3.976491	FUT2	fucosyltransferase 2 (secretor status included)	BC001899
218273_s_at	0.83312	7.3489607	8.92473	2.78E-16	6.02E-15	26.34211	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	NM_018444
209774_x_at	0.83296	8.9446793	3.858572	0.0001535	0.0004634	0.036617	CXCL2	chemokine (C-X-C motif) ligand 2	M57731
225991_at	0.83282	8.1246758	11.89365	4.67E-25	4.97E-23	46.26826	TMEM41A	transmembrane protein 41A	BE644935
204105_s_at	0.83245	5.7901007	4.603083	7.36E-06	2.83E-05	2.922498	NRCAM	neuronal cell adhesion molecule	NM_005010
1554414_a_at	0.83237	7.4140221	9.892546	4.65E-19	1.64E-17	32.63974	OSGIN2	oxidative stress induced growth inhibitor family member 2	BC031054
216237_s_at	0.83231	8.5200939	10.83751	7.39E-22	4.18E-20	38.99587	MCM5	minichromosome maintenance complex component 5	AA807529
235907_at	0.83228	7.7277554	11.19343	6.28E-23	4.37E-21	41.43031	TMEM33	transmembrane protein 33	BE245080
205296_at	0.83213	5.7008721	11.95501	3.04E-25	3.34E-23	46.69479	RBL1	retinoblastoma-like 1 (p107)	AL365505
210821_x_at	0.83197	6.9749921	12.77609	9.12E-28	1.68E-25	52.43109	CENPA	centromere protein A	BC002703
229812_at	0.8312	6.7810819	9.509376	6.01E-18	1.74E-16	30.11695	USP48	ubiquitin specific peptidase 48	BE645018
201479_at	0.83111	10.218167	12.95123	2.63E-28	5.54E-26	53.66017	DKC1	dyskeratosis congenita 1, dyskerin	NM_001363
223651_x_at	0.83109	5.5347855	10.32865	2.43E-20	1.05E-18	35.55153	CDC23	cell division cycle 23 homolog (S. cerevisiae)	BC005258
209679_s_at	0.83107	8.9078773	6.847772	8.88E-11	7.63E-10	13.90185	LOC57228	small trans-membrane and glycosylated protein	BC003379
205402_x_at	0.83105	8.5063607	3.704159	0.0002739	0.000787	-0.50762	PRSS2	protease, serine, 2 (trypsin 2)	NM_002770
204734_at	0.83058	5.0366676	7.067915	2.52E-11	2.37E-10	15.13332	KRT15	keratin 15	NM_002275
223649_s_at	0.83053	9.0248004	13.58842	2.81E-30	1.00E-27	58.14126	SLC25A39	solute carrier family 25, member 39	AF317711
228485_s_at	0.83052	6.6556122	8.579631	2.55E-15	4.69E-14	24.16195	SLC44A1	solute carrier family 44, member 1	AW165999
201251_at	0.83048	10.23041	12.30674	2.54E-26	3.41E-24	49.146	PKM2	pyruvate kinase, muscle	NM_002654
215966_x_at	0.83044	5.2493042	8.997818	1.73E-16	3.88E-15	26.80864	GK3P	glycerol kinase 3 pseudogene	AA292874
219061_s_at	0.83029	8.7521051	11.08838	1.30E-22	8.59E-21	40.70983	LAGE3	L antigen family, member 3	NM_006014
209893_s_at	0.83017	7.2379395	8.554195	2.99E-15	5.46E-14	24.00279	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	M58596
209624_s_at	0.83003	6.9678804	10.13871	8.82E-20	3.47E-18	34.27838	MCCC2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	AB050049
212619_at	0.82999	5.5586822	9.991479	2.39E-19	8.84E-18	33.29672	TMEM194A	transmembrane protein 194A	AW205215
218340_s_at	0.82957	6.8668124	7.395549	3.71E-12	4.04E-11	17.00876	UBA6	ubiquitin-like modifier activating enzyme 6	NM_018227
235026_at	0.8294	6.2186998	9.394244	1.29E-17	3.52E-16	29.36611	C12orf66	chromosome 12 open reading frame 66	AI885871

205260_s_at	0.82931	7.0443609	10.05251	1.58E-19	6.00E-18	33.70311	ACYP1	acylphosphatase 1, erythrocyte (common) type	NM_001107
209238_at	0.82879	9.059114	8.210228	2.61E-14	4.01E-13	21.87268	STX3	syntaxin 3	BE966922
1554553_s_at	0.82872	7.3544644	12.88705	4.15E-28	8.26E-26	53.20958	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	BC014974
206242_at	0.82855	7.8807635	4.661443	5.71E-06	2.24E-05	3.166336	TM4SF5	transmembrane 4 L six family member 5	NM_003963
213088_s_at	0.82813	9.3203904	11.06602	1.52E-22	9.84E-21	40.55668	DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	BE551340
227787_s_at	0.82753	8.2455906	10.06032	1.50E-19	5.70E-18	33.75515	MED30	mediator complex subunit 30	AI026938
243010_at	0.82727	6.064055	9.30797	2.27E-17	5.98E-16	28.80578	MSI2	musashi homolog 2 (Drosophila)	BE000929
223103_at	0.8272	9.5033164	5.739272	3.46E-08	1.94E-07	8.09223	STARD10	StAR-related lipid transfer (START) domain containing 10	AF151810
229634_at	0.82648	5.8759384	5.666969	4.98E-08	2.73E-07	7.738013	TMEM139	transmembrane protein 139	AI627262
226319_s_at	0.82623	9.3501425	11.09225	1.27E-22	8.38E-21	40.73633	THOC4	THO complex 4	AF047002
225829_at	0.82608	6.9823513	7.994705	9.94E-14	1.38E-12	20.56002	PDZD8	PDZ domain containing 8	BE552184
207079_s_at	0.82604	7.6287144	9.196537	4.73E-17	1.17E-15	28.08508	MED6	mediator complex subunit 6	NM_005466
225850_at	0.82537	10.054758	9.840633	6.59E-19	2.25E-17	32.29588	SFT2D1	SFT2 domain containing 1	BF975327
226187_at	0.82536	7.246519	6.94114	5.22E-11	4.66E-10	14.42124	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	AW304313
223491_at	0.82512	7.7845587	11.08214	1.36E-22	8.93E-21	40.66708	COMMD2	COMM domain containing 2	BC001228
208527_x_at	0.82453	7.619897	8.454868	5.62E-15	9.78E-14	23.38341	HIST1H2BC	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	NM_003523
221922_at	0.82452	8.1673991	7.884494	1.96E-13	2.61E-12	19.89569	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	AW195581
219434_at	0.82435	6.2767445	5.610837	6.60E-08	3.55E-07	7.465258	TREM1	triggering receptor expressed on myeloid cells 1	NM_018643
200889_s_at	0.82413	9.3180408	11.03204	1.93E-22	1.22E-20	40.32407	SSR1	signal sequence receptor, alpha	AI016620
205733_at	0.82383	7.0466933	7.709266	5.68E-13	7.00E-12	18.84951	BLM	Bloom syndrome	NM_000057
212978_at	0.82375	7.7099326	10.7364	1.48E-21	8.00E-20	38.30784	LRRC8B	leucine rich repeat containing 8 family, member B	AU146004
225237_s_at	0.8235	7.07568	8.056493	6.79E-14	9.70E-13	20.93453	MSI2	musashi homolog 2 (Drosophila)	BF435123
213310_at	0.82284	6.4537279	8.189278	2.98E-14	4.53E-13	21.74431	EIF2C2	Eukaryotic translation initiation factor 2C, 2 (EIF2C2), mRNA	AI613483
204415_at	0.82273	9.5042935	6.139256	4.34E-09	2.84E-08	10.10877	IFI6	interferon, alpha-inducible protein 6	NM_022873
204427_s_at	0.82271	10.066922	9.378089	1.43E-17	3.89E-16	29.26104	TMED2	transmembrane emp24 domain trafficking protein 2	NM_006815
236026_at	0.82259	5.6448054	9.976262	2.64E-19	9.74E-18	33.19552	GPATCH2	G patch domain containing 2	AA160529
36742_at	0.82255	8.2073667	6.305758	1.78E-09	1.24E-08	10.97562	TRIM15	tripartite motif-containing 15	U34249
229181_s_at	0.82254	7.9350697	12.91686	3.35E-28	6.81E-26	53.41885	CEP27	centrosomal protein 27kDa	AI248305
218342_s_at	0.82203	8.1756212	9.800393	8.63E-19	2.89E-17	32.02978	ERMP1	endoplasmic reticulum metalloproteinase 1	NM_024896
208209_s_at	0.82203	7.3523425	4.659984	5.74E-06	2.25E-05	3.16021	C4BPB	complement component 4 binding protein, beta	NM_000716
1568596_a_at	0.8218	7.3219428	8.830668	5.10E-16	1.06E-14	25.74412	TROAP	trophinin associated protein (tastin)	AI199355
239346_at	0.82177	7.5120344	10.05643	1.54E-19	5.85E-18	33.7292	0	0	AI097560
218602_s_at	0.82142	5.0746617	10.14819	8.27E-20	3.27E-18	34.34176	FAM29A	family with sequence similarity 29, member A	NM_017645
45633_at	0.82091	5.5633614	11.14986	8.50E-23	5.78E-21	41.13128	GIN53	GIN5 complex subunit 3 (Psf3 homolog)	AI421812
226926_at	0.8209	6.1142759	4.976797	1.38E-06	6.03E-06	4.526111	DMKN	dermokine	AA706316
205429_s_at	0.82049	5.1227996	6.919557	5.90E-11	5.23E-10	14.3008	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	NM_016447
241937_s_at	0.82044	7.2282829	9.383766	1.38E-17	3.75E-16	29.29795	WDR4	WD repeat domain 4	AA577678
221539_at	0.8203	8.9611399	9.361681	1.60E-17	4.31E-16	29.15439	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	AB044548
204976_s_at	0.82026	8.1056674	8.258648	1.93E-14	3.03E-13	22.16998	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	AK023637

209608_s at	0.81985	8.2787701	11.08346	1.35E-22	8.86E-21	40.67608	ACAT2	acetyl-Coenzyme A acetyltransferase 2	BC000408
211162_x at	0.81978	6.6159419	6.806696	1.12E-10	9.46E-10	13.67473	SCD	stearoyl-CoA desaturase (delta-9- desaturase)	AF116616
223397_s at	0.81978	8.0606889	11.23208	4.80E-23	3.41E-21	41.69578	NIP7	nuclear import 7 homolog (S. cerevisiae)	AF161528
235247_at	0.81971	5.2325655	9.737905	1.31E-18	4.25E-17	31.61731	0	0	AI224578
219125_s at	0.81961	8.6082988	10.94739	3.46E-22	2.08E-20	39.74536	RAG1AP1	recombination activating gene 1 activating protein 1	NM_018845
218567_x at	0.81935	8.043724	10.21169	5.38E-20	2.20E-18	34.76673	DPP3	dipeptidyl-peptidase 3	NM_005700
218792_s at	0.81929	7.106949	6.762622	1.44E-10	1.19E-09	13.43198	BSPRY	B-box and SPRY domain containing	NM_017688
218282_at	0.81929	7.8611655	12.00619	2.12E-25	2.38E-23	47.05083	EDEM2	ER degradation enhancer, mannosidase alpha-like 2	NM_018217
212105_s at	0.8188	6.4013209	7.815728	2.98E-13	3.86E-12	19.48364	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	BF313832
1569253_at	0.8186	3.7580102	11.37037	1.83E-23	1.42E-21	42.64726	INTS4	integrator complex subunit 4	BC018672
202736_s at	0.81822	9.3536294	12.27816	3.10E-26	4.11E-24	48.9465	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	AA112507
200910_at	0.81803	10.847053	14.10023	7.32E-32	4.59E-29	61.74604	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	NM_005998
203714_s at	0.81789	8.5674392	10.82813	7.89E-22	4.46E-20	38.93196	TBCE	tubulin folding cofactor E	NM_003193
218556_at	0.81665	9.6202115	10.43225	1.20E-20	5.43E-19	36.24893	ORMDL2	ORM1-like 2 (S. cerevisiae)	NM_014182
208343_s at	0.81656	4.3055529	5.69866	4.24E-08	2.35E-07	7.892867	NR5A2	nuclear receptor subfamily 5, group A, member 2	AF146343
241342_at	0.8164	7.4767187	6.954984	4.82E-11	4.33E-10	14.49862	TMEM65	transmembrane protein 65	BG288115
235476_at	0.81599	6.9666538	7.602679	1.08E-12	1.27E-11	18.21936	TRIM59	tripartite motif-containing 59	AW182459
212175_s at	0.81562	9.2513478	11.06442	1.54E-22	9.93E-21	40.54573	AK2	adenylate kinase 2	AL513611
215395_x at	0.81542	8.4043448	5.531434	9.79E-08	5.13E-07	7.082816	PRSS1 /// T	protease, serine, 1 (trypsin 1) /// trypsinogen C	U66061
211478_s at	0.8152	5.9838695	4.018815	8.26E-05	0.0002627	0.621583	DPP4	dipeptidyl-peptidase 4	M74777
208165_s at	0.8149	6.5076289	4.83152	2.68E-06	1.11E-05	3.890945	PRSS16	protease, serine, 16 (thymus)	NM_005865
206924_at	0.81489	4.6716076	4.252865	3.23E-05	0.0001108	1.512143	IL11	interleukin 11	NM_000641
202706_s at	0.81464	8.2143306	13.57246	3.15E-30	1.10E-27	58.02891	UMPS	uridine monophosphate synthetase	D86227
205229_s at	0.81463	5.7550456	4.624561	6.70E-06	2.60E-05	3.011949	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	AA669336
201287_s at	0.81432	9.8201514	5.633317	5.90E-08	3.19E-07	7.574256	SDC1	syndecan 1	NM_002997
212474_at	0.81423	8.7084557	10.27919	3.40E-20	1.45E-18	35.21931	AVL9	AVL9 homolog (S. cerevisiae)	D87682
242722_at	0.81421	9.0899983	5.322735	2.71E-07	1.33E-06	6.096872	LMO7	LIM domain 7	AA100793
241031_at	0.81419	7.0128284	3.745156	0.0002353	0.0006851	-0.36501	FAM148A	family with sequence similarity 148, member A	BE218239
225766_s at	0.81402	8.5503616	10.52164	6.49E-21	3.06E-19	36.85234	TNPO1	transportin 1	AA527296
233655_s at	0.81398	5.767958	10.54068	5.70E-21	2.71E-19	36.98106	FAM29A	family with sequence similarity 29, member A	AK022964
243000_at	0.81267	5.768916	6.433555	8.90E-10	6.49E-09	11.65145	CDK6	cyclin-dependent kinase 6	AW194766
1557129_a at	0.81262	4.5970402	7.75326	4.35E-13	5.48E-12	19.11099	FAM111B	family with sequence similarity 111, member B	AA960844
204172_at	0.8126	8.0778695	10.33793	2.28E-20	9.92E-19	35.61395	CPOX	coproporphyrinogen oxidase	NM_000097
203721_s at	0.81251	9.8617931	12.76809	9.65E-28	1.75E-25	52.37499	UTP18	UTP18, small subunit (SSU) processome component, homolog (yeast)	NM_016001
37950_at	0.81227	8.0296982	9.688442	1.82E-18	5.75E-17	31.29148	PREP	prolyl endopeptidase	X74496
225447_at	0.81212	8.4690502	8.920684	2.85E-16	6.16E-15	26.31633	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	AA613031
200868_s at	0.81194	8.9662935	10.59948	3.81E-21	1.88E-19	37.37897	RNF114	ring finger protein 114	NM_018683
218826_at	0.81189	7.3182762	6.945585	5.09E-11	4.56E-10	14.44608	SLC35F2	solute carrier family 35, member F2	NM_017515
204252_at	0.81148	8.2758119	11.67471	2.18E-24	2.04E-22	44.7495	CDK2	cyclin-dependent kinase 2	M68520
204147_s at	0.81138	7.3323122	13.25432	3.04E-29	7.87E-27	55.79016	TFDP1	transcription factor Dp-1	NM_007111
222736_s at	0.81133	7.2530837	10.75821	1.28E-21	6.99E-20	38.45615	TMEM38B	transmembrane protein 38B	BC000049
201252_at	0.81113	9.6852327	13.22431	3.77E-29	9.48E-27	55.5791	PSMC4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	NM_006503
206316_s at	0.81083	6.3329096	10.6798	2.19E-21	1.13E-19	37.92349	KNTC1	kinetochore associated 1	NM_014708
201231_s at	0.81068	11.489036	14.59918	2.09E-33	2.15E-30	65.25966	ENO1	enolase 1, (alpha)	NM_001428
230772_at	0.81042	8.5504189	5.327106	2.66E-07	1.30E-06	6.11723	0	0	AA639753
203087_s at	0.81008	7.9924192	10.25391	4.04E-20	1.69E-18	35.0497	KIF2A	kinesin heavy chain member 2A	NM_004520
201399_s at	0.81003	10.424376	10.47859	8.72E-21	4.03E-19	36.56155	TRAM1	translocation associated membrane protein 1	NM_014294

205479_s_at	0.80965	8.5108705	6.182831	3.44E-09	2.28E-08	10.33411	PLAU	plasminogen activator, urokinase	NM_002658
217772_s_at	0.80945	10.323198	13.01497	1.67E-28	3.69E-25	54.1078	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	NM_014342
219531_at	0.80868	5.70217	8.576365	2.60E-15	4.78E-14	24.1415	CEP72	centrosomal protein 72kDa	NM_018140
208916_at	0.80844	8.1412029	9.969002	2.78E-19	1.02E-17	33.14726	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	AF105230
205687_at	0.80828	7.1110041	9.875492	5.21E-19	1.82E-17	32.5267	UBFD1	ubiquitin family domain containing 1	NM_019116
1554242_a_at	0.80825	4.5400243	5.758775	3.13E-08	1.77E-07	8.188326	COCH	coagulation factor C homolog, cochlin (Limulus polyphemus)	BC007230
225375_at	0.80805	7.5934932	13.9733	1.81E-31	9.41E-29	60.85198	TMEM199	transmembrane protein 199	AW975808
219461_at	0.80799	5.5228473	8.193327	2.90E-14	4.43E-13	21.76911	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	AJ236915
209426_s_at	0.80792	7.2271851	5.709581	4.02E-08	2.24E-07	7.946377	AMACR	alpha-methylacyl-CoA racemase	AF047020
202528_at	0.8077	8.9279662	5.663164	5.07E-08	2.78E-07	7.719463	GALE	UDP-galactose-4-epimerase	NM_000403
228171_s_at	0.80757	6.8356602	9.517162	5.71E-18	1.65E-16	30.16785	PLEKHG4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	AI056683
211150_s_at	0.80745	7.8083528	11.04729	1.73E-22	1.11E-20	40.42845	DLAT	dihydrolipoamide S-acetyltransferase	J03866
228868_x_at	0.80726	7.7772395	7.322485	5.71E-12	6.00E-11	16.58625	CDT1	Chromatin licensing and DNA replication factor 1, mRNA (cDNA clone IMAGE:4329262)	AW075105
205191_at	0.80679	8.0040944	9.02772	1.42E-16	3.24E-15	26.99997	RP2	retinitis pigmentosa 2 (X-linked recessive)	NM_006915
218897_at	0.80678	7.1596858	11.45797	9.92E-24	8.11E-22	43.25118	TMEM177	transmembrane protein 177	NM_030577
232158_x_at	0.80625	5.6179811	7.530251	1.67E-12	1.91E-11	17.79392	NPAL1	NIPA-like domain containing 1	AU158253
235350_at	0.80581	6.7175272	4.288902	2.78E-05	9.66E-05	1.653011	C4orf19	chromosome 4 open reading frame 19	AI935586
228463_at	0.80575	8.1791223	3.898111	0.000132	0.0004036	0.179055	FOXA3	forkhead box A3	R99562
204426_at	0.8057	9.0862727	9.834375	6.87E-19	2.34E-17	32.25448	TMED2	transmembrane emp24 domain trafficking protein 2	NM_006815
219402_s_at	0.80561	10.00524	11.91563	4.00E-25	4.29E-23	46.42103	DERL1	Der1-like domain family, member 1	NM_024295
202223_at	0.80555	9.27525	11.77624	1.07E-24	1.05E-22	45.4532	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	NM_002219
210317_s_at	0.80547	8.3371128	8.737664	9.27E-16	1.83E-14	25.15558	YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	U28936
222583_s_at	0.80487	6.8159001	10.63462	2.99E-21	1.51E-19	37.61705	NUP50	nucleoporin 50kDa	AF116624
238028_at	0.80475	6.4470896	6.103794	5.23E-09	3.38E-08	9.926177	LOC100128	hypothetical protein LOC100128918	BE379393
225520_at	0.80458	7.6864919	9.142533	6.73E-17	1.62E-15	27.73706	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	AL133260
217188_s_at	0.80429	8.0074692	10.0706	1.40E-19	5.36E-18	33.82367	C14orf1	chromosome 14 open reading frame 1	AC007182
219031_s_at	0.8042	8.6227182	10.24033	4.43E-20	1.85E-18	34.95861	NIP7	nuclear import 7 homolog (S. cerevisiae)	NM_016101
227021_at	0.80397	6.4249866	9.062443	1.14E-16	2.63E-15	27.22248	AOF1	amine oxidase (flavin containing) domain 1	BE348688
228221_at	0.80388	8.1021059	5.453356	1.44E-07	7.34E-07	6.710664	SLC44A3	solute carrier family 44, member 3	AA809640
242037_at	0.80385	5.5363438	7.483443	2.20E-12	2.48E-11	17.52018	ASPH	Aspartyl(asparaginyl)beta-hydroxylase [human, hepatoblastoma cell line HepG2, mRNA Partial, 2324 nt]	AA543030
211363_s_at	0.80336	5.5861473	8.786927	6.75E-16	1.37E-14	25.46697	MTAP	methylthioadenosine phosphorylase	AF109294

								histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	
208180_s_at	0.8031	4.8880517	6.292963	1.91E-09	1.32E-08	10.90845	HIST1H4A		NM_003543
1555785_a_at	0.80304	5.2726157	9.276933	2.79E-17	7.22E-16	28.6047	XRN1	5'-3' exoribonuclease 1	AY137776
205895_s_at	0.803	7.8172153	11.15147	8.40E-23	5.73E-21	41.14233	NOLC1	nucleolar and coiled-body phosphoprotein 1	NM_004741
234464_s_at	0.80265	6.6072484	9.85406	6.02E-19	2.07E-17	32.38476	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	AK021607
235099_at	0.80257	7.9533532	7.017024	3.38E-11	3.12E-10	14.84654	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	AW080832
235515_at	0.80242	5.5090178	6.188603	3.34E-09	2.22E-08	10.36404	C19orf46	chromosome 19 open reading frame 46	AA827649
212789_at	0.80235	8.066231	11.68816	1.98E-24	1.87E-22	44.84269	NCAPD3	non-SMC condensin II complex, subunit D3	AI796581
223021_x_at	0.80193	8.3287686	11.68894	1.97E-24	1.87E-22	44.84812	VTAT1	Vps20-associated 1 homolog (S. cerevisiae)	BF241590
212378_at	0.80177	8.5567029	12.70354	1.53E-27	2.68E-25	51.92241	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	NM_000819
235644_at	0.80177	5.1242918	11.78668	9.92E-25	9.88E-23	45.52561	CCDC138	coiled-coil domain containing 138	BF213953
211848_s_at	0.80113	6.2688892	4.632127	6.49E-06	2.52E-05	3.04354	CEACAM7	carcinoembryonic antigen-related cell adhesion molecule 7	AF006623
205628_at	0.8007	6.0069503	11.03923	1.83E-22	1.16E-20	40.3733	LOC100134	hypothetical protein LOC100134172 /// primase, DNA, polypeptide 2 (58kDa)	NM_000947
235763_at	0.80065	3.9389418	4.362521	2.05E-05	7.28E-05	1.943854	SLC44A5	solute carrier family 44, member 5	AA001450
209507_at	0.80051	9.8157833	11.83785	6.92E-25	7.10E-23	45.88076	RPA3	replication protein A3, 14kDa	BC005264
201558_at	0.80043	9.7359604	11.61891	3.22E-24	2.90E-22	44.3633	RAE1	RAE1 RNA export 1 homolog (S. pombe)	NM_003610
205807_s_at	0.80035	8.605559	7.429167	3.04E-12	3.35E-11	17.20396	TUFT1	tuftelin 1	NM_020127
203208_s_at	0.8003	9.7595366	11.61229	3.37E-24	3.02E-22	44.31749	MTFR1	mitochondrial fission regulator 1	NM_014637
206536_s_at	0.80024	5.5376254	11.08663	1.32E-22	8.68E-21	40.6978	XIAP	X-linked inhibitor of apoptosis	U32974
204203_at	0.79977	8.4357202	8.530772	3.47E-15	6.28E-14	23.85644	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	NM_001806
1555943_at	0.79956	6.3823742	11.90834	4.22E-25	4.51E-23	46.37037	PGAM5	phosphoglycerate mutase family member 5	CA307621
231779_at	0.79951	7.5320454	6.49847	6.24E-10	4.68E-09	11.99815	IRAK2	interleukin-1 receptor-associated kinase 2	AI246590
232112_at	0.79933	5.1193272	9.713508	1.54E-18	4.92E-17	31.45652	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	AW504453
218622_at	0.79924	9.3881906	12.2073	5.12E-26	6.54E-24	48.45202	NUP37	nucleoporin 37kDa	NM_024057
225686_at	0.79915	7.2335057	9.252458	3.28E-17	8.34E-16	28.44632	FAM33A	family with sequence similarity 33, member A	BE048371
234672_s_at	0.79909	9.2027311	12.44057	9.84E-27	1.44E-24	50.08125	TMEM48	transmembrane protein 48	AI354612
220442_at	0.79892	7.4004455	6.142206	4.27E-09	2.79E-08	10.12398	GALNT4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 4 (GalNAc-T4) /// WD repeat domain 51B	NM_003774
209626_s_at	0.79884	7.6485945	7.381052	4.04E-12	4.37E-11	16.92473	OSBPL3	oxysterol binding protein-like 3	AI202969

209719_x_at	0.79876	4.4786101	4.507431	1.11E-05	4.14E-05	2.528235	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	U19556
222750_s_at	0.79788	8.57204	7.420248	3.21E-12	3.52E-11	17.15212	SRD5A3	steroid 5 alpha-reductase 3	BC002480
239818_x_at	0.79736	4.8572805	6.540885	4.94E-10	3.77E-09	12.22591	TRIB1	tribbles homolog 1 (Drosophila)	AA576947
208658_at	0.79725	9.0781179	7.71093	5.62E-13	6.93E-12	18.85939	PDIA4	protein disulfide isomerase family A, member 4	BC000425
223570_at	0.79692	5.7016969	11.35019	2.11E-23	1.61E-21	42.50825	MCM10	minichromosome maintenance complex component 10	AL136840
218398_at	0.79669	8.8925644	10.44536	1.09E-20	5.00E-19	36.33735	MRPS30	mitochondrial ribosomal protein S30	NM_016640
1559827_at	0.79651	5.2112372	5.032292	1.07E-06	4.76E-06	4.772619	LOC401074	hypothetical LOC401074	BC039495
217185_s_at	0.79636	7.5886027	12.17162	6.59E-26	8.20E-24	48.20314	LOC442240	similar to zinc finger protein 259	Z95118
203715_at	0.79614	6.6643266	10.55926	5.02E-21	2.40E-19	37.1067	TBCE	/// zinc finger protein 259	NM_003193
227140_at	0.79576	9.1218919	3.793702	0.0001962	0.0005806	-0.19437	0	tubulin folding cofactor E	AI343467
202005_at	0.79569	9.4019553	6.099522	5.35E-09	3.45E-08	9.904229	ST14	suppression of tumorigenicity 14 (colon carcinoma)	NM_021978
1554451_s_at	0.79567	6.7914949	10.86186	6.25E-22	3.59E-20	39.16178	DNAJC14	DnaJ (Hsp40) homolog, subfamily C, member 14	AF141342
207543_s_at	0.79563	9.1804846	8.396283	8.13E-15	1.37E-13	23.01969	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	NM_000917
213454_at	0.79545	7.6294582	10.48496	8.34E-21	3.87E-19	36.60459	APITD1 ///	apoptosis-inducing, TAF9-like domain 1 /// cortistatin	AL578583
224913_s_at	0.79543	8.9170425	11.80394	8.78E-25	8.87E-23	45.6454	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	AA877820
214006_s_at	0.79542	7.2638388	13.14531	6.61E-29	1.58E-26	55.02369	GGCX	gamma-glutamyl carboxylase	BE325952
224715_at	0.79495	8.6779167	9.095966	9.12E-17	2.16E-15	27.43764	WDR34	WD repeat domain 34	BG338983
1554095_at	0.79472	6.0832421	9.850778	6.15E-19	2.11E-17	32.36303	RBM33	RNA binding motif protein 33	BC011923
240303_at	0.79469	8.3553678	3.802593	0.0001898	0.0005629	-0.16291	TMC5	Transmembrane channel-like 5, mRNA (cDNA clone IMAGE:5265527)	BG484769
216652_s_at	0.79457	7.6955797	9.564363	4.17E-18	1.24E-16	30.47676	DR1	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	AL137673
207396_s_at	0.79448	8.423679	13.5138	4.79E-30	1.58E-27	57.61591	ALG3	asparagine-linked glycosylation 3, alpha-1,3- mannosyltransferase homolog (S. cerevisiae)	NM_005787
203032_s_at	0.79421	7.072843	7.43733	-2.90E-12	3.20E-11	17.25144	FH	fumarate hydratase	AI363836
201301_s_at	0.79405	11.791601	6.970754	4.41E-11	3.99E-10	14.58688	ANXA4	annexin A4	BC000182
212766_s_at	0.79388	8.5060162	11.66017	2.41E-24	2.23E-22	44.64884	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	AW294587
206613_s_at	0.79361	5.8921005	8.821013	5.42E-16	1.12E-14	25.68289	TAF1A	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	NM_005681
202483_s_at	0.79325	10.411731	14.01093	1.38E-31	7.70E-29	61.117	RANBP1	RAN binding protein 1	NM_002882
203234_at	0.79318	7.1134622	9.022543	1.47E-16	3.34E-15	26.96683	UPP1	uridine phosphorylase 1	NM_003364
219296_at	0.79304	8.3180704	8.372545	9.44E-15	1.57E-13	22.87266	ZDHHC13	zinc finger, DHHC-type containing 13	NM_019028
225261_x_at	0.79268	9.515188	12.10042	1.09E-25	1.29E-23	47.70691	TH1L	TH1-like (Drosophila)	AJ238376
1552472_a_at	0.79229	6.4845834	10.10339	1.12E-19	4.35E-18	34.04249	ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	NM_012287
201633_s_at	0.7922	8.2760234	9.557127	4.38E-18	1.29E-16	30.42937	CYB5B	cytochrome b5 type B (outer mitochondrial membrane)	AW235051
238662_at	0.79211	7.2444937	9.82725	7.21E-19	2.45E-17	32.20734	ATPBD4	ATP binding domain 4	BE884544
235694_at	0.79199	5.5424627	9.261818	3.08E-17	7.91E-16	28.50687	TCFL5	transcription factor-like 5 (basic helix-loop-helix)	N49233
225739_at	0.79188	6.9489366	9.095237	9.17E-17	2.17E-15	27.43295	RAB11FIP4	RAB11 family interacting protein 4 (class II)	BF064276
208696_at	0.79162	10.663317	13.00451	1.80E-28	3.88E-26	54.03431	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	AF275798
1554351_a_at	0.79159	7.7499478	9.495739	6.58E-18	1.89E-16	30.02784	TIPRL	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	BC009506
223100_s_at	0.79155	9.6244193	11.27796	3.48E-23	2.55E-21	42.01115	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	BC000025
202487_s_at	0.79155	10.569297	14.00237	1.47E-31	8.03E-29	61.05676	H2AFV	H2A histone family, member V	NM_012412

201555_at	0.79145	9.2366227	11.87797	5.22E-25	5.50E-23	46.15935	MCM3	minichromosome maintenance complex component 3	NM_002388
206085_s_at	0.79112	5.051048	7.515239	1.82E-12	2.08E-11	17.70602	CTH	cystathionase (cystathionine gamma-lyase)	NM_001902
1552256_a_at	0.791	8.1908205	8.433555	6.43E-15	1.10E-13	23.25096	SCARB1	scavenger receptor class B, member 1	NM_005505
232195_at	0.79077	5.2734391	5.32543	2.68E-07	1.31E-06	6.109424	GPR158	G protein-coupled receptor 158	R41459
202904_s_at	0.7907	7.4425929	9.679168	1.94E-18	6.09E-17	31.23045	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_012322
206918_s_at	0.79038	9.024569	8.834573	4.97E-16	1.03E-14	25.76889	CPNE1	copine I	NM_003915
201664_at	0.79015	9.6174532	11.35942	1.98E-23	1.53E-21	42.57179	SMC4	structural maintenance of chromosomes 4	AL136877
235113_at	0.79008	8.3417119	9.808265	8.18E-19	2.74E-17	32.08181	PPIL5	peptidylprolyl isomerase (cyclophilin)-like 5	AA742244
229064_s_at	0.78981	6.2742179	9.941601	3.34E-19	1.21E-17	32.96522	RCAN3	RCAN family member 3	BE670097
212445_s_at	0.78969	8.0709769	7.458598	2.55E-12	2.85E-11	17.37527	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	AI357376
227143_s_at	0.78953	8.4727974	11.39509	1.54E-23	1.21E-21	42.81755	BID	BH3 interacting domain death agonist	AA706658
202539_s_at	0.78946	8.1686645	8.056909	6.77E-14	9.68E-13	20.93706	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	AL518627
201066_at	0.78916	10.792189	10.39023	1.59E-20	7.09E-19	35.96583	CYC1	cytochrome c-1	NM_001916
202691_at	0.7891	8.3967161	10.46217	9.75E-21	4.48E-19	36.45076	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	NM_006938
222250_s_at	0.78895	7.337403	13.22188	3.83E-29	9.58E-27	55.562	INTS7	Integrator complex subunit 7	AK001363
208002_s_at	0.7889	9.229501	9.621862	2.84E-18	8.69E-17	30.85383	ACOT7	acyl-CoA thioesterase 7	NM_007274
222392_x_at	0.78888	11.83029	7.375073	4.19E-12	4.51E-11	16.89011	PERP	PERP, TP53 apoptosis effector	AJ251830
219161_s_at	0.78825	9.4727174	9.201967	4.56E-17	1.14E-15	28.12012	CKLF	chemokine-like factor	NM_016951
205774_at	0.78808	7.2871069	5.989272	9.54E-09	5.89E-08	9.341508	F12	coagulation factor XII (Hageman factor)	NM_000505
220386_s_at	0.78778	7.7273491	9.660585	2.20E-18	6.83E-17	31.10823	EML4	echinoderm microtubule associated protein like 4	NM_019063
1554899_s_at	0.78778	8.0767316	4.624232	6.71E-06	2.60E-05	3.010575	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	BC020763
210337_s_at	0.78759	8.3819458	10.70283	1.87E-21	9.82E-20	38.07982	ACLY	ATP citrate lyase	U18197
223845_at	0.78753	6.293801	7.886896	1.93E-13	2.58E-12	19.91012	FLJ20674	hypothetical protein FLJ20674	BC001437
206976_s_at	0.78753	10.282296	10.07705	1.34E-19	5.14E-18	33.86674	HSPH1	heat shock 105kDa/110kDa protein 1	NM_006644
236279_at	0.78745	7.0991902	5.134571	6.65E-07	3.05E-05	5.232468	0	0	N23258
1555829_at	0.78741	5.6015939	9.739863	1.29E-18	4.20E-17	31.63022	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	BC001224
219715_s_at	0.7873	7.6786352	13.25789	2.96E-29	7.82E-27	55.81526	TDP1	tyrosyl-DNA phosphodiesterase 1	NM_018319
1557455_s_at	0.78673	6.491468	8.735637	9.39E-16	1.85E-14	25.14278	MOSPD1	motile sperm domain containing 1	AF086333
1565162_s_at	0.78624	9.1776557	3.925593	0.0001187	0.0003663	0.278795	MGST1	microsomal glutathione S-transferase 1	D16947
204750_s_at	0.78618	7.2890488	4.221606	3.67E-05	0.0001245	1.390755	DSC2	desmocollin 2	BF196457
228181_at	0.78614	7.2362182	8.268861	1.81E-14	2.86E-13	22.23279	SLC30A1	solute carrier family 30 (zinc transporter), member 1	AI553933
227455_at	0.78612	7.4056355	9.256793	3.18E-17	8.14E-16	28.47436	C6orf136	chromosome 6 open reading frame 136	BF224092
219017_at	0.78566	8.9972855	5.373777	2.12E-07	1.05E-06	6.335395	ETNK1	ethanolamine kinase 1	NM_018638
218737_at	0.78536	5.7138975	10.76033	1.26E-21	6.90E-20	38.47054	SBNO1	strawberry notch homolog 1 (Drosophila)	NM_018183
204317_at	0.78525	4.8591292	11.25725	4.03E-23	2.90E-21	41.86873	GTSE1	G-2 and S-phase expressed 1	BF305380
201772_at	0.78513	9.8883017	10.90295	4.70E-22	2.77E-20	39.442	AZIN1	antizyme inhibitor 1	NM_015878
219189_at	0.78508	6.8169679	9.560608	4.28E-18	1.26E-16	30.45216	FBXL6	F-box and leucine-rich repeat protein 6	NM_024555
213913_s_at	0.78508	6.038004	6.491456	6.48E-10	4.85E-09	11.96058	TBC1D30	TBC1 domain family, member 30	AW134976
218829_s_at	0.78481	7.8311004	8.59473	2.31E-15	4.29E-14	24.25653	CHD7	chromodomain helicase DNA binding protein 7	NM_017780
218479_s_at	0.78463	5.6526852	10.78862	1.04E-21	5.73E-20	38.66299	XPO4	exportin 4	NM_022459
1554761_a_at	0.78443	6.5403489	12.06161	1.43E-25	1.66E-23	47.4366	HEATR2	HEAT repeat containing 2	BC010850

203545_at	0.78418	8.7299902	10.53562	5.90E-21	2.80E-19	36.94687	ALG8	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (<i>S. cerevisiae</i>)	NM_024079
241455_at	0.78407	6.0232963	5.947158	1.19E-08	7.22E-08	9.128437	0		AW135306
223308_s_at	0.78377	6.9876206	11.86812	5.59E-25	5.85E-23	46.09094	WDR5	WD repeat domain 5	AL521101
218681_s_at	0.78354	8.7123515	9.49353	6.68E-18	1.91E-16	30.0134	SDF2L1	stromal cell-derived factor 2-like 1	NM_022044
228123_s_at	0.78346	9.1229073	10.06944	1.41E-19	5.39E-18	33.81595	ABHD12	abhydrolase domain containing 12	AW303865
224578_at	0.78346	9.8544796	13	1.86E-28	3.99E-26	54.00266	RCC2	regulator of chromosome condensation 2	AB040903
224204_x_at	0.78329	7.418258	8.386675	8.64E-15	1.45E-13	22.96016	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	AF231339
1558014_s_at	0.78316	6.5016829	6.352594	1.38E-09	9.76E-09	11.22226	FAR1	fatty acyl CoA reductase 1	BG261090
225203_at	0.78299	7.6876417	7.363709	4.48E-12	4.79E-11	16.82434	PPP1R16A	protein phosphatase 1, regulatory (inhibitor) subunit 16A	AI742931
209279_s_at	0.78291	7.285971	10.91674	4.28E-22	2.53E-20	39.5361	NSDHL	NAD(P) dependent steroid dehydrogenase-like	BC000245
214581_x_at	0.78281	8.4102408	6.693545	2.12E-10	1.71E-09	13.05352	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	BE568134
213984_at	0.78267	4.988003	8.93247	2.64E-16	5.75E-15	26.39144	PDS5A	PDS5, regulator of cohesion maintenance, homolog A (<i>S. cerevisiae</i>)	AW991219
202823_at	0.78265	7.4518531	9.355258	1.67E-17	4.48E-16	29.11266	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	N89607
222590_s_at	0.78261	6.4364253	12.86372	4.89E-28	9.65E-26	53.04586	NLK	nemo-like kinase	AF180819
221827_at	0.78251	9.9017714	9.022911	1.47E-16	3.34E-15	26.96919	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	BE788439
203816_at	0.78246	7.5766177	12.93701	2.91E-28	6.01E-26	53.56031	DGUOK	deoxyguanosine kinase	NM_001929
226817_at	0.78241	9.1404707	4.612984	7.05E-06	2.72E-05	2.963693	DSC2	desmocollin 2	AU154691
219888_at	0.78236	6.8940665	5.999574	9.05E-09	5.60E-08	9.39379	SPAG4	sperm associated antigen 4	NM_003116
201521_s_at	0.78155	8.1389888	11.80017	9.02E-25	9.07E-23	45.6192	NCBP2	nuclear cap binding protein subunit 2, 20kDa	NM_007362
215977_x_at	0.7815	6.5676198	8.91162	3.02E-16	6.51E-15	26.2586	GK	glycerol kinase	X68285
235363_at	0.78098	5.3130056	7.574918	1.28E-12	1.49E-11	18.05603	0		BF108778
242473_at	0.78092	4.9989269	10.04246	1.69E-19	6.39E-18	33.63613	TRAF4	TNF receptor-associated factor 4	BF000155
1555310_a_at	0.78059	6.5487974	6.956644	4.78E-11	4.30E-10	14.50791	PAK6	p21 protein (Cdc42/Rac)-activated kinase 6	BC035596
205078_at	0.77978	8.0662694	7.861049	2.26E-13	2.99E-12	19.755	PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	NM_002643
212330_at	0.77892	9.6263099	12.58247	3.60E-27	5.87E-25	51.07425	TFDP1	transcription factor Dp-1	R60866
1557910_at	0.77891	11.256081	9.275273	2.82E-17	7.29E-16	28.59396	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	BG612458
1555736_a_at	0.77886	7.8578647	10.50439	7.30E-21	3.41E-19	36.73577	AGTRAP	angiotensin II receptor-associated protein	AF165187
218180_s_at	0.77862	8.2389333	7.53811	1.59E-12	1.83E-11	17.83997	EPS8L2	EPS8-like 2	NM_022772
218365_s_at	0.77859	7.2934966	10.23089	4.72E-20	1.96E-18	34.89535	DARS2	aspartyl-tRNA synthetase 2, mitochondrial	AI765051
218392_x_at	0.77857	7.5452816	8.278077	1.71E-14	2.72E-13	22.28952	SFXN1	sideroflexin 1	NM_022754
205761_s_at	0.77854	7.0687627	9.046828	1.26E-16	2.90E-15	27.12237	DUS4L	dihydrouridine synthase 4-like (<i>S. cerevisiae</i>)	AW242981
216607_s_at	0.77849	8.8974545	7.024644	3.23E-11	3.00E-10	14.8894	CYP51A1	cytochrome P450, family 51, subfamily A, polypeptide 1	U40053
206704_at	0.77838	6.0236699	9.241544	3.52E-17	8.92E-16	28.37575	CLCN5	chloride channel 5	NM_000084
208300_at	0.77837	7.1194228	4.725054	4.31E-06	1.73E-05	3.434924	PTPRH	protein tyrosine phosphatase, receptor type, H	NM_002842
218448_at	0.77836	8.9079492	12.04408	1.62E-25	1.85E-23	47.31451	C20orf11	chromosome 20 open reading frame 11	NM_017896
204678_s_at	0.77824	8.6849213	4.569149	8.53E-06	3.24E-05	2.781861	KCNK1	potassium channel, subfamily K, member 1	U90065
226943_at	0.77824	7.1203053	10.25204	4.09E-20	1.71E-18	35.03714	C12orf73	chromosome 12 open reading frame 73	AA287457
243529_at	0.77805	6.0298129	11.87986	5.15E-25	5.44E-23	46.1725	MARS2	methionyl-tRNA synthetase 2, mitochondrial	BE542381
222396_at	0.77797	9.2898838	7.617274	9.89E-13	1.17E-11	18.30536	HN1	hematological and neurological expressed 1	AF060925
207180_s_at	0.77794	9.0847862	8.125195	4.44E-14	6.57E-13	21.35268	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	NM_006410

241224_x_at	0.77783	5.1226094	4.626618	6.64E-06	2.58E-05	3.020533	DSCR8	Down syndrome critical region gene 8	AA770014
208694_at	0.77774	9.342955	10.2085	5.49E-20	2.25E-18	34.74535	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	U47077
205767_at	0.77768	4.749077	3.913812	0.0001242	0.0003819	0.235965	EREG	epiregulin	NM_001432
227818_at	0.77765	6.4047232	12.84231	5.70E-28	1.09E-25	52.89567	CCDC21	coiled-coil domain containing 21	AL133609
225177_at	0.7776	9.0659377	6.110539	5.05E-09	3.27E-08	9.96085	RAB11FIP1	RAB11 family interacting protein 1 (class I)	AA143793
222404_x_at	0.77749	10.90931	10.0696	1.41E-19	5.39E-18	33.81702	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	AI984229
1555788_a_at	0.77732	5.4011621	9.054932	1.19E-16	2.76E-15	27.17432	TRIB3	tribbles homolog 3 (Drosophila)	AF250311
231008_at	0.77684	7.2378101	3.843789	0.0001624	0.0004884	-0.01632	UNC5CL	Unc-5 homolog C (C. elegans)-like, mRNA (cDNA clone MGC:34763 IMAGE:5189247)	AI733001
206205_at	0.77662	5.8629244	10.54445	5.55E-21	2.65E-19	37.00656	MPHOSPH9	M-phase phosphoprotein 9	NM_022782
1568838_at	0.77653	4.0310463	7.072527	2.45E-11	2.31E-10	15.15937	hCG_17428	hCG_1742852 /// similar to hCG1742852	AI015847
219399_at	0.77648	7.5677243	8.174578	3.26E-14	4.93E-13	21.65434	LIN7C	lin-7 homolog C (C. elegans)	NM_018362
215227_x_at	0.77648	9.7812439	13.01447	1.68E-28	3.69E-26	54.10432	ACP1	acid phosphatase 1, soluble	BG035989
203313_s_at	0.77637	9.2011949	9.490667	6.80E-18	1.94E-16	29.9947	TGIF1	TGFB-induced factor homeobox 1	NM_003244
200730_s_at	0.77637	9.1561768	6.86593	8.01E-11	6.93E-10	14.00253	PTP4A1	protein tyrosine phosphatase type IVA, member 1	BF576710
201644_at	0.77632	9.8648712	7.221508	1.03E-11	1.04E-10	16.00632	TSTA3	tissue specific transplantation antigen P35B	NM_003313
202671_s_at	0.77582	9.0912511	8.874664	3.84E-16	8.11E-15	26.02348	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	NM_003681
215165_x_at	0.7758	8.5834818	13.1362	7.05E-29	1.67E-26	54.95966	UMPS	uridine monophosphate synthetase	AL080099
203028_s_at	0.77561	11.658117	8.690671	1.25E-15	2.42E-14	24.85925	CYBA	cytochrome b-245, alpha polypeptide	NM_000101
205990_s_at	0.77533	8.6238842	4.916574	1.82E-06	7.78E-06	4.261017	WNT5A	wingless-type MMTV integration site family, member 5A	NM_003392
206788_s_at	0.77467	7.2363996	10.70917	1.79E-21	9.42E-20	38.12289	CBFB	core-binding factor, beta subunit	AF294326
1555037_a_at	0.77454	10.652529	8.706945	1.13E-15	2.20E-14	24.96179	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	BC012846
209317_at	0.77432	8.1936394	10.8894	5.17E-22	3.01E-20	39.3496	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	AF008442
207740_s_at	0.7741	6.9014119	12.51727	5.72E-27	8.87E-25	50.61782	NUP62	nucleoporin 62kDa	NM_012346
218720_x_at	0.77407	7.708654	5.631629	5.95E-08	3.22E-07	7.566062	LOC652900	similar to seizure related 6 homolog (mouse)-like 2 isoform 1 /// seizure related 6 homolog (mouse)-like 2	NM_012410
211056_s_at	0.77333	7.0943912	8.192407	2.92E-14	4.45E-13	21.76348	SRD5A1	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	BC006373
212815_at	0.77326	8.0902975	10.87538	5.69E-22	3.30E-20	39.25399	ASCC3	activating signal cointegrator 1 complex subunit 3	AA156961
225865_x_at	0.77315	9.7923477	11.79463	9.38E-25	9.38E-23	45.58078	TH1L	TH1-like (Drosophila)	AJ238374
222532_at	0.77306	8.596887	9.77854	9.99E-19	3.31E-17	31.88543	SRPRB	signal recognition particle receptor, B subunit	BF983948
221665_s_at	0.77278	6.8809691	5.259242	3.68E-07	1.77E-06	5.802554	EPS8L1	EPS8-like 1	BC004907
235117_at	0.77268	7.3371406	6.66629	2.46E-10	1.98E-09	12.90487	CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	AI191897
233878_s_at	0.77202	8.053246	8.774272	7.33E-16	1.47E-14	25.3869	XRN2	5'-3' exoribonuclease 2	BE536170
218872_at	0.77183	8.7021315	3.762196	0.0002208	0.0006469	-0.30533	TESC	tescalcin	NM_017899
1554915_a_at	0.77174	6.3895387	9.520315	5.59E-18	1.62E-16	30.18847	PDE12	phosphodiesterase 12	BC034978
205351_at	0.77171	7.3406221	9.578776	3.79E-18	1.13E-16	30.5712	GGCX	gamma-glutamyl carboxylase	NM_000821
200935_at	0.77168	7.4851194	10.17291	7.00E-20	2.81E-18	34.50711	CALR	calreticulin	NM_004343
206302_s_at	0.77128	9.000177	7.123559	1.83E-11	1.76E-10	15.44831	NUDT4 ///	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// pseudogene 1	NM_019094
204416_x_at	0.77097	9.4095817	4.212302	3.81E-05	0.0001288	1.35477	APOC1	apolipoprotein C-I	NM_001645
200658_s_at	0.77069	9.7255068	12.4644	8.31E-27	1.24E-24	50.24793	PHB	prohibitin	AL560017

225438_at	0.7703	4.6447585	10.26131	3.84E-20	1.62E-18	35.09932	NUDCD1	NudC domain containing 1	BF445343
210543_s_at	0.77001	7.8501703	11.55148	5.16E-24	4.46E-22	43.897	PRKDC	protein kinase, DNA-activated, catalytic polypeptide	U34994
235588_at	0.76963	6.3003699	8.369716	9.61E-15	1.59E-13	22.85515	ESCO2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	AA740849
203284_s_at	0.76922	8.3088462	9.164476	5.83E-17	1.42E-15	27.87837	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	AW151887
224461_s_at	0.76901	7.5407699	8.262428	1.89E-14	2.97E-13	22.19322	AIFM2	apoptosis-inducing factor, mitochondrion-associated, 2	BC006121
204799_at	0.76895	6.803626	10.74815	1.37E-21	7.45E-20	38.38771	ZBED4	zinc finger, BED-type containing 4	NM_014838
1559826_a_at	0.76886	4.9253469	7.100264	2.09E-11	2.00E-10	15.31626	LOC401074	hypothetical LOC401074	BC039495
225864_at	0.76871	9.4493302	6.971102	4.40E-11	3.98E-10	14.58883	FAM84B	family with sequence similarity 84, member B	AL039862
227296_at	0.76846	6.4751771	9.275886	2.81E-17	7.26E-16	28.59792	MFS03	major facilitator superfamily domain containing 3	AA523543
231769_at	0.76824	8.3915803	7.337602	5.23E-12	5.52E-11	16.67347	FBX06	F-box protein 6	AF129536
208394_x_at	0.76812	5.4630382	6.890452	6.97E-11	6.10E-10	14.13874	ESM1	endothelial cell-specific molecule 1	NM_007036
223079_s_at	0.76785	6.8600627	5.550634	8.90E-08	4.69E-07	7.174926	GLS	glutaminase	AI828035
218172_s_at	0.76753	8.9901382	10.06574	1.45E-19	5.52E-18	33.79125	DERL1	Der1-like domain family, member 1	NM_018630
238015_at	0.76751	6.0743395	9.086277	9.72E-17	2.29E-15	27.37542	C4orf46	chromosome 4 open reading frame 46	BE620598
227916_x_at	0.76738	8.3014388	12.57719	3.74E-27	6.06E-25	51.03732	EXOSC3	exosome component 3	AA747303
222569_at	0.76666	7.1043189	14.69939	1.02E-33	1.27E-30	65.96488	UGCG1	UDP-glucose ceramide glucosyltransferase-like 1	AU153746
227759_at	0.76628	6.1541469	6.396796	1.09E-09	7.80E-09	11.45614	PCSK9	proprotein convertase subtilisin/kexin type 9	W92036
234000_s_at	0.76627	10.818142	10.25653	3.96E-20	1.67E-18	35.06727	PTPLAD1	protein tyrosine phosphatase-like A domain containing 1	AJ271091
225161_at	0.7662	8.5965753	10.94919	3.42E-22	2.06E-20	39.75768	GFM1	G elongation factor, mitochondrial 1	AI659020
235583_at	0.76618	6.2710599	6.297834	1.86E-09	1.29E-08	10.93401	ILDR1	immunoglobulin-like domain containing receptor 1	AI821661
231227_at	0.76608	5.1551495	5.745279	3.35E-08	1.89E-07	8.121799	0	0	AI703321
203743_s_at	0.76595	9.2017427	10.69454	1.98E-21	1.03E-19	38.02354	TDG	thymine-DNA glycosylase	NM_003211
219573_at	0.76584	7.2735591	8.197144	2.83E-14	4.33E-13	21.79249	LRRC16A	leucine rich repeat containing 16A	NM_017640
211450_s_at	0.76573	7.538777	7.768737	3.96E-13	5.02E-12	19.20317	MSH6	mutS homolog 6 (E. coli)	D89646
204826_at	0.76553	7.1627605	11.89885	4.51E-25	4.80E-23	46.30439	CCNF	cyclin F	NM_001761
202540_s_at	0.76529	8.364199	8.292308	1.56E-14	2.50E-13	22.37716	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	NM_000859
222555_s_at	0.76495	7.9139788	11.01844	2.12E-22	1.33E-20	40.23103	MRPL44	mitochondrial ribosomal protein L44	AI338045
201821_s_at	0.7649	9.3393706	9.610469	3.07E-18	9.33E-17	30.77905	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	BC004439
226686_at	0.76425	7.7019569	11.30799	2.83E-23	2.10E-21	42.21772	CISD2	CDGS iron sulfur domain 2	AI188518
210639_s_at	0.76425	7.822973	9.924862	3.74E-19	1.34E-17	32.85409	ATG5	ATG5 autophagy related 5 homolog (S. cerevisiae)	AF293841
214698_at	0.76418	6.715814	12.85486	5.21E-28	1.02E-25	52.98373	ROD1	ROD1 regulator of differentiation 1 (S. pombe)	AW190873
212657_s_at	0.76405	8.7817025	3.721281	0.0002571	0.0007429	-0.44822	IL1RN	interleukin 1 receptor antagonist	U65590
241898_at	0.76398	6.6398488	5.037145	1.05E-06	4.66E-06	4.794276	0	0	AA991267
227042_at	0.76385	7.2336587	11.04091	1.81E-22	1.15E-20	40.38479	YDJC	YdjC homolog (bacterial)	BE218514
235542_at	0.76374	7.4921528	9.661546	2.18E-18	6.80E-17	31.11455	TET3	tet oncogene family member 3	BF675754
213301_x_at	0.76365	8.3373947	8.193658	2.90E-14	4.42E-13	21.77114	TRIM24	tripartite motif-containing 24	AL538264
218151_x_at	0.76364	8.7907864	10.23189	4.69E-20	1.95E-18	34.90204	GPR172A	G protein-coupled receptor 172A	NM_024531
219032_x_at	0.76358	8.617795	6.928311	5.62E-11	4.99E-10	14.34962	OPN3	opsin 3	NM_014322
203176_s_at	0.76356	8.4699371	11.67803	2.13E-24	2.00E-22	44.77254	TFAM	transcription factor A, mitochondrial	BE552470
232510_s_at	0.76334	9.168957	10.14408	8.51E-20	3.35E-18	34.31427	DPP3	dipeptidyl-peptidase 3	AW250952
224888_at	0.76323	7.4825719	11.60632	3.51E-24	3.15E-22	44.27618	SELI	selenoprotein I	AB051511
218605_at	0.76319	8.9640624	10.66286	2.46E-21	1.26E-19	37.80855	TFB2M	transcription factor B2, mitochondrial	NM_022366

203557_s_at	0.7628	8.849366	9.917319	3.93E-19	1.41E-17	32.80404	PC8D1	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	NM_000281
228441_s_at	0.76278	4.5327076	10.87217	5.82E-22	3.36E-20	39.23208	0		BE550153
235253_at	0.76273	7.018563	9.065386	1.11E-16	2.59E-15	27.24135	RAD1	RAD1 homolog (S. pombe)	AI742925
232155_at	0.76273	5.7262922	7.726865	5.11E-13	6.34E-12	18.95401	KIAA1618	KIAA1618	AK023113
208097_s_at	0.76269	8.6310085	8.211062	2.60E-14	4.00E-13	21.8778	TXNDC1	thioredoxin domain containing 1	NM_030755
205490_x_at	0.76257	7.9251807	5.368546	2.17E-07	1.08E-06	6.310871	GJB3	gap junction protein, beta 3, 31kDa	BF060667
204717_s_at	0.76232	5.6504457	7.729553	5.02E-13	6.24E-12	18.96999	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	AF034102
239010_at	0.76212	4.0344673	6.33193	1.55E-09	1.08E-08	11.11329	FLJ39632	CDNA clone IMAGE:5270501	AI744280
1556429_a_at	0.76208	4.1586137	9.529696	5.25E-18	1.53E-16	30.24983	WDR67	WD repeat domain 67	BC026969
208744_x_at	0.76203	9.4079652	9.857875	5.87E-19	2.02E-17	32.41002	HSPH1	heat shock 105kDa/110kDa protein 1	BG403660
208447_s_at	0.76188	7.0618449	8.463814	5.31E-15	9.30E-14	23.43906	PRPS1	phosphoribosyl pyrophosphate synthetase 1	NM_002764
202740_at	0.76183	8.7335757	6.294912	1.89E-09	1.31E-08	10.91868	ACY1	aminoacylase 1	NM_000666
210511_s_at	0.76166	7.4829592	3.900082	0.000131	0.0004008	0.186189	INHBA	inhibin, beta A	M13436
200078_s_at	0.76136	10.713843	11.35687	2.01E-23	1.56E-21	42.55422	ATP6V0B	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	BC005876
210540_s_at	0.76121	8.1190179	6.729086	1.73E-10	1.42E-09	13.24794	B4GALT4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	BC004523
208368_s_at	0.76115	5.5470626	9.793525	9.03E-19	3.01E-17	31.9844	BRCA2	breast cancer 2, early onset	NM_000059
205169_at	0.76074	6.9090434	9.915156	3.99E-19	1.43E-17	32.78968	RBBP5	retinoblastoma binding protein 5	NM_005057
238805_at	0.76045	6.3557797	5.173257	5.54E-07	2.58E-06	5.408254	C11orf52	chromosome 11 open reading frame 52	AA991551
216243_s_at	0.76036	6.342587	6.295961	1.88E-09	1.30E-08	10.92418	IL1RN	interleukin 1 receptor antagonist	BE563442
203124_s_at	0.76021	8.1738985	7.885072	1.95E-13	2.60E-12	19.89916	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	NM_000617
211212_s_at	0.75996	6.4803684	9.149612	6.43E-17	1.55E-15	27.78263	ORC5L	origin recognition complex, subunit 5-like (yeast)	AF081459
1558292_s_at	0.75969	7.2186788	8.972626	2.04E-16	4.53E-15	26.64765	PIGW	phosphatidylinositol glycan anchor biosynthesis, class W	BF037819
238632_at	0.75968	5.1108113	5.002677	1.23E-06	5.40E-06	4.640802	0		AI631657
1553220_at	0.75951	5.0617967	9.732903	1.36E-18	4.38E-17	31.58434	FAM117B	family with sequence similarity 117, member B	NM_173511
226610_at	0.75922	8.7618168	6.491488	6.48E-10	4.85E-09	11.96075	CENPV	centromere protein V	AA722878
208523_x_at	0.75917	6.0715135	7.981981	1.08E-13	1.49E-12	20.48308	HIST1H2BC	histone cluster 1, H2bc /// histone cluster 1, H2be /// histone cluster 1, H2bf /// histone cluster 1, H2bg /// histone cluster 1, H2bi	NM_003525
203165_s_at	0.75912	7.4323862	8.62426	1.92E-15	3.60E-14	24.44172	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	NM_004733
209836_x_at	0.759	9.8671993	10.53413	5.96E-21	2.82E-19	36.93675	BOLA2 /// B	bolA homolog 2 (E. coli) /// bolA homolog 2B (E. coli)	AF060511
203023_at	0.75898	7.5050398	9.910205	4.13E-19	1.47E-17	32.75684	NOP16	NOP16 nucleolar protein homolog (yeast)	NM_016391
218420_s_at	0.75828	7.0357143	10.57588	4.48E-21	2.17E-19	37.2192	C13orf23	chromosome 13 open reading frame 23	NM_025138
222402_at	0.75822	7.495755	8.564225	2.81E-15	5.13E-14	24.06553	POMP	proteasome maturation protein	BC003390
225694_at	0.75803	7.7699263	11.48377	8.29E-24	6.89E-22	43.4293	CRKRS	Cdc2-related kinase, arginine/serine-rich	AI823766
225006_x_at	0.7573	9.7794761	11.54406	5.44E-24	4.68E-22	43.84569	TH1L	TH1-like (Drosophila)	AJ238379
208837_at	0.75728	9.5909206	8.685923	1.29E-15	2.49E-14	24.82935	TMED3	transmembrane emp24 protein transport domain containing 3	BC000027
1554835_a_at	0.75694	6.3935883	8.167295	3.41E-14	5.15E-13	21.6098	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	BC028058
202597_at	0.75674	8.7502945	5.283496	3.28E-07	1.58E-06	5.914671	IRF6	interferon regulatory factor 6	AU144284

234942_s_at	0.75666	8.7983193	9.826771	7.23E-19	2.46E-17	32.20417	DNTTIP1	deoxynucleotidyltransferase, terminal, interacting protein 1	AK025220
201091_s_at	0.75632	10.357308	11.87038	5.51E-25	5.79E-23	46.10666	CBX3 /// LOC	chromobox homolog 3 (HP1 gamma homolog, Drosophila) /// similar to chromobox homolog 3	BE748755
223151_at	0.75617	9.5965951	10.50044	7.50E-21	3.50E-19	36.70914	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	BC004169
209186_at	0.75605	10.959668	10.73272	1.52E-21	8.18E-20	38.28286	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	M23114
220056_at	0.75596	6.9236569	5.540957	9.34E-08	4.91E-07	7.128473	IL22RA1	Interleukin 22 receptor, alpha 1	NM_021258
219037_at	0.75594	8.1285304	9.712316	1.56E-18	4.96E-17	31.44867	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	NM_016052
208511_at	0.75559	6.1635606	11.21025	5.58E-23	3.92E-21	41.54581	PTTG3	pituitary tumor-transforming 3	NM_021000
220585_at	0.75553	5.5956533	7.505688	1.93E-12	2.19E-11	17.65015	HKDC1	hexokinase domain containing 1	NM_025130
204108_at	0.7552	7.3962548	10.89897	4.84E-22	2.84E-20	39.41486	NFYA	nuclear transcription factor Y, alpha	AL031778
238756_at	0.75511	7.3427258	6.186599	3.37E-09	2.24E-08	10.35365	GAS2L3	PIG-A-II=glycoinositol phospholipid anchor synthetic element [human, paroxysmal nocturnal hemoglobinuria patient, B lymphocytes, mRNA Partial, 1599 nt]	AI860012
1567080_s_at	0.75482	7.3702466	12.77126	9.43E-28	1.72E-25	52.39727	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	D17218
236979_at	0.75465	7.7428683	4.705605	4.70E-06	1.87E-05	3.352493	BCL2L15	BCL2-like 15	AI821801
225578_at	0.75444	8.7951792	9.92921	3.63E-19	1.30E-17	32.88295	C13orf37	chromosome 13 open reading frame 37	AI885466
219513_s_at	0.75429	5.9247655	6.000563	9.00E-09	5.57E-08	9.398809	SH2D3A	SH2 domain containing 3A	NM_005490
218817_at	0.75426	7.3786265	8.485535	4.63E-15	8.21E-14	23.57429	SPCS3	signal peptidase complex subunit 3; homolog (S. cerevisiae)	NM_021928
1558105_a_at	0.75396	5.4487881	6.045533	7.11E-09	4.48E-08	9.62778	0	0	AK096921
209680_s_at	0.7537	7.4774332	10.58853	4.10E-21	2.01E-19	37.30484	KIFC1	kinesin family member C1	BC000712
203830_at	0.75369	6.1570536	9.506327	6.13E-18	1.77E-16	30.09702	C17orf75	chromosome 17 open reading frame 75	NM_022344
222500_at	0.75326	8.6980432	8.677068	1.37E-15	2.62E-14	24.77361	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	BC003048
220668_s_at	0.75294	6.176151	8.279163	1.70E-14	2.70E-13	22.2962	DNMT3B	DNA (cytosine-5)-methyltransferase 3 beta	NM_006892
205309_at	0.75283	5.7846546	6.533682	5.14E-10	3.91E-09	12.18716	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	NM_014474
220230_s_at	0.75251	6.6720635	6.858547	8.35E-11	7.20E-10	13.96157	CYB5R2	cytochrome b5 reductase 2	NM_016229
201043_s_at	0.75241	7.9781519	10.46327	9.68E-21	4.45E-19	36.45817	ANP32A ///	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A /// hypothetical protein LOC100128146	NM_006305
242996_at	0.75234	4.4737418	9.547125	4.68E-18	1.37E-16	30.36388	MTRF1	mitochondrial translational release factor 1	AI341686
224521_s_at	0.75219	5.2169585	11.06799	1.50E-22	9.73E-21	40.57016	CCDC77	coiled-coil domain containing 77	BC006444
231856_at	0.75216	6.1164603	5.595724	7.11E-08	3.80E-07	7.392162	KIAA1244	KIAA1244	AB033070
1553928_at	0.75198	6.7681616	7.688123	6.45E-13	7.87E-12	18.72413	ELMOD2	ELMO/CED-12 domain containing 2	NM_153702
222147_s_at	0.75164	6.2656331	12.57456	3.81E-27	6.15E-25	51.01887	ACTR5	ARPS actin-related protein 5 homolog (yeast)	AL133519
210085_s_at	0.75129	5.8675599	7.502903	1.96E-12	2.23E-11	17.63387	ANXA9	annexin A9	AF230929
1557411_s_at	0.75109	7.6416511	6.46409	7.53E-10	5.57E-09	11.81425	SLC25A43	solute carrier family 25, member 43	AK094254
217834_s_at	0.75077	8.9849879	11.22586	5.01E-23	3.54E-21	41.65305	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	NM_006372
210779_x_at	0.75031	6.6446453	10.95479	3.29E-22	1.99E-20	39.79589	SIP1	survival of motor neuron protein interacting protein 1	AB037701
223057_s_at	0.74996	7.5214842	10.99989	2.41E-22	1.49E-20	40.10417	XPO5	exportin 5	BC000129
231973_s_at	0.74991	6.6976898	9.161217	5.96E-17	1.45E-15	27.85737	ANAPC1	anaphase promoting complex subunit 1	AK001223
209080_x_at	0.74971	9.7191687	11.73408	1.43E-24	1.38E-22	45.16088	GLRX3	glutaredoxin 3	AF118652

218783_at	0.74929	5.8465921	8.713822	1.08E-15	2.11E-14	25.00515	INTS7	integrator complex subunit 7	AL133049
225759_x_at	0.74912	6.3598118	6.858615	8.35E-11	7.20E-10	13.96195	CLMN	calmin (calponin-like, transmembrane)	AK023828
223861_at	0.74905	3.9187523	4.028586	7.95E-05	0.0002536	0.657908	HORMAD1	HORMA domain containing 1	AL136755
218695_at	0.74902	8.6258165	11.89206	4.73E-25	5.01E-23	46.25726	EXOSC4	exosome component 4	NM_019037
238578_at	0.74867	4.7725114	11.10259	1.18E-22	7.85E-21	40.80718	TMEM182	transmembrane protein 182	BF574691
220789_s_at	0.74855	8.501085	12.27129	3.26E-26	4.27E-24	48.8985	TBRG4	transforming growth factor beta regulator 4	NM_004749
204608_at	0.74839	9.3846209	7.041349	2.94E-11	2.74E-10	14.98346	ASL	argininosuccinate lyase	NM_000048
201193_at	0.74832	11.748863	8.669726	1.43E-15	2.74E-14	24.72741	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	NM_005896
228977_at	0.74827	7.7139316	5.818759	2.30E-08	1.33E-07	8.485344	LOC729680	hypothetical protein LOC729680	AI669535
215071_s_at	0.74816	9.3095838	6.289983	1.94E-09	1.34E-08	10.89282	HIST1H2AC	histone cluster 1, H2ac	AL353759
211810_s_at	0.74806	6.0077945	7.390778	3.82E-12	4.14E-11	16.98109	GALC	galactosylceramidase	D25284
223156_at	0.74801	9.624824	10.82095	8.29E-22	4.67E-20	38.88307	MRPS23	mitochondrial ribosomal protein S23	BC000242
1553535_a_at	0.74755	7.7517077	13.68647	1.40E-30	5.42E-28	58.83166	RANGAP1	Ran GTPase activating protein 1	NM_002883
218867_s_at	0.74692	7.557148	11.00105	2.39E-22	1.48E-20	40.11207	C12orf49	chromosome 12 open reading frame 49	NM_024738
225468_at	0.74673	7.2789672	8.950683	2.35E-16	5.15E-15	26.50759	PATL1	protein associated with topoisomerase II homolog 1 (yeast)	AI761804
219439_at	0.74671	8.4902951	7.33666	5.26E-12	5.55E-11	16.66803	C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	NM_020156
225047_at	0.74663	5.7266415	10.28725	3.22E-20	1.37E-18	35.27345	NUPL1	nucleoporin like 1	AF113020
228505_s_at	0.74645	6.1990248	10.39189	1.58E-20	7.03E-19	35.977	TMEM170A	transmembrane protein 170A	N49836
222443_s_at	0.74606	9.4801867	13.34615	1.58E-29	4.55E-27	56.4361	RBM8A	RNA binding motif protein 8A	AF182415
216593_s_at	0.74603	7.8069124	9.44537	9.18E-18	2.57E-16	29.6991	PIGC	phosphatidylinositol glycan anchor biosynthesis, class C	AB000359
213424_at	0.74591	5.8383157	5.814064	2.36E-08	1.36E-07	8.462019	KIAA0895	KIAA0895	AB020702
226611_s_at	0.74589	8.8277665	5.917693	1.38E-08	8.32E-08	8.979989	CENPV	centromere protein V	AA722878
211935_at	0.74576	11.458178	9.487594	6.94E-18	1.98E-16	29.97463	ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	D31885
226777_at	0.74562	5.5450483	3.839984	0.0001647	0.0004947	-0.02992	0	0	AA147933
226064_s_at	0.74546	7.2209073	5.804847	2.47E-08	1.42E-07	8.416264	DGAT2	diacylglycerol O-acyltransferase homolog 2 (mouse)	AW469523
219858_s_at	0.74534	6.8109579	7.540114	1.57E-12	1.81E-11	17.85172	MFSD6	major facilitator superfamily domain containing 6	NM_017694
203283_s_at	0.74531	7.5508381	9.131944	7.21E-17	1.73E-15	27.66892	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	AK023260
211015_s_at	0.74527	8.8343662	10.89516	4.97E-22	2.91E-20	39.38889	HSPA4	heat shock 70kDa protein 4	L12723
235136_at	0.74511	6.5809895	7.425541	3.11E-12	3.42E-11	17.18288	ORMDL3	ORM1-like 3 (S. cerevisiae)	BF337528
205401_at	0.74504	7.6466564	9.590085	3.52E-18	1.06E-16	30.64534	AGPS	alkylglycerone phosphate synthase	NM_003659
223172_s_at	0.74449	7.7858001	9.076562	1.04E-16	2.42E-15	27.31306	MTP18	mitochondrial protein 18 kDa	AF060924
203015_s_at	0.74486	5.9403542	8.823865	5.33E-16	1.10E-14	25.70097	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	AW136988
229801_at	0.74452	7.6699832	6.85044	8.75E-11	7.52E-10	13.91663	C10orf47	chromosome 10 open reading frame 47	AI640157
203626_s_at	0.74413	5.3623939	9.822418	7.44E-19	2.52E-17	32.17538	SKP2	S-phase kinase-associated protein 2 (p45)	NM_005983
204932_at	0.74404	4.9163799	3.725937	0.0002527	0.0007311	-0.43203	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b	BF433902
202275_at	0.74372	7.4888511	9.831507	7.00E-19	2.39E-17	32.2355	G6PD	glucose-6-phosphate dehydrogenase	NM_000402
230563_at	0.74364	6.6437624	3.987137	9.35E-05	0.0002942	0.50433	RASGEF1A	RasGEF domain family, member 1A	BF446578
203612_at	0.7435	7.8841096	11.17093	7.34E-23	5.05E-21	41.27582	BYSL	bystin-like	NM_004053
204740_at	0.74349	7.0654751	9.305712	2.31E-17	6.06E-16	28.79114	CNKSR1	connector enhancer of kinase suppressor of Ras 1	NM_006314
226355_at	0.74348	6.4945255	9.797284	8.81E-19	2.94E-17	32.00924	WDR51A	WD repeat domain 51A	AW001089
226952_at	0.74327	7.5711205	9.610673	3.07E-18	9.33E-17	30.78039	EAF1	ELL associated factor 1	AU149385
223874_at	0.7432	6.0193835	7.023445	3.26E-11	3.01E-10	14.88265	ARP11	actin-related Arp11	AB039791
225836_s_at	0.74319	6.5287928	9.230251	3.79E-17	9.54E-16	28.30276	C12orf32	chromosome 12 open reading frame 32	AL528840
227786_at	0.74289	7.7054726	9.581943	3.71E-18	1.11E-16	30.59196	MED30	mediator complex subunit 30	AI026938
238755_at	0.74277	5.7844001	4.020062	8.22E-05	0.0002615	0.626215	0	0	AA876179
218035_s_at	0.74236	10.329888	5.082871	8.47E-07	3.83E-06	4.99913	RBM47	RNA binding motif protein 47	NM_019027

209448_at	0.74231	9.8438106	7.289071	6.95E-12	7.18E-11	16.39383	HTATIP2	HIV-1/Tat interactive protein 2, 30kDa	BC002439
213427_at	0.74217	7.9231181	8.457492	5.53E-15	9.63E-14	23.39974	RPP40	ribonuclease P/MRP 40kDa subunit	NM_006638
219177_at	0.74213	7.7501676	9.648309	2.39E-18	7.38E-17	31.02754	BXDC2	brix domain containing 2	NM_018321
216591_s_at	0.74213	9.1853835	9.910791	4.11E-19	1.46E-17	32.76073	hCG_17769	hCG1776980 /// succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	AF080579
229061_s_at	0.74144	6.6558389	8.298531	1.50E-14	2.41E-13	22.4155	SLC25A13	solute carrier family 25, member 13 (citrin)	AW268880
211804_s_at	0.74117	6.7907376	10.92111	4.15E-22	2.46E-20	39.56593	CDK2	cyclin-dependent kinase 2	AB012305
215093_at	0.74092	7.2952021	9.695043	1.75E-18	5.52E-17	31.33492	NSDHL	NAD(P)-dependent steroid dehydrogenase-like	U82671
221781_s_at	0.74045	7.990017	8.448243	5.86E-15	1.01E-13	23.34223	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	BG168666
219219_at	0.73996	7.7342741	12.29579	2.74E-26	3.66E-24	49.06958	TMEM160	transmembrane protein 160	NM_017854
209369_at	0.73994	9.6236874	4.224124	3.63E-05	0.0001233	1.400504	ANXA3	annexin A3	M63310
205483_s_at	0.73982	10.060656	5.992984	9.36E-09	5.78E-08	9.360338	ISG15	ISG15 ubiquitin-like modifier	NM_005101
225750_at	0.73969	9.7457641	8.243243	2.13E-14	3.31E-13	22.0753	0	0	BE966748
211681_s_at	0.73953	6.491396	7.671756	7.12E-13	8.63E-12	18.62721	PDLIM5	PDZ and LIM domain 5	AF116705
208691_at	0.73932	11.687382	8.53783	3.32E-15	6.02E-14	23.90052	TFRC	transferrin receptor (p90, CD71)	BC001188
212898_at	0.7393	7.4365755	9.903112	4.33E-19	1.53E-17	32.70979	KIAA0406	KIAA0406	AB007866
212321_at	0.73929	7.7815626	10.1333	9.15E-20	3.59E-18	34.24222	SGPL1	sphingosine-1-phosphate lyase 1	AB033078
229526_at	0.73917	6.05208	6.941511	5.21E-11	4.66E-10	14.42331	AQP11	aquaporin 11	AI886656
206445_s_at	0.73913	10.462228	12.58069	3.65E-27	5.93E-25	51.06179	PRMT1	protein arginine methyltransferase 1	NM_001536
218119_at	0.73886	8.8170746	10.48767	8.19E-21	3.81E-19	36.62285	TIMM23 ///	translocase of inner mitochondrial membrane 23 homolog (yeast) /// translocase of inner mitochondrial membrane 23 homolog B (yeast)	NM_006327
208084_at	0.7388	5.7103921	5.843847	2.03E-08	1.19E-07	8.610218	ITG86	integrin, beta 6	NM_000888
242458_at	0.73867	4.9947997	9.099356	8.92E-17	2.12E-15	27.45941	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	AA721230
239647_at	0.73862	4.9834911	6.129117	4.58E-09	2.98E-08	10.05648	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13	AA677272
221750_at	0.73848	7.8495583	6.587569	3.82E-10	2.96E-09	12.47769	HMGCS1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	BG035985
204238_s_at	0.73807	8.9741482	8.466239	5.23E-15	9.18E-14	23.45415	C6orf108	chromosome 6 open reading frame 108	NM_006443
201853_s_at	0.73798	9.2721775	7.85853	2.29E-13	3.03E-12	19.73989	CDC25B	cell division cycle 25 homolog B (S. pombe)	NM_021873
207813_s_at	0.73793	6.4798542	8.315574	1.35E-14	2.18E-13	22.5206	FDXR	ferredoxin reductase	NM_004110
202638_s_at	0.73785	7.5917665	5.299289	3.04E-07	1.48E-06	5.987881	ICAM1	intercellular adhesion molecule 1	NM_000201
211754_s_at	0.7377	7.5182877	9.937611	3.43E-19	1.24E-17	32.93873	SLC25A17	solute carrier family 25 (mitochondrial carrier; peroxisomal membrane protein, 34kDa), member 17	BC005957
209799_at	0.73749	6.8663375	8.970764	2.06E-16	4.58E-15	26.63577	PRKAA1	protein kinase, AMP-activated, alpha 1 catalytic subunit	AF100763
204330_s_at	0.73737	5.0559924	11.34713	2.15E-23	1.64E-21	42.48716	MRPS12	mitochondrial ribosomal protein S12	AA587905
204973_at	0.73734	7.9254197	5.957047	1.13E-08	6.89E-08	9.178375	GJB1	gap junction protein, beta 1, 32kDa	NM_000166
214681_at	0.73701	6.8180138	7.04969	2.80E-11	2.62E-10	15.03048	GK	glycerol kinase	AI830490
201456_s_at	0.73699	8.9454964	10.68159	2.17E-21	1.12E-19	37.93561	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	AU160695
210005_at	0.73697	6.5332356	9.084353	9.84E-17	2.31E-15	27.36307	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	D32051
226446_at	0.73632	7.6380175	4.864952	2.30E-06	9.67E-06	4.035798	HES6	hairy and enhancer of split 6 (Drosophila)	AW249678

207668_x_at	0.73623	11.114146	12.4758	7.67E-27	1.15E-24	50.3277	PDIA6	protein disulfide isomerase family A, member 6	NM_005742
1569454_a_at	0.7362	3.8569185	4.098959	6.02E-05	0.0001964	0.921742	LOC283352	hypothetical protein LOC283352	BG475827
210293_s_at	0.7362	9.4832434	9.901427	4.38E-19	1.55E-17	32.69862	SEC23B	Sec23 homolog B (S. cerevisiae)	BC005032
1563111_a_at	0.73618	7.4738935	7.814618	3.00E-13	3.88E-12	19.47701	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	AK000529
216685_s_at	0.73617	6.0870228	8.207482	2.66E-14	4.08E-13	21.85584	MTAP	methylthioadenosine phosphorylase	AF216650
1555639_a_at	0.736	5.5141994	10.22081	5.05E-20	2.08E-18	34.82779	RBM14	RNA binding motif protein 14	AF315633
235651_at	0.73578	7.8533826	4.133492	5.24E-05	0.000173	1.052625	0	0	AV741130
225519_at	0.73575	9.637414	11.9659	2.81E-25	3.10E-23	46.77049	PPP4R2	protein phosphatase 4, regulatory subunit 2	AA206408
214214_s_at	0.73556	10.451266	11.08041	1.38E-22	9.01E-21	40.65524	C1QBP	complement component 1, q subcomponent binding protein	AU151801
217445_s_at	0.73556	4.9304558	9.33775	1.87E-17	4.98E-16	28.99897	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	AF008655
1558045_a_at	0.73528	5.1568082	9.066243	1.11E-16	2.57E-15	27.24685	LOC441528	hypothetical protein LOC441528	BC017239
226914_at	0.73504	8.0284801	11.24552	4.37E-23	3.13E-21	41.78809	ARPC5L	actin related protein 2/3 complex, subunit 5-like	AU158936
216488_s_at	0.73476	6.4788187	12.58545	3.53E-27	5.77E-25	51.09512	ATP11A	ATPase, class VI, type 11A	AL161996
231270_at	0.73472	7.8893435	4.303123	2.63E-05	9.15E-05	1.708876	CA13	carbonic anhydrase XIII	BF111998
1554417_s_at	0.7347	7.9659694	10.68475	2.12E-21	1.10E-19	37.95707	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	AY113699
209585_s_at	0.73459	7.7656443	8.100501	5.17E-14	7.55E-13	21.20218	MINPP1	multiple inositol polyphosphate histidine phosphatase, 1	AF084943
209720_s_at	0.73455	3.4818558	4.585262	7.95E-06	3.04E-05	2.848536	SERPINB3	serpin peptidase inhibitor, clade B (ovalbumin), member 3	BC005224
222697_s_at	0.73454	7.6039515	9.333026	1.93E-17	5.13E-16	28.96831	ABHD10	abhydrolase domain containing 10	AI521709
231914_at	0.73442	7.3447379	8.791209	6.57E-16	1.34E-14	25.49408	NUDT14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	W24623
229208_at	0.73435	5.9355466	12.05314	1.52E-25	1.75E-23	47.37762	CEP27	centrosomal protein 27kDa	AK022939
202886_s_at	0.73429	6.9079582	7.80291	3.22E-13	4.15E-12	19.40705	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	M65254
207169_x_at	0.73428	9.3799453	6.475829	7.06E-10	5.25E-09	11.87697	DDR1	discoidin domain receptor tyrosine kinase 1	NM_001954
214264_s_at	0.73414	7.2344365	8.861953	4.17E-16	8.76E-15	25.9427	C14orf143	chromosome 14 open reading frame 143	AI656610
202433_at	0.73411	9.0906274	9.276483	2.80E-17	7.24E-16	28.60179	SLC35B1	solute carrier family 35, member B1	NM_005827
244567_at	0.73403	3.526984	4.635983	6.38E-06	2.48E-05	3.059658	0	0	BG165613
210519_s_at	0.73396	10.613294	3.880885	0.000141	0.0004288	0.116845	NQO1	NAD(P)H dehydrogenase, quinone 1	BC000906
242013_at	0.73389	6.6039561	4.119081	5.55E-05	0.0001824	0.997894	BCL2L15	BCL2-like 15	BF445012
220083_x_at	0.73355	6.2359535	11.12811	9.88E-23	6.67E-21	40.98208	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	NM_016017
223054_at	0.73342	9.9855406	11.99072	2.36E-25	2.63E-23	46.94318	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	BC001144
209052_s_at	0.73337	5.7873657	11.67026	2.25E-24	2.09E-22	44.71869	WHSC1	Wolf-Hirschhorn syndrome candidate 1	BF111870
218027_at	0.73336	10.189834	10.76173	1.25E-21	6.84E-20	38.48005	MRPL15	mitochondrial ribosomal protein L15	NM_014175
220603_s_at	0.73321	6.2213136	8.302386	1.47E-14	2.36E-13	22.43926	MCTP2	multiple C2 domains, transmembrane 2	NM_018349
222572_at	0.73301	9.459936	8.124621	4.45E-14	6.58E-13	21.34918	PPM2C	protein phosphatase 2C, magnesium-dependent, catalytic subunit	BG542521
235707_at	0.73294	4.7328752	10.99469	2.49E-22	1.54E-20	40.0686	LOC221710	hypothetical protein LOC221710	AW994270

214359_s_at	0.7329	11.143583	10.6254	3.19E-21	1.59E-19	37.55455	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	AI218219
211016_x_at	0.73279	7.3426771	9.392814	1.30E-17	3.55E-16	29.3568	HSPA4	heat shock 70kDa protein 4	BC002526
219404_at	0.73277	8.2355869	4.434509	1.52E-05	5.51E-05	2.232202	EPS8L3	EPS8-like 3	NM_024526
201327_s_at	0.73268	10.479091	13.15883	6.00E-29	1.45E-26	55.11875	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	NM_001762
205137_x_at	0.73259	7.9902265	4.639497	6.28E-06	2.45E-05	3.074353	USH1C	Usher syndrome 1C (autosomal recessive, severe)	NM_005709
1555281_x_at	0.73247	6.0204367	8.780311	7.05E-16	1.42E-14	25.42511	ARMC8	armadillo repeat containing 8	BC007934
224956_at	0.73235	8.4108528	10.73349	1.51E-21	8.14E-20	38.28807	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	AI743689
226520_at	0.73217	8.6033962	8.156124	3.66E-14	5.50E-13	21.5415	0	0	AI831506
205924_at	0.7319	5.6357176	6.926933	5.66E-11	5.03E-10	14.34193	RAB3B	RAB3B, member RAS oncogene family	BC005035
242517_at	0.73173	4.8091395	5.153388	6.08E-07	2.81E-06	5.317841	KISS1R	KISS1 receptor	AI819198
204956_at	0.73149	4.8250084	7.773709	3.84E-13	4.88E-12	19.23281	MTAP	methylthioadenosine phosphorylase	NM_002451
205129_at	0.73144	7.2113977	9.357627	1.64E-17	4.41E-16	29.12805	NPM3	nucleophosmin/nucleoplasmin, 3	NM_006993
225253_s_at	0.73132	9.2552799	11.17983	6.90E-23	4.76E-21	41.3369	METTL2A	methyltransferase like 2A /// methyltransferase like 2B	AI632244
236193_at	0.73111	5.7526919	5.779479	2.82E-08	1.61E-07	8.290594	HIST1H2BC	histone cluster 1, H2bc	AA037483
226403_at	0.73075	8.6335049	4.72071	4.39E-06	1.76E-05	3.416489	TMC4	transmembrane channel-like 4	BE645551
217968_at	0.7304	8.0350973	13.04343	1.36E-28	3.09E-26	54.30776	TSSC1	tumor suppressing subtransferable candidate 1	NM_003310
207239_s_at	0.73028	6.8864272	10.75508	1.31E-21	7.14E-20	38.43488	PCTK1	PCTAIRE protein kinase 1	NM_006201
1568617_a_at	0.73021	6.3583976	6.394766	1.10E-09	7.88E-09	11.44537	KIAA1543	KIAA1543	BC020431
201275_at	0.73019	9.6191167	11.51439	6.69E-24	5.70E-22	43.64071	FDPS	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)	NM_002004
213435_at	0.73018	6.0251	5.548612	8.99E-08	4.74E-07	7.165217	SATB2	SATB homeobox 2	AB028957
208698_s_at	0.73009	9.475268	10.26307	3.79E-20	1.61E-18	35.11117	NONO	non-POU domain containing, octamer-binding	L14599
1555906_s_at	0.73	8.3622849	8.871416	3.92E-16	8.28E-15	26.00283	C3orf23	chromosome 3 open reading frame 23	AI147556
202737_s_at	0.72998	9.6480413	11.05282	1.67E-22	1.07E-20	40.46627	LSM4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	NM_012321
227220_at	0.72989	7.5674756	9.876628	5.17E-19	1.81E-17	32.53423	NFXL1	nuclear transcription factor, X-box binding-like 1	AI743731
206919_at	0.72969	4.3378368	8.28166	1.67E-14	2.66E-13	22.31157	ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	NM_021795
230021_at	0.72959	5.6662536	12.05845	1.46E-25	1.69E-23	47.41455	C15orf42	chromosome 15 open reading frame 42	AI638593
205264_at	0.72954	7.4063639	10.26098	3.85E-20	1.63E-18	35.09714	CD3EAP	CD3e molecule, epsilon associated protein	NM_012099
218557_at	0.72939	9.2291845	10.98032	2.75E-22	1.69E-20	39.97033	NIT2	nitrilase family, member 2	NM_020202
208310_s_at	0.72931	9.3211089	10.62255	3.25E-21	1.62E-19	37.53526	C7orf28A	chromosome 7 open reading frame 28A /// chromosome 7 open reading frame 28B	NM_007085
214173_x_at	0.72906	9.5727751	7.469777	2.39E-12	2.68E-11	17.44044	C19orf2	chromosome 19 open reading frame 2	AW514900
207549_x_at	0.72894	9.0053504	9.136369	7.01E-17	1.68E-15	27.69739	CD46	CD46 molecule, complement regulatory protein	NM_002389
224247_s_at	0.72884	8.6957206	8.763411	7.86E-16	1.57E-14	25.31823	MRPS10	mitochondrial ribosomal protein S10	AF277180
224447_s_at	0.72882	10.078058	6.42961	9.09E-10	6.62E-09	11.63045	C17orf37	chromosome 17 open reading frame 37	BC006006
227935_s_at	0.7288	7.3972766	8.322936	1.29E-14	2.09E-13	22.56602	PCGF5	polycomb group ring finger 5	AA522681
209885_at	0.72878	7.3306847	6.16035	3.88E-09	2.55E-08	10.21772	RHOD	ras homolog gene family, member D	BC001338
238065_at	0.7285	5.6819256	10.47441	8.97E-21	4.14E-19	36.53338	TPM3	tropomyosin 3	BG337831
217983_s_at	0.7285	11.031572	7.642466	8.50E-13	1.02E-11	18.45402	RNASET2	ribonuclease T2	NM_003730
200825_s_at	0.72846	9.7936734	10.57837	4.40E-21	2.14E-19	37.23604	HYOU1	hypoxia up-regulated 1	NM_006389
225470_at	0.72839	8.6976352	10.88074	5.49E-22	3.18E-20	39.29053	NUP35	nucleoporin 35kDa	AL529634
224392_s_at	0.72832	6.1857594	6.823532	1.02E-10	8.65E-10	13.76772	OPN3	opsin 3	AF303588
1552696_at	0.72821	4.7091591	10.95292	3.33E-22	2.01E-20	39.78313	NIPA1	non imprinted in Prader-Willi/Angelman syndrome 1	NM_144599
238686_at	0.728	6.9644267	8.237683	2.20E-14	3.42E-13	22.04115	FBXO3	F-box protein 3	AA130258

226649_at	0.72792	7.5534487	5.959865	1.11E-08	6.79E-08	9.192615	PANK1	pantothenate kinase 1	AI373299
206533_at	0.72785	4.8326946	7.999462	9.65E-14	1.35E-12	20.5888	CHRNA5	cholinergic receptor, nicotinic, alpha 5	NM_000745
224416_s_at	0.72776	6.9240247	9.297656	2.43E-17	6.37E-16	28.73893	MED28	mediator complex subunit 28	AF358829
235037_at	0.72771	8.4209771	11.2268	4.98E-23	3.52E-21	41.65949	TMEM41A	transmembrane protein 41A	AA371513
225088_at	0.72758	6.3747595	8.408151	7.55E-15	1.28E-13	23.09328	C16orf63	chromosome 16 open reading frame 63	BG546917
218343_s_at	0.72751	8.0790147	11.0093	2.25E-22	1.41E-20	40.1685	GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	NM_012086
238562_at	0.72738	4.489924	8.491822	4.45E-15	7.92E-14	23.61346	0	0	BE542779
219099_at	0.72716	8.3857423	9.144292	6.65E-17	1.60E-15	27.74838	C12orf5	chromosome 12 open reading frame 5	NM_020375
201504_s_at	0.72677	8.2249954	10.17803	6.76E-20	2.72E-18	34.54134	TSN	translin	AI435302
233337_s_at	0.72675	7.6859164	5.235885	4.11E-07	1.96E-06	5.694958	LOC652900	similar to seizure related 6 homolog (mouse)-like 2 isoform 1 /// seizure related 6 homolog (mouse)-like 2	AF131749
205555_s_at	0.72668	6.0810775	7.638062	8.73E-13	1.04E-11	18.42802	MSX2	msh homeobox 2	D31771
217871_s_at	0.72666	12.347625	11.19205	6.34E-23	4.40E-21	41.42079	LOC284889	hypothetical protein LOC284889 /// macrophage migration inhibitory factor (glycosylation-inhibiting factor)	NM_002415
1554321_a at	0.72631	6.3952577	10.51276	6.90E-21	3.24E-19	36.79235	NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	BC018471
206653_at	0.72623	5.218133	7.352955	4.77E-12	5.08E-11	16.76216	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	BF062139
204624_at	0.72616	6.9231745	4.814218	2.90E-06	1.20E-05	3.816284	ATP7B	ATPase, Cu++ transporting, beta polypeptide	NM_000053
210253_at	0.72606	6.5619546	6.89122	6.94E-11	6.08E-10	14.14301	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	AF092095
215780_s_at	0.72602	10.061518	7.697117	6.11E-13	7.49E-12	18.77744	hCG_16446	SET translocation (myeloid leukemia-associated) pseudogene /// SET nuclear oncogene	Z95126
244563_at	0.72599	5.5398862	8.492301	4.43E-15	7.90E-14	23.61644	QSER1	glutamine and serine rich 1	BG026723
203608_at	0.72581	7.7884042	4.854616	2.41E-06	1.01E-05	3.990931	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	AL031230
205449_at	0.72576	8.2486556	9.209535	4.34E-17	1.08E-15	28.16896	SAC3D1	SAC3 domain containing 1	NM_013299
204459_at	0.72566	7.9087676	10.98183	2.73E-22	1.67E-20	39.9807	CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	NM_001325
230294_at	0.72562	6.169298	9.190953	4.90E-17	1.21E-15	28.04905	0	0	AV714462
218647_s_at	0.72548	8.734844	11.02816	1.98E-22	1.25E-20	40.29753	YRDC	yrnC domain containing (E. coli)	NM_024640
208623_s_at	0.72547	10.788679	6.285483	1.99E-09	1.37E-08	10.86922	EZR	ezrin	J05021
201201_at	0.72534	12.12376	9.688793	1.82E-18	5.74E-17	31.29379	CSTB	cystatin B (stefin B)	NM_000100
222765_x_at	0.72507	6.8482405	7.534918	1.62E-12	1.87E-11	17.82127	ESF1	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	AL161659
218842_at	0.72402	8.0778241	9.7086	1.59E-18	5.07E-17	31.4242	RPAP3	RNA polymerase II associated protein 3	NM_024604
215150_at	0.72391	4.8302158	8.491581	4.45E-15	7.93E-14	23.61196	YOD1	YOD1 OTU deubiquitinating enzyme 1 homolog (S. cerevisiae)	AF090896
205519_at	0.7238	5.3128756	10.58835	4.11E-21	2.01E-19	37.30362	WDR76	WD repeat domain 76	NM_024908
201971_s_at	0.72367	7.9045701	8.553646	3.00E-15	5.48E-14	23.99936	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	NM_001690
57703_at	0.72312	5.6973208	11.24739	4.31E-23	3.10E-21	41.80095	SENPS	SUMO1/sentrin specific peptidase 5	N32782
204109_s_at	0.72262	6.0787555	10.00842	2.13E-19	7.94E-18	33.40945	NFYA	nuclear transcription factor Y, alpha	NM_002505
216266_s_at	0.72259	7.9136397	8.624281	1.91E-15	3.60E-14	24.44185	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	AK025637
238010_at	0.72254	6.262155	8.503542	4.13E-15	7.37E-14	23.68651	C1orf174	chromosome 1 open reading frame 174	BF970340
202089_s_at	0.7223	8.3463382	6.982424	4.12E-11	3.75E-10	14.65227	SLC39A6	solute carrier family 39 (zinc transporter), member 6	NM_012319
224509_s_at	0.72195	7.0838802	9.500254	6.38E-18	1.84E-16	30.05733	RTN4IP1	reticulon 4 interacting protein 1	BC006399
205763_s_at	0.72195	8.3555937	10.36592	1.88E-20	8.30E-19	35.80222	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	NM_006773

1563646_a_at	0.72176	5.6262226	9.284331	2.66E-17	6.91E-16	28.65261	TMEM67	transmembrane protein 67	AK092244
238821_at	0.72172	6.0345325	9.919046	3.89E-19	1.39E-17	32.8155	CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	AI826277
228654_at	0.7213	7.7928954	5.466371	1.35E-07	6.91E-07	6.772428	SPIN4	spindlin family, member 4	AU145277
220161_s_at	0.72122	9.2725515	4.158879	4.73E-05	0.0001574	1.14943	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	NM_019114
1553338_at	0.72107	5.8947542	9.135895	7.03E-17	1.69E-15	27.69434	C1orf55	chromosome 1 open reading frame 55	NM_152608
218595_s_at	0.72099	8.7226736	10.56793	4.73E-21	2.27E-19	37.16537	HEATR1	HEAT repeat containing 1	NM_018072
228124_at	0.7207	8.1701466	8.070459	6.23E-14	8.97E-13	21.01939	ABHD12	abhydrolase domain containing 12	AW303865
201943_s_at	0.72067	8.6032193	6.438585	8.66E-10	6.33E-09	11.67823	CPD	carboxypeptidase D	NM_001304
230782_at	0.72061	5.5758249	6.169233	3.70E-09	2.44E-08	10.26367	SORD	sorbitol dehydrogenase	AV699883
204113_at	0.72042	6.1253063	9.82405	7.36E-19	2.50E-17	32.18618	CUGBP1	CUG triplet repeat, RNA binding protein 1	NM_006560
229927_at	0.7203	4.5409828	4.527196	1.02E-05	3.83E-05	2.609153	LEMD1	LEM domain containing 1	BE222220
214193_s_at	0.72011	7.1019686	8.801243	6.16E-16	1.26E-14	25.55762	C1orf107	chromosome 1 open reading frame 107	AI770084
225904_at	0.72006	7.6168086	8.837616	4.87E-16	1.02E-14	25.78819	C1orf96	chromosome 1 open reading frame 96	N64686
201323_at	0.72004	8.9619304	11.47716	8.68E-24	7.17E-22	43.38363	EBNA1BP2	EBNA1 binding protein 2	NM_006824
218111_s_at	0.72002	7.4062481	7.798631	3.30E-13	4.25E-12	19.38149	CMAS	cytidine monophosphate N-acetylneuraminic acid synthetase	NM_018686
223158_s_at	0.72	8.64281	9.066729	1.10E-16	2.57E-15	27.24997	NEK6	NIMA (never in mitosis gene a)-related kinase 6	BE616825
222507_s_at	0.71997	8.5158453	8.142392	3.99E-14	5.97E-13	21.45763	TMEM9B	TMEM9 domain family, member B	AI188389
205240_at	0.7199	7.5656261	7.847559	2.45E-13	3.22E-12	19.67414	GPSM2	G-protein signaling modulator 2 (AGS3-like, C. elegans)	NM_013296
208651_x_at	0.71975	10.718382	3.803822	0.0001889	0.0005606	-0.15855	CD24	CD24 molecule	M58664
208424_s_at	0.71957	7.9553073	11.90665	4.27E-25	4.55E-23	46.3586	CIAPIN1	cytokine induced apoptosis inhibitor 1	NM_020313
201400_at	0.71948	11.533816	12.39349	1.37E-26	1.95E-24	49.75215	PSMB3	proteasome (prosome, macropain) subunit, beta type, 3	NM_002795
204107_at	0.71942	6.4589164	12.40214	1.29E-26	1.85E-24	49.81258	NFYA	nuclear transcription factor Y, alpha	BF445142
225158_at	0.71926	8.7548033	9.757327	1.15E-18	3.78E-17	31.74541	GFM1	G elongation factor, mitochondrial 1	BF978647
226609_at	0.71915	8.0002585	8.422113	6.91E-15	1.17E-13	23.17991	DCBLD1	discoidin, CUB and LCCL domain containing 1	N22751
208337_s_at	0.71906	4.6261924	6.94607	5.07E-11	4.55E-10	14.44879	NR5A2	nuclear receptor subfamily 5, group A, member 2	NM_003822
239697_x_at	0.7189	3.9181844	6.293965	1.90E-09	1.31E-08	10.91371	C3orf67	chromosome 3 open reading frame 67	AA521262
226060_at	0.71876	7.3610326	13.00879	1.74E-28	3.80E-26	54.06441	RFT1	RFT1 homolog (S. cerevisiae)	BF475369
229845_at	0.71874	6.434646	9.951563	3.12E-19	1.14E-17	33.03138	MAPKAP1	mitogen-activated protein kinase associated protein 1	BF939919
201169_s_at	0.71873	7.233312	6.444215	8.40E-10	6.15E-09	11.70823	BHLHE40	basic helix-loop-helix family, member e40	BG326045
214130_s_at	0.71861	6.2696905	6.98689	4.02E-11	3.66E-10	14.67732	PDE4DIP	phosphodiesterase 4D interacting protein	AI821791
227474_at	0.71853	6.7246854	4.438757	1.49E-05	5.42E-05	2.249341	LOC654433	CDNA clone IMAGE:4826696	AY007128
202613_at	0.71845	7.5757117	9.232689	3.73E-17	9.41E-16	28.31852	CTPS	CTP synthase	NM_001905
228378_at	0.71833	7.1264779	8.084402	5.71E-14	8.27E-13	21.10418	C12orf29	chromosome 12 open reading frame 29	BF439204
203407_at	0.71799	7.9073749	5.07654	8.72E-07	3.94E-06	4.970683	PPL	periplakin	NM_002705
209545_s_at	0.71795	8.8602174	9.088457	9.58E-17	2.26E-15	27.38942	RIPK2	receptor-interacting serine-threonine kinase 2	AF064824
209146_at	0.71787	9.7409897	6.173582	3.61E-09	2.39E-08	10.28619	SC4MOL	sterol-C4-methyl oxidase-like	AV704962
220172_at	0.71706	4.9214368	9.93885	3.40E-19	1.23E-17	32.94695	C2orf37	chromosome 2 open reading frame 37	NM_025000
219465_at	0.71691	4.1748287	3.752593	0.0002288	0.0006683	-0.33899	APOA2	apolipoprotein A-II	NM_001643
205598_at	0.71676	5.3598479	12.6177	2.81E-27	4.67E-25	51.32096	TRAIP	TRAF interacting protein	NM_005879
216574_s_at	0.71672	6.0050368	11.2157	5.38E-23	3.78E-21	41.58325	hCG_20244	rcRPE /// ribulose-5-phosphate-3-epimerase	JO4742
230093_at	0.71668	6.5251862	5.611183	6.59E-08	3.54E-07	7.466935	RSPH1	radial spoke head 1 homolog (Chlamydomonas)	AI683428
1554433_a_at	0.71667	7.5597593	8.703644	1.15E-15	2.24E-14	24.94099	ZNF146	zinc finger protein 146	BC005154
225736_at	0.71624	7.5921805	12.34202	1.98E-26	2.73E-24	49.39243	FBXO22	F-box protein 22	BE966247
39402_at	0.71611	8.0723339	3.813083	0.0001824	0.0005429	-0.12571	IL1B	interleukin 1, beta	M15330

218281_at	0.71577	8.9575639	10.95322	3.32E-22	2.01E-20	39.78523	MRPL48	mitochondrial ribosomal protein L48	NM_016055
200837_at	0.71576	10.296421	11.67049	2.24E-24	2.09E-22	44.72033	BCAP31	B-cell receptor-associated protein 31	NM_005745
213320_at	0.71572	7.9333327	9.25334	3.26E-17	8.29E-16	28.45203	PRMT3	protein arginine methyltransferase 3	AL551971
1557448_a_at	0.71552	4.48439	7.534243	1.63E-12	1.87E-11	17.81731	0	0	AI393041
1554466_a_at	0.71544	8.1807885	11.05544	1.64E-22	1.05E-20	40.48424	C16orf13	chromosome 16 open reading frame 13	BC007207
209927_s_at	0.71538	7.1636494	13.1258	7.59E-29	1.79E-26	54.88651	C1orf77	chromosome 1 open reading frame 77	AF261137
227828_s_at	0.71529	5.4867057	6.091177	5.59E-09	3.59E-08	9.861388	FAM176A	family with sequence similarity 176, member A	AV700753
225833_at	0.71505	5.8776862	11.53558	5.77E-24	4.95E-22	43.78713	DAGLB	diacylglycerol lipase, beta	BE795104
200820_at	0.71504	10.162524	11.44961	1.05E-23	8.54E-22	43.19354	PSMD8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	NM_002812
205778_at	0.71503	6.2047681	3.908303	0.0001269	0.0003894	0.215977	KLK7	kallikrein-related peptidase 7	NM_005046
1559190_s_at	0.71495	6.3470422	6.848734	8.83E-11	7.59E-10	13.90718	RDH13	CDNA PSEC0082 fis, clone NT2RP2004966, highly similar to Retinol dehydrogenase 13 (EC 1.1.1.1-)	AL833150
206307_s_at	0.71434	6.102638	4.242705	3.37E-05	0.000115	1.472604	FOXD1	forkhead box D1	NM_004472
203405_at	0.71434	9.1265647	8.763454	7.86E-16	1.57E-14	25.3185	PSMG1	proteasome (prosome, macropain) assembly chaperone 1	NM_003720
224762_at	0.71423	8.0519823	5.17864	5.40E-07	2.52E-06	5.43279	KIAA0746	KIAA0746 protein /// serine incorporator 2	AA872583
214590_s_at	0.71404	6.3404678	7.066552	2.54E-11	2.39E-10	15.12563	UBE2D1	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	AL545760
201115_at	0.714	8.7577027	13.08399	1.02E-28	2.35E-26	54.59269	POLD2	polymerase (DNA directed), delta 2, regulatory subunit 50kDa	NM_006230
236451_at	0.71371	3.9801573	7.347335	4.94E-12	5.24E-11	16.72968	0	0	AA825510
204186_s_at	0.71369	8.3020656	8.321033	1.31E-14	2.12E-13	22.55428	PPID	peptidylprolyl isomerase D	AI014573
219558_at	0.71355	7.618871	10.79777	9.73E-22	5.39E-20	38.72523	ATP13A3	ATPase type 13A3	NM_024524
208955_at	0.7132	7.2059738	8.138002	4.10E-14	6.11E-13	21.43082	DUT	deoxyuridine triphosphatase	AB049113
226320_at	0.71289	9.0893585	11.23948	4.56E-23	3.25E-21	41.74658	THOC4	THO complex 4	AF047002
204558_at	0.71286	6.3962004	9.04464	1.27E-16	2.94E-15	27.10835	RAD54L	RAD54-like (S. cerevisiae)	NM_003579
223076_s_at	0.71285	8.6669177	11.63565	2.86E-24	2.60E-22	44.47908	NSUN2	NOL1/NOP2/Sun domain family, member 2	BC001041
229954_at	0.71278	6.6484477	5.367377	2.19E-07	1.09E-06	6.305397	0	0	AI025415
209449_at	0.71277	8.5413581	11.08968	1.29E-22	8.52E-21	40.71874	LSM2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	AF196468
217786_at	0.71269	8.8660754	11.49211	7.82E-24	6.55E-22	43.48682	PRMT5	protein arginine methyltransferase 5	NM_006109
225075_at	0.71253	8.5943212	12.3071	2.53E-26	3.41E-24	49.14857	PDRG1	p53 and DNA damage regulated 1	AL031658
211115_x_at	0.71252	7.1385291	10.14827	8.27E-20	3.27E-18	34.34228	SIP1	survival of motor neuron protein interacting protein 1	AB037703
235955_at	0.71231	6.0287986	5.461184	1.38E-07	7.07E-07	6.747797	MARVELD2	MARVEL domain containing 2	N57927
222925_at	0.71231	4.7791417	4.271956	2.99E-05	0.0001031	1.586645	DCDC2	doublecortin domain containing 2	AW444617
225119_at	0.71219	8.3936057	8.357879	1.04E-14	1.71E-13	22.78191	CHMP4B	chromatin modifying protein 4B	AW299290
213667_at	0.71206	6.6291489	7.821226	2.88E-13	3.74E-12	19.51652	SRCAP	Snf2-related CREBBP activator protein	AB002307
201457_x_at	0.71155	9.9134156	8.844107	4.67E-16	9.75E-15	25.82938	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	AF081496
222932_at	0.71154	5.1968261	7.349965	4.86E-12	5.16E-11	16.74488	EHF	ets homologous factor	AF203977
230244_at	0.71146	5.5039708	4.930801	1.71E-06	7.32E-06	4.323415	C2orf82	chromosome 2 open reading frame 82	AI871385
218454_at	0.71135	10.210451	5.348757	2.39E-07	1.18E-06	6.218264	FLJ22662	hypothetical protein FLJ22662	NM_024829
230259_at	0.71128	7.2392139	8.032339	7.88E-14	1.12E-12	20.78795	C10orf125	chromosome 10 open reading frame 125	AI471699
218776_s_at	0.71115	8.0646332	9.68629	1.85E-18	5.83E-17	31.27731	TMEM62	transmembrane protein 62	NM_024956
218566_s_at	0.71093	8.9230416	9.004787	1.65E-16	3.72E-15	26.85321	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	NM_012124
208675_s_at	0.71051	11.276901	12.20492	5.21E-26	6.63E-24	48.4354	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	D29643

213346_at	0.71039	6.7879926	8.387008	8.62E-15	1.45E-13	22.96222	C13orf27	chromosome 13 open reading frame 27	BE748563
226482_s_at	0.71018	8.9941301	6.645124	2.77E-10	2.20E-09	12.7897	hCG_20857	thiosulfate sulfurtransferase KAT, putative /// KAT protein	AI814545
202183_s_at	0.71006	7.4407487	11.51523	6.65E-24	5.67E-22	43.64649	KIF22	kinesin family member 22	NM_007317
225943_at	0.70996	7.042048	9.332992	1.93E-17	5.13E-16	28.96808	NLN	neurolysin (metallopeptidase M3 family)	BF222737
218593_at	0.70968	7.7996163	13.19856	4.52E-29	1.11E-26	55.39801	RBM28	RNA binding motif protein 28	NM_018077
201114_x_at	0.70965	11.20116	13.00855	1.75E-28	3.80E-26	54.06271	PSMA7	proteasome (prosome, macropain) subunit, alpha type, 7	NM_002792
230532_at	0.70961	7.5315888	9.60036	3.28E-18	9.92E-17	30.71272	CXorf38	chromosome X open reading frame 38	BF001685
210156_s_at	0.7096	9.0009874	10.89071	5.12E-22	2.99E-20	39.3585	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	D25547
226134_s_at	0.70945	8.2098962	7.706572	5.77E-13	7.11E-12	18.83352	0	0	AI978754
209744_x_at	0.7094	7.9035273	11.20819	5.66E-23	3.97E-21	41.53166	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	AB056663
221802_s_at	0.70936	8.2980842	6.535558	5.09E-10	3.87E-09	12.19725	KIAA1598	KIAA1598	AU157109
58696_at	0.7093	8.9798155	11.7712	1.11E-24	1.09E-22	45.41825	EXOSC4	exosome component 4	AL039469
223055_s_at	0.70925	6.8742135	10.23052	4.73E-20	1.96E-18	34.89288	XPO5	exportin 5	AF271159
1555292_at	0.70913	4.3497728	7.536985	1.60E-12	1.85E-11	17.83338	FAM40B	family with sequence similarity 40, member B	BC019064
202924_s_at	0.70896	6.688216	9.195885	4.75E-17	1.17E-15	28.08087	PLAGL2	pleiomorphic adenoma gene-like 2	AL562280
218051_s_at	0.70882	7.5935499	6.490351	6.52E-10	4.88E-09	11.95466	NT5DC2	5'-nucleotidase domain containing 2	NM_022908
208152_s_at	0.7088	10.021368	9.885027	4.89E-19	1.71E-17	32.58989	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	NM_004728
229545_at	0.70825	7.8433251	5.700353	4.21E-08	2.33E-07	7.90116	FERMT1	fermitin family homolog 1 (Drosophila)	BF591031
208639_x_at	0.70816	11.105338	12.1299	8.85E-26	1.07E-23	47.91232	PDIA6	protein disulfide isomerase family A, member 6	BC001312
219960_s_at	0.70811	8.5657026	9.539292	4.93E-18	1.44E-16	30.31261	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	NM_015984
219330_at	0.70782	6.7964945	9.344772	1.78E-17	4.78E-16	29.04456	VANGL1	vang-like 1 (van gogh, Drosophila)	NM_024062
223478_at	0.70764	7.2599238	11.04653	1.74E-22	1.11E-20	40.42322	TIMM8B	translocase of inner mitochondrial membrane 8 homolog B (yeast)	AF165967
218187_s_at	0.70764	8.2796758	7.970693	1.15E-13	1.59E-12	20.41487	C8orf33	chromosome 8 open reading frame 33	NM_023080
201543_s_at	0.7076	8.8059582	9.308676	2.26E-17	5.96E-16	28.81036	SAR1A	SAR1 homolog A (S. cerevisiae)	NM_020150
233565_s_at	0.70757	9.2179693	4.125302	5.41E-05	0.0001784	1.021497	SDCBP2	syndecan binding protein (syntenin) 2	AL136531
214711_at	0.70652	7.4034041	9.18743	5.02E-17	1.23E-15	28.02633	GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	BE568184
218046_s_at	0.70626	9.2911669	10.69224	2.01E-21	1.05E-19	38.00796	MRPS16	mitochondrial ribosomal protein S16	NM_016065
221550_at	0.70621	6.7485383	9.196437	4.73E-17	1.17E-15	28.08443	COX15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	BC002382
224468_s_at	0.70618	8.1171508	9.408584	1.17E-17	3.22E-16	29.45944	C19orf48	chromosome 19 open reading frame 48	BC006151
236140_at	0.70579	7.3040038	7.614818	1.00E-12	1.19E-11	18.29089	GCLM	glutamate-cysteine ligase, modifier subunit	AI753488
224185_at	0.70553	5.0906688	9.369324	1.52E-17	4.11E-16	29.20406	0	0	U58658
214097_at	0.70541	8.5333169	6.569319	4.22E-10	3.26E-09	12.37913	RPS21	ribosomal protein S21	AW024383
211501_s_at	0.70532	8.9377122	11.56208	4.79E-24	4.17E-22	43.97022	EIF3B	eukaryotic translation initiation factor 3, subunit B	BC001173
211599_x_at	0.70492	7.7421526	7.465277	2.45E-12	2.74E-11	17.4142	MET	met proto-oncogene (hepatocyte growth factor receptor)	U19348
201281_at	0.70479	9.3845954	12.59325	3.34E-27	5.47E-25	51.14974	ADRM1	adhesion regulating molecule 1	NM_007002
242618_at	0.70468	4.9325392	9.072088	1.07E-16	2.49E-15	27.28435	HCG18	HLA complex group 18	AA430072
219742_at	0.70423	5.9538129	9.537603	4.98E-18	1.46E-16	30.30156	PRR7	proline rich 7 (synaptic)	NM_030567
218434_s_at	0.70413	8.2403713	7.68993	6.38E-13	7.79E-12	18.73484	AACS	acetoacetyl-CoA synthetase	NM_023928

224839_s_at	0.70399	7.0404608	5.551661	8.86E-08	4.67E-07	7.179861	GPT2	glutamic pyruvate transaminase (alanine aminotransferase) 2	BG328998
231871_at	0.70387	6.7201789	8.238068	2.20E-14	3.41E-13	22.04351	GPR180	G protein-coupled receptor 180	AU160685
212125_at	0.70368	7.5860911	12.84296	5.67E-28	1.09E-25	52.90017	RANGAP1	Ran GTPase activating protein 1	NM_002883
223258_s_at	0.70354	6.7088846	9.085914	9.74E-17	2.29E-15	27.37309	KIAA1333	KIAA1333	BC000973
227046_at	0.70332	8.1123425	5.597912	7.04E-08	3.77E-07	7.402737	SLC39A11	solute carrier family 39 (metal ion transporter), member 11	BF062384
240983_s_at	0.70321	6.3466537	8.452679	5.70E-15	9.89E-14	23.3698	CARS	cysteinyl-tRNA synthetase	AW292273
225707_at	0.70318	8.8109321	10.87575	5.68E-22	3.29E-20	39.25645	ARL6IP6	ADP-ribosylation-like factor 6 interacting protein 6	AL581082
206515_at	0.70284	5.7973993	3.727289	0.0002514	0.0007277	-0.42733	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	NM_000896
207515_s_at	0.70268	8.0541429	10.62565	3.18E-21	1.59E-19	37.55625	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	NM_004875
235003_at	0.70265	7.5232918	8.429059	6.61E-15	1.13E-13	23.22303	UHK1	U2AF homology motif (UHM) kinase 1	AI249980
201930_at	0.70248	9.8362225	11.2514	4.19E-23	3.02E-21	41.82852	MCM6	minichromosome maintenance complex component 6	NM_005915
1558693_s_at	0.70218	7.9752414	8.354131	1.06E-14	1.75E-13	22.75874	C1orf85	chromosome 1 open reading frame 85	AW090182
209796_s_at	0.70166	9.7690223	10.7164	1.70E-21	9.02E-20	38.17199	CNPY2	canopy 2 homolog (zebrafish)	BC001027
201459_at	0.70166	9.7818582	12.22611	4.48E-26	5.79E-24	48.58323	RUVBL2	RuvB-like 2 (E. coli)	NM_006666
209892_at	0.70163	8.4329095	5.113384	7.34E-07	3.35E-06	5.136626	FUT4	fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific)	AF305083
227545_at	0.70155	7.2985056	8.809469	5.84E-16	1.20E-14	25.60972	0	0	AI686314
208824_x_at	0.70151	7.7144403	10.41162	1.38E-20	6.20E-19	36.10991	PCTK1	PCTAIRE protein kinase 1	BC001048
207628_s_at	0.70121	9.7458407	10.5838	4.24E-21	2.07E-19	37.2728	WBSR22	Williams Beuren syndrome chromosome region 22	NM_017528
218538_s_at	0.70113	7.7738016	8.786195	6.79E-16	1.38E-14	25.46234	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	NM_020662
219649_at	0.70112	8.3496746	8.949842	2.36E-16	5.17E-15	26.50222	ALG6	asparagine-linked glycosylation 6, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	NM_013339
200846_s_at	0.70082	10.616588	11.49404	7.71E-24	6.47E-22	43.50018	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	NM_002708
203219_s_at	0.70082	8.5300084	10.60438	3.68E-21	1.82E-19	37.41214	APRT	adenine phosphoribosyltransferase	NM_000485
228810_at	0.70076	6.8922045	8.093722	5.39E-14	7.85E-13	21.1609	CCNYL1	cyclin Y-like 1	AW135279
222654_at	0.70059	8.4769662	7.475365	2.31E-12	2.60E-11	17.47303	IMPAD1	inositol monophosphatase domain containing 1	AI302253
213582_at	0.70058	4.495211	10.74295	1.42E-21	7.70E-20	38.35236	ATP11A	Homo sapiens, clone IMAGE:4427831, mRNA	BF439472
213330_s_at	0.70031	9.4597169	13.5078	5.00E-30	1.62E-27	57.5737	STIP1	stress-induced-phosphoprotein 1 similar to MCT /// solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	BE886580
206600_s_at	0.70017	7.2518209	4.838338	2.60E-06	1.08E-05	3.92042	LOC100133		NM_004695
219080_s_at	0.69996	7.3154365	8.550367	3.07E-15	5.59E-14	23.97886	CTPS2	CTP synthase II	NM_019857
200875_s_at	0.6999	9.97405	9.171981	5.55E-17	1.36E-15	27.92673	NOP56	NOP56 ribonucleoprotein homolog (yeast)	NM_006392
210177_at	0.69965	7.2595198	6.085804	5.75E-09	3.69E-08	9.833827	TRIM15	tripartite motif-containing 15	U34249
229091_s_at	0.69963	6.0348919	7.648636	8.19E-13	9.84E-12	18.49048	CCNJ	cyclin J	AU154786
203593_at	0.69926	9.5512919	7.684111	6.61E-13	8.04E-12	18.70036	CD2AP	CD2-associated protein	NM_012120
201286_at	0.6991	9.1320762	4.811545	2.93E-06	1.21E-05	3.804772	SDC1	syndecan 1	Z48199
210813_s_at	0.69887	6.3488611	7.147889	1.59E-11	1.55E-10	15.58649	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	BC005259
235407_at	0.69874	6.9552599	11.4237	1.26E-23	1.01E-21	43.01478	0	0	BG435723
204299_at	0.69864	7.9057795	9.951985	3.12E-19	1.13E-17	33.03418	FUSIP1 ///	FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1	NM_021993
202129_s_at	0.69846	8.2057386	6.271101	2.15E-09	1.47E-08	10.79389	RIOK3	RIO kinase 3 (yeast)	AW006290

219015_s_at	0.69809	7.9689577	8.034908	7.76E-14	1.10E-12	20.80353	ALG13	asparagine-linked glycosylation 13 homolog (<i>S. cerevisiae</i>)	NM_018466
223234_at	0.69808	8.2213882	8.886118	3.56E-16	7.57E-15	26.09631	MAD2L2	MAD2 mitotic arrest deficient-like 2 (yeast)	AF080398
215017_s_at	0.69806	8.8336834	7.650076	8.12E-13	9.76E-12	18.49898	FNBP1L	formin binding protein 1-like	AW270932
1555434_a_at	0.69803	6.8942073	6.628504	3.04E-10	2.40E-09	12.69942	SLC39A14	solute carrier family 39 (zinc transporter), member 14	BC015770
216602_s_at	0.69783	8.0062229	11.48024	8.49E-24	7.04E-22	43.4049	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	AD000092
239138_at	0.69769	5.0754158	8.117491	4.65E-14	6.85E-13	21.3057	0	0	H16725
219959_at	0.69769	7.4190382	4.583289	8.02E-06	3.07E-05	2.84036	MOCOS	molybdenum cofactor sulfurase	NM_017947
207414_s_at	0.6976	7.2189185	6.385545	1.16E-09	8.27E-09	11.3965	PCSK6	proprotein convertase subtilisin/kexin type 6	NM_002570
218777_at	0.69747	7.5514819	10.7749	1.14E-21	6.27E-20	38.56966	REEP4	receptor accessory protein 4	NM_025232
227904_at	0.69731	6.6760715	10.61677	3.38E-21	1.68E-19	37.49611	AZI2	5-azacytidine induced 2	BF000175
218866_s_at	0.69724	8.3632442	9.644865	2.44E-18	7.54E-17	31.00491	POLR3K	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa	NM_016310
1564064_a_at	0.69724	7.2248902	8.117801	4.64E-14	6.84E-13	21.30759	ATP11B	ATPase, class VI, type 11B	AK093727
204905_s_at	0.69718	8.4050353	8.931567	2.66E-16	5.78E-15	26.38568	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	NM_004280
228053_s_at	0.69687	10.446413	11.57381	4.41E-24	3.86E-22	44.05131	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)	BF965064
208680_at	0.69677	12.079402	13.40621	1.03E-29	3.16E-27	56.85869	PRDX1	peroxiredoxin 1	L19184
210164_at	0.69672	7.3304026	4.555393	9.05E-06	3.42E-05	2.72509	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	J03189
218689_at	0.69663	8.1950461	8.507129	4.03E-15	7.22E-14	23.70888	FANCF	Fanconi anemia, complementation group F	NM_022725
232296_s_at	0.69663	7.0973954	11.70943	1.71E-24	1.63E-22	44.99004	GFM1	G elongation factor, mitochondrial 1	AK000780
202296_s_at	0.69645	10.159124	10.09573	1.18E-19	4.56E-18	33.99135	RER1	RER1 retention in endoplasmic reticulum 1 homolog (<i>S. cerevisiae</i>)	NM_007033
202178_at	0.69644	8.0995956	7.244934	9.01E-12	9.12E-11	16.14045	PRKCZ	protein kinase C, zeta	NM_002744
219016_at	0.69644	8.0392083	11.41637	1.33E-23	1.05E-21	42.96427	FASTKD5	FAST kinase domains 5	NM_021826
223363_at	0.6964	8.3995579	11.11953	1.05E-22	7.03E-21	40.9233	PSMG3	proteasome (prosome, macropain) assembly chaperone 3	BC004308
226242_at	0.69639	9.2040041	9.359828	1.62E-17	4.35E-16	29.14235	C1orf131	chromosome 1 open reading frame 131	BF515750
228061_at	0.69624	6.2319741	8.02399	8.30E-14	1.17E-12	20.73734	CCDC126	coiled-coil domain containing 126	BF062262
219303_at	0.69624	7.7013571	7.021194	3.30E-11	3.05E-10	14.86999	RNF219	ring finger protein 219	NM_024546
229886_at	0.69617	6.178059	7.950302	1.31E-13	1.79E-12	20.2918	C5orf34	chromosome 5 open reading frame 34	AA502768
1554339_a_at	0.69614	5.0355046	7.795016	3.38E-13	4.33E-12	19.35991	COG3	component of oligomeric golgi complex 3	BC038953
235947_at	0.69612	4.3183472	3.729934	0.000249	0.0007209	-0.41812	0	0	AA922273
201477_s_at	0.69608	9.7375659	11.1628	7.77E-23	5.32E-21	41.22005	RRM1	ribonucleotide reductase M1	NM_001033
65588_at	0.69586	8.0522794	7.450135	2.69E-12	2.98E-11	17.32597	LOC388796	hypothetical LOC388796	AA827892
215380_s_at	0.69579	10.78239	11.00801	2.27E-22	1.41E-20	40.15968	GGCT	gamma-glutamyl cyclotransferase	AK021779
1552660_a_at	0.69564	6.3325977	8.048596	7.13E-14	1.02E-12	20.88659	C5orf22	chromosome 5 open reading frame 22	BC021215
202830_s_at	0.69563	7.771616	8.606879	2.14E-15	3.99E-14	24.33268	SLC37A4	solute carrier family 37 (glucose-6-phosphate transporter), member 4	NM_001467
1558750_a_at	0.69549	4.6677726	8.849688	4.51E-16	9.42E-15	25.86481	0	0	BG109249
228347_at	0.69543	5.2862401	4.558468	8.93E-06	3.38E-05	2.737769	SIX1	SIX homeobox 1	N79004
225201_s_at	0.69536	9.9722484	10.98543	2.66E-22	1.64E-20	40.00528	MRPL14	mitochondrial ribosomal protein L14	BF569593
211713_x_at	0.69524	7.4679116	8.887175	3.54E-16	7.53E-15	26.10303	KIAA0101	KIAA0101	BC005832
203946_s_at	0.69521	5.8005745	5.357291	2.30E-07	1.14E-06	6.25817	ARG2	arginase, type II	U75667
200700_s_at	0.69516	11.026024	8.953554	2.30E-16	5.07E-15	26.52591	KDEL2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	NM_006854
41660_at	0.69511	5.6962064	8.118202	4.63E-14	6.83E-13	21.31003	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, <i>Drosophila</i>)	AL031588

207732_s_at	0.69511	6.8657334	8.67479	1.39E-15	2.66E-14	24.75927	DLG3	discs, large homolog 3 (Drosophila)	NM_021120
225418_at	0.69508	8.7659333	7.715951	5.45E-13	6.73E-12	18.88919	PVRL2	poliovirus receptor-related 2 (herpesvirus entry mediator B)	AI520949
219301_s_at	0.69499	4.8683938	6.395714	1.09E-09	7.84E-09	11.4504	CNTNAP2	contactin associated protein-like 2	AU144598
202697_at	0.69497	8.710911	9.480379	7.28E-18	2.06E-16	29.92752	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	NM_007006
203536_s_at	0.69487	8.2828557	13.76991	7.72E-31	3.29E-28	59.41929	CIAO1	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	NM_004804
205278_at	0.69481	3.7459557	5.254194	3.77E-07	1.81E-06	5.77927	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	NM_000817
211404_s_at	0.69468	9.5784152	8.66479	1.48E-15	2.82E-14	24.69636	APLP2	amyloid beta (A4) precursor-like protein 2	BC004371
1568593_a_at	0.69459	6.5877934	6.564403	4.34E-10	3.34E-09	12.35261	NUDT16P	nudix (nucleoside diphosphate linked moiety X)-type motif 16 pseudogene	CA431328
221561_at	0.69454	7.7631534	5.497752	1.16E-07	5.98E-07	6.921796	SOAT1	sterol O-acyltransferase 1	L21934
203007_x_at	0.69448	10.07733	11.19285	6.30E-23	4.38E-21	41.42632	LYPLA1	lysophospholipase I	AF077198
205235_s_at	0.69435	6.9696197	10.54073	5.69E-21	2.71E-19	36.98137	KIF20B	kinesin family member 20B	NM_016195
200895_s_at	0.69379	9.0350853	9.780524	9.86E-19	3.27E-17	31.89853	FKBP4	FK506 binding protein 4, 59kDa	NM_002014
235022_at	0.69378	7.3598843	9.126018	7.50E-17	1.79E-15	27.6308	C18orf19	chromosome 18 open reading frame 19	BE326738
201704_at	0.69365	8.9984511	8.373185	9.41E-15	1.56E-13	22.87662	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative function)	NM_001247
217859_s_at	0.69364	6.2317759	8.434075	6.41E-15	1.10E-13	23.25419	SLC39A9	solute carrier family 39 (zinc transporter), member 9	NM_018375
242871_at	0.69357	6.1509724	4.051172	7.27E-05	0.0002334	0.742163	PAQR5	progesterin and adipoQ receptor family member V	AI934557
224615_x_at	0.69345	9.1811422	10.81466	8.66E-22	4.85E-20	38.84024	HM13	histocompatibility (minor) 13	AL110115
204649_at	0.69344	6.9097503	10.10413	1.11E-19	4.33E-18	34.04738	TROAP	trophinin associated protein (tastin)	NM_005480
222029_x_at	0.69341	8.1974887	12.38507	1.46E-26	2.05E-24	49.6933	PFDN6	prefoldin subunit 6	NM_014260
214484_s_at	0.69304	8.2929893	8.441809	6.10E-15	1.05E-13	23.30223	SIGMAR1	sigma non-opioid intracellular receptor 1	AF226604
210371_s_at	0.69292	9.599473	9.501983	6.31E-18	1.82E-16	30.06863	RBBP4	retinoblastoma binding protein 4	BC003092
223254_s_at	0.69291	7.5641329	8.057177	6.76E-14	9.67E-13	20.93869	KIAA1333	KIAA1333	AA887053
224437_s_at	0.69273	8.9247537	9.896492	4.53E-19	1.60E-17	32.6659	VTA1	Vps20-associated 1 homolog (S. cerevisiae)	BC005937
200635_s_at	0.69255	9.102498	7.48909	2.13E-12	2.41E-11	17.55315	PTPRF	protein tyrosine phosphatase, receptor type, F	AU145351
217809_at	0.69243	11.143126	9.428826	1.02E-17	2.84E-16	29.59127	BZW2	basic leucine zipper and W2 domains 2	NM_014038
201819_at	0.69222	7.4069426	7.374976	4.19E-12	4.52E-11	16.88955	SCARB1	scavenger receptor class B, member 1	NM_005505
212680_x_at	0.69203	8.9553163	10.96652	3.03E-22	1.84E-20	39.87607	PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	BE305165
221927_s_at	0.69191	8.818246	6.516953	5.64E-10	4.26E-09	12.09728	ABHD11	abhydrolase domain containing 11	AI923458
214507_s_at	0.69159	7.502221	12.15263	7.54E-26	9.23E-24	48.07073	EXOSC2	exosome component 2	NM_014285
200638_s_at	0.69158	11.990793	11.08465	1.34E-22	8.79E-21	40.68427	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	BC003623
202307_s_at	0.69133	9.6564403	6.852632	8.64E-11	7.44E-10	13.92878	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	NM_000593
211574_s_at	0.69131	8.551162	8.708105	1.12E-15	2.18E-14	24.9691	CD46	CD46 molecule, complement regulatory protein	D84105
210233_at	0.69113	4.9710054	8.853588	4.40E-16	9.21E-15	25.88957	IL1RAP	interleukin 1 receptor accessory protein	AF167343
232893_at	0.69088	4.9656666	9.559733	4.30E-18	1.27E-16	30.44644	LMBRD2	LMBR1 domain containing 2	AL137370
219470_x_at	0.69073	6.3026583	7.652546	8.00E-13	9.62E-12	18.51358	CCNJ	cyclin J	NM_019084
204836_at	0.69049	5.5368009	5.573738	7.94E-08	4.22E-07	7.286078	GLDC	glycine dehydrogenase (decarboxylating)	NM_000170

1553528_a_at	0.69035	6.3819631	9.186178	5.06E-17	1.24E-15	28.01826	TAF5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	NM_139052
1554086_at	0.69021	4.9335383	10.1835	6.51E-20	2.63E-18	34.57793	TUBGCP3	tubulin, gamma complex associated protein 3	BC007763
200750_s_at	0.6902	11.571753	12.07824	1.27E-25	1.49E-23	47.55241	RAN	RAN, member RAS oncogene family	AF054183
228624_at	0.69015	7.9720511	5.686553	4.51E-08	2.49E-07	7.833633	TMEM144	transmembrane protein 144	AI432488
219003_s_at	0.69004	6.8851004	6.786536	1.26E-10	1.05E-09	13.56357	MANEA	mannosidase, endo-alpha	NM_024641
208952_s_at	0.68989	8.1511873	9.562863	4.21E-18	1.25E-16	30.46694	LARP5	La ribonucleoprotein domain family, member 5	AA811923
232103_at	0.68988	7.8353562	6.117023	4.88E-09	3.17E-08	9.994207	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	AI439695
208777_s_at	0.68986	10.053358	12.16772	6.77E-26	8.41E-24	48.17596	PSMD11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	AF001212
222881_at	0.68961	5.1626507	6.862915	8.15E-11	7.04E-10	13.9858	HPSE	heparanase	AF155510
238762_at	0.68959	7.2588847	5.831415	2.16E-08	1.26E-07	8.54829	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	AA702016
204233_s_at	0.68938	7.5750184	7.039911	2.96E-11	2.76E-10	14.97536	CHKA	choline kinase alpha	AI991328
225252_at	0.68933	9.2412982	9.883727	4.93E-19	1.73E-17	32.58128	SRXN1	sulfiredoxin 1 homolog (S. cerevisiae)	AL121758
243507_s_at	0.68918	6.1097707	9.784511	9.60E-19	3.19E-17	31.92486	C20orf196	chromosome 20 open reading frame 196	AV715251
201912_s_at	0.68916	9.196648	9.162339	5.91E-17	1.44E-15	27.8646	GSPT1	G1 to S phase transition 1	NM_002094
209704_at	0.68915	6.1480355	8.653368	1.59E-15	3.02E-14	24.62455	MTF2	metal response element binding transcription factor 2	AL523380
229128_s_at	0.68886	8.5029235	4.720692	4.39E-06	1.76E-05	3.416414	0	0	AI697657
218336_at	0.68871	9.8782433	11.58592	4.05E-24	3.57E-22	44.13507	PFDN2	prefoldin subunit 2	NM_012394
209615_s_at	0.68867	6.6572638	8.43938	6.20E-15	1.07E-13	23.28714	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1	U51120
201942_s_at	0.68863	7.134019	6.972299	4.37E-11	3.95E-10	14.59554	CPD	carboxypeptidase D	D85390
204679_at	0.68857	9.6928127	3.781511	0.0002054	0.0006054	-0.2374	KCNK1	potassium channel, subfamily K, member 1	NM_002245
206214_at	0.68813	8.0123082	4.15241	4.86E-05	0.0001612	1.124714	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	NM_005084
209509_s_at	0.6881	8.5553224	9.787567	9.40E-19	3.13E-17	31.94504	DPAGT1	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase)	BC000325
217916_s_at	0.68774	9.230709	11.33242	2.38E-23	1.80E-21	42.3859	FAM49B	family with sequence similarity 49, member B	NM_016623
207717_s_at	0.68767	8.0258959	4.79536	3.15E-06	1.29E-05	3.735157	PKP2	plakophilin 2	NM_004572
202726_at	0.68761	7.2769937	10.7204	1.66E-21	8.79E-20	38.19914	LIG1	ligase I, DNA, ATP-dependent	NM_000234
235057_at	0.68757	5.4495774	6.81835	1.05E-10	8.89E-10	13.73909	ITCH	Itchy E3 ubiquitin protein ligase homolog (mouse)	AW089307
236313_at	0.68752	7.3037076	4.00816	8.61E-05	0.0002725	0.582056	CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	AW444761
222645_s_at	0.68719	6.5341859	10.22185	5.02E-20	2.07E-18	34.83481	KCTD5	potassium channel tetramerisation domain containing 5	AA872593
226584_s_at	0.68717	6.5230976	9.910125	4.13E-19	1.47E-17	32.75631	FAM110A	family with sequence similarity 110, member A	AL118502
202852_s_at	0.68702	8.4109762	11.30782	2.83E-23	2.10E-21	42.21658	FLJ11506	alpha- and gamma-adaptin-binding protein p34	NM_024666
214095_at	0.68697	6.9676016	9.398356	1.25E-17	3.43E-16	29.39287	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	AW190316
210663_s_at	0.68697	6.9415187	4.804708	3.02E-06	1.24E-05	3.77534	KYNU	kynureninase (L-kynurenine hydrolase)	BC000879
1555279_at	0.68688	5.8280012	8.940401	2.51E-16	5.47E-15	26.44201	ARMC8	armadillo repeat containing 8	BC007934
212070_at	0.68664	9.7560841	6.582408	3.93E-10	3.04E-09	12.4498	GPR56	G protein-coupled receptor 56	AL554008
225799_at	0.68642	9.3831517	6.97762	4.24E-11	3.84E-10	14.62535	LOC541471	hypothetical LOC541471 /// non-protein coding RNA 152	BF209337
212268_at	0.68622	10.127011	5.45663	1.42E-07	7.23E-07	6.72619	SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1	NM_030666
210904_s_at	0.68618	8.2936292	6.06424	6.44E-09	4.10E-08	9.723379	IL13RA1	interleukin 13 receptor, alpha 1	U81380

200973_s_at	0.68584	10.320673	7.149446	1.57E-11	1.53E-10	15.59535	TSPAN3	tetraspanin 3	NM_005724
202961_s_at	0.68582	11.632532	11.41102	1.38E-23	1.09E-21	42.92739	ATP5J2	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit F2	NM_004889
231882_at	0.68567	6.1567719	5.113435	7.34E-07	3.35E-06	5.136856	FLJ39632 //	hypothetical LOC642477 /// similar to double homeobox A	AL530703
225060_at	0.6856	9.6958967	8.487628	4.57E-15	8.11E-14	23.58733	LRP11	low density lipoprotein receptor-related protein 11	BF696304
222883_at	0.68536	7.0021732	10.3425	2.21E-20	9.65E-19	35.64464	C1orf163	chromosome 1 open reading frame 163	NM_023077
218884_s_at	0.68526	5.4036583	8.247264	2.07E-14	3.24E-13	22.1	GUF1	GUF1 GTPase homolog (S. cerevisiae)	NM_021927
208876_s_at	0.68515	6.5166033	10.02275	1.93E-19	7.24E-18	33.50482	PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	AI076186
218219_s_at	0.68513	7.7483756	8.954102	2.30E-16	5.05E-15	26.5294	LANCL2	LanC lantibiotic synthetase component C-like 2 (bacterial)	NM_018697
214522_x_at	0.68512	5.377115	9.924197	3.76E-19	1.35E-17	32.84968	HIST1H2AD	histone cluster 1, H2ad /// histone cluster 1, H3d	NM_021065
208926_at	0.68475	8.601523	4.964963	1.46E-06	6.34E-06	4.473819	NEU1	sialidase 1 (lysosomal sialidase)	U84246
1555460_a_at	0.68455	6.7962018	6.844815	9.03E-11	7.75E-10	13.88547	SLC39A6	solute carrier family 39 (zinc transporter), member 6	BC039498
210405_x_at	0.68444	6.7354838	8.117646	4.65E-14	6.85E-13	21.30664	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	AF153687
215177_s_at	0.68392	8.7945097	6.264654	2.22E-09	1.52E-08	10.76017	ITGA6	integrin, alpha 6	AV733308
221256_s_at	0.6839	7.999837	6.496369	6.31E-10	4.73E-09	11.98689	HDHD3	haloacid dehalogenase-like hydrolase domain containing 3	NM_031219
209389_x_at	0.68389	11.025626	10.62944	3.10E-21	1.56E-19	37.58192	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	M15887
209302_at	0.68385	9.6622359	12.30725	2.53E-26	3.41E-24	49.14958	POLR2H	polymerase (RNA) II (DNA directed) polypeptide H	U37689
1555734_x_at	0.68376	5.213728	7.510831	1.87E-12	2.13E-11	17.68023	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	AF393369
1553689_s_at	0.68366	6.5741686	9.863151	5.66E-19	1.96E-17	32.44496	METTL6	methyltransferase like 6	NM_152396
206558_at	0.68365	6.2986458	6.328781	1.57E-09	1.10E-08	11.0967	SIM2	single-minded homolog 2 (Drosophila)	NM_005069
223575_at	0.68361	5.2952331	7.467444	2.42E-12	2.71E-11	17.42683	KIAA1549	KIAA1549	AL136736
202883_s_at	0.6836	8.2349734	7.857276	2.31E-13	3.05E-12	19.73237	PPP2R1B	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	T79584
217790_s_at	0.68356	7.5898525	8.753009	8.40E-16	1.67E-14	25.25249	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	NM_007107
236937_at	0.68355	4.6294818	8.770041	7.53E-16	1.51E-14	25.36015	VP58	CDNA clone IMAGE:4733107	BF108423
235387_at	0.68352	6.6026454	9.583882	3.66E-18	1.10E-16	30.60467	GSTCD	glutathione S-transferase, C-terminal domain containing	AA740875
203622_s_at	0.68351	9.0151698	10.80791	9.07E-22	5.06E-20	38.79425	PNO1	partner of NOB1 homolog (S. cerevisiae)	NM_020143
200922_at	0.68337	8.765482	10.00349	2.20E-19	8.18E-18	33.37666	KDELRL1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	NM_006801
221970_s_at	0.68313	9.1188306	12.11878	9.57E-26	1.15E-23	47.83481	NOL11	nucleolar protein 11	AU158148
212449_s_at	0.68305	10.83206	11.41901	1.30E-23	1.04E-21	42.98246	LYPLA1	lysophospholipase I	BG288007
204224_s_at	0.68286	9.0859451	6.396696	1.09E-09	7.80E-09	11.45561	GCH1	GTP cyclohydrolase 1	NM_000161
210896_s_at	0.68281	9.2713993	5.222343	4.39E-07	2.08E-06	5.632741	ASPH	aspartate beta-hydroxylase	AF306765
208436_s_at	0.6828	8.3948356	7.073993	2.43E-11	2.30E-10	15.16766	IRF7	interferon regulatory factor 7	NM_004030
210678_s_at	0.68258	8.0457301	7.734257	4.88E-13	6.09E-12	18.99795	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	U56418
228648_at	0.68239	7.258484	4.876572	2.19E-06	9.20E-06	4.086334	LRG1	leucine-rich alpha-2-glycoprotein 1	AA622495
214452_at	0.68232	4.7462185	5.028902	1.09E-06	4.83E-06	4.757499	BCAT1	branched chain aminotransferase 1, cytosolic	NM_005504
223246_s_at	0.68225	6.7187738	9.63102	2.68E-18	8.22E-17	30.91396	STRBP	spermatid perinuclear RNA binding protein	BC002693
225887_at	0.6816	7.8616041	8.717049	1.06E-15	2.07E-14	25.0255	C13orf23	chromosome 13 open reading frame 23	AL522406
229983_at	0.68153	7.0236419	9.655634	2.27E-18	7.04E-17	31.07569	TIGD2	tigger transposable element derived 2	AI610112
208750_s_at	0.68133	10.472935	11.31493	2.69E-23	2.01E-21	42.2655	ARF1	ADP-ribosylation factor 1	AA580004

37079_at	0.68124	5.3448328	10.63799	2.92E-21	1.48E-19	37.63988	YDD19	YDD19 protein	U82319
213391_at	0.68104	8.1475454	7.693826	6.23E-13	7.62E-12	18.75794	DPY19L4	dpy-19-like 4 (C. elegans)	AI669947
236028_at	0.68082	3.6304369	7.041619	2.93E-11	2.74E-10	14.98498	IBSP	integrin-binding sialoprotein	BE466675
215733_x_at	0.68079	5.1637231	3.737119	0.0002424	0.0007037	-0.39307	CTAG2	cancer/testis antigen 2	AI012833
206669_at	0.68048	5.2847926	6.481319	6.85E-10	5.11E-09	11.90633	GAD1	glutamate decarboxylase 1 (brain, 67kDa)	NM_013445
204391_x_at	0.68042	8.2453873	7.844086	2.50E-13	3.29E-12	19.65333	TRIM24	tripartite motif-containing 24	NM_015905
1558507_at	0.68041	5.7609298	11.17612	7.08E-23	4.88E-21	41.31149	C1orf53	chromosome 1 open reading frame 53	BI832220
209482_at	0.68033	8.9633936	10.72095	1.65E-21	8.76E-20	38.20289	POP7	processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae)	BC001430
241726_at	0.68004	5.9039334	5.244332	3.95E-07	1.89E-06	5.733827		0	AI682088
208934_s_at	0.68002	7.927515	10.17532	6.88E-20	2.77E-18	34.52323	LGALS8	lectin, galactoside-binding, soluble, 8	AF342815
204727_at	0.68	4.2194966	10.56827	4.71E-21	2.27E-19	37.16769	WDHD1	WD repeat and HMG-box DNA binding protein 1	AW772140
209806_at	0.67999	10.916468	5.446133	1.49E-07	7.58E-07	6.676433	HIST1H2BK	histone cluster 1, H2bk	BC000893
205420_at	0.67997	7.2540277	6.912486	6.15E-11	5.43E-10	14.26139	PEX7	peroxisomal biogenesis factor 7	NM_000288
1555751_a_at	0.67958	7.9109645	11.59352	3.84E-24	3.42E-22	44.18764	GEMIN7	gem (nuclear organelle) associated protein 7	AY114106
226473_at	0.67947	6.1718195	5.8252	2.23E-08	1.29E-07	8.51737	CBX2	chromobox homolog 2 (Pc class homolog, Drosophila)	BE514414
218028_at	0.67934	9.2750122	10.57846	4.40E-21	2.14E-19	37.23666	ELOVL1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	NM_016031
201689_s_at	0.67934	10.093831	5.024715	1.11E-06	4.92E-06	4.738834	TPD52	tumor protein D52	BE974098
234983_at	0.67933	9.0865756	7.427257	3.08E-12	3.38E-11	17.19286		0	BE893995
221712_s_at	0.67922	7.9746501	10.85308	6.64E-22	3.78E-20	39.10196	WDR74	WD repeat domain 74	BC006351
204341_at	0.67909	8.041206	5.666025	5.00E-08	2.74E-07	7.733407	TRIM16	tripartite motif-containing 16	NM_006470
212720_at	0.67907	8.6358698	8.525399	3.59E-15	6.48E-14	23.82288	PAPOLA	poly(A) polymerase alpha	AI670847
223506_at	0.67906	7.2648211	10.75455	1.31E-21	7.16E-20	38.43125	ZC3H8	zinc finger CCCH-type containing 8	AF334161
218853_s_at	0.67897	7.9269032	7.06764	2.52E-11	2.38E-10	15.13177	MOSPD1	motile sperm domain containing 1	NM_019556
200987_x_at	0.67889	8.7483271	11.32959	2.43E-23	1.84E-21	42.36639	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	AA758755
225717_at	0.6788	6.4830768	7.209272	1.11E-11	1.11E-10	15.93637	KIAA1715	KIAA1715	AI814587
224785_at	0.67879	7.4717011	10.59094	4.04E-21	1.99E-19	37.32113	FAM100B	family with sequence similarity 100, member B	AI024869
1553219_a_at	0.67858	4.7670474	8.955972	2.27E-16	5.00E-15	26.54134	AMMECR1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	NM_015365
1555522_s_at	0.67845	7.7773963	11.18986	6.43E-23	4.47E-21	41.40576	MEMO1	mediator of cell motility 1	BC036262
1552312_a_at	0.67845	6.3047094	6.661474	2.53E-10	2.02E-09	12.87864	MFAP3	microfibrillar-associated protein 3	NM_005927
219633_at	0.67832	6.8935014	9.639406	2.53E-18	7.81E-17	30.96904	TTPAL	tocopherol (alpha) transfer protein-like	NM_024331
233656_s_at	0.67823	7.8918483	8.397868	8.05E-15	1.35E-13	23.02952	VP54	vacuolar protein sorting 54 homolog (S. cerevisiae)	AL359939
229236_s_at	0.6782	7.8891341	9.213912	4.22E-17	1.06E-15	28.19722	SFXN4	sideroflexin 4	AI346445
207265_s_at	0.67808	8.9897411	5.315501	2.81E-07	1.37E-06	6.063205	KDEL3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	NM_016657
223878_at	0.67805	4.2036344	6.191249	3.29E-09	2.19E-08	10.37777	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	BC005273
203650_at	0.67805	8.3941429	5.653529	5.33E-08	2.91E-07	7.672527	PROCR	protein C receptor, endothelial (EPCR)	NM_006404
212832_s_at	0.67797	8.7078428	12.54342	4.75E-27	7.45E-25	50.8009	CKAP5	cytoskeleton associated protein 5	AI143124
206303_s_at	0.6778	8.044015	7.539309	1.58E-12	1.82E-11	17.847	NUDT4 ///	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	AF191653
205648_at	0.67777	6.2066433	4.733396	4.15E-06	1.67E-05	3.470359	WNT2	wingless-type MMTV integration site family member 2	NM_003391
1554533_at	0.6777	4.0798845	7.002118	3.68E-11	3.38E-10	14.76278	C2	complement component 2	BC029781

210749_x_at	0.67751	10.160653	6.051459	6.89E-09	4.36E-08	9.658041	DDR1	discoidin domain receptor tyrosine kinase 1	L11315
202200_s_at	0.67748	9.64095	9.955041	3.05E-19	1.11E-17	33.05449	SRPK1	SFRS protein kinase 1	NM_008137
204039_at	0.67742	8.1756974	4.120546	5.52E-05	0.0001814	1.003449	CEBPA	CCAAT/enhancer binding protein (C/EBP), alpha	NM_004364
201755_at	0.67742	7.1125647	10.52928	6.16E-21	2.91E-19	36.90402	MCM5	minichromosome maintenance complex component 5	NM_006739
203094_at	0.67729	8.5763049	10.14935	8.21E-20	3.25E-18	34.34953	MAD2L1BP	MAD2L1 binding protein	NM_014628
205618_at	0.67711	7.5688483	5.177933	5.42E-07	2.53E-06	5.42957	PRRG1	proline rich Gla (G-carboxyglutamic acid) 1	NM_000950
224483_s_at	0.67708	4.6376637	10.46464	9.59E-21	4.41E-19	36.46743	MFSD9	major facilitator superfamily domain containing 9	BC006242
219178_at	0.67701	6.269999	10.35732	2.00E-20	8.78E-19	35.74433	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	NM_024638
212541_at	0.67691	8.1259323	12.39816	1.33E-26	1.89E-24	49.78475	FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae)	AL562282
208864_s_at	0.67687	11.638881	8.890249	3.47E-16	7.40E-15	26.12258	TXN	thioredoxin	AF313911
221040_at	0.67629	4.0770277	6.840202	9.27E-11	7.93E-10	13.85993	CAPN10	calpain 10	NM_023089
224944_at	0.67623	9.9946104	9.926987	3.69E-19	1.32E-17	32.86819	TMPO	thymopoietin	AL566034
209125_at	0.67584	3.9857912	4.29014	2.77E-05	9.61E-05	1.657868	KRT6A	keratin 6A	J00269
232322_x_at	0.67573	9.4076055	4.884113	2.11E-06	8.92E-06	4.119177	STARD10	STAR-related lipid transfer (START) domain containing 10	D60944
219166_at	0.67553	7.5299648	7.827332	2.77E-13	3.61E-12	19.55304	C14orf104	chromosome 14 open reading frame 104	NM_018139
223993_s_at	0.67551	11.011221	10.89587	4.94E-22	2.90E-20	39.39371	CNIH4	cornichon homolog 4 (Drosophila)	AL136930
234290_x_at	0.67527	7.7539985	4.965221	1.46E-06	6.33E-06	4.474959	MYH14	myosin, heavy chain 14	BC000676
32723_at	0.67527	7.636699	10.36714	1.87E-20	8.24E-19	35.81039	CSTF1	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	L02547
218096_at	0.67518	9.081604	7.36459	4.46E-12	4.77E-11	16.82943	AGPAT5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	NM_018361
219745_at	0.67505	6.1625778	8.734132	9.48E-16	1.87E-14	25.13328	TMEM180	transmembrane protein 180	NM_024789
224608_s_at	0.67481	9.4639365	12.41478	1.18E-26	1.71E-24	49.90096	VPS25	vacuolar protein sorting 25 homolog (S. cerevisiae)	AL528911
203828_s_at	0.67479	9.7525231	5.460822	1.39E-07	7.09E-07	6.746081	IL32	interleukin 32	NM_004221
1554148_a_at	0.67469	7.2501915	9.798761	8.72E-19	2.91E-17	32.019	SLC33A1	solute carrier family 33 (acetyl-CoA transporter), member 1	BC014416
205067_at	0.67466	8.1357122	3.772268	0.0002126	0.0006249	-0.26994	IL1B	Interleukin 1, beta	NM_000576
202824_s_at	0.67464	10.778539	12.73635	1.21E-27	2.14E-25	52.15243	TCEB1	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	NM_005648
1554441_a_at	0.6744	7.356397	9.433564	9.93E-18	2.76E-16	29.62214	WAPAL	wings apart-like homolog (Drosophila)	AF479418
215084_s_at	0.67429	8.2731162	10.70159	1.89E-21	9.90E-20	38.07141	LRRC42	leucine rich repeat containing 42	AL031427
242019_at	0.67427	5.1694834	6.02745	7.82E-09	4.89E-08	9.535569	LASS6	LAG1 homolog, ceramide synthase 6	BG257755
213889_at	0.67427	6.350431	8.946201	2.42E-16	5.29E-15	26.479	PIGL	phosphatidylinositol glycan anchor biosynthesis, class L	A1742901
225099_at	0.674	8.4148141	10.7293	1.56E-21	8.34E-20	38.25964	FBXO45	F-box protein 45	AA126445
236219_at	0.67379	5.1986529	4.519362	1.06E-05	3.95E-05	2.577048	0	0	AI452512
44065_at	0.67378	6.7607884	10.5927	3.99E-21	1.96E-19	37.33307	C12orf52	chromosome 12 open reading frame 52	AI937468
201298_s_at	0.67376	9.2298896	10.23982	4.44E-20	1.85E-18	34.9552	MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	BC003398
228987_at	0.67353	6.4739624	8.18039	3.15E-14	4.77E-13	21.6899	0	0	AA156238
236622_at	0.67353	5.2959268	8.792835	6.50E-16	1.32E-14	25.50437	PIGM	phosphatidylinositol glycan anchor biosynthesis, class M	AI761712
219653_at	0.6735	6.6310815	10.79821	9.70E-22	5.38E-20	38.72825	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	NM_014054
202475_at	0.6735	10.354679	12.11799	9.62E-26	1.15E-23	47.82934	TMEM147	transmembrane protein 147	NM_006326
206245_s_at	0.67349	9.5756746	7.685995	6.54E-13	7.96E-12	18.71152	IVNS1ABP	influenza virus NS1A binding protein	NM_005469
229242_at	0.67337	7.8572477	5.128481	6.84E-07	3.13E-06	5.204888	0	0	BF439063
201381_x_at	0.67335	10.362305	12.56493	4.08E-27	6.51E-25	50.95143	CACYBP	calcyclin binding protein	AF057356
213929_at	0.67329	6.2519652	4.543271	9.53E-06	3.59E-05	2.675177	0	0	AL050204
226946_at	0.67325	7.1488059	6.545783	4.81E-10	3.68E-09	12.25227	C5orf33	chromosome 5 open reading frame 33	AI453203

1553510_s_at	0.67297	7.4493267	10.86026	6.32E-22	3.62E-20	39.15091	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	NM_005444
219800_s_at	0.67287	4.4892727	8.876632	3.79E-16	8.02E-15	26.03599	THNSL1	threonine synthase-like 1 (S. cerevisiae)	NM_024838
211563_s_at	0.67276	8.3798611	6.306156	1.78E-09	1.23E-08	10.97771	C19orf2	chromosome 19 open reading frame 2	AB006572
201037_at	0.67269	9.6947994	7.35505	4.72E-12	5.02E-11	16.77427	PFKP	phosphofructokinase, platelet	NM_002627
232861_at	0.67254	5.0543574	9.456923	8.51E-18	2.39E-16	29.77444	PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	AB037769
210978_s_at	0.67244	10.787195	8.956322	2.26E-16	4.99E-15	26.54357	TAGLN2	transgelin 2	BC002616
226907_at	0.67224	5.4098039	4.097469	6.05E-05	0.0001975	0.916117	PPP1R14C	protein phosphatase 1, regulatory (inhibitor) subunit 14C	N32557
224407_s_at	0.67214	5.7097478	6.311832	1.72E-09	1.20E-08	11.00753	RP6-213H1	serine/threonine protein kinase MST4	AF344882
226345_at	0.67208	8.8638328	8.331539	1.22E-14	2.00E-13	22.61914	0		0 AW270158
1554575_a_at	0.67206	6.7779196	10.57038	4.65E-21	2.25E-19	37.18198	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	BC017801
209971_x_at	0.67184	9.6512714	11.61529	3.30E-24	2.96E-22	44.33821	JTV1	JTV1 gene	AI928526
228302_x_at	0.6718	7.4290641	4.365138	2.03E-05	7.21E-05	1.954269	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	AW162846
210513_s_at	0.67176	7.4843927	7.594783	1.13E-12	1.33E-11	18.17287	VEGFA	vascular endothelial growth factor A	AF091352
204305_at	0.67167	7.7839075	9.264846	3.02E-17	7.76E-16	28.52647	MIPEP	mitochondrial intermediate peptidase	NM_005932
226750_at	0.67166	6.8429219	7.13136	1.75E-11	1.69E-10	15.49258	LARP2	La ribonucleoprotein domain family, member 2	AI767732
209666_s_at	0.67165	7.8826191	8.630946	1.84E-15	3.46E-14	24.48369	CHUK	conserved helix-loop-helix ubiquitous kinase	AF080157
219703_at	0.67158	5.9394063	6.169492	3.69E-09	2.44E-08	10.26501	MNS1	meiosis-specific nuclear structural 1	NM_018365
202906_s_at	0.67118	8.4978243	7.702547	5.91E-13	7.27E-12	18.80965	NBN	nibrin	AF049895
232437_at	0.67096	5.1780018	11.2574	4.02E-23	2.90E-21	41.86978	CPSF3L	cleavage and polyadenylation specific factor 3-like	AA732590
228846_at	0.67084	8.4094757	4.631067	6.52E-06	2.53E-05	3.039113	MXD1	MAX dimerization protein 1	AW071793
222748_s_at	0.67036	6.1726903	9.490776	5.80E-18	1.94E-15	29.99542	TXNL4B	thioredoxin-like 4B	AW194729
226432_at	0.66988	7.8616276	5.857436	1.89E-08	1.11E-07	8.678015	ETNK1	ethanolamine kinase 1	AI276880
223898_at	0.66982	5.3146491	7.987164	1.04E-13	1.45E-12	20.51441	ZNF670	zinc finger protein 670	BC005360
214336_s_at	0.6698	7.0971435	6.71201	1.91E-10	1.56E-09	13.15445	COPA	coatamer protein complex, subunit alpha	AI621079
209208_at	0.66962	8.8694903	8.966974	2.11E-16	4.68E-15	26.61157	MPDU1	mannose-P-dolichol utilization defect 1	AF059752
208613_s_at	0.66952	8.5326769	6.98089	4.16E-11	3.78E-10	14.64367	FLNB	filamin B, beta (actin binding protein 278)	AV712733
230166_at	0.66948	5.6028113	7.688154	6.45E-13	7.87E-12	18.72432	KIAA1958	KIAA1958	BG026236
218979_at	0.66936	7.7625344	8.317814	1.33E-14	2.15E-13	22.53442	RMI1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	NM_024945
224972_at	0.66915	9.4803213	10.51234	6.92E-21	3.25E-19	36.78951	ROMO1	reactive oxygen species modulator 1	BF381837
229676_at	0.66908	7.4806156	7.338731	5.19E-12	5.49E-11	16.67999	PAPD1	Clone peg2041 hypothetical protein (FJ10486)	AA400998
204981_at	0.66904	8.5672549	4.437864	1.49E-05	5.44E-05	2.245735	SLC22A18	solute carrier family 22, member 18	NM_002555
202488_s_at	0.66884	8.9035036	4.894495	2.02E-06	8.53E-06	4.164464	FXVD3	FXVD domain containing ion transport regulator 3	NM_005971
1559946_s_at	0.66878	10.105559	11.46106	9.71E-24	7.96E-22	43.27252	RUVBL2	RuvB-like 2 (E. coli)	AI860098
224598_at	0.66869	10.150702	7.272125	7.68E-12	7.88E-11	16.29644	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	BF570193
225994_at	0.66861	7.7762543	8.775015	7.29E-16	1.47E-14	25.39161	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	AK023583
200598_s_at	0.6686	11.253655	10.39168	1.58E-20	7.03E-19	35.97562	HSP90B1	heat shock protein 90kDa beta (Grp94), member 1	AI582238
200853_at	0.66859	11.303993	11.71044	1.69E-24	1.62E-22	44.99707	H2AFZ	H2A histone family, member Z	NM_002106
224613_s_at	0.66842	6.7459109	10.63278	3.03E-21	1.53E-19	37.60456	DNAJC5	DnaJ (Hsp40) homolog, subfamily C, member 5	BF115518
225580_at	0.66813	7.8252034	8.30902	1.41E-14	2.27E-13	22.48017	MRPL50	mitochondrial ribosomal protein L50	BG028213
239202_at	0.66802	5.3658372	6.37475	1.23E-09	8.73E-09	11.33935	0		0 BE552383

214096_s_at	0.66786	10.082372	8.929165	2.70E-16	5.86E-15	26.37038	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	AW190316
202869_at	0.66784	8.5814394	4.820489	2.82E-06	1.17E-05	3.843319	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	NM_016816
1556613_s_at	0.66759	6.1883718	7.461497	2.51E-12	2.80E-11	17.39216	LOC203107	hypothetical protein LOC203107	BC038568
219212_at	0.66738	8.5635604	9.429966	1.02E-17	2.82E-16	29.5987	HSPA14	heat shock 70kDa protein 14	NM_016299
205704_s_at	0.66733	6.9506849	8.662402	1.50E-15	2.86E-14	24.68135	ATP6VOA2	ATPase, H+ transporting, lysosomal VO subunit a2	NM_012463
215207_x_at	0.66732	5.5786843	9.829278	7.11E-19	2.42E-17	32.22076	LOC646208	nuclear undecaprenyl pyrophosphate synthase 1 pseudogene /// nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae) /// YDD19 protein	BF695847
221620_s_at	0.66729	8.3116757	9.742738	1.27E-18	4.12E-17	31.64918	APOO	apolipoprotein O	AF061264
235931_at	0.66726	6.9767297	8.351726	1.08E-14	1.77E-13	22.74387	FAM119A	family with sequence similarity 119, member A	AI332764
212902_at	0.6672	6.9096193	6.897885	6.68E-11	5.87E-10	14.18009	SEC24A	SEC24 family, member A (S. cerevisiae)	BE645231
239355_at	0.66688	8.5491677	9.873384	5.29E-19	1.84E-17	32.51274	0	0	BF675979
1554794_a_at	0.66681	5.1475837	9.783942	9.63E-19	3.20E-17	31.9211	UBE3C	ubiquitin protein ligase E3C	BC014029
224746_at	0.66645	9.1532995	7.514632	1.83E-12	2.09E-11	17.70247	KIAA1522	KIAA1522	AB040955
208659_at	0.66644	12.04305	12.00522	2.13E-25	2.39E-23	47.04402	CLIC1	chloride intracellular channel 1	AF034607
233588_x_at	0.66643	8.4606359	11.86889	5.56E-25	5.83E-23	46.09625	PFDN6	prefoldin subunit 6	BE561798
225485_at	0.66606	6.1429851	6.708611	1.94E-10	1.58E-09	13.13585	TSGA14	testis specific, 14	AJ278890
205321_at	0.66585	8.5948353	4.755596	3.76E-06	1.53E-05	3.564914	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	NM_001415
213082_s_at	0.66576	7.741652	7.982364	1.07E-13	1.49E-12	20.48539	SLC35D2	solute carrier family 35, member D2	AJ005866
241371_at	0.66567	6.7029562	7.12834	1.78E-11	1.72E-10	15.47544	0	0	AW451259
231918_s_at	0.66562	6.5777988	8.179726	3.16E-14	4.79E-13	21.68584	GFM2	G elongation factor, mitochondrial 2	AK025314
212621_at	0.66552	7.3286274	8.139652	4.05E-14	6.05E-13	21.44089	TMEM194A	transmembrane protein 194A	AB006624
229616_s_at	0.66526	5.5042535	6.943931	5.14E-11	4.60E-10	14.43684	GRAMD2	GRAM domain containing 2	AU158463
202138_x_at	0.66505	9.8324501	11.42474	1.25E-23	1.01E-21	43.02197	JTV1	JTV1 gene	NM_006303
203594_at	0.66478	9.1106555	9.379315	1.42E-17	3.86E-16	29.26901	RTCD1	RNA terminal phosphate cyclase domain 1	NM_003729
224654_at	0.66478	10.194753	10.22757	4.83E-20	2.00E-18	34.87312	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	BG164358
210048_at	0.6647	6.9125363	8.901744	3.22E-16	6.91E-15	26.19573	NAPG	N-ethylmaleimide-sensitive factor attachment protein, gamma	BC001889
209108_at	0.66459	8.8008728	5.079403	8.60E-07	3.89E-06	4.983545	TSPAN6	tetraspanin 6	AF053453
225649_s_at	0.66456	9.833286	9.596421	3.37E-18	1.02E-16	30.68689	STK35	serine/threonine kinase 35	AA001414
221703_at	0.66454	4.0419737	9.480523	7.28E-18	2.06E-16	29.92846	BRIP1	BRCA1 interacting protein C-terminal helicase 1	AF360549
222456_s_at	0.66434	6.9122084	4.659113	5.76E-06	2.26E-05	3.156553	LIMA1	LIM domain and actin binding 1	BF197289
204866_at	0.66415	7.4556435	7.176847	1.34E-11	1.32E-10	15.75133	PHF16	PHD finger protein 16	NM_014735
239078_at	0.6641	5.8683784	6.661729	2.53E-10	2.02E-09	12.88003	C1orf58	chromosome 1 open reading frame 58	BG500291
208931_s_at	0.66408	7.7711209	10.72157	1.64E-21	8.74E-20	38.20712	ILF3	interleukin enhancer binding factor 3, 90kDa	AF147209
243292_at	0.66406	6.1793273	4.885395	2.10E-06	8.87E-06	4.124766	FAM132A	family with sequence similarity 132, member A	BF589994
213425_at	0.66378	7.3566834	4.012466	8.47E-05	0.0002685	0.598018	WNT5A	wingless-type MMTV integration site family, member 5A	AI968085
213393_at	0.66374	6.363053	7.75396	4.33E-13	5.46E-12	19.11516	0	0	AI767210
235153_at	0.66365	6.3265616	4.748881	3.88E-06	1.57E-05	3.536278	RNF183	ring finger protein 183	BE796148
201584_s_at	0.66325	9.8301491	9.003684	1.66E-16	3.74E-15	26.84615	DDX39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	NM_005804
222506_at	0.6632	5.9887084	8.618503	1.99E-15	3.72E-14	24.40559	LMBR1	limb region 1 homolog (mouse)	AF107454
202058_s_at	0.66293	6.8724592	7.767381	3.99E-13	5.06E-12	19.19509	KPNA1	karyopherin alpha 1 (importin alpha 5)	BC002374

204588_s_at	0.66287	8.9681335	6.335834	1.51E-09	1.06E-08	11.13386	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	NM_003982
213822_s_at	0.66279	6.8495513	8.714991	1.07E-15	2.10E-14	25.01252	UBE3B	ubiquitin protein ligase E3B	BE856776
210093_s_at	0.66276	8.8647997	11.68031	2.09E-24	1.97E-22	44.78833	MAGOH	mago-nashi homolog, proliferation-associated (Drosophila)	AF067173
208779_x_at	0.66273	9.4152374	6.124962	4.68E-09	3.05E-08	10.03508	DDR1	discoidin domain receptor tyrosine kinase 1	L20817
201377_at	0.66267	8.6543762	11.12424	1.02E-22	6.84E-21	40.95559	UBAP2L	ubiquitin associated protein 2-like	NM_014847
221291_at	0.66264	5.538987	7.638126	8.72E-13	1.04E-11	18.42839	ULBP2	UL16 binding protein 2	NM_025217
219890_at	0.66249	4.9145569	5.161347	5.86E-07	2.71E-06	5.354029	CLEC5A	C-type lectin domain family 5, member A	NM_013252
213470_s_at	0.66233	6.4740937	5.586433	7.45E-08	3.97E-07	7.347293	HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 (H)	BF983406
1554539_a_at	0.66231	6.5291756	5.503993	1.12E-07	5.81E-07	6.951574	RHOF	ras homolog gene family, member F (in filopodia)	BC018208
200867_at	0.66224	8.7835418	10.51911	6.60E-21	3.11E-19	36.83527	RNF114	ring finger protein 114	AL031685
212115_at	0.66218	9.7329271	9.428776	1.02E-17	2.84E-16	29.59095	HN1L	hematological and neurological expressed 1-like	AK023154
222393_s_at	0.66213	8.6687586	8.221287	2.44E-14	3.76E-13	21.9405	NAT13	N-acetyltransferase 13 (GCN5-related)	AU149868
214358_at	0.66212	6.0441465	8.47931	4.81E-15	8.51E-14	23.53551	ACACA	acetyl-Coenzyme A carboxylase alpha	AW188201
203564_at	0.66207	7.4119524	9.427699	1.03E-17	2.86E-16	29.58393	FANCG	Fanconi anemia, complementation group G	NM_004629
208828_at	0.66206	9.3171949	9.869455	5.43E-19	1.88E-17	32.48672	POLE3	polymerase (DNA directed), epsilon 3 (p17 subunit)	BC004170
219750_at	0.66188	4.7212872	5.996562	9.19E-09	5.68E-08	9.378497	TMEM144	transmembrane protein 144	NM_018342
210665_at	0.66184	5.9441141	3.712972	0.0002651	0.0007641	-0.47708	TFPI	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	AF021834
216969_s_at	0.66175	6.1554002	13.21737	3.96E-29	9.73E-27	55.53028	KIF22	kinesin family member 22	AC002301
215747_s_at	0.66171	6.9964955	12.02126	1.90E-25	2.15E-23	47.1557	RCC1 /// SN	regulator of chromosome condensation 1 /// SNHG3-RCC1 readthrough transcript	X06130
228733_at	0.66167	7.2024402	11.3511	2.09E-23	1.61E-21	42.51446	PUSL1	pseudouridylate synthase-like 1	AU154793
234749_s_at	0.66151	5.5571144	10.55157	5.29E-21	2.53E-19	37.05469	WDR51A	WD repeat domain 51A	AL117629
226431_at	0.66136	7.6178751	6.897534	6.69E-11	5.88E-10	14.17813	FAM117B	family with sequence similarity 117, member B	AK025007
216521_s_at	0.66131	6.9661577	7.616987	9.91E-13	1.18E-11	18.30367	BRCC3	BRCA1/BRCA2-containing complex, subunit 3	S72931
223040_at	0.66118	9.9488959	12.18923	5.82E-26	7.29E-24	48.32594	NAT5	N-acetyltransferase 5 (GCN5-related, putative)	BC005181
224511_s_at	0.66096	10.925254	10.22405	4.94E-20	2.04E-18	34.84949	TXNDC17	thioredoxin domain containing 17	BC006405
232105_at	0.66091	5.304735	5.226078	4.31E-07	2.05E-06	5.649888	0	0	AU148391
243372_at	0.66086	4.9476221	7.604371	1.07E-12	1.26E-11	18.22933	HSPD1 /// H4	heat shock 60kDa protein 1 (chaperonin) /// heat shock 60kDa protein 1 (chaperonin) pseudogene	AW674195
223532_at	0.66067	6.9544003	10.88346	5.38E-22	3.13E-20	39.30908	ANKRD39	ankyrin repeat domain 39	AF151034
238598_s_at	0.66056	4.6869276	8.88836	3.51E-16	7.48E-15	26.11057	0	0	BE962709
209027_s_at	0.6603	9.5152001	8.519071	3.74E-15	6.73E-14	23.78339	ABI1	abl-interactor 1	BF673013
203672_x_at	0.66014	8.5256704	8.062069	6.56E-14	9.41E-13	20.96841	TPMT	thiopurine S-methyltransferase	U12387
201876_at	0.66001	10.401369	6.287883	1.96E-09	1.35E-08	10.88181	PON2	paraoxonase 2	NM_000305
200890_s_at	0.65973	8.9470972	8.56057	2.87E-15	5.25E-14	24.04266	SSR1	signal sequence receptor, alpha	AW006345
205691_at	0.65971	6.2841395	4.492058	1.19E-05	4.40E-05	2.465501	SYNGR3	synaptogyrin 3	NM_004209
222385_x_at	0.65962	8.7243193	8.860692	4.20E-16	8.82E-15	25.93469	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	AF346602
204485_s_at	0.65951	8.7093136	4.905799	1.91E-06	8.14E-06	4.213856	TOM1L1	target of myb1 (chicken)-like 1	NM_005486
220104_at	0.65947	5.7828569	7.791425	3.45E-13	4.42E-12	19.33848	ZC3HAV1	zinc finger CCCH-type, antiviral 1	NM_020119
220153_at	0.65933	6.7046389	9.349951	1.72E-17	4.63E-16	29.07818	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	NM_020354
238460_at	0.65929	4.5852821	4.641061	6.24E-06	2.43E-05	3.080895	FAM83A	family with sequence similarity 83, member A	AI590662
223819_x_at	0.65928	8.4160004	12.1127	9.99E-26	1.19E-23	47.79247	COMMD5	COMM domain containing 5	BC003055

210386_s_at	0.65919	9.1594051	13.14264	6.73E-29	1.61E-26	55.00491	MTX1	metaxin 1	BC001906
210175_at	0.65874	6.8219362	9.082613	9.95E-17	2.34E-15	27.3519	C2orf3	chromosome 2 open reading frame 3	BC000853
208932_at	0.65872	9.7852143	13.25519	3.02E-29	7.87E-27	55.79628	PPP4C	protein phosphatase 4 (formerly X), catalytic subunit	BC001416
218424_s_at	0.65867	8.2979184	6.03589	7.48E-09	4.70E-08	9.578582	STEAP3	STEAP family member 3	NM_018234
215033_at	0.65851	4.555936	6.272515	2.13E-09	1.46E-08	10.8013	TM4SF1	transmembrane 4 L six family member 1	AI189753
210087_s_at	0.65817	7.9366725	8.400998	7.89E-15	1.33E-13	23.04892	MPZL1	myelin protein zero-like 1	AF095727
207782_s_at	0.65817	8.1139041	10.13018	9.35E-20	3.66E-18	34.22142	PSEN1	presenilin 1	NM_007319
219208_at	0.6581	3.9884605	11.15565	8.16E-23	5.57E-21	41.171	FBXO11	F-box protein 11	NM_025133
209294_x_at	0.65792	6.9152467	7.99614	9.85E-14	1.37E-12	20.5687	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	BC001281
202418_at	0.65766	10.135809	9.407531	1.18E-17	3.24E-16	29.45258	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	NM_020470
212312_at	0.65763	9.5748357	9.777093	1.01E-18	3.34E-17	31.87588	BCL2L1	BCL2-like 1	AL117381
228996_at	0.65754	5.6615301	7.538469	1.59E-12	1.83E-11	17.84208	RC3H1	ring finger and CCCH-type zinc finger domains 1	AW205418
219797_at	0.6573	6.5726034	5.768925	2.97E-08	1.69E-07	8.238428	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	NM_012214
64408_s_at	0.65713	8.9049524	3.719304	0.000259	0.0007478	-0.4551	CALML4	calmodulin-like 4	AW025529
214430_at	0.65696	8.7260189	9.613904	3.00E-18	9.14E-17	30.80159	GLA	galactosidase, alpha	NM_000169
212072_s_at	0.65671	9.5260158	11.06836	1.50E-22	9.72E-21	40.57271	CSNK2A1	casein kinase 2, alpha 1 polypeptide	AL049761
203605_at	0.65663	8.9239464	9.496714	6.54E-18	1.88E-16	30.03421	SRP54	signal recognition particle 54kDa	NM_003136
225837_at	0.65659	8.2580128	8.631266	1.83E-15	3.45E-14	24.4857	C12orf32	chromosome 12 open reading frame 32	AL577977
205032_at	0.65654	7.9271132	6.890471	6.97E-11	6.10E-10	14.13885	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	NM_002203
1552977_a_at	0.65651	7.5658291	6.685736	1.29E-15	2.49E-14	24.82817	CNPY3	canopy 3 homolog (zebrafish)	NM_006586
215243_s_at	0.6564	7.1288757	4.754312	3.79E-06	1.53E-05	3.559437	GJB3	gap junction protein, beta 3, 31kDa	AF099730
222592_s_at	0.6563	9.5204927	4.193207	4.12E-05	0.0001385	1.28112	ACSL5	acyl-CoA synthetase long-chain family member 5	AW173691
231953_at	0.65628	4.7075021	9.766136	1.09E-18	3.57E-17	31.80354	BPTF	bromodomain PHD finger transcription factor	AK027184
212396_s_at	0.65627	7.959506	10.4055	1.44E-20	6.44E-19	36.05869	KIAA0090	KIAA0090	AI143233
228051_at	0.65626	7.5728753	4.067333	6.82E-05	0.0002202	0.802694	LOC202451	hypothetical protein LOC202451	AI979261
225103_at	0.65613	8.606103	11.86763	5.61E-25	5.85E-23	46.08754	MRPL38	mitochondrial ribosomal protein L38	BE855557
219624_at	0.6561	5.2359081	8.664123	1.48E-15	2.84E-14	24.69217	BAG4	BCL2-associated athanogene 4	NM_004874
204117_at	0.65584	8.8835677	8.637677	1.76E-15	3.32E-14	24.52595	PREP	prolyl endopeptidase	NM_002726
222602_at	0.65563	8.2011216	9.432206	1.00E-17	2.78E-16	29.6133	UBA6	ubiquitin-like modifier activating enzyme 6	AW296050
201923_at	0.65554	11.466647	8.392002	8.35E-15	1.40E-13	22.99316	PRDX4	peroxiredoxin 4	NM_006406
205135_s_at	0.65548	6.6284711	9.448018	9.02E-18	2.52E-16	29.71637	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	AL049842
212340_at	0.65525	7.3994232	10.1665	7.31E-20	2.93E-18	34.46419	YIPF6	Yip1 domain family, member 6	BE673723
238867_at	0.65492	5.039203	10.03682	1.76E-19	6.61E-18	33.59856	TMEM182	transmembrane protein 182	AI298041
235269_at	0.65489	6.4521404	5.79249	2.64E-08	1.51E-07	8.355	FAM83F	family with sequence similarity 83, member F	BE786265
1558164_s_at	0.65487	4.9110147	9.716453	1.51E-18	4.84E-17	31.47592	PEX13	peroxisomal biogenesis factor 13	BC040953
223798_at	0.65476	6.9816567	4.935984	1.67E-06	7.16E-06	4.346181	SLC41A2	solute carrier family 41, member 2	AL136828
213237_at	0.65466	6.68564	8.490987	4.47E-15	7.95E-14	23.60825	C16orf88	chromosome 16 open reading frame 88	AI652058
210546_x_at	0.65465	4.6448806	3.667955	0.0003129	0.0008899	-0.63242	CTAG1A ///	cancer/testis antigen 1A ///	U87459
215728_s_at	0.65442	7.1362768	8.997166	1.74E-16	3.89E-15	26.80447	ACOT7	cancer/testis antigen 1B	AL031848
217289_s_at	0.65442	7.0795817	9.019077	1.51E-16	3.41E-15	26.94464	SLC37A4	acyl-CoA thioesterase 7	AF097831
1553801_a_at	0.65436	5.2479501	8.100266	5.18E-14	7.56E-13	21.20074	C14orf126	solute carrier family 37 (glucose-6-phosphate transporter), member 4	NM_080664
229426_at	0.65433	6.3878246	9.576661	3.84E-18	1.15E-16	30.55734	COX5A	chromosome 14 open reading frame 126	BF196691
								cytochrome c oxidase subunit Va	

225638_at	0.65433	8.8517148	11.15107	8.43E-23	5.74E-21	41.13959	C1orf31	chromosome 1 open reading frame 31	AI564054
218793_s_at	0.65423	7.6764241	5.661482	5.12E-08	2.80E-07	7.711263	SCML1	sex comb on midleg-like 1 (Drosophila)	NM_006746
200607_s_at	0.65416	9.5167211	9.313708	2.19E-17	5.79E-16	28.84299	RAD21	RAD21 homolog (S. pombe)	BG289967
226461_at	0.65405	6.5951412	6.749001	1.55E-10	1.28E-09	13.35716	HOXB9	homeobox B9	AA204719
222821_s_at	0.65365	7.787706	11.02042	2.09E-22	1.31E-20	40.24456	GEMIN7	gem (nuclear organelle) associated protein 7	AL530748
1553956_at	0.65346	7.0459877	8.039038	7.56E-14	1.07E-12	20.82859	ALS2CR4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	BG194770
238794_at	0.65339	6.5595152	5.832808	2.14E-08	1.25E-07	8.555228	C10orf78	chromosome 10 open reading frame 78	N23586
218704_at	0.65334	7.2028778	4.687777	5.08E-06	2.01E-05	3.277174	RNF43	ring finger protein 43	NM_017763
210104_at	0.65307	8.0138123	10.14287	8.58E-20	3.38E-18	34.30619	MED6	mediator complex subunit 6	AF074723
218326_s_at	0.65302	8.5426187	5.108881	7.50E-07	3.42E-06	5.116292	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	NM_018490
212527_at	0.65279	7.777301	9.561948	4.24E-18	1.25E-16	30.46094	FAM152B	family with sequence similarity 152, member B	BF057059
226264_at	0.65264	6.6861421	8.86866	3.99E-16	8.42E-15	25.98532	SUSD1	sushi domain containing 1	AL137432
218702_at	0.65253	6.9693619	10.23473	4.60E-20	1.91E-18	34.92106	SARS2	seryl-tRNA synthetase 2, mitochondrial	NM_017827
218193_s_at	0.65219	8.6242888	8.890213	3.47E-16	7.40E-15	26.12235	GOLT1B	golgi transport 1 homolog B (S. cerevisiae)	NM_016072
227718_at	0.65214	7.1777397	8.112011	4.81E-14	7.07E-13	21.2723	PURB	purine-rich element binding protein B	BF337790
203931_s_at	0.65213	9.1010171	11.32583	2.50E-23	1.88E-21	42.34051	MRPL12	mitochondrial ribosomal protein L12	NM_002949
224368_s_at	0.65212	7.3229945	7.787998	3.52E-13	4.50E-12	19.31802	NDRG3	NDRG family member 3	AF251054
202684_s_at	0.65209	5.6941387	9.979698	2.58E-19	9.54E-18	33.21837	RNMT	RNA (guanine-7-) methyltransferase	AB020966
204393_s_at	0.65205	5.2919816	4.845974	2.51E-06	1.05E-05	3.953475	ACPP	acid phosphatase, prostate	NM_001099
211603_s_at	0.65205	6.8424725	6.886688	7.12E-11	6.22E-10	14.11781	ETV4	ets variant 4	U35622
238629_x_at	0.65205	5.7379149	5.465061	1.36E-07	6.95E-07	6.766203	0	0	AI240943
222386_s_at	0.65203	10.105226	10.89135	5.10E-22	2.98E-20	39.36284	COPZ1	coatamer protein complex, subunit zeta 1	AB047848
201420_s_at	0.65202	8.1489375	9.699356	1.70E-18	5.37E-17	31.36332	WDR77	WD repeat domain 77	BF975273
203125_x_at	0.65195	7.3518392	9.19253	4.85E-17	1.20E-15	28.05923	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	AF046997
210470_x_at	0.65172	9.607593	10.14267	8.59E-20	3.38E-18	34.30489	NONO	non-POU domain containing, octamer-binding	BC003129
223542_at	0.65155	6.4646016	7.628067	9.27E-13	1.11E-11	18.36902	ANKRD32	ankyrin repeat domain 32	AL136560
222768_s_at	0.65155	8.0052696	9.202205	4.55E-17	1.13E-15	28.12165	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	BE897074
202199_s_at	0.65154	7.2897219	10.48227	8.50E-21	3.94E-19	36.58639	SRPK1	SFRS protein kinase 1	AW082913
212264_s_at	0.65144	8.4854093	9.19769	4.69E-17	1.16E-15	28.09252	WAPAL	wings apart-like homolog (Drosophila)	BE645850
1556064_at	0.65132	5.5758887	8.01897	8.56E-14	1.20E-12	20.70692	LOC284926	hypothetical protein LOC284926	BQ575161
202955_s_at	0.65106	7.8700551	9.93331	3.53E-19	1.27E-17	32.91017	ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	AF084520
214700_x_at	0.651	7.0973914	9.831237	7.02E-19	2.39E-17	32.23371	RIF1	RAP1 interacting factor homolog (yeast)	AK000323
218670_at	0.65082	7.1897766	10.62599	3.17E-21	1.59E-19	37.55854	PUS1	pseudouridylate synthase 1	NM_025215
212871_at	0.65068	7.6235866	11.28149	3.40E-23	2.50E-21	42.03545	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	NM_003668
219038_at	0.65059	7.7898156	6.412224	1.00E-09	7.22E-09	11.53802	MORC4	MORC family CW-type zinc finger 4	NM_024657
209233_at	0.65057	9.4134158	11.06245	1.56E-22	1.01E-20	40.5322	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)	U72514
1552617_a_at	0.65056	8.5186159	9.711808	1.56E-18	4.97E-17	31.44532	RFWD2	ring finger and WD repeat domain 2	NM_022457
200636_s_at	0.65034	10.349018	6.979037	4.20E-11	3.82E-10	14.63329	PTPRF	protein tyrosine phosphatase, receptor type, F	NM_002840
214527_s_at	0.6502	8.922635	8.653773	1.59E-15	3.01E-14	24.62709	PQB1	polyglutamine binding protein 1	AB041836
209853_s_at	0.65014	8.364753	11.3487	2.13E-23	1.63E-21	42.49796	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	BC002684

1554036_at	0.65008	4.7865297	7.451501	2.66E-12	2.96E-11	17.33393	ZBTB24	zinc finger and BTB domain containing 24	BC036731
232591_s_at	0.65004	8.1583574	6.26904	2.17E-09	1.49E-08	10.78311	TMEM30A	transmembrane protein 30A	AK022883
204769_s_at	0.64999	7.4095989	5.814104	2.36E-08	1.36E-07	8.462217	TAP2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	M74447
226608_at	0.64989	6.0918138	6.927221	5.65E-11	5.02E-10	14.34354	C16orf87	chromosome 16 open reading frame 87	AW157311
219217_at	0.64987	8.8404245	9.399534	1.24E-17	3.41E-16	29.40053	NARS2	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	NM_024678
215044_s_at	0.6498	6.9270716	10.32555	2.48E-20	1.07E-18	35.53071	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	AI571996
217301_x_at	0.64977	9.2627173	8.681038	1.33E-15	2.56E-14	24.7986	RBBP4	retinoblastoma binding protein 4	X71810
202546_at	0.64955	10.738615	6.156297	3.96E-09	2.60E-08	10.19676	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	NM_003761
225568_at	0.64949	8.8181429	8.013221	8.87E-14	1.24E-12	20.6721	KIAA1984	KIAA1984 /// transmembrane protein 141	BE728983
201411_s_at	0.64936	9.1713992	10.35767	1.99E-20	8.77E-19	35.74667	PLEKH82	pleckstrin homology domain containing, family B (evectins) member 2	NM_017958
208308_s_at	0.64934	10.749765	9.793761	9.02E-19	3.01E-17	31.98596	GPI /// LOC	glucose phosphate isomerase /// similar to Glucose phosphate isomerase	NM_000175
223586_at	0.64933	7.2650851	6.827798	9.94E-11	8.46E-10	13.79131	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	AF256215
222163_s_at	0.64926	8.4397745	8.850303	4.49E-16	9.39E-15	25.86872	SPATA5L1	spermatogenesis associated 5-like 1	BE890973
214481_at	0.64922	4.8373216	8.694036	1.23E-15	2.37E-14	24.88045	HIST1H2AM	Histone cluster 1, H2am (HIST1H2AM), mRNA	NM_003514
202278_s_at	0.6488	7.729681	9.973893	2.69E-19	9.88E-18	33.17977	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	NM_006415
221845_s_at	0.64858	7.0714684	10.90769	4.55E-22	2.69E-20	39.47435	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	AI655698
203702_s_at	0.64836	7.0306342	9.445187	9.19E-18	2.57E-16	29.69791	TTL4	tubulin tyrosine ligase-like family, member 4	AL043927
209653_at	0.64831	7.4743736	7.075085	2.42E-11	2.28E-10	15.17383	KPNA4	karyopherin alpha 4 (importin alpha 3)	U93240
213741_s_at	0.64813	6.781551	7.416017	3.29E-12	3.60E-11	17.12755	KPNA1	karyopherin alpha 1 (importin alpha 5)	BF575685
208967_s_at	0.64804	9.685043	11.33254	2.38E-23	1.80E-21	42.38672	AK2	adenylate kinase 2	U39945
226597_at	0.64785	7.1532753	4.013541	8.43E-05	0.0002675	0.602008	REEP6	receptor accessory protein 6	AI348159
220189_s_at	0.64778	8.757068	7.466362	2.44E-12	2.73E-11	17.42052	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	NM_014275
203856_at	0.64766	8.1060196	9.256108	3.20E-17	8.17E-16	28.46993	VRK1	vaccinia related kinase 1	NM_003384
229666_s_at	0.64748	7.0285809	6.567797	4.26E-10	3.28E-09	12.37092	CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	AI653037
217754_at	0.64738	8.3518044	12.88635	4.17E-28	8.27E-26	53.20468	DDX56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	NM_019082
222767_s_at	0.64702	7.8005832	9.71562	1.52E-18	4.86E-17	31.47044	C12orf49	chromosome 12 open reading frame 49	AW872378
1558143_a_at	0.64698	7.6064076	7.539143	1.58E-12	1.82E-11	17.84603	BCL2L11	BCL2-like 11 (apoptosis facilitator)	AK027160
218507_at	0.64697	8.1018441	5.746067	3.34E-08	1.88E-07	8.125682	HIG2	hypoxia-inducible protein 2	NM_013332
1558015_s_at	0.6469	8.3419602	6.677676	2.31E-10	1.85E-09	12.96692	ACTR2	ARP2 actin-related protein 2 homolog (yeast)	BU175810
215947_s_at	0.6468	9.2716275	11.47891	8.57E-24	7.09E-22	43.39571	FAM135A	family with sequence similarity 136, member A	AF090094
224173_s_at	0.64678	6.2057505	8.18266	3.10E-14	4.71E-13	21.7038	MRPL30	mitochondrial ribosomal protein L30	BC000217
202667_s_at	0.64672	7.7876076	9.221812	4.01E-17	1.00E-15	28.24824	SLC39A7	solute carrier family 39 (zinc transporter), member 7	NM_006979
228439_at	0.64671	7.3379356	4.849144	2.48E-06	1.03E-05	3.967206	BATF2	basic leucine zipper transcription factor, ATF-like 2	AW083820
222735_at	0.64661	7.9800839	6.676762	2.32E-10	1.87E-09	12.96194	TMEM38B	transmembrane protein 38B	AW452608
222398_s_at	0.64659	9.9176889	14.19327	3.77E-32	2.67E-29	62.40148	EFTUD2	elongation factor Tu GTP binding domain containing 2	BC002360
212709_at	0.64653	7.8033201	8.646046	1.67E-15	3.16E-14	24.57853	NUP160	nucleoporin 160kDa	D83781
209445_x_at	0.64627	8.1595335	10.19459	6.04E-20	2.46E-18	34.65221	C7orf44	chromosome 7 open reading frame 44	AI765280

204460_s_at	0.64618	7.9748272	8.780921	7.02E-16	1.42E-14	25.42897	RAD1	RAD1 homolog (S. pombe)	AF074717
226565_at	0.64616	7.560965	6.073825	6.13E-09	3.91E-08	9.772441	TMEM99	transmembrane protein 99	AW054855
231955_s_at	0.64603	7.302661	5.990176	9.50E-09	5.86E-08	9.346094	HIBADH	3-hydroxyisobutyrate dehydrogenase	AC007130
223369_at	0.6456	7.4998272	10.19853	5.88E-20	2.39E-18	34.67856	METTL1A	methyltransferase like 11A	BC001396
210186_s_at	0.64557	9.0299129	9.614909	2.98E-18	9.09E-17	30.80819	FKBP1A	FK506 binding protein 1A, 12kDa	BC005147
235033_at	0.6455	6.374049	7.659633	7.66E-13	9.24E-12	18.55548	NPEPL1	CDNA FLJ55989 complete cds, highly similar to Probable aminopeptidase NPEPL1 (EC 3.4.11.-)	AL577823
215549_x_at	0.64539	7.5720034	7.508086	1.90E-12	2.17E-11	17.66417	CTAGE4	CTAGE family, member 4	AC005587
216032_s_at	0.64537	10.599306	9.777569	1.01E-18	3.33E-17	31.87902	ERGIC3	ERGIC and golgi 3	AF091085
230448_at	0.6453	6.9454607	8.79413	6.45E-16	1.31E-14	25.51257	SLC38A10	solute carrier family 38, member 10	AI869717
1564520_s_at	0.64492	8.3322207	9.872817	5.31E-19	1.84E-17	32.50898	PRMT5	protein arginine methyltransferase 5	AK027737
201489_at	0.64485	9.6068202	8.124586	4.45E-14	6.58E-13	21.34896	PPIF	peptidylprolyl isomerase F	BC005020
225100_at	0.64484	6.6002347	9.543002	4.81E-18	1.41E-16	30.33689	FBXO45	F-box protein 45	BF590021
201920_at	0.64467	9.1672642	7.562883	1.37E-12	1.60E-11	17.98532	SLC20A1	solute carrier family 20 (phosphate transporter), member 1	NM_005415
218608_at	0.64442	6.7463977	10.26347	3.78E-20	1.60E-18	35.1138	ATP13A2	ATPase type 13A2	NM_022089
232977_x_at	0.64409	7.6948941	4.994112	1.28E-06	5.60E-06	4.602793	MYH14	myosin, heavy chain 14	BC004396
222206_s_at	0.64398	7.5426059	7.196727	1.19E-11	1.18E-10	15.86472	NCLN	nicalin homolog (zebrafish)	AA781143
207325_x_at	0.64379	4.5610226	4.044035	7.48E-05	0.0002396	0.715495	MAGEA1	melanoma antigen family A, 1 (directs expression of antigen MZ2-E)	NM_004988
1555226_s_at	0.64377	10.466155	10.04338	1.68E-19	6.35E-18	33.64226	C1orf43	chromosome 1 open reading frame 43	BC008306
214734_at	0.64364	6.9651154	4.652378	5.94E-06	2.33E-05	3.128301	EXPH5	exophilin 5	AB014524
224695_at	0.64363	9.1700819	12.64901	2.25E-27	3.81E-25	51.5403	C2orf29	chromosome 2 open reading frame 29	AK024221
209163_at	0.6433	8.6814133	6.54781	4.75E-10	3.64E-09	12.26318	CYB561	cytochrome b-561	AL514271
205329_s_at	0.64324	7.4987636	9.461931	8.23E-18	2.32E-16	29.80711	SNX4	sorting nexin 4	NM_003794
217791_s_at	0.64322	9.0481582	8.820102	5.46E-16	1.12E-14	25.67712	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	NM_002860
205216_s_at	0.64308	5.0234946	4.480193	1.25E-05	4.61E-05	2.417199	APOH	apolipoprotein H (beta-2-glycoprotein I)	NM_000042
1555427_s_at	0.64303	7.3179383	9.508267	6.05E-18	1.75E-16	30.1097	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	AY034482
217850_at	0.64302	9.3321784	9.946304	3.24E-19	1.18E-17	32.99645	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	NM_014366
200644_at	0.64296	11.461161	7.490886	2.11E-12	2.38E-11	17.56364	MARCKSL1	MARCKS-like 1	NM_023009
207456_at	0.64283	4.9016962	5.570732	8.06E-08	4.28E-07	7.271596	HNF4G	hepatocyte nuclear factor 4, gamma	NM_004133
222212_s_at	0.64281	10.379197	10.01825	1.99E-19	7.45E-18	33.47484	LASS2	LAG1 homolog, ceramide synthase 2	AK001105
204433_s_at	0.64267	7.4158598	9.35762	1.64E-17	4.41E-16	29.128	SPATA2	spermatogenesis associated 2	U28164
221597_s_at	0.64264	9.3784061	10.90489	4.64E-22	2.73E-20	39.45521	TMEM208	transmembrane protein 208	BC003080
240277_at	0.6425	6.8777042	5.842935	2.04E-08	1.19E-07	8.605672	SLC30A7	Zinc transporter ZNT7 (ZNT7)	AI740796
205568_at	0.64245	6.8425171	4.372297	1.97E-05	7.01E-05	1.982783	AQP9	aquaporin 9	NM_020980
208968_s_at	0.64227	9.3517699	10.86151	6.26E-22	3.59E-20	39.15941	CIAPIN1	cytokine induced apoptosis inhibitor 1	BC002568
226631_at	0.64191	7.3280274	8.008991	9.10E-14	1.27E-12	20.64648	METTL10	methyltransferase like 10	C06331
205572_at	0.64186	6.3803327	5.258032	3.70E-07	1.78E-06	5.796974	ANGPT2	angiopoietin 2	NM_001147
225612_s_at	0.64186	9.6210696	5.267505	3.54E-07	1.70E-06	5.840707	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	BE672260
212297_at	0.64166	9.2204828	8.305702	1.44E-14	2.31E-13	22.45971	ATP13A3	ATPase type 13A3	BF218804
213789_at	0.64166	6.5928033	8.282518	1.66E-14	2.65E-13	22.31685	0	0	N58493
1559861_at	0.64133	5.2040964	7.022619	3.27E-11	3.03E-10	14.87801	0	0	BC042913
213857_s_at	0.64126	10.998025	8.294206	1.55E-14	2.47E-13	22.38885	CD47	CD47 molecule	BG230614
203739_at	0.641	8.9120406	6.7663	1.41E-10	1.17E-09	13.4522	ZNF217	zinc finger protein 217	NM_006526
233208_x_at	0.641	7.2283041	10.88852	5.20E-22	3.03E-20	39.34354	CPSF2	cleavage and polyadenylation specific factor 2, 100kDa	AA583986
211576_s_at	0.64081	7.1710583	9.721382	1.46E-18	4.70E-17	31.5084	SLC19A1	solute carrier family 19 (folate transporter), member 1	BC003068
229400_at	0.64071	4.5767356	4.901734	1.95E-06	8.28E-06	4.196081	HOXD10	homeobox D10	AW299531
229744_at	0.64058	7.6218726	6.343103	1.46E-09	1.02E-08	11.17218	SSFA2	Cleavage signal 1 protein	AL556611

225036_at	0.6404	10.362458	10.99416	2.50E-22	1.55E-20	40.06498	SHB /// TOR	Src homology 2 domain containing adaptor protein B /// translocase of outer mitochondrial membrane 5 homolog (yeast)	BF969806
211337_s_at	0.6403	6.8816225	9.25055	3.32E-17	8.43E-16	28.43398	TUBGCP4	tubulin, gamma complex associated protein 4	BC000966
221485_at	0.64026	9.5650645	8.468823	5.14E-15	9.05E-14	23.47023	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	AL035683
231967_at	0.63981	5.317579	7.77136	3.90E-13	4.95E-12	19.2188	PHF20L1	PHD finger protein 20-like 1	AI913146
217010_s_at	0.63965	4.5760789	7.447043	2.74E-12	3.03E-11	17.30797	CDC25C	cell division cycle 25 homolog C (S. pombe)	AF277724
219874_at	0.63946	6.872607	6.113678	4.97E-09	3.22E-08	9.976995	SLC12A8	solute carrier family 12 (potassium/chloride transporters), member 8	NM_024628
209162_s_at	0.63942	8.6323088	12.10173	1.08E-25	1.28E-23	47.71605	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	U82756
205395_s_at	0.63919	7.2305061	7.408024	3.45E-12	3.77E-11	17.08114	MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	NM_005590
227180_at	0.63904	7.8204975	4.465389	1.33E-05	4.89E-05	2.357083	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	AW138767
213201_s_at	0.63899	6.1124133	5.314761	2.82E-07	1.38E-06	6.059763	TNNT1	troponin T type 1 (skeletal, slow)	AJ011712
205209_at	0.63898	7.1622132	7.871809	2.11E-13	2.81E-12	19.81954	ACVR1B	activin A receptor, type IB	BC000254
225872_at	0.63873	9.3811445	6.942729	5.17E-11	4.63E-10	14.43012	SLC35F5	solute carrier family 35, member F5	AA044835
219305_x_at	0.63847	6.8473323	5.576007	7.85E-08	4.17E-07	7.297009	FBXO2	F-box protein 2	NM_012168
1554883_a_at	0.63823	5.4410043	7.441352	2.83E-12	3.13E-11	17.27484	ERCC8	excision repair cross-complementing rodent repair deficiency, complementation group 8	BC009793
239069_s_at	0.63822	7.8719065	4.692131	4.99E-06	1.98E-05	3.295546	0	0	BF691045
222231_s_at	0.63814	10.456373	8.007781	9.17E-14	1.28E-12	20.63915	LRRCS9	leucine rich repeat containing 59	AK025328
206288_at	0.63809	6.1106771	7.124539	1.82E-11	1.75E-10	15.45387	PGGT1B	protein geranylgeranyltransferase type I, beta subunit	NM_005023
202264_s_at	0.63797	8.3874062	10.45085	1.05E-20	4.82E-19	36.37439	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	NM_006114
213491_x_at	0.63769	12.183374	11.86795	5.60E-25	5.85E-23	46.08974	RPN2	ribophorin II	AL514285
223361_at	0.63745	9.3303889	6.02599	7.88E-09	4.92E-08	9.528129	C6orf115	chromosome 6 open reading frame 115	AF116682
210445_at	0.6373	6.1127533	4.14715	4.96E-05	0.0001644	1.104641	FABP6	fatty acid binding protein 6, ileal	U19869
218582_at	0.63704	8.140272	9.285928	2.63E-17	6.84E-16	28.66295	MARCH5	membrane-associated ring finger (C3HC4) 5	NM_017824
222993_at	0.63681	9.2395333	13.03764	1.42E-28	3.21E-26	54.26704	MRPL37	mitochondrial ribosomal protein L37	AF325707
221761_at	0.63674	8.6804179	9.234094	3.70E-17	9.33E-16	28.3276	ADSS	adenylosuccinate synthase	AA628948
200881_s_at	0.6365	11.088241	10.61637	3.39E-21	1.68E-19	37.4934	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	NM_001539
218356_at	0.63633	8.5067265	10.94853	3.43E-22	2.06E-20	39.75318	FTSJ2	FtsJ homolog 2 (E. coli)	NM_013393
212168_at	0.63593	8.9162892	11.6296	2.99E-24	2.70E-22	44.43725	CPNE1 /// R	copine I /// RNA binding motif protein 12	AL514547
214827_at	0.63586	3.8374146	6.757297	1.48E-10	1.23E-09	13.40272	PARD6B	par-6 partitioning defective 6 homolog beta (C. elegans)	AL031680
224387_at	0.63562	7.4433712	10.72993	1.55E-21	8.31E-20	38.26393	COMMD5	COMM domain containing 5	AF290195
220094_s_at	0.6355	9.0609109	8.2524	2.01E-14	3.15E-13	22.13157	CCDC90A	coiled-coil domain containing 90A	NM_022102
211747_s_at	0.63543	10.485841	11.20952	5.61E-23	3.93E-21	41.5408	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	BC005938
222451_s_at	0.63528	8.8421679	6.555412	4.56E-10	3.50E-09	12.30413	ZDHHC9	zinc finger, DHHC-type containing 9	BC003128
219023_at	0.63519	7.4077634	8.816914	5.57E-16	1.15E-14	25.65691	C4orf16	chromosome 4 open reading frame 16	NM_018569
200990_at	0.63516	9.9258424	10.50572	7.24E-21	3.39E-19	36.74477	TRIM28	tripartite motif-containing 28	NM_005762
201415_at	0.63495	9.0827229	9.020727	1.49E-16	3.38E-15	26.9552	GSS	glutathione synthetase	NM_000178

								ribosomal RNA processing 9, small subunit (SSU) processome component, homolog (yeast)	NM_004704
204133_at	0.63493	6.8428826	10.97993	2.76E-22	1.69E-20	39.96772	RRP9	nucleoporin 205kDa	AW008531
212247_at	0.63472	8.4049392	11.35006	2.11E-23	1.61E-21	42.50734	NUP205	replication protein A1, 70kDa	NM_002945
201529_s_at	0.63467	8.6366193	8.274697	1.75E-14	2.77E-13	22.26871	RPA1	phosphatidylinositol glycan anchor biosynthesis, class O	BC001030
209998_at	0.63448	7.7744709	10.12396	9.75E-20	3.81E-18	34.17988	PIGO	topoisomerase (DNA) I, mitochondrial	AW592604
225802_at	0.63437	7.4430279	7.750509	4.42E-13	5.56E-12	19.09462	TOP1MT	colled-coil domain containing 86	NM_024098
203119_at	0.63427	8.0910728	10.39848	1.51E-20	6.73E-19	36.02138	CCDC86	malignant T cell amplified sequence 1	NM_014060
218163_at	0.63423	9.9157502	8.979252	1.95E-16	4.34E-15	26.68998	MCTS1	poly-U binding splicing factor 60KDa	AF217197
209899_s_at	0.63409	9.8957191	12.13828	8.34E-26	1.02E-23	47.97072	PUF60	nuclear transport factor 2	NM_005796
202397_at	0.63406	9.8353925	9.195516	4.76E-17	1.17E-15	28.07849	NUTF2	ubiquitin-conjugating enzyme E2W (putative)	AK024050
222657_s_at	0.63405	8.6986365	10.37366	1.78E-20	7.89E-19	35.85432	UBE2W	cortactin	BG475299
214073_at	0.63403	6.7894807	6.453588	7.98E-10	5.87E-09	11.7582	CTTN	ribosomal protein S6 kinase, 90kDa, polypeptide 1	NM_002953
203379_at	0.63399	7.887805	5.701261	4.19E-08	2.33E-07	7.905606	RPS6KA1	GTPase activating protein (SH3 domain) binding protein 1	NM_005754
201514_s_at	0.63394	8.7075088	10.56389	4.86E-21	2.33E-19	37.13807	G3BP1	small nuclear ribonucleoprotein polypeptide E	NM_003094
203316_s_at	0.63393	11.257712	12.11895	9.56E-26	1.15E-23	47.83602	SNRPE	TBC1 domain family, member 8B (with GRAM domain)	BC017978
1563272_at	0.63388	4.7516662	8.6255	1.90E-15	3.57E-14	24.4495	TBC1D8B	cathepsin C	AI246687
225647_s_at	0.63387	9.3909164	4.823322	2.78E-06	1.15E-05	3.855543	CTSC	mediator complex subunit 24	AI023317
213043_s_at	0.63384	7.6212964	6.587753	3.81E-10	2.96E-09	12.47869	MED24	zinc finger protein 697	AW003092
227080_at	0.63377	6.914454	7.149291	1.57E-11	1.53E-10	15.59447	ZNF697	tumor necrosis factor receptor superfamily, member 10a	NM_003844
1552648_a_at	0.63377	7.4277893	6.933649	5.45E-11	4.85E-10	14.37941	TNFRSF10A	transmembrane protein 209	AI807036
235158_at	0.6337	7.6901063	8.691464	1.25E-15	2.41E-14	24.86425	TMEM209	zinc finger protein 92	TS2999
235170_at	0.6335	7.5455492	8.46228	5.36E-15	9.38E-14	23.42952	ZNF92	CDNA FLJ53118 complete cds, highly similar to Protein FAM82B	BE962867
229843_at	0.63349	5.4488985	5.144138	6.35E-07	2.93E-06	5.275847	FAM82B	GrpE-like 1, mitochondrial (E. coli)	AL542571
212432_at	0.63336	8.5946123	9.799269	8.69E-19	2.91E-17	32.02235	GRPEL1	RAB7A, member RAS oncogene family	BG261416
211960_s_at	0.63332	9.5410663	8.977774	1.97E-16	4.38E-15	26.68053	RAB7A	poly(A) binding protein interacting protein 1	NM_006451
208051_s_at	0.63326	9.4144625	6.791582	1.22E-10	1.02E-09	13.59138	PAIP1	TBCC domain containing 1	NM_018138
206451_at	0.63319	7.3226313	8.328193	1.25E-14	2.03E-13	22.59848	TBCCD1	survival of motor neuron protein interacting protein 1	AB037702
211114_x_at	0.63314	6.6915845	10.44944	1.06E-20	4.87E-19	36.36491	SIP1	fatty acid synthase	AI954041
212218_s_at	0.63306	7.5871072	7.777794	3.75E-13	4.77E-12	19.25716	FASN		AI926924
239253_at	0.633	3.7806745	6.769543	1.38E-10	1.15E-09	13.47004	0	selenophosphate synthetase 1	BC000941
208941_s_at	0.63293	8.1619949	9.251309	3.30E-17	8.40E-16	28.43889	SEPHS1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	H93026
57163_at	0.6328	9.4579172	9.64726	2.40E-18	7.43E-17	31.02065	ELOVL1	actin related protein 2/3 complex, subunit 5-like	BC000018
223101_s_at	0.63268	8.3064576	11.63893	2.80E-24	2.54E-22	44.5018	ARPC5L	sequestosome 1	N30649
213112_s_at	0.63253	7.205991	8.124411	4.46E-14	6.59E-13	21.3479	SQSTM1	ferredoxin 1	M18003
203647_s_at	0.63246	9.6610689	8.419706	7.02E-15	1.19E-13	23.16497	FDX1	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	NM_005034
202635_s_at	0.63243	9.7541819	9.518712	5.65E-18	1.64E-16	30.17798	POLR2K	fibronectin type III and SPRY domain containing 1-like	H07986
242586_at	0.63241	4.7786765	5.131423	6.75E-07	3.09E-06	5.218209	FSD1L	phosphatidylinositol-specific phospholipase C, X domain containing 2	AW170015
235230_at	0.63239	5.3048115	6.549143	4.72E-10	3.61E-09	12.27036	PLCXD2	casein kinase 2, alpha 1 polypeptide	AI161318
212075_s_at	0.6323	8.7245812	9.912237	4.07E-19	1.45E-17	32.77032	CSNK2A1	transcriptional adaptor 1 (HF1) homolog, yeast-like	AI760812
225455_at	0.63227	8.0509979	7.722079	5.26E-13	6.51E-12	18.92558	TADA1L	ring finger protein 170	NM_030954
220985_s_at	0.63221	7.300389	7.042411	2.92E-11	2.72E-10	14.98944	RNF170	mitofusin 1	NM_017927
207098_s_at	0.632	8.1742263	8.0124	8.91E-14	1.25E-12	20.66712	MFN1		

235168_at	0.63198	6.8985227	7.561981	1.38E-12	1.60E-11	17.98002	PIGM	phosphatidylinositol glycan anchor biosynthesis, class M	AI701594
222546_s_at	0.63176	5.4591239	8.420393	6.98E-15	1.19E-13	23.16924	EPS8L2	EPS8-like 2	AW204755
234730_s_at	0.63175	5.3747612	8.681835	1.33E-15	2.55E-14	24.80362	RIPK4	receptor-interacting serine-threonine kinase 4	AP001743
226997_at	0.6315	7.0889878	4.585924	7.93E-06	3.03E-05	2.85128	ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif, 12, mRNA (cDNA clone IMAGE:40147204)	W74476
210854_x_at	0.63146	8.0258475	5.206355	4.73E-07	2.23E-06	5.559447	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	U17986
231843_at	0.63142	6.4224949	11.71668	1.62E-24	1.56E-22	45.0403	DDX55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	AB046815
219447_s_at	0.6314	7.5183422	12.19678	5.52E-26	6.99E-24	48.37859	SLC35C2	solute carrier family 35, member C2	NM_015945
201695_s_at	0.63122	9.3058835	6.660243	2.55E-10	2.04E-09	12.87194	NP	nucleoside phosphorylase	NM_000270
201947_s_at	0.63116	11.38983	10.38915	1.61E-20	7.14E-19	35.95859	CCT2	chaperonin containing TCP1, subunit 2 (beta)	NM_006431
227609_at	0.63093	8.9928241	4.76807	3.56E-06	1.45E-05	3.618197	EPSTI1	epithelial stromal interaction 1 (breast)	AA633203
229099_at	0.63073	7.6720127	10.51617	6.74E-21	3.17E-19	36.81536	C11orf83	chromosome 11 open reading frame 83	AW051379
212729_at	0.63072	7.2276737	8.216597	2.51E-14	3.87E-13	21.91174	DLG3	discs, large homolog 3 (Drosophila)	AI916274
1555137_a_at	0.63054	6.0854453	5.253085	3.79E-07	1.82E-06	5.774157	FGD6	FYVE, RhoGEF and PH domain containing 6	BC013319
208743_s_at	0.6305	11.092791	10.16009	7.63E-20	3.04E-18	34.42135	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	BC001359
202407_s_at	0.6305	7.6330083	9.606704	3.15E-18	9.54E-17	30.75435	PRPF31	PRP31 pre-mRNA processing factor 31 homolog (S. cerevisiae)	BF342707
1554080_at	0.63047	6.6317929	7.35757	4.65E-12	4.95E-11	16.78884	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	BC007102
216483_s_at	0.6302	9.3750717	9.146059	6.58E-17	1.59E-15	27.75976	C19orf10	chromosome 19 open reading frame 10	AC005339
201209_at	0.63018	10.82248	9.781982	9.76E-19	3.24E-17	31.90816	HDAC1	histone deacetylase 1	NM_004964
226150_at	0.63014	9.2121893	6.050896	6.91E-09	4.37E-08	9.655165	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	BF111651
219283_at	0.63009	9.1751591	9.483215	7.15E-18	2.03E-16	29.94603	C1GALT1C1	C1GALT1-specific chaperone 1	NM_014158
222412_s_at	0.63009	8.6524287	7.808243	3.11E-13	4.03E-12	19.43891	SSR3	signal sequence receptor, gamma (translocon-associated protein gamma)	AW150923
208928_at	0.63003	8.4593807	8.270318	1.79E-14	2.84E-13	22.24176	POR	P450 (cytochrome) oxidoreductase	AF258341
222269_at	0.62989	6.1837461	7.913199	1.64E-13	2.22E-12	20.06826	APOOL	apolipoprotein O-like	W87634
33304_at	0.62989	8.9906849	4.666211	5.59E-06	2.20E-05	3.186367	ISG20	interferon stimulated exonuclease gene 20kDa	U88964
224410_s_at	0.62988	7.0757671	7.531125	1.66E-12	1.91E-11	17.79904	LMBR1	limb region 1 homolog (mouse)	AF348513
213370_s_at	0.62968	7.3376504	9.723797	1.44E-18	4.63E-17	31.52432	SFMBT1	Scm-like with four mbt domains 1	BF057298
214308_s_at	0.62962	6.6380638	4.361303	2.06E-05	7.31E-05	1.939009	HGD /// LO	homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase like	AI478172
219226_at	0.6296	7.2454943	10.44344	1.11E-20	5.06E-19	36.32441	CRKRS	Cdc2-related kinase, arginine/serine-rich	NM_016507
202558_s_at	0.62946	7.9798341	6.294668	1.89E-09	1.31E-08	10.9174	HSPA13	heat shock protein 70kDa family, member 13	NM_006948
218594_at	0.62938	8.5916985	9.557283	4.37E-18	1.29E-16	30.43039	HEATR1	HEAT repeat containing 1	NM_018072
225401_at	0.62929	8.8461457	7.941164	1.38E-13	1.89E-12	20.23669	C1orf85	chromosome 1 open reading frame 85	BF977145
222270_at	0.62904	4.8055893	8.316034	1.35E-14	2.18E-13	22.52344	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	BG540048

222699_s_at	0.62897	8.1849466	7.970925	1.15E-13	1.59E-12	20.41628	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	BF439250
212246_at	0.62853	8.2203084	7.90355	1.74E-13	2.35E-12	20.01022	MCFD2	multiple coagulation factor deficiency 2	BE880828
208336_s_at	0.62849	9.5225171	9.461033	8.28E-18	2.33E-16	29.80126	GPSN2	glycoprotein, synaptic 2	NM_004868
209231_s_at	0.62835	7.8252312	6.938981	5.28E-11	4.72E-10	14.40918	DCTN5	dynactin 5 (p25)	AI038068
202416_at	0.62833	8.80602	11.22862	4.91E-23	3.48E-21	41.67202	DNAJC7	DnaJ (Hsp40) homolog, subfamily C, member 7	NM_003315
231880_at	0.62816	4.4371449	6.975926	4.28E-11	3.88E-10	14.61586	FAM40B	family with sequence similarity 40, member B	AB032996
225616_at	0.62808	7.0130689	11.42241	1.27E-23	1.02E-21	43.00595	SPRYD4	SPRY domain containing 4	AI570493
1552304_at	0.62798	4.2773799	9.955798	3.04E-19	1.11E-17	33.05952	ALG10	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (S. pombe)	NM_032834
220144_s_at	0.62762	5.6837913	6.763496	1.43E-10	1.19E-09	13.43679	ANKRD5	ankyrin repeat domain 5	NM_022096
217942_at	0.62752	10.126946	8.674136	1.39E-15	2.67E-14	24.75516	MRPS35	mitochondrial ribosomal protein S35	NM_021821
211623_s_at	0.62747	10.871654	9.457154	8.49E-18	2.39E-16	29.77595	FBL	fibrillarin	M30448
213461_at	0.62746	6.8580976	6.955785	4.80E-11	4.32E-10	14.5031	NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	AI800983
1554008_at	0.62725	6.7450064	4.945421	1.60E-05	6.88E-06	4.387683	OSMR	oncostatin M receptor	BC010943
1564220_a_at	0.62691	4.0011289	4.073178	6.66E-05	0.0002155	0.82464	0	0	AK096932
229232_at	0.62677	7.4770378	9.01284	1.57E-16	3.54E-15	26.90473	LRRC57	leucine rich repeat containing 57	AW135740
235256_s_at	0.62661	8.3430658	6.478279	6.97E-10	5.19E-09	11.89007	GALM	galactose mutarotase (aldose 1-epimerase)	BE788984
227606_s_at	0.6266	6.905435	6.535132	5.10E-10	3.88E-09	12.19496	STAMBPL1	STAM binding protein-like 1	AI638611
223271_s_at	0.62643	8.0300056	7.952938	1.29E-13	1.76E-12	20.30769	CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	AF161543
222678_s_at	0.62636	7.1753011	6.266377	2.20E-09	1.51E-08	10.76918	DCUN1D1	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	BF057821
209935_at	0.62626	7.226408	7.345977	4.98E-12	5.27E-11	16.72184	ATP2C1	ATPase, Ca++ transporting, type 2C, member 1	AF225981
218218_at	0.62608	7.4700113	7.36077	4.56E-12	4.87E-11	16.80734	APPL2	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 2	NM_018171
221020_s_at	0.62591	9.2667479	8.384105	8.78E-15	1.47E-13	22.94424	SLC25A32	solute carrier family 25, member 32	NM_030780
218724_s_at	0.62585	6.3097217	7.301837	5.45E-12	6.71E-11	16.46729	TGIF2	TGFB-induced factor homeobox 2	NM_021809
1552740_at	0.6253	4.3765307	10.0525	1.58E-19	6.00E-18	33.70303	C2orf15	chromosome 2 open reading frame 15	NM_144706
210056_at	0.62519	7.2776805	5.601566	6.91E-08	3.71E-07	7.420403	RND1	Rho family GTPase 1	U69563
225666_at	0.62494	8.2234104	5.909917	1.44E-08	8.65E-08	8.940898	TMTC4	transmembrane and tetratricopeptide repeat containing 4	D80480
236381_s_at	0.62489	6.9842766	9.361068	1.60E-17	4.32E-16	29.1504	WDR8	WD repeat domain 8	AW572779
219326_s_at	0.62485	7.3266081	8.322058	1.30E-14	2.10E-13	22.56061	B3GNT2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	NM_006577
220106_at	0.62479	6.1574281	3.905861	0.0001281	0.0003926	0.207123	NPC1L1	NPC1 (Niemann-Pick disease, type C1, gene)-like 1	NM_013389
224535_s_at	0.62461	8.1465906	10.80931	8.98E-22	5.02E-20	38.80378	MRP63	mitochondrial ribosomal protein 63	AB049957
226063_at	0.62457	7.898105	9.415631	1.12E-17	3.08E-16	29.50533	LOC100128	hypothetical protein. LOC100128155 /// vav 2 guanine nucleotide exchange factor	AA481141
209040_s_at	0.62435	10.322169	7.062838	2.60E-11	2.44E-10	15.10465	PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	U17496
224595_at	0.62431	9.5648832	6.215463	2.89E-09	1.94E-08	10.50357	SLC44A1	solute carrier family 44, member 1	AK022549

1564494_s_at	0.62419	9.5325311	6.027571	7.81E-09	4.88E-08	9.536182	P4HB	prolyl 4-hydroxylase, beta polypeptide	AK075503
1561254_at	0.62403	4.5786084	5.956437	1.13E-08	6.91E-08	9.175294	tcag7.1188	hypothetical LOC340340	BC040593
206884_s_at	0.624	4.1306024	3.834742	0.0001681	0.0005036	-0.04863	SCEL	scellin	NM_003843
235389_at	0.62398	6.5889721	8.712505	1.09E-15	2.13E-14	24.99684	PHF20	PHD finger protein 20	BG168139
223198_x_at	0.62393	8.3989432	12.19561	5.56E-26	7.03E-24	48.37047	COMMD5	COMM domain containing 5	BC002672
217408_at	0.62385	9.7943931	9.889049	4.76E-19	1.67E-17	32.61655	MRPS18B	mitochondrial ribosomal protein S18B	AL050361
202674_s_at	0.62382	5.2412075	5.414321	1.74E-07	8.77E-07	6.526073	LMO7	LIM domain 7	NM_005358
223808_s_at	0.62376	8.6511875	9.164774	5.82E-17	1.42E-15	27.88028	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	AF277187
204025_s_at	0.62356	7.6000925	8.662747	1.50E-15	2.86E-14	24.68351	PDCD2	programmed cell death 2	NM_002598
203215_s_at	0.62349	9.4092113	6.347006	1.42E-09	1.00E-08	11.19277	MYO6	myosin VI	AA877789
215905_s_at	0.62348	8.2176863	11.24681	4.33E-23	3.11E-21	41.79597	SNRNP40	small nuclear ribonucleoprotein 40kDa (U5)	AL157420
218291_at	0.62347	9.1241708	11.03535	1.88E-22	1.19E-20	40.34671	ROBLD3	roadblock domain containing 3	NM_014017
204883_s_at	0.62335	8.0640139	10.92892	3.93E-22	2.35E-20	39.61928	HUS1	HUS1 checkpoint homolog (S. pombe)	AI968626
211672_s_at	0.62309	9.1104	7.749826	4.44E-13	5.58E-12	19.09055	ARPC4 /// T3	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member	AF019888
214347_s_at	0.62302	5.9637931	4.285793	2.82E-05	9.78E-05	1.64082	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	AW772056
238526_at	0.6228	5.4292658	6.848637	8.84E-11	7.59E-10	13.90665	RAB3IP	RAB3A interacting protein (rabn3)	AL119897
212348_s_at	0.62277	8.5861777	9.468619	7.87E-18	2.22E-16	29.85075	AOF2	amine oxidase (flavin containing) domain 2	AB011173
230641_at	0.62266	6.4264752	5.843348	2.03E-08	1.19E-07	8.607734	0	0	AI792670
203805_s_at	0.62261	6.1575341	8.92357	2.80E-16	6.06E-15	26.33472	FANCA	Fanconi anemia, complementation group A	AW083279
205072_s_at	0.62255	5.5382083	6.841826	9.18E-11	7.87E-10	13.86892	KRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	NM_022406
1568643_a_at	0.6224	5.7343316	7.353538	4.76E-12	5.06E-11	16.76553	0	0	BC032795
204700_x_at	0.62239	7.7626155	8.161278	3.54E-14	5.34E-13	21.57301	C1orf107	chromosome 1 open reading frame 107	NM_014388
225901_at	0.62238	7.26484	9.036624	1.34E-16	3.08E-15	27.057	PTPMT1	protein tyrosine phosphatase, mitochondrial 1	AI440338
204175_at	0.62235	8.6762946	9.478983	7.35E-18	2.08E-16	29.9184	ZNF593	zinc finger protein 593	NM_015871
229304_s_at	0.6223	5.7879037	8.7871	6.75E-16	1.37E-14	25.46807	MLF1IP	MLF1 interacting protein	AA460299
205180_s_at	0.62223	7.0455079	7.318224	5.86E-12	6.14E-11	16.56168	ADAM8	ADAM metalloproteinase domain 8	NM_001109
223298_s_at	0.62212	9.9112369	7.843196	2.52E-13	3.30E-12	19.64801	NT5C3	5'-nucleotidase, cytosolic III	AF312735
231835_at	0.62212	9.2140128	6.234997	2.60E-09	1.77E-08	10.6053	C1orf93	chromosome 1 open reading frame 93	AL359575
225024_at	0.62193	7.6791865	11.35878	1.98E-23	1.54E-21	42.56739	RPRD1B	regulation of nuclear pre-mRNA domain containing 1B	AL117521
209980_s_at	0.62181	7.0088946	8.062548	6.54E-14	9.38E-13	20.97132	SHMT1	serine hydroxymethyltransferase 1 (soluble)	L23928
210754_s_at	0.62172	8.9499929	7.510888	1.87E-12	2.13E-11	17.68056	LYN	v-src-1 Yamaguchi sarcoma viral related oncogene homolog	M79321
224455_s_at	0.6215	6.7623802	11.42795	1.22E-23	9.85E-22	43.04409	ADPGK	ADP-dependent glucokinase	BC006112
219029_at	0.62146	8.1018501	6.549319	4.71E-10	3.61E-09	12.27131	C5orf28	chromosome 5 open reading frame 28	NM_022483
221514_at	0.62135	7.9821024	8.058902	6.69E-14	9.58E-13	20.94917	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	BC001149
242538_at	0.62121	4.7516564	11.4948	7.67E-24	6.45E-22	43.50541	TFDP1	Transcription factor Dp-1, mRNA (cDNA clone IMAGE:5274257)	AW007021
210174_at	0.621	6.0036581	4.376435	1.94E-05	6.90E-05	1.999285	NR5A2	nuclear receptor subfamily 5, group A, member 2	AF228413
226707_at	0.62098	8.992872	5.356392	2.31E-07	1.14E-06	6.253965	NAPRT1	nicotinate phosphoribosyltransferase domain containing 1	AI925574
201297_s_at	0.62098	7.7107442	8.19528	2.87E-14	4.38E-13	21.78107	MOBK1B	MOB1, Mps One Binder kinase activator-like 1B (yeast)	AK023321
223231_at	0.62087	8.8684305	7.543817	1.54E-12	1.78E-11	17.87343	TATDN1	TatD DNase domain containing 1	AF212250
212365_at	0.62076	8.5901489	6.216656	2.87E-09	1.93E-08	10.50978	MYO1B	myosin 1B	BF215996

228923_at	0.62067	5.7031671	4.791059	3.21E-06	1.32E-05	3.716688	S100A6	S100 calcium binding protein A6	AW166825
1553959_a_at	0.62057	8.5000227	9.032972	1.38E-16	3.15E-15	27.0336	B3GALT6	UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6	N95564
230655_at	0.62049	6.1127789	5.694569	4.33E-08	2.40E-07	7.872846	0	0	AW025928
236009_at	0.62041	5.7456148	5.547231	9.05E-08	4.77E-07	7.158582	0	0	AI767250
209064_x_at	0.62036	9.5668335	6.985864	4.04E-11	3.68E-10	14.67156	PAIP1	poly(A) binding protein interacting protein 1	AL136920
215723_s_at	0.62025	5.3611266	5.107633	7.54E-07	3.43E-06	5.11066	PLD1	phospholipase D1, phosphatidylcholine-specific	AI276230
225419_at	0.62017	9.2981816	12.12397	9.22E-26	1.11E-23	47.87101	C7orf11	chromosome 7 open reading frame 11	AI869704
1553423_a_at	0.62007	4.3967698	5.265817	3.57E-07	1.72E-06	5.832909	SLFN13	schlafen family member 13	NM_144682
230370_x_at	0.62005	7.8869465	7.124703	1.81E-11	1.75E-10	15.4548	STYXL1	serine/threonine/tyrosine interacting-like 1	AI244335
208907_s_at	0.61998	8.7755721	10.47254	9.08E-21	4.19E-19	36.52072	MRPS18B	mitochondrial ribosomal protein S18B	BC005373
1552613_s_at	0.61998	6.9651142	6.407952	1.02E-09	7.38E-09	11.51533	CDC42SE2	CDC42 small effector 2	NM_020240
228851_s_at	0.61962	7.600675	8.888029	3.52E-16	7.50E-15	26.10846	ENSA	endosulfine alpha	AV726322
1555167_s_at	0.61961	7.8017784	4.880269	2.15E-06	9.06E-06	4.102432	NAMPT	nicotinamide phosphoribosyltransferase	BC020691
218455_at	0.61957	7.2951971	9.040642	1.31E-16	3.00E-15	27.08274	NFS1	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	NM_021100
205664_at	0.61946	8.0200611	7.245538	8.98E-12	9.09E-11	16.14391	KIN	KIN, antigenic determinant of recA protein homolog (mouse)	NM_012311
204616_at	0.61943	9.9165847	8.144823	3.93E-14	5.89E-13	21.47247	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	NM_006002
213399_x_at	0.61935	12.248545	11.70594	1.75E-24	1.66E-22	44.96589	RPN2	ribophorin II	AI560720
221637_s_at	0.61934	9.4879928	11.04758	1.73E-22	1.11E-20	40.43043	C11orf48	chromosome 11 open reading frame 48	BC001434
1554594_at	0.61927	4.1771564	8.064597	6.46E-14	9.27E-13	20.98377	ARHGAP27	Rho GTPase activating protein 27 /// hypothetical protein LOC201175	AF258593
218385_at	0.61873	8.361646	8.925313	2.77E-16	6.00E-15	26.34583	MRPS18A	mitochondrial ribosomal protein S18A	NM_018135
1553698_a_at	0.61859	3.8024297	9.272057	2.88E-17	7.43E-16	28.57313	C1orf96	chromosome 1 open reading frame 96	NM_145257
208977_x_at	0.6184	11.502627	10.19021	6.22E-20	2.52E-18	34.62284	TUBB2C	tubulin, beta 2C	BC004188
217094_s_at	0.61835	7.1653344	10.95217	3.35E-22	2.02E-20	39.77804	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	AL109923
226733_at	0.61823	7.3577868	4.36496	2.03E-05	7.21E-05	1.953559	PFKFB2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	AA587884
205770_at	0.61813	7.9459372	6.620093	3.19E-10	2.51E-09	12.65379	GSR	glutathione reductase	NM_000637
222824_at	0.61811	7.9249734	6.013669	8.40E-09	5.23E-08	9.465419	0	0	AW237290
223441_at	0.61797	8.8400038	5.85898	1.87E-08	1.10E-07	8.685728	SLC17A5	solute carrier family 17 (anion/sugar transporter), member 5	AK026921
229276_at	0.61794	5.9016333	5.383705	2.02E-07	1.01E-06	6.38199	IGSF9	immunoglobulin superfamily, member 9	AB037776
218474_s_at	0.61789	8.8815806	7.969059	1.16E-13	1.61E-12	20.405	KCTD5	potassium channel tetramerisation domain containing 5	NM_018992
208726_s_at	0.61784	11.438368	12.48132	7.37E-27	1.12E-24	50.36632	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	BC000461
201196_s_at	0.6178	8.9139131	8.511283	3.93E-15	7.05E-14	23.73479	AMD1	adenosylmethionine decarboxylase 1	M21154
205010_at	0.61752	7.0842028	10.93565	3.75E-22	2.25E-20	39.66523	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	NM_019067
201458_s_at	0.61744	9.6358305	10.62281	3.24E-21	1.62E-19	37.53704	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	NM_004725
221082_s_at	0.61729	6.9583086	9.809859	8.10E-19	2.71E-17	32.09234	NDRG3	NDRG family member 3	NM_022477
222825_at	0.61729	7.3236677	6.982179	4.13E-11	3.75E-10	14.6509	OTUD6B	OTU domain containing 6B	BF435752
208700_s_at	0.61705	10.490305	9.762964	1.11E-18	3.65E-17	31.78261	TKT	transketolase	L12711
205622_at	0.61702	7.3322622	9.803104	8.47E-19	2.84E-17	32.04769	SMPD2	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase)	NM_003080

212220_at	0.61693	7.2748573	7.68677	6.51E-13	7.92E-12	18.71612	PSME4	proteasome (prosome, macropain) activator subunit 4	AI972268
218477_at	0.61667	10.170123	7.535555	1.61E-12	1.86E-11	17.825	TMEM14A	transmembrane protein 14A	NM_014051
225114_at	0.61649	8.2075668	6.696301	2.08E-10	1.69E-09	13.06857	AGPS	alkylglycerone phosphate synthase	AA127674
201188_s_at	0.61636	8.0664713	6.56363	4.36E-10	3.35E-09	12.34844	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	D26351
208699_x_at	0.61634	9.7376339	9.690186	1.80E-18	5.69E-17	31.30296	TKT	transketolase	BF696840
243840_at	0.61633	4.7983236	12.30326	2.60E-26	3.48E-24	49.12176	0	0	BF691634
209267_s_at	0.616	8.0087822	3.820692	0.0001772	0.0005287	-0.09867	SLC39A8	solute carrier family 39 (zinc transporter), member 8	AB040120
231730_at	0.61566	5.2030142	6.903182	6.48E-11	5.70E-10	14.20957	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	NM_016955
242417_at	0.61564	6.940907	5.167881	5.68E-07	2.64E-06	5.383765	LOC283278	hypothetical protein LOC283278	AI690465
204455_at	0.61523	4.1396114	5.283181	3.28E-07	1.59E-06	5.913213	DST	dystonin	NM_001723
208270_s_at	0.61516	9.5210987	8.741951	9.02E-16	1.79E-14	25.18265	RNPEP	arginyl aminopeptidase (aminopeptidase B)	NM_020216
227349_at	0.61511	5.186579	7.96907	1.16E-13	1.61E-12	20.40507	HELLS	helicase, lymphoid-specific	AI807356
222470_s_at	0.615	5.8917253	9.264786	3.02E-17	7.76E-16	28.52608	UQCC	ubiquinol-cytochrome c reductase complex chaperone	AA033998
212792_at	0.61494	8.058512	7.439328	2.86E-12	3.16E-11	17.26306	DPY19L1	dpy-19-like 1 (C. elegans)	AB020684
202595_s_at	0.61484	8.9530027	8.471598	5.05E-15	8.91E-14	23.4875	LEPROTL1	leptin receptor overlapping transcript-like 1	AF161461
210541_s_at	0.61465	8.0936185	9.823172	7.41E-19	2.51E-17	32.18037	TRIM27	tripartite motif-containing 27	AF230394
242905_at	0.61462	5.922242	9.158235	6.07E-17	1.48E-15	27.83816	PNO1	partner of NOB1 homolog (S. cerevisiae)	AV733347
209743_s_at	0.61444	6.9607193	7.776935	3.77E-13	4.79E-12	19.25204	ITCH	Itchy E3 ubiquitin protein ligase homolog (mouse)	AI989677
226524_at	0.6144	7.8397665	8.455167	5.61E-15	9.76E-14	23.38527	C3orf38	chromosome 3 open reading frame 38	AI458735
237690_at	0.61412	3.6114354	6.260305	2.27E-09	1.55E-08	10.73742	GPR115	G protein-coupled receptor 115	W67511
203911_at	0.61409	7.5734069	4.19307	4.12E-05	0.0001386	1.280594	RAP1GAP	RAP1 GTPase activating protein	NM_002885
205077_s_at	0.61396	8.8778973	8.566297	2.77E-15	5.07E-14	24.07849	PIGF	phosphatidylinositol glycan anchor biosynthesis, class F	NM_002643
1555826_at	0.61391	5.7972709	8.146122	3.89E-14	5.84E-13	21.4804	EPR1	effector cell peptidase receptor 1 (non-protein coding)	BQ021146
218159_at	0.6139	9.0433522	10.60102	3.77E-21	1.86E-19	37.3894	DDRKG1	DDRKG domain containing 1	NM_023935
223159_s_at	0.61373	7.4258407	7.134049	1.72E-11	1.67E-10	15.50786	NEK6	NIMA (never in mitosis gene a)-related kinase 6	BC000101
242116_x_at	0.61348	3.651397	9.296332	2.46E-17	6.42E-16	28.73035	0	0	AL566906
222140_s_at	0.61347	8.1920823	9.560137	4.29E-18	1.27E-16	30.44908	GPR89A ///	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	AK021758
227105_at	0.61346	7.7312652	6.794373	1.20E-10	1.01E-09	13.60676	CSPP1	centrosome and spindle pole associated protein 1	AI400587
213696_s_at	0.61345	8.2844533	12.30354	2.59E-26	3.48E-24	49.1237	MED8	mediator complex subunit 8	AA421957
1552641_s_at	0.61343	6.5463844	10.97712	2.82E-22	1.72E-20	39.9485	ATAD3A ///	ATPase family, AAA domain containing 3A /// ATPase family, AAA domain containing 3B /// ATPase family, AAA domain containing 3C /// similar to AAA-ATPase TOB3	NM_031921
216212_s_at	0.61308	8.570701	9.699316	1.70E-18	5.37E-17	31.36306	DKC1	dyskeratosis congenita 1, dyskerin	AJ010395
210243_s_at	0.61305	8.1631637	10.72858	1.57E-21	8.36E-20	38.25471	B4GALT3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	AF038661
223330_s_at	0.61296	7.5064987	8.433871	6.41E-15	1.10E-13	23.25292	SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	BC000911
211136_s_at	0.6128	8.4367479	10.54352	5.59E-21	2.66E-19	37.00029	CLPTM1	cleft lip and palate associated transmembrane protein 1	BC004865
204809_at	0.6128	8.0291048	8.44985	5.80E-15	1.00E-13	23.35222	CLPX	CipX caseinolytic peptidase X homolog (E. coli)	NM_006660
217909_s_at	0.61277	8.9384028	8.82573	5.26E-16	1.09E-14	25.7128	MLX	MAX-like protein X	BF056105
238045_at	0.61266	5.0715764	8.144621	3.93E-14	5.89E-13	21.47124	TMEM65	transmembrane protein 65	BG167675

214431_at	0.61266	9.1125962	10.87221	5.82E-22	3.36E-20	39.23235	GMPS	guanine morphosphate synthetase	NM_003875
242753_x_at	0.61258	4.133515	9.024354	1.45E-16	3.31E-15	26.97842	C4orf16	chromosome 4 open reading frame 16	AI394199
202370_s_at	0.61216	9.5671764	9.618044	2.92E-18	8.91E-17	30.82876	CBFB	core-binding factor, beta subunit	NM_001755
203462_x_at	0.61209	10.432243	9.952241	3.11E-19	1.13E-17	33.03589	EIF3B	eukaryotic translation initiation factor 3, subunit B	NM_003751
213412_at	0.61208	7.2098158	4.829473	2.70E-06	1.12E-05	3.882097	TJP3	tight junction protein 3 (zona occludens 3)	NM_014428
91826_at	0.61201	8.3967126	4.261702	3.11E-05	0.0001071	1.546594	EPS8L1	EPS8-like 1	AI219073
235413_at	0.61176	7.4790653	7.745355	4.56E-13	5.73E-12	19.06395	GGCX	gamma-glutamyl carboxylase	AW191608
205627_at	0.61166	6.1624574	4.127688	5.36E-05	0.0001768	1.030562	CDA	cytidine deaminase	NM_001785
222011_s_at	0.61155	7.7611436	6.943381	5.15E-11	4.61E-10	14.43376	TCP1	t-complex 1	BF224073
202854_at	0.61153	10.227266	8.352427	1.07E-14	1.76E-13	22.74821	HPRT1	hypoxanthine phosphoribosyltransferase 1	NM_000194
218757_s_at	0.61119	8.1716817	6.5701	4.20E-10	3.24E-09	12.38334	UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	NM_023010
222979_s_at	0.61107	9.5850697	10.16329	7.47E-20	2.98E-18	34.44275	SURF4	surfeit 4	AF078866
205238_at	0.61107	6.6137593	8.171411	3.33E-14	5.03E-13	21.63497	TRMT2B	TRM2 tRNA methyltransferase 2 homolog B (S. cerevisiae)	NM_024917
218014_at	0.61094	8.5956982	11.58742	4.01E-24	3.55E-22	44.14547	NUP85	nucleoporin 85kDa	NM_024844
243299_at	0.61064	5.6752887	6.985751	4.04E-11	3.68E-10	14.67093	0	0	AW167087
204698_at	0.61058	9.1287946	4.293091	2.74E-05	9.50E-05	1.669451	ISG20	interferon stimulated exonuclease gene 20kDa	NM_002201
1555971_s_at	0.6105	8.4359292	8.799467	6.23E-16	1.27E-14	25.54637	FBXO28	F-box protein 28	AU154086
201771_at	0.61047	9.3833088	12.33492	2.08E-26	2.86E-24	49.34289	SCAMP3	secretory carrier membrane protein 3	NM_005698
229835_s_at	0.61045	7.3333305	6.812814	1.08E-10	9.15E-10	13.70851	0	0	AA004210
203040_s_at	0.61023	8.2724641	9.866134	5.55E-19	1.92E-17	32.46471	HMBS	hydroxymethylbilane synthase	NM_000190
239302_s_at	0.61017	6.3751335	4.803515	3.04E-06	1.25E-05	3.770209	0	0	AA931539
206052_s_at	0.6101	9.7518803	9.487393	6.95E-18	1.98E-16	29.97332	SLBP	stem-loop binding protein	NM_006527
1554472_a_at	0.61007	5.526231	8.073125	6.13E-14	8.83E-13	21.0356	PHF20L1	PHD finger protein 20-like 1	BC015211
242807_at	0.61001	5.1930271	4.926236	1.74E-06	7.46E-06	4.303378	FSD1L	fibronectin type III and SPRY domain containing 1-like	AI970348
238465_at	0.60999	6.3740403	4.429963	1.55E-05	5.62E-05	2.21388	C5orf35	chromosome 5 open reading frame 35	AI265933
205347_s_at	0.60995	5.4135114	3.750912	0.0002303	0.0006719	-0.34487	MGC39900	thymosin beta15b /// thymosin beta 15a	NM_021992
205071_x_at	0.60993	6.8974845	6.7612	1.45E-10	1.20E-09	13.42417	XRCC4	X-ray repair complementing defective repair in Chinese hamster cells 4	AB017445
208721_s_at	0.60986	7.5522918	9.277987	2.77E-17	7.18E-16	28.61153	ANAPC5	anaphase promoting complex subunit 5	BF967271
209577_at	0.60974	7.2451449	8.351045	1.08E-14	1.78E-13	22.73966	PCYT2	phosphate cytidyltransferase 2, ethanolamine	BC000351
209020_at	0.60967	8.4108315	8.356121	1.05E-14	1.73E-13	22.77105	C20orf111	chromosome 20 open reading frame 111	AF217514
214875_x_at	0.60964	9.5792694	7.843332	2.51E-13	3.30E-12	19.64882	APLP2	amyloid beta (A4) precursor-like protein 2	AW001847
218384_at	0.60957	9.2761667	8.728396	9.84E-16	1.94E-14	25.09708	CARHSP1	calcium regulated heat stable protein 1, 24kDa	NM_014316
221079_s_at	0.60946	7.2832546	7.725608	5.14E-13	6.38E-12	18.94655	METTL2A	methyltransferase like 2A /// methyltransferase like 2B	NM_018396
201271_s_at	0.60924	9.2486793	11.97313	2.67E-25	2.95E-23	46.82079	RALY	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))	NM_016732
1554052_at	0.60901	6.391762	8.836649	4.90E-16	1.02E-14	25.78206	CNOT1	CCR4-NOT transcription complex, subunit 1	BC040523
228205_at	0.60897	5.2421747	8.886317	3.56E-16	7.57E-15	26.09757	TKT	transketolase	AU152969
207852_at	0.60882	4.0020093	4.979668	1.37E-06	5.95E-06	4.538812	CXCL5	chemokine (C-X-C motif) ligand 5	NM_002994
227680_at	0.60874	7.7648291	9.525849	5.39E-18	1.56E-16	30.22456	ZNF326	zinc finger protein 326	AI057121
202352_s_at	0.60869	9.6073679	9.971331	2.73E-19	1.00E-17	33.16275	PSMD12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	AI446530
203415_at	0.60863	10.025979	9.453407	8.71E-18	2.44E-16	29.75151	PDCD6	programmed cell death 6	NM_013232
225614_at	0.60862	7.7833292	9.502593	6.29E-18	1.81E-16	30.07262	SAAL1	serum amyloid A-like 1	AI815207
221741_s_at	0.60858	10.008389	10.77158	1.17E-21	6.41E-20	38.54703	YTHDF1	YTH domain family, member 1	AL096828

225754_at	0.60853	7.111377	9.181903	5.20E-17	1.28E-15	27.99069	AP1G1	adaptor-related protein complex 1, gamma 1 subunit	AA142984
204812_at	0.60847	7.9558772	12.3127	2.43E-26	3.30E-24	49.18763	ZW10	ZW10, kinetochore associated, homolog (Drosophila)	NM_004724
244261_at	0.60822	6.7278329	5.070046	8.99E-07	4.05E-05	4.941527	IL28RA	interleukin 28 receptor, alpha (interferon, lambda receptor)	AW340139
209589_s_at	0.60812	7.3713424	4.448062	1.43E-05	5.23E-05	2.286922	EPHB2	EPH receptor B2	AF025304
219075_at	0.60812	6.1343891	11.54032	5.58E-24	4.80E-22	43.81984	YIPF2	Yip1 domain family, member 2	NM_024029
222417_s_at	0.6081	9.9362389	9.869225	5.44E-19	1.88E-17	32.48519	SNX5	sorting nexin 5	AF121855
238448_at	0.60801	5.5892078	9.972162	2.72E-19	9.98E-18	33.16827	MRPL19	mitochondrial ribosomal protein L19	BE544070
223489_x_at	0.60797	6.9248756	11.46813	9.24E-24	7.61E-22	43.32135	EXOSC3	exosome component 3	AW015573
223339_at	0.60787	7.2554996	5.964067	1.09E-08	6.66E-08	9.21386	ATPIF1	ATPase inhibitory factor 1	BC001867
235096_at	0.60774	7.4405117	10.5046	7.29E-21	3.41E-19	36.73722	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	AA074729
207121_s_at	0.60774	10.122943	9.164225	5.84E-17	1.42E-15	27.87675	MAPK6	mitogen-activated protein kinase 6	NM_002748
226329_s_at	0.6077	8.4829017	7.27908	7.37E-12	7.58E-11	16.33639	MITD1	MIT, microtubule interacting and transport, domain containing 1	BF055289
209393_s_at	0.60764	9.0302748	11.79747	9.19E-25	9.23E-23	45.60048	EIF4E2	eukaryotic translation initiation factor 4E family member 2	AF047695
1554508_at	0.60736	5.333192	6.489051	6.57E-10	4.91E-09	11.94771	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	BC029917
214443_at	0.6073	5.4594645	10.85846	6.40E-22	3.66E-20	39.13861	PVR	poliovirus receptor	NM_006505
207891_s_at	0.6073	6.262337	9.244827	3.44E-17	8.74E-16	28.39697	TREX2 /// U	three prime repair exonuclease 2	NM_017518
201433_s_at	0.60723	10.210363	10.72595	1.60E-21	8.49E-20	38.23687	PTDSS1	phosphatidylserine synthase 1	NM_014754
203693_s_at	0.60715	7.828327	8.0974	5.27E-14	7.69E-13	21.18329	E2F3	E2F transcription factor 3	NM_001949
203484_at	0.60713	10.688503	10.70965	1.78E-21	9.40E-20	38.12614	SEC61G	Sec61 gamma subunit	NM_014302
223069_s_at	0.60688	6.8534016	9.024767	1.45E-16	3.30E-15	26.98106	EML4	echinoderm microtubule associated protein like 4	AF177377
224460_s_at	0.60687	5.717201	9.608341	3.11E-18	9.46E-17	30.76509	L2HGDH	L-2-hydroxyglutarate dehydrogenase	BC006117
220987_s_at	0.60679	7.3301496	5.189571	5.13E-07	2.40E-06	5.482686	C11orf17 //	chromosome 11 open reading frame 17 /// NUA family, SNF1-like kinase, 2	NM_030952
204952_at	0.60665	6.4509945	5.82459	2.24E-08	1.30E-07	8.514335	LYPD3	LY6/PLAUR domain containing 3	NM_014400
209974_s_at	0.60661	10.471814	10.42478	1.26E-20	5.70E-19	36.19858	BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast)	AF047473
205512_s_at	0.60649	8.5140088	8.571379	2.68E-15	4.92E-14	24.11029	AIFM1	apoptosis-inducing factor, mitochondrion-associated, 1	NM_004208
1554485_s_at	0.60632	7.3995128	3.847868	0.0001599	0.0004814	-0.00173	TMEM37	transmembrane protein 37	BI825302
226121_at	0.60611	7.7249285	7.599748	1.10E-12	1.29E-11	18.2021	DHRS13	dehydrogenase/reductase (SDR family) member 13	AI076793
219615_s_at	0.60604	7.181695	4.547161	9.38E-06	3.54E-05	2.69118	KCNK5	potassium channel, subfamily K, member 5	NM_003740
227019_at	0.60603	6.2418306	6.346599	1.43E-09	1.01E-08	11.19062	C1orf226	chromosome 1 open reading frame 226	AA129774
203203_s_at	0.60593	7.9415379	7.70586	5.80E-13	7.13E-12	18.8293	KRR1	KRR1, small subunit (SSU) processome component, homolog (yeast)	NM_007043
219673_at	0.60577	7.1111219	7.659398	7.68E-13	9.25E-12	18.55409	MCM9	minichromosome maintenance complex component 9	NM_017696
41858_at	0.60574	7.9431101	8.80054	6.19E-16	1.26E-14	25.55316	FRAG1	FGF receptor activating protein 1	AL049261
204207_s_at	0.60572	7.0226406	8.686247	1.29E-15	2.48E-14	24.8314	RNGTT	RNA guanylyltransferase and 5'-phosphatase	AB012142
202903_at	0.60567	6.3811882	8.087587	5.60E-14	8.12E-13	21.12356	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	AU153477
204761_at	0.60567	6.9511435	7.197688	1.19E-11	1.18E-10	15.87021	USP6NL	USP6 N-terminal like	NM_014688
222354_at	0.60559	6.1268368	5.936181	1.26E-08	7.62E-08	9.073075	F11R	F11 receptor	AW675655
202272_s_at	0.60546	8.7340686	8.985463	1.87E-16	4.18E-15	26.72966	FBXO28	F-box protein 28	NM_015176

32837_at	0.60541	9.466816	6.416053	9.79E-10	7.09E-09	11.55836	AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	U56418
220525_s_at	0.60531	9.2528832	12.41234	1.20E-26	1.74E-24	49.88387	AUP1	ancient ubiquitous protein 1	NM_012103
216283_s_at	0.60528	5.8672309	8.621456	1.95E-15	3.66E-14	24.42412	PVR	poliovirus receptor	X64116
205566_at	0.60525	8.0524391	5.859777	1.87E-08	1.10E-07	8.689706	ABHD2	abhydrolase domain-containing 2	NM_007011
218848_at	0.60524	7.0512425	10.14718	8.33E-20	3.29E-18	34.33501	THOC6	THO complex 6 homolog (Drosophila)	NM_024339
202071_at	0.60512	11.036056	5.540143	9.38E-08	4.93E-07	7.124568	SDC4	syndecan 4	NM_002999
225898_at	0.60509	8.0753873	7.13718	1.69E-11	1.64E-10	15.52564	WDR54	WD repeat domain 54	AK023015
203352_at	0.60494	6.2359671	9.084562	9.83E-17	2.31E-15	27.36441	ORC4L	origin recognition complex, subunit 4-like (yeast)	NM_002552
1568627_at	0.60494	4.3340835	11.40485	1.44E-23	1.14E-21	42.88487	SMEK2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	BC032531
223413_s_at	0.60481	8.3634316	9.186024	5.06E-17	1.24E-15	28.01727	LYAR	Ly1 antibody reactive homolog (mouse)	AW958593
213897_s_at	0.60478	9.0472172	9.734977	1.34E-18	4.32E-17	31.59801	MRPL23	mitochondrial ribosomal protein L23	AI832239
201589_at	0.6046	9.8402895	9.484708	7.08E-18	2.01E-16	29.95578	SMC1A	structural maintenance of chromosomes 1A	D80000
226796_at	0.60451	6.6144642	7.354219	4.74E-12	5.04E-11	16.76946	LOC116236	hypothetical protein LOC116236	AI817418
202952_s_at	0.6045	5.4692361	4.016292	8.34E-05	0.000265	0.612215	ADAM12	ADAM metalloproteinase domain 12	NM_003474
226294_x_at	0.60444	9.4673672	10.07201	1.39E-19	5.31E-18	33.83311	FAM91A1	family with sequence similarity 91, member A1	AI245517
211721_s_at	0.60429	5.6483753	5.917953	1.38E-08	8.31E-08	8.981295	ZNF551	zinc finger protein 551	BC005868
201233_at	0.60424	7.7828573	12.97713	2.19E-28	4.66E-26	53.84206	PSMD13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	NM_002817
1555830_s_at	0.60418	5.8350445	5.647575	5.49E-08	2.99E-07	7.643551	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	BC001224
227224_at	0.60414	7.8968154	6.20478	3.06E-09	2.05E-08	10.44803	RALGPS2	Ral GEF with PH domain and SH3 binding motif 2	AW003297
218401_s_at	0.60407	7.2652646	5.173187	5.54E-07	2.58E-06	5.407935	ZNF281	zinc finger protein 281	NM_012482
201463_s_at	0.60403	11.265996	11.48941	7.97E-24	6.65E-22	43.4682	LOC100133	similar to transaldolase /// transaldolase 1	NM_006755
223639_s_at	0.604	8.8099824	10.25417	4.03E-20	1.69E-18	35.05145	ZNRD1	zinc ribbon domain containing 1	AF230337
200824_at	0.60377	11.232587	7.65267	7.99E-13	9.61E-12	18.51432	GSTP1	glutathione S-transferase pi 1	NM_000852
202633_at	0.60363	8.7053511	9.815832	7.78E-19	2.62E-17	32.13183	TOPBP1	topoisomerase (DNA) II binding protein 1	NM_007027
213951_s_at	0.60349	6.3679197	8.745613	8.81E-16	1.75E-14	25.20577	PSMC3IP	PSMC3 interacting protein	BE964655
202937_x_at	0.60344	7.596927	9.50979	5.99E-18	1.73E-16	30.11965	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	AL022316
210885_s_at	0.60343	6.1266912	7.346939	4.95E-12	5.25E-11	16.72739	TRIM15	tripartite motif-containing 15	AF220133
228773_at	0.60336	6.7068608	8.802739	6.10E-16	1.25E-14	25.56709	0	0	AI200538
230966_at	0.60333	6.4098422	5.887658	1.62E-08	9.63E-08	8.829198	IL4I1	interleukin 4 induced 1	AI859620
208799_at	0.60331	10.006766	11.94764	3.20E-25	3.48E-23	46.64355	PSMB5	proteasome (prosome, macropain) subunit, beta type, 5	BC004146
221452_s_at	0.60329	10.310226	8.145202	3.92E-14	5.88E-13	21.47478	TMEM14B	transmembrane protein 14B	NM_030969
202847_at	0.60304	7.93778	5.903532	1.49E-08	8.93E-08	8.908828	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	NM_004563
225583_at	0.603	8.660406	7.999151	9.67E-14	1.35E-12	20.58692	UXS1	UDP-glucuronate decarboxylase 1	AL573637
218511_s_at	0.60292	8.4308222	8.776578	7.22E-16	1.45E-14	25.4015	PNPO	pyridoxamine 5'-phosphate oxidase	NM_018129
204857_at	0.60249	7.012887	6.913142	6.12E-11	5.41E-10	14.26504	MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast)	NM_003550
226988_s_at	0.60247	7.4258523	4.744661	3.95E-06	1.60E-05	3.518296	MYH14	myosin, heavy chain 14	AI709055
201435_s_at	0.6024	9.1014642	8.425772	6.75E-15	1.15E-13	23.20262	EIF4E	eukaryotic translation initiation factor 4E	AW268640
206920_s_at	0.60232	6.9232912	10.31625	2.64E-20	1.14E-18	35.46819	GLE1	GLE1 RNA export mediator homolog (yeast)	NM_001499
217996_at	0.60224	9.1662396	3.816096	0.0001803	0.0005372	-0.11501	PHLDA1	pleckstrin homology-like domain, family A, member 1	AA576961
224221_s_at	0.60195	4.3102499	4.533411	9.95E-06	3.73E-05	2.634658	VAV3	vav 3 guanine nucleotide exchange factor	AF118886

216836_s_at	0.60194	9.3234681	4.111018	5.73E-05	0.0001878	0.967343	ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	X03363
224998_at	0.60179	8.3033471	5.385773	2.00E-07	9.99E-07	6.391701	CMTM4	CKLF-like MARVEL transmembrane domain containing 4	AK000855
203957_at	0.60175	7.5202422	8.945587	2.43E-16	5.30E-15	26.47508	E2F6	E2F transcription factor 6	NM_001952
1554452_a_at	0.60174	8.4209498	4.810775	2.94E-06	1.21E-05	3.801454	HIG2	hypoxia-inducible protein 2	BC001863
1563900_at	0.60174	4.1013019	6.653975	2.64E-10	2.10E-09	12.83783	FAM83B	family with sequence similarity 83, member B	AK055204
217970_s_at	0.6017	8.1057091	9.448064	9.02E-18	2.52E-16	29.71667	CNOT6	CCR4-NOT transcription complex, subunit 6	NM_015455
208921_s_at	0.60167	11.280523	7.10866	1.99E-11	1.91E-10	15.36382	SRI	sorcin	L12387
225644_at	0.60165	8.3739191	7.724519	5.18E-13	6.42E-12	18.94008	CCDC117	coiled-coil domain containing 117	BF060776
212475_at	0.60165	6.7462737	9.540323	4.89E-18	1.44E-16	30.31936	AVL9	AVL9 homolog (S. cerevisiae)	AI797458
227374_at	0.60157	7.3169136	9.558109	4.35E-18	1.28E-16	30.4358	EARS2	glutamyl-tRNA synthetase 2, mitochondrial (putative)	AA833716
223566_s_at	0.60143	6.6884431	7.423788	3.14E-12	3.45E-11	17.1727	BCOR	BCL6 co-repressor	AF317391
213017_at	0.60139	9.4736333	6.013409	8.41E-09	5.23E-08	9.4641	ABHD3	abhydrolase domain containing 3	AL534702
210396_s_at	0.60131	9.5664104	6.655395	2.62E-10	2.09E-09	12.84555	BOLA2 /// L	bolA homolog 2 (E. coli) /// PI-3-kinase-related kinase SMG-1 pseudogene /// PI-3-kinase-related kinase SMG-1 pseudogene	AF271775
230522_s_at	0.6011	5.1350811	7.61687	9.91E-13	1.18E-11	18.30298	C9orf100	chromosome 9 open reading frame 100	BG028209
226882_x_at	0.60073	6.4580193	7.402722	3.56E-12	3.88E-11	17.05037	WDR4	WD repeat domain 4	AI861913
212862_at	0.60061	8.2777437	8.664303	1.48E-15	2.83E-14	24.6933	CDS2	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 2	AL568982
229068_at	0.60061	6.9355153	7.226431	1.00E-11	1.01E-10	16.03449	CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	BF197357
223451_s_at	0.60057	8.5579722	7.478501	2.27E-12	2.55E-11	17.49133	CKLF	chemokine-like factor	AF096895
211906_s_at	0.60054	3.4227571	4.231041	3.53E-05	0.0001201	1.427313	SERPINB4	serpin peptidase inhibitor, clade B (ovalbumin), member 4	AB046400
219901_at	0.60049	6.6808935	4.92348	1.77E-06	7.55E-06	4.291287	FGD6	FYVE, RhoGEF and PH domain containing 6	NM_018351
233979_s_at	0.60044	5.4124365	5.438283	1.55E-07	7.86E-07	6.639269	ESPN	espin	AI927458
226089_at	0.60032	6.718645	7.844639	2.49E-13	3.28E-12	19.65665	RABL3	RAB, member of RAS oncogene family-like 3	AI742028
223120_at	0.60027	9.4955716	9.265849	3.00E-17	7.71E-16	28.53295	FUCA2	fucosidase, alpha-L-2, plasma	BC003060
204385_at	0.60022	7.0920134	5.250306	3.84E-07	1.84E-06	5.761348	KYNU	kynureninase (L-kynurenine hydrolase)	NM_003937
225597_at	0.59979	7.9455304	6.37133	1.25E-09	8.88E-09	11.32126	SLC45A4	solute carrier family 45, member 4	AI346128
205527_s_at	0.59979	7.1724058	9.018589	1.51E-16	3.42E-15	26.94152	GEMIN4	gem (nuclear organelle) associated protein 4	NM_015487
223978_s_at	0.59978	9.7315855	7.63935	8.66E-13	1.04E-11	18.43562	CRLS1	cardiolipin synthase 1	AF241784
203867_s_at	0.59959	7.1718121	9.300356	2.39E-17	6.26E-16	28.75643	NLE1	notchless homolog 1 (Drosophila)	NM_018096
215078_at	0.59959	4.020288	5.168799	5.66E-07	2.63E-06	5.387946	SOD2	superoxide dismutase 2, mitochondrial	AL050388
227653_at	0.59945	6.927816	9.348025	1.75E-17	4.68E-16	29.06568	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	AI168767
222601_at	0.59932	7.5082394	8.77172	7.45E-16	1.49E-14	25.37077	UBA6	ubiquitin-like modifier activating enzyme 6	AI457479
219518_s_at	0.5993	6.5814063	4.699476	4.83E-05	1.92E-05	3.326574	ELL3	elongation factor RNA polymerase II-like 3	NM_025165
215458_s_at	0.59925	5.8946837	7.709112	5.68E-13	7.00E-12	18.84859	SMURF1	SMAD specific E3 ubiquitin protein ligase 1	AF199354
235573_at	0.59911	6.1802908	7.196396	1.20E-11	1.19E-10	15.86283	0	0	AL536101
221666_s_at	0.5991	9.4233311	5.433066	1.59E-07	8.05E-07	6.614594	PYCARD	PYD and CARD domain containing	BC004470
227245_at	0.59906	6.8934101	9.20566	4.45E-17	1.11E-15	28.14395	C12orf30	chromosome 12 open reading frame 30	AW511198
33307_at	0.59903	7.6948036	9.497538	6.50E-18	1.87E-16	30.03959	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	AL022316

235013_at	0.59901	8.1701376	8.204478	2.71E-14	4.15E-13	21.83743	SLC31A1	solute carrier family 31 (copper transporters), member 1	AI754064
208953_at	0.5989	8.265445	7.416207	3.28E-12	3.60E-11	17.12865	LARP5	La ribonucleoprotein domain family, member 5	AU154358
204228_at	0.59881	9.2250879	10.74266	1.42E-21	7.71E-20	38.35044	PPIH	peptidylprolyl isomerase H (cyclophilin H)	NM_006347
214144_at	0.59862	6.4131308	8.09709	5.28E-14	7.70E-13	21.18141	POLR2D	polymerase (RNA) II (DNA directed) polypeptide D	BF432147
225944_at	0.59857	6.6051277	6.640343	2.85E-10	2.26E-09	12.76371	NLN	neurolysin (metallopeptidase M3 family)	AW006938
223681_s_at	0.59847	7.3482282	5.650225	5.42E-08	2.95E-07	7.656444	INADL	InaD-like (Drosophila)	AB044807
212556_at	0.59824	8.8581656	9.488463	6.90E-18	1.97E-16	29.9803	SCRIB	scribbled homolog (Drosophila)	AI469403
218275_at	0.59819	6.5460334	7.622341	9.59E-13	1.14E-11	18.33524	SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	NM_012140
212107_s_at	0.59817	8.0114573	7.486574	2.16E-12	2.44E-11	17.53846	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	BE561014
1555039_a_at	0.59815	5.2356154	6.926004	5.69E-11	5.05E-10	14.33675	ABCC4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	AY133679
202673_at	0.59813	11.006643	10.72899	1.56E-21	8.34E-20	38.2575	DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	NM_003859
217736_s_at	0.59799	10.0616	9.715152	1.53E-18	4.88E-17	31.46735	EIF2AK1	eukaryotic translation initiation factor 2-alpha kinase 1	NM_014413
222923_s_at	0.5979	7.3700445	4.467626	1.32E-05	4.84E-05	2.366154	KCNE3	potassium voltage-gated channel, Isk-related family, member 3	AF302494
224314_s_at	0.5979	6.9356913	6.998454	3.76E-11	3.44E-10	14.7422	EGLN1	egl nine homolog 1 (C. elegans)	AF277174
205670_at	0.59789	6.1857878	6.93068	5.54E-11	4.93E-10	14.36284	GAL3ST1	galactose-3-O-sulfotransferase 1	NM_004861
200943_at	0.59785	11.133077	10.50474	7.29E-21	3.41E-19	36.73814	HMGNL	high-mobility group nucleosome binding domain 1	NM_004965
201708_s_at	0.5977	8.1881411	8.50833	4.00E-15	7.17E-14	23.71637	NIPSNAP1	nipsnap homolog 1 (C. elegans)	AW083371
223540_at	0.59765	6.7632273	6.399835	1.07E-09	7.68E-09	11.47226	PVRL4	poliovirus receptor-related 4	AF160477
203927_at	0.59762	7.4855408	7.288655	6.97E-12	7.20E-11	16.39144	NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	NM_004556
48808_at	0.59752	7.7023912	8.032696	7.86E-14	1.11E-12	20.79012	DHFR	dihydrofolate reductase	AI144299
225599_s_at	0.59751	7.3697815	5.749815	3.28E-08	1.85E-07	8.144145	C8orf83	chromosome 8 open reading frame 83	AW303300
227012_at	0.59744	7.9490355	7.258898	8.30E-12	8.46E-11	16.22052	SLC25A40	solute carrier family 25, member 40	AI823986
213912_at	0.59738	5.3549037	5.796581	2.58E-08	1.48E-07	8.37527	FLI41278	hypothetical gene supported by AK123272 /// TBC1 domain family, member 30	AW134976
200766_at	0.59733	9.1584453	7.375217	4.19E-12	4.51E-11	16.89094	CTSD	cathepsin D	NM_001909
1559590_at	0.59729	3.7730763	7.00739	3.57E-11	3.28E-10	14.79239	CHDH	choline dehydrogenase	AA609488
210410_s_at	0.59726	5.8694897	6.94261	5.18E-11	4.63E-10	14.42946	C6orf26	chromosome 6 open reading frame 26 /// mutS homolog 5 (E. coli)	AF034759
212200_at	0.59726	7.0862223	7.144571	1.62E-11	1.57E-10	15.56763	ANKLE2	ankyrin repeat and LEM domain containing 2	AK025933
211797_s_at	0.59712	6.8178137	8.663648	1.49E-15	2.84E-14	24.68918	NFYC	nuclear transcription factor Y, gamma	U62296
231200_at	0.597	5.2931871	9.659864	2.21E-18	6.85E-17	31.10349	LSM14B	LSM14B, SCD6 homolog B (S. cerevisiae)	BG222606
206261_at	0.59699	7.345053	6.882117	7.31E-11	6.37E-10	14.09241	ZNF239	zinc finger protein 239	NM_005674
214512_s_at	0.59694	10.971707	9.154332	6.23E-17	1.51E-15	27.81302	SUB1	SUB1 homolog (S. cerevisiae)	NM_006713
209605_at	0.59687	10.203051	4.619843	6.84E-06	2.65E-05	2.992273	TST	thiosulfate sulfurtransferase (rhodanese)	D87292
202411_at	0.59679	11.333287	4.379514	1.91E-05	6.82E-05	2.011568	IFI27	interferon, alpha-inducible protein 27	NM_005532
235440_at	0.59661	6.7037668	9.62275	2.83E-18	8.65E-17	30.85966	SPTY2D1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	BE780878

206752_s_at	0.59655	6.118486	8.001687	9.52E-14	1.33E-12	20.60226	DFFB	DNA fragmentation factor, 40kDa, beta polypeptide (caspase-activated DNase)	NM_004402
215739_s_at	0.5965	4.9117089	7.467046	2.43E-12	2.72E-11	17.42451	TUBGCP3	tubulin, gamma complex associated protein 3	AJ003062
1558522_at	0.59635	3.9940649	6.989517	3.96E-11	3.61E-10	14.69205	0	0	BC013077
206675_s_at	0.59627	4.8865876	6.724921	1.77E-10	1.46E-09	13.22512	SKIL	SKI-like oncogene	NM_005414
218774_at	0.59621	7.9408578	9.757481	1.15E-18	3.77E-17	31.74643	DCPS	decapping enzyme, scavenger	NM_014026
214830_at	0.59594	7.3479019	5.716345	3.88E-08	2.17E-07	7.979556	SLC38A6	solute carrier family 38, member 6	AI537540
203342_at	0.59589	8.4660302	10.65891	2.53E-21	1.29E-19	37.78173	TIMM17B	translocase of inner mitochondrial membrane 17 homolog B (yeast)	NM_005834
204859_s_at	0.59587	6.8111537	7.889939	1.89E-13	2.53E-12	19.9284	APAF1	apoptotic peptidase activating factor 1	NM_013229
200790_at	0.59582	11.177471	6.631287	2.99E-10	2.37E-09	12.71453	ODC1	ornithine decarboxylase 1	NM_002539
203377_s_at	0.59551	6.0388696	7.832431	2.69E-13	3.51E-12	19.58355	CDC40	cell division cycle 40 homolog (S. cerevisiae)	NM_015891
213843_x_at	0.59535	8.022224	4.670599	5.48E-06	2.16E-05	3.204815	SLC6A8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	AW276522
219376_at	0.59508	6.5346934	6.85128	8.70E-11	7.49E-10	13.92129	ZNF322B	zinc finger protein 322B	NM_024639
203669_s_at	0.59507	8.4518692	5.617243	6.39E-08	3.44E-07	7.496288	OGAT1 ///	diacylglycerol O-acyltransferase homolog 1 (mouse) /// similar to diacylglycerol O-acyltransferase homolog 1 (mouse)	NM_012079
222931_s_at	0.59489	6.598077	7.18258	1.30E-11	1.28E-10	15.78401	THNSL1	threonine synthase-like 1 (S. cerevisiae)	AI809864
212339_at	0.59484	6.8236313	5.410193	1.78E-07	8.94E-07	6.506611	EPB41L1	erythrocyte membrane protein band 4.1-like 1	AL121895
203634_s_at	0.5947	5.2858405	6.44636	8.30E-10	6.08E-09	11.71966	CPT1A	carnitine palmitoyltransferase 1A (liver)	NM_001876
213807_x_at	0.59456	6.9609956	6.36116	1.32E-09	9.35E-09	11.2675	MET	met proto-oncogene (hepatocyte growth factor receptor)	BE870509
222551_s_at	0.59436	7.4534918	8.836641	4.90E-16	1.02E-14	25.78201	C8orf33	chromosome 8 open reading frame 33	AI197841
225648_at	0.59432	7.2781516	10.53043	6.11E-21	2.89E-19	36.91178	STK35	serine/threonine kinase 35	AA001414
222343_at	0.59425	4.799327	10.89054	5.13E-22	2.99E-20	39.35736	BCL2L11	BCL2-like 11 (apoptosis facilitator)	AA629050
200896_x_at	0.59417	11.055798	10.24712	4.23E-20	1.77E-18	35.00416	HDGF	hepatoma-derived growth factor (high-mobility group protein 1-like)	NM_004494
226026_at	0.59415	8.1712488	7.496061	2.04E-12	2.32E-11	17.59388	DIRC2	disrupted in renal carcinoma 2	AI147467
210010_s_at	0.59413	8.2314402	7.059742	2.64E-11	2.48E-10	15.08718	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	U25147
232164_s_at	0.59409	8.4500871	3.666877	0.0003141	0.0008931	-0.63612	EPPK1	epiplakin 1	AL137725
223480_s_at	0.59401	10.414616	11.83493	7.06E-25	7.24E-23	45.86045	MRPL47	mitochondrial ribosomal protein L47	AI189156
208580_x_at	0.59398	6.9866128	9.070288	1.08E-16	2.51E-15	27.2728	HIST1H4A	histone cluster 1, H4a /// histone cluster 1, H4b /// histone cluster 1, H4c /// histone cluster 1, H4d /// histone cluster 1, H4e /// histone cluster 1, H4f /// histone cluster 1, H4h /// histone cluster 1, H4i /// histone cluster 1, H4j /// histone cluster 1, H4k /// histone cluster 1, H4l /// histone cluster 2, H4a /// histone cluster 2, H4b /// histone cluster 4, H4	NM_021968

201003_x_at	0.59395	9.3418124	8.263189	1.88E-14	2.95E-13	22.1979	RNPEP ///	arginyl aminopeptidase (aminopeptidase B) /// transmembrane protein 189 /// TMEM189-UBE2V1 readthrough transcript /// ubiquitin-conjugating enzyme E2 variant 1 /// ubiquitin-conjugating enzyme E2 variant 1 pseudogene 2	NM_003349
200692_s_at	0.59383	9.806256	9.677163	1.97E-18	6.16E-17	31.21726	HSPA9	heat shock 70kDa protein 9 (mortalin)	NM_004134
218800_at	0.59379	5.1712369	5.498059	1.15E-07	5.97E-07	6.923259	SRD5A3	steroid 5 alpha-reductase 3	NM_024592
208309_s_at	0.59368	6.9864609	6.733961	1.69E-10	1.39E-09	13.27466	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	NM_006785
218533_s_at	0.59345	8.3641825	10.09322	1.20E-19	4.63E-18	33.97457	UCKL1	uridine-cytidine kinase 1-like 1	NM_017859
235287_at	0.59345	4.789645	4.360307	2.07E-05	7.34E-05	1.93505	CDK6	cyclin-dependent kinase 6	AW192700
228095_at	0.59343	9.0625814	8.830265	5.11E-16	1.06E-14	25.74156	PHF14	PHD finger protein 14	AA608749
231033_at	0.59334	4.9508117	4.25073	3.26E-05	0.0001117	1.503828	0	0	AI819863
1554102_a_at	0.59333	6.1001103	8.228284	2.33E-14	3.61E-13	21.98344	TMTC4	transmembrane and tetratricopeptide repeat containing 4	BC018707
218721_s_at	0.59329	8.5981522	7.79714	3.33E-13	4.28E-12	19.37259	C1orf27	chromosome 1 open reading frame 27	NM_017847
222442_s_at	0.59325	8.4564934	7.287985	7.00E-12	7.22E-11	16.38759	ARL8B	ADP-ribosylation factor-like 8B	AW055237
218389_s_at	0.59319	9.864827	10.29409	3.07E-20	1.31E-18	35.31938	APH1A	anterior pharynx defective 1 homolog A (C. elegans)	NM_016022
203517_at	0.59314	8.9583093	10.96903	2.98E-22	1.82E-20	39.8932	MTX2	metaxin 2	NM_006554
204514_at	0.59313	7.7575715	11.16682	7.55E-23	5.18E-21	41.24767	DPH2	DPH2 homolog (S. cerevisiae)	NM_001384
201970_s_at	0.59312	9.4079702	11.80352	8.81E-25	8.88E-23	45.64246	NASP	nuclear autoantigenic sperm protein (histone-binding)	NM_002482
213823_at	0.593	6.2967672	5.169034	5.65E-07	2.63E-06	5.389013	HOXA11	homeobox A11	H94842
231576_at	0.59288	7.8592321	4.539264	9.70E-06	3.65E-05	2.6587	0	0	AA829940
202929_s_at	0.59286	9.1321724	8.006148	9.26E-14	1.29E-12	20.62927	DDT	D-dopachrome tautomerase	NM_001355
221826_at	0.59281	6.2877928	7.891521	1.87E-13	2.51E-12	19.93791	ANGEL2	angel homolog 2 (Drosophila)	BE671941
218133_s_at	0.59266	8.7583903	11.34951	2.12E-23	1.62E-21	42.50352	NIF3L1	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	NM_021824
209864_at	0.59264	8.3528264	6.937203	5.34E-11	4.76E-10	14.39925	FRAT2	frequently rearranged in advanced T-cell lymphomas 2	AB045118
202843_at	0.59264	7.1910248	5.138296	6.53E-07	3.00E-06	5.249351	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	NM_012328
202246_s_at	0.59264	10.105283	9.47574	7.51E-18	2.12E-16	29.89723	CDK4	cyclin-dependent kinase 4	NM_000075
212250_at	0.5926	10.163567	9.590193	3.51E-18	1.06E-16	30.64604	MTDH	metadherin	AV700332
208758_at	0.59259	10.015208	10.59653	3.88E-21	1.92E-19	37.35901	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	D89976
226375_at	0.59227	7.8684281	7.019996	3.32E-11	3.07E-10	14.86325	0	0	AW206440
225142_at	0.59225	6.3986924	6.323512	1.62E-09	1.13E-08	11.06897	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	AW294022
223221_at	0.59212	8.1220444	9.773126	1.04E-18	3.42E-17	31.84968	SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	AF183424
225527_at	0.59212	8.6192589	7.491626	2.10E-12	2.37E-11	17.56796	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	BE622659
201417_at	0.59209	10.572588	5.878332	1.70E-08	1.01E-07	8.78249	SOX4	SRY (sex determining region Y)-box 4	AL136179
224610_at	0.59203	8.874373	7.609247	1.04E-12	1.23E-11	18.25805	SNHG1	small nucleolar RNA host gene 1 (non-protein coding)	AL530869
1552417_a_at	0.59193	5.9343858	7.373838	4.22E-12	4.54E-11	16.88296	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	NM_152905
209161_at	0.59192	8.99257	11.23132	4.82E-23	3.42E-21	41.69055	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	AI184802
227477_at	0.59184	8.3306299	9.433043	9.96E-18	2.77E-16	29.61875	ZMYND19	zinc finger, MYND-type containing 19	AL565563
218893_at	0.59182	8.4083428	9.485306	7.05E-18	2.01E-16	29.95969	ISOC2	isochorismatase domain containing 2	NM_024710
1553167_a_at	0.59173	5.1898333	6.187479	3.36E-09	2.23E-08	10.35821	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	BC023539

227008_at	0.59172	7.9124116	9.3548	1.67E-17	4.49E-16	29.10968	HDDC3	HD domain containing 3	AI393309
208840_s_at	0.59163	8.4888581	6.467853	7.38E-10	5.47E-09	11.83434	G3BP2	GTPase activating protein (SH3 domain) binding protein 2	AU149503
214011_s_at	0.59144	9.5435942	8.710801	1.10E-15	2.15E-14	24.9861	NOP16	NOP16 nucleolar protein homolog (yeast)	BE314601
201001_s_at	0.59128	9.8062309	10.22707	4.84E-20	2.00E-18	34.86974	TMEM189	TMEM189-UBE2V1 readthrough transcript /// ubiquitin-conjugating enzyme E2 variant 1	BG164064
225827_at	0.59102	8.3444671	6.799389	1.17E-10	9.83E-10	13.63442	EIF2C2	eukaryotic translation initiation factor 2C, 2	AI832074
214741_at	0.59102	7.6585651	6.542883	4.88E-10	3.73E-09	12.23666	ZNF131	zinc finger protein 131	AW968301
212171_x_at	0.59101	8.5493278	6.615971	3.26E-10	2.56E-09	12.63144	VEGFA	vascular endothelial growth factor A	H95344
1554513_s_at	0.591	4.6269913	7.0802	2.35E-11	2.22E-10	15.20274	CCDC123	coiled-coil domain containing 123	BC032307
217959_s_at	0.59081	9.4512623	7.687729	6.47E-13	7.88E-12	18.7218	TRAPPC4	trafficking protein particle complex 4	NM_016146
223516_s_at	0.5907	9.9647341	9.838739	6.67E-19	2.28E-17	32.28335	PRICKLE4	prickle homolog 4 (Drosophila) /// translocase of outer mitochondrial membrane 6 homolog (yeast)	AF216754
201913_s_at	0.59069	8.915246	8.789727	6.63E-16	1.35E-14	25.4847	COASY	Coenzyme A synthase	NM_025233
212656_at	0.5906	8.467245	12.81317	7.01E-28	1.32E-25	52.69118	TSFM	Ts translation elongation factor, mitochondrial	AF110399
218732_at	0.5906	8.8415463	9.930843	3.59E-19	1.29E-17	32.89379	PTRH2	peptidyl-tRNA hydrolase 2	NM_016077
242786_at	0.59055	5.353962	7.177325	1.34E-11	1.32E-10	15.75406	0	0	AI521166
202562_s_at	0.59048	8.6695771	9.452201	8.78E-18	2.46E-16	29.74364	C14orf1	chromosome 14 open reading frame 1	AL136658
202675_at	0.59043	9.5784666	9.738419	1.31E-18	4.24E-17	31.6207	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (lp)	NM_003000
203194_s_at	0.59029	7.3629476	10.58571	4.18E-21	2.05E-19	37.28575	NUP98	nucleoporin 98kDa	AA527238
218768_at	0.59024	9.1121831	7.666011	7.38E-13	8.91E-12	18.59321	NUP107	nucleoporin 107kDa	NM_020401
209882_at	0.59017	7.5969821	7.378925	4.10E-12	4.42E-11	16.91242	RIT1	Ras-like without CAAX 1	AF084462
226193_x_at	0.59007	10.329103	10.48646	8.26E-21	3.83E-19	36.6147	CBWD1	COBW domain containing 1 /// COBW domain containing 2 /// COBW domain containing 3 /// COBW domain containing 5 /// COBW domain containing 6	AV709992
201587_s_at	0.58995	9.9428663	8.899532	3.27E-16	7.00E-15	26.18165	IRAK1	interleukin-1 receptor-associated kinase 1	NM_001569
220329_s_at	0.58992	6.9681468	7.319509	5.82E-12	6.10E-11	16.56909	RMND1	required for meiotic nuclear division 1 homolog (S. cerevisiae)	NM_017909
219575_s_at	0.58988	8.0728769	10.45318	1.04E-20	4.75E-19	36.39013	COG8	component of oligomeric golgi complex 8 /// peptide deformylase (mitochondrial)	NM_022341
202535_at	0.58969	8.7217347	8.751554	8.48E-16	1.69E-14	25.2433	FADD	Fas (TNFRSF6)-associated via death domain	NM_003824
202900_s_at	0.58967	9.0185439	8.762579	7.90E-16	1.58E-14	25.31297	NUP88	nucleoporin 88kDa	NM_002532
1556242_a_at	0.58963	7.2764907	8.092147	5.44E-14	7.91E-13	21.15131	0	0	BC040715
218118_s_at	0.58957	9.307075	9.894499	4.59E-19	1.62E-17	32.65268	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	NM_006327
235346_at	0.58934	8.5833239	5.989887	9.51E-09	5.87E-08	9.344629	FUNDC1	FUN14 domain containing 1	BF033615
203123_s_at	0.5892	8.4181623	6.868664	7.89E-11	6.84E-10	14.0177	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	AU154469
215812_s_at	0.58905	7.8011466	6.085711	5.76E-09	3.69E-08	9.833349	LOC653562	hypothetical LOC653562 /// solute carrier family 6 (neurotransmitter transporter, creatine), member 10 (pseudogene) /// solute carrier family 6 (neurotransmitter transporter, creatine), member 8	U41163
215450_at	0.58896	6.9221644	7.905929	1.72E-13	2.32E-12	20.02452	0	0	W87901
213892_s_at	0.58894	9.1931741	8.422367	6.90E-15	1.17E-13	23.18149	APRT	adenine phosphoribosyltransferase	AA927724
218944_at	0.58884	6.9765225	8.433184	6.44E-15	1.11E-13	23.24865	PYCR1	pyrroline-5-carboxylate reductase-like	NM_023078

201491_at	0.58879	9.8988197	10.12436	9.72E-20	3.80E-18	34.18253	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	NM_012111
242706_s_at	0.58875	6.489702	6.419752	9.60E-10	6.96E-09	11.57802	MED23	mediator complex subunit 23	AW959449
214882_s_at	0.58869	10.250535	11.32597	2.49E-23	1.88E-21	42.3415	SFRS2	splicing factor, arginine/serine-rich 2	BG254869
210816_s_at	0.58866	6.1816343	8.85204	4.44E-16	9.30E-15	25.87975	CYB561	cytochrome b-561	BC000021
212590_at	0.58862	7.8348045	4.190241	4.17E-05	0.00014	1.269706	RRAS2	related RAS viral (r-ras) oncogene homolog 2	AI431643
225037_at	0.58859	8.5493918	9.724386	1.44E-18	4.61E-17	31.5282	SLC35C2	solute carrier family 35, member C2	AL518563
203577_at	0.58844	6.9855079	10.71522	1.72E-21	9.08E-20	38.16397	GTF2H4	general transcription factor IIH, polypeptide 4, 52kDa	NM_001517
1554251_at	0.58836	6.5172054	6.368315	1.27E-09	9.02E-09	11.30532	HP1BP3	heterochromatin protein 1, binding protein 3	BC022342
214463_x_at	0.58836	7.4153978	8.404857	7.70E-15	1.30E-13	23.07285	HIST1H4J	histone cluster 1, H4j	NM_003541
208456_s_at	0.58836	6.8967372	4.123059	5.46E-05	0.0001798	1.012984	RRAS2	related RAS viral (r-ras) oncogene homolog 2	NM_012250
217831_s_at	0.58823	8.118581	10.92079	4.16E-22	2.47E-20	39.56375	NSFL1C	NSFL1 (p97) cofactor (p47)	NM_016143
242140_at	0.5881	7.9633573	5.766626	3.01E-08	1.71E-07	8.227075	0	0	AA635618
228543_at	0.58809	8.9226393	6.171456	3.66E-09	2.42E-08	10.27518	CSR2BP	CSR2 binding protein	AA780252
209790_s_at	0.58798	8.7966199	6.957921	4.74E-11	4.27E-10	14.51505	CASP6	caspase 6, apoptosis-related cysteine peptidase	BC000305
206656_s_at	0.58794	10.110917	8.900091	3.26E-16	6.98E-15	26.18521	C20orf3	chromosome 20 open reading frame 3	BC000353
219904_at	0.58792	5.699563	9.210155	4.32E-17	1.08E-15	28.17297	ZSCAN5A	zinc finger and SCAN domain containing 5A	NM_024303
235260_s_at	0.58788	6.9456612	6.698841	2.05E-10	1.67E-09	13.08245	PACRGL	PARK2 co-regulated-like	AA398590
203252_at	0.58778	8.7470743	7.651162	8.07E-13	9.70E-12	18.5054	CDK2AP2	cyclin-dependent kinase 2 associated protein 2	NM_005851
226710_at	0.58778	8.5263061	7.30807	6.22E-12	6.48E-11	16.50318	C8orf82	chromosome 8 open reading frame 82	AI199072
202857_at	0.58771	10.952751	9.819703	7.58E-19	2.56E-17	32.15743	CNPY2	canopy 2 homolog (zebrafish)	NM_014255
225126_at	0.58769	7.5485322	8.293546	1.55E-14	2.48E-13	22.38478	MRRF	mitochondrial ribosome recycling factor	BF438352
203765_at	0.58761	8.1895883	6.744543	1.59E-10	1.31E-09	13.33269	GCA	grancalcin, EF-hand calcium binding protein	NM_012198
222939_s_at	0.58753	6.1369919	3.869327	0.0001473	0.0004464	0.075238	SLC16A10	solute carrier family 16, member 10 (aromatic amino acid transporter)	N30257
201512_s_at	0.58747	8.6735382	9.147355	6.52E-17	1.58E-15	27.7681	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A [S. cerevisiae]	BC003633
211089_s_at	0.58738	5.9508146	5.878915	1.69E-08	1.00E-07	8.785405	NEK3	NIMA (never in mitosis gene a)-related kinase 3	Z25434
201898_s_at	0.58728	9.384924	9.944604	3.27E-19	1.19E-17	32.98516	UBE2A	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	AI126625
1568600_at	0.58721	5.9070778	5.022976	1.12E-06	4.95E-06	4.731089	CALML4	calmodulin-like 4	AA741090
208852_s_at	0.58719	10.157972	8.038327	7.60E-14	1.08E-12	20.82427	CANX	calnexin	AI761759
220642_x_at	0.58697	8.2734843	10.33454	2.33E-20	1.01E-18	35.5911	GPR89A ///	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	NM_016334
206016_at	0.58682	7.1488197	8.028436	8.07E-14	1.14E-12	20.76429	CCDC22	coiled-coil domain containing 22	NM_014008
203417_at	0.58677	8.3548948	3.741929	0.0002381	0.0006925	-0.37628	MFAP2	microfibrillar-associated protein 2	NM_017459
227790_at	0.58671	5.5728816	8.094137	5.38E-14	7.83E-13	21.16343	UBE2CBP	ubiquitin-conjugating enzyme E2C binding protein	AV692609
200892_s_at	0.5867	9.7396776	10.62397	3.22E-21	1.61E-19	37.54489	SFRS10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	BC000451
201128_s_at	0.58663	10.542448	8.263916	1.87E-14	2.94E-13	22.20238	ACLY	ATP citrate lyase	NM_001096
1007_s_at	0.58652	10.539967	6.04886	6.99E-09	4.41E-08	9.644768	DDR1	discoidin domain receptor tyrosine kinase 1	U48705
222759_at	0.58629	8.0632809	7.695421	6.18E-13	7.56E-12	18.76739	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	BC002522
243042_at	0.58619	6.0520009	6.119272	4.82E-09	3.13E-08	10.00578	FAM73A	family with sequence similarity 73, member A	BE645144
238539_at	0.58618	6.311162	8.945648	2.42E-16	5.30E-15	26.47547	HPS3	Hermansky-Pudlak syndrome 3	BG163294
203359_s_at	0.58613	9.0903417	9.282892	2.68E-17	6.97E-16	28.64329	MYCBP	c-myc binding protein	AL525412

226503_at	0.58606	7.0525386	8.040298	7.50E-14	1.07E-12	20.83623	RIF1	RAP1 interacting factor homolog (yeast)	BE504653
236598_at	0.58605	5.1146791	6.643236	2.80E-10	2.23E-09	12.77943	0	0	BF432065
201376_s_at	0.58603	9.4516911	10.48717	8.22E-21	3.82E-19	36.61952	HNRNPF	heterogeneous nuclear ribonucleoprotein F	AI591354
200769_s_at	0.58587	7.5605202	6.172018	3.64E-09	2.41E-08	10.27809	MAT2A	methionine adenosyltransferase II, alpha	NM_005911
212016_s_at	0.58585	7.9552575	11.46435	9.49E-24	7.81E-22	43.29526	PTBP1	polypyrimidine tract binding protein 1	AA679988
213124_at	0.58582	6.5049827	8.609576	2.10E-15	3.93E-14	24.34959	ZNF473	zinc finger protein 473	BG538800
223056_s_at	0.58574	8.6418678	9.052828	1.21E-16	2.80E-15	27.16083	XPO5	exportin 5	AF298880
235688_s_at	0.58571	6.0227602	8.387946	8.57E-15	1.44E-13	22.96803	TRAF4	TNF receptor-associated factor 4	AI992283
200751_s_at	0.58563	10.435987	9.288125	2.59E-17	6.76E-16	28.67718	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	BE898861
225210_s_at	0.58554	9.0920693	7.960975	1.22E-13	1.68E-12	20.3562	FAM103A1	family with sequence similarity 103, member A1	AW025216
205977_s_at	0.58551	7.6414618	5.890218	1.60E-08	9.51E-08	8.842029	EPHA1	EPH receptor A1	NM_005232
217167_x_at	0.58549	6.5640177	7.169849	1.40E-11	1.37E-10	15.71146	GK	glycerol kinase	AI252550
231399_at	0.58528	5.0504159	5.508424	1.10E-07	5.70E-07	6.972737	RAB3IP	RAB3A interacting protein (rabin3)	BE671491
200838_at	0.58525	11.493273	6.379165	1.20E-09	8.54E-09	11.36272	CTSB	cathepsin B	NM_001908
218331_s_at	0.58524	8.8126822	7.742926	4.63E-13	5.80E-12	19.0495	C10orf18	chromosome 10 open reading frame 18	NM_017782

Figure 13

Metabolic-subtype up-regulated genes

ID	logFC	AveExpr	t	P.Value	adj.P.Val	B	Gene Symb	Gene Title	GeneBank_ACC
220191_at	4.60637	7.7518899	7.568906	1.33E-12	7.45E-12	18.0329	GKN1	gastrokine 1	NM_019617
238222_at	4.44625	7.2435922	8.175409	3.26E-14	2.40E-13	21.66953	GKN2	gastrokine 2	AI821357
206334_at	3.83302	7.5600178	6.847086	8.93E-11	3.76E-10	13.91247	LIPF	lipase, gastric	NM_004190
213265_at	3.716	7.7798869	7.730506	5.01E-13	3.00E-12	18.98732	PGA3 /// PG	A) /// pepsinogen 4, group I (pepsinogen A) /// pepsinogen 5,	AI570199
207033_at	3.41311	5.6048021	8.19274	2.92E-14	2.17E-13	21.77555	GIF	gastric intrinsic factor (vitamin B	NM_005142
207546_at	3.23308	5.1127969	9.307116	2.30E-17	3.15E-16	28.80583	ATP4B	ATPase, H+/K+ exchanging, beta	NM_000705
238383_at	3.11019	5.8001214	7.648528	8.22E-13	4.77E-12	18.50178	C6orf58	chromosome 6 open reading frame	AI857688
214385_s_at	3.08153	8.708118	7.532215	1.65E-12	9.14E-12	17.81775	MUC5AC	mucin 5AC, oligomeric mucus/gel-	AI521646
1555236_a_at	2.91523	9.168527	5.536562	9.55E-08	2.63E-07	7.125079	PGC	progastricsin (pepsinogen C)	BC042578
214303_x_at	2.8805	8.6094619	8.484406	4.68E-15	4.02E-14	23.5762	MUC5AC	mucin 5AC, oligomeric mucus/gel-	AW192795
205261_at	2.72051	9.9225886	5.476495	1.28E-07	3.48E-07	6.838359	PGC	progastricsin (pepsinogen C)	NM_002630
231646_at	2.71897	7.2163182	6.616717	3.25E-10	1.26E-09	12.65055	DPCR1	diffuse panbronchiolitis critical	AW473496
207139_at	2.69433	5.7546223	10.23945	4.48E-20	1.14E-18	34.95401	ATP4A	ATPase, H+/K+ exchanging, alpha	NM_000704
214476_at	2.68029	10.171745	6.426502	9.26E-10	3.35E-09	11.62949	TFF2	trefoil factor 2	NM_005423
243764_at	2.67934	8.1626224	6.181552	3.47E-09	1.16E-08	10.34368	VSIG1	V-set and immunoglobulin domain	AW085312
205319_at	2.64669	7.6001628	6.857155	8.43E-11	3.56E-10	13.96825	PSCA	prostate stem cell antigen	NM_005672
241137_at	2.60967	7.1166098	6.713701	1.89E-10	7.61E-10	13.17849	DPCR1	diffuse panbronchiolitis critical	AW338320
226960_at	2.6087	8.1789546	7.655532	7.88E-13	4.59E-12	18.54315	CXCL17	chemokine (C-X-C motif) ligand 17	AW471176
226147_s_at	2.58743	10.57029	5.759291	3.12E-08	9.17E-08	8.20807	PIGR	polymeric immunoglobulin	AA838075
203240_at	2.54172	8.1485546	7.858521	2.30E-13	1.46E-12	19.75107	FCGBP /// L	/// similar to IgGfC-binding protein precursor (FcgammaBP) (Fcgamma-	NM_003890
202018_s_at	2.53128	8.5136245	6.612521	3.33E-10	1.29E-09	12.62782	LTF	lactotransferrin	NM_002343
210143_at	2.45691	9.3475657	5.367066	2.19E-07	5.76E-07	6.321979	ANXA10	annexin A10	AF196478
1565666_s_at	2.3546	5.2492232	7.655209	7.89E-13	4.60E-12	18.54124	LOC100133	(Gastric mucin-6) /// similar to Mucin-6 precursor (Gastric mucin-	AW864944
213953_at	2.27946	7.9104709	4.866507	2.29E-06	5.25E-06	4.061561	KRT20	keratin 20	AI732381
214133_at	2.26087	7.4931141	10.91087	4.49E-22	1.87E-20	39.4939	LOC100133	similar to Mucin-6 precursor	AI611214
206561_s_at	2.21731	9.377678	4.713282	4.54E-06	1.00E-05	3.404267	AKR1B10	aldo-keto reductase family 1,	NM_020299
205343_at	2.1912	7.4279752	6.616291	3.26E-10	1.26E-09	12.64824	SULT1C2	sulfotransferase family, cytosolic,	NM_001056
207912_s_at	2.1904	5.1886009	4.178768	4.37E-05	8.50E-05	1.245739	DAZ1 /// D	deleted in azoospermia 2 /// deleted in azoospermia 3 ///	NM_004081
205009_at	2.16022	11.289692	4.794856	3.16E-06	7.11E-06	3.752119	TFF1	trefoil factor 1	NM_003225
213921_at	2.15954	6.4718647	6.178665	3.52E-09	1.17E-08	10.32873	SST	somatostatin	NM_001048
221095_s_at	2.11634	6.778295	9.754042	1.18E-18	2.14E-17	31.72733	KCNE2	potassium voltage-gated channel,	NM_005136
229030_at	2.08173	7.6397627	8.076529	6.02E-14	4.24E-13	21.06676	CAPN8	calpain 8	AW242997
229659_s_at	2.04926	9.0097692	5.685883	4.53E-08	1.30E-07	7.847724	0	0	BE501712
211470_s_at	2.04797	8.5875596	5.521685	1.03E-07	2.82E-07	7.053852	SULT1C2	sulfotransferase family, cytosolic,	AF186255
205979_at	2.02234	5.4773214	6.426184	9.28E-10	3.36E-09	11.6278	SCGB2A1	secretoglobulin, family 2A, member	NM_002407
226067_at	2.01978	8.1336879	4.748372	3.89E-06	8.66E-06	3.553319	C20orf114	chromosome 20 open reading	AL355392
217187_at	2.00157	7.3419341	9.236871	3.65E-17	4.80E-16	28.35144	MUC5AC	mucin 5AC, oligomeric mucus/gel-forming	Z34282
234370_at	1.98119	6.2948892	6.677847	2.31E-10	9.18E-10	12.98275	VSIG1	V-set and immunoglobulin domain containing 1	AL031177
208063_s_at	1.97774	6.2151708	8.908408	3.10E-16	3.37E-15	26.24542	CAPN9	calpain 9	NM_006615
214046_at	1.96973	5.4540007	5.706254	4.09E-08	1.18E-07	7.947386	FUT9	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	AA017721
205342_s_at	1.94381	8.2784827	5.251653	3.82E-07	9.71E-07	5.785832	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	AF026303
207249_s_at	1.93148	5.6775405	6.438297	8.69E-10	3.16E-09	11.69224	SLC28A2	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2	NM_004212
214235_at	1.90539	7.4654233	8.099788	5.21E-14	3.70E-13	21.20821	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	X90579
232578_at	1.89169	9.2458394	3.74134	0.0002387	0.000423	-0.35762	CLDN18	claudin 18	BG547464
229152_at	1.87756	6.2278214	5.73438	3.55E-08	1.03E-07	8.085414	C4orf7	chromosome 4 open reading frame 7	AI718421
211357_s_at	1.85392	6.9264322	5.228955	4.26E-07	1.08E-06	5.681424	ALDOB	aldolase B, fructose-bisphosphate	BC005314
226248_s_at	1.84652	8.3958733	5.670885	4.89E-08	1.40E-07	7.774511	KIAA1324	KIAA1324	AI565067
217238_s_at	1.84302	6.1299354	4.872984	2.22E-06	5.10E-06	4.089708	ALDOB	aldolase B, fructose-bisphosphate family with sequence similarity 3,	AK026411
227676_at	1.8372	8.0225614	6.589788	3.78E-10	1.45E-09	12.50483	FAM3D	member D	AW001287
213456_at	1.83711	6.6746778	6.136942	4.40E-09	1.44E-08	10.11314	SOSTDC1	sclerostin domain containing 1	AI927000
209752_at	1.83681	9.4665144	3.576104	0.0004367	0.0007485	-0.92331	REG1A	regenerating islet-derived 1 alpha	AF172331
214135_at	1.8288	10.901612	4.611786	7.09E-06	1.53E-05	2.978148	CLDN18	claudin 18	BE551219

204705_x_at	1.81672	7.5628775	6.27814	2.07E-09	7.12E-09	10.84571	ALDOB	aldolase B, fructose-bisphosphate	NM_000035
205765_at	1.80852	8.2610887	5.612326	6.55E-08	1.84E-07	7.489994	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	NM_000777
205927_s_at	1.80575	10.766058	4.439489	1.49E-05	3.07E-05	2.272017	CTSE	cathepsin E	NM_001910
207392_x_at	1.79735	6.699554	6.796805	1.19E-10	4.90E-10	13.63473	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	NM_001076
205513_at	1.75836	7.9258064	4.354674	2.12E-05	4.29E-05	1.932514	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	NM_001062
214324_at	1.75679	5.9917705	6.046293	7.09E-09	2.27E-08	9.648193	GP2	glycoprotein 2 (zymogen granule membrane)	BF222483
228592_at	1.75259	6.3206274	5.256128	3.74E-07	9.52E-07	5.806457	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	AW474852
219564_at	1.74698	4.0495244	7.802838	3.23E-13	2.00E-12	19.41804	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	NM_018658
228232_s_at	1.73434	8.5100609	5.967626	1.07E-08	3.34E-08	9.248578	VSIG2	V-set and immunoglobulin domain containing 2	NM_014312
236001_at	1.70287	7.9670915	9.242805	3.51E-17	4.62E-16	28.38977	LOC400573	hypothetical gene supported by BC015790; BC041634	BF446940
227194_at	1.70279	8.1350861	4.527957	1.02E-05	2.15E-05	2.631858	FAM3B	family with sequence similarity 3, member B	BF106962
228969_at	1.70166	9.8681929	5.561489	8.44E-08	2.34E-07	7.244738	AGR2	anterior gradient homolog 2 (Xenopus laevis)	AI922323
210641_at	1.69812	5.6673167	7.73033	5.01E-13	3.00E-12	18.98527	CAPN9	calpain 9	AB038463
208126_s_at	1.685	7.5826284	5.79041	2.67E-08	7.90E-08	8.361827	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	NM_000772
229070_at	1.68241	7.238746	5.087417	8.29E-07	2.02E-06	5.038168	C6orf105	chromosome 6 open reading frame 105	AA470369
205623_at	1.65533	7.2131732	7.249929	8.77E-12	4.31E-11	16.1823	ALDH3A1	aldehyde dehydrogenase 3 family, member A1	NM_000691
205267_at	1.64082	7.9339753	5.707211	4.07E-08	1.18E-07	7.952074	POU2AF1	POU class 2 associating factor 1	NM_006235
223862_at	1.63917	5.5351607	7.144682	1.62E-11	7.63E-11	15.58181	GHRL	ghrelin/obestatin prepropeptide	AB035700
228004_at	1.63742	7.246197	6.61444	3.29E-10	1.27E-09	12.63822	C20orf56	chromosome 20 open reading frame 56	AL121722
229254_at	1.63635	7.2359455	5.753659	3.21E-08	9.42E-08	8.180308	MFSD4	major facilitator superfamily domain containing 4	BE550027
210065_s_at	1.61148	6.1605386	5.288356	3.20E-07	8.23E-07	5.955381	UPK1B	uropiakin 1B	AB002155
239370_at	1.61146	7.428256	5.417614	1.71E-07	4.57E-07	6.559545	0	0	AW081982
228058_at	1.60414	8.1704351	5.458359	1.40E-07	3.79E-07	6.752245	LOC124220	similar to common salivary protein 1	AI559190
214234_s_at	1.59271	8.2740219	5.75907	3.13E-08	9.18E-08	8.206978	CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5	X90579
242271_at	1.59074	5.5356113	6.970531	4.42E-11	1.95E-10	14.5997	SLC26A9	solute carrier family 26, member 9	AI932662
210064_s_at	1.58411	5.7491682	5.646206	5.53E-08	1.57E-07	7.654342	UPK1B	uropiakin 1B	NM_006952
219727_at	1.5818	6.9198754	4.921089	1.79E-06	4.15E-06	4.299709	DUOX2	dual oxidase 2	NM_014080
205544_s_at	1.56748	6.1522059	6.404041	1.05E-09	3.76E-09	11.51021	CR2	complement component (3d/Epstein Barr virus) receptor 2	NM_001877
206262_at	1.56418	8.7931388	4.095111	6.11E-05	0.0001166	0.927459	ADH1C	alcohol dehydrogenase 1C (class I), gamma polypeptide	NM_000669
205199_at	1.55625	7.6105583	6.63038	3.01E-10	1.17E-09	12.72463	CA9	carbonic anhydrase IX	NM_001216
206212_at	1.55354	6.0061843	8.64863	1.65E-15	1.54E-14	24.60307	CPA2	carboxypeptidase A2 (pancreatic)	NM_001869
1564333_a_at	1.54875	7.0753346	12.15032	7.74E-26	8.74E-24	48.0455	PSAPL1	prosaposin-like 1	AK097698
215118_s_at	1.54026	5.6033943	6.630064	3.02E-10	1.17E-09	12.72292	IGHG1	Immunoglobulin lambda heavy chain	AW519168
208473_s_at	1.53541	6.6641575	5.041597	1.03E-06	2.47E-06	4.832839	GP2	glycoprotein 2 (zymogen granule membrane)	NM_016295
229177_at	1.52914	6.4768309	6.901032	6.57E-11	2.83E-10	14.21187	C16orf89	chromosome 16 open reading frame 89	AI823572
210381_s_at	1.52646	5.4799743	9.369645	1.52E-17	2.16E-16	29.21146	CCKBR	cholecystokinin B receptor	BC000740
207981_s_at	1.52492	5.1315148	5.559518	8.53E-08	2.36E-07	7.235263	ESRRG	estrogen-related receptor gamma	NM_001438
216687_x_at	1.52375	5.8654975	7.494049	2.07E-12	1.13E-11	17.59457	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15	U06641
208138_at	1.5116	6.7048498	5.893061	1.57E-08	4.81E-08	8.873179	GAST	gastrin	NM_000805
226228_at	1.51025	3.7110491	6.790232	1.23E-10	5.08E-10	13.59852	AQP4	aquaporin 4	T15657
220468_at	1.49528	8.2475121	4.429499	1.55E-05	3.19E-05	2.231748	ARL14	ADP-ribosylation factor-like 14	NM_D25047

203453_at	1.49505	8.4224844	4.717696	4.46E-06	9.84E-06	3.422969	SCNN1A	sodium channel, nonvoltage-gated 1 alpha	NM_001038
209966_x_at	1.48606	5.4700195	6.876532	7.56E-11	3.22E-10	14.07571	ESRRG	estrogen-related receptor gamma	AF094518
206691_s_at	1.47707	6.1701243	7.399629	3.63E-12	1.90E-11	17.04517	PDIA2	protein disulfide isomerase family A, member 2	NM_006849
206239_s_at	1.46819	11.772926	3.80827	0.0001858	0.0003336	-0.12215	SPINK1	serine peptidase inhibitor, Kazal type 1	NM_003122
204351_at	1.46691	11.586355	4.077168	6.56E-05	0.0001247	0.859903	S100P	S100 calcium binding protein P	NM_005980
219956_at	1.46653	8.3879872	6.504081	6.06E-10	2.25E-09	12.0436	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	NM_007210
222484_s_at	1.45473	8.9545241	4.710583	4.60E-06	1.01E-05	3.39284	CXCL14	chemokine (C-X-C motif) ligand 14	AF144103
214070_s_at	1.44163	8.1807585	5.479025	1.27E-07	3.44E-07	6.850391	ATP10B	ATPase, class V, type 10B	AW006935
212827_at	1.43497	6.7014569	5.541487	9.32E-08	2.57E-07	7.148692	IGHM	immunoglobulin heavy constant mu	X17115
231211_s_at	1.43418	6.0725561	11.60129	3.68E-24	2.56E-22	44.23542	LOC541469	hypothetical protein LOC541469	AI254026
210107_at	1.43263	5.5514467	5.089738	8.20E-07	2.00E-06	5.048606	CLCA1	chloride channel regulator 1	AF127036
240304_s_at	1.43228	10.646622	4.901614	1.95E-06	4.51E-06	4.214497	TMC5	transmembrane channel-like 5	BG484769
227742_at	1.42686	7.4923006	4.909901	1.88E-06	4.35E-06	4.250721	CLIC6	chloride intracellular channel 6	AI638295
221133_s_at	1.42038	9.0833993	3.550753	0.0004783	0.000815	-1.00812	CLDN18	claudin 18	NM_016369
215103_at	1.41745	6.2442737	4.962003	1.48E-06	3.48E-06	4.479584	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18	AW192911
209309_at	1.4173	7.105601	4.596522	7.58E-06	1.62E-05	2.91471	AZGP1	alpha-2-glycoprotein 1, zinc-binding	D90427
204378_at	1.40784	7.3637617	5.72638	3.69E-08	1.07E-07	8.046107	BCAS1	breast carcinoma amplified sequence 1	NM_003657
1552834_at	1.40352	5.9900938	8.65616	1.57E-15	1.47E-14	24.65037	B3GNT6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	BC025357
221122_at	1.39323	6.4502524	5.621093	6.27E-08	1.77E-07	7.532452	HRASL52	HRAS-like suppressor 2	NM_017878
209301_at	1.39159	10.171667	3.742611	0.0002376	0.0004211	-0.35318	CA2	carbonic anhydrase II	M36532
203924_at	1.38935	8.1489148	3.914978	0.0001237	0.000227	0.260692	GSTA1	glutathione S-transferase alpha 1	NM_000846
204919_at	1.38789	5.8920152	6.238163	2.56E-09	8.71E-09	10.63787	PRR4	proline rich 4 (lacrima)	NM_007244
242093_at	1.37595	6.4892653	5.186636	5.20E-07	1.30E-06	5.487684	SYTL5	synaptotagmin-like 5	AW263497
204272_at	1.35367	11.124708	3.703153	0.000275	0.0004837	-0.49033	LGALS4	lectin, galactoside-binding, soluble, 4	NM_006149
220639_at	1.34575	7.2140797	3.551943	0.0004762	0.0008118	-1.00415	TM4SF20	transmembrane 4 L six family member 20	NM_024795
1554970_at	1.34154	4.1512107	10.80581	9.27E-22	3.58E-20	38.77837	PDILT	protein disulfide isomerase-like protein of the testis	BC042607
208281_x_at	1.34117	5.3209562	3.633752	0.0003546	0.000615	-0.72849	DAZ1 /// DAZL	deleted in azoospermia 1 /// deleted in azoospermia 2 /// deleted in azoospermia 3 /// deleted in azoospermia 4 /// similar to deleted in azoospermia-like	NM_020364
218002_s_at	1.33637	8.789147	4.405057	1.72E-05	3.51E-05	2.133542	CXCL14	chemokine (C-X-C motif) ligand 14	NM_004887
221874_at	1.31781	6.6076732	4.828304	2.72E-06	6.17E-06	3.896119	KIAA1324	KIAA1324	AB037745
236430_at	1.3158	5.0905684	5.188876	5.15E-07	1.29E-06	5.497908	TMED6	transmembrane emp24 protein transport domain containing 6	AA708152
237466_s_at	1.31033	5.1208245	8.899288	3.29E-16	3.56E-15	26.1874	HHIP	hedgehog interacting protein	AW444502
228303_at	1.30178	7.4932723	7.194025	1.22E-11	5.84E-11	15.8627	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	AW014155
1553986_at	1.29932	7.8631062	5.753395	3.22E-08	9.43E-08	8.179003	RASEF	RAS and EF-hand domain containing	BC023566
206681_x_at	1.29549	6.8123852	5.833984	2.13E-08	6.40E-08	8.578108	GP2	glycoprotein 2 (zymogen granule membrane)	NM_001502
205403_at	1.29433	8.2429926	4.977228	1.38E-06	3.26E-06	4.546819	IL1R2	interleukin 1 receptor, type II	NM_004633
235638_at	1.28557	6.6717337	4.911015	1.87E-06	4.33E-06	4.255596	RASSF6	Ras association (RalGDS/AF-6) domain family member 6	AI167789
223895_s_at	1.28373	6.6286784	8.173359	3.30E-14	2.43E-13	21.65699	EPN3	epsin 3	BC001038

207601_at	1.27607	6.7593051	7.34752	4.94E-12	2.53E-11	16.74366	SULT1B1	sulfotransferase family, cytosolic, 1B, member 1	NM_014465
155654_at	1.27452	5.1719487	11.11159	1.12E-22	5.41E-21	40.86563	TRIM50	tripartite motif-containing 50	AK057366
215129_at	1.27451	6.0779363	5.14066	6.46E-07	1.59E-06	5.278561	PIK3C2G	phosphoinositide-3-kinase, class 2, gamma polypeptide	AJ000008
229369_at	1.2696	7.68948	6.692845	2.13E-10	8.50E-10	13.05455	VSIG2	V-set and immunoglobulin domain containing 2	AI201858
229147_at	1.26594	8.3676947	4.660651	5.73E-06	1.25E-05	3.182371	0	0	AW070877
206002_at	1.26285	5.259561	6.509254	5.89E-10	2.19E-09	12.07132	GPR64	G protein-coupled receptor 64	NM_005756
243780_at	1.25846	5.3653135	5.36009	2.27E-07	5.94E-07	6.289326	0	0	AW575863
205969_at	1.25781	7.5006744	4.256924	3.18E-05	6.29E-05	1.547966	AADAC	arylacetamide deacetylase (esterase)	NM_001086
230585_at	1.25252	4.6219159	9.192593	4.87E-17	6.25E-16	28.06572	0	0	AI632692
1554182_at	1.24851	4.4528239	11.44637	1.09E-23	6.81E-22	43.16612	TRIM73	tripartite motif-containing 73 /// tripartite motif-containing 74	BC033871
205470_s_at	1.24523	7.0766792	4.87218	2.23E-06	5.12E-06	4.086215	KLK11	kallikrein-related peptidase 11	NM_006853
210619_s_at	1.24329	6.8908158	6.776401	1.33E-10	5.47E-10	13.52239	HYAL1	hyaluronoglucosaminidase 1	AF173154
227725_at	1.24144	8.5741579	4.3569	2.10E-05	4.26E-05	1.941357	ST6GALNAC	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylglucosaminide alpha-2,6-sialyltransferase 1	Y11339
235591_at	1.23629	6.2966337	4.208616	3.87E-05	7.58E-05	1.360607	SSTR1	somatostatin receptor 1	R62424
238385_at	1.23588	4.1571189	7.643714	8.46E-13	4.91E-12	18.47335	C6orf58	CDNA FLJ50045 complete cds	BF825703
219580_s_at	1.23136	9.2132018	4.306121	2.59E-05	5.19E-05	1.740601	TMC5	transmembrane channel-like 5	NM_024780
234709_at	1.22975	4.4920353	6.266905	2.20E-09	7.54E-09	10.78793	CAPN13	calpain 13	AK026692
211372_s_at	1.22541	7.3238037	5.293366	3.13E-07	8.05E-07	5.978593	IL1R2	interleukin 1 receptor, type II	U64094
204673_at	1.22482	6.0630858	4.815822	2.88E-06	6.51E-06	3.842291	MUC2	mucln 2, oligomeric mucus/gel-forming	NM_002457
239832_at	1.22068	5.8273796	9.481573	7.26E-18	1.11E-16	29.94013	0	0	AI264135
227782_at	1.21894	7.3666499	7.988423	1.04E-13	6.99E-13	20.5328	ZBTB7C	zinc finger and BTB domain containing 7C	AI278995
227306_at	1.21304	6.547515	5.198542	4.92E-07	1.23E-06	5.542067	0	0	AK024898
203559_s_at	1.21253	8.5774062	3.783412	0.000204	0.0003643	-0.21003	ABP1	amiloride binding protein 1 (amine oxidase (copper-containing))	NM_001091
211600_at	1.21073	11.924113	10.66465	2.45E-21	8.52E-20	37.81985	PTPRO	protein tyrosine phosphatase, receptor type, O	U20489
201468_s_at	1.20837	10.55367	5.484468	1.24E-07	3.36E-07	6.876284	NQO1	NAD(P)H dehydrogenase, quinone 1	NM_000903
205049_s_at	1.20292	6.8263252	6.47619	7.06E-10	2.60E-09	11.89434	CD79A	CD79a molecule, immunoglobulin-associated alpha	NM_001783
219429_at	1.20269	7.9348676	4.836899	2.62E-06	5.95E-06	3.933253	FA2H	fatty acid 2-hydroxylase	NM_024306
207158_at	1.19995	6.03541	5.949541	1.18E-08	3.65E-08	9.157223	APOBEC1	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	NM_001644
205464_at	1.18884	4.6412691	12.99437	1.96E-28	5.30E-26	53.94872	SCNN1B	sodium channel, nonvoltage-gated 1, beta	NM_000336
230615_at	1.18701	7.4623502	6.239736	2.54E-09	8.65E-09	10.64607	DUOXA2	dual oxidase maturation factor 2	AI821606
209173_at	1.18622	12.590001	3.617241	0.0003765	0.0006506	-0.78457	AGR2	anterior gradient homolog 2 (Xenopus laevis)	AF088867
207222_at	1.18605	8.2702854	4.518432	1.06E-05	2.23E-05	2.592834	PLA2G10	phospholipase A2, group X	NM_003561
219476_at	1.18491	8.3166474	4.120183	5.53E-05	0.0001061	1.02228	C1orf116	chromosome 1 open reading frame 116	NM_024115
231982_at	1.18286	8.9557411	3.997508	8.98E-05	0.0001678	0.563011	LOC284422	similar to HSPC323	AF161441
210356_x_at	1.18061	5.9085371	4.923338	1.77E-06	4.11E-06	4.309565	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	BC002807
243582_at	1.17657	6.694639	6.451652	8.07E-10	2.95E-09	11.76338	SH3RF2	SH3 domain containing ring finger 2	AW082633
202831_at	1.16426	11.195457	3.976523	9.75E-05	0.0001812	0.485629	GPX2	glutathione peroxidase 2 (gastrointestinal)	NM_002083
210103_s_at	1.1628	7.3501347	5.60169	6.91E-08	1.94E-07	7.438547	FOXA2	forkhead box A2	AB028021
222245_s_at	1.16218	7.3587915	9.965157	2.87E-19	5.97E-18	33.12431	FER1L4	fer-1-like 4 (C. elegans)	AF218012
209374_s_at	1.16203	9.9974453	3.683251	0.0002959	0.0005183	-0.55903	IGHM	immunoglobulin heavy constant mu	BC001872
202525_at	1.1556	8.6331241	4.492216	1.19E-05	2.48E-05	2.485782	PRSS8	protease, serine, 8	NM_002773
206844_at	1.15505	5.3862478	8.76495	7.81E-16	7.80E-15	25.33581	FBP2	fructose-1,6-bisphosphatase 2	NM_003837
229150_at	1.15452	6.329551	7.562835	1.37E-12	7.71E-12	17.99726	0	0	AI810764

220017_x_at	1.15419	6.7836781	7.428122	3.07E-12	1.62E-11	17.21055	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	NM_000771
212592_at	1.1497	10.631894	3.500315	0.0005722	0.0009659	-1.17526	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	AV733266
205997_at	1.14868	7.7892751	4.582176	8.06E-06	1.72E-05	2.855242	ADAM28	ADAM metalloproteinase domain 28	NM_021778
1568513_x_at	1.14495	9.2836027	12.61245	2.95E-27	5.44E-25	51.27225	IL23A	T cell receptor beta chain (TCRBV8S1-TCRBJ1S5)	AJ296370
217418_x_at	1.14376	5.7938386	4.805785	3.01E-06	6.79E-06	3.799085	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	X12530
234723_x_at	1.14251	8.1282063	8.558588	2.92E-15	2.61E-14	24.03893	0	0	AK024881
228708_at	1.14162	9.5699507	4.646732	6.09E-06	1.32E-05	3.124023	RAB27B	Small GTP-binding protein Rab27b	BF438386
218211_s_at	1.14068	9.6567135	5.417521	1.72E-07	4.57E-07	6.559107	MLPH	melanophilin	NM_024101
205929_at	1.13707	7.3759572	4.475376	1.28E-05	2.65E-05	2.417286	GPA33	glycoprotein A33 (transmembrane)	NM_005814
226553_at	1.13064	9.36274	5.630496	5.98E-08	1.69E-07	7.578044	TMPSR2	transmembrane protease, serine 2	AI660243
209950_s_at	1.12921	7.8735272	5.373814	2.12E-07	5.58E-07	6.353599	VILL	villin-like	BC004300
210119_at	1.12741	5.8875335	5.347536	2.41E-07	6.29E-07	6.231105	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	U73191
238197_at	1.12693	4.83301	5.266438	3.56E-07	9.09E-07	5.854023	GATA5	GATA binding protein 5	N72525
222915_s_at	1.12596	5.8499269	8.142591	3.99E-14	2.89E-13	21.46906	BANK1	B-cell scaffold protein with ankyrin repeats 1	AA811540
220421_at	1.12314	7.4140886	4.856208	2.40E-06	5.48E-06	4.016856	BTNL8 /// L	butyrophilin-like 8 /// similar to B7h.4	NM_024850
220177_s_at	1.12114	7.3669478	3.785755	0.0002022	0.0003613	-0.20177	TMPSR3	transmembrane protease, serine 3	NM_024022
1552797_s_at	1.11423	7.6205174	4.249768	3.27E-05	6.46E-05	1.5201	PROM2	prominin 2	NM_144707
214421_x_at	1.11232	5.8759653	7.684935	6.60E-13	3.88E-12	18.71706	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	AV652420
236118_at	1.11192	6.8046744	6.674453	2.36E-10	9.35E-10	12.96426	LOC100128	LOC728473	N63706
231278_at	1.11147	6.2630699	8.800379	6.22E-16	6.33E-15	25.55985	0	0	BF063966
220068_at	1.11121	5.7314713	7.685443	6.58E-13	3.87E-12	18.72007	VPREB3	pre-B lymphocyte 3	NM_013378
221008_s_at	1.1097	3.5661063	7.071883	2.47E-11	1.13E-10	15.16949	AGXT2L1	alanine-glyoxylate aminotransferase 2-like 1	NM_031279
228806_at	1.10844	5.6567144	7.359515	4.60E-12	2.36E-11	16.81296	RORC	RAR-related orphan receptor C	AI218580
238750_at	1.1056	7.3285688	4.682456	5.21E-06	1.14E-05	3.274061	0	0	AW083576
1555854_at	1.10491	4.985034	5.3824	2.03E-07	5.37E-07	6.393869	0	0	AA594609
1560199_x_at	1.09947	6.6996163	11.67318	2.22E-24	1.67E-22	44.73262	LOC728153	similar to FAM133B protein	AU120130
1552870_s_at	1.09937	4.4245738	4.658912	5.77E-06	1.26E-05	3.175076	C1orf125	chromosome 1 open reading frame 125	NM_144696
235372_at	1.09735	6.384265	8.743991	8.94E-16	8.81E-15	25.20346	FCRLA	Fc receptor-like A	AW575245
234562_x_at	1.09513	5.8596735	8.225423	2.38E-14	1.80E-13	21.9758	LOC728678	PREDICTED: Homo sapiens misc_RNA (LOC728678), miscRNA	AK000115
204519_s_at	1.09297	8.8453188	4.960692	1.49E-06	3.50E-06	4.473803	PLLP	plasma membrane proteolipid (plasmolipin)	NM_015993
233463_at	1.08696	4.9177018	8.303948	1.46E-14	1.15E-13	22.45853	RASSF6	Ras association (RalGDS/AF-6) domain family member 6	AU157324
230135_at	1.08264	5.5411964	5.47638	1.29E-07	3.48E-07	6.837815	0	0	AI822137
225165_at	1.08197	8.4304677	3.855307	0.0001555	0.0002818	0.045481	PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B	AK024593
209995_s_at	1.08096	6.2255233	6.581719	3.95E-10	1.51E-09	12.46124	TCL1A	T-cell leukemia/lymphoma 1A	BC003574
213693_s_at	1.0711	11.219226	4.724399	4.33E-06	9.57E-06	3.451394	MUC1	mucin 1, cell surface associated	AI610859
209699_x_at	1.07005	9.7810678	4.795242	3.16E-06	7.10E-06	3.753776	AKR1C2	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	U05598
229909_at	1.06834	6.9317349	9.680556	1.93E-18	3.32E-17	31.24351	B4GALNT3	beta-1,4-N-acetyl-galactosaminyl transferase 3	AI654238
205999_x_at	1.06708	7.0177418	6.371795	1.25E-09	4.44E-09	11.33944	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	AF182273

33323_r_at	1.06651	11.001069	3.863376	0.0001508	0.0002737	0.074418	SFN	stratifin	X57348
227475_at	1.06571	11.108946	3.547541	0.0004838	0.0008238	-1.01882	FOXQ1	forkhead box Q1	AI676059
1561346_at	1.06402	7.9341696	12.66217	2.07E-27	4.11E-25	51.62029	0		0 AW303888
237654_at	1.06348	6.5642088	8.43448	6.41E-15	5.37E-14	23.26584	C14orf50	chromosome 14 open reading frame 50	AA400298
227320_at	1.06339	8.325001	5.256932	3.72E-07	9.48E-07	5.810162	FAM101A	family with sequence similarity 101, member A	AW264333
203908_at	1.0615	7.8371761	3.577769	0.0004341	0.0007442	-0.91772	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	NM_003759
1553798_a_at	1.06069	4.0912786	8.790801	6.62E-16	6.70E-15	25.49924	FBXL13	F-box and leucine-rich repeat protein 13	NM_145032
238942_at	1.0517	4.5742178	13.61519	2.36E-30	1.20E-27	58.31127	0		0 AI248760
222257_s_at	1.04804	6.4222677	3.749677	0.0002314	0.0004107	-0.32848	ACE2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	AK026461
39318_at	1.04379	6.0169453	6.594321	3.68E-10	1.41E-09	12.52933	TCL1A	T-cell leukemia/lymphoma 1A	X82240
1568634_a_at	1.0427	5.2314576	5.327374	2.66E-07	6.90E-07	6.136601	LRRC66	leucine rich repeat containing 66	BU620718
204437_s_at	1.04134	6.3021941	4.144649	5.01E-05	9.67E-05	1.115276	FOLR1	folate receptor 1 (adult)	NM_016725
228360_at	1.03443	7.0483521	4.782768	3.34E-06	7.49E-06	3.700275	LYPD6B	LY6/PLAUR domain containing 6B	BF060747
204697_s_at	1.03368	6.3805459	4.862425	2.33E-06	5.34E-06	4.043833	CHGA	chromogranin A (parathyroid secretory protein 1)	NM_001275
220192_x_at	1.0278	7.8345383	7.062197	2.61E-11	1.19E-10	15.11483	SPDEF	SAM pointed domain containing ets transcription factor	NM_012391
206398_s_at	1.02289	6.1318462	6.623068	3.14E-10	1.22E-09	12.68498	CD19	CD19 molecule	NM_001770
236225_at	1.02244	6.3648498	5.269573	3.51E-07	8.96E-07	5.8685	GGT6	gamma-glutamyltransferase 6	AI697028
205776_at	1.01951	7.2742882	4.816468	2.87E-06	6.49E-06	3.845072	FMO5	flavin containing monooxygenase 5	NM_001461
241640_at	1.01906	6.6569424	15.68559	9.41E-37	1.18E-32	72.85451	BCAP29	B-cell receptor-associated protein 29	BG149769
213874_at	1.01396	6.75938	5.579861	7.71E-08	2.15E-07	7.333183	SERPINA4	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 4	NM_006215
220351_at	1.0131	6.510198	4.517679	1.06E-05	2.24E-05	2.589755	CCRL1	chemokine (C-C motif) receptor-like 1	NM_016557
40284_at	1.01309	7.9087228	4.245267	3.33E-05	6.58E-05	1.502591	FOXA2	forkhead box A2	AB028021
207638_at	1.00614	3.8110352	3.72604	0.0002526	0.0004464	-0.41093	PRSS7	protease, serine, 7 (enterokinase)	NM_002772
1568598_at	1.00542	6.0460218	9.388618	1.34E-17	1.93E-16	29.33474	KAZALD1	Kazal-type serine peptidase inhibitor domain 1, mRNA (cDNA clone MGC:13129 IMAGE:4122366)	BF434771
233867_at	1.00539	6.5717617	8.257989	1.94E-14	1.50E-13	22.17573	0		0 AK000119
220723_s_at	1.00211	4.2626677	13.20283	4.45E-29	1.47E-26	55.41231	FLJ21511	hypothetical protein FLJ21511	NM_025087
242998_at	0.99989	5.722649	6.19173	3.29E-09	1.10E-08	10.39644	RDH12	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)	AI796235
206539_s_at	0.99894	7.1627716	12.79555	8.04E-28	1.82E-25	52.55448	CYP4F12	cytochrome P450, family 4, subfamily F, polypeptide 12	NM_023944
208037_s_at	0.9917	7.0110129	11.98753	2.44E-25	2.39E-23	46.91281	MADCAM1	mucosal vascular addressin cell adhesion molecule 1	NM_007164
205757_at	0.98903	6.5801831	9.732433	1.37E-18	2.43E-17	31.58492	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	NM_001249
204073_s_at	0.98586	8.0567124	5.369353	2.17E-07	5.70E-07	6.33269	C11orf9	chromosome 11 open reading frame 9	NM_013279
220940_at	0.98293	6.9679052	6.793542	1.21E-10	4.99E-10	13.61675	ANKRD36B	ankyrin repeat domain 36B	NM_025190
229740_at	0.98165	6.8287543	12.26783	3.38E-26	4.36E-24	48.86457	LOC643008	PP12104	BF478120
228865_at	0.98126	8.2972529	4.077798	6.55E-05	0.0001244	0.862268	C1orf116	chromosome 1 open reading frame 116	AA622392
1555786_s_at	0.97909	8.4068694	8.502641	4.17E-15	3.62E-14	23.68977	CUEDC1	CUE domain containing 1	BC008034
206548_at	0.97813	4.6082838	7.356772	4.68E-12	2.40E-11	16.79711	hCG_17762	hypothetical protein FLJ23556	NM_024880
221969_at	0.97731	6.1051837	5.416558	1.72E-07	4.59E-07	6.554565	0		0 BF510692
207356_at	0.97583	6.0479378	6.355235	1.36E-09	4.83E-09	11.25196	DEFB4	defensin, beta 4	NM_004942
220630_s_at	0.97488	4.9508821	7.339446	5.18E-12	2.64E-11	16.69706	CH1A	chitinase, acidic	NM_021797
216381_x_at	0.97391	9.0975489	5.421939	1.68E-07	4.48E-07	6.579948	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	AL035413
228463_at	0.9729	8.1791223	4.033264	7.81E-05	0.0001469	0.695658	FOXA3	forkhead box A3	R99562
207847_s_at	0.96898	10.041733	3.990758	9.22E-05	0.000172	0.538084	MUC1	mucin 1, cell surface associated	NM_002456

235350_at	0.96667	6.7175272	4.408431	1.69E-05	3.47E-05	2.147072	C4orf19	chromosome 4 open reading frame 19	AI935586
234756_at	0.96389	4.1987553	10.90897	4.55E-22	1.89E-20	39.48097	CACNG8	calcium channel, voltage-dependent, gamma subunit 8	AF288388
240200_at	0.96332	5.765136	9.622726	2.84E-18	4.71E-17	30.86369	SULT1C2	sulfotransferase family, cytosolic, 1C, member 2	AI307799
211116_at	0.96292	5.0909022	7.147584	1.59E-11	7.51E-11	15.5983	SLC9A2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	AF073299
231734_at	0.96251	6.0681537	3.663797	0.0003178	0.0005546	-0.62587	RBP2	retinol binding protein 2, cellular	NM_004164
207200_at	0.96134	4.9458285	4.646093	6.11E-06	1.32E-05	3.12135	OTC	ornithine carbamoyltransferase	NM_000531
205509_at	0.96104	4.3581287	4.927748	1.73E-06	4.03E-06	4.328903	CPB1	carboxypeptidase B1 (tissue)	NM_001871
244341_at	0.96098	5.6761425	7.528788	1.69E-12	9.32E-12	17.79769	0	0	AA827728
214465_at	0.96035	5.3055647	3.981746	9.55E-05	0.0001778	0.504855	ORM1 /// C	Orosomucoid 1 /// orosomucoid 2	NM_000608
204151_x_at	0.95524	10.305118	4.298113	2.68E-05	5.36E-05	1.709121	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	NM_001353
224254_x_at	0.95524	6.7878659	6.88028	7.40E-11	3.15E-10	14.09652	0	0	AF116695
213611_at	0.95517	6.7062012	5.064301	9.24E-07	2.23E-06	4.934401	AQP5	aquaporin 5	BF726531
227226_at	0.9462	6.7101583	4.587296	7.89E-06	1.69E-05	2.87645	MRAP2	melanocortin 2 receptor accessory protein 2	AA418816
1556336_at	0.94393	6.3034702	8.935329	2.60E-16	2.87E-15	26.41682	CCBL2 /// L	cysteine conjugate-beta lyase 2 /// similar to RNA binding motif protein, X-linked /// RNA binding motif protein, X-linked	AA460960
221241_s_at	0.94245	7.3508972	4.597779	7.54E-06	1.62E-05	2.91993	BCL2L14	BCL2-like 14 (apoptosis facilitator)	NM_030766
220030_at	0.94144	5.90679	3.724211	0.0002544	0.0004492	-0.41729	STYK1	serine/threonine/tyrosine kinase 1	NM_018423
227946_at	0.94116	7.4504678	8.284398	1.65E-14	1.28E-13	22.33813	OSBPL7	oxysterol binding protein-like 7	AI955239
1556352_at	0.9397	5.9972044	10.16728	7.31E-20	1.76E-18	34.47107	0	0	AI692624
216661_x_at	0.93929	6.1995865	7.139846	1.67E-11	7.84E-11	15.55434	CYP2C9	Putative CYP2C9 gene [human, liver, mRNA, 1814 nt]	M15331
1568249_at	0.93891	6.2955486	11.23259	4.82E-23	2.56E-21	41.69541	LOC388796	hypothetical LOC388796 /// small nucleolar RNA, H/ACA box 71B	Y11166
219543_at	0.93865	8.5385625	4.201013	3.99E-05	7.80E-05	1.331285	PBLD	phenazine biosynthesis-like protein domain containing	NM_022129
236098_at	0.93861	7.375433	4.688309	5.07E-06	1.11E-05	3.298731	hCG_16438	hypothetical LOC100130933	AA429598
216025_x_at	0.93576	6.5101708	7.210304	1.11E-11	5.35E-11	15.95561	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9	M21940
1564069_at	0.9354	6.7347148	9.980297	2.59E-19	5.44E-18	33.22488	0	0	AK093987
216379_x_at	0.93386	12.651811	4.295297	2.71E-05	5.42E-05	1.698062	CD24	CD24 molecule	AK000168
205671_s_at	0.92931	6.4659487	6.488096	6.61E-10	2.44E-09	11.958	HLA-DQB	major histocompatibility complex, class II, DQ beta	NM_002120
230378_at	0.92712	6.2137697	6.165202	3.78E-09	1.25E-08	10.25905	SCGB3A1	secretoglobulin, family 3A, member 1	AA742697
229223_at	0.92682	6.7778739	6.608724	3.40E-10	1.31E-09	12.60726	0	0	AI038402
219667_s_at	0.92658	5.7736954	4.180156	4.34E-05	8.45E-05	1.251068	BANK1	B-cell scaffold protein with ankyrin repeats 1	NM_017935
242055_at	0.92504	5.1605054	8.645654	1.68E-15	1.56E-14	24.58438	0	0	AW136397
205297_s_at	0.92439	6.5340506	7.15706	1.51E-11	7.14E-11	15.65216	CD79B	CD79b molecule, immunoglobulin-associated beta	NM_000626
233152_x_at	0.92277	4.8271788	8.638475	1.76E-15	1.63E-14	24.53932	0	0	AL049979
217014_s_at	0.92231	6.4680783	4.788677	3.25E-06	7.30E-06	3.725607	AZGP1 /// A	alpha-2-glycoprotein 1, zinc-binding /// alpha-2-glycoprotein 1, zinc-binding pseudogene 1	AC004522
231978_at	0.9218	4.6130038	6.902783	6.51E-11	2.80E-10	14.22161	TPCN2	two pore segment channel 2	AI137479
206988_at	0.91987	5.3188205	4.39515	1.79E-05	3.66E-05	2.093863	CCL25	chemokine (C-C motif) ligand 25	NM_005624
1556510_at	0.91963	4.4427174	9.935948	3.49E-19	7.15E-18	32.93042	0	0	BC030753
204777_s_at	0.91947	6.1791515	4.84472	2.53E-06	5.76E-06	3.967085	MAL	mal, T-cell differentiation protein	NM_002371
211916_s_at	0.9188	7.0997364	4.833856	2.65E-06	6.03E-06	3.920101	MYO1A	myosin IA	AF009961

242372_s_at	0.9182	5.3831006	4.735105	4.13E-06	9.15E-06	3.496862	MFS4	major facilitator superfamily domain containing 4	AL542291
266_s_at	0.91633	11.25408	3.969689	0.0001001	0.0001859	0.460504	CD24	CD24 molecule	L33930
233565_s_at	0.91626	9.2179693	4.610527	7.13E-06	1.53E-05	2.972909	SDCBP2	syndecan binding protein (syntenin) 2	AL136531
219395_at	0.91574	7.986144	5.094373	8.03E-07	1.96E-06	5.069465	RBM35B	RNA binding motif protein 35B	NM_024939
210652_s_at	0.91416	7.6070386	3.885927	0.0001383	0.0002522	0.155562	TTC39A	tetratricopeptide repeat domain 39A	BC004399
238543_x_at	0.91244	5.9457261	13.68954	1.39E-30	7.74E-28	58.83434	MDGA1	MAM domain containing glycosylphosphatidylinositol anchor 1	BF724151
243149_at	0.91233	4.8268814	7.332289	5.41E-12	2.74E-11	16.65577	0	0	AI467945
204750_s_at	0.91056	7.2890488	4.175874	4.42E-05	8.59E-05	1.234641	DSC2	desmocollin 2	BF196457
244875_at	0.90525	6.0470146	11.38682	1.65E-23	9.88E-22	42.75589	0	0	AA548751
214404_x_at	0.90354	7.9130816	8.075626	6.05E-14	4.26E-13	21.06127	SPDEF	SAM pointed domain containing ets transcription factor	AI435670
213036_x_at	0.90304	8.5924224	5.761041	3.10E-08	9.09E-08	8.216703	ATP2A3	ATPase, Ca++ transporting, ubiquitous	Y15724
204213_at	0.89855	7.5955469	4.142433	5.06E-05	9.75E-05	1.106834	PIGR	polymeric immunoglobulin receptor	NM_002644
231496_at	0.89811	4.1883406	6.513236	5.76E-10	2.15E-09	12.09267	FCAMR	Fc receptor, IgA, IgM, high affinity	AW028140
231275_at	0.89402	5.3239841	14.01792	1.34E-31	1.17E-28	61.14501	LOC100129	similar to FLJ42875 protein	AW271608
215712_s_at	0.8934	5.587718	13.3528	1.53E-29	5.88E-27	56.46617	IGFALS	insulin-like growth factor binding protein, acid labile subunit	AW338791
204875_s_at	0.89308	9.5924495	3.847855	0.0001599	0.0002895	0.018806	GMD5	GDP-mannose 4,6-dehydratase	NM_001500
206286_s_at	0.89284	6.3917641	4.283171	2.85E-05	5.68E-05	1.650508	TDGF1 /// T	teratocarcinoma-derived growth factor 1 /// teratocarcinoma-derived growth factor 3, pseudogene	NM_003212
225491_at	0.89243	4.5561854	7.156695	1.51E-11	7.16E-11	15.65009	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	AL157452
230682_x_at	0.8908	7.2200416	12.27594	3.19E-26	4.14E-24	48.92112	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	BF515888
1566848_x_at	0.88868	6.3709017	8.94531	2.44E-16	2.71E-15	26.48043	0	0	BC034050
209771_x_at	0.88807	12.489784	4.220342	3.69E-05	7.24E-05	1.40592	CD24	CD24 molecule	AA761181
239597_at	0.88574	6.7379263	6.099218	5.37E-09	1.74E-08	9.91907	0	0	AA993566
215100_at	0.88313	5.5858212	7.619349	9.79E-13	5.63E-12	18.32964	C6orf105	chromosome 6 open reading frame 105	AL022724
1564444_at	0.88164	4.2213409	10.03733	1.76E-19	3.84E-18	33.60422	LOC100130	hypothetical LOC100130264	AK097497
242071_x_at	0.88066	5.5540962	11.20168	5.98E-23	3.10E-21	41.48327	ITGAB	Integrin, alpha 8	BF446919
206119_at	0.87901	4.8468459	7.748554	4.49E-13	2.71E-12	19.09459	BHMT	betaine-homocysteine methyltransferase	NM_001713
205185_at	0.87805	6.4664039	3.864394	0.0001502	0.0002727	0.078071	SPINK5	serine peptidase inhibitor, Kazal type 5	NM_006846
224707_at	0.87481	12.167868	5.654929	5.29E-08	1.51E-07	7.696771	C5orf32	chromosome 5 open reading frame 32	AL522667
1553396_a_at	0.87391	5.6908968	9.182121	5.22E-17	6.64E-16	27.99822	CCDC13	coiled-coil domain containing 13	NM_144719
1566957_at	0.87153	5.2526867	11.1327	9.65E-23	4.73E-21	41.01025	0	0	AL137719
1569428_at	0.87151	5.3085078	15.87896	2.39E-37	4.35E-33	74.20544	LOC100129	hypothetical protein LOC100129087 /// within bgcn homolog (Drosophila)	BC008292
1565483_at	0.87121	6.4472249	9.865393	5.61E-19	1.10E-17	32.46288	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	AF277897
206469_x_at	0.87018	9.1287217	5.155495	6.03E-07	1.49E-06	5.345883	AKR7A3	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	NM_012067
239136_at	0.8684	5.1762627	9.375828	1.46E-17	2.08E-16	29.25162	hCG_18182	hCG1818231	AI871120
239196_at	0.86829	8.3127683	4.391992	1.81E-05	3.70E-05	2.08123	ANKRD22	ankyrin repeat domain 22	AI097229
213059_at	0.86822	9.2202629	4.840209	2.58E-06	5.87E-06	3.947566	CREB3L1	cAMP responsive element binding protein 3-like 1	AF055009
236083_at	0.86794	6.163752	4.716472	4.48E-06	9.89E-06	3.417783	BCL2L15	BCL2-like 15	AI685244
214372_x_at	0.8671	9.2708854	8.84233	4.75E-16	4.94E-15	25.82564	ERN2	endoplasmic reticulum to nucleus signaling 2	AI732416

220312_at	0.86517	6.5634634	7.636892	8.81E-13	5.10E-12	18.43309	FAM83E	family with sequence similarity 83, member E	NM_017708
205632_s_at	0.86479	8.6259216	3.763741	0.0002196	0.0003908	-0.27921	PIP5K1B	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	NM_003558
1554516_at	0.86436	7.3016691	10.20844	5.53E-20	1.37E-18	34.7464	LOC203274	CDNA FLJ31544 fis, clone NT2RI2000865	BC011779
1553071_a_at	0.86315	4.8599271	11.14914	8.61E-23	4.28E-21	41.12291	MYOZ3	myozenin 3	NM_133371
235245_at	0.86301	7.7017443	7.722579	5.25E-13	3.14E-12	18.94025	TMEM92	transmembrane protein 92	AI990471
219327_s_at	0.8628	8.3451147	6.46895	7.35E-10	2.70E-09	11.85567	GPRC5C	G protein-coupled receptor, family C, group 5, member C	NM_022036
219450_at	0.8615	7.3510254	3.757092	0.0002251	0.0004001	-0.30252	C4orf19	chromosome 4 open reading frame 19	NM_018302
205971_s_at	0.85455	3.8365166	5.791923	2.65E-08	7.84E-08	8.369314	CTRB1 /// C	chymotrypsinogen B1 /// chymotrypsinogen B2	NM_001906
214088_s_at	0.85321	7.9292016	4.026694	8.01E-05	0.0001506	0.671208	FUT3	fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis blood group)	AW080549
1557658_at	0.8517	4.652279	8.520527	3.72E-15	3.26E-14	23.80128	0	0	BE503598
1561044_at	0.85032	6.3247366	9.181364	5.25E-17	6.67E-16	27.99334	0	0	BC039493
230238_at	0.84961	6.7759239	3.551256	0.0004774	0.0008136	-1.00644	ANKRD43	ankyrin repeat domain 43	AI744123
211465_x_at	0.84719	8.715584	7.229065	9.91E-12	4.83E-11	16.06285	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	U27335
207522_s_at	0.84629	7.9882864	4.740284	4.03E-06	8.95E-06	3.518883	ATP2A3	ATPase, Ca++ transporting, ubiquitous	NM_005173
235592_at	0.84576	5.5526737	5.490995	1.20E-07	3.25E-07	6.907363	0	0	AW960145
242874_at	0.84534	6.3084675	6.091345	5.59E-09	1.81E-08	9.878673	0	0	AI741506
238943_at	0.84405	5.9397483	10.60049	3.81E-21	1.26E-19	37.38527	FIBCD1	fibrinogen C domain containing 1	BF792773
1556267_at	0.84357	4.3963191	8.533261	3.43E-15	3.03E-14	23.88073	C12orf28	chromosome 12 open reading frame 28	AK057785
1566887_x_at	0.84332	8.2678672	8.515907	3.83E-15	3.35E-14	23.77247	0	0	AY094612
208147_s_at	0.84228	3.6023262	6.245963	2.46E-09	8.38E-09	10.67855	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	NM_030878
217207_s_at	0.83966	6.9218717	9.220585	4.06E-17	5.29E-16	28.24628	BTNL3	butyrophilin-like 3	AK025267
221131_at	0.83879	5.442059	3.910879	0.0001257	0.0002304	0.245819	A4GNT	alpha-1,4-N-acetylglucosaminyltransferase	NM_016161
241161_at	0.83781	5.3152081	11.61163	3.42E-24	2.41E-22	44.30692	0	0	T70280
243349_at	0.83618	6.164118	5.291053	3.16E-07	8.13E-07	5.967877	KIAA1324	KIAA1324	AI672868
241994_at	0.83556	6.1901568	3.512346	0.0005483	0.0009278	-1.13559	XDH	xanthine dehydrogenase	BC260086
1556994_at	0.83533	4.9831362	9.781473	9.85E-19	1.81E-17	31.90826	0	0	BC042991
1555779_a_at	0.83423	7.0941457	5.793473	2.62E-08	7.78E-08	8.376991	CD79A	CD79a molecule, immunoglobulin-associated alpha	M74721
206337_at	0.83287	6.8679692	3.733465	0.0002458	0.0004348	-0.38508	CCR7	chemokine (C-C motif) receptor 7	NM_001838
216419_at	0.83279	5.2725068	10.78818	1.05E-21	3.99E-20	38.65848	CROCC	ciliary rootlet coiled-coil, rootletin	AK026910
205660_at	0.83259	7.4656925	4.509894	1.10E-05	2.31E-05	2.557916	OASL	2'-5'-oligoadenylate synthetase-like	NM_003733
208161_s_at	0.83254	9.1113567	4.661567	5.71E-06	1.24E-05	3.186219	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_020037
220161_s_at	0.83201	9.2725515	4.096339	6.08E-05	0.0001161	0.932093	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	NM_019114
91826_at	0.83059	8.3967126	5.023143	1.12E-06	2.67E-06	4.750547	EPS8L1	EPS8-like 1	AI219073
220059_at	0.83049	4.6458305	4.847177	2.50E-06	5.70E-06	3.97772	STAP1	signal transducing adaptor family member 1	NM_012108
232083_at	0.8266	6.918866	5.271385	3.48E-07	8.89E-07	5.876872	KIF16B	kinesin family member 16B	AB046810
1552383_at	0.82642	6.8181158	12.52631	5.42E-27	9.14E-25	50.66973	FAM71A	family with sequence similarity 71, member A	NM_153606
207003_at	0.824	6.1398204	6.143589	4.24E-09	1.40E-08	10.14741	GUCA2A	guanylate cyclase activator 2A (guanylin)	NM_002098
1552930_at	0.8238	6.7747325	7.743377	4.63E-13	2.79E-12	19.06381	MMEL1	membrane metallo-endopeptidase-like 1	NM_033467
217137_x_at	0.82354	5.7964127	9.454371	8.70E-18	1.30E-16	29.76274	0	0	K00627
205709_s_at	0.82191	8.9534528	3.55079	0.0004782	0.0008149	-1.008	CDS1	CDP-diacylglycerol synthase (phosphatidate cytidyltransferase) 1	NM_001263
225299_at	0.82182	7.5293542	3.645476	0.0003398	0.0005906	-0.68853	MYO5B	myosin VB	AB032945
1561079_at	0.82103	4.4358404	7.122548	1.84E-11	8.60E-11	15.45618	ANKRD28	ankyrin repeat domain 28	BC035170

227862_at	0.82091	9.3273005	3.762365	0.0002207	0.0003927	-0.28404	C1orf225	chromosome 1 open reading frame 225	AA037766
1552872_at	0.82068	5.178198	9.625256	2.80E-18	4.64E-17	30.88029	NCRNA0010	non-protein coding RNA 105	NM_025091
214106_s_at	0.82018	9.0078773	4.603824	7.34E-06	1.58E-05	2.945038	GMD5	GDP-mannose 4,6-dehydratase	AI762113
235651_at	0.81955	7.8533826	3.920115	0.0001213	0.0002228	0.279353	0	0	AV741130
208651_x_at	0.81707	10.718382	3.683459	0.0002956	0.000518	-0.55831	CD24	CD24 molecule	M58664
229467_at	0.81666	6.4087244	9.632986	2.66E-18	4.43E-17	30.93102	PCBP2	HnRNP-E2 mRNA	AA504356
244678_at	0.81589	3.5249933	8.630065	1.85E-15	1.71E-14	24.48654	0	0	BE220208
214594_x_at	0.81578	8.3438844	7.954771	1.27E-13	8.46E-13	20.32965	ATP8B1	ATPase, class I, type 8B, member 1	BG252666
1558814_s_at	0.81542	5.0648693	9.396689	1.27E-17	1.83E-16	29.38722	TMED5	transmembrane emp24 protein transport domain containing 5	B1561660
204130_at	0.81384	6.3723252	5.073245	8.86E-07	2.15E-06	4.974506	HSD11B2	hydroxysteroid (11-beta) dehydrogenase 2	NM_000196
242773_at	0.81359	6.435999	4.515766	1.07E-05	2.26E-05	2.581925	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1	AI274308
232245_at	0.81174	4.9004785	11.23452	4.76E-23	2.53E-21	41.70868	SLC25A34	solute carrier family 25, member 34	AU151211
205455_at	0.81148	7.6235691	4.823692	2.78E-06	6.29E-06	3.876217	MST1R	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	NM_002447
206043_s_at	0.81118	6.8907186	4.33989	2.26E-05	4.55E-05	1.873891	ATP2C2	ATPase, Ca++ transporting, type 2C, member 2	NM_014861
223385_at	0.81062	7.8889473	4.088747	6.27E-05	0.0001195	0.903468	CYP251	cytochrome P450, family 2, subfamily 5, polypeptide 1	AF335278
235871_at	0.81062	7.4687091	3.84504	0.0001617	0.0002924	0.008739	LIPH	lipase, member H	AA088857
235965_at	0.81035	6.6301617	5.263771	3.60E-07	9.20E-07	5.841711	0	0	BF513674
1556797_at	0.80942	6.1938953	11.77353	1.10E-24	8.97E-23	45.4275	LOC386597	hypothetical protein LOC386597	AK090737
204401_at	0.80801	7.8223353	4.244917	3.34E-05	6.58E-05	1.501231	KCNN4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	NM_002250
210399_x_at	0.80761	7.9934671	5.809224	2.42E-08	7.21E-08	8.455067	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	U27336
210328_at	0.80691	4.8515824	12.64854	2.28E-27	4.48E-25	51.52485	GNMT	glycine N-methyltransferase	AF101477
213285_at	0.80683	9.1066895	4.038509	7.65E-05	0.0001441	0.715199	TMEM30B	transmembrane protein 30B	AV691491
222675_s_at	0.80666	8.1217127	5.42664	1.64E-07	4.38E-07	6.602139	BAIAP2L1	BAI1-associated protein 2-like 1	AA628400
244120_at	0.80535	4.01866	11.8862	4.98E-25	4.44E-23	46.20895	LOC340178	hypothetical protein LOC340178	AW183280
244355_at	0.80523	4.4110613	12.16761	6.85E-26	7.91E-24	48.16593	AVL9	KIAA0241 gene	AI090310
210239_at	0.80293	4.8429063	6.032357	7.63E-09	2.43E-08	9.577136	IRX5	Iroquois homeobox 5	U90304
244753_at	0.80251	6.7201929	6.018673	8.19E-09	2.60E-08	9.507471	0	0	BF000430
211695_x_at	0.8011	7.3936216	3.982877	9.51E-05	0.0001771	0.509021	MUC1	mucin 1, cell surface associated	AF348143
228984_at	0.80105	5.455531	11.16693	7.61E-23	3.83E-21	41.24488	ATPGD1	ATP-grasp domain containing 1	AB037815
224062_x_at	0.80083	5.450654	11.649	2.63E-24	1.91E-22	44.56533	KLK4	kallikrein-related peptidase 4	AF113140
235525_at	0.80006	6.0679245	13.36427	1.41E-29	5.50E-27	56.54675	0	0	BF513712
1560878_at	0.79981	7.2678687	10.95683	3.27E-22	1.41E-20	39.80746	SYT15	synaptotagmin XV	AI971263
233938_at	0.79956	6.3107731	9.793232	9.10E-19	1.69E-17	31.98587	C11orf86	chromosome 11 open reading frame 86	AK026328
1554039_at	0.79849	6.975935	9.899815	4.45E-19	8.89E-18	32.69084	C14orf159	chromosome 14 open reading frame 159	BC009182
210519_s_at	0.79753	10.613294	3.586311	0.000421	0.000723	-0.88902	NQO1	NAD(P)H dehydrogenase, quinone 1	BC000906
229499_at	0.7962	7.0083142	9.923381	3.80E-19	7.70E-18	32.84707	CAPN13	calpain 13	AI762355
230318_at	0.79583	6.0288061	4.037211	7.69E-05	0.0001448	0.710362	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 1	T62088
205505_at	0.79472	6.9481472	4.297004	2.69E-05	5.38E-05	1.704765	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransferase)	NM_001490
207202_s_at	0.79364	5.7556921	3.538888	0.000499	0.0008482	-1.04763	NR112	nuclear receptor subfamily 1, group 1, member 2	NM_003889

210739_x_at	0.7933	6.5055587	6.396732	1.09E-09	3.90E-09	11.47145	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	AF069510
232428_at	0.79175	5.7646511	5.06238	9.32E-07	2.25E-06	4.925794	MOGAT2	monoacylglycerol O-acyltransferase 2	AK000245
232867_at	0.7917	5.7698807	15.03969	9.23E-35	3.36E-31	68.32921	0	0	AW204620
238830_at	0.79095	5.2368933	11.6682	2.30E-24	1.70E-22	44.69817	SOS2	Guanine nucleotide releasing factor (SOS2)	BE675872
236279_at	0.78994	7.0991902	4.328673	2.36E-05	4.75E-05	1.82952	0	0	N23258
238884_at	0.78961	6.2781876	7.098107	2.12E-11	9.82E-11	15.31773	0	0	AW195351
205221_at	0.78855	6.9748269	3.657301	0.0003254	0.0005672	-0.64812	HGD /// LO	homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase	NM_000187
214723_x_at	0.78749	5.8617924	5.554191	8.75E-08	2.42E-07	7.209668	ANKRD36	ankyrin repeat domain 36	AB046861
206602_s_at	0.78711	4.2047461	10.07592	1.36E-19	3.06E-18	33.86122	HOXD3	homeobox D3	NM_006898
1555753_x_at	0.78616	4.3795155	8.692207	1.25E-15	1.19E-14	24.87706	0	0	U92815
213622_at	0.78614	6.1929068	6.524339	5.42E-10	2.03E-09	12.15226	COL9A2	collagen, type IX, alpha 2	AI733465
237254_at	0.78374	5.2569613	11.20001	6.05E-23	3.13E-21	41.47176	SLC5A11	solute carrier family 5 (sodium/glucose cotransporter), member 11	AA772233
207251_at	0.78361	4.603304	4.829134	2.71E-06	6.15E-06	3.899702	MEP1B	meprin A, beta	NM_005925
210301_at	0.78304	5.9733221	7.211778	1.10E-11	5.30E-11	15.96403	XDH	xanthine dehydrogenase	U06117
1558784_at	0.78156	7.0243203	12.08796	1.20E-25	1.27E-23	47.61131	0	0	BG540230
220075_s_at	0.78095	5.6364284	3.55181	0.0004765	0.0008122	-1.00459	MUPCDH	mucin-like protocadherin	NM_017717
207899_at	0.77941	4.2370663	4.650057	6.00E-06	1.30E-05	3.13795	GIP	gastric inhibitory polypeptide	NM_004123
206126_at	0.77821	4.8154069	9.187947	5.02E-17	6.42E-16	28.03577	CXCR5	chemokine (C-X-C motif) receptor 5	NM_001716
232541_at	0.7779	5.7329223	3.754778	0.000227	0.0004034	-0.31063	0	0	AK000106
223194_s_at	0.77673	8.2274086	5.4504	1.46E-07	3.93E-07	6.714518	SLC22A23	solute carrier family 22, member 23	AL512737
1556914_at	0.77518	5.4373188	11.27815	3.51E-23	1.93E-21	42.00834	0	0	BC031235
209696_at	0.77493	8.813223	4.166084	4.60E-05	8.91E-05	1.197136	FBP1	fructose-1,6-bisphosphatase 1	D26054
1559948_at	0.77482	4.4744778	10.12525	9.72E-20	2.27E-18	34.19028	0	0	AK000454
214142_at	0.77362	5.8447183	6.642715	2.81E-10	1.10E-09	12.7916	JCLN	jacalin-like lectin domain containing	AI732905
231554_at	0.77277	5.168937	12.55517	4.42E-27	7.72E-25	50.87151	TPD52L3	tumor protein D52-like 3	AI041556
211910_at	0.77275	5.2070929	11.19957	6.07E-23	3.13E-21	41.4688	0	0	U87229
228599_at	0.77209	4.3485597	4.395528	1.79E-05	3.65E-05	2.095376	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	AI862674
210597_x_at	0.77196	7.5618436	11.43092	1.21E-23	7.47E-22	43.05963	PRB1	proline-rich protein BstNI subfamily 1	K03206
220724_at	0.7706	3.4015942	9.648941	2.39E-18	4.02E-17	31.03577	FLI21511	hypothetical protein FLI21511	NM_025087
238827_at	0.7704	6.1535669	10.6677	2.40E-21	8.37E-20	37.84055	0	0	BE843544
1558662_s_at	0.77025	6.7311828	4.100259	5.99E-05	0.0001144	0.946891	BANK1	B-cell scaffold protein with ankyrin repeats 1	BG200452
229638_at	0.76967	5.9798979	4.125514	5.41E-05	0.000104	1.042504	IRX3	iroquois homeobox 3	AI681917
241540_at	0.76931	5.7338864	10.31821	2.62E-20	7.07E-19	35.48226	0	0	AA767283
221286_s_at	0.76919	7.8326579	3.746492	0.0002342	0.0004154	-0.33962	MGC29506	hypothetical protein MGC29506	NM_016459
216849_at	0.76784	5.7216852	11.80159	9.02E-25	7.57E-23	45.62199	0	0	AL080233
239595_at	0.76742	5.1118599	6.499217	6.22E-10	2.31E-09	12.01753	GPX2	glutathione peroxidase 2 (gastrointestinal)	AA569032
1559436_x_at	0.76662	8.3440515	7.84074	2.56E-13	1.61E-12	19.64459	0	0	AL832061
219404_at	0.76658	8.2355869	3.927392	0.0001179	0.0002169	0.305822	EPS8L3	EPS8-like 3	NM_024526
233696_at	0.76628	5.6564817	13.2372	3.48E-29	1.18E-26	55.6538	0	0	AK025010
1556340_at	0.76561	7.2713954	12.94058	2.87E-28	7.26E-26	53.57139	MAPK12	mitogen-activated protein kinase 12	AK098058
204971_at	0.76522	8.48731	3.550543	0.0004786	0.0008155	-1.00882	CSTA	cystatin A (stefin A)	NM_005213
202752_x_at	0.76465	8.0795774	8.018642	8.60E-14	5.90E-13	20.7156	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	NM_012244
207057_at	0.76271	7.0335488	4.087945	6.29E-05	0.0001198	0.900451	SLC16A7	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	NM_004731

1555962_at	0.76214	7.1449468	3.71669	0.0002615	0.0004614	-0.44342	B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	CA503291
35148_at	0.76152	7.6268215	5.270808	3.49E-07	8.91E-07	5.874209	TJP3	tight junction protein 3 (zona occludens 3)	AC005954
213813_x_at	0.76149	6.9511272	8.757296	8.21E-16	8.17E-15	25.28746	0		0 AI345238
233658_at	0.76128	6.3234138	9.404377	1.21E-17	1.75E-16	29.43721	0		0 AK022413
239156_at	0.76034	4.8503601	7.313751	6.03E-12	3.03E-11	16.54893	0		0 AW615179
241436_at	0.76004	3.260864	6.442724	8.48E-10	3.09E-09	11.71581	SCNN1G	sodium channel, nonvoltage-gated 1, gamma	AI985987
239673_at	0.75975	4.3343474	7.245881	8.98E-12	4.40E-11	16.1591	0		0 AW080999
243238_at	0.7592	4.2638538	12.64227	2.39E-27	4.62E-25	51.48097	PYGB	(xsr) mRNA, 290bp	AA601213
1556012_at	0.75864	5.7418488	5.994858	9.28E-09	2.92E-08	9.3865	KLHDC7A	kelch domain containing 7A	BM976939
234632_x_at	0.75855	4.073606	4.762142	3.66E-06	8.17E-06	3.61205	0		0 AK026267
1569202_x_at	0.75768	6.4242521	11.90842	4.26E-25	3.86E-23	46.36319	0		0 BF847120
1553657_at	0.75758	6.4840243	10.88776	5.27E-22	2.15E-20	39.33637	VWA3A	von Willebrand factor A domain containing 3A	NM_173615
235141_at	0.75687	8.7998719	3.985463	9.41E-05	0.0001754	0.518554	MARVELD2	MARVEL domain containing 2	AW009562
237073_at	0.75335	4.2924422	7.571751	1.30E-12	7.33E-12	18.04961	0		0 BF062674
233486_at	0.75323	6.6768267	10.78443	1.07E-21	4.07E-20	38.633	LOC729940	similar to hCG2036908	AA573826
211912_at	0.75294	3.9126534	13.34562	1.61E-29	6.10E-27	56.41571	MERTK	c-mer proto-oncogene tyrosine kinase	L08961
238359_at	0.75148	5.4674117	12.76325	1.01E-27	2.22E-25	52.32815	0		0 BE786383
238878_at	0.75107	4.7608295	3.754867	0.000227	0.0004033	-0.31032	ARX	aristaless related homeobox	AA496211
211494_s_at	0.75038	6.0134012	4.347823	2.18E-05	4.41E-05	1.905328	SLC4A4	solute carrier family 4, sodium bicarbonate cotransporter, member 4	AF157492
225822_at	0.75038	8.4656893	3.688715	0.00029	0.0005088	-0.5402	TMEM125	transmembrane protein 125	AV709406
208072_s_at	0.74995	8.1085107	10.5423	5.67E-21	1.80E-19	36.99182	DGKD	diacylglycerol kinase, delta 130kDa	NM_003648
240809_at	0.74811	4.737071	9.501235	6.38E-18	9.80E-17	30.06848	C21orf121	chromosome 21 open reading frame 121	AI138282
209453_at	0.7481	8.1810748	7.245324	9.01E-12	4.41E-11	16.15592	SLC9A1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	M81768
208468_at	0.7454	4.8420428	10.89529	5.00E-22	2.05E-20	39.3877	SOX21	SRY (sex determining region Y)-box 21	NM_007084
226903_s_at	0.74528	5.2033232	13.98719	1.66E-31	1.40E-28	60.92874	SLC6A10P	CDNA clone IMAGE:40015586 /// Creatine transporter	AI820043
221992_at	0.74512	7.5434905	7.880833	2.01E-13	1.29E-12	19.88486	LOC440348	similar to nuclear pore complex interacting protein	AI925734
204581_at	0.74486	5.3583923	8.848368	4.57E-16	4.78E-15	25.86394	CD22	CD22 molecule	NM_001771
241477_at	0.74367	5.6748879	11.18739	6.60E-23	3.37E-21	41.38521	NEIL1	nei endonuclease VIII-like 1 (E. coli)	BF194999
217080_s_at	0.74345	5.2865515	4.594648	7.64E-06	1.64E-05	2.906933	HOMER2	homer homolog 2 (Drosophila)	Y19026
243755_at	0.74281	4.1707839	7.45692	2.59E-12	1.38E-11	17.37806	PRLR	prolactin receptor	AI628734
1555173_at	0.74188	4.7815269	4.98782	1.32E-06	3.11E-06	4.593684	STX19	syntaxin 19	BC034696
229023_at	0.74119	5.3007824	11.62206	3.18E-24	2.25E-22	44.37904	SFT2D3	SFT2 domain containing 3	BF590323
206297_at	0.74067	5.1697108	8.46555	5.27E-15	4.49E-14	23.45888	CTRC	chymotrypsin C (caldecrin)	NM_007272
225726_s_at	0.74065	7.0818589	4.817977	2.85E-06	6.45E-06	3.851575	PLEKHH1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	AB033026
1568663_a_at	0.74046	4.1685799	9.328479	2.00E-17	2.77E-16	28.9443	0		0 BC032951
1552367_a_at	0.74024	5.7677152	3.787629	0.0002008	0.0003589	-0.19516	SCIN	scinderin	AF276507
204015_s_at	0.73826	8.1864795	3.817864	0.0001792	0.0003225	-0.08811	DUSP4	dual specificity phosphatase 4	BC002671
240422_at	0.73799	5.3860835	4.408322	1.69E-05	3.47E-05	2.146634	0		0 AI935710
220609_at	0.73764	5.3960138	7.645856	8.35E-13	4.85E-12	18.486	LOC202181	hypothetical protein LOC202181	NM_024651
1570430_at	0.73761	4.335168	14.30534	1.72E-32	2.30E-29	63.16752	0		0 BC015783
210961_s_at	0.73735	3.881393	8.885088	3.60E-16	3.87E-15	26.09712	ADRA1D	adrenergic, alpha-1D-, receptor	M76446
206410_at	0.73699	7.4431345	4.74111	4.02E-06	8.92E-06	3.522399	NROB2	nuclear receptor subfamily 0, group B, member 2	NM_021969
231203_at	0.73632	6.4283128	10.37512	1.78E-20	5.00E-19	35.86476	LOC100129	similar to hCG1651427	BF059208
237604_at	0.73533	4.4530681	10.22139	5.07E-20	1.27E-18	34.83305	LOC415056	BC038740, mRNA (cDNA clone IMAGE:5268434)	AA906413
207693_at	0.73512	4.9480319	9.396531	1.27E-17	1.84E-16	29.38619	CACNB4	calcium channel, voltage-dependent, beta 4 subunit	NM_000726
240971_x_at	0.73488	5.5809289	6.034335	7.55E-09	2.40E-08	9.587214	0		0 AI950451
1555616_at	0.7344	4.7946995	11.05079	1.70E-22	7.87E-21	40.44949	0		0 BC009519
221665_s_at	0.73408	6.8809691	4.174143	4.45E-05	8.64E-05	1.228004	EPS8L1	EPS8-like 1	BC004907
240074_at	0.73407	4.7478706	8.730828	9.72E-16	9.53E-15	25.12041	0		0 AW014249

231647_s_at	0.73325	4.1503498	3.942949	0.0001111	0.000205	0.362551	FCRL5	Fc receptor-like 5	AW241983
240297_at	0.73289	4.7455662	14.51099	3.98E-33	7.76E-30	64.61415	0		0 AA605090
1556721_at	0.73197	4.5244596	7.594502	1.14E-12	6.46E-12	18.18334	FLJ33706	hypothetical protein FLJ33706	AK091025
215588_x_at	0.73167	8.6429897	7.665097	7.44E-13	4.35E-12	18.59968	RIOK3	RIO kinase 3 (yeast)	AK024958
234791_at	0.73126	4.4841712	9.100379	8.90E-17	1.08E-15	27.47246	GSX1	GS homeobox 1	AL390738
232522_at	0.7306	5.6868669	9.770507	1.06E-18	1.93E-17	31.83591	0		0 AK025137
1554992_at	0.72964	5.0535089	11.01339	2.21E-22	9.89E-21	40.19382	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1	BC040275
1569001_at	0.72933	5.8713427	11.73405	1.45E-24	1.16E-22	45.15398	BMP1	bone morphogenetic protein 1	AF318323
232684_at	0.72904	6.0128461	8.182746	3.11E-14	2.30E-13	21.7144	LOC253264	hypothetical protein LOC253264	AK023445
215565_at	0.72852	4.7950663	4.35055	2.16E-05	4.36E-05	1.916143	DTNB	dystrobrevin, beta	AK022277
240827_at	0.72844	4.5900656	11.17557	7.17E-23	3.63E-21	41.30413	FLJ45983	hypothetical LOC399717	AA846824
215685_s_at	0.72823	5.3856714	11.35661	2.03E-23	1.19E-21	42.54789	DLX2	distal-less homeobox 2	BE792224
217269_s_at	0.72716	5.9058372	5.077662	8.68E-07	2.11E-06	4.994336	PRSS7	protease, serine, 7 (enterokinase)	AP001672
206310_at	0.72586	5.3656433	7.168067	1.41E-11	6.73E-11	15.71479	SPINK2	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	NM_021114
227134_at	0.72565	7.8269034	4.032515	7.83E-05	0.0001474	0.692868	SYTL1	synaptotagmin-like 1	AI341537
238134_at	0.72563	4.9602847	6.535449	5.10E-10	1.92E-09	12.21195	0		0 AW885748
202528_at	0.72559	8.9279662	4.213459	3.79E-05	7.44E-05	1.379311	GALE	UDP-galactose-4-epimerase	NM_000403
206293_at	0.72526	3.7654345	4.119919	5.53E-05	0.0001062	1.021278	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	U08024
238366_at	0.72477	6.0535056	12.97711	2.21E-28	5.87E-26	53.82762	NCRNA000	P40	AW015512
231463_at	0.72444	4.9257738	7.980603	1.09E-13	7.31E-13	20.48555	CNTD1	cyclin N-terminal domain containing 1	AA868514
244890_at	0.72403	5.3022868	12.12617	9.18E-26	1.01E-23	47.87731	0		0 AI264671
207412_x_at	0.72396	5.6884785	4.273639	2.97E-05	5.89E-05	1.613207	CELP	carboxyl ester lipase pseudogene	NM_001808
211217_s_at	0.72319	7.3701875	11.0704	1.49E-22	6.94E-21	40.58365	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	AF051426
227850_x_at	0.72269	9.4837875	3.815245	0.000181	0.0003254	-0.09741	CDC42EP5	CDC42 effector protein (Rho GTPase binding) 5	AW084544
233483_at	0.72185	5.8132874	15.40676	6.80E-36	4.64E-32	70.90318	TBC1D27	TBC1 domain family, member 27	AK024458
207752_x_at	0.72183	7.1315311	10.35073	2.10E-20	5.79E-19	35.70071	PRB1 /// PR	proline-rich protein BstNI subfamily 1 /// proline-rich protein BstNI subfamily 2	NM_005039
241677_x_at	0.72016	4.2883875	13.64756	1.87E-30	9.84E-28	58.53896	0		0 AI792698
205861_at	0.72012	6.073802	4.244936	3.34E-05	6.58E-05	1.501305	SPIB	Spi-B transcription factor (Spi-1/PU.1 related)	NM_003121
207067_s_at	0.72009	6.0285579	6.091292	5.60E-09	1.81E-08	9.878403	HDC	histidine decarboxylase	NM_002112
220209_at	0.72001	5.9334028	9.233871	3.72E-17	4.89E-16	28.33206	PYY2	peptide YY, 2 (seminalplasmin)	NM_021093
228691_at	0.71897	6.251012	9.863446	5.68E-19	1.11E-17	32.44999	BICD1	Bicaudal-D (BICD) mRNA, alternatively spliced	AI694946
229358_at	0.71811	7.0424926	4.407484	1.70E-05	3.48E-05	2.143272	IHH	Indian hedgehog homolog (Drosophila)	AA628967
211531_x_at	0.71747	7.5497441	10.88158	5.50E-22	2.23E-20	39.29428	PRB1 /// PR	proline-rich protein BstNI subfamily 1 /// proline-rich protein BstNI subfamily 2	K03205
1565105_at	0.71728	3.5671697	8.452963	5.71E-15	4.83E-14	23.38064	0		0 U61086
243981_at	0.71713	4.3714128	5.45169	1.45E-07	3.90E-07	6.720632	STK4	serine/threonine kinase 4	AI763206
215967_s_at	0.71676	5.410882	7.202137	1.16E-11	5.59E-11	15.90898	LY9	lymphocyte antigen 9	AL582804
1555653_at	0.71659	12.73848	9.048997	1.24E-16	1.47E-15	27.14296	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	BC012090
237111_at	0.71592	4.5358709	7.833646	2.68E-13	1.68E-12	19.60214	FLJ44450	hypothetical gene supported by AK126414	AW118588
208367_x_at	0.71564	5.1821729	6.532241	5.19E-10	1.95E-09	12.19471	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	NM_000776
237662_at	0.71435	4.6518347	11.29485	3.13E-23	1.73E-21	42.12313	LOC646522	CDNA clone IMAGE:5223914	BE858657
1560782_at	0.71432	5.3182019	12.02835	1.83E-25	1.85E-23	47.19662	0		0 BC035326
235663_at	0.71383	6.3914624	12.57836	3.75E-27	6.70E-25	51.03372	0		0 AI313160
232440_at	0.71369	4.9287319	11.29726	3.07E-23	1.71E-21	42.13971	ZDHHC13	HIP3RP mRNA for huntingtin interacting protein HIP3RP	AU155198

228518_at	0.71357	5.8227704	5.115288	7.28E-07	1.78E-06	5.163767	IGH@ /// IGmu	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant	AW575313
238177_at	0.71356	6.0474217	5.374723	2.11E-07	5.56E-07	6.35786	SLC6A19	solute carrier family 6 (neutral amino acid transporter), member 19	AA873542
1565320_at	0.71304	4.8347069	9.351199	1.72E-17	2.42E-16	29.09169	RBMV3AP	RNA binding motif protein, Y-linked, family 3, member A pseudogene	U94386
233908_x_at	0.71263	5.0932654	10.78153	1.10E-21	4.14E-20	38.61328	0		AK022112
239122_at	0.71233	5.5912249	12.06814	1.38E-25	1.43E-23	47.47341	0		AI638155
218035_s_at	0.71227	10.329888	4.084047	6.39E-05	0.0001216	0.885772	RBM47	RNA binding motif protein 47	NM_019027
224135_at	0.71179	4.9496569	11.48943	8.04E-24	5.20E-22	43.46308	WDR87	WD repeat domain 87	AY026504
237345_at	0.71132	6.6964741	12.16903	6.78E-26	7.85E-24	48.17585	0		AW087759
215856_at	0.71121	6.9596185	6.814712	1.07E-10	4.46E-10	13.7335	SIGLEC15	sialic acid binding Ig-like lectin 15	AK025833
1562586_at	0.71112	5.3320964	11.58336	4.17E-24	2.87E-22	44.11154	0		BC037164
1569867_at	0.71109	5.1419496	10.01966	1.99E-19	4.27E-18	33.4866	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	BC041011
242733_at	0.71027	5.1447239	9.852066	6.14E-19	1.19E-17	32.3747	0		AI457588
208165_s_at	0.70997	6.5076289	3.508807	0.0005552	0.0009391	-1.14727	PRSS16	protease, serine, 16 (thymus)	NM_005865
216092_s_at	0.70952	7.9623529	6.558382	4.49E-10	1.70E-09	12.33537	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	AL365347
229922_at	0.70937	5.0488197	10.31491	2.68E-20	7.22E-19	35.46012	GPRIN1	G protein regulated inducer of neurite outgrowth 1	AI052709
236263_at	0.70914	6.437522	6.29203	1.92E-09	6.64E-09	10.91948	SHH	Sonic hedgehog protein (SHH)	AI192528
220186_s_at	0.70879	7.5033445	4.535418	9.87E-06	2.08E-05	2.662467	PCDH24	protocadherin 24	NM_017675
234785_at	0.70754	4.1455401	10.0941	1.20E-19	2.74E-18	33.98248	0		AK025047
241855_s_at	0.70701	3.8817094	11.50036	7.45E-24	4.85E-22	43.53848	0		AA960963
240861_at	0.70696	5.3380507	5.898247	1.53E-08	4.69E-08	8.899181	0		BF433219
214599_at	0.70676	4.2482457	8.933773	2.63E-16	2.90E-15	26.40691	IVL	involucrin	NM_005547
220923_s_at	0.70627	6.1652758	14.81938	4.43E-34	1.21E-30	66.78202	PNMA3	paraneoplastic antigen MA3	NM_013364
211806_s_at	0.70595	5.8459162	6.469802	7.31E-10	2.68E-09	11.86022	KCNJ15	potassium inwardly-rectifying channel, subfamily J, member 15	D87291
228939_at	0.70568	4.9761117	11.40694	1.43E-23	8.69E-22	42.89445	OAF	CDNA FLJ11658 fis, clone HEMBA1004577	AU145346
243437_at	0.70547	4.4604513	9.651186	2.35E-18	3.97E-17	31.05051	GCC1	Full length Insert cDNA clone ZA83B04	N75454
235661_at	0.70523	5.1500763	7.147577	1.59E-11	7.51E-11	15.59826	0		T99553
210906_x_at	0.7052	3.3815202	8.002387	9.51E-14	6.47E-13	20.61723	AQP4	aquaporin 4	U34846
209558_s_at	0.70427	8.225679	5.786304	2.72E-08	8.05E-08	8.341502	HIP1R	huntingtin interacting protein 1 related	AB013384
1556814_a_at	0.70403	4.4730401	6.113204	4.98E-09	1.63E-08	9.990925	0		AF086143
207633_s_at	0.70376	3.9508001	8.46004	5.46E-15	4.63E-14	23.42462	MUSK	muscle, skeletal, receptor tyrosine kinase	NM_005592
244548_at	0.70376	4.8725386	7.023679	3.26E-11	1.47E-10	14.89788	0		AI189587
234285_at	0.70373	5.434726	11.55529	5.07E-24	3.42E-22	43.91766	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	AL021366
222102_at	0.70282	4.7973678	10.63208	3.07E-21	1.04E-19	37.59915	GSTA3	glutathione S-transferase alpha 3	NM_000847
1554183_s_at	0.70239	7.0869031	12.32584	2.24E-26	3.08E-24	49.26928	TRIM73 ///	tripartite motif-containing 73 /// tripartite motif-containing 74	BC033871
208300_at	0.70216	7.1194228	3.564359	0.0004555	0.0007789	-0.96267	PTPRH	protein tyrosine phosphatase, receptor type, H	NM_002842
228892_at	0.7016	6.0000881	6.686714	2.20E-10	8.77E-10	13.0311	SH3RF2	SH3 domain containing ring finger 2	AI807681
243842_at	0.70146	5.2870219	8.424706	6.82E-15	5.68E-14	23.20518	0		BE463896
224355_s_at	0.70144	6.3155111	3.585128	0.0004228	0.0007259	-0.89299	MS4A8B	membrane-spanning 4-domains, subfamily A, member 8B	AF237905
229599_at	0.70125	8.9180283	5.127243	6.88E-07	1.69E-06	5.217799	LOC440335	hypothetical gene supported by BC022385; BC035868; BC048326	AA675917
241486_at	0.70115	6.0330106	10.91851	4.26E-22	1.78E-20	39.546	0		BE222186
1559276_at	0.70109	4.0150653	10.95562	3.29E-22	1.41E-20	39.79921	LOC728606	hypothetical LOC728606	AK056805
1553264_a_at	0.70094	6.1214349	8.593369	2.34E-15	2.13E-14	24.25652	SYN1	synapsin I	NM_006950

240669_at	0.70008	5.4332389	9.141212	6.82E-17	8.49E-16	27.73486	0	0	AW450171
213412_at	0.69983	7.2098158	4.708227	4.65E-06	1.02E-05	3.38287	TJP3	tight junction protein 3 (zona occludens 3)	NM_014428
219695_at	0.69953	6.4899877	6.03672	7.46E-09	2.38E-08	9.599366	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	NM_024703
217251_x_at	0.6995	5.0847206	9.695298	1.75E-18	3.03E-17	31.34047	IVD	Clone ds1-1 immunoglobulin lambda chain VJ region, (IGL)	AF043583
1555849_a_at	0.69905	4.1085085	9.623753	2.82E-18	4.68E-17	30.87043	LOC100170	hypothetical LOC100170229	BG720339
218779_x_at	0.69889	7.3801258	4.653802	5.90E-06	1.28E-05	3.153643	EPS8L1	EPS8-like 1	NM_017729
1565583_at	0.69792	5.659183	10.58805	4.15E-21	1.35E-19	37.3011	ZSCAN5A	zinc finger and SCAN domain containing 5A	AW469591
230956_at	0.69755	6.5748019	6.238904	2.55E-09	8.68E-09	10.64173	FLJ45803	FLJ45803 protein	AI347581
1566643_a_at	0.69734	4.7949976	9.815804	7.83E-19	1.48E-17	32.13495	0	0	BC022568
1570364_at	0.69727	3.6592785	12.71559	1.42E-27	2.97E-25	51.99432	ZNF709	zinc finger protein 709	BI830259
213441_x_at	0.69708	7.9584165	9.273459	2.87E-17	3.85E-16	28.58794	SPDEF	SAM pointed domain containing ets transcription factor	AI745526
236725_at	0.69679	6.0810908	7.207018	1.13E-11	5.44E-11	15.93685	WWC1	WW and C2 domain containing 1	H09245
241140_at	0.6967	4.6496648	7.344804	5.02E-12	2.56E-11	16.72798	LMO7	LIM domain 7	AA702962
232699_at	0.69598	4.9857562	13.85992	4.12E-31	2.96E-28	60.03312	0	0	AK021990
215538_at	0.69558	4.5463786	9.619557	2.90E-18	4.80E-17	30.8429	LARGE	like-glycosyltransferase	BF057493
1555323_at	0.69524	5.3869681	10.6914	2.04E-21	7.23E-20	38.00123	ABCB9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	BC017348
241918_at	0.69478	6.86511	12.31402	2.44E-26	3.30E-24	49.18678	ANO7	anoctamin 7	AI299378
1559870_at	0.6944	6.2803773	10.78809	1.05E-21	3.99E-20	38.65791	LOC100129	hypothetical protein. LOC100129129	BC038546
1556442_x_at	0.69422	7.7030604	11.93662	3.49E-25	3.24E-23	46.55904	0	0	AU159357
1561214_at	0.69367	4.9750289	12.11589	9.87E-26	1.07E-23	47.8058	0	0	BC041869
235892_at	0.69289	4.2654854	4.906647	1.91E-06	4.41E-06	4.236492	0	0	AI620881
1555754_s_at	0.69277	7.2329203	12.27571	3.19E-26	4.14E-24	48.91951	ATN1	atrophin 1	Z22814
234540_at	0.69277	3.3319459	8.938366	2.55E-16	2.82E-15	26.43618	GCNT7	glucosaminyl (N-acetyl) transferase family member 7	AL109806
229004_at	0.69212	5.8935471	4.280202	2.89E-05	5.75E-05	1.638883	0	0	AI970797
236033_at	0.69194	5.8278987	10.68846	2.08E-21	7.34E-20	37.98127	ASB12	ankyrin repeat and SOCS box-containing 12	AA349954
231245_s_at	0.69192	4.1684731	10.6539	2.64E-21	9.06E-20	37.74701	0	0	AW294061
236736_at	0.69187	5.7057699	13.9061	2.97E-31	2.25E-28	60.35813	0	0	AW274301
1560391_at	0.69173	3.9141562	7.070412	2.49E-11	1.14E-10	15.16119	0	0	AL832404
1554222_at	0.69136	6.3248992	10.70982	1.80E-21	6.46E-20	38.12624	MGC45922	hypothetical gene MGC45922	BC033237
230813_at	0.69109	6.7987317	10.90745	4.60E-22	1.90E-20	39.4706	LEPREL1	leprecan-like 1	BF434223
228051_at	0.69098	7.5728753	3.63251	0.0003562	0.0006176	-0.73272	LOC202451	hypothetical protein LOC202451	AI979261
211442_x_at	0.69082	6.4487567	9.160636	6.01E-17	7.55E-16	27.85985	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	AF280111
235632_at	0.69073	3.9372984	9.611186	3.07E-18	5.05E-17	30.788	0	0	AI638195
1556584_at	0.69069	5.0522182	12.98481	2.10E-28	5.61E-26	53.88165	0	0	BC041995
244357_at	0.6893	5.5430949	5.963878	1.09E-08	3.40E-08	9.229628	0	0	T90760
231644_at	0.68894	4.8662197	5.067392	9.11E-07	2.20E-06	4.948254	0	0	AW016812
225458_at	0.68859	6.6643885	3.701998	0.0002761	0.0004856	-0.49433	LOC25845	hypothetical LOC25845	BF528646
1556796_at	0.68779	4.3040389	11.40458	1.45E-23	8.80E-22	42.87817	0	0	AW187990
239576_at	0.68754	6.0927712	7.847683	2.46E-13	1.55E-12	19.68615	MTUS1	Full length insert cDNA clone ZD67D11	AI028661
215184_at	0.68753	6.3858687	9.861027	5.78E-19	1.13E-17	32.43399	DAPK2	death-associated protein kinase 2	AK026801
205141_at	0.68751	8.4554112	4.212229	3.81E-05	7.47E-05	1.374558	ANG	angiogenin, ribonuclease, RNase A family, 5	NM_001145
223910_at	0.68715	7.0582356	9.417686	1.11E-17	1.62E-16	29.52381	ERN2	endoplasmic reticulum to nucleus signaling 2	AB047079
240262_at	0.68703	4.8283607	6.608669	3.40E-10	1.31E-09	12.60696	0	0	AI251870
236976_at	0.687	4.7532394	7.341463	5.12E-12	2.61E-11	16.70869	FANCA	Fanconi anemia, complementation group A	AI569792
242885_at	0.68602	5.567747	13.7812	7.23E-31	4.70E-28	59.47923	0	0	BG163756
244197_x_at	0.68563	7.6063616	6.281666	2.03E-09	7.00E-09	10.86517	0	0	AI859990
221350_at	0.68549	5.3939215	8.944771	2.45E-16	2.72E-15	26.47699	HOXC8	homeobox C8	NM_022658
229583_at	0.68546	5.520569	11.78146	1.04E-24	8.54E-23	45.4825	0	0	AA457049
206292_s_at	0.68527	4.1632502	5.199766	4.89E-07	1.23E-06	5.547664	SULT2A1	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	NM_003167

1558327_at	0.68522	5.5535343	11.87383	5.43E-25	4.78E-23	46.12313	ZDHC18	zinc finger, DHHC-type containing 18	AW408051
1560119_at	0.68516	5.054424	7.311637	6.10E-12	3.07E-11	16.53675	LOC389634	hypothetical LOC389634	AK074886
241368_at	0.68456	5.6716368	9.952461	3.12E-19	6.46E-18	33.04001	LSDP5	lipid storage droplet protein 5	AI190693
205019_s_at	0.68454	7.0561906	7.733422	4.92E-13	2.95E-12	19.00464	VIPR1	vasoactive intestinal peptide receptor 1	NM_004624
232424_at	0.68452	5.427734	4.04378	7.49E-05	0.0001413	0.734858	PRDM16	PR domain containing 16	AI623202
219610_at	0.68435	7.1162783	8.539463	3.30E-15	2.93E-14	23.91945	RGNEF	Rho-guanine nucleotide exchange factor	NM_022448
216603_at	0.68379	5.875516	9.349402	1.74E-17	2.44E-16	29.08003	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	AL365343
1569200_at	0.68374	8.0316609	11.3299	2.45E-23	1.40E-21	42.3641	0	0	BF847120
1564164_at	0.68343	4.5994516	6.668975	2.43E-10	9.62E-10	12.93442	DENND1B	DENN/MADD domain containing 1B	AL831839
223663_at	0.68329	7.6799536	13.15182	6.39E-29	2.01E-26	55.05407	CCDC88B	coiled-coil domain containing 88B	AL136799
243820_at	0.6831	5.6728561	9.934189	3.53E-19	7.22E-18	32.91876	LOC401463	hypothetical gene supported by BC025555; BC050012	U80755
1554400_at	0.68246	5.8261097	8.854517	4.39E-16	4.61E-15	25.9036	TCTE3	t-complex-associated-testis-expressed 3	AF519569
229241_at	0.68237	5.3192632	8.086933	5.64E-14	3.99E-13	21.13001	LDHD	lactate dehydrogenase D	AI623801
230772_at	0.68141	8.6504189	3.704714	0.0002734	0.0004811	-0.48493	0	0	AA639753
234116_at	0.68111	4.3395206	10.91565	4.34E-22	1.81E-20	39.52654	GJD4	gap junction protein, delta 4, 40.1kDa	AI742624
225966_at	0.68103	4.9735999	11.18922	6.52E-23	3.33E-21	41.39773	C17orf89	chromosome 17 open reading frame 89 /// similar to hCG19906	BF683512
1553512_at	0.68075	4.4464891	7.864234	2.22E-13	1.41E-12	19.7853	HOXC12	homeobox C12	NM_173860
240104_at	0.68072	5.488844	9.82176	7.52E-19	1.43E-17	32.17431	0	0	AI917371
213706_at	0.67997	6.5188403	4.420673	1.61E-05	3.30E-05	2.196236	GPD1	glycerol-3-phosphate dehydrogenase 1 (soluble)	AI368018
237805_at	0.67992	3.7474876	9.73867	1.31E-18	2.34E-17	31.62602	LOC729296	PREDICTED: Homo sapiens similar to hCG2017976 (LOC729296), mRNA	AI684717
1554517_x_at	0.67983	7.3297992	9.969118	2.79E-19	5.83E-18	33.15062	LOC203274	CDNA FLJ31544 fis, clone NT2RI2000865	BC011779
237104_at	0.67979	4.4835448	7.406284	3.49E-12	1.83E-11	17.08377	0	0	BE675415
232465_at	0.67919	5.8842475	9.321213	2.09E-17	2.90E-16	28.89719	0	0	AK021749
213350_at	0.67816	7.5937043	7.997189	9.82E-14	6.66E-13	20.58579	RPS11	Ribosomal protein S11	BF680255
220871_at	0.67754	5.0341234	11.86196	5.90E-25	5.16E-23	46.04073	0	0	NM_018513
243280_at	0.6769	6.0802225	11.08754	1.32E-22	6.25E-21	40.70099	0	0	AW444619
220373_at	0.67681	5.1440572	9.701886	1.68E-18	2.91E-17	31.38381	DCHS2	dachsous 2 (Drosophila)	NM_017639
223990_at	0.67662	6.0773174	12.78898	8.42E-28	1.89E-25	52.50845	C4orf17	chromosome 4 open reading frame 17	AL136838
232290_at	0.67652	5.8161749	9.028862	1.42E-16	1.65E-15	27.01405	0	0	BE815259
220727_at	0.6761	6.3868389	8.644076	1.69E-15	1.58E-14	24.57448	KCNK10	potassium channel, subfamily K, member 10	NM_021161
1552749_a_at	0.67513	7.7003235	13.96278	1.98E-31	1.61E-28	60.75701	KLC3	kinesin light chain 3	NM_145275
236516_at	0.67494	5.5661831	10.04769	1.64E-19	3.62E-18	33.67317	0	0	BE674844
1565358_at	0.67472	5.8153921	3.684554	0.0002945	0.000516	-0.55454	RARA	retinoic acid receptor, alpha	AI417079
210922_at	0.67464	4.982202	12.77421	9.35E-28	2.09E-25	52.405	0	0	BC000772
220561_at	0.67441	6.0444353	11.19005	6.48E-23	3.32E-21	41.40346	IGF2AS	insulin-like growth factor 2 antisense	NM_016412
233741_at	0.67278	5.5437837	9.127502	7.46E-17	9.21E-16	27.6467	FTCD	formiminotransferase cyclodeaminase	AL109817
212925_at	0.67277	9.7584208	3.743242	0.000237	0.0004202	-0.35097	C19orf21	chromosome 19 open reading frame 21	AA143765
207063_at	0.67274	4.1777772	5.368244	2.18E-07	5.73E-07	6.327499	CYorf14	chromosome Y open reading frame 14	NM_018542
237093_at	0.6727	5.6565899	9.870983	5.40E-19	1.06E-17	32.49988	0	0	AI568751
1564281_at	0.67253	6.5846719	10.63122	3.08E-21	1.04E-19	37.59335	LOC285708	hypothetical protein LOC285708	AK092078
1556507_at	0.67137	8.5029847	11.68507	2.04E-24	1.56E-22	44.8149	0	0	BC038725
233702_x_at	0.67134	9.2854594	8.648657	1.65E-15	1.54E-14	24.60325	0	0	AK024599
221668_s_at	0.67121	4.700392	8.560121	2.89E-15	2.59E-14	24.04851	DNAI2	dynein, axonemal, intermediate chain 2	AF250288
1558412_at	0.67111	7.078472	7.158179	1.50E-11	7.10E-11	15.65853	LOC113230	hypothetical protein LOC113230	BC011002
1559167_x_at	0.67071	8.3538113	11.50948	6.99E-24	4.58E-22	43.60144	MPV17L	MPV17 mitochondrial membrane protein-like	AK096918

1555763_x_at	0.67018	6.4624962	6.853663	8.60E-11	3.63E-10	13.9489	MKL1	MKL1 mRNA, 5' untranslated region, partial sequence; alternatively spliced	AF364036
239107_at	0.67014	5.8464211	10.1711	7.13E-20	1.71E-18	34.49658	ZNF280D	zinc finger protein 280D	AA725587
1570266_x_at	0.67012	8.1771228	9.579546	3.79E-18	6.10E-17	30.58063	0	0	BC015108
221655_x_at	0.66956	7.1732717	4.843803	2.54E-06	5.78E-06	3.963114	EPS8L1	EPS8-like 1	AF282167
231107_at	0.66948	4.4856648	9.062354	1.14E-16	1.36E-15	27.22854	0	0	AI492822
205998_x_at	0.66932	6.2863985	11.68399	2.06E-24	1.57E-22	44.80743	CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4	NM_017460
206160_at	0.66903	5.6049568	7.026435	3.21E-11	1.45E-10	14.91337	APOBEC2	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2	NM_006789
1559882_at	0.66831	4.6984258	5.25837	3.70E-07	9.42E-07	5.816793	SAMHD1	Full length insert cDNA clone YP80A10	AF147427
232500_at	0.66774	6.4451097	5.834023	2.13E-08	6.40E-08	8.578302	C20orf74	chromosome 20 open reading frame 74	AL121896
230525_at	0.66742	6.0396305	12.95871	2.52E-28	6.50E-26	53.69856	LOC283875	hypothetical protein LOC283875	AI762077
241045_at	0.66722	5.5345926	10.62869	3.14E-21	1.06E-19	37.57623	JMJD5	jumonji domain containing 5	AW589664
1553499_s_at	0.66665	6.236337	12.21457	4.92E-26	6.01E-24	48.49317	SERPINA9	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	AY185496
1561171_a_at	0.66654	6.0236523	12.01909	1.95E-25	1.96E-23	47.13222	FLJ36131	hypothetical protein FLJ36131 /// hypothetical protein LOC100131452 /// transmembrane domain-containing protein ENSP00000320207-like /// hypothetical protein LOC100132566 /// hypothetical protein LOC100132727 /// hypothetical LOC729272	AK093450
232360_at	0.66603	5.5629479	5.584537	7.53E-08	2.10E-07	7.355727	EHF	ets homologous factor	AA565141
1552615_at	0.66564	7.9985976	10.97622	2.86E-22	1.24E-20	39.93985	ACACB	acetyl-Coenzyme A carboxylase beta	NM_001093
228898_s_at	0.66543	5.5344275	9.066539	1.11E-16	1.32E-15	27.25536	SMARCB1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	AW135031
216975_x_at	0.66496	5.5148014	11.01873	2.13E-22	9.55E-21	40.23028	NPAS1	neuronal PAS domain protein 1	U51628
220396_at	0.66447	6.3875365	12.94954	2.69E-28	6.87E-26	53.6342	0	0	NM_018520
204704_s_at	0.66427	3.5685488	3.631801	0.0003571	0.0006189	-0.73513	ALDOB	aldolase B, fructose-bisphosphate	BF195998
213509_x_at	0.66338	9.4872243	3.726087	0.0002526	0.0004464	-0.41077	CES2	carboxylesterase 2 (intestine, liver)	AW157619
219562_at	0.66336	5.8688323	5.287227	3.22E-07	8.27E-07	5.950155	RAB26	RAB26, member RAS oncogene family	NM_014353
1559638_at	0.66324	7.590946	11.5289	6.10E-24	4.04E-22	43.73543	C1orf200	chromosome 1 open reading frame 200	AA827203
207106_s_at	0.66317	5.0891059	7.374147	4.22E-12	2.18E-11	16.89758	LTK	leukocyte receptor tyrosine kinase	NM_002344
231732_at	0.66304	5.8241406	7.148791	1.58E-11	7.47E-11	15.60516	SMPD3	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	NM_018667
1565484_x_at	0.66176	6.2954012	8.372789	9.46E-15	7.68E-14	22.88354	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	AF277897
1555585_a_at	0.66145	3.6749059	11.74988	1.30E-24	1.04E-22	45.26368	FAM71B	family with sequence similarity 71, member B	AF465821
206237_s_at	0.66142	5.2945959	6.632926	2.97E-10	1.16E-09	12.73845	NRG1	neuregulin 1	NM_013957
229668_at	0.66087	5.9992056	12.64256	2.38E-27	4.62E-25	51.48296	LOC90393	hypothetical protein LOC90393	AI022626
227885_at	0.66073	5.1446745	13.4021	1.08E-29	4.36E-27	56.8127	LOC400236	Full length insert cDNA clone ZD64H08	AW138940
204909_at	0.66049	5.7197546	8.558037	2.93E-15	2.62E-14	24.03548	DDX6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	NM_004397
216910_at	0.66019	5.5882094	4.127627	5.37E-05	0.0001031	1.050527	XPNPEP2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	AF195953

219028_at	0.65989	6.3118917	9.6747	2.01E-18	3.44E-17	31.20501	HIPK2	homeodomain interacting protein kinase 2	NM_022740
244387_at	0.6594	5.4711582	5.153522	6.08E-07	1.51E-06	5.336918	0		0 AW979271
207284_s_at	0.65886	4.3926788	9.138261	6.95E-17	8.63E-16	27.71588	ASPH	aspartate beta-hydroxylase	NM_020164
205874_at	0.65849	6.4799838	4.877596	2.18E-06	5.00E-06	4.109774	ITPKA	inositol 1,4,5-trisphosphate 3-kinase A	NM_002220
224258_at	0.65791	4.2149762	10.60651	3.65E-21	1.21E-19	37.42604	ELP1P	endozepine-like peptide 1 pseudogene	AF229803
227014_at	0.65748	7.5934549	3.854589	0.0001559	0.0002825	0.04291	ASPHD2	aspartate beta-hydroxylase domain containing 2	BE550881
1566630_at	0.65721	5.2014748	13.7242	1.09E-30	6.37E-28	59.07818	LOC100134	similar to protein phosphatase 2 (formerly 2A), regulatory subunit B, beta	AL834280
214206_at	0.65714	4.6940391	7.946597	1.34E-13	8.86E-13	20.28037	PPIL6	peptidylprolyl isomerase (cyclophilin)-like 6	AI739480
244696_at	0.6563	5.6809624	11.6909	1.96E-24	1.50E-22	44.85526	0		0 AI033582
238072_at	0.65579	5.3851703	14.35796	1.18E-32	1.75E-29	63.53771	0		0 AI073865
1552354_at	0.65559	4.9697516	9.140462	6.85E-17	8.52E-16	27.73003	C19orf26	chromosome 19 open reading frame 26	NM_152769
233091_at	0.65555	4.7243674	12.15999	7.23E-26	8.25E-24	48.11288	ATAD3B	ATPase family, AAA domain containing 3B	AB033099
244475_at	0.65545	5.1131486	10.59782	3.88E-21	1.27E-19	37.36722	0		0 AW296024
219597_s_at	0.65536	5.4624443	5.90739	1.46E-08	4.49E-08	8.945059	DUOX1	dual oxidase 1	NM_017434
234439_at	0.6553	4.5172315	14.82428	4.27E-34	1.21E-30	66.81646	0		0 AK001097
242913_at	0.65529	5.4323229	4.557692	8.96E-06	1.90E-05	2.754099	CLIC6	chloride intracellular channel 6	AW816405
240770_at	0.6552	6.4269713	4.770871	3.52E-06	7.87E-06	3.649348	TMEM171	transmembrane protein 171	AW058459
216374_at	0.65504	3.9397135	9.974034	2.70E-19	5.65E-18	33.18328	LOC728137	similar to testis specific protein, Y-linked 1 /// similar to testis specific protein, Y-linked 1 /// similar to testis specific protein, Y-linked 1 /// testis specific protein, Y-linked	AC005986
228428_at	0.65475	4.6513399	8.90743	3.12E-16	3.39E-15	26.23919	FAM102A	CDNA FLJ37031 fis, clone BRACE2011199	AA521285
240754_at	0.65433	5.4568152	8.944071	2.46E-16	2.73E-15	26.47253	LOC284933	hypothetical protein LOC284933	AI382197
239996_x_at	0.65401	6.6027501	14.03658	1.17E-31	1.05E-28	61.27636	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	AI671237
1554379_a_at	0.65339	5.9173867	10.58507	4.23E-21	1.38E-19	37.28095	TP73	tumor protein p73	AB055066
1566550_at	0.65325	3.8588926	10.85137	6.77E-22	2.69E-20	39.0885	0		0 AL137307
240242_at	0.6527	4.876564	5.22826	4.27E-07	1.08E-06	5.67823	0		0 BE222843
236286_at	0.65225	6.1636903	14.76824	6.37E-34	1.66E-30	66.42268	PROCA1	proline-rich cyclin A1-interacting protein	AI887588
239027_at	0.65218	6.1068499	7.655216	7.89E-13	4.60E-12	18.54128	DOCK8	dedicator of cytokinesis 8	AV760561
207778_at	0.65177	4.8728322	9.886094	4.88E-19	9.68E-18	32.59994	REG1P	regenerating islet-derived 1 pseudogene	NM_006508
209443_at	0.65162	6.5347892	4.002854	8.80E-05	0.0001644	0.582779	SERPINA5	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 5	J02639
227393_at	0.65121	7.3464632	6.984851	4.07E-11	1.81E-10	14.6799	ANO9	anoctamin 9	AW084755
1552819_at	0.65115	4.4369005	9.801947	8.59E-19	1.61E-17	32.04342	C21orf86	chromosome 21 open reading frame 86	NM_153454
1566931_at	0.65099	5.4313724	8.691987	1.25E-15	1.19E-14	24.87568	TFB2M	Transcription factor B2, mitochondrial, mRNA (cDNA clone IMAGE:5311413)	BC042010
243233_at	0.65087	5.415306	5.956587	1.13E-08	3.52E-08	9.192794	0		0 AI701943
236547_at	0.65076	3.9961839	8.761091	8.01E-16	7.98E-15	25.31143	0		0 AI161428
215863_at	0.65034	5.9043272	10.96743	3.04E-22	1.32E-20	39.87984	TFR2	transferrin receptor 2	AK022002
244409_at	0.65031	5.7926054	15.31856	1.27E-35	6.95E-32	70.28516	CCDC154	CDNA clone IMAGE:4111037	AW612232
1569002_x_at	0.65015	5.8697067	11.72619	1.53E-24	1.22E-22	45.09953	BMP1	bone morphogenetic protein 1	AF318323
241488_at	0.65015	4.7725763	13.03687	1.45E-28	4.10E-26	54.24698	0		0 AI822112
1557656_at	0.64965	6.5503521	13.7514	8.94E-31	5.42E-28	59.26951	LOC400238	hypothetical gene supported by AK093266	AK093266
204810_s_at	0.64962	4.7147072	7.614422	1.01E-12	5.79E-12	18.3006	CKM	creatine kinase, muscle	NM_001824
216594_x_at	0.64919	9.9670621	3.569598	0.0004471	0.0007651	-0.94513	AKR1C1	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	S68290
206255_at	0.64916	4.5766516	6.02505	7.93E-09	2.52E-08	9.539926	BLK	B lymphoid tyrosine kinase	NM_001715

1566106_at	0.64914	3.6639647	8.845252	4.66E-16	4.86E-15	25.84418	0	AK091277
226403_at	0.64896	8.6335049	3.502559	0.0005676	0.0009589	-1.16787	TMC4	transmembrane channel-like 4
77508_r_at	0.64866	7.1976142	14.4493	6.18E-33	1.02E-29	64.18026	LOC100133	similar to RABEP2 protein /// rabaptin, RAB GTPase binding effector protein 2
221164_x_at	0.6485	6.3223705	5.085881	8.35E-07	2.03E-06	5.031263	CHST5	carbohydrate (N- acetylglucosamine 6-O) sulfotransferase 5
208390_s_at	0.64839	6.7680934	13.69941	1.29E-30	7.37E-28	58.90375	GLP1R	glucagon-like peptide 1 receptor
235730_at	0.64821	4.7421495	7.006391	3.60E-11	1.61E-10	14.80074	0	AA830545
238095_at	0.64804	4.3142003	6.845963	8.99E-11	3.78E-10	13.90626	GATA5	GATA binding protein 5
1558525_at	0.64778	5.0250445	10.17894	6.76E-20	1.64E-18	34.54904	LOC283901	hypothetical protein LOC283901
237497_at	0.64768	6.5218428	9.738107	1.32E-18	2.35E-17	31.62231	0	N69098
242966_x_at	0.64764	4.7884964	8.282279	1.67E-14	1.30E-13	22.32509	0	AW341515
224501_at	0.64756	5.8018597	15.19751	3.01E-35	1.49E-31	69.43648	C1orf170	chromosome 1 open reading frame 170
1552582_at	0.64728	3.5977295	8.156032	3.67E-14	2.68E-13	21.55112	ABCC13	ATP-binding cassette, sub-family C (CFTR/MRP), member 13
237360_at	0.64724	4.5375555	8.702455	1.17E-15	1.12E-14	24.94159	ACTRT2	actin-related protein T2
1569607_s_at	0.64696	6.5278909	4.574208	8.35E-06	1.78E-05	2.82228	ANKRD20A	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family, member A2 /// ankyrin repeat domain 20 family, member A3 /// ankyrin repeat domain 20 family, member A4 /// chromosome 21 open reading frame 81 /// hypothetical protein LOC100132733 /// similar to ankyrin repeat domain 20 family, member A2 /// hypothetical LOC643187 /// similar to ankyrin repeat domain 20A /// hypothetical LOC653436 /// similar to ankyrin repeat domain 20 family, member A1 /// similar to FLJ00310 protein
1568986_x_at	0.64642	7.3298182	13.79746	6.44E-31	4.34E-28	59.59361	PIGT	phosphatidylinositol glycan anchor biosynthesis, class T
1569579_at	0.64622	5.572166	10.30286	2.91E-20	7.77E-19	35.37924	0	AW450527
203029_s_at	0.64565	7.6563021	3.576374	0.0004363	0.0007478	-0.92241	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2
1560178_at	0.64524	4.2245397	8.322695	1.30E-14	1.03E-13	22.5741	0	B1821213
211253_x_at	0.645	5.9949783	7.907602	1.70E-13	1.10E-12	20.04564	PYY	peptide YY
241769_at	0.64483	6.5924325	4.542127	9.58E-06	2.03E-05	2.690029	0	AW962458
242619_x_at	0.64458	5.7032514	11.01144	2.24E-22	1.00E-20	40.18045	0	H82831
233402_at	0.64458	4.3636411	9.06317	1.13E-16	1.35E-15	27.23377	0	AU159414
208486_at	0.64452	5.0467199	11.00033	2.42E-22	1.07E-20	40.10457	DRD5	dopamine receptor D5
218931_at	0.64417	7.5288128	5.528539	9.94E-08	2.73E-07	7.086653	RAB17	RAB17, member RAS oncogene family
1552857_a_at	0.64411	4.2640533	10.31658	2.65E-20	7.14E-19	35.47129	HTR6	5-hydroxytryptamine (serotonin) receptor 6
225513_at	0.64396	6.2370903	13.59448	2.73E-30	1.33E-27	58.16557	SCRN2	secernin 2
243834_at	0.6439	5.6136147	9.928481	3.67E-19	7.48E-18	32.88089	TNRC6A	trinucleotide repeat containing 6A
1552915_at	0.64375	4.8784328	9.834854	6.89E-19	1.32E-17	32.26086	IL28A	interleukin 28A (interferon, lambda 2)
232169_x_at	0.643	7.4196646	6.547666	4.77E-10	1.80E-09	12.27766	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH- coenzyme Q reductase)
233700_at	0.64294	4.344376	7.982353	1.08E-13	7.24E-13	20.49612	0	AK025291
234422_at	0.64218	4.6877613	10.51237	6.97E-21	2.16E-19	36.78966	0	AF060169
244665_at	0.64213	5.409458	6.636051	2.92E-10	1.14E-09	12.75541	0	AI056776
237763_at	0.64211	4.4669463	14.25626	2.45E-32	2.97E-29	62.82222	0	BE670795
220344_at	0.64202	6.3284313	11.26131	3.95E-23	2.15E-21	41.89264	C11orf16	chromosome 11 open reading frame 16

229555_at	0.64147	7.585219	4.925953	1.75E-06	4.06E-06	4.321029	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl/galactosaminyltransferase 5 (GalNAc-T5)	AI633503
207051_at	0.64128	5.7927019	6.79397	1.21E-10	4.98E-10	13.61911	SLC17A4	solute carrier family 17 (sodium phosphate), member 4	NM_005495
242359_at	0.64101	4.9154282	12.45178	9.20E-27	1.41E-24	50.14874	0	0	AI021939
1553808_a_at	0.6406	4.8866436	4.544956	9.47E-06	2.00E-05	2.701661	NKX2-3	NK2 transcription factor related, locus 3 (Drosophila)	NM_145285
236139_at	0.64021	4.7610608	9.067482	1.10E-16	1.32E-15	27.26141	0	0	BE671815
223775_at	0.64018	4.0367696	5.42076	1.69E-07	4.50E-07	6.574384	HHIP	hedgehog interacting protein	AY009951
241439_at	0.63994	3.820531	7.414078	3.33E-12	1.75E-11	17.12899	0	0	BE675448
1565701_at	0.63993	5.1407332	11.33692	2.33E-23	1.34E-21	42.41243	0	0	AL832624
223611_s_at	0.6397	7.352144	3.679934	0.0002995	0.0005242	-0.57045	LNX1	ligand of numb-protein X 1	AI738919
211996_s_at	0.63898	8.1954638	5.129914	6.80E-07	1.67E-06	5.229886	LOC100132	similar to Uncharacterized protein KIAA0220 /// PI-3-kinase-related kinase SMG-1 isoform 1 homolog /// nuclear pore complex interacting protein pseudogene	BG256504
1559303_at	0.6389	4.009585	11.44505	1.10E-23	6.85E-22	43.15705	0	0	AK055100
220515_at	0.63858	4.4114951	10.50336	7.41E-21	2.28E-19	36.7288	DUSP21	dual specificity phosphatase 21	NM_022076
231401_s_at	0.63856	5.3261344	10.07943	1.33E-19	3.00E-18	33.88461	0	0	AI871586
210505_at	0.63833	4.2377881	8.935174	2.61E-16	2.88E-15	26.41584	ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	U07821
223753_s_at	0.63819	4.2846887	4.918768	1.81E-06	4.19E-06	4.28954	CFC1 /// CF	cripto, FRL-1, cryptic family 1 ///	AF312769
221318_at	0.63808	4.5265606	10.73617	1.50E-21	5.48E-20	38.3051	NEUROD4	cripto, FRL-1, cryptic family 1B neurogenic differentiation 4	NM_021191
238018_at	0.6379	4.2440216	4.475771	1.27E-05	2.65E-05	2.418888	FAM150B	family with sequence similarity 150, member B	BF449053
238837_at	0.63784	5.0095294	10.06004	1.51E-19	3.37E-18	33.75543	PHF8	CDNA FLJ11634 fis, clone HEMBA1004275, moderately similar to Homo sapiens PHD-finger protein (GRCS) mRNA	BE676640
1562751_at	0.63741	4.704264	10.43773	1.16E-20	3.39E-19	36.28621	0	0	BC042499
244216_at	0.63662	5.2115532	12.67388	1.91E-27	3.83E-25	51.70224	0	0	BF439270
233895_at	0.63642	5.9260913	12.14876	7.83E-26	8.82E-24	48.03462	ANKRD24	ankyrin repeat domain 24	AC005578
1559491_at	0.63628	5.2496895	11.31667	2.68E-23	1.51E-21	42.27312	0	0	AL390180
232121_at	0.63626	4.8986061	13.26197	2.92E-29	1.02E-26	55.82783	TRDMT1	tRNA aspartic acid methyltransferase 1	AK021659
242110_at	0.63598	5.333202	4.188754	4.19E-05	8.18E-05	1.284096	0	0	AV735587
237779_at	0.6358	6.4129951	13.66629	1.64E-30	8.69E-28	58.67075	0	0	AW188090
224079_at	0.63573	6.2564316	13.08162	1.05E-28	3.11E-26	54.5611	IL17C	interleukin 17C	AF152099
211682_x_at	0.63567	5.8409546	4.594588	7.64E-06	1.64E-05	2.906683	UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28	AF177272
238406_x_at	0.63567	7.239305	12.11389	1.00E-25	1.09E-23	47.79182	SEZ6L2	seizure related 6 homolog (mouse)-like 2	AI734001
206797_at	0.63564	5.878966	3.592582	0.0004116	0.0007077	-0.8679	NAT2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	NM_000015
240963_x_at	0.6356	6.1755362	15.56569	1.08E-36	1.18E-32	72.71535	LOC100131	hypothetical protein LOC100131347	BF434274
1559977_a_at	0.6353	5.8167438	10.03139	1.83E-19	3.98E-18	33.56467	SLC25A34	solute carrier family 25, member 34	AL832282
237603_at	0.63503	4.1415449	8.517954	3.78E-15	3.31E-14	23.78523	C1orf100	chromosome 1 open reading frame 100	AI122828
211843_x_at	0.63482	7.4971008	6.223104	2.78E-09	9.40E-09	10.55944	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7	AF315325
237099_at	0.63432	4.8380838	8.72301	1.02E-15	9.99E-15	25.07111	C20orf70	chromosome 20 open reading frame 70	AI218468
230709_x_at	0.63417	4.4991017	7.7568	4.27E-13	2.59E-12	19.14364	ZBTB7A	TTF-I interacting peptide 21	AI763405
239720_at	0.63367	6.3102542	12.15834	7.32E-26	8.32E-24	48.1014	GLP-1	GATA like protein-1	AI923985
1561393_at	0.63303	5.1830304	8.899322	3.29E-16	3.56E-15	26.18762	0	0	AW014122
206892_at	0.633	5.9819573	13.79467	6.57E-31	4.37E-28	59.57401	AMHR2	anti-Mullerian hormone receptor, type II	NM_020547
204487_s_at	0.63205	7.8699016	5.097054	7.93E-07	1.93E-06	5.081536	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	NM_000218
1561421_a_at	0.63196	6.0040866	6.420322	9.58E-10	3.46E-09	11.59664	0	0	AK057259

220377_at	0.63137	6.1622671	7.390872	3.83E-12	1.99E-11	15.99442	FAM30A	family with sequence similarity 30, member A	NM_014151
224406_s_at	0.63134	6.4215516	6.005572	8.78E-09	2.77E-08	9.440885	FCRL5	Fc receptor-like 5	AF343664
1563685_at	0.63127	3.6429672	9.445574	9.22E-18	1.37E-16	29.70541	LOC285422	hypothetical protein LOC285422	AL832228
1562657_a_at	0.63127	5.2359503	11.42147	1.29E-23	7.92E-22	42.99453	C10orf90	chromosome 10 open reading frame 90	AK093093
221084_at	0.63107	4.3425295	9.876136	5.22E-19	1.03E-17	32.534	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	NM_006028
210068_s_at	0.63081	3.751157	6.881005	7.37E-11	3.14E-10	14.10055	AQP4	aquaporin 4	U63622
1569105_at	0.63031	8.3507345	13.00278	1.84E-28	5.09E-26	54.00779	SETD5	SET domain containing 5	BI087313
205391_x_at	0.63008	5.4522445	9.067731	1.10E-16	1.31E-15	27.26301	ANK1	ankyrin 1, erythrocytic	M28880
1559702_at	0.63	4.7644042	8.306041	1.44E-14	1.13E-13	22.47142			0 AF143879
234882_at	0.62988	6.0577931	12.34417	1.97E-26	2.77E-24	49.3972			0 X76785
242068_at	0.62985	4.9095921	4.816731	2.87E-06	6.48E-06	3.846209			0 AA608834
1557817_a_at	0.62977	6.6943496	14.16743	4.61E-32	4.93E-29	62.19715	LOC100131	HSPC103	AF161366
210850_s_at	0.62933	4.3731131	7.180214	1.32E-11	6.29E-11	15.78396	ELK1	ELK1, member of ETS oncogene family	AF000672
226292_at	0.62933	8.4509343	4.467294	1.32E-05	2.74E-05	2.384485	CAPN5	calpain 5	BF195709
208573_s_at	0.62919	4.5609808	10.29244	3.13E-20	8.27E-19	35.3093	OR2H2	olfactory receptor, family 2, subfamily H, member 2	NM_007160
1554050_at	0.6291	6.934408	10.87491	5.76E-22	2.33E-20	39.2488	SMPDL3B	sphingomyelin phosphodiesterase, acid-like 3B	BC014444
208268_at	0.62847	4.7068948	4.395027	1.79E-05	3.66E-05	2.093369	ADAM28	ADAM metalloproteinase domain 28	NM_021777
229341_at	0.62832	6.3890948	6.498064	6.26E-10	2.32E-09	12.01136	TFCP2L1	transcription factor CP2-like 1	AW195353
235595_at	0.62764	6.531573	14.69515	1.07E-33	2.34E-30	65.90902	ARHGEF2	Homo sapiens, clone IMAGE:4636257, mRNA	AW299534
206151_x_at	0.62746	5.4774488	5.655625	5.28E-08	1.50E-07	7.700161	ELA3B	elastase 3B, pancreatic	NM_007352
221232_s_at	0.62743	4.8582394	9.483389	7.18E-18	1.09E-16	29.95198	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)	NM_020349
234425_at	0.6268	5.4985588	12.98246	2.13E-28	5.68E-26	53.86518			0 AF233648
230191_at	0.62678	5.9758489	11.9402	3.40E-25	3.17E-23	46.58394	TTBK1	tau tubulin kinase 1	H04790
235446_at	0.62665	5.3173029	9.544444	4.79E-18	7.55E-17	30.35087			0 AW856618
202488_s_at	0.62656	8.9035036	3.838433	0.0001658	0.0002994	-0.01486	FXD3	FXD domain containing ion transport regulator 3	NM_005971
1553372_at	0.62633	4.1818987	8.708108	1.12E-15	1.09E-14	24.9772	FLJ23865	hypothetical protein FLJ23865	NM_152669
237475_x_at	0.62605	8.9109515	6.346649	1.43E-09	5.04E-09	11.20667	CCDC152	coiled-coil domain containing 152	AI151104
230489_at	0.62587	6.4237418	7.598408	1.11E-12	6.33E-12	18.20632	CD5	CD5 molecule	AI797836
238645_at	0.62581	5.4971055	12.58453	3.59E-27	6.43E-25	51.07688			0 AW361623
1558007_s_at	0.62563	4.9806677	9.969761	2.78E-19	5.80E-18	33.15489			0 BC024748
220905_at	0.62533	6.0314919	8.534005	3.41E-15	3.02E-14	23.88538			0 NM_025007
235400_at	0.62526	3.7703473	5.164973	5.76E-07	1.43E-06	5.388972	FCRLA	Fc receptor-like A	AL560266
242810_x_at	0.62492	6.5793504	14.75155	7.17E-34	1.70E-30	66.30542			0 BF125537
1563074_at	0.62491	5.5764861	11.0013	2.40E-22	1.06E-20	40.11117	LOC255654	hypothetical protein LOC255654	BC039539
1560642_at	0.62473	3.607937	7.340595	5.15E-12	2.62E-11	16.70369			0 BI461667
242022_at	0.62468	5.838798	8.706938	1.13E-15	1.10E-14	24.96983			0 BF883581
1553946_at	0.62467	4.6386435	10.21513	5.29E-20	1.32E-18	34.79113	DCD	dermcidin	NM_053283
230880_at	0.62404	5.6706387	9.802291	8.57E-19	1.60E-17	32.04569	KIAA1652	KIAA1652 protein	AW450772
219707_at	0.62388	6.5671759	12.38113	1.52E-26	2.23E-24	49.65523	CPNE7	copine VII	NM_014427
206324_s_at	0.62385	5.902078	9.258265	3.17E-17	4.21E-16	28.48969	DAPK2	death-associated protein kinase 2	NM_014326
1553444_a_at	0.62332	6.1090885	10.26745	3.70E-20	9.62E-19	35.14166	C1orf127	chromosome 1 open reading frame 127	NM_173507
220780_at	0.62325	5.3046773	9.438795	9.64E-18	1.42E-16	29.66125	PLA2G3	phospholipase A2, group III	NM_015715
229548_at	0.62298	5.4089789	9.875631	5.24E-19	1.03E-17	32.53066			0 BG231709
211441_x_at	0.62294	6.3992664	8.559366	2.91E-15	2.60E-14	24.04379	CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43	AF280113
1556046_a_at	0.62277	6.221607	13.26879	2.78E-29	9.86E-27	55.87572	LOC157627	hypothetical LOC157627	AL832535
227556_at	0.62256	10.805103	3.687401	0.0002914	0.000511	-0.54473	NME7	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	AI094580
209919_x_at	0.62236	7.7018671	4.31865	2.46E-05	4.94E-05	1.789953	GGT1	gamma-glutamyltransferase 1	L20490
205914_s_at	0.6222	4.8184077	8.916553	2.94E-16	3.21E-15	26.29725	GRIN1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	NM_007327
220714_at	0.62206	5.6434321	14.12435	6.26E-32	6.33E-29	61.89398	PRDM14	PR domain containing 14	NM_024504
232977_x_at	0.6211	7.6948941	4.037509	7.68E-05	0.0001447	0.71147	MYH14	myosin, heavy chain 14	BC004396

213486_at	0.62054	5.1113103	9.111189	8.30E-17	1.02E-15	27.54188	COPG2IT1	coatamer protein complex, subunit gamma 2, intronic transcript 1	BF435376
242695_at	0.62034	5.5640562	5.872433	1.75E-08	5.32E-08	8.769912	0		BF512254
243653_at	0.62034	4.8668009	9.929575	3.64E-19	7.43E-18	32.88815	SHROOM3	CDNA FLJ55531 complete cds, highly similar to Homo sapiens shroom (SHRM), mRNA	AA236863
240831_at	0.62029	5.267543	9.033204	1.38E-16	1.61E-15	27.04184	0		AW070342
215788_at	0.62006	6.1778224	12.20913	5.11E-26	6.19E-24	48.4553	C1orf222	chromosome 1 open reading frame 222	AL137547
1560137_at	0.62	4.8786257	10.85043	6.82E-22	2.70E-20	39.08204	0		AW118011
237220_at	0.61986	5.4090659	13.42182	9.36E-30	3.90E-27	56.95133	0		AW135348
1554616_at	0.61977	6.3090989	10.84997	6.84E-22	2.71E-20	39.07894	SERPIN8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	BC034528
236580_at	0.61963	5.2661484	10.18958	6.29E-20	1.54E-18	34.62018	0		AI703052
225280_x_at	0.6195	8.0766448	5.477834	1.28E-07	3.46E-07	6.844725	ARSD	arylsulfatase D	N51673
225981_at	0.61949	7.395373	6.171627	3.66E-09	1.21E-08	10.29229	C17orf28	chromosome 17 open reading frame 28	AW139549
1568719_s_at	0.61948	6.134655	8.287238	1.62E-14	1.26E-13	22.35562	SLC22A23	solute carrier family 22, member 23	BC038748
207131_x_at	0.61947	7.5533628	4.148156	4.94E-05	9.54E-05	1.128644	GGT1	gamma-glutamyltransferase 1	NM_013430
236775_s_at	0.61928	4.3837947	7.300924	6.50E-12	3.26E-11	16.47509	0		AI733792
225496_s_at	0.61889	9.7339183	4.174333	4.45E-05	8.64E-05	1.228732	SYTL2	synaptotagmin-like 2	N21426
208352_x_at	0.61883	5.8404986	10.40453	1.46E-20	4.17E-19	36.0626	ANK1	ankyrin 1, erythrocytic	NM_020479
231123_at	0.61875	3.962807	8.495832	4.35E-15	3.76E-14	23.64735	TRIM36	tripartite motif-containing 36	AI028170
239869_at	0.61874	5.8048484	12.36148	1.74E-26	2.48E-24	49.51803	0		BF001965
1555374_at	0.61871	6.5423337	13.31652	1.98E-29	7.31E-27	56.21115	0		AB071393
212659_s_at	0.61831	7.0645285	5.427596	1.63E-07	4.36E-07	6.606658	IL1RN	interleukin 1 receptor antagonist	AW083357
221083_at	0.61808	5.4932643	10.74831	1.38E-21	5.08E-20	38.38751	KCNQ4	potassium voltage-gated channel, KQT-like subfamily, member 4	NM_004700
1561355_at	0.61793	6.5085942	10.24347	4.36E-20	1.11E-18	34.98097	LOC692247	hypothetical locus LOC692247	AA975897
1563138_at	0.61777	4.8547354	11.51189	6.87E-24	4.50E-22	43.61804	0		BC029470
237283_at	0.6173	5.210895	10.32078	2.58E-20	6.96E-19	35.4995	0		AW573124
1562844_at	0.61719	4.1934958	12.22725	4.50E-26	5.56E-24	48.58167	LOC339822	hypothetical protein LOC339822	BC043553
1558438_a_at	0.61699	5.9302188	6.309306	1.75E-09	6.09E-09	11.01014	IGHG1	Immunoglobulin lambda heavy chain	S55277
219752_at	0.61695	7.2074251	5.231548	4.20E-07	1.06E-06	5.693335	RASAL1	RAS protein activator like 1 (GAP1 like)	NM_004658
221176_x_at	0.61688	6.5449908	11.10275	1.19E-22	5.71E-21	40.8051	WBSCR23	Williams-Beuren syndrome chromosome region 23	NM_025042
213975_s_at	0.61678	12.467808	4.108408	5.79E-05	0.0001109	0.977685	LYZ	lysozyme (renal amyloidosis)	AV711904
220743_at	0.61678	5.8383638	12.86444	4.93E-28	1.18E-25	53.03742	0		NM_014117
232828_at	0.61657	5.3549971	9.281809	2.71E-17	3.67E-16	28.64197	0		AK025806
203673_at	0.61604	5.5513399	10.02907	1.86E-19	4.03E-18	33.54924	TG	thyroglobulin	NM_003235
226988_s_at	0.61601	7.4258523	4.093536	6.15E-05	0.0001173	0.921519	MYH14	myosin, heavy chain 14	AI709055
204637_at	0.61588	4.9338286	4.883523	2.12E-06	4.88E-06	4.135578	CGA	glycoprotein hormones, alpha polypeptide	NM_000735
239341_at	0.61566	5.2212263	9.781476	9.85E-19	1.81E-17	31.90828	0		AI122709
228818_at	0.61557	4.4073924	8.019245	8.57E-14	5.88E-13	20.71925	0		BF110792
232925_at	0.61551	4.77751	5.994744	9.29E-09	2.92E-08	9.38592	0		AU156822
230245_s_at	0.61548	6.2388008	4.440596	1.48E-05	3.05E-05	2.276485	LOC283663	hypothetical LOC283663	AI926479
228888_at	0.61545	6.7012989	12.98576	2.08E-28	5.60E-26	53.88833	STAC2	SH3 and cysteine rich domain 2	AI821472
208389_s_at	0.61523	4.5881035	11.90931	4.23E-25	3.84E-23	46.36943	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	NM_004171
1558324_a_at	0.61482	4.9865466	8.499282	4.26E-15	3.69E-14	23.66884	TMEM72	transmembrane protein 72	BC029135
1559754_at	0.61422	5.1906997	12.30042	2.68E-26	3.58E-24	49.09187	LTB	Lymphotoxin beta isoform variant, alternatively spliced	BC018898
243462_s_at	0.61403	4.8113574	5.603897	6.84E-08	1.92E-07	7.449217	0		BF590303
206792_x_at	0.61398	9.4649399	7.517786	1.80E-12	9.91E-12	17.7333	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	NM_000923
205821_at	0.61391	6.7916647	4.148662	4.93E-05	9.52E-05	1.130577	KLRK1	killer cell lectin-like receptor subfamily K, member 1	NM_007360
213177_at	0.61363	6.1303243	10.80422	9.38E-22	3.61E-20	38.76755	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	AB028989

213900_at	0.61362	6.4854015	4.251216	3.25E-05	6.43E-05	1.525737	C9orf61	chromosome 9 open reading frame 61	AA524029
242497_at	0.61343	4.5111438	9.252944	3.28E-17	4.35E-16	28.45529	TRAFD1	Fin29	AI694735
221226_s_at	0.61318	5.1321641	12.37032	1.64E-26	2.37E-24	49.57974	ACCN4	amiloride-sensitive cation channel 4, pituitary	NM_018674
219835_at	0.61298	4.9921955	9.194118	4.83E-17	6.20E-16	28.07554	PRDM8	PR domain containing 8	NM_020226
235741_at	0.61283	5.4439753	13.00752	1.78E-28	4.95E-26	54.04098	PPIA	CDNA: FUJ22916 fis, clone KATO6406, highly similar to HSCYCR Human mRNA for T-cell cyclophilin	AA457033
208266_at	0.61271	4.2834505	9.059371	1.16E-16	1.38E-15	27.20943	C8orf17	chromosome 8 open reading frame 17	NM_020237
223662_x_at	0.61262	7.3870381	8.653191	1.60E-15	1.50E-14	24.63172	DDX59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	AL136611
1555617_x_at	0.61248	4.8141186	10.78132	1.10E-21	4.14E-20	38.61188	0	0	BC009519
231482_at	0.61219	4.3296466	11.9387	3.44E-25	3.20E-23	46.57354	0	0	AW274257
1563255_at	0.6121	5.1469253	12.68927	1.71E-27	3.48E-25	51.81	LOC728883	CDNA clone IMAGE:4836904	BC033360
219946_x_at	0.61188	8.5752653	4.440309	1.48E-05	3.06E-05	2.275326	MYH14	myosin, heavy chain 14	NM_024729
229330_at	0.61164	4.6366849	8.604742	2.18E-15	1.99E-14	24.32777	0	0	BF109947
241715_x_at	0.61141	6.1985108	9.798622	8.78E-19	1.64E-17	32.02146	ACPT	acid phosphatase, testicular	AA861388
231044_at	0.61139	5.0043437	8.406039	7.67E-15	6.34E-14	23.08942	C1orf194	chromosome 1 open reading frame 194	AI652292
1560089_at	0.61098	7.4619099	3.917277	0.0001226	0.0002251	0.269041	LOC286208	hypothetical protein LOC286208	AL833509
214371_at	0.61059	5.0228603	11.32869	2.47E-23	1.41E-21	42.35578	TSSK2	testis-specific serine kinase 2	AI652441
244157_x_at	0.61057	6.2810936	14.75357	7.07E-34	1.70E-30	66.31961	0	0	BF514597
211484_s_at	0.61048	5.5059516	10.2797	3.41E-20	8.95E-19	35.22386	DSCAM	Down syndrome cell adhesion molecule	AF023450
207502_at	0.61022	4.7264053	6.406559	1.03E-09	3.71E-09	11.52357	GUCA2B	guanylate cyclase activator 2B (uroguanylin)	NM_007102
210448_s_at	0.61012	7.2003428	4.342685	2.23E-05	4.50E-05	1.884963	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	U49396
1553367_a_at	0.61011	5.7199221	7.705327	5.83E-13	3.46E-12	18.83789	COX6B2	cytochrome c oxidase subunit VIb polypeptide 2 (testis)	NM_144613
234290_x_at	0.60994	7.7539985	3.742398	0.0002378	0.0004214	-0.35392	MYH14	myosin, heavy chain 14	BC000676
220318_at	0.60985	6.5630922	4.588814	7.83E-06	1.68E-05	2.882738	EPN3	epsin 3	NM_017957
244733_at	0.60966	4.5584876	14.30114	1.78E-32	2.31E-29	63.13799	0	0	BF110847
224001_at	0.60954	5.0653594	10.76811	1.20E-21	4.51E-20	38.5221	FAM135B	family with sequence similarity 135, member B	AF131744
1556883_a_at	0.60939	3.6497674	8.679051	1.35E-15	1.29E-14	24.79428	LOC440896	hypothetical gene LOC440896	AK055091
208109_s_at	0.60909	4.4032159	4.880206	2.15E-06	4.95E-06	4.121133	C15orf5	chromosome 15 open reading frame 5	NM_030944
236857_at	0.6089	4.6484836	10.18841	6.34E-20	1.55E-18	34.61236	0	0	AW206279
219194_at	0.60882	7.3512747	4.081195	6.46E-05	0.0001229	0.875041	SEMA4G	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	NM_017893
232396_at	0.60824	5.3324532	7.940211	1.39E-13	9.18E-13	20.24189	0	0	AV711227
221390_s_at	0.60815	6.5066245	11.78085	1.04E-24	8.57E-23	45.47827	MTMR8	myotubularin related protein 8	NM_004686
217616_at	0.60812	3.8527145	10.27753	3.46E-20	9.07E-19	35.20931	0	0	AV763520
222901_s_at	0.60788	3.677231	9.695955	1.75E-18	3.02E-17	31.34479	KCNJ16	potassium inwardly-rectifying channel, subfamily J, member 16	AF153815
1556764_s_at	0.60776	4.1156519	9.170243	5.64E-17	7.13E-16	27.9217	0	0	AI452799
221404_at	0.60755	4.7485132	10.85866	6.44E-22	2.57E-20	39.13813	IL1F6	interleukin 1 family, member 6 (epsilon)	NM_014440
208284_x_at	0.60746	7.5710549	4.630853	6.53E-06	1.41E-05	3.05763	GGT1	gamma-glutamyltransferase 1	NM_013421
231025_at	0.60663	5.0473548	8.471397	5.08E-15	4.34E-14	23.49525	0	0	AI796794
237742_at	0.60656	4.9835858	7.934465	1.44E-13	9.49E-13	20.20728	0	0	AW138840
243279_at	0.60601	5.0908025	9.695083	1.76E-18	3.04E-17	31.33905	0	0	AI417007
1554938_a_at	0.606	5.4820644	6.627377	3.06E-10	1.19E-09	12.70834	ACOT11	acyl-CoA thioesterase 11	AF416922
1569409_x_at	0.60589	6.692498	9.286835	2.63E-17	3.56E-16	28.6745	0	0	BC037812
211885_x_at	0.60583	5.7112854	4.547444	9.37E-06	1.98E-05	2.711894	FUT6	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)	U27332
222483_at	0.60569	8.4744447	5.319915	2.75E-07	7.14E-07	6.101881	EFHD2	EF-hand domain family, member D2	AW664179
1563453_at	0.60529	4.7337521	11.57256	4.49E-24	3.06E-22	44.03694	0	0	AL833544
1561817_at	0.60526	3.642	6.180476	3.49E-09	1.16E-08	10.3381	0	0	BF681305
244880_at	0.60511	4.5507451	6.508432	5.91E-10	2.20E-09	12.06692	0	0	AA969517
215067_x_at	0.60476	6.5950792	7.589596	1.17E-12	6.64E-12	18.15448	PRDX2	peroxiredoxin 2	AU147942

208208_at	0.60465	4.5265832	9.467438	7.98E-18	1.20E-16	29.84793	MYH13	myosin, heavy chain 13, skeletal muscle	NM_003802
228877_at	0.60456	5.2153314	6.65966	2.56E-10	1.01E-09	12.88371	RGL3	ral guanine nucleotide dissociation stimulator-like 3	AI379517
237108_x_at	0.60448	6.8685342	13.43313	8.63E-30	3.68E-27	57.03086	FLI42875	hypothetical LOC440556	AW611845
208239_at	0.60423	3.9768201	9.018231	1.52E-16	1.76E-15	26.94604	FOXE1	forkhead box E1 (thyroid transcription factor 2)	NM_012185
1569834_at	0.60405	6.6603452	12.36295	1.72E-26	2.46E-24	49.52828	0	0	BC029533
207915_at	0.60387	4.2909463	8.039616	7.56E-14	5.24E-13	20.84269	0	0	NM_005377
233593_at	0.6035	4.2946131	12.22184	4.67E-26	5.75E-24	48.54386	0	0	AL117437
234667_at	0.60347	4.1532075	8.576731	2.60E-15	2.35E-14	24.15238	0	0	AK026861
1570451_at	0.60331	4.319409	8.683434	1.32E-15	1.25E-14	24.82186	C1orf61	chromosome 1 open reading frame 61	BC010558
238666_at	0.60313	5.0295601	5.464847	1.36E-07	3.67E-07	6.783026	0	0	BF438300
206213_at	0.60304	5.9823879	11.59847	3.75E-24	2.60E-22	44.21598	WNT10B	wingless-type MMTV integration site family, member 10B	NM_003394
207140_at	0.60301	5.1689571	6.056299	6.73E-09	2.16E-08	9.69928	ALPI	alkaline phosphatase, intestinal	NM_001631
1563587_at	0.60301	4.4024578	9.27108	2.91E-17	3.90E-16	28.57255	CDH4	cadherin 4, type 1, R-cadherin (retinal)	AL834206
207641_at	0.60295	5.9820555	11.12991	9.84E-23	4.81E-21	40.99118	TNFRSF13B	tumor necrosis factor receptor superfamily, member 13B	NM_012452
242373_at	0.60295	5.4568377	13.84041	4.74E-31	3.32E-28	59.89586	0	0	AI733144
229021_at	0.60278	6.0160068	7.88265	1.98E-13	1.27E-12	19.89577	0	0	AK026984
222896_at	0.60261	6.66746	4.910456	1.88E-06	4.34E-06	4.25315	TMEM38A	transmembrane protein 38A	AA196034
214357_at	0.60237	4.6642221	9.280424	2.74E-17	3.70E-16	28.63301	C1orf105	chromosome 1 open reading frame 105	AL035295
207820_at	0.60202	4.8520105	3.713851	0.0002643	0.000466	-0.45327	ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide	NM_000667
219398_at	0.602	6.9842139	3.889015	0.0001367	0.0002495	0.166704	CIDEA	cell death-inducing DFFA-like effector c	NM_022094
216119_s_at	0.60198	5.2354595	10.12274	9.89E-20	2.31E-18	34.17354	SPEF1	sperm flagellar 1	AL109804
224087_at	0.60173	5.1688996	12.01375	2.03E-25	2.03E-23	47.09512	0	0	AF116621
238088_at	0.60166	3.8822719	7.919325	1.58E-13	1.03E-12	20.11614	LOC100129	hypothetical protein LOC100129194	BF511954
231695_at	0.60162	4.4133753	10.05436	1.57E-19	3.48E-18	33.71758	0	0	AA001390
1556542_a_at	0.60153	3.965587	9.298925	2.43E-17	3.32E-16	28.75278	0	0	AF086077
210080_x_at	0.60135	4.870081	4.620033	6.84E-06	1.47E-05	3.012495	ELA3A	elastase 3A, pancreatic	D00306
1566157_x_at	0.60117	5.5954404	7.930211	1.48E-13	9.72E-13	20.18166	0	0	BC029166
215066_at	0.60113	4.786127	9.471055	7.79E-18	1.18E-16	29.87152	PTPRF	protein tyrosine phosphatase, receptor type, F	AU158443
243454_at	0.60112	5.61584	9.521252	5.58E-18	8.70E-17	30.19924	0	0	AW207866
1566134_at	0.60109	6.4353461	12.36479	1.70E-26	2.43E-24	49.54111	CARHSP1	MRNA; cDNA DKFZp547G1014 (from clone DKFZp547G1014)	AL832316
1556942_at	0.60103	3.7545966	9.077438	1.03E-16	1.24E-15	27.32525	0	0	AL832732
215628_x_at	0.60073	7.5241451	6.553477	4.61E-10	1.75E-09	12.30895	0	0	AL049285
1561342_at	0.60068	3.9835715	8.421139	6.98E-15	5.80E-14	23.18305	LOC150005	hypothetical protein LOC150005	AI677840
1554201_at	0.60035	6.9405975	8.979408	1.96E-16	2.21E-15	26.69795	CABP4	calcium binding protein 4	BC033167
1568617_a_at	0.59996	6.3583976	4.27694	2.93E-05	5.82E-05	1.62612	KIAA1543	KIAA1543	BC020431
227015_at	0.59969	6.3998036	4.364129	2.04E-05	4.13E-05	1.970096	ASPHD2	aspartate beta-hydroxylase domain containing 2	Z99714
1552884_at	0.59964	5.989051	4.676771	5.34E-06	1.17E-05	3.250125	NKX6-3	NK6 homeobox 3	NM_152568
220074_at	0.59944	6.1343625	5.165498	5.75E-07	1.43E-06	5.39136	MUPCDH	mucin-like protocadherin	NM_017717
232367_x_at	0.59929	7.3195878	11.30575	2.90E-23	1.62E-21	42.19805	ZNF598	zinc finger protein 598	BG341703
233939_at	0.59907	6.0708802	13.29895	2.24E-29	8.10E-27	56.08769	REXO1	REX1, RNA exonuclease 1 homolog (S. cerevisiae) (REXO1), mRNA	AL117522
234291_s_at	0.59886	6.5063892	3.95151	0.0001074	0.0001987	0.393847	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20	AL389979
235084_x_at	0.59871	7.194041	6.973763	4.34E-11	1.92E-10	14.61779	0	0	AI809831
244497_at	0.59867	5.6397815	8.680164	1.35E-15	1.28E-14	24.80128	LOC100129	hypothetical protein LOC100129907	AI650407
231338_at	0.59858	6.7880656	13.09474	9.59E-29	2.88E-26	54.65327	C15orf55	chromosome 15 open reading frame 55	AL040313

								homogentisate 1,2-dioxygenase (homogentisate oxidase) /// similar to homogentisate 1,2-dioxygenase /// homogentisate 1,2-dioxygenase	
214307_at	0.59835	5.8730559	3.739465	0.0002404	0.0004257	-0.36416	HGD /// LO	like	AI478172
234834_at	0.59835	5.3008034	12.34745	1.92E-26	2.71E-24	49.42011	0		AF233648
227739_at	0.59824	7.7591832	9.304445	2.34E-17	3.20E-16	28.78853	LOC648245	hypothetical LOC648245	AI417537
235633_at	0.59815	4.0241968	9.1173	7.97E-17	9.78E-16	27.58114	0		AW361634
211417_x_at	0.5981	7.7384462	4.650807	5.98E-06	1.30E-05	3.141091	GGT1	gamma-glutamyltransferase 1	L20493
								eukaryotic translation initiation factor 4E	
237718_at	0.59803	4.8233111	7.766781	4.02E-13	2.45E-12	19.20306	EIF4E		AA913840
239920_at	0.59801	5.7920845	11.69996	1.84E-24	1.42E-22	44.91793	UBTF	Upstream binding factor (hUBF)	BF436302
244408_at	0.59794	5.0371617	10.61827	3.37E-21	1.13E-19	37.50567	0		AA927995
								Serologically defined colon cancer antigen 8, mRNA (cDNA clone IMAGE:5301251)	
243963_at	0.59762	5.5438059	5.570445	8.08E-08	2.24E-07	7.287828	SDCCAG8		AI473707
235091_at	0.59762	5.3402471	12.61514	2.89E-27	5.40E-25	51.29106	PDE12	Clone 23960 mRNA sequence	BF515943
								YLP motif containing 1, mRNA (cDNA clone IMAGE:3835908)	
1557065_at	0.59755	6.0014366	8.095542	5.35E-14	3.79E-13	21.18237	YLP1		AA927802
230694_at	0.59752	3.9550032	10.88069	5.53E-22	2.25E-20	39.2882	0		AI340341
1557835_at	0.59736	4.2502162	8.177859	3.21E-14	2.36E-13	21.68451	0		AW474420
208224_at	0.5969	5.8121165	12.01053	2.07E-25	2.06E-23	47.07268	HOXB1	homeobox B1	NM_002144
								chromosome 12 open reading frame 53	
1553566_at	0.59681	5.5729837	9.646196	2.43E-18	4.08E-17	31.01774	C12orf53		NM_153685
								chromosome 1 open reading frame 223	
230969_at	0.59666	4.7510311	10.95585	3.29E-22	1.41E-20	39.80081	C1orf223		AW138142
								YSK4 Sps1/Ste20-related kinase homolog (S. cerevisiae)	
221180_at	0.59638	6.4152737	13.51293	4.89E-30	2.26E-27	57.59202	YSK4	family with sequence similarity 171, member A2	NM_025052
235544_x_at	0.59592	4.8464736	9.882362	5.01E-19	9.89E-18	32.57522	FAM171A2		AI888199
243603_at	0.5956	5.6419138	12.31176	2.48E-26	3.33E-24	49.17102	0		AI973041
206634_at	0.59552	4.5943619	8.099743	5.21E-14	3.70E-13	21.20794	SIX3	SIX homeobox 3	NM_005413
233484_at	0.59533	4.2932752	11.0808	1.38E-22	6.52E-21	40.65488	0		AF131844
								glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	
243265_at	0.59529	3.7548971	8.297597	1.52E-14	1.19E-13	22.4194	GAD2		AW444497
1559377_at	0.59528	3.2370246	9.270335	2.93E-17	3.92E-16	28.56774	0		AV736725
208256_at	0.59521	4.2178667	10.20863	5.53E-20	1.37E-18	34.74764	EFNA2	ephrin-A2	NM_001405
								growth factor receptor-bound protein 2	
228572_at	0.5951	6.9759417	10.40271	1.47E-20	4.21E-19	36.05035	GRB2		AI653267
								chromosome 10 open reading frame 41	
237044_s_at	0.59498	6.1752068	11.91094	4.18E-25	3.81E-23	46.3807	C10orf41		AI480142
222485_at	0.59444	5.7555748	12.22383	4.61E-26	5.68E-24	48.55772	FKBP3	FK506 binding protein 3, 25kDa	M90820
233135_at	0.59383	4.7605185	9.451056	8.89E-18	1.32E-16	29.74114	0		AF131787
201766_at	0.5938	4.3560667	10.45313	1.04E-20	3.10E-19	36.39	ELAC2	elaC homolog 2 (E. coli)	AF304370
								tubulin tyrosine ligase-like family, member 6	
230924_at	0.59379	5.4435633	5.656381	5.26E-08	1.50E-07	7.703843	TTL6		AI698574
1560659_at	0.59366	5.7221654	7.187103	1.27E-11	6.06E-11	15.82322	0		AL832439
227537_s_at	0.59366	4.6803816	10.94001	3.67E-22	1.56E-20	39.69271	SP3	Sp3 transcription factor	AW173024
210637_at	0.59361	4.9740738	10.44509	1.10E-20	3.25E-19	36.33583	TACR1	tachykinin receptor 1	M81797
								arachidonate 15-lipoxygenase, type B	
206714_at	0.5936	5.1186656	7.133946	1.72E-11	8.09E-11	15.52085	ALOX15B		NM_001141
237307_at	0.59355	5.37376	11.01973	2.11E-22	9.50E-21	40.23711	0		AW299734
240284_x_at	0.59342	5.8467045	5.97385	1.04E-08	3.24E-08	9.280061	EMG1	C2f	AA863389
1554950_at	0.59307	4.3934333	8.501587	4.19E-15	3.64E-14	23.6832	ACAN	aggrecan	BC036445
208173_at	0.59299	4.2564155	7.532374	1.65E-12	9.14E-12	17.81868	IFNB1	interferon, beta 1, fibroblast	NM_002176
								hypothetical protein	
237266_at	0.59296	6.4910689	10.43475	1.18E-20	3.46E-19	36.26612	LOC100133	LOC100133686	BE552347
								hypothetical protein	
1557263_s_at	0.59285	6.2258996	10.09144	1.22E-19	2.78E-18	33.96472	LOC100131	LOC100131731	AK092855
								tripartite motif-containing pseudogene 1	
232464_at	0.59277	5.0024373	13.17162	5.55E-29	1.78E-26	55.19308	TRIMP1		AF230412
								H1 histone family, member N, testis-specific	
238373_at	0.59267	5.1084909	9.47431	7.62E-18	1.15E-16	29.89275	H1FNT		AW665295

216881_x at	0.59254	5.4572605	10.86549	6.14E-22	2.46E-20	39.18461	PRB1 /// PR	proline-rich protein BstNI subfamily 1 /// proline-rich protein BstNI subfamily 4 /// proline-rich protein HaeIII subfamily 1 /// proline-rich protein HaeIII subfamily 2 /// proline rich 4 (lacrima)	X07882
206694_at	0.59247	5.1025855	8.667161	1.46E-15	1.38E-14	24.71951	PNLIPRP1	pancreatic lipase-related protein 1	NM_006229
1563405_at	0.59229	6.0318499	11.32192	2.59E-23	1.47E-21	42.30926	ATP4B	ATPase, H+/K+ exchanging, beta polypeptide	BC042846
229524_at	0.59223	4.382925	7.660731	7.63E-13	4.46E-12	18.57387	KIAA0494	KIAA0494, mRNA (cDNA clone MGC:1949 IMAGE:3139273)	AI040880
207087_x at	0.59223	5.704757	10.04114	1.72E-19	3.76E-18	33.62959	ANK1	ankyrin 1, erythrocytic	NM_020478
220006_at	0.59205	5.4550457	9.308998	2.27E-17	3.12E-16	28.81802	CCDC48	coiled-coil domain containing 48	NM_024768
220965_s at	0.59196	6.0146122	9.936972	3.47E-19	7.11E-18	32.93722	RSHL1	radial spokehead-like 1	NM_030785
241548_at	0.5917	4.0556375	12.83768	5.96E-28	1.39E-25	52.8498	0	0	AW468777
216736_at	0.59163	5.4614973	9.884581	4.93E-19	9.77E-18	32.58992	TM6SF2	transmembrane 6 superfamily member 2	AK024515
1556333_at	0.5912	3.990605	10.0438	1.69E-19	3.70E-18	33.64725	0	0	AI339536
206323_x at	0.59089	10.396505	6.172189	3.65E-09	1.21E-08	10.2952	OPHN1	oligophrenin 1	NM_002547
205124_at	0.59084	4.6060326	8.814885	5.67E-16	5.81E-15	25.65169	MEF2B	myocyte enhancer factor 2B	NM_005919
236041_at	0.59057	4.8715499	9.350056	1.73E-17	2.43E-16	29.08427	0	0	AW967916
1555405_at	0.59057	3.2985402	10.94664	3.51E-22	1.50E-20	39.73796	UBE3C	ubiquitin protein ligase E3C	BC026241
233689_at	0.59028	5.0059885	8.587183	2.43E-15	2.21E-14	24.2178	0	0	AK026816
222159_at	0.59027	5.5021801	12.6206	2.78E-27	5.24E-25	51.3293	0	0	AK023058
1570040_at	0.59006	4.6275974	8.721672	1.03E-15	1.01E-14	25.06268	0	0	BC039334
236601_at	0.58996	4.2373651	8.115188	4.73E-14	3.39E-13	21.30198	LOC100133	hypothetical protein LOC100133474	BF508918
231670_at	0.58966	4.6036559	7.604489	1.07E-12	6.12E-12	18.24211	0	0	AA057519
1565671_a at	0.58955	4.7925713	7.757384	4.25E-13	2.58E-12	19.14712	LOC391142	hypothetical gene supported by AJ249778; NM_001531	BF515734
241944_x at	0.58911	5.9965302	11.74498	1.34E-24	1.08E-22	45.22968	0	0	BF508371
215126_at	0.5891	4.2359184	6.64317	2.81E-10	1.10E-09	12.79406	0	0	AL109716
222333_at	0.58901	6.7971568	11.17159	7.37E-23	3.73E-21	41.27683	ALS2CL	ALS2 C-terminal like	AV661533
211173_at	0.58883	5.6777774	7.300637	6.51E-12	3.26E-11	16.47344	CCKAR	cholecystokinin A receptor	D85606
211845_at	0.58868	4.8166018	10.42055	1.31E-20	3.77E-19	36.17049	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	AF110314
204674_at	0.58868	7.2473857	4.523	1.04E-05	2.19E-05	2.61154	LRMP	lymphoid-restricted membrane protein	NM_006152
241493_at	0.58867	4.4550598	13.0733	1.12E-28	3.28E-26	54.50272	0	0	AW811910
242720_at	0.58866	4.5498099	7.858238	2.30E-13	1.46E-12	19.74937	ITI4	Inter-alpha (globulin) inhibitor H4 (plasma kallikrein-sensitive glycoprotein)	A/004137
223372_at	0.58827	4.3266927	11.35868	2.00E-23	1.18E-21	42.56216	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	BF116164
220645_at	0.58811	5.268101	9.929868	3.64E-19	7.42E-18	32.89009	FAM55D	family with sequence similarity 55, member D	NM_017678
232322_x at	0.588	9.4076055	3.540569	0.000496	0.0008434	-1.04204	STARD10	StAR-related lipid transfer (START) domain containing 10	D60944
1553880_at	0.58793	4.8495776	9.923388	3.80E-19	7.70E-18	32.84711	C10orf91	chromosome 10 open reading frame 91	NM_173541
211693_at	0.5879	6.3598691	14.98587	1.34E-34	4.32E-31	67.95842	IGHG1	immunoglobulin lambda heavy chain	AF343666
224762_at	0.58776	8.0519823	3.526333	0.0005218	0.000885	-1.08931	KIAA0746	KIAA0746 protein /// serine incorporator 2	AA872583
209641_s at	0.58743	7.7143309	3.969406	0.0001002	0.0001861	0.459465	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	AF009670
223870_at	0.58714	4.7409503	8.915035	2.97E-16	3.24E-15	26.28759	FBXW10	F-box and WD repeat domain containing 10	AL136822
1554129_a at	0.5871	5.6030377	11.04488	1.78E-22	8.14E-21	40.40912	ADIG	adipogenin	BC029594
235095_at	0.58698	6.797088	5.860617	1.86E-08	5.63E-08	8.710872	CCDC64B	coiled-coil domain containing 64B	AW139399
238715_at	0.58696	6.0369117	11.42876	1.23E-23	7.56E-22	43.0448	LOC646014	CDNA clone IMAGE:4798235	BF110180
236114_at	0.58694	5.0325884	5.284317	3.27E-07	8.38E-07	5.936681	0	0	AI798118
1565527_x at	0.58671	4.138338	7.402272	3.58E-12	1.87E-11	17.06049	TCP1112	Clone 1503-7E mRNA sequence	AF306673
243534_at	0.58639	5.8554688	8.696109	1.21E-15	1.17E-14	24.90163	CC2D2B ///	coiled-coil and C2 domain containing 2B /// hypothetical protein LOC100131720	AA877128

228258_at	0.58628	6.9785644	5.391081	1.95E-07	5.16E-07	6.434637	TBC1D10C	TBC1 domain family, member 10C	AW008519
239030_at	0.58624	4.2448111	11.02649	2.02E-22	9.11E-21	40.28337	0	0	BF439137
206998_x_at	0.58614	6.481505	11.41189	1.38E-23	8.43E-22	42.92855	PRB3	proline-rich protein BstNI subfamily 3	NM_006249
215545_at	0.58606	5.7337287	10.51031	7.06E-21	2.18E-19	36.77571	0	0	AK024185
210326_at	0.5859	5.6630008	9.296069	2.47E-17	3.37E-16	28.73428	AGXT	alanine-glyoxylate aminotransferase	D13368
238949_at	0.5856	8.2163294	6.395024	1.10E-09	3.94E-09	11.4624	RNF145	ring finger protein 145	BF681162
230603_at	0.58558	5.0830486	10.75935	1.28E-21	4.76E-20	38.46252	COL27A1	collagen, type XXVII, alpha 1	W94813
1565107_x_at	0.58532	3.5859464	8.998281	1.73E-16	1.97E-15	26.81849	0	0	U61086
243135_x_at	0.58518	5.4612781	14.01715	1.34E-31	1.17E-28	61.13958	0	0	R26456
242354_at	0.58504	7.2016938	4.07492	6.62E-05	0.0001258	0.851457	0	0	AI191905

Figure 14

Hypermethylated in invasive-subtype								
ID	beta_dif	AveExpr	t	P.Value	adj.P.Val	B	Gene	GeneBank_Acc
cg161757 25	0.18582	0.49117673	5.680235	7.59E-08	2.16E-05	7.40509	TCF1	NM_000545.3
cg223467 65	0.182713	0.52633278	6.34716	2.90E-09	4.05E-06	10.5812	UNC5CL	NM_173561.1
cg061948 08	0.176592	0.54137949	5.836512	3.60E-08	1.40E-05	8.13061	MGC9712	NM_152689.2
cg266086 67	0.174848	0.61782145	5.41408	2.66E-07	5.07E-05	6.19136	MGC11257	NM_032350.3
cg011191 35	0.173222	0.51838825	6.292793	3.82E-09	4.30E-06	10.3148	C1orf116	NM_023938.4
cg154843 75	0.17236	0.47219031	6.446914	1.75E-09	4.05E-06	11.0733	SAA1	NM_199161.1
cg084110 49	0.169686	0.60632492	5.658894	8.39E-08	2.27E-05	7.30695	SERPINB5	NM_002639.2
cg224873 22	0.167838	0.6526185	5.537722	1.48E-07	3.51E-05	6.75414	IL20RA	NM_014432.2
cg107840 90	0.164264	0.5425396	5.226712	6.20E-07	8.64E-05	5.37071	CLDN18	NM_001002026.2
cg254336 48	0.163872	0.64703617	5.019842	1.56E-06	0.0001516	4.48018	S100A14	NM_020672.1
cg129076 44	0.162558	0.50920708	6.234981	5.09E-09	4.95E-06	10.0329	SAA2	NM_030754.2
cg015805 68	0.162299	0.63304755	6.029288	1.41E-08	8.68E-06	9.0418	LAMB3	NM_000228.2
cg208377 35	0.161493	0.63523777	5.220774	6.37E-07	8.69E-05	5.34481	SERPINB5	NM_002639.2
cg177415 72	0.160842	0.65144623	5.181865	7.58E-07	9.34E-05	5.17559	CFB	NM_001710.4
cg024421 61	0.160743	0.52353885	5.824628	3.81E-08	1.46E-05	8.07502	PI3	NM_002638.2
cg153204 74	0.160261	0.51475352	5.900863	2.63E-08	1.18E-05	8.43282	UBD	NM_006398.2
cg091952 71	0.160063	0.52441304	5.026056	1.52E-06	0.0001494	4.50657	RNF186	NM_019062.1
cg210941 54	0.15959	0.58362649	5.117232	1.01E-06	0.0001127	4.89637	TNFSF11	NM_003701.2
cg124913 68	0.158608	0.54372553	4.957001	2.05E-06	0.0001793	4.21455	LOC196549	NM_145293.2
cg077859 36	0.158159	0.60473111	6.158347	7.46E-09	5.99E-06	9.66143	GPR39	NM_001508.1
cg155603 37	0.157587	0.55185124	5.466208	2.07E-07	4.14E-05	6.43145	HYAL4	NM_012269.1
cg033874 97	0.157098	0.56228483	5.772986	4.88E-08	1.76E-05	7.83424	C20orf179	NM_001014977.1
cg054986 81	0.154922	0.65963055	5.199364	7.01E-07	9.01E-05	5.25159	SRC	NM_005417.3
cg214784 37	0.154685	0.61936453	5.160127	8.36E-07	0.0001007	5.08141	CTSE	NM_001910.2
cg154221 47	0.154428	0.6199431	5.260317	5.32E-07	7.85E-05	5.51766	SERPINB5	NM_002639.2

cg154858 59	0.154204	0.52240997	5.971829	1.87E-08	1.01E-05	8.76838	C1orf116	NM_023938.4
cg172987 04	0.153512	0.56110565	4.300435	3.19E-05	0.0013315	1.58488	CLDN18	NM_001002026.2
cg102077 45	0.153225	0.38608156	5.5292	1.54E-07	3.59E-05	6.71555	C12orf36	NM_182558.1
cg025378 38	0.153199	0.54465945	5.981325	1.78E-08	9.89E-06	8.81346	C20orf151	NM_080833.1
cg161730 67	0.152879	0.57554492	5.382905	3.04E-07	5.44E-05	6.05897	SDCBP2	NM_015685.3
cg063942 29	0.152116	0.52079691	4.812154	3.85E-06	0.0002806	3.61126	LGALS4	NM_006149.2
cg123026 21	0.151953	0.59241425	4.539408	1.21E-05	0.0006509	2.51027	SLC28A1	NM_004213.3
cg002088 30	0.150085	0.5563797	5.941759	2.16E-08	1.06E-05	8.62591	LAMC2	NM_005562.1
cg276105 61	0.150039	0.61815485	4.348556	2.63E-05	0.0011531	1.76819	SLC2A10	NM_030777.3
cg197171 50	0.149216	0.44504022	5.736836	5.80E-08	1.92E-05	7.66647	HNF4A	NM_000457.3
cg166395 95	0.148755	0.55326228	5.65882	8.40E-08	2.27E-05	7.30661	SRI	NM_198901.1
cg021486 42	0.148616	0.38403198	5.46768	2.06E-07	4.14E-05	6.43806	RGPD5	NM_032260.2
cg006986 88	0.148041	0.55943769	5.25141	5.54E-07	7.99E-05	5.47865	SULT2B1	NM_177973.1
cg056599 47	0.147547	0.52772858	5.64929	8.78E-08	2.32E-05	7.26286	C4BPB	NM_000716.3
cg212015 72	0.147359	0.48474509	5.755853	5.29E-08	1.81E-05	7.75464	AGR2	NM_006408.2
cg148987 79	0.14723	0.67877769	4.800373	4.04E-06	0.0002922	3.56275	STK31	NM_031414.2
cg159136 71	0.145991	0.47071257	5.702907	6.81E-08	2.03E-05	7.50959	TMEM105	NM_178520.2
cg276007 94	0.14545	0.58415146	4.335731	2.77E-05	0.001204	1.71918	PNLIPRP1	NM_006229.1
cg036849 77	0.145376	0.55759688	4.533137	1.24E-05	0.0006626	2.48551	GRB7	NM_005310.2
cg255275 47	0.14509	0.59429596	5.019308	1.56E-06	0.0001516	4.47791	PLOD3	NM_001084.4
cg005159 05	0.145036	0.70829079	5.097234	1.11E-06	0.0001199	4.81047	EPS8L3	NM_024526.2
cg072077 89	0.14484	0.51591936	5.472707	2.01E-07	4.12E-05	6.46066	CRISPLD2	NM_031476.1
cg263776 77	0.144597	0.62763963	4.684204	6.62E-06	0.0004138	3.08896	FURIN	NM_002569.2
cg049471 57	0.143827	0.41486631	5.415293	2.62E-07	5.03E-05	6.20335	TMC6	NM_007267.5
cg078977 01	0.143527	0.56288911	5.393395	2.90E-07	5.35E-05	6.10567	ABP1	NM_001091.2
cg049944 56	0.143472	0.62914738	5.6476	8.85E-08	2.32E-05	7.25511	RNF186	NM_019062.1
cg238345 93	0.143211	0.46981034	5.754543	5.33E-08	1.81E-05	7.74856	HNF4A	NM_000457.3
cg090815 44	0.143209	0.59006507	5.144184	8.98E-07	0.0001037	5.01252	MUC13	NM_033049.2

cg224388 10	0.142727	0.53468973	5.8925	2.74E-08	1.18E-05	8.39344	LCN2	NM_005564.2
cg222669 67	0.142607	0.5242969	5.901025	2.63E-08	1.18E-05	8.43358	S100P	NM_005980.2
cg118006 72	0.142377	0.51697954	4.93038	2.31E-06	0.0001936	4.10274	SLC39A4	NM_130849.1
cg136889 66	0.141474	0.35349879	6.564896	9.61E-10	3.07E-06	11.6606	TM4SF4	NM_004617.2
cg232132 17	0.140942	0.36719663	6.304964	3.59E-09	4.30E-06	10.3743	DEGS1	NM_144780.1
cg183681 25	0.140526	0.68404032	5.771013	4.92E-08	1.76E-05	7.82506	TMED6	NM_144676.1
cg032921 49	0.14031	0.64779752	5.210811	6.66E-07	8.82E-05	5.3014	CBLC	NM_012116.2
cg126191 62	0.14017	0.5433988	4.791095	4.21E-06	0.0003002	3.5246	FXVD4	NM_173160.2
cg240242 14	0.139827	0.62737766	4.903174	2.61E-06	0.000206	3.98927	BTNL8	NM_024850.1
cg216854 27	0.139447	0.59109434	5.124472	9.81E-07	0.0001105	4.92753	SGK2	NM_016276.3
cg161766 00	0.139107	0.38819624	5.448019	2.25E-07	4.42E-05	6.3498	FRK	NM_002031.2
cg081240 30	0.138829	0.44835314	5.556866	1.36E-07	3.24E-05	6.84097	TM4SF1	NM_014220.2
cg208703 62	0.138685	0.54938096	5.138723	9.20E-07	0.000105	4.98895	CCIN	NM_005893.1
cg084958 78	0.138128	0.66919242	4.909492	2.53E-06	0.0002015	4.01529	SERPINA4	NM_006215.2
cg004127 72	0.137699	0.66156917	5.393558	2.90E-07	5.35E-05	6.1064	C19orf33	NM_033520.1
cg032702 04	0.137423	0.5707089	5.085827	1.16E-06	0.0001244	4.76157	DDR1	NM_001954.3
cg007444 33	0.1367	0.55670997	5.249063	5.60E-07	8.02E-05	5.46837	CXADR	NM_001338.3
cg209165 23	0.136643	0.44128595	4.869689	3.00E-06	0.0002298	3.84939	VHL	NT_022517.17
cg099881 16	0.136614	0.6531546	4.612707	8.94E-06	0.0005136	2.80156	MGC52423	NM_182517.1
cg026338 17	0.136587	0.58703807	5.133882	9.40E-07	0.0001069	4.96808	FXVD3	NM_021910.1
cg058286 24	0.136537	0.64945532	4.960481	2.02E-06	0.0001786	4.2292	REG1A	NM_002909.3
cg065182 71	0.136181	0.634412	5.439784	2.34E-07	4.56E-05	6.3129	ADH6	NM_000672.2
cg169868 46	0.135469	0.42026062	4.956729	2.06E-06	0.0001793	4.21341	SCGB2A1	NM_002407.1
cg274201 23	0.135425	0.42650902	5.329609	3.88E-07	6.39E-05	5.82262	FSHB	NM_000510.2
cg222891 15	0.13517	0.72349314	4.516746	1.33E-05	0.0006921	2.42091	MUCDHL	NM_021924.2
cg159379 58	0.135102	0.68963208	5.27082	5.12E-07	7.66E-05	5.56218	UNQ473	NM_198477.1
cg214848 34	0.134195	0.56357272	5.891089	2.76E-08	1.18E-05	8.38679	PTK6	NM_005975.2
cg260919 81	0.133309	0.6301108	5.128429	9.63E-07	0.000109	4.94458	LCT	NM_002299.2

cg168795 96	0.133178	0.52538806	4.537178	1.22E-05	0.0006556	2.50146	CYP3A5	NM_000777.2
cg044577 94	0.133051	0.5194326	4.100002	7.00E-05	0.0024027	0.8383	CTSE	NM_001910.2
cg096431 86	0.133021	0.69630256	4.977406	1.88E-06	0.0001698	4.30055	GPX2	NM_002083.2
cg008084 92	0.133017	0.61581285	4.713746	5.85E-06	0.0003777	3.20866	REG4	NM_032044.2
cg039776 57	0.132955	0.52853631	5.992903	1.68E-08	9.89E-06	8.86848	LAMB3	NM_000228.2
cg271328 14	0.132539	0.48407115	5.211867	6.63E-07	8.82E-05	5.306	C20orf79	NM_178483.2
cg137189 60	0.131833	0.56048638	4.60135	9.37E-06	0.0005319	2.7562	RNASE1	NM_198232.1
cg112045 62	0.131611	0.59559091	5.096849	1.11E-06	0.0001199	4.80882	C10orf81	NM_024889.3
cg161484 54	0.130926	0.61140806	5.421002	2.55E-07	4.93E-05	6.22886	TMED6	NM_144676.1
cg095847 11	0.130832	0.47272599	5.954835	2.03E-08	1.04E-05	8.68781	HPR	NM_020995.3
cg015661 70	0.13083	0.4249487	5.32947	3.89E-07	6.39E-05	5.82201	CAPN2	NM_001748.3
cg076650 60	0.130814	0.38650608	6.428854	1.92E-09	4.05E-06	10.9839	C19orf33	NM_033520.1
cg206955 87	0.130449	0.58901939	5.711545	6.54E-08	1.97E-05	7.54947	TMPRSS11F	NM_207407.1
cg040016 68	0.13039	0.72629557	5.236873	5.92E-07	8.34E-05	5.41508	GPR56	NM_201525.1
cg090017 77	0.130377	0.337393	5.522588	1.59E-07	3.59E-05	6.68563	FUT3	NM_000149.1
cg124939 06	0.130376	0.61441772	4.219698	4.39E-05	0.0016979	1.28084	MMP26	NM_021801.3
cg082618 41	0.129726	0.63155041	5.186375	7.43E-07	9.34E-05	5.19516	FLJ90586	NM_153345.1
cg004801 15	0.129709	0.57784154	4.756795	4.87E-06	0.0003322	3.38404	FXD3	NM_021910.1
cg117834 97	0.129662	0.6488174	3.96286	0.000118	0.0034951	0.34355	IL1RN	NM_000577.3
cg010536 21	0.129137	0.61755673	4.211962	4.53E-05	0.0017308	1.25194	APOA2	NM_001643.1
cg159969 47	0.129031	0.65033327	4.732684	5.40E-06	0.0003564	3.28567	L2HGDH	NM_024884.1
cg074122 54	0.128693	0.56969096	5.58455	1.19E-07	2.94E-05	6.96689	FLJ14816	NM_032845.1
cg157033 57	0.128689	0.42283874	6.229697	5.23E-09	4.95E-06	10.0072	LINC	XM_930227.1
cg189407 63	0.128687	0.31679979	5.311722	4.21E-07	6.72E-05	5.74364	XBP1	NM_005080.2
cg204161 79	0.128464	0.61468497	5.471544	2.02E-07	4.12E-05	6.45543	C6orf71	NM_203395.1
cg198141 16	0.128299	0.35176999	4.208588	4.59E-05	0.0017514	1.23935	KCNAB2	NM_003636.2
cg070847 09	0.128073	0.70042714	4.151717	5.73E-05	0.002064	1.02828	Gcom1	NM_001018090.1
cg130190 92	0.12791	0.62198064	4.556349	1.13E-05	0.0006134	2.57729	PDZK1	NM_002614.3

cg124565 10	0.127809	0.57013887	4.578053	1.03E-05	0.0005733	2.66342	TFF2	NM_005423.3
cg274965 06	0.127651	0.58010016	4.793851	4.18E-06	0.0003002	3.53238	TGM5	NM_201631.1
cg175827 77	0.127472	0.61939109	4.728179	5.50E-06	0.0003606	3.26733	EFNA3	NM_004952.3
cg231115 44	0.12718	0.57878305	5.37341	3.18E-07	5.57E-05	6.01675	REG1A	NM_002909.3
cg135532 04	0.127044	0.46566738	4.719424	5.71E-06	0.0003714	3.23172	CNKSR1	NM_006314.1
cg160196 20	0.12703	0.5574866	5.275864	4.96E-07	7.46E-05	5.58585	MEP1A	NM_005588.1
cg170308 20	0.126952	0.66121558	4.150144	5.79E-05	0.0020794	1.02119	MSMB	NM_002443.2
cg181194 07	0.126692	0.39747164	5.725427	6.12E-08	1.94E-05	7.61365	CFLAR	NM_003879.3
cg198076 85	0.126671	0.55973458	4.984364	1.82E-06	0.0001676	4.32993	HSD17B2	NM_002153.1
cg216430 45	0.126605	0.67241731	5.042804	1.41E-06	0.0001408	4.57781	CCL20	NM_004591.1
cg004914 04	0.126371	0.59258672	5.57817	1.23E-07	2.98E-05	6.93783	EPS8L3	NM_024526.2
cg077059 08	0.126233	0.53613452	4.267562	3.64E-05	0.0014708	1.46055	SPDEF	NM_012391.1
cg188331 40	0.12623	0.46158057	5.481875	1.93E-07	4.06E-05	6.50191	HABP2	NM_004132.2
cg166488 41	0.125768	0.48495256	5.142992	9.03E-07	0.0001037	5.00737	C8A	NM_000562.1
cg134242 29	0.125671	0.52372227	5.276282	4.95E-07	7.46E-05	5.58768	CPA3	NM_001870.1
cg184626 53	0.125465	0.47199656	3.995219	0.0001044	0.0031825	0.45909	DEFB119	NM_153289.2
cg242725 59	0.125252	0.59053843	4.71147	5.90E-06	0.0003795	3.19942	LOC116123	NM_138784.1
cg214328 42	0.125181	0.30686399	6.548691	1.04E-09	3.07E-06	11.5796	CSF3	NM_000759.2
cg097997 14	0.125146	0.55385799	4.271255	3.60E-05	0.0014577	1.47283	PDZD3	NM_024791.2
cg262598 65	0.124715	0.71326067	4.934316	2.27E-06	0.0001919	4.11924	LOC124220	NM_145252.1
cg003254 91	0.124407	0.41982852	6.383972	2.41E-09	4.05E-06	10.7623	FN5	NM_020179.1
cg048287 92	0.124355	0.62487408	4.703497	6.11E-06	0.0003878	3.16707	MX2	NM_002463.1
cg231811 33	0.124306	0.39317568	6.411511	2.10E-09	4.05E-06	10.8982	CEACAM3	NM_001815.1
cg095395 38	0.124096	0.44439946	5.751294	5.41E-08	1.81E-05	7.73349	C20orf42	NM_017671.3
cg005468 97	0.123977	0.50001521	5.782879	4.65E-08	1.71E-05	7.88026	LOC284837	NM_194310.1
cg258568 11	0.123645	0.41515189	5.0036	1.67E-06	0.0001601	4.4113	SPRR3	NM_005416.1
cg249286 87	0.123614	0.66588504	4.214061	4.49E-05	0.0017241	1.25978	EPHX1	NM_000120.2
cg043842 08	0.123502	0.45418916	4.478789	1.56E-05	0.0007894	2.27418	FCGR3A	NM_000569.6

cg209934 03	0.123221	0.51181124	5.20949	6.70E-07	8.83E-05	5.29564	EPB41L1	NM_012156.2
cg123972 74	0.122921	0.41469933	5.613723	1.04E-07	2.64E-05	7.09999	TINAG	NM_014464.2
cg135207 15	0.12289	0.6656216	5.956752	2.01E-08	1.04E-05	8.69689	C21orf129	NM_152506.1
cg003117 68	0.1227	0.51189837	5.207648	6.75E-07	8.85E-05	5.28763	TSTA3	NM_003313.2
cg273839 56	0.122678	0.63917803	4.229444	4.23E-05	0.0016517	1.3173	FLJ13265	NM_024877.1
cg200593 12	0.122502	0.69804172	4.793613	4.16E-06	0.0002996	3.53495	NGEF	NM_019850.1
cg187668 47	0.121873	0.54726865	5.721212	6.24E-08	1.94E-05	7.59416	ACMSD	NM_138326.1
cg167456 04	0.121795	0.46136761	5.717439	6.36E-08	1.94E-05	7.57671	CASP10	NM_001230.3
cg215789 06	0.121775	0.69181679	4.183599	5.06E-05	0.0018829	1.14633	SLC5A4	NM_014227.1
cg160977 72	0.12177	0.48151983	4.65031	7.64E-06	0.0004608	2.95231	LYZ	NM_000239.1
cg256454 62	0.121489	0.61691338	5.202403	6.97E-07	9.01E-05	5.26365	GPR56	NM_201525.1
cg274623 98	0.121255	0.67049724	4.561822	1.12E-05	0.0006119	2.59367	C1orf181	NM_017953.2
cg246417 37	0.121133	0.41853482	4.42093	1.97E-05	0.0009516	2.04678	DENND2D	NM_024901.3
cg203852 29	0.121078	0.43956316	5.053944	1.34E-06	0.0001363	4.62529	ALKBH	NM_006020.1
cg236969 49	0.12098	0.37856881	4.95575	2.07E-06	0.0001793	4.20929	LAMC2	NM_005562.1
cg162724 20	0.120961	0.55800039	4.533981	1.24E-05	0.0006616	2.48884	PNLIPRP2	NM_005396.3
cg127883 13	0.120789	0.65841041	4.56334	1.10E-05	0.000603	2.605	MST1	NM_020998.2
cg184376 33	0.120751	0.60779716	5.188996	7.34E-07	9.33E-05	5.20654	ITGB6	NM_000888.3
cg136159 63	0.120527	0.29159884	6.45912	1.65E-09	4.05E-06	11.1338	CCR6	NM_004367.3
cg234642 69	0.120474	0.46868397	4.718918	5.72E-06	0.0003714	3.22967	UGT1A3	NM_019093.2
cg144447 10	0.120461	0.56616844	5.396792	2.85E-07	5.35E-05	6.1208	PDPK1	NM_031268.4
cg117623 46	0.120436	0.60773004	4.261266	3.73E-05	0.001492	1.43683	HKDC1	NM_025130.2
cg177381 94	0.120413	0.42559446	5.154975	8.69E-07	0.0001028	5.05292	GK2	NM_033214.2
cg112612 64	0.120401	0.58499924	5.007225	1.65E-06	0.0001582	4.42666	PTPRH	NM_002842.2
cg276226 10	0.120075	0.47575007	4.222202	4.35E-05	0.0016869	1.2902	OR1G1	NM_003555.1
cg203733 26	0.119994	0.44322308	5.810131	4.08E-08	1.54E-05	8.00729	HSD17B2	NM_002153.1
cg174635 27	0.119989	0.5471091	4.925687	2.35E-06	0.0001936	4.08307	SGK2	NM_016276.3
cg035488 57	0.119776	0.42050307	5.461258	2.12E-07	4.19E-05	6.40921	FFAR2	NM_005306.1

cg190250 34	0.119774	0.63655727	5.053694	1.34E-06	0.0001363	4.62422	FUT2	NM_000511.3
cg029069 39	0.119765	0.67903374	5.062403	1.29E-06	0.0001342	4.66139	HNMT	NM_006895.2
cg155828 91	0.119655	0.50554477	5.566364	1.30E-07	3.13E-05	6.88413	TAAR1	NM_138327.1
cg242926 12	0.119634	0.38779468	5.318085	4.09E-07	6.65E-05	5.77172	DEFB1	NM_005218.3
cg243639 55	0.119252	0.57513729	4.711778	5.90E-06	0.0003795	3.20066	FLJ14054	NM_024563.2
cg209805 92	0.119242	0.72139254	4.357405	2.54E-05	0.0011261	1.80206	MEP1A	NM_005588.1
cg026436 67	0.119234	0.70202046	4.7541	4.93E-06	0.0003337	3.37303	TFF1	NM_003225.2
cg185420 98	0.119229	0.73336595	4.555592	1.13E-05	0.0006138	2.57429	FLJ36445	NM_153233.1
cg058592 64	0.119223	0.37839004	4.834911	3.49E-06	0.0002587	3.70521	MAPK13	NM_002754.3
cg068505 26	0.119064	0.39108998	5.224971	6.25E-07	8.66E-05	5.36311	MGC15523	NM_138570.1
cg037238 45	0.119021	0.66799095	4.322464	2.92E-05	0.0012411	1.6686	BTNL8	NM_024850.1
cg095085 56	0.119011	0.71319716	4.362602	2.49E-05	0.0011157	1.82198	PSORS1C2	NM_014069.1
cg132592 90	0.119008	0.6135269	4.251054	3.88E-05	0.0015418	1.39839	CSF2	NM_000758.2
cg251825 23	0.118958	0.52433261	4.65567	7.47E-06	0.0004547	2.97387	C1orf24	NM_022083.1
cg034213 00	0.118913	0.69260503	4.730821	5.44E-06	0.0003575	3.27808	SFN	NM_006142.3
cg256121 45	0.118794	0.72376538	4.282219	3.43E-05	0.0014028	1.51589	STK31	NM_031414.2
cg267184 20	0.118513	0.61279447	4.621914	8.60E-06	0.0005029	2.83839	C12orf59	NM_153022.1
cg274120 93	0.11846	0.5718019	3.910057	0.0001438	0.0039789	0.15663	CAPN9	NM_006615.2
cg223353 40	0.11838	0.50138399	5.758934	5.22E-08	1.81E-05	7.76895	PTPN6	NM_002831.3
cg243550 48	0.118295	0.44285439	4.874294	2.94E-06	0.0002266	3.86853	CTSG	NM_001911.2
cg095330 63	0.118199	0.46227825	4.887725	2.78E-06	0.0002169	3.92445	ALDH8A1	NM_022568.2
cg184143 81	0.118005	0.35625308	5.223352	6.29E-07	8.67E-05	5.35605	EHF	NM_012153.3
cg146595 47	0.118005	0.54958777	4.148378	5.80E-05	0.0020832	1.01596	RETNLB	NM_032579.1
cg140348 70	0.117981	0.41680428	6.142823	8.05E-09	6.27E-06	9.5865	SFTPG	NM_205854.1
cg026711 71	0.117775	0.45317591	5.530336	1.54E-07	3.59E-05	6.72069	RPH3AL	NM_006987.2
cg193461 93	0.117742	0.60921963	3.89176	0.0001539	0.0041806	0.09232	UROS	NM_000375.1
cg270438 73	0.117639	0.5910573	4.363752	2.48E-05	0.0011125	1.82639	CDH18	NM_004934.2
cg239683 83	0.11761	0.66692129	3.785811	0.0002272	0.0055406	-0.27525	ZNF572	NM_152412.1

cg103217 23	0.117402	0.7048582	3.786381	0.0002274	0.0055406	-0.26891	PDZK1	NM_002614.3
cg079185 09	0.11734	0.56435626	4.497668	1.44E-05	0.0007364	2.34594	ICAM2	NM_000873.2
cg103688 42	0.117118	0.39357712	4.979265	1.86E-06	0.000169	4.3084	C10orf81	NM_024889.3
cg059583 52	0.116907	0.56399563	4.439689	1.82E-05	0.0008908	2.11956	RNASE1	NM_198232.1
cg084584 87	0.11689	0.59743043	3.666226	0.0003496	0.0075651	-0.68021	SFTPD	NM_003019.4
cg000759 67	0.116742	0.59885612	4.662328	7.26E-06	0.0004442	3.00068	STRA6	NM_022369.2
cg109293 87	0.116461	0.68564526	3.999419	0.0001028	0.0031469	0.47414	ITIH4	NM_002218.3
cg006686 85	0.116321	0.72749697	3.829775	0.0001935	0.0049182	-0.12372	SLC39A5	NM_173596.1
cg113008 09	0.116303	0.37804605	6.572812	9.23E-10	3.07E-06	11.7002	SGPP2	NM_152386.2
cg103582 12	0.116252	0.5409432	5.064689	1.28E-06	0.0001339	4.67115	ASCIZ	NM_015251.2
cg140035 12	0.116163	0.4908664	6.091666	1.04E-08	6.74E-06	9.34034	PLGLB2	NM_002665.3
cg151490 98	0.116118	0.63548234	4.688329	6.51E-06	0.0004086	3.10565	SULT2B1	NM_177973.1
cg238773 85	0.115989	0.57622944	4.516279	1.33E-05	0.0006921	2.41907	GCNT3	NM_004751.1
cg274040 50	0.11596	0.33690804	5.504917	1.73E-07	3.74E-05	6.60578	PRODH2	NM_021232.1
cg083146 60	0.115845	0.7352996	4.357363	2.54E-05	0.0011261	1.8019	PKP3	NM_007183.2
cg045777 15	0.115842	0.70854041	5.303773	4.37E-07	6.89E-05	5.7086	SPINK1	NM_003122.2
cg102871 37	0.115715	0.58807475	4.527627	1.27E-05	0.0006711	2.46378	P2RY2	NM_002564.2
cg156522 12	0.11563	0.60649217	4.514352	1.34E-05	0.0006963	2.41149	FLJ90586	NM_153345.1
cg023994 55	0.115569	0.71689402	4.328806	2.85E-05	0.0012277	1.69276	SRI	NM_198901.1
cg109688 15	0.115497	0.56715361	3.9507	0.0001235	0.0035996	0.30033	BPIL1	NM_025227.1
cg128558 51	0.115492	0.62273067	4.619474	8.69E-06	0.0005058	2.82862	PGC	NM_002630.1
cg203992 52	0.115459	0.68120866	3.875839	0.0001633	0.0043411	0.03657	EBPL	NM_032565.1
cg144173 29	0.115338	0.33089868	5.182189	7.57E-07	9.34E-05	5.17699	SLC16A3	NM_004207.1
cg217472 71	0.115338	0.28857357	6.32933	3.18E-09	4.21E-06	10.4937	AIP	NM_003977.1
cg139441 41	0.115274	0.50527135	5.983386	1.76E-08	9.89E-06	8.82325	PRSS2	NM_002770.2
cg265144 92	0.115153	0.31119702	4.957026	2.05E-06	0.0001793	4.21466	GPR132	NM_013345.2
cg061233 46	0.115061	0.42123608	4.905857	2.57E-06	0.0002035	4.0001	ATP4A	NM_000704.2
cg108783 07	0.115054	0.52469788	5.077635	1.21E-06	0.0001279	4.7265	ATAD4	NM_024320.2

cg177978 15	0.114915	0.48396518	4.771468	4.58E-06	0.0003171	3.44408	RAB11FIP2	NM_014904.1
cg024900 34	0.114897	0.50495086	4.056742	8.26E-05	0.0027019	0.6808	MEST	NM_177524.1
cg235959 27	0.114711	0.50674827	4.373713	2.38E-05	0.0010798	1.86463	MYL5	NM_002477.1
cg267994 74	0.114685	0.41004903	6.365028	2.65E-09	4.05E-06	10.6691	CASP8	NM_001228.3
cg091550 25	0.114609	0.6723316	4.875556	2.93E-06	0.000226	3.87378	SLC39A4	NM_130849.1
cg053160 65	0.114557	0.31388901	6.171773	6.98E-09	5.78E-06	9.72632	MLZE	NM_031415.1
cg265303 41	0.114289	0.55194363	3.86431	0.0001704	0.0044855	-0.0037	TNFRSF10A	NM_003844.2
cg204376 04	0.113904	0.47610724	4.851193	3.27E-06	0.0002481	3.77323	ANXA9	NM_003568.1
cg272103 90	0.113879	0.376243	5.21595	6.51E-07	8.79E-05	5.32378	TOM1L1	NM_005486.1
cg142520 59	0.113847	0.49593584	4.628115	8.38E-06	0.0004933	2.86322	TECTA	NM_005422.1
cg267388 80	0.113825	0.55882704	4.994243	1.74E-06	0.0001636	4.37169	DPP6	NM_001936.2
cg045050 23	0.113822	0.52326739	3.888624	0.0001557	0.004208	0.08133	SPRR1A	NM_005987.2
cg246075 35	0.113733	0.5802911	4.499219	1.43E-05	0.0007346	2.35203	CDH26	NM_177980.1
cg128186 99	0.113617	0.63496089	4.59531	9.61E-06	0.0005416	2.73211	C6orf32	NM_015864.2
cg095412 48	0.11355	0.486529	5.054649	1.34E-06	0.0001363	4.6283	MYO1A	NM_005379.2
cg150212 92	0.113465	0.723626	3.860671	0.0001727	0.0045282	-0.01638	PIK3R1	NM_181523.1
cg208950 28	0.113426	0.65800087	4.079867	7.56E-05	0.0025427	0.76483	CDH26	NM_177980.1
cg207752 54	0.113406	0.72015096	4.466286	1.64E-05	0.0008205	2.22313	PROM2	NM_144707.1
cg163240 18	0.113127	0.55230114	5.145062	8.94E-07	0.0001037	5.01631	RBED1	NM_032213.3
cg071098 01	0.113091	0.45984133	5.196219	7.11E-07	9.10E-05	5.23792	C3orf60	NM_199069.1
cg172045 57	0.113036	0.59339328	5.163069	8.25E-07	9.98E-05	5.09414	FLJ14816	NM_032845.1
cg189173 78	0.112985	0.42156789	4.434589	1.86E-05	0.0009078	2.09975	BCAS1	NM_003657.1
cg176287 17	0.11298	0.65304185	3.778873	0.0002331	0.0056219	-0.29903	HECW1	NM_015052.2
cg057900 38	0.11292	0.52553142	4.528288	1.27E-05	0.0006706	2.46638	TRPV3	NM_145068.2
cg168691 08	0.112759	0.48211365	4.737571	5.32E-06	0.0003547	3.30226	VHL	NT_022517.17
cg272213 38	0.112676	0.76263595	4.880451	2.87E-06	0.0002219	3.89415	KDEL2	NM_006854.2
cg108833 52	0.112531	0.74360547	3.749645	0.0002591	0.0060919	-0.39884		0
cg251194 15	0.112455	0.54624059	3.975949	0.0001123	0.0033609	0.39019	MNDA	NM_002432.1

cg250729 62	0.112415	0.52475981	5.239526	5.85E-07	8.28E-05	5.42667	MGC35295	NM_152717.1
cg244083 13	0.112384	0.40226995	4.941851	2.19E-06	0.000187	4.15087	BCL2	NT_025028.13
cg116396 51	0.112309	0.57740252	4.053927	8.35E-05	0.0027177	0.6706	HKDC1	NM_025130.2
cg026354 07	0.112212	0.53208514	5.112441	1.03E-06	0.0001142	4.87577	SH3TC1	NM_018986.2
cg247650 79	0.111987	0.41320644	3.875112	0.0001637	0.0043444	0.03402	CDH1	NT_010498.15
cg099370 39	0.111978	0.24342278	5.152338	8.66E-07	0.0001028	5.04774	BATF	NM_006399.2
cg201899 37	0.111704	0.6074047	3.90562	0.0001462	0.0040242	0.14101	L2HGDH	NM_024884.1
cg136960 12	0.111652	0.66541039	4.054501	8.33E-05	0.0027177	0.67268	BPIL1	NM_025227.1
cg261641 84	0.111535	0.68204367	3.739101	0.0002692	0.0062504	-0.43469	FCN2	NM_004108.2
cg159100 79	0.111516	0.45424901	5.168324	8.06E-07	9.79E-05	5.11689	RNASE3	NM_002935.2
cg030037 45	0.111468	0.38746284	4.384532	2.28E-05	0.0010464	1.90624	UNQ473	NM_198477.1
cg018354 89	0.111341	0.5086622	4.557639	1.12E-05	0.0006128	2.5824	KRT8	NM_002273.2
cg240127 08	0.111234	0.47104396	5.392692	2.91E-07	5.35E-05	6.10254	HDHD3	NM_031219.2
cg045670 09	0.111099	0.61481342	3.592676	0.0004534	0.0091887	-0.92397	FCGR3B	NM_000570.2
cg149404 20	0.111015	0.60480484	4.384244	2.28E-05	0.0010464	1.90513	IQCF2	NM_203424.1
cg069421 10	0.111006	0.60774144	4.151908	5.73E-05	0.002064	1.02899	INT1	XM_931325.1
cg191112 62	0.11095	0.46497257	4.718363	5.73E-06	0.0003714	3.22741	IGSF9	NM_020789.2
cg164135 35	0.110923	0.75357115	4.995572	1.73E-06	0.0001636	4.37731	TKTL2	NM_032136.3
cg062049 48	0.110921	0.2688341	6.366537	2.63E-09	4.05E-06	10.6765	MARK2	NM_017490.1
cg120191 09	0.110904	0.54575281	3.827719	0.000195	0.004946	-0.13084	AZGP1	NM_001185.2
cg250414 39	0.110685	0.41788779	5.047883	1.38E-06	0.0001385	4.59945	HYLS1	NM_145014.1
cg098010 65	0.110409	0.45108752	5.054231	1.34E-06	0.0001363	4.62651	FAT2	NM_001447.1
cg103182 58	0.110344	0.51064918	4.707128	6.01E-06	0.0003842	3.1818	RIPK3	NM_006871.2
cg244264 05	0.110338	0.38570698	5.94739	2.10E-08	1.05E-05	8.65256	AGR2	NM_006408.2
cg048370 71	0.110326	0.44586618	5.145637	8.92E-07	0.0001037	5.01879	NOXA1	NM_006647.1
cg155037 52	0.110324	0.41070999	4.931203	2.30E-06	0.0001936	4.10619	ST6GALNAC1	NM_018414.2
cg270150 47	0.110246	0.60688965	4.906066	2.56E-06	0.0002035	4.00097	DMBT1	NM_004406.1
cg083194 04	0.110139	0.38960744	5.253254	5.50E-07	7.99E-05	5.48672	THRB	NM_000461.2

cg058200 87	0.109913	0.42262027	4.868973	3.01E-06	0.0002298	3.84641	ATP13A4	NM_032279.2
cg246210 42	0.109891	0.44786534	5.51958	1.62E-07	3.59E-05	6.67203	SERPINA1	NM_000295.3
cg082680 99	0.109889	0.63134689	3.877555	0.0001622	0.0043225	0.04257	OLFM1	NM_014279.2
cg006795 56	0.109778	0.3826898	5.471047	2.02E-07	4.12E-05	6.4532	TRIM31	NM_007028.3
cg222130 42	0.109532	0.60011634	4.219641	4.39E-05	0.0016979	1.28063	CPA2	NM_001869.1
cg021318 53	0.109415	0.39289214	4.991987	1.76E-06	0.0001638	4.36215	FLJ23235	NM_024943.1
cg148942 16	0.109377	0.49560861	4.662679	7.25E-06	0.0004442	3.0021	CATSPER1	NM_053054.2
cg143334 54	0.109348	0.35528171	6.107225	9.60E-09	6.69E-06	9.41508	SFN	NM_006142.3
cg271902 39	0.109271	0.42861049	5.007566	1.65E-06	0.0001582	4.42811	CLEC2A	NM_207375.1
cg208116 07	0.109155	0.63368034	4.480391	1.54E-05	0.0007835	2.27825	SMPD2	NM_003080.1
cg018885 66	0.108874	0.23142025	5.011979	1.61E-06	0.000156	4.44682	MEST	NT_007933.14
cg068009 62	0.108765	0.29126032	6.843222	2.28E-10	2.01E-06	13.0676	TM4SF1	NM_014220.2
cg164834 66	0.108625	0.63272225	3.944005	0.0001266	0.0036456	0.27658	C20orf186	NM_182519.1
cg013480 86	0.108604	0.36261267	4.393276	2.20E-05	0.0010296	1.93992	RGS14	NM_006480.4
cg021968 05	0.108353	0.50102336	4.758203	4.84E-06	0.0003314	3.3898	CSF2	NM_000758.2
cg159835 20	0.108278	0.54160739	4.218557	4.41E-05	0.0017013	1.27657	GPT	NM_005309.1
cg158560 55	0.108132	0.29255882	6.351016	2.85E-09	4.05E-06	10.6002	ZNF511	NM_145806.2
cg051873 22	0.1081	0.70470114	3.692995	0.0003177	0.0070349	-0.59049	CARD14	NM_024110.2
cg159835 38	0.108078	0.58590834	3.886025	0.0001572	0.004231	0.07222	SEMA4A	NM_022367.2
cg041117 61	0.108075	0.40997744	5.583145	1.20E-07	2.94E-05	6.96048	CCR3	NM_001837.2
cg204851 65	0.107954	0.55699639	4.056195	8.28E-05	0.0027042	0.67882	WFDC12	NM_080869.1
cg167310 16	0.107854	0.74579619	4.141135	5.97E-05	0.002131	0.98926	LGALS4	NM_006149.2
cg104123 12	0.107847	0.54345839	4.917498	2.44E-06	0.0001975	4.04878	FLJ36004	NM_152590.1
cg158409 85	0.10782	0.42190142	6.210758	5.75E-09	5.04E-06	9.91519	OSBPL10	NM_017784.3
cg208280 84	0.107738	0.66344368	4.942877	2.18E-06	0.000187	4.15518	KIAA1199	NM_018689.1
cg199983 28	0.10772	0.66087362	4.67806	6.80E-06	0.0004216	3.06414	LOC90580	NM_138358.2
cg012148 47	0.107531	0.55945528	4.78301	4.36E-06	0.0003068	3.4914	TMPRSS3	NM_024022.1
cg079558 87	0.107431	0.65277039	4.389797	2.23E-05	0.0010405	1.92651	KIAA0802	NM_015210.1

cg185524 13	0.107154	0.32706466	4.695468	6.32E-06	0.0003983	3.13453	DARC	NM_002036.2
cg110969 93	0.107127	0.37037045	6.085366	1.07E-08	6.75E-06	9.31011	ACY3	NM_080658.1
cg033439 42	0.107069	0.50137018	4.156484	5.62E-05	0.0020324	1.04589	SLC39A5	NM_173596.1
cg211053 18	0.106967	0.55261257	4.666634	7.13E-06	0.0004403	3.01804	ITGB6	NM_000888.3
cg261919 51	0.106683	0.46334698	5.178073	7.71E-07	9.46E-05	5.15914	RNASE2	NM_002934.2
cg216046 15	0.106588	0.24062022	6.090433	1.04E-08	6.74E-06	9.33442	SYTL1	NM_032872.1
cg041170 29	0.106584	0.5940758	3.852867	0.0001777	0.0046285	-0.04356	UROS	NM_000375.1
cg267678 97	0.106531	0.65687892	4.204787	4.68E-05	0.0017777	1.22834	XDH	NM_000379.2
cg236254 58	0.106447	0.74984866	4.466691	1.63E-05	0.0008205	2.22471	AFAR3	NM_201252.1
cg243311 62	0.106341	0.5572274	4.854684	3.20E-06	0.0002437	3.78709	SYT8	NM_138567.2
cg236133 17	0.106269	0.6050207	4.404554	2.10E-05	0.0009924	1.98344	LARP1	NM_033551.2
cg137970 31	0.106234	0.61547335	3.747966	0.0002614	0.0061213	-0.40482	NIPSNAP1	NM_003634.1
cg245129 73	0.10623	0.62564097	3.904155	0.000147	0.0040378	0.13586	MUC1	NM_002456.4
cg028337 25	0.106112	0.41403685	4.563981	1.09E-05	0.0006027	2.60754	ISG20L2	NM_030980.1
cg210666 36	0.106017	0.31787607	5.259734	5.34E-07	7.85E-05	5.5151	TM4SF5	NM_003963.2
cg218174 50	0.105987	0.60319493	4.406154	2.09E-05	0.0009896	1.98962	PIG38	NM_017993.1
cg253910 23	0.105895	0.47900405	4.63571	8.12E-06	0.0004854	2.89367	BTNL2	NM_019602.1
cg011092 19	0.105834	0.51853808	3.987442	0.0001075	0.0032624	0.43126	RASGRP3	NM_170672.1
cg049565 11	0.105787	0.38813144	5.059794	1.31E-06	0.0001352	4.65025	PTPN6	NM_002831.3
cg101508 13	0.105752	0.28649736	6.889196	1.79E-10	2.01E-06	13.3028	KIAA0746	NM_015187.1
cg216156 63	0.105713	0.63640945	4.61601	8.82E-06	0.0005098	2.81476	MGC35048	NM_153208.1
cg199872 19	0.105454	0.70027622	3.885979	0.0001572	0.004231	0.07206	FLJ32011	NM_182516.1
cg038176 21	0.105338	0.57094553	5.527011	1.63E-07	3.59E-05	6.68449	ACF	NM_014576.2
cg031167 40	0.105262	0.66609608	4.018282	9.57E-05	0.0030136	0.54189	TSPAN4	NM_003271.4
cg250812 01	0.10522	0.73302105	4.237267	4.10E-05	0.0016111	1.34662	FXD4	NM_173160.2
cg136440 52	0.105201	0.68151647	4.264812	3.68E-05	0.0014802	1.45018	PAQR4	NM_152341.2
cg092057 51	0.105122	0.68612616	3.704077	0.0003054	0.0068718	-0.55318	NALP6	NM_138329.1
cg098161 80	0.104654	0.57298038	5.149945	8.75E-07	0.000103	5.0374	GC	NM_000583.2

cg242113 88	0.104486	0.61562959	4.508009	1.38E-05	0.0007133	2.38655	AIF1	NM_032955.1
cg073375 98	0.104479	0.50633751	4.993687	1.75E-06	0.0001636	4.36934	ANXA9	NM_003568.1
cg199103 82	0.104475	0.67719791	3.639657	0.0003842	0.0080955	-0.76873	FABP1	NM_001443.1
cg215504 42	0.104445	0.55351295	4.081697	7.51E-05	0.0025305	0.77149	FLJ36445	NM_153233.1
cg254065 18	0.104435	0.4686872	3.807792	0.0002097	0.0052453	-0.19966	DAK	NM_015533.2
cg201319 68	0.104335	0.3865882	4.528288	1.27E-05	0.0006706	2.46638	CCDC47	NM_020198.1
cg136762 15	0.104214	0.26725852	5.504109	1.74E-07	3.74E-05	6.60214	AHR	NM_001621.2
cg275137 64	0.104167	0.58067299	4.000616	0.0001023	0.0031398	0.47843	EFCAB3	NM_173503.1
cg052447 66	0.103901	0.64053878	3.914135	0.0001416	0.0039312	0.17099	GSTP1	NM_000852.2
cg003922 57	0.103864	0.38623576	4.614658	8.91E-06	0.0005132	2.80652	ISG20L2	NM_030980.1
cg031025 16	0.10384	0.51537031	5.896521	2.69E-08	1.18E-05	8.41237	LINCR	XM_930227.1
cg004662 49	0.103827	0.40844458	5.526307	1.57E-07	3.59E-05	6.70245	MGC15523	NM_138570.1
cg040578 58	0.103753	0.53350092	4.338642	2.75E-05	0.0011997	1.733	UNQ9391	NM_198464.1
cg183124 29	0.103715	0.4794591	5.386823	2.99E-07	5.41E-05	6.0764	SLC10A2	NM_000452.1
cg244276 60	0.10357	0.52225275	3.824712	0.0001971	0.0049866	-0.14124	PNPLA2	NM_020376.2
cg239785 57	0.103533	0.57145625	4.324771	2.90E-05	0.0012359	1.67739	SMPD2	NM_003080.1
cg265451 62	0.10342	0.4397651	4.408214	2.07E-05	0.0009832	1.99758	LGICZ1	NM_180990.2
cg270900 87	0.103372	0.39508974	6.211098	5.74E-09	5.04E-06	9.91684	TINAG	NM_014464.2
cg144018 37	0.103357	0.51620964	3.616432	0.0004171	0.0086302	-0.84568	GPR154	NM_207173.1
cg133647 56	0.103327	0.66422338	4.323452	2.91E-05	0.0012382	1.67236	CYP3A43	NM_022820.3
cg128271 88	0.10327	0.40431672	5.754135	5.34E-08	1.81E-05	7.74667	FGA	NM_000508.3
cg130385 60	0.103238	0.69216845	3.999408	0.0001028	0.0031469	0.4741	FLJ22555	NM_024520.1
cg148266 83	0.103223	0.51590972	4.076243	7.67E-05	0.0025641	0.75164	SPRR2D	NM_006945.3
cg179989 64	0.10316	0.21243066	5.874769	2.99E-08	1.24E-05	8.31004	MARK2	NM_017490.1
cg122372 69	0.103112	0.49061503	5.088284	1.15E-06	0.0001235	4.77209	SLN	NM_003063.1
cg073273 47	0.102918	0.46961894	4.039815	8.81E-05	0.0028402	0.61954	AQP8	NM_001169.2
cg227181 39	0.102784	0.72045268	3.693937	0.0003167	0.007023	-0.58732	HMGCS2	NM_005518.2
cg118712 80	0.102724	0.71328129	3.742804	0.0002656	0.0062005	-0.42211	SLC16A7	NM_004731.3

cg152286 39	0.102705	0.48151074	4.156632	5.62E-05	0.0020324	1.04644	PLA2G4E	NM_198442.1
cg144813 39	0.10261	0.63547655	4.026836	9.26E-05	0.0029482	0.5727	KCNJ1	NM_000220.2
cg019416 19	0.1026	0.55792128	4.772841	4.55E-06	0.0003171	3.44971	MEP1B	NM_005925.1
cg125479 30	0.1025	0.56602643	4.321585	2.93E-05	0.0012434	1.66525	WFDC6	NM_080827.1
cg136035 51	0.102489	0.5286919	4.81649	3.77E-06	0.0002769	3.62913	ABP1	NM_001091.2
cg203126 87	0.102478	0.52026344	3.739732	0.0002686	0.0062458	-0.43255	DEFB118	NM_054112.1
cg105253 72	0.102458	0.59506675	4.997533	1.72E-06	0.0001633	4.38561	WISP3	NM_003880.2
cg212817 99	0.10228	0.58132455	4.018236	9.57E-05	0.0030136	0.54172	DYRK2	NM_003583.2
cg021929 65	0.102257	0.5430078	3.703208	0.0003063	0.0068757	-0.55611	SLC3A1	NM_000341.2
cg006893 40	0.102211	0.35961786	4.271855	3.58E-05	0.0014505	1.47675	RTKN	NM_033046.2
cg242696 57	0.101958	0.52548721	4.416606	2.00E-05	0.0009606	2.03004	F7	NM_000131.2
cg135074 29	0.101886	0.48432314	4.925287	2.36E-06	0.0001936	4.08139	KLHDC7A	NM_152375.1
cg172592 65	0.101872	0.62058406	4.463631	1.65E-05	0.0008263	2.21278	HYLS1	NM_145014.1
cg066502 60	0.101865	0.63438161	3.725746	0.0002825	0.0064665	-0.47998	NR0B2	NM_021969.1
cg130155 34	0.10177	0.36992581	6.12009	9.01E-09	6.45E-06	9.47697	ST6GALNAC1	NM_018414.2
cg194217 52	0.101727	0.38785598	4.229933	4.22E-05	0.0016509	1.31914	SLC6A18	NM_182632.1
cg249494 88	0.101664	0.51628634	3.623332	0.000407	0.0084557	-0.82287	DNTT	NM_004088.3
cg255118 07	0.101611	0.3945295	4.70928	5.96E-06	0.0003821	3.19053	MMP7	NM_002423.3
cg111471 93	0.101573	0.41564494	4.21632	4.45E-05	0.0017113	1.26822	HPCAL1	NM_002149.2
cg004110 97	0.101502	0.38885848	5.730039	5.99E-08	1.94E-05	7.63499	MGC9712	NM_152689.2
cg201610 89	0.101459	0.50386811	4.471909	1.60E-05	0.0008065	2.24509	IFI27	NM_005532.3
cg194858 04	0.101438	0.570621	4.283645	3.41E-05	0.0013997	1.52129	NGEF	NM_019850.1
cg170952 79	0.101424	0.53042181	4.972019	1.92E-06	0.0001721	4.27782	APOH	NM_000042.1
cg164467 83	0.101421	0.52718763	4.462534	1.66E-05	0.0008273	2.20849	MRGPRX4	NM_054032.2
cg240884 38	0.101405	0.27752581	3.691751	0.0003192	0.0070444	-0.59467	URP2	NM_031471.4
cg129512 82	0.101343	0.2899924	4.383639	2.29E-05	0.0010464	1.9028	ASGR2	NM_001181.2
cg197958 98	0.101323	0.52867238	3.607857	0.0004299	0.0088192	-0.87399	KIAA1984	NM_032874.2
cg035621 20	0.101308	0.40508747	3.81883	0.0002014	0.0050759	-0.16158	WISP2	NM_003881.2

cg039968 22	0.101078	0.32966398	5.676979	7.71E-08	2.17E-05	7.3901	RASSF6	NM_201431.1
cg104149 46	0.101078	0.490747	3.906432	0.0001457	0.0040162	0.14387	MS4A2	NM_000139.2
cg066920 50	0.101073	0.67171823	3.595848	0.0004484	0.0091218	-0.91354	SFRP5	NM_003015.2
cg209107 46	0.101046	0.56327872	4.760383	4.80E-06	0.0003292	3.39871	BBOX1	NM_003986.1
cg224154 72	0.101031	0.63463143	4.388669	2.24E-05	0.0010416	1.92217	SLC5A7	NM_021815.2
cg178907 64	0.100943	0.40481893	4.492069	1.47E-05	0.0007492	2.32398	ITIH4	NM_002218.3
cg056563 64	0.100907	0.24022662	5.872478	3.02E-08	1.24E-05	8.29927	VAMP8	NM_003761.2
cg226274 27	0.100745	0.64682606	4.096817	7.09E-05	0.0024245	0.82666	C11orf9	NM_013279.1
cg029155 44	0.100617	0.47833105	4.929128	2.32E-06	0.0001936	4.09749	PSMAL	NM_153696.2
cg196901 01	0.100581	0.75790992	4.013646	9.74E-05	0.0030485	0.52521	DHX57	NM_144995.2
cg078101 56	0.100522	0.58715477	4.172161	5.29E-05	0.0019485	1.1039	PDZK1IP1	NM_005764.3
cg036091 02	0.100466	0.43224849	4.740031	5.23E-06	0.0003507	3.31561	MUC5B	XM_039877.12
cg094252 28	0.100397	0.63032327	4.848708	3.29E-06	0.0002481	3.76232	CCL20	NM_004591.1
cg197560 68	0.100347	0.49096826	4.186482	5.00E-05	0.0018666	1.15704	CYP2B6	NM_000767.4
cg168623 61	0.100344	0.51435438	4.936115	2.25E-06	0.000191	4.12679	XDH	NM_000379.2
cg151752 66	0.100255	0.50289878	4.233917	4.15E-05	0.00163	1.33406	CDH12	NM_004061.2
cg237321 82	0.100119	0.5163638	5.244683	5.71E-07	8.14E-05	5.44921	C21orf84	NM_153752.1
cg266564 52	0.100079	0.64617222	4.117649	6.54E-05	0.0022876	0.90292	HABP2	NM_004132.2
cg204068 78	0.100067	0.59530266	4.679447	6.80E-06	0.0004216	3.06666	NR5A2	NM_003822.3
cg007506 06	0.100028	0.49257178	4.038294	8.87E-05	0.0028514	0.61404	CDA	NM_001785.1
cg148931 29	0.100007	0.66643792	3.733942	0.0002743	0.0063387	-0.4522	CARD14	NM_024110.2
cg230920 86	0.100001	0.62396627	4.756377	4.88E-06	0.0003322	3.38233	CES7	NM_145024.1

Figure 15

Hypomethylated in invasive-subtype								
ID	beta_dif	AveExpr	t	P.Value	adj.P.Val	B	Gene	GeneBank_Acc
cg028445 45	-0.101005942	0.491116	-4.409459	2.06E-05	0.00098	2.002395	GCM2	NM_004752.1
cg250472 80	-0.101125889	0.425005	-3.958474	0.0001199	0.0035453	0.327949	HOXA9	NM_152739.2
cg003638 13	-0.102115769	0.537464	-4.6278	8.44E-06	0.0004945	2.86356	HOM-TES-103	NM_015438.1
cg077524 20	-0.102479122	0.398149	-4.077013	7.65E-05	0.0025641	0.754441	CDKN2A	NT_008413.17
cg194665 63	-0.103365916	0.511383	-5.03206	1.48E-06	0.0001466	4.532088	SPARCL1	NM_004684.2
cg149180 82	-0.103785686	0.768199	-5.722549	6.20E-08	1.94E-05	7.60034	KCNAB3	NM_004732.2
cg108945 12	-0.104177533	0.704685	-5.952531	2.05E-08	1.04E-05	8.676895	ACTA2	NM_001613.1
cg204426 97	-0.105067009	0.578406	-4.07015	7.85E-05	0.0026083	0.729478	LRRC17	NM_005824.1
cg172413 10	-0.105354773	0.446123	-3.924069	0.0001364	0.0038363	0.206037	BARHL2	NM_020063.1
cg215427 93	-0.105501078	0.530567	-3.7973	0.0002179	0.0054017	-0.235789	ADRA2B	NM_000682.4
cg229338 47	-0.106043526	0.37112	-4.295029	3.26E-05	0.0013558	1.564384	MRGPRF	NM_145015.2
cg039343 54	-0.106152124	0.73029	-6.205584	5.90E-09	5.04E-06	9.890082	C1QTNF3	NM_181435.4
cg013818 46	-0.106577202	0.563098	-3.754416	0.0002547	0.0060018	-0.382593	HOXA9	NM_152739.2
cg102362 39	-0.107501751	0.455587	-4.739149	5.25E-06	0.0003512	3.31201	SULT1C2	NM_006588.2
cg162321 26	-0.108344699	0.4394	-3.790032	0.0002238	0.0054931	-0.260762	SLC5A7	NM_021815.2
cg036624 59	-0.108478688	0.699037	-6.785391	3.08E-10	2.04E-06	12.77282	IL11RA	NM_004512.3
cg212011 09	-0.108742404	0.693439	-6.257991	4.54E-09	4.63E-06	10.14491	ANKRD25	NM_015493.4
cg222898 37	-0.109308925	0.437739	-4.630993	8.28E-06	0.0004896	2.874755	CA3	NM_005181.2
cg019881 29	-0.109826288	0.623355	-3.727405	0.0002808	0.0064413	-0.474361	ADHFE1	NM_144650.1
cg123747 21	-0.111398089	0.525082	-3.696645	0.0003136	0.0069974	-0.57821	PRAC	NM_032391.2
cg108955 43	-0.111512723	0.28413	-4.321191	2.94E-05	0.0012434	1.663754	CDKN2A	NT_008413.17
cg127277 95	-0.11187947	0.246915	-3.593922	0.0004515	0.0091695	-0.919875	PDGFRB	NM_002609.3
cg043967 91	-0.112343335	0.491087	-4.274223	3.54E-05	0.0014391	1.485687	SHANK2	NM_012309.1
cg055216 96	-0.11464914	0.457591	-4.07594	7.68E-05	0.0025641	0.750535	SLC2A14	NM_153449.2
cg112131 50	-0.115217219	0.600736	-5.14258	9.04E-07	0.0001037	5.005596	ANGPTL2	NM_012098.2

cg258020 93	-0.11577371	0.55524	-3.574103	0.0004839	0.0096591	-0.984876	SPAG6	NM_012443.2
cg005736 06	-0.116059184	0.578023	-4.158545	5.58E-05	0.0020244	1.053506	COL6A3	NM_004369.2
cg068129 77	-0.117489609	0.539637	-4.190289	4.93E-05	0.0018495	1.171192	C10orf59	NM_00103170 9.1
cg013544 73	-0.120280876	0.536634	-4.069847	7.86E-05	0.0026083	0.728375	HOXA9	NM_152739.2
cg052211 67	-0.120507428	0.321466	-4.012143	9.79E-05	0.0030623	0.519812	ZNF560	NM_152476.1
cg242154 43	-0.122817895	0.512594	-4.993009	1.75E-06	0.0001636	4.366476	TCF21	NM_003206.2
cg187509 60	-0.123414845	0.414829	-4.174933	5.23E-05	0.001931	1.114175	HOXD4	NM_014621.2
cg235718 57	-0.123595002	0.579509	-4.790654	4.22E-06	0.0003002	3.52279	BIRC4BP	NM_017523.2
cg177061 73	-0.125614983	0.518238	-5.524428	1.58E-07	3.59E-05	6.693951	C16orf30	NM_024600.1
cg069811 82	-0.127600664	0.443616	-4.305571	3.13E-05	0.0013067	1.604368	C10orf59	NM_00103170 9.1
cg103624 75	-0.129941974	0.665092	-4.972258	1.92E-06	0.0001721	4.278831	SHANK2	NM_012309.1
cg238572 26	-0.129959661	0.345426	-3.808157	0.0002094	0.0052433	-0.198406	ZNF671	NM_024833.1
cg203115 01	-0.130334002	0.426995	-3.7316	0.0002766	0.0063869	-0.460143	APC	NT_034772.5
cg130357 43	-0.130872984	0.535942	-4.88367	2.83E-06	0.0002197	3.907552	PRRT1	NM_030651.2
cg008423 51	-0.131005897	0.481098	-4.706307	6.03E-06	0.0003842	3.178465	TJP2	NM_201629.1
cg243324 22	-0.131442333	0.377335	-4.171908	5.30E-05	0.0019485	1.102964	APC	NM_000038.3
cg262673 10	-0.13146725	0.306016	-4.279243	3.47E-05	0.0014151	1.504645	DHRS10	NM_016246.2
cg016838 83	-0.131632177	0.522838	-4.91857	2.44E-06	0.0001975	4.049178	CMTM2	NM_144673.2
cg243358 95	-0.13163705	0.508822	-5.216672	6.48E-07	8.79E-05	5.326929	COX7A1	NM_001864.2
cg150206 45	-0.132602909	0.400843	-3.875584	0.0001634	0.0043411	0.035674	APC	NM_000038.3
cg069588 29	-0.133067661	0.601855	-4.949743	2.12E-06	0.0001834	4.184026	CHAD	NM_001267.1
cg038741 99	-0.133368693	0.348442	-3.80882	0.0002089	0.0052355	-0.196121	HOXD12	NM_021193.2
cg013353 67	-0.134895511	0.49058	-4.230825	4.21E-05	0.0016476	1.322476	C12orf34	NM_032829.1
cg216346 02	-0.136227642	0.451729	-4.044981	8.64E-05	0.0028018	0.638211	APC	NM_000038.3
cg203086 79	-0.136978142	0.333598	-4.491793	1.47E-05	0.0007492	2.322904	FRZB	NM_001463.2
cg090997 44	-0.138471309	0.323275	-4.192606	4.89E-05	0.0018391	1.179808	CDKN2A	NT_008413.17
cg186749 80	-0.140485358	0.434377	-4.628929	8.35E-06	0.0004927	2.866485	CA3	NM_005181.2
cg086687 90	-0.14069338	0.471989	-4.569026	1.07E-05	0.0005915	2.627558	ZNF154	NM_003444.1

cg014935 17	-0.143279851	0.480046	-5.212234	6.62E-07	8.82E-05	5.307595	HOM-TES- 103	NM_015438.1
cg217906 26	-0.148269412	0.470127	-3.949565	0.000124	0.0036017	0.296299	ZNF154	NM_003444.1
cg149914 87	-0.148609709	0.540831	-3.894046	0.0001526	0.0041537	0.100344	HOXD9	NM_014213.2
cg077780 29	-0.149026219	0.361239	-4.3328	2.81E-05	0.0012142	1.707996	HOXA9	NM_152739.2
cg261135 12	-0.154789551	0.350771	-4.058359	8.21E-05	0.0026908	0.686666	VILL	NM_015873.2
cg227408 35	-0.155085674	0.644663	-6.090424	1.04E-08	6.74E-06	9.33438	DDR2	NM_006182.2
cg169702 32	-0.155859437	0.524028	-4.187277	4.99E-05	0.0018635	1.159997	APC	NT_034772.5
cg053452 86	-0.168656572	0.493707	-5.091168	1.14E-06	0.0001224	4.784454	MDFI	NM_005586.2
cg271887 03	-0.192322416	0.547225	-5.379898	3.08E-07	5.48E-05	6.045594	FAIM2	NM_012306.2

Figure 16

Hypermethylated in proliferative-subtype								
ID	beta_dif	AveExpr	t	P.Value	adj.P.Val	B	Gene	GeneBank_Acc
cg21790626	0.191074	0.47012689	5.545484	1.43E-07	2.44E-05	6.75775	ZNF154	NM_003444.1
cg08668790	0.17616	0.47198899	6.285347	3.96E-09	2.72E-06	10.2491	ZNF154	NM_003444.1
cg27188703	0.175692	0.54722515	5.058539	1.31E-06	9.22E-05	4.61196	FAIM2	NM_012306.2
cg09099744	0.169253	0.32327529	5.548562	1.41E-07	2.43E-05	6.77172	CDKN2A	NT_008413.17
cg07778029	0.169171	0.36123919	5.255369	5.44E-07	5.12E-05	5.46358	HOXA9	NM_152739.2
cg23857226	0.165725	0.34542585	5.261589	5.29E-07	5.08E-05	5.49085	ZNF671	NM_024833.1
cg16970232	0.164251	0.52402792	4.647199	7.74E-06	0.0002835	2.90583	APC	NT_034772.5
cg12874092	0.164093	0.33214203	3.976442	0.0001121	0.0019043	0.35647	VIM	NM_003380.2
cg03874199	0.158097	0.34844152	4.827066	3.61E-06	0.0001749	3.63925	HOXD12	NM_021193.2
cg14991487	0.157556	0.5408314	4.34377	2.68E-05	0.0006871	1.7152	HOXD9	NM_014213.2
cg20311501	0.155889	0.42699469	4.77318	4.54E-06	0.0002018	3.41743	APC	NT_034772.5
cg25438963	0.155727	0.23661413	4.661466	7.29E-06	0.000273	2.96327	HIST1H3C	NM_003531.2
cg08090772	0.155094	0.38886913	5.266395	5.18E-07	5.01E-05	5.51193	ADHFE1	NM_144650.1
cg24332422	0.154973	0.37733543	5.283277	4.80E-07	4.77E-05	5.58609	APC	NM_000038.3
cg15020645	0.154161	0.4008429	4.806007	3.95E-06	0.0001854	3.55235	APC	NM_000038.3
cg13577076	0.153819	0.5287834	4.12242	6.42E-05	0.001285	0.88525	PRKAR1B	NM_002735.1
cg20308679	0.150603	0.33359775	5.253147	5.50E-07	5.13E-05	5.45385	FRZB	NM_001463.2
cg05345286	0.150391	0.49370673	4.659383	7.35E-06	0.0002744	2.95487	MDFI	NM_005586.2
cg06981182	0.146368	0.4436161	5.286216	4.73E-07	4.77E-05	5.59902	C10orf59	NM_001031709.1
cg10362475	0.146336	0.66509159	6.024376	1.44E-08	5.62E-06	8.98824	SHANK2	NM_012309.1
cg17602451	0.146032	0.346653	4.776764	4.47E-06	0.0002001	3.43213	BCL2	NT_025028.13
cg21634602	0.145897	0.45172948	4.569207	1.07E-05	0.0003515	2.59411	APC	NM_000038.3
cg24446548	0.144994	0.48049246	3.464112	0.0007079	0.0075235	-1.37666	TWIST1	NM_000474.3
cg06812977	0.144	0.53963723	5.563763	1.31E-07	2.34E-05	6.84078	C10orf59	NM_001031709.1
cg18674980	0.142493	0.43437661	4.924343	2.37E-06	0.0001345	4.04416	CA3	NM_005181.2
cg19246110	0.141745	0.40161715	3.790905	0.0002231	0.0031935	-0.29363	ZNF671	NM_024833.1

cg014935 17	0.14093	0.48004616	5.354413	3.47E-07	3.95E-05	5.90031	HOM-TES-103	NM_015438.1
cg123747 21	0.138499	0.52508241	4.944556	2.17E-06	0.0001302	4.129	PRAC	NM_032391.2
cg012952 03	0.13849	0.448848	3.741787	0.0002666	0.0036441	-0.46153	PRDM14	NM_024504.2
cg202862 00	0.137658	0.35974919	3.704315	0.0003051	0.004028	-0.58841	EYA4	NM_004100.2
cg010495 30	0.137475	0.44364271	3.516795	0.0005906	0.0065423	-1.20754	BMP3	NM_001201.1
cg242154 43	0.137286	0.51259424	5.99464	1.67E-08	6.00E-06	8.84653	TCF21	NM_003206.2
cg157318 15	0.136494	0.49473822	4.725727	5.56E-06	0.0002254	3.22357	C1orf188	NM_173795.2
cg046604 10	0.135307	0.30883835	3.727431	0.0002808	0.0037922	-0.51026	VILL	NM_015873.2
cg243358 95	0.13527	0.50882174	5.652466	8.65E-08	1.78E-05	7.24618	COX7A1	NM_001864.2
cg203304 72	0.134316	0.35719712	3.853279	0.0001774	0.0027089	-0.07786	EYA4	NT_025741.14
cg261135 12	0.134131	0.35077072	3.616231	0.0004174	0.0050499	-0.88255	VILL	NM_015873.2
cg019881 29	0.133627	0.62335525	4.863646	3.08E-06	0.0001552	3.79084	ADHFE1	NM_144650.1
cg013353 67	0.133534	0.49058017	4.371221	2.40E-05	0.0006357	1.82043	C12orf34	NM_032829.1
cg199884 49	0.133402	0.43727468	4.20861	4.59E-05	0.0010206	1.20444	BNC1	NM_001717.2
cg258020 93	0.132422	0.55524006	4.333836	2.79E-05	0.0007095	1.67724	SPAG6	NM_012443.2
cg155408 20	0.131868	0.44477745	4.660004	7.33E-06	0.0002743	2.95738	EOMES	NM_005442.2
cg052211 67	0.131144	0.32146598	4.615292	8.84E-06	0.0003086	2.77784	ZNF560	NM_152476.1
cg016838 83	0.130022	0.52283805	5.071747	1.25E-06	8.96E-05	4.66421	CMTM2	NM_144673.2
cg043967 91	0.128845	0.49108655	5.244397	5.72E-07	5.28E-05	5.41553	SHANK2	NM_012309.1
cg194028 85	0.1288	0.34803769	3.837948	0.0001878	0.0028207	-0.13116	PTPRO	NM_002848.2
cg187509 60	0.128007	0.41482875	4.54904	1.16E-05	0.0003736	2.51414	HOXD4	NM_014621.2
cg220292 75	0.127449	0.46886949	3.387505	0.0009179	0.0090852	-1.61874	FLJ25477	NM_199138.1
cg008423 51	0.127447	0.48109831	4.769096	4.62E-06	0.000204	3.40069	TJP2	NM_201629.1
cg183498 35	0.127238	0.34561254	3.722357	0.000286	0.0038445	-0.52745	VIPR2	NM_003382.3
cg209598 66	0.126682	0.44274125	3.842849	0.0001844	0.0027877	-0.11414	AJAP1	NM_018836.2
cg150871 47	0.126457	0.35001121	4.80081	4.04E-06	0.0001876	3.53095	LRRC4	NM_022143.3
cg108955 43	0.126379	0.28413	5.230238	6.10E-07	5.48E-05	5.35363	CDKN2A	NT_008413.17
cg069588 29	0.125176	0.60185522	4.822694	3.67E-06	0.0001763	3.62119	CHAD	NM_001267.1

cg076361 78	0.124979	0.14148165	4.803464	3.99E-06	0.0001864	3.54188	HIST1H3C	NM_003531.2
cg189526 47	0.12429	0.41797053	3.888567	0.0001557	0.0024683	0.04546	BNC1	NM_001717.2
cg013544 73	0.123894	0.53663449	4.397306	2.16E-05	0.0005886	1.92089	HOXA9	NM_152739.2
cg261625 82	0.123502	0.47559628	3.633447	0.0003927	0.0048382	-0.82552	KCNA6	NM_002235.2
cg197513 00	0.122456	0.32534831	4.979536	1.86E-06	0.0001157	4.2764	ST8SIA5	NM_013305.3
cg212502 96	0.12239	0.18921135	3.937071	0.00013	0.0021544	0.21644	HIST1H2BB	NM_021062.2
cg229338 47	0.121409	0.37112031	5.260488	5.32E-07	5.09E-05	5.48602	MRGPRF	NM_145015.2
cg222898 37	0.121218	0.43773896	5.480767	1.94E-07	2.94E-05	6.46516	CA3	NM_005181.2
cg258752 13	0.121107	0.40116948	3.565581	0.0004985	0.0057964	-1.04903	FLJ37549	NM_152605.2
cg204917 07	0.120506	0.39025763	4.029037	9.18E-05	0.0016547	0.54525	PPYR1	NM_005972.3
cg039430 81	0.120454	0.39721143	3.846005	0.0001823	0.002762	-0.10317	TCERG1L	NM_174937.1
cg002404 32	0.120351	0.24223207	3.937031	0.00013	0.0021544	0.2163	TWIST1	NM_000474.3
cg026223 16	0.119744	0.23073733	3.803283	0.0002132	0.0030909	-0.25104	ZNF96	NM_014724.2
cg051591 88	0.118224	0.27243395	3.818243	0.0002018	0.0029688	-0.19941	HIST1H4F	NM_003540.3
cg073070 78	0.118024	0.32664654	3.695759	0.0003146	0.004121	-0.61724	TUBB6	NM_032525.1
cg174835 10	0.117424	0.31320936	3.417107	0.0008338	0.0085019	-1.52127	GNB4	NM_021629.2
cg077524 20	0.117051	0.39814927	4.965167	1.98E-06	0.0001221	4.21577	CDKN2A	NT_008413.17
cg128806 58	0.116756	0.38376105	4.166609	5.41E-05	0.0011448	1.04825	CDO1	NM_001801.2
cg069087 78	0.116216	0.50805784	4.815221	3.79E-06	0.0001808	3.59034	SPAG6	NM_012443.2
cg104572 47	0.116154	0.30683746	4.822677	3.68E-06	0.0001763	3.62112	PRDM14	NM_024504.2
cg187228 41	0.116006	0.39789151	4.155199	5.65E-05	0.0011779	1.00604	PHOX2A	NM_005169.2
cg013818 46	0.114526	0.56309775	4.24854	3.92E-05	0.0009097	1.35404	HOXA9	NM_152739.2
cg271967 45	0.11443	0.38787897	3.45642	0.0007267	0.0076593	-1.40117	PTPRO	NM_002848.2
cg096435 44	0.113932	0.48815645	3.877612	0.0001622	0.0025372	0.00708	ZNF177	NM_003451.1
cg267803 33	0.113749	0.22821876	5.40625	2.73E-07	3.46E-05	6.131	ACOT4	NM_152331.2
cg250472 80	0.113231	0.42500456	4.703622	6.10E-06	0.0002398	3.13374	HOXA9	NM_152739.2
cg115406 92	0.113102	0.41158034	6.28178	4.03E-09	2.72E-06	10.2317	SIM1	NM_005068.2
cg219075 79	0.112709	0.36134045	4.632792	8.22E-06	0.0002959	2.84796	TBX5	NM_080718.1

cg215917 42	0.112007	0.44746151	4.613148	8.92E-06	0.0003089	2.76926	HOXD10	NM_002148.2
cg113947 85	0.110789	0.40250223	4.051334	8.44E-05	0.0015613	0.62588	LTC4S	NM_145867.1
cg120737 79	0.11031	0.35450308	4.386863	2.26E-05	0.0006065	1.88062	CRYGD	NM_006891.2
cg128658 37	0.110249	0.37797291	5.38804	2.97E-07	3.61E-05	6.04979	SIM1	NM_005068.2
cg267212 64	0.109975	0.41476376	3.592634	0.0004535	0.0054091	-0.96035	GALR1	NM_001480.2
cg055080 84	0.109631	0.37419172	5.07403	1.23E-06	8.93E-05	4.67819	ZNF667	NM_022103.2
cg082609 59	0.109595	0.28842175	3.61942	0.0004127	0.0050125	-0.872	HIST1H4F	NM_003540.3
cg126993 71	0.109457	0.37511906	4.000429	0.0001024	0.0017923	0.44232	GALR1	NM_001480.2
cg227408 35	0.108205	0.64466286	4.162528	5.49E-05	0.0011576	1.03314	DDR2	NM_006182.2
cg061511 65	0.107795	0.45800324	3.545957	0.0005338	0.0060837	-1.11301	VSX1	NM_014588.4
cg022128 36	0.107515	0.45793632	6.876408	1.92E-10	9.94E-07	13.2101	LY86	NM_004271.3
cg216025 20	0.107358	0.36578837	3.791722	0.0002262	0.0032292	-0.27937	BCL2	NT_025028.13
cg237643 81	0.107332	0.22017112	3.352537	0.0010321	0.0099101	-1.72772	ATRNL1	NM_207303.1
cg266561 35	0.107246	0.39908041	4.066968	7.97E-05	0.0015074	0.68218	EYA4	NM_004100.2
cg181455 05	0.107192	0.28323854	3.501664	0.0006223	0.0068357	-1.25633	GREM1	NM_013372.5
cg028445 45	0.106933	0.49111634	4.927164	2.34E-06	0.0001341	4.05598	GCM2	NM_004752.1
cg231294 78	0.106816	0.28353531	3.712069	0.0002967	0.0039453	-0.56224	ST8SIA5	NM_013305.3
cg104869 98	0.106815	0.40967083	3.993022	0.0001053	0.0018226	0.41577	GALR1	NM_001480.2
cg000058 47	0.106534	0.44517371	4.891453	2.75E-06	0.0001459	3.90553	HOXD3	NM_006898.4
cg223413 10	0.106245	0.48295456	3.695101	0.0003153	0.0041246	-0.61945	ZNF541	NM_032255.1
cg003638 13	0.106032	0.5374636	5.089456	1.15E-06	8.54E-05	4.73998	HOM-TES-103	NM_015438.1
cg044549 51	0.105937	0.34401356	4.320898	2.94E-05	0.0007337	1.6279	UNQ739	NM_198570.1
cg149044 64	0.105795	0.22686411	3.589913	0.0004578	0.005433	-0.96929	NELL2	NM_006159.1
cg079355 68	0.105702	0.41961022	3.806247	0.0002109	0.0030676	-0.24082	MLNR	NM_001507.1
cg172413 10	0.105534	0.44612335	4.106187	6.83E-05	0.0013457	0.82571	BARHL2	NM_020063.1
cg139912 33	0.105155	0.28868545	4.235956	4.12E-05	0.0009461	1.30678	GAS7	NM_003644.2
cg130357 43	0.104986	0.53594164	3.970767	0.0001145	0.0019355	0.33621	PRRT1	NM_030651.2
cg054366 58	0.104253	0.33063957	3.386743	0.0009219	0.0091115	-1.61756	PRKCB1	NM_002738.5

cg010096 64	0.104222	0.56564593	3.771309	0.0002396	0.0033571	-0.36082	TRH	NM_007117.1
cg262673 10	0.103837	0.30601569	3.440992	0.000766	0.0079581	-1.4502	DHRS10	NM_016246.2
cg140469 86	0.103785	0.15766331	3.804756	0.0002126	0.0030844	-0.24573	RCSD1	NM_052862.2
cg193259 85	0.103635	0.35502205	4.934311	2.27E-06	0.0001334	4.08597	HOXD13	NM_000523.2
cg235632 34	0.1036	0.43156452	4.024774	9.33E-05	0.0016749	0.52988	PCDHGB7	NM_018927.2
cg018052 82	0.103389	0.51654489	3.80583	0.0002112	0.0030689	-0.24226	EYA4	NT_025741.14
cg115007 97	0.103341	0.44510864	3.41246	0.0008438	0.0085695	-1.54038	DLX5	NT_007933.14
cg062697 53	0.103152	0.28996131	4.259131	3.76E-05	0.0008799	1.3939	MSC	NM_005098.2
cg175603 32	0.103145	0.43228977	4.419994	1.98E-05	0.0005525	2.00948	BOLL	NM_033030.3
cg126141 05	0.102922	0.41051574	3.808488	0.0002098	0.0030543	-0.23043	NPY	NM_000905.2
cg026200 13	0.102604	0.56525171	4.593222	9.69E-06	0.0003262	2.68968	MLNR	NM_001507.1
cg140376 65	0.102437	0.42962978	3.488337	0.0006528	0.007078	-1.29828	PXDN	XM_935180.1
cg164952 65	0.102228	0.30937005	3.949178	0.0001242	0.0020753	0.25938	HOXB5	NM_002147.2
cg070546 41	0.102222	0.53123826	4.066758	7.95E-05	0.0015055	0.68185	WDR52	NM_018338.2
cg121272 82	0.102107	0.52655441	4.756326	4.88E-06	0.0002088	3.34842	HOXD4	NM_014621.2
cg141161 22	0.102013	0.23636054	3.691189	0.0003198	0.0041704	-0.63261	CART1	NM_006982.1
cg265905 37	0.101963	0.26223308	3.44673	0.0007511	0.0078542	-1.43199	KCNA1	NM_000217.1
cg153431 19	0.101918	0.39456994	3.81055	0.0002076	0.0030314	-0.22598	GALR1	NM_001480.2
cg215427 93	0.101752	0.53056734	3.808932	0.0002088	0.0030427	-0.23156	ADRA2B	NM_000682.4
cg241998 34	0.10164	0.45377664	3.924215	0.0001364	0.0022405	0.17096	POU4F2	NM_004575.1
cg212388 18	0.101507	0.46472346	4.008383	9.93E-05	0.0017482	0.47088	GAL3ST3	NM_033036.1
cg116537 09	0.10146	0.35488084	5.3526	3.50E-07	3.95E-05	5.89226	CDKN2A	NT_008413.17
cg156076 72	0.101018	0.4631843	4.542751	1.19E-05	0.0003795	2.48925	OTX2	NM_021728.2
cg115381 28	0.100495	0.24421826	3.978307	0.0001113	0.0018974	0.36313	ZNF354C	NM_014594.1
cg222436 62	0.100493	0.14739321	3.83289	0.0001913	0.0028632	-0.14871	ATP6V1C2	NM_144583.2
cg081183 11	0.100335	0.41380795	3.619844	0.0004121	0.0050111	-0.8706	SALL3	NM_171999.1

Figure 17

Hypomethylated in proliferative-subtype								
ID	beta_dif	AveExpr	t	P.Value	adj.P.Val	B	Gene	GeneBank_Acc
cg01883966	-0.100043318	0.7859187	-3.901937	0.0001482	0.0023916	0.092422	STK19	NM_032454.1
cg01671881	-0.100055982	0.6179723	-3.675355	0.0003392	0.0043615	-0.685249	C20orf71	NM_178466.2
cg01598642	-0.100065012	0.7160566	-4.55573	1.13E-05	0.0003654	2.540641	HBG1	NM_000559.2
cg11554605	-0.100075218	0.6381739	-3.944754	0.0001263	0.0021047	0.243678	ASB4	NM_145872.1
cg17129388	-0.100099289	0.5189682	-4.116348	6.59E-05	0.0013105	0.862378	NGFR	NM_002507.1
cg08878744	-0.100209086	0.4080681	-4.047754	8.55E-05	0.0015707	0.612907	LCE1B	NM_178349.1
cg07236190	-0.10022001	0.6181344	-3.745439	0.0002631	0.0036144	-0.449103	AMDHD1	NM_152435.1
cg07327347	-0.100334066	0.4696189	-4.101438	6.96E-05	0.0013585	0.808323	AQP8	NM_001169.2
cg12237269	-0.100348506	0.490615	-5.160049	8.36E-07	6.79E-05	5.04842	SLN	NM_003063.1
cg01617750	-0.100433805	0.6049298	-4.560881	1.11E-05	0.0003603	2.561062	CMTM8	NM_178868.3
cg16762386	-0.10047875	0.5444829	-4.135199	6.11E-05	0.0012398	0.932249	NR0B2	NM_021969.1
cg24389359	-0.100532282	0.560962	-4.888975	2.76E-06	0.0001462	3.896281	CCDC63	NM_152591.1
cg25341653	-0.100558432	0.7658828	-4.77161	4.57E-06	0.0002029	3.410994	ELMO3	NM_024712.2
cg14934821	-0.10063871	0.5860271	-3.366831	0.0009839	0.0095666	-1.683287	GPSM1	NM_015597.2
cg04117029	-0.10067187	0.5940758	-3.776509	0.0002351	0.0033117	-0.343023	UROS	NM_000375.1
cg18913951	-0.100731165	0.7984734	-3.992213	0.0001056	0.0018246	0.41287	TMEM45B	NM_138788.2
cg17463527	-0.100740908	0.5471091	-4.213058	4.51E-05	0.0010095	1.221049	SGK2	NM_016276.3
cg20916523	-0.100800242	0.441286	-3.610222	0.0004263	0.0051345	-0.902399	VHL	NT_022517.17
cg01532771	-0.100826576	0.6356666	-4.780003	4.41E-06	0.0001994	3.445422	CLEC4M	NM_014257.3
cg02311163	-0.100832391	0.7426634	-4.448813	1.76E-05	0.0005051	2.120591	SEMG2	NM_003008.2
cg25659818	-0.100840081	0.5917501	-4.261219	3.73E-05	0.0008757	1.401771	CCL4	NM_002984.1
cg24166628	-0.100902448	0.6791835	-4.602187	9.34E-06	0.0003179	2.725455	TNNC1	NM_003280.1
cg07109801	-0.100925251	0.4598413	-4.757519	4.86E-06	0.0002085	3.353295	C3orf60	NM_199069.1
cg25133753	-0.100927873	0.3748278	-4.722591	5.66E-06	0.0002273	3.208144	WFDC11	NM_147197.2
cg02100848	-0.10095044	0.6995796	-4.575794	1.04E-05	0.0003446	2.620291	C3orf32	NM_015931.1
cg13588835	-0.101051399	0.5890859	-4.890094	2.75E-06	0.0001459	3.900949	LGALS7	NM_002307.1

cg041117 61	-0.101141313	0.4099774	-5.400241	2.81E-07	3.51E-05	6.104189	CCR3	NM_001837.2
cg064686 95	-0.101198861	0.7357871	-4.167039	5.40E-05	0.0011448	1.049846	CCDC42	NM_144681.1
cg056740 36	-0.101250613	0.704809	-4.213952	4.49E-05	0.0010088	1.224391	OR3A3	NM_012373.1
cg275923 18	-0.101318827	0.7829002	-3.441447	0.0007648	0.0079571	-1.448757	HEMGN	NM_197978.1
cg175827 77	-0.101363747	0.6193911	-3.813152	0.0002056	0.0030109	-0.216997	EFNA3	NM_004952.3
cg117191 57	-0.101455482	0.5198987	-5.533634	1.51E-07	2.50E-05	6.70401	PITPNA	NM_006224.2
cg092722 56	-0.101483708	0.5787784	-5.263979	5.23E-07	5.04E-05	5.50133	AKR1C4	NM_001818.2
cg067930 62	-0.10151749	0.6462125	-4.122166	6.42E-05	0.0012853	0.884317	CNTNAP4	NM_033401.2
cg172881 21	-0.101606083	0.5943245	-4.609947	9.04E-06	0.0003109	2.756458	DEFB103A	NM_018661.2
cg189922 01	-0.101640287	0.6657396	-4.115151	6.60E-05	0.0013107	0.858566	DPPA2	NM_138815.2
cg168691 08	-0.101663411	0.4821137	-4.394478	2.20E-05	0.0005956	1.908538	VHL	NT_022517.17
cg117593 78	-0.101681688	0.6503505	-4.198206	4.78E-05	0.0010479	1.165637	DPPA2	NM_138815.2
cg231105 14	-0.101764909	0.4810344	-4.937592	2.24E-06	0.0001325	4.099743	LCE3E	NM_178435.2
cg272199 73	-0.101812835	0.434828	-5.160108	8.36E-07	6.79E-05	5.048674	GNRHR	NM_000406.2
cg136960 12	-0.10181956	0.6654104	-3.821535	0.0001994	0.0029508	-0.18803	BPIL1	NM_025227.1
cg048370 71	-0.101946889	0.4458662	-4.907785	2.54E-06	0.0001398	3.974834	NOXA1	NM_006647.1
cg118469 68	-0.102019886	0.6089813	-4.765321	4.70E-06	0.0002061	3.385227	PLUNC	NM_016583.2
cg242764 91	-0.102036388	0.6965107	-4.610647	9.02E-06	0.0003105	2.75926	C14orf11	NM_018453.2
cg251121 91	-0.10219568	0.4874587	-4.098222	7.05E-05	0.0013724	0.796561	RORC	NM_005060.3
cg102077 45	-0.102287067	0.3860816	-3.635811	0.0003895	0.0048183	-0.817669	C12orf36	NM_182558.1
cg069736 52	-0.10228731	0.6782769	-3.872951	0.000165	0.0025708	-0.009228	BRCA1	NM_007294.2
cg140620 83	-0.102358059	0.6706042	-4.815371	3.79E-06	0.0001808	3.590961	KRTAP13-4	NM_181600.1
cg063533 45	-0.102393397	0.467905	-4.640562	7.96E-06	0.0002891	2.879156	OR51B4	NM_033179.1
cg102126 21	-0.102411472	0.4687322	-4.631189	8.27E-06	0.0002959	2.841527	HMGCS2	NM_005518.2
cg266614 81	-0.102466987	0.7240937	-4.024246	9.35E-05	0.001675	0.527976	IL10RA	NM_001558.2
cg058200 87	-0.102553892	0.4226203	-4.699817	6.20E-06	0.0002426	3.118305	ATP13A4	NM_032279.2
cg079508 03	-0.102600724	0.7098765	-3.976499	0.0001121	0.0019043	0.356673	CD1A	NM_001763.1
cg236966 18	-0.102619066	0.4646293	-6.890985	1.77E-10	9.94E-07	13.28479	SERPINB1 0	NM_005024.1

cg091200 35	-0.102652905	0.7080344	-4.417135	2.01E-05	0.000556	1.996046	CYP11B1	NM_000497.3
cg103310 38	-0.10269943	0.6322243	-4.919154	2.42E-06	0.0001353	4.022413	TNR	NM_003285.1
cg201610 89	-0.102700513	0.5038681	-4.7433	5.16E-06	0.0002141	3.295199	IFI27	NM_005532.3
cg177919 36	-0.102711252	0.7379618	-6.308068	3.53E-09	2.70E-06	10.36033	SLC37A4	NM_001467.3
cg163240 18	-0.102822202	0.5523011	-4.813261	3.83E-06	0.0001814	3.582256	RBED1	NM_032213.3
cg029926 47	-0.10282944	0.6418024	-4.328253	2.86E-05	0.0007216	1.655932	DDX52	NM_152300.2
cg095330 63	-0.102899661	0.4622782	-4.356828	2.55E-05	0.0006675	1.76519	ALDH8A1	NM_022568.2
cg144628 30	-0.10291771	0.5907393	-5.4276	2.48E-07	3.26E-05	6.226441	TRDN	NM_006073.1
cg042826 22	-0.1029415	0.5146193	-5.04758	1.38E-06	9.44E-05	4.565199	FAM71C	NM_153364.1
cg061233 46	-0.103007521	0.4212361	-4.514396	1.34E-05	0.0004122	2.377371	ATP4A	NM_000704.2
cg047210 98	-0.103047211	0.5142548	-4.143056	5.93E-05	0.001213	0.961202	CACNG3	NM_006539.2
cg058105 50	-0.103163353	0.6438504	-4.029157	9.18E-05	0.0016547	0.545687	DEFB106A	NM_152251.2
cg259463 74	-0.103186408	0.5115922	-4.438578	1.83E-05	0.0005204	2.080768	IL22RA1	NM_021258.2
cg208280 84	-0.10332025	0.6634437	-4.925911	2.35E-06	0.0001342	4.05073	KIAA1199	NM_018689.1
cg170952 79	-0.103354673	0.5304218	-5.326333	3.94E-07	4.23E-05	5.775943	APOH	NM_000042.1
cg160763 28	-0.10335607	0.3757849	-4.963566	2.05E-06	0.0001251	4.198354	TACSTD1	NM_002354.1
cg216156 63	-0.103395643	0.6364094	-4.706461	6.03E-06	0.0002375	3.145259	MGC3504 8	NM_153208.1
cg249142 44	-0.103580104	0.7313019	-4.471043	1.60E-05	0.0004747	2.207314	RTN4IP1	NM_032730.3
cg129675 60	-0.103602355	0.6786051	-4.061034	8.13E-05	0.0015284	0.661062	LYSMD4	NM_152449.2
cg059583 52	-0.103611453	0.5639956	-4.047907	8.55E-05	0.0015707	0.613464	RNASE1	NM_198232.1
cg228792 89	-0.103651821	0.5644502	-4.862662	3.09E-06	0.0001552	3.786755	NID1	NM_002508.1
cg002835 35	-0.103729405	0.521831	-5.563417	1.32E-07	2.34E-05	6.839211	ANXA13	NM_004306.2
cg173570 62	-0.103753099	0.5773708	-5.099875	1.09E-06	8.27E-05	4.788978	FCN1	NM_002003.2
cg194649 44	-0.10375687	0.4329205	-4.475253	1.58E-05	0.0004687	2.223774	FCGR1A	NM_000566.2
cg092057 51	-0.103996611	0.6861262	-3.820929	0.0001999	0.0029524	-0.190127	NALP6	NM_138329.1
cg147574 92	-0.104025497	0.5879988	-5.30783	4.29E-07	4.47E-05	5.694233	DDX49	NM_019070.3
cg242696 57	-0.104111875	0.5254872	-4.731463	5.42E-06	0.0002214	3.246927	F7	NM_000131.2
cg039983 48	-0.104195318	0.6235923	-4.578484	1.03E-05	0.0003425	2.630986	TMCO5	NM_152453.2

cg150212 92	-0.104258218	0.723626	-3.671129	0.0003435	0.0043979	-0.699913	PIK3R1	NM_181523.1
cg133973 79	-0.104377337	0.6964119	-4.159577	5.56E-05	0.0011635	1.022224	OR2C3	NM_198074.3
cg098379 43	-0.104389446	0.6009297	-5.512134	1.67E-07	2.67E-05	6.6067	ZIM2	NT_011109.15
cg168791 15	-0.10443282	0.5687795	-5.422272	2.54E-07	3.30E-05	6.202603	APOBEC1	NM_005889.2
cg240633 82	-0.104546844	0.6848819	-5.47558	1.98E-07	2.95E-05	6.441806	MAS1L	NM_052967.1
cg276257 32	-0.104590438	0.6839317	-5.024635	1.53E-06	0.0001001	4.467511	TBC1D13	NM_018201.2
cg064447 81	-0.104681611	0.6247061	-5.581994	1.21E-07	2.25E-05	6.923773	TCF1	NM_000545.3
cg029925 96	-0.104721905	0.7008202	-4.803048	4.00E-06	0.0001864	3.540162	MGC2701 6	NM_144979.2
cg026114 19	-0.104738211	0.4292341	-4.015859	9.75E-05	0.0017244	0.504373	KCNK17	NM_031460.2
cg105334 34	-0.104746534	0.6626685	-5.924873	2.34E-08	7.57E-06	8.515651	SERPINB3	NM_006919.1
cg077473 36	-0.10476706	0.5340506	-4.492975	1.47E-05	0.0004429	2.293191	C11orf38	NM_212555.1
cg246424 68	-0.104807624	0.548374	-5.072072	1.24E-06	8.96E-05	4.669807	MGC3336 7	NM_144602.2
cg136947 49	-0.105083992	0.7188679	-4.209824	4.57E-05	0.0010173	1.20897	SCN4A	NM_000334.3
cg168942 11	-0.10518992	0.5698284	-4.528449	1.27E-05	0.0003945	2.432757	SYN3	NM_003490.2
cg139542 92	-0.105210808	0.8254405	-3.816724	0.000203	0.002979	-0.204662	ZFR	NM_016107.3
cg133141 67	-0.105259694	0.8175365	-4.721845	5.65E-06	0.0002271	3.207772	C9orf84	NM_173521.2
cg036003 18	-0.105278871	0.2956266	-5.841815	3.50E-08	9.67E-06	8.124749	SFTPD	NM_003019.4
cg214142 51	-0.105296996	0.378034	-5.333049	3.82E-07	4.15E-05	5.80565	OR12D2	NM_013936.2
cg199872 19	-0.105299499	0.7002762	-4.0516	8.43E-05	0.0015613	0.626842	FLJ32011	NM_182516.1
cg130422 88	-0.105329809	0.722008	-4.654734	7.50E-06	0.0002781	2.936149	ANPEP	NM_001150.1
cg250414 39	-0.105367209	0.4178878	-4.986903	1.80E-06	0.0001128	4.307538	HYLS1	NM_145014.1
cg141142 67	-0.105381576	0.4878235	-5.630855	9.58E-08	1.91E-05	7.147037	SP3	NM_003111.3
cg020342 22	-0.105418257	0.6321173	-4.454318	1.72E-05	0.0004961	2.142036	DQX1	NM_133637.1
cg098710 43	-0.105545521	0.4359515	-5.460887	2.12E-07	3.04E-05	6.375724	PKHD1	NM_138694.2
cg001347 87	-0.105545616	0.6314082	-5.239867	5.84E-07	5.34E-05	5.395715	MYH1	NM_005963.2
cg100712 75	-0.105545684	0.5889673	-4.127595	6.29E-05	0.0012633	0.904267	MYT1	NM_004535.2
cg206764 75	-0.105551041	0.5787422	-4.202138	4.71E-05	0.001037	1.180291	LCE3D	NM_032563.1
cg233827 41	-0.105740497	0.6025369	-4.52845	1.27E-05	0.0003945	2.432761	PPP1R14D	NM_017726.6

cg225108 22	-0.105752156	0.6430263	-4.062641	8.08E-05	0.0015229	0.666896	OR1E2	NM_003554.1
cg242223 24	-0.105865121	0.7313387	-4.631721	8.26E-06	0.0002959	2.843661	TNFSF11	NM_003701.2
cg222130 42	-0.105896318	0.6001163	-4.244448	3.99E-05	0.0009226	1.33866	CPA2	NM_001869.1
cg091550 25	-0.105961075	0.6723316	-4.656492	7.44E-06	0.0002771	2.943229	SLC39A4	NM_130849.1
cg155828 91	-0.106058007	0.5055448	-5.045604	1.39E-06	9.50E-05	4.556775	TAAR1	NM_138327.1
cg031025 16	-0.106231827	0.5153703	-6.377695	2.49E-09	2.44E-06	10.70244	LINCR	XM_930227.1
cg268622 86	-0.106284632	0.7197775	-4.074545	7.72E-05	0.0014685	0.710177	NCL	NM_005381.2
cg103474 18	-0.106479206	0.7057059	-4.69143	6.42E-06	0.0002488	3.084323	ZNF436	NM_030634.1
cg039051 44	-0.106490171	0.5840691	-5.091384	1.14E-06	8.43E-05	4.752536	MPDZ	NM_003829.1
cg062772 77	-0.106532286	0.6521491	-3.762243	0.0002476	0.0034493	-0.391819	NR1I3	NM_005122.2
cg274120 93	-0.106544169	0.5718019	-3.631422	0.0003956	0.0048639	-0.832237	CAPN9	NM_006615.2
cg089479 64	-0.106660456	0.6778734	-4.77874	4.44E-06	0.0001996	3.440237	CX62	NM_032602.1
cg232132 17	-0.10666098	0.3671966	-4.710664	5.92E-06	0.0002349	3.162323	DEGS1	NM_144780.1
cg169536 12	-0.10666978	0.6670759	-4.472661	1.59E-05	0.0004727	2.213639	DNAJB8	NM_153330.2
cg263857 43	-0.106682201	0.7835555	-3.783261	0.0002294	0.0032608	-0.319876	IMP4	NM_033416.1
cg209672 20	-0.106841324	0.6318346	-4.570456	1.07E-05	0.0003514	2.599072	GCM1	NM_003643.2
cg108628 48	-0.106951028	0.5779184	-3.829664	0.0001936	0.0028859	-0.159888	GNMT	NT_007592.14
cg021929 65	-0.10698578	0.5430078	-4.065324	8.00E-05	0.0015105	0.676643	SLC3A1	NM_000341.2
cg186922 73	-0.106994019	0.7299706	-4.104521	6.88E-05	0.0013484	0.819608	TNNT2	NM_000364.2
cg062049 48	-0.107032175	0.2688341	-6.393361	2.30E-09	2.34E-06	10.7797	MARK2	NM_017490.1
cg033295 72	-0.107077838	0.7239532	-4.930086	2.31E-06	0.0001341	4.068235	FCRL5	NM_031281.1
cg222021 41	-0.107082436	0.5557436	-3.676243	0.0003373	0.0043415	-0.682784	FCGR3A	NM_000569.6
cg023301 06	-0.107139565	0.6780072	-3.469676	0.0006945	0.0074204	-1.358896	MGMT	NM_002412.2
cg195542 94	-0.107232479	0.5510299	-5.309633	4.25E-07	4.45E-05	5.702183	VN1R2	NM_173856.1
cg255143 04	-0.107282183	0.608278	-3.930846	0.000133	0.0021938	0.194404	PSEN2	NM_000447.1
cg145473 35	-0.107286069	0.7565279	-4.289793	3.33E-05	0.0008026	1.509742	ATP2B2	NM_001683.2
cg242113 88	-0.107299321	0.6156296	-4.863313	3.09E-06	0.0001552	3.78946	AIF1	NM_032955.1
cg235959 27	-0.107309373	0.5067483	-4.238284	4.08E-05	0.0009404	1.315511	MYL5	NM_002477.1

cg196850 66	-0.107314206	0.7499841	-3.974923	0.0001127	0.0019115	0.351044	ACTL8	NM_030812.1
cg051555 95	-0.107446262	0.3654888	-5.335672	3.78E-07	4.13E-05	5.817255	ANXA4	NM_001153.2
cg138616 44	-0.107485903	0.7113761	-4.559169	1.12E-05	0.000362	2.554275	PIWIL1	NM_004764.3
cg049621 34	-0.107498874	0.6076904	-5.426352	2.49E-07	3.26E-05	6.220856	TRIM51	NM_032681.1
cg236254 58	-0.107519376	0.7498487	-4.725923	5.55E-06	0.0002254	3.224365	AFAR3	NM_201252.1
cg225859 88	-0.107592247	0.587016	-4.279079	3.47E-05	0.0008284	1.469191	PVRL4	NM_030916.1
cg002042 62	-0.107622601	0.6834643	-4.925597	2.36E-06	0.0001342	4.049411	ECH1	NM_001398.2
cg192976 88	-0.107635829	0.6011959	-3.91712	0.00014	0.0022879	0.145907	INSL4	NM_002195.1
cg247511 29	-0.10767174	0.6408527	-4.124517	6.37E-05	0.0012775	0.892952	GNMT	NM_018960.4
cg014267 43	-0.107715315	0.5848552	-4.270386	3.60E-05	0.0008529	1.436348	FAM20B	NM_014864.2
cg069421 10	-0.107779792	0.6077414	-4.196333	4.81E-05	0.0010521	1.158661	INT1	XM_931325.1
cg259952 12	-0.107844606	0.6972273	-4.479079	1.55E-05	0.0004646	2.238744	SCN7A	NM_002976.1
cg245129 73	-0.107926628	0.625641	-4.150526	5.76E-05	0.0011911	0.98877	MUC1	NM_002456.4
cg026711 71	-0.108126301	0.4531759	-5.227979	6.16E-07	5.51E-05	5.343763	RPH3AL	NM_006987.2
cg237321 82	-0.108145721	0.5163638	-6.048796	1.28E-08	5.30E-06	9.104933	C21orf84	NM_153752.1
cg155440 36	-0.10815826	0.5682309	-6.150024	7.77E-09	3.88E-06	9.591523	CLDN4	NM_001305.3
cg250812 01	-0.108282661	0.733021	-4.576876	1.04E-05	0.0003435	2.624592	FXD4	NM_173160.2
cg254880 21	-0.108485823	0.6976873	-4.612419	8.95E-06	0.0003094	2.766343	EPB41L2	NM_001431.1
cg095558 79	-0.10851146	0.7747199	-5.387118	2.98E-07	3.61E-05	6.04569	GRIK5	NM_002088.3
cg051873 22	-0.108536992	0.7047011	-3.872323	0.0001654	0.0025753	-0.011421	CARD14	NM_024110.2
cg219486 55	-0.108543448	0.7870917	-4.56	1.11E-05	0.0003612	2.557568	SMCP	NM_030663.2
cg004740 04	-0.108614458	0.6234012	-5.581724	1.21E-07	2.25E-05	6.922546	IFNA14	NM_002172.1
cg132592 90	-0.108640675	0.6135269	-4.009066	9.91E-05	0.0017468	0.473338	CSF2	NM_000758.2
cg211227 74	-0.108682104	0.6981844	-4.901047	2.62E-06	0.0001417	3.946669	SARDH	NM_007101.2
cg069064 35	-0.108735815	0.5540562	-4.37809	2.34E-05	0.0006214	1.846843	FLJ25773	NM_182560.1
cg123489 70	-0.108763387	0.7315283	-4.724751	5.61E-06	0.0002266	3.219244	SLC24A2	NM_020344.1
cg239785 57	-0.108875845	0.5714563	-4.792101	4.19E-06	0.0001926	3.495117	SMPD2	NM_003080.1
cg045050 23	-0.108876008	0.5232674	-3.865107	0.0001699	0.0026157	-0.03663	SPRR1A	NM_005987.2

cg079558 87	-0.108915552	0.6527704	-4.663282	7.23E-06	0.0002721	2.970592	KIAA0802	NM_015210.1
cg035488 57	-0.108962753	0.4205031	-5.108031	1.06E-06	8.03E-05	4.824022	FFAR2	NM_005306.1
cg119205 19	-0.108992596	0.7112503	-3.868257	0.0001679	0.002599	-0.02563	MAP1LC3 A	NM_181509.1
cg036091 02	-0.10910584	0.4322485	-5.475287	1.98E-07	2.95E-05	6.440488	MUC5B	XM_039877.1 2
cg203830 64	-0.109109447	0.6606318	-4.143418	5.92E-05	0.001213	0.962539	BFSP2	NM_003571.2
cg234133 07	-0.109111784	0.56568	-3.911663	0.0001438	0.0023347	0.131556	LCE1F	NM_178354.1
cg221618 74	-0.109147921	0.6639879	-5.245025	5.70E-07	5.28E-05	5.41828	TRPM6	NM_017662.3
cg272912 31	-0.109215858	0.7701888	-4.573147	1.05E-05	0.000348	2.609766	SSNA1	NM_003731.1
cg093267 02	-0.109248426	0.7845456	-5.542805	1.45E-07	2.44E-05	6.745593	SLC22A11	NM_018484.2
cg139505 58	-0.109283358	0.5636837	-4.729126	5.48E-06	0.0002232	3.237407	BLOC1S3	NM_212550.1
cg216243 59	-0.109285086	0.566938	-5.400757	2.80E-07	3.51E-05	6.106487	FFAR3	NM_005304.2
cg140348 70	-0.109313396	0.4168043	-5.860495	3.20E-08	9.12E-06	8.212379	SFTPG	NM_205854.1
cg054453 26	-0.109407631	0.6780892	-4.149502	5.78E-05	0.0011938	0.984989	TM4SF19	NM_138461.1
cg066502 60	-0.109472142	0.6343816	-4.215721	4.46E-05	0.0010041	1.231	NR0B2	NM_021969.1
cg077457 25	-0.109622867	0.548181	-5.676964	7.70E-08	1.65E-05	7.358838	PSG3	NM_021016.2
cg140234 51	-0.10969186	0.6778205	-4.90074	2.62E-06	0.0001417	3.945386	GPLD1	NM_001503.2
cg129716 94	-0.109727842	0.5192866	-4.814809	3.80E-06	0.0001808	3.58864	CD72	NM_001782.1
cg131196 09	-0.109728578	0.5533747	-4.313005	3.05E-05	0.0007534	1.599059	APOC2	NM_000483.3
cg080744 77	-0.109734465	0.5106152	-5.542821	1.45E-07	2.44E-05	6.745668	TNS4	NM_032865.3
cg066460 21	-0.109753105	0.5066381	-4.423515	1.95E-05	0.0005442	2.02229	RAB4A	NM_004578.2
cg049471 57	-0.109814861	0.4148663	-4.140229	5.99E-05	0.0012226	0.95078	TMC6	NM_007267.5
cg123972 74	-0.109819322	0.4146993	-5.135239	9.34E-07	7.37E-05	4.9412	TINAG	NM_014464.2
cg216242 82	-0.109870583	0.7817252	-4.385446	2.27E-05	0.0006087	1.875161	LOC12225 8	NM_145248.2
cg191397 29	-0.109892198	0.511562	-4.912381	2.49E-06	0.0001385	3.994058	SULT2A1	NM_003167.2
cg097997 14	-0.109900347	0.553858	-3.843242	0.0001847	0.00279	-0.110195	PDZD3	NM_024791.2
cg250729 62	-0.109963579	0.5247598	-5.347032	3.59E-07	3.99E-05	5.867575	MGC3529 5	NM_152717.1
cg077059 08	-0.110107278	0.5361345	-3.825959	0.0001962	0.0029147	-0.172721	SPDEF	NM_012391.1
cg189675 33	-0.110145721	0.5283252	-5.886443	2.82E-08	8.70E-06	8.334379	KLK6	NM_002774.3

cg168795 96	-0.110207569	0.5253881	-3.830671	0.0001928	0.0028841	-0.156398	CYP3A5	NM_000777.2
cg002458 78	-0.110290366	0.7272182	-5.210676	6.66E-07	5.82E-05	5.268289	H-plk	NM_015852.1
cg116953 58	-0.1103426	0.6369641	-4.732151	5.41E-06	0.0002211	3.249729	MAPK15	NM_139021.1
cg136440 52	-0.110344064	0.6815165	-4.709759	5.95E-06	0.0002354	3.158648	PAQR4	NM_152341.2
cg133206 83	-0.110369241	0.674956	-4.175367	5.23E-05	0.0011153	1.080722	RHOBTB1	NM_014836.3
cg135875 52	-0.110370396	0.6710983	-4.716624	5.78E-06	0.0002304	3.186539	SCNN1D	NM_002978.2
cg123807 64	-0.110421503	0.4778872	-4.259951	3.75E-05	0.0008778	1.396993	IL19	NM_013371.2
cg212836 80	-0.110602146	0.5983576	-4.582132	1.02E-05	0.0003378	2.645504	SH3BP5	NM_004844.2
cg165754 08	-0.110604544	0.7707829	-4.432576	1.88E-05	0.000531	2.057449	MMP1	NM_002421.2
cg069854 15	-0.110666423	0.7775386	-4.348541	2.63E-05	0.0006767	1.73345	C10orf39	NM_194303.1
cg219067 16	-0.110778802	0.7788559	-4.632427	8.23E-06	0.0002959	2.846495	TP73	NT_004321.17
cg187053 01	-0.110873981	0.5105974	-5.060967	1.30E-06	9.18E-05	4.622333	NDUFAF1	NM_016013.2
cg204851 65	-0.110882569	0.5569964	-4.368224	2.43E-05	0.0006403	1.808916	WFDC12	NM_080869.1
cg157033 57	-0.11109069	0.4228387	-5.445296	2.28E-07	3.15E-05	6.305729	LINCR	XM_930227.1
cg253910 23	-0.111257149	0.4790041	-5.141365	9.09E-07	7.30E-05	4.967644	BTNL2	NM_019602.1
cg095412 48	-0.111468452	0.486529	-5.178965	7.68E-07	6.48E-05	5.130401	MYO1A	NM_005379.2
cg224779 71	-0.111473508	0.5901417	-4.786977	4.28E-06	0.0001952	3.474059	C1QB	NM_000491.2
cg184143 81	-0.111639577	0.3562531	-5.121516	9.93E-07	7.69E-05	4.882045	EHF	NM_012153.3
cg160977 72	-0.111749084	0.4815198	-4.406453	2.09E-05	0.0005725	1.95623	LYZ	NM_000239.1
cg003254 91	-0.111877172	0.4198285	-5.861751	3.18E-08	9.12E-06	8.218274	FN5	NM_020179.1
cg033439 42	-0.111931895	0.5013702	-4.569746	1.07E-05	0.0003515	2.596252	SLC39A5	NM_173596.1
cg012148 47	-0.112014594	0.5594553	-5.255796	5.43E-07	5.12E-05	5.465453	TMPRSS3	NM_024022.1
cg109688 15	-0.112030538	0.5671536	-3.988159	0.0001072	0.0018443	0.398356	BPIL1	NM_025227.1
cg248162 98	-0.112141897	0.5917808	-4.563848	1.10E-05	0.0003576	2.572836	PTH	NM_000315.2
cg211053 18	-0.112193875	0.5526126	-5.166297	8.13E-07	6.66E-05	5.075475	ITGB6	NM_000888.3
cg258568 11	-0.112289135	0.4151519	-4.679016	6.77E-06	0.000258	3.034104	SPRR3	NM_005416.1
cg157612 33	-0.112318957	0.6616724	-5.473721	2.00E-07	2.96E-05	6.433438	FLJ22555	NM_024520.1
cg144447 10	-0.11234599	0.5661684	-5.200632	6.97E-07	5.99E-05	5.224551	PDPK1	NM_031268.4

cg224244 44	-0.1124401	0.6392412	-4.423389	1.95E-05	0.0005442	2.021803	TOLLIP	NM_019009.2
cg264249 56	-0.112604732	0.7003658	-4.540255	1.21E-05	0.0003825	2.479387	GRM4	NM_000841.1
cg256454 62	-0.112690767	0.6169134	-5.010478	1.64E-06	0.0001049	4.403474	GPR56	NM_201525.1
cg015661 70	-0.112691376	0.4249487	-4.679091	6.77E-06	0.000258	3.034408	CAPN2	NM_001748.3
cg105163 59	-0.112750929	0.7788734	-3.569068	0.0004925	0.0057515	-1.03763	SLC35C1	NM_018389.3
cg199983 28	-0.112791952	0.6608736	-5.168856	8.04E-07	6.63E-05	5.086564	LOC90580	NM_138358.2
cg095085 56	-0.112811549	0.7131972	-4.291181	3.31E-05	0.0008004	1.515	PSORS1C2	NM_014069.1
cg002731 24	-0.112886375	0.6845561	-4.613116	8.92E-06	0.0003089	2.769132	NOLA2	NM_017838.3
cg166488 41	-0.113015732	0.4849526	-4.747919	5.06E-06	0.000212	3.314057	C8A	NM_000562.1
cg204068 78	-0.113082721	0.5953027	-5.648576	8.91E-08	1.81E-05	7.223088	NR5A2	NM_003822.3
cg120191 09	-0.113163245	0.5457528	-4.087997	7.33E-05	0.0014146	0.759207	AZGP1	NM_001185.2
cg011092 19	-0.113172716	0.5185381	-4.494469	1.46E-05	0.0004422	2.299054	RASGRP3	NM_170672.1
cg227804 75	-0.113265357	0.5385348	-5.459637	2.13E-07	3.04E-05	6.370107	CBLC	NM_012116.2
cg074092 00	-0.11342874	0.4223076	-4.86134	3.11E-06	0.0001555	3.781263	FLJ40919	NM_182508.1
cg094402 43	-0.113455024	0.675087	-5.055728	1.33E-06	9.25E-05	4.599959	PTPRD	NM_130391.1
cg071508 30	-0.113478015	0.7836545	-4.170921	5.32E-05	0.0011311	1.064232	NOS2A	NM_000625.3
cg094223 55	-0.1134865	0.7472643	-5.016292	1.58E-06	0.0001023	4.432067	CABP5	NM_019855.3
cg203733 26	-0.113507366	0.4432231	-5.691711	7.18E-08	1.59E-05	7.426805	HSD17B2	NM_002153.1
cg153016 94	-0.113570481	0.7255899	-5.426662	2.49E-07	3.26E-05	6.222245	STRN3	NM_014574.2
cg011442 51	-0.11359716	0.6452324	-4.668183	7.09E-06	0.0002673	2.990359	KLK9	NM_012315.1
cg172592 65	-0.113648009	0.6205841	-5.310677	4.23E-07	4.45E-05	5.706793	HYLS1	NM_145014.1
cg104123 12	-0.113766354	0.5434584	-5.491306	1.84E-07	2.84E-05	6.512658	FLJ36004	NM_152590.1
cg195808 10	-0.113848589	0.4617126	-5.361268	3.36E-07	3.87E-05	5.930727	RAB25	NM_020387.1
cg242926 12	-0.113931044	0.3877947	-5.25522	5.45E-07	5.12E-05	5.462929	DEFB1	NM_005218.3
cg274010 95	-0.11394244	0.4196044	-5.421047	2.55E-07	3.30E-05	6.197125	ZNF324	NM_014347.1
cg213121 48	-0.114070618	0.5795237	-4.617025	8.78E-06	0.0003067	2.784775	LCE2D	NM_178430.2
cg248351 59	-0.11409285	0.4855601	-5.140556	9.13E-07	7.30E-05	4.964148	RNF43	NM_017763.3
cg196901 01	-0.114121369	0.7579099	-4.846205	3.32E-06	0.0001632	3.718464	DHX57	NM_144995.2

cg271001 23	-0.114177575	0.7967016	-4.618526	8.72E-06	0.0003059	2.790781	SERPINB8	NM_198833.1
cg113104 96	-0.114181289	0.6183752	-4.154826	5.66E-05	0.0011786	1.004657	PNLIPRP2	NM_005396.3
cg140035 12	-0.114448907	0.4908664	-6.281695	4.03E-09	2.72E-06	10.23128	PLGLB2	NM_002665.3
cg219307 12	-0.114584705	0.4961949	-4.301097	3.18E-05	0.0007779	1.552606	FLJ40235	NM_173635.1
cg097050 62	-0.114617855	0.5883071	-5.616957	1.02E-07	1.99E-05	7.083408	SLC22A11	NM_018484.2
cg236211 15	-0.11467537	0.5789361	-5.76119	5.16E-08	1.31E-05	7.748487	PRKCABP	NM_012407.2
cg190250 34	-0.114704532	0.6365573	-5.028065	1.50E-06	9.92E-05	4.482093	FUT2	NM_000511.3
cg099718 11	-0.114815713	0.7180399	-4.41223	2.04E-05	0.0005612	1.978577	CST7	NM_003650.2
cg098161 80	-0.114835772	0.5729804	-6.052288	1.26E-08	5.29E-06	9.121641	GC	NM_000583.2
cg045777 15	-0.114884078	0.7085404	-5.504176	1.74E-07	2.75E-05	6.570741	SPINK1	NM_003122.2
cg164467 83	-0.114890088	0.5271876	-5.408251	2.71E-07	3.45E-05	6.139938	MRGPRX4	NM_054032.2
cg188702 31	-0.114985299	0.6354838	-5.058469	1.31E-06	9.22E-05	4.611664	C1orf87	NM_152377.1
cg117834 97	-0.114990447	0.6488174	-3.623462	0.0004068	0.0049602	-0.858619	IL1RN	NM_000577.3
cg003117 68	-0.115135309	0.5118984	-5.056896	1.32E-06	9.23E-05	4.604945	TSTA3	NM_003313.2
cg089998 95	-0.115237228	0.5039952	-4.024095	9.36E-05	0.001675	0.527431	SLC22A18 AS	NM_007105.1
cg197958 98	-0.115336567	0.5286724	-4.352478	2.59E-05	0.0006719	1.748523	KIAA1984	NM_032874.2
cg252143 46	-0.115341258	0.6882753	-4.260361	3.74E-05	0.0008777	1.39854	NR1B3	NM_005122.2
cg105031 38	-0.115354852	0.6059238	-5.171186	7.96E-07	6.61E-05	5.096661	CNTN4	NM_175607.1
cg054061 01	-0.115388033	0.7707311	-3.818204	0.0002019	0.0029688	-0.199548	C21orf6	NM_016940.1
cg101269 23	-0.115577477	0.7575542	-4.856706	3.17E-06	0.0001577	3.762023	NKG7	NM_005601.3
cg108783 07	-0.115621782	0.5246979	-5.351104	3.52E-07	3.95E-05	5.885627	ATAD4	NM_024320.2
cg090760 77	-0.115715317	0.6103914	-4.046176	8.60E-05	0.0015747	0.607196	FLJ33860	NM_173644.1
cg198726 81	-0.115961888	0.5824781	-4.424263	1.94E-05	0.0005442	2.025191	SLC7A7	NM_003982.2
cg147094 81	-0.116144384	0.6691451	-5.2945	4.56E-07	4.64E-05	5.635479	HK3	NM_002115.1
cg250331 44	-0.116150763	0.7832297	-4.723553	5.61E-06	0.0002266	3.214719	FLJ00060	NM_033206.1
cg274040 50	-0.116271544	0.336908	-5.794102	4.41E-08	1.19E-05	7.901697	PRODH2	NM_021232.1
cg083146 60	-0.116437291	0.7352996	-4.582515	1.01E-05	0.0003377	2.647028	PKP3	NM_007183.2
cg126191 62	-0.116459468	0.5433988	-4.054566	8.33E-05	0.0015486	0.637592	FXD4	NM_173160.2

cg07908874	-0.11646691	0.6559776	-4.852158	3.24E-06	0.00016	3.743148	TUBGCP2	NM_006659.1
cg13424229	-0.116567518	0.5237223	-5.053134	1.35E-06	9.33E-05	4.588888	CPA3	NM_001870.1
cg10358212	-0.11663935	0.5409432	-5.326965	3.93E-07	4.23E-05	5.778738	ASCIZ	NM_015251.2
cg19346193	-0.116795017	0.6092196	-4.027797	9.23E-05	0.0016603	0.54078	UROS	NM_000375.1
cg26023389	-0.116934034	0.6171272	-4.625807	8.46E-06	0.0002988	2.819948	GCM1	NM_003643.2
cg22228134	-0.117168388	0.6859401	-4.886889	2.79E-06	0.0001468	3.887584	GZMH	NM_033423.2
cg04574507	-0.117205032	0.5762202	-5.388312	2.97E-07	3.61E-05	6.051005	CD1B	NM_001764.1
cg20059312	-0.117221554	0.6980417	-4.765167	4.70E-06	0.0002061	3.384597	NGEF	NM_019850.1
cg00062776	-0.117224739	0.8593224	-5.036024	1.45E-06	9.73E-05	4.515961	TULP2	NM_003323.1
cg26767897	-0.117282003	0.6568789	-4.938421	2.24E-06	0.0001326	4.099638	XDH	NM_000379.2
cg14481339	-0.117343229	0.6354765	-4.907997	2.54E-06	0.0001398	3.97572	KCNJ1	NM_000220.2
cg22539738	-0.117367633	0.7315882	-3.756111	0.0002531	0.0035047	-0.412746	KIAA1704	NM_018559.2
cg24331162	-0.117393909	0.5572274	-5.728548	6.03E-08	1.44E-05	7.597059	SYT8	NM_138567.2
cg21431536	-0.11750642	0.5499552	-5.907571	2.55E-08	7.95E-06	8.43395	LGR8	NM_130806.2
cg02148642	-0.117557409	0.384032	-4.347845	2.64E-05	0.0006777	1.730786	RGPDS	NM_032260.2
cg17003970	-0.117557634	0.7888248	-4.476067	1.57E-05	0.0004677	2.226957	CHFR	NT_024477.13
cg06643227	-0.117606723	0.8055647	-4.318104	2.98E-05	0.0007392	1.617257	C9orf84	NM_173521.2
cg10055471	-0.117613155	0.8179237	-4.611559	8.98E-06	0.0003097	2.762907	NROB2	NM_021969.1
cg07918509	-0.117665097	0.5643563	-4.719246	5.71E-06	0.0002285	3.197199	ICAM2	NM_000873.2
cg04806409	-0.117691017	0.6099434	-4.217811	4.43E-05	0.0009976	1.238814	TFF3	NM_003226.2
cg06319346	-0.117739954	0.7028759	-5.592261	1.15E-07	2.19E-05	6.970588	CHRFAM7A	NM_139320.1
cg02906939	-0.117755691	0.6790337	-5.196797	7.09E-07	6.06E-05	5.207871	HNMT	NM_006895.2
cg24363955	-0.117804542	0.5751373	-4.860852	3.12E-06	0.0001555	3.779236	FLJ14054	NM_024563.2
cg03116740	-0.118098693	0.6660961	-4.788885	4.25E-06	0.000194	3.481899	TSPAN4	NM_003271.4
cg06690548	-0.118178467	0.790839	-5.232819	6.03E-07	5.45E-05	5.364906	SLC7A11	NM_014331.2
cg17797815	-0.118240602	0.4839652	-5.166086	8.14E-07	6.66E-05	5.074559	RAB11FIP2	NM_014904.1
cg15996947	-0.1182553	0.6503333	-4.476619	1.57E-05	0.0004672	2.229118	L2HGDH	NM_024884.1
cg21281799	-0.118255591	0.5813245	-4.960444	2.02E-06	0.000124	4.195862	DYRK2	NM_003583.2

cg23181133	-0.11829089	0.3931757	-6.323813	3.26E-09	2.70E-06	10.43751	CEACAM3	NM_001815.1
cg02825709	-0.118499542	0.6485327	-5.579166	1.22E-07	2.25E-05	6.91089	ZNF75A	NM_153028.1
cg21550442	-0.118537056	0.5535129	-4.933973	2.27E-06	0.0001334	4.084548	FLJ36445	NM_153233.1
cg09037813	-0.118625052	0.597465	-4.099716	7.01E-05	0.0013655	0.802026	LRRFIP1	NM_004735.2
cg21817450	-0.118805575	0.6031949	-5.268888	5.12E-07	4.97E-05	5.522871	PIG38	NM_017993.1
cg03817621	-0.118815625	0.5709455	-6.824107	2.73E-10	9.94E-07	12.87732	ACF	NM_014576.2
cg03364504	-0.118833462	0.6899362	-4.287643	3.36E-05	0.000808	1.501595	FLJ36116	XR_000536.1
cg09243900	-0.118862078	0.5416389	-5.309574	4.25E-07	4.45E-05	5.701926	RAB25	NM_020387.1
cg15669228	-0.119022964	0.5852285	-5.709889	6.59E-08	1.49E-05	7.510738	IFNA8	NM_002170.2
cg26457013	-0.119150673	0.6601179	-4.531853	1.25E-05	0.0003908	2.446191	TMEM86B	NM_173804.3
cg26530341	-0.119181334	0.5519436	-4.229881	4.22E-05	0.0009645	1.283998	TNFRSF10A	NM_003844.2
cg00491404	-0.119190551	0.5925867	-5.446818	2.26E-07	3.14E-05	6.312555	EPS8L3	NM_024526.2
cg04995095	-0.119231717	0.4656664	-4.929721	2.31E-06	0.0001341	4.066707	CD300E	NM_181449.1
cg20189937	-0.119237389	0.6074047	-4.390878	2.22E-05	0.0006004	1.896096	L2HGDH	NM_024884.1
cg23464269	-0.119481912	0.468684	-4.890809	2.74E-06	0.0001459	3.90393	UGT1A3	NM_019093.2
cg25612480	-0.119528142	0.5831921	-5.916059	2.45E-08	7.81E-06	8.474016	UBE2V2	NM_003350.2
cg14252059	-0.119684432	0.4959358	-5.136364	9.30E-07	7.37E-05	4.946054	TECTA	NM_005422.1
cg27043873	-0.119732069	0.5910573	-4.656208	7.45E-06	0.0002771	2.942086	CDH18	NM_004934.2
cg09134726	-0.119794709	0.5958367	-4.371207	2.40E-05	0.0006357	1.820378	PRTN3	NM_002777.3
cg12456510	-0.120081087	0.5701389	-4.456717	1.70E-05	0.0004927	2.151387	TFF2	NM_005423.3
cg20811607	-0.120165185	0.6336803	-5.247191	5.65E-07	5.25E-05	5.427764	SMPD2	NM_003080.1
cg10929387	-0.12024346	0.6856453	-4.331524	2.82E-05	0.0007133	1.66841	ITIH4	NM_002218.3
cg25214366	-0.120272182	0.5894663	-4.301129	3.18E-05	0.0007779	1.552727	DEFB103A	NM_018661.2
cg16413535	-0.120281233	0.7535712	-5.774646	4.84E-08	1.26E-05	7.811062	TKTL2	NM_032136.3
cg24765079	-0.120340541	0.4132064	-4.38888	2.24E-05	0.000604	1.888392	CDH1	NT_010498.15
cg01772980	-0.120598523	0.6183646	-5.098288	1.10E-06	8.27E-05	4.782163	SCGB1D1	NM_006552.1
cg24580782	-0.120787409	0.805551	-5.066034	1.27E-06	9.01E-05	4.643987	NROB2	NM_021969.1
cg22658979	-0.120799141	0.6916922	-5.208812	6.72E-07	5.85E-05	5.260169	MMP13	NM_002427.2

cg055013 57	-0.120895274	0.5742506	-5.99969	1.63E-08	6.00E-06	8.87057	HIPK3	NM_005734.2
cg027196 34	-0.120927216	0.6972204	-5.022873	1.54E-06	0.0001004	4.460022	SLC22A18 AS	NM_007105.1
cg261919 51	-0.121080841	0.463347	-6.355882	2.78E-09	2.53E-06	10.59504	RNASE2	NM_002934.2
cg044577 94	-0.121093906	0.5194326	-3.855436	0.000176	0.002689	-0.070353	CTSE	NM_001910.2
cg164834 66	-0.121330442	0.6327223	-4.672467	6.96E-06	0.0002641	3.007648	C20orf186	NM_182519.1
cg251825 23	-0.121405974	0.5243326	-4.989503	1.78E-06	0.0001121	4.318536	C1orf24	NM_022083.1
cg030037 45	-0.121421337	0.3874628	-5.065854	1.27E-06	9.01E-05	4.643215	UNQ473	NM_198477.1
cg159379 58	-0.12153523	0.6896321	-4.895256	2.70E-06	0.0001444	3.919098	UNQ473	NM_198477.1
cg243550 48	-0.121726939	0.4428544	-5.280687	4.85E-07	4.77E-05	5.574702	CTSG	NM_001911.2
cg081240 30	-0.121837838	0.4483531	-4.978622	1.87E-06	0.0001159	4.272543	TM4SF1	NM_014220.2
cg208950 28	-0.121910187	0.6580009	-4.628753	8.36E-06	0.0002968	2.831756	CDH26	NM_177980.1
cg274201 23	-0.121992266	0.426509	-4.930103	2.31E-06	0.0001341	4.068308	FSHB	NM_000510.2
cg130385 60	-0.122093134	0.6921685	-5.069489	1.25E-06	8.96E-05	4.658759	FLJ22555	NM_024520.1
cg128186 99	-0.122144072	0.6349609	-5.236679	5.92E-07	5.37E-05	5.381777	C6orf32	NM_015864.2
cg249286 87	-0.122194638	0.665885	-4.346796	2.65E-05	0.0006795	1.726771	EPHX1	NM_000120.2
cg068480 73	-0.122251604	0.4347192	-4.753411	4.94E-06	0.0002097	3.3365	FBXO44	NM_00101476 5.1
cg166070 65	-0.122254582	0.6664937	-4.920164	2.41E-06	0.0001351	4.026642	TP73	NT_004321.17
cg169868 46	-0.122386074	0.4202606	-4.608122	9.11E-06	0.0003122	2.749166	SCGB2A1	NM_002407.1
cg273418 60	-0.122387478	0.8222873	-5.37498	3.15E-07	3.70E-05	5.991663	OR2L13	NM_175911.2
cg185347 30	-0.122526872	0.6074445	-4.650924	7.66E-06	0.0002814	2.920768	CABP5	NM_019855.3
cg152417 08	-0.122583532	0.7267215	-4.555987	1.13E-05	0.0003654	2.541658	CNOT6	NM_015455.3
cg128674 48	-0.122715292	0.721479	-5.43576	2.38E-07	3.23E-05	6.262983	ODF2	NM_002540.3
cg146968 70	-0.122755518	0.6287189	-3.848689	0.0001805	0.0027415	-0.093839	FCER1A	NM_002001.2
cg146033 45	-0.122765159	0.3646356	-5.479021	1.95E-07	2.94E-05	6.457299	BTBD3	NM_181443.1
cg179075 67	-0.122798631	0.4468312	-4.538831	1.21E-05	0.0003843	2.473756	HAMP	NM_021175.2
cg110619 75	-0.122856008	0.7290808	-4.757377	4.86E-06	0.0002085	3.352716	SIRPB2	NM_018556.2
cg092077 18	-0.122934686	0.7357251	-4.634766	8.15E-06	0.0002945	2.855881	CYP1A2	NM_000761.3
cg102871 37	-0.123364942	0.5880747	-5.105607	1.07E-06	8.09E-05	4.813603	P2RY2	NM_002564.2

cg160196 20	-0.123633828	0.5574866	-5.351592	3.51E-07	3.95E-05	5.887793	MEP1A	NM_005588.1
cg270150 47	-0.12363654	0.6068897	-5.907558	2.55E-08	7.95E-06	8.433893	DMBT1	NM_004406.1
cg129700 84	-0.123665295	0.4615341	-5.036516	1.45E-06	9.73E-05	4.518053	ELF3	NM_004433.3
cg199103 82	-0.12387395	0.6771979	-4.602415	9.33E-06	0.0003179	2.726365	FABP1	NM_001443.1
cg087752 30	-0.123897725	0.4920491	-5.626487	9.78E-08	1.92E-05	7.127027	C11orf52	NM_080659.1
cg112612 64	-0.123956377	0.5849992	-5.431817	2.43E-07	3.25E-05	6.245321	PTPRH	NM_002842.2
cg042454 02	-0.124213647	0.4995845	-4.65277	7.56E-06	0.0002792	2.928247	C19orf21	NM_173481.2
cg094488 75	-0.124217396	0.5582027	-5.523002	1.59E-07	2.58E-05	6.655859	ABCC2	NM_000392.1
cg167310 16	-0.124246392	0.7457962	-5.098722	1.10E-06	8.27E-05	4.784028	LGALS4	NM_006149.2
cg203992 52	-0.124316912	0.6812087	-4.39964	2.14E-05	0.0005843	1.929905	EBPL	NM_032565.1
cg276531 34	-0.124386813	0.5859682	-5.075917	1.22E-06	8.90E-05	4.68626	A2ML1	NM_144670.2
cg103217 23	-0.124409893	0.7048582	-4.241029	4.06E-05	0.0009348	1.324871	PDZK1	NM_002614.3
cg074477 73	-0.124437462	0.5798924	-4.927485	2.34E-06	0.0001341	4.057329	AKR7A3	NM_012067.2
cg159100 79	-0.124447111	0.454249	-6.206948	5.86E-09	3.43E-06	9.867167	RNASE3	NM_002935.2
cg137972 82	-0.124509855	0.6656879	-5.555278	1.37E-07	2.37E-05	6.802218	CARD10	NM_014550.3
cg239841 30	-0.124524161	0.6441716	-4.949996	2.12E-06	0.0001278	4.151876	0	0
cg048287 92	-0.124572478	0.6248741	-4.932293	2.29E-06	0.0001338	4.077497	MX2	NM_002463.1
cg238773 85	-0.124628492	0.5762294	-5.139897	9.15E-07	7.30E-05	4.961304	GCNT3	NM_004751.1
cg267388 80	-0.124641486	0.558827	-5.843661	3.47E-08	9.67E-06	8.133404	DPP6	NM_001936.2
cg240127 08	-0.124794515	0.471044	-6.542312	1.08E-09	1.59E-06	11.51932	HDHD3	NM_031219.2
cg006264 66	-0.12483479	0.48507	-6.163095	7.28E-09	3.88E-06	9.654693	GNS	NM_002076.2
cg185420 98	-0.124847506	0.733366	-5.029878	1.49E-06	9.90E-05	4.489804	FLJ36445	NM_153233.1
cg039776 57	-0.124990972	0.5285363	-5.824137	3.82E-08	1.04E-05	8.041981	LAMB3	NM_000228.2
cg187668 47	-0.125023252	0.5472687	-6.203626	5.96E-09	3.43E-06	9.851043	ACMSD	NM_138326.1
cg021682 91	-0.125150332	0.6162524	-5.25619	5.42E-07	5.12E-05	5.467179	CDH13	NT_010498.15
cg029984 25	-0.125196215	0.6662377	-5.222632	6.31E-07	5.57E-05	5.320423	ADAM21	NM_003813.2
cg198076 85	-0.125234388	0.5597346	-5.149704	8.76E-07	7.05E-05	5.00367	HSD17B2	NM_002153.1
cg076650 60	-0.125313491	0.3865061	-6.395494	2.27E-09	2.34E-06	10.79023	C19orf33	NM_033520.1

cg231115 44	-0.12531401	0.578783	-5.533405	1.51E-07	2.50E-05	6.702976	REG1A	NM_002909.3
cg091952 71	-0.125326656	0.524413	-3.971567	0.0001142	0.0019322	0.339069	RNF186	NM_019062.1
cg135207 15	-0.125612574	0.6656216	-6.43786	1.84E-09	2.03E-06	10.99971	C21orf129	NM_152506.1
cg090815 44	-0.125725908	0.5900651	-4.622603	8.58E-06	0.0003025	2.807108	MUC13	NM_033049.2
cg271328 14	-0.125799737	0.4840712	-5.1302	9.56E-07	7.47E-05	4.919469	C20orf79	NM_178483.2
cg077110 97	-0.125827693	0.7435273	-4.547373	1.18E-05	0.0003752	2.505556	GML	NM_002066.1
cg095395 38	-0.125923513	0.4443995	-6.151185	7.73E-09	3.88E-06	9.597131	C20orf42	NM_017671.3
cg263905 26	-0.126003796	0.6665097	-4.545781	1.18E-05	0.0003752	2.50124	FLG	NM_002016.1
cg136889 66	-0.126095415	0.3534988	-5.954507	2.03E-08	6.89E-06	8.655918	TM4SF4	NM_004617.2
cg256121 45	-0.126196912	0.7237654	-4.799967	4.05E-06	0.0001879	3.527479	STK31	NM_031414.2
cg244276 60	-0.126458401	0.5222528	-5.019853	1.56E-06	0.0001012	4.447192	PNPLA2	NM_020376.2
cg222681 64	-0.126634985	0.5086399	-4.133558	6.15E-05	0.001243	0.926206	TRHR	NM_003301.1
cg148266 83	-0.12692142	0.5159097	-5.420969	2.55E-07	3.30E-05	6.196773	SPRR2D	NM_006945.3
cg026436 67	-0.127304696	0.7020205	-5.380194	3.08E-07	3.67E-05	6.01486	TFF1	NM_003225.2
cg246075 35	-0.127457205	0.5802911	-5.384636	3.02E-07	3.63E-05	6.034634	CDH26	NM_177980.1
cg274965 06	-0.128131532	0.5801002	-5.020467	1.57E-06	0.0001014	4.448107	TGM5	NM_201631.1
cg095847 11	-0.128339932	0.472726	-6.104819	9.72E-09	4.52E-06	9.373655	HPR	NM_020995.3
cg177415 72	-0.128597863	0.6514462	-4.184398	5.04E-05	0.0010845	1.114258	CFB	NM_001710.4
cg006893 40	-0.12868868	0.3596179	-5.87438	2.99E-08	9.12E-06	8.27762	RTKN	NM_033046.2
cg156522 12	-0.12927751	0.6064922	-5.388382	2.97E-07	3.61E-05	6.051317	FLJ90586	NM_153345.1
cg146595 47	-0.129327009	0.5495878	-4.816903	3.77E-06	0.0001804	3.597282	RETNLB	NM_032579.1
cg188331 40	-0.129402687	0.4615806	-5.930811	2.28E-08	7.57E-06	8.543726	HABP2	NM_004132.2
cg172045 57	-0.130058228	0.5933933	-6.449172	1.73E-09	2.00E-06	11.05577	FLJ14816	NM_032845.1
cg191112 62	-0.130151007	0.4649726	-5.993787	1.68E-08	6.00E-06	8.842469	IGSF9	NM_020789.2
cg208703 62	-0.130273997	0.549381	-4.996912	1.72E-06	0.000109	4.349895	CCIN	NM_005893.1
cg037238 45	-0.130282866	0.6679909	-5.020099	1.56E-06	0.0001012	4.448235	BTNL8	NM_024850.1
cg082618 41	-0.130335406	0.6315504	-5.466157	2.07E-07	3.03E-05	6.399411	FLJ90586	NM_153345.1
cg228090 47	-0.130337271	0.4710904	-4.724462	5.62E-06	0.0002266	3.218071	RPL31	NM_000993.2

cg186781 21	-0.130616713	0.5595585	-4.195948	4.82E-05	0.0010528	1.157225	SEC61A2	NM_018144.2
cg276226 10	-0.130766446	0.4757501	-4.869784	3.00E-06	0.0001525	3.816359	OR1G1	NM_003555.1
cg010746 40	-0.130822714	0.6413372	-5.695516	7.06E-08	1.57E-05	7.444362	IFNA17	NM_021268.1
cg052447 66	-0.130826264	0.6405388	-5.338813	3.72E-07	4.11E-05	5.831162	GSTP1	NM_000852.2
cg272213 38	-0.130922454	0.7626359	-6.143064	8.04E-09	3.95E-06	9.557918	KDELR2	NM_006854.2
cg184376 33	-0.131292231	0.6077972	-6.030847	1.40E-08	5.53E-06	9.019141	ITGB6	NM_000888.3
cg240276 79	-0.131300618	0.7229574	-5.300134	4.48E-07	4.63E-05	5.657152	SLC2A7	NM_207420.1
cg005468 97	-0.131368649	0.5000152	-6.541641	1.08E-09	1.59E-06	11.51597	LOC28483 7	NM_194310.1
cg276105 61	-0.131382552	0.6181548	-3.913726	0.0001418	0.0023071	0.133935	SLC2A10	NM_030777.3
cg204376 04	-0.131551759	0.4761072	-6.093938	1.04E-08	4.67E-06	9.310955	ANXA9	NM_003568.1
cg221901 14	-0.131720703	0.7780177	-4.813179	3.83E-06	0.0001814	3.581917	NALP8	NM_176811.2
cg151490 98	-0.13175584	0.6354823	-5.710912	6.56E-08	1.49E-05	7.515466	SULT2B1	NM_177973.1
cg118712 80	-0.131761251	0.7132813	-5.199862	6.99E-07	5.99E-05	5.221201	SLC16A7	NM_004731.3
cg272103 90	-0.132074401	0.376243	-6.589538	8.47E-10	1.58E-06	11.7557	TOM1L1	NM_005486.1
cg034213 00	-0.132433174	0.692605	-5.634906	9.40E-08	1.90E-05	7.165603	SFN	NM_006142.3
cg040016 68	-0.13309256	0.7262956	-5.628333	9.70E-08	1.92E-05	7.135482	GPR56	NM_201525.1
cg161766 00	-0.133163026	0.3881962	-5.416905	2.60E-07	3.33E-05	6.178601	FRK	NM_002031.2
cg199828 60	-0.133222209	0.5967395	-5.71474	6.44E-08	1.48E-05	7.533163	IFNA21	NM_002175.1
cg023994 55	-0.133341574	0.716894	-5.353935	3.47E-07	3.95E-05	5.898183	SRI	NM_198901.1
cg018354 89	-0.133367436	0.5086622	-5.925603	2.34E-08	7.57E-06	8.519104	KRT8	NM_002273.2
cg127883 13	-0.133397483	0.6584104	-5.369672	3.23E-07	3.75E-05	5.968065	MST1	NM_020998.2
cg084958 78	-0.133453985	0.6691924	-4.935664	2.25E-06	0.000133	4.091644	SERPINA4	NM_006215.2
cg214848 34	-0.133661851	0.5635727	-6.156687	7.52E-09	3.88E-06	9.623712	PTK6	NM_005975.2
cg118006 72	-0.133726035	0.5169795	-4.795298	4.13E-06	0.0001907	3.508267	SLC39A4	NM_130849.1
cg240242 14	-0.133773774	0.6273777	-4.899203	2.66E-06	0.0001426	3.935558	BTNL8	NM_024850.1
cg216854 27	-0.133794882	0.5910943	-5.109676	1.05E-06	8.02E-05	4.831097	SGK2	NM_016276.3
cg148942 16	-0.133937973	0.4956086	-6.248027	4.77E-09	3.01E-06	10.06697	CATSPER1	NM_053054.2
cg137189 60	-0.13396711	0.5604864	-4.905222	2.57E-06	0.0001407	3.964117	RNASE1	NM_198232.1

cg150510 63	-0.134352863	0.7203555	-4.77635	4.48E-06	0.0002001	3.430432	0	0
cg204161 79	-0.134564481	0.614685	-6.082295	1.09E-08	4.71E-06	9.265445	C6orf71	NM_203395.1
cg251194 15	-0.134575979	0.5462406	-5.109006	1.05E-06	8.02E-05	4.828213	MNDA	NM_002432.1
cg167722 07	-0.134736024	0.6539493	-4.681576	6.70E-06	0.000257	3.044451	MYT1	NM_004535.2
cg197171 50	-0.134857888	0.4450402	-5.317485	4.10E-07	4.37E-05	5.736845	HNF4A	NM_000457.3
cg224388 10	-0.135181886	0.5346897	-5.780823	4.70E-08	1.26E-05	7.839816	LCN2	NM_005564.2
cg189173 78	-0.135265737	0.4215679	-5.748158	5.49E-08	1.37E-05	7.687968	BCAS1	NM_003657.1
cg275137 64	-0.135273401	0.580673	-5.67765	7.68E-08	1.65E-05	7.361998	EFCAB3	NM_173503.1
cg238345 93	-0.1353426	0.4698103	-5.631213	9.57E-08	1.91E-05	7.148679	HNF4A	NM_000457.3
cg006686 85	-0.135369226	0.727497	-4.75189	4.97E-06	0.0002104	3.330282	SLC39A5	NM_173596.1
cg267184 20	-0.135378588	0.6127945	-5.671405	7.91E-08	1.68E-05	7.333248	C12orf59	NM_153022.1
cg072077 89	-0.135396239	0.5159194	-5.28755	4.70E-07	4.75E-05	5.604887	CRISPLD2	NM_031476.1
cg206955 87	-0.135535315	0.5890194	-6.294613	3.78E-09	2.72E-06	10.29445	TMPRSS1 1F	NM_207407.1
cg124913 68	-0.135612336	0.5437255	-4.32707	2.87E-05	0.0007241	1.651419	LOC19654 9	NM_145293.2
cg008084 92	-0.135683775	0.6158129	-5.049881	1.37E-06	9.44E-05	4.575011	REG4	NM_032044.2
cg248248 40	-0.136247562	0.6857554	-5.270986	5.07E-07	4.94E-05	5.532086	SHANK1	NM_016148.1
cg116396 51	-0.136542836	0.5774025	-5.315962	4.13E-07	4.38E-05	5.730119	HKDC1	NM_025130.2
cg161120 50	-0.136567232	0.6930024	-4.739475	5.24E-06	0.0002163	3.279591	ENOSF1	NM_017512.2
cg229830 92	-0.136592824	0.7385397	-4.517452	1.33E-05	0.0004087	2.389402	KRT25A	NM_181534.2
cg082680 99	-0.13664126	0.6313469	-5.205874	6.81E-07	5.91E-05	5.24737	OLFM1	NM_014279.2
cg032702 04	-0.137230666	0.5707089	-5.319198	4.07E-07	4.35E-05	5.744411	DDR1	NM_001954.3
cg239683 83	-0.137500495	0.6669213	-4.719664	5.70E-06	0.0002285	3.198901	ZNF572	NM_152412.1
cg094183 21	-0.137896052	0.4205436	-6.176864	6.80E-09	3.83E-06	9.721313	DYRK4	NM_003845.1
cg112045 62	-0.138204131	0.5955909	-5.667473	8.06E-08	1.69E-05	7.315154	C10orf81	NM_024889.3
cg154797 52	-0.138252305	0.7691488	-5.3917	2.92E-07	3.61E-05	6.066102	FFAR2	NM_005306.1
cg215789 06	-0.138403275	0.6918168	-5.072057	1.24E-06	8.96E-05	4.669742	SLC5A4	NM_014227.1
cg135532 04	-0.138582156	0.4656674	-5.479803	1.94E-07	2.94E-05	6.460819	CNKSR1	NM_006314.1
cg056599 47	-0.13880513	0.5277286	-5.498349	1.78E-07	2.79E-05	6.544434	C4BPB	NM_000716.3

cg000759 67	-0.139110125	0.5988561	-6.03452	1.37E-08	5.51E-06	9.036682	STRA6	NM_022369.2
cg203126 87	-0.139442718	0.5202634	-5.579729	1.22E-07	2.25E-05	6.913457	DEFB118	NM_054112.1
cg273839 56	-0.140237519	0.639178	-5.166032	8.14E-07	6.66E-05	5.074326	FLJ13265	NM_024877.1
cg255275 47	-0.140449852	0.594296	-5.057712	1.32E-06	9.22E-05	4.608429	PLOD3	NM_001084.4
cg058286 24	-0.140471494	0.6494553	-5.375227	3.15E-07	3.70E-05	5.992761	REG1A	NM_002909.3
cg216430 45	-0.140569342	0.6724173	-6.007249	1.57E-08	5.94E-06	8.906573	CCL20	NM_004591.1
cg118842 43	-0.140577788	0.6785193	-5.066766	1.27E-06	9.01E-05	4.647116	FCN2	NM_004108.2
cg209805 92	-0.141516623	0.7213925	-5.579843	1.22E-07	2.25E-05	6.913976	MEP1A	NM_005588.1
cg242725 59	-0.141712208	0.5905384	-5.720649	6.26E-08	1.48E-05	7.560494	LOC11612 3	NM_138784.1
cg176287 17	-0.141740292	0.6530419	-5.117152	1.01E-06	7.80E-05	4.863258	HECW1	NM_015052.2
cg070847 09	-0.141812208	0.7004271	-4.879245	2.88E-06	0.0001505	3.855731	Gcom1	NM_00101809 0.1
cg159136 71	-0.141846616	0.4707126	-5.77494	4.83E-08	1.26E-05	7.812428	TMEM105	NM_178520.2
cg170308 20	-0.142001548	0.6612156	-4.916824	2.46E-06	0.0001374	4.011456	MSMB	NM_002443.2
cg212015 72	-0.142061641	0.4847451	-5.772553	4.89E-08	1.26E-05	7.801322	AGR2	NM_006408.2
cg024900 34	-0.142163775	0.5049509	-5.434004	2.40E-07	3.23E-05	6.255116	MEST	NM_177524.1
cg096431 86	-0.143176368	0.6963026	-5.699995	6.91E-08	1.55E-05	7.465033	GPX2	NM_002083.2
cg074122 54	-0.1436172	0.569691	-6.747366	3.75E-10	9.94E-07	12.552	FLJ14816	NM_032845.1
cg065182 71	-0.144607563	0.634412	-6.150998	7.73E-09	3.88E-06	9.596229	ADH6	NM_000672.2
cg099881 16	-0.144945013	0.6531546	-5.175116	7.82E-07	6.55E-05	5.113701	MGC5242 3	NM_182517.1
cg025378 38	-0.145005458	0.5446595	-5.862509	3.17E-08	9.12E-06	8.221835	C20orf151	NM_080833.1
cg062552 27	-0.145528541	0.7649582	-5.328737	3.90E-07	4.21E-05	5.786571	NPBWR2	NM_005286.2
cg130190 92	-0.145615204	0.6219806	-5.562354	1.32E-07	2.34E-05	6.83438	PDZK1	NM_002614.3
cg183681 25	-0.145778086	0.6840403	-6.350088	2.86E-09	2.53E-06	10.56655	TMED6	NM_144676.1
cg072209 39	-0.146178544	0.4681265	-4.418549	1.99E-05	0.0005526	2.003043	SLC22A12	NM_144585.2
cg010536 21	-0.146364131	0.6175567	-5.091509	1.14E-06	8.43E-05	4.753072	APOA2	NM_001643.1
cg276007 94	-0.146407887	0.5841515	-4.567187	1.08E-05	0.0003536	2.58609	PNLIPRP1	NM_006229.1
cg153204 74	-0.146967702	0.5147535	-5.563235	1.32E-07	2.34E-05	6.838384	UBD	NM_006398.2
cg137970 31	-0.146968241	0.6154733	-5.687244	7.42E-08	1.62E-05	7.400735	NIPSNAP1	NM_003634.1

cg002088 30	-0.147839084	0.5563797	-6.123447	8.86E-09	4.27E-06	9.463324	LAMC2	NM_005562.1
cg049944 56	-0.147911229	0.6291474	-6.15986	7.40E-09	3.88E-06	9.639049	RNF186	NM_019062.1
cg149404 20	-0.148078285	0.6048048	-6.510568	1.27E-09	1.68E-06	11.36094	IQCF2	NM_203424.1
cg261641 84	-0.148978714	0.6820437	-5.453998	2.19E-07	3.07E-05	6.344783	FCN2	NM_004108.2
cg063942 29	-0.149302924	0.5207969	-4.927802	2.33E-06	0.0001341	4.058658	LGAL54	NM_006149.2
cg222669 67	-0.149330597	0.5242969	-6.579354	8.92E-10	1.58E-06	11.70465	S100P	NM_005980.2
cg114359 43	-0.149386403	0.6138295	-5.285386	4.75E-07	4.77E-05	5.595369	SERPINB1 2	NM_080474.1
cg024421 61	-0.149677342	0.5235389	-5.596355	1.13E-07	2.16E-05	6.98927	PI3	NM_002638.2
cg117623 46	-0.149821619	0.60773	-5.771311	4.92E-08	1.26E-05	7.795545	HKDC1	NM_025130.2
cg078977 01	-0.149936628	0.5628891	-5.971495	1.87E-08	6.43E-06	8.73651	ABP1	NM_001091.2
cg161484 54	-0.149962997	0.6114081	-6.762068	3.48E-10	9.94E-07	12.62666	TMED6	NM_144676.1
cg205569 88	-0.150130503	0.6866559	-5.675978	7.74E-08	1.65E-05	7.354297	CCL1	NM_002981.1
cg045670 09	-0.150189958	0.6148134	-5.295542	4.54E-07	4.64E-05	5.640069	FCGR3B	NM_000570.2
cg161730 67	-0.150488754	0.5755449	-5.536676	1.49E-07	2.50E-05	6.717801	SDCBP2	NM_015685.3
cg260919 81	-0.150706582	0.6301108	-6.258424	4.53E-09	2.93E-06	10.11766	LCT	NM_002299.2
cg154858 59	-0.150840794	0.52241	-6.10055	9.92E-09	4.53E-06	9.353129	C1orf116	NM_023938.4
cg148987 79	-0.150853695	0.6787777	-5.172102	7.92E-07	6.60E-05	5.100632	STK31	NM_031414.2
cg222891 15	-0.151022339	0.7234931	-5.386995	2.98E-07	3.61E-05	6.045139	MUCDHL	NM_021924.2
cg155603 37	-0.152183646	0.5518512	-5.493231	1.83E-07	2.83E-05	6.521343	HYAL4	NM_012269.1
cg007444 33	-0.152585879	0.55671	-6.312886	3.45E-09	2.70E-06	10.38393	CXADR	NM_001338.3
cg032921 49	-0.153782714	0.6477975	-6.119292	9.05E-09	4.28E-06	9.443309	CBLC	NM_012116.2
cg274623 98	-0.154339767	0.6704972	-6.357803	2.84E-09	2.53E-06	10.58357	C1orf181	NM_017953.2
cg031093 16	-0.154996408	0.7120351	-5.300818	4.43E-07	4.60E-05	5.663314	ZNF80	NM_007136.1
cg124939 06	-0.155427934	0.6144177	-5.42006	2.56E-07	3.30E-05	6.192707	MMP26	NM_021801.3
cg108833 52	-0.156271165	0.7436055	-5.738256	5.76E-08	1.40E-05	7.64204	0	0
cg166395 95	-0.156330962	0.5532623	-6.326269	3.22E-09	2.70E-06	10.44956	SRI	NM_198901.1
cg107840 90	-0.157019683	0.5425396	-5.188405	7.36E-07	6.25E-05	5.171388	CLDN18	NM_00100202 6.2
cg214784 37	-0.15763486	0.6193645	-5.532817	1.52E-07	2.50E-05	6.70031	CTSE	NM_001910.2

cg184626 53	-0.158061987	0.4719966	-5.462655	2.10E-07	3.04E-05	6.383668	DEFB119	NM_153289.2
cg004127 72	-0.158942034	0.6615692	-6.793786	2.95E-10	9.94E-07	12.78801	C19orf33	NM_033520.1
cg172987 04	-0.159221957	0.5611056	-4.688688	6.50E-06	0.0002509	3.073221	CLDN18	NM_00100202 6.2
cg006986 88	-0.15960568	0.5594377	-6.042431	1.32E-08	5.38E-06	9.074491	SULT2B1	NM_177973.1
cg005159 05	-0.159864939	0.7082908	-6.020715	1.47E-08	5.64E-06	8.970776	EPS8L3	NM_024526.2
cg061948 08	-0.160162098	0.5413795	-5.430421	2.44E-07	3.25E-05	6.239072	MGC9712	NM_152689.2
cg043842 08	-0.160189997	0.4541892	-6.474317	1.55E-09	1.87E-06	11.16719	FCGR3A	NM_000569.6
cg182233 79	-0.160416454	0.5764279	-5.369965	3.23E-07	3.75E-05	5.969367	BPIL3	NM_174897.1
cg263776 77	-0.160697909	0.6276396	-5.561831	1.33E-07	2.34E-05	6.832001	FURIN	NM_002569.2
cg077859 36	-0.16091198	0.6047311	-6.622863	7.14E-10	1.45E-06	11.92303	GPR39	NM_001508.1
cg266086 67	-0.161310411	0.6178215	-5.128956	9.68E-07	7.53E-05	4.911866	MGC1125 7	NM_032350.3
cg033874 97	-0.161491581	0.5622848	-6.278272	4.10E-09	2.72E-06	10.21455	C20orf179	NM_00101497 7.1
cg236969 49	-0.162189765	0.3785688	-7.567521	4.77E-12	6.32E-08	16.83178	LAMC2	NM_005562.1
cg026338 17	-0.162248046	0.5870381	-6.682576	5.25E-10	1.16E-06	12.22395	FXYD3	NM_021910.1
cg123026 21	-0.1641423	0.5924142	-5.200175	6.98E-07	5.99E-05	5.222566	SLC28A1	NM_004213.3
cg004801 15	-0.165645793	0.5778415	-6.749493	3.71E-10	9.94E-07	12.5628	FXYD3	NM_021910.1
cg224873 22	-0.165662554	0.6526185	-5.716679	6.38E-08	1.48E-05	7.542131	IL20RA	NM_014432.2
cg084584 87	-0.168379424	0.5974304	-5.854513	3.30E-08	9.29E-06	8.184296	SFTPD	NM_003019.4
cg015805 68	-0.169683738	0.6330476	-6.715577	4.42E-10	1.07E-06	12.39084	LAMB3	NM_000228.2
cg154221 47	-0.170195852	0.6199431	-6.224994	5.35E-09	3.22E-06	9.95485	SERPINB5	NM_002639.2
cg011191 35	-0.170293323	0.5183883	-6.473521	1.53E-09	1.87E-06	11.17661	C1orf116	NM_023938.4
cg036849 77	-0.1703138	0.5575969	-5.730599	5.97E-08	1.44E-05	7.606559	GRB7	NM_005310.2
cg084110 49	-0.170424856	0.6063249	-5.971849	1.87E-08	6.43E-06	8.738191	SERPINB5	NM_002639.2
cg210941 54	-0.174712288	0.5836265	-5.994088	1.67E-08	6.00E-06	8.843903	TNFSF11	NM_003701.2
cg254336 48	-0.175580891	0.6470362	-5.718592	6.32E-08	1.48E-05	7.550978	S100A14	NM_020672.1
cg208377 35	-0.17590703	0.6352378	-6.083745	1.08E-08	4.71E-06	9.272403	SERPINB5	NM_002639.2
cg161757 25	-0.1760158	0.4911767	-5.574785	1.25E-07	2.28E-05	6.890939	TCF1	NM_000545.3
cg054986 81	-0.179284118	0.6596305	-6.547858	1.05E-09	1.59E-06	11.54704	SRC	NM_005417.3

cg223467 65	-0.179558095	0.5263328	-6.527057	1.17E-09	1.63E-06	11.44316	UNC5CL	NM_173561.1
cg129076 44	-0.181784514	0.5092071	-7.635137	3.30E-12	6.32E-08	17.19412	SAA2	NM_030754.2
cg154843 75	-0.183397842	0.4721903	-7.383915	1.29E-11	1.14E-07	15.85468	SAA1	NM_199161.1

Figure 18**Invasive subtype vs proliferative subtype**

probeset	GeneName	Inv1_Pro2	t
201496_x_at	MYH11	1	16.78624612
222722_at	OGN	1	15.86875576
209613_s_at	ADH1B	1	14.94898083
223623_at	C2orf40	1	15.92992939
218730_s_at	OGN	1	17.86620622
202992_at	C7	1	18.42541061
225720_at	SYNPO2	1	17.15146732
212730_at	SYNM	1	17.14849823
227662_at	SYNPO2	1	16.29354535
225894_at	SYNPO2	1	18.00011767
202222_s_at	DES	1	15.09544164
228202_at	PLN	1	17.19582839
225895_at	SYNPO2	1	15.8400793
205475_at	SCRG1	1	16.37777896
209612_s_at	ADH1B	1	14.54097857
204938_s_at	PLN	1	16.80419329
204719_at	ABCA8	1	16.82392921
210299_s_at	FHL1	1	19.26382637
226303_at	PGM5	1	17.86749716
228133_s_at	MYH11	1	17.7564569
204940_at	PLN	1	17.09147837
228504_at		0	22.68041227
227827_at		0	15.57893475
204939_s_at	PLN	1	16.36436826
227826_s_at		0	15.33224205
225721_at	SYNPO2	1	17.8099863
228750_at		0	18.91272925
203951_at	CNN1	1	15.95525618
232298_at	hCG_1806964	1	17.9240204
231773_at	ANGPTL1	1	20.7301424
220595_at	PDZRN4	1	18.62420966
201497_x_at	MYH11	1	15.38958246
203766_s_at	LMOD1	1	18.59105674
214505_s_at	FHL1	1	19.99556557
202037_s_at	SFRP1	1	16.2523822
201539_s_at	FHL1	1	20.07840961
218087_s_at	SORBS1	1	17.24539622
237206_at	MYOCD	1	16.54700257
209763_at	CHRD1	1	15.62332708
202274_at	ACTG2	1	14.07912014
238751_at		0	15.59982669
228885_at	MAMDC2	1	21.74275045
205433_at	BCHE	1	15.0977277
210298_x_at	FHL1	1	19.73198976
214027_x_at	DES /// FAM48A	1	15.72673726
226304_at	HSPB6	1	21.74771488
203296_s_at	ATP1A2	1	19.52415407
202920_at	ANK2	1	18.51622312

212805_at	PRUNE2	1	15.68229925
1556325_at	FILIP1	1	20.47712718
235183_at	0	1	19.06368796
225381_at	LOC399959	1	16.2474567
202036_s_at	SFRP1	1	16.40633859
229461_x_at	NEGR1	1	19.85165725
227061_at	0	1	15.01198178
209687_at	CXCL12	1	15.25580432
243278_at	FOXP2	1	17.55484122
205357_s_at	AGTR1	1	17.23640908
219230_at	TMEM100	1	17.48728883
209541_at	IGF1	1	14.42255129
219772_s_at	SMPX	1	12.81291158
236141_at	NBLA00301	1	17.75173339
201495_x_at	MYH11	1	17.62537696
209540_at	IGF1	1	15.11747741
224339_s_at	ANGPTL1	1	20.55419122
206201_s_at	MEOX2	1	17.18042642
228854_at	0	1	17.04911332
221584_s_at	KCNMA1	1	16.2478521
223395_at	ABI3BP	1	14.21913756
213371_at	LDB3	1	17.08034188
218934_s_at	HSPB7	1	17.80904651
1552309_a_at	NEXN	1	17.4916624
235759_at	0	1	17.3814491
235201_at	FOXP2	1	18.56661289
222717_at	SDPR	1	19.41217031
211276_at	TCEAL2	1	14.11125334
206552_s_at	TAC1	1	13.08697677
206577_at	VIP	1	13.05071926
226103_at	NEXN	1	18.05667036
212865_s_at	COL14A1	1	17.10203083
239183_at	ANGPTL1	1	19.93038317
1570515_a_at	FILIP1	1	18.08437994
209948_at	KCNMB1	1	16.20546223
221667_s_at	HSPB8	1	17.41740811
214767_s_at	HSPB6	1	19.84400564
227727_at	MGRPRF	1	18.5724737
201540_at	FHL1	1	17.31567637
219791_s_at	NBLA00301	1	16.8137827
229649_at	NRXN3	1	13.19983341
201058_s_at	MYL9	1	17.02016464
202555_s_at	MYLK	1	16.6196559
204793_at	GPRASP1	1	22.67402682
229288_at	EPHA7	1	13.56109878
225782_at	MSRB3	1	18.46804219
223235_s_at	SMOC2	1	14.10884562
212806_at	PRUNE2	1	15.77515536
204894_s_at	AOC3	1	19.25717594
202437_s_at	CYP1B1	1	12.320695

222043_at	CLU	1	15.9946876
207961_x_at	MYH11	1	16.3657032
235503_at	ASB5	1	12.6058345
244745_at	RERG	1	18.5806123
1569956_at	MYLK	1	16.24691321
1558828_s_at	LOC728264	1	18.52526492
201957_at	PPP1R12B	1	17.76650112
215306_at	0	1	20.55656456
204776_at	THBS4	1	13.11520943
210198_s_at	PLP1	1	16.25073471
203980_at	FABP4	1	11.24927282
206898_at	CDH19	1	14.07669626
230130_at	0	1	16.13092668
213068_at	DPT	1	11.65782806
237169_at	0	1	14.4813217
233496_s_at	CFL2	1	17.61861721
219685_at	TMEM35	1	16.25427405
223468_s_at	RGMA	1	18.65495717
204284_at	PPP1R3C	1	14.96790892
207390_s_at	SMTN	1	17.51482345
205498_at	GHR	1	20.59926989
229339_at	0	1	16.92366895
213438_at	NFASC	1	16.45134193
221583_s_at	KCNMA1	1	15.40491945
230595_at	LOC572558	1	18.3585719
221276_s_at	SYNC	1	16.41283397
213993_at	SPON1	1	15.98171409
228728_at	C7orf58	1	19.82686536
209283_at	CRYAB	1	20.75181716
227197_at	SGEF	1	14.89313512
217967_s_at	FAM129A	1	18.08449403
238533_at	EPHA7	1	13.21572145
209170_s_at	GPM6B	1	15.639392
213791_at	PENK	1	12.50961693
226834_at	0	1	15.28387533
225242_s_at	CCDC80	1	13.09800303
208335_s_at	DARC	1	14.21757836
227758_at	RERG	1	18.84758635
205782_at	FGF7	1	17.0703644
202436_s_at	CYP1B1	1	12.49866186
204955_at	SRPX	1	15.54876207
243357_at	NEGR1	1	21.35898987
230087_at	PRIMA1	1	17.65684927
211562_s_at	LMOD1	1	17.9122082
209242_at	PEG3	1	18.43545957
225990_at	BOC	1	21.99174038
236038_at	0	1	21.09004688
244108_at	SYNPO2	1	17.14097869
201525_at	APOD	1	11.29916743
204796_at	EML1	1	18.4458159

213413_at	STON1	1	18.29649313
206070_s_at	EPHA3	1	13.96015858
205907_s_at	OMD	1	13.21483066
229127_at	JAM2	1	19.52245958
221748_s_at	TNS1	1	18.44099158
202995_s_at	FBLN1	1	13.50327185
223122_s_at	SFRP2	1	8.733775742
204424_s_at	LMO3	1	17.68444993
202291_s_at	MGP	1	14.30020611
229800_at	DCLK1	1	15.72665757
1557961_s_at	LOC100127983	1	18.14800761
220794_at	GREM2	1	12.57016643
228802_at	RBPM52	1	16.89719324
209167_at	GPM6B	1	14.82679179
227084_at	DTNA	1	15.08157618
221747_at	TNS1	1	20.61677659
239349_at	C1QTNF7	1	17.213969
204154_at	CDO1	1	19.57653114
204364_s_at	REEP1	1	11.02702303
213994_s_at	SPON1	1	13.9883327
238447_at	RBMS3	1	18.14009549
208131_s_at	PTGIS	1	14.34462947
212713_at	MFAP4	1	16.25614115
225790_at	MSRB3	1	19.10929815
205399_at	DCLK1	1	18.8402229
228107_at	LOC100127983	1	15.89579945
202035_s_at	SFRP1	1	15.56895026
219778_at	ZFPM2	1	17.28127962
229504_at	0	1	16.99761751
1554127_s_at	MSRB3	1	18.74271516
201843_s_at	EFEMP1	1	13.00439532
236304_at	0	1	14.89057909
227529_s_at	AKAP12	1	16.77766031
204359_at	FLRT2	1	14.56206821
238592_at	PDLIM3	1	16.39032818
228224_at	PRELP	1	18.7499995
235570_at	0	1	20.57708342
218711_s_at	SDPR	1	20.92597133
224352_s_at	CFL2	1	17.59449677
221207_s_at	NBEA	1	15.41135862
205795_at	NRXN3	1	12.61299901
205908_s_at	OMD	1	14.04968441
242447_at	C3orf70	1	12.82582671
201431_s_at	DPYSL3	1	16.67644635
222513_s_at	SORBS1	1	17.09087237
223987_at	CHRD12	1	11.876859
202435_s_at	CYP1B1	1	12.71722989
232119_at	SYNPO2	1	16.89125403
210221_at	CHRNA3	1	13.15592458
209621_s_at	PDLIM3	1	15.95162907

222877_at	0	1	14.90127046
214724_at	DIXDC1	1	21.4609757
204083_s_at	TPM2	1	15.84654664
239262_at	0	1	20.26972412
228640_at	PCDH7	1	11.81041988
202994_s_at	FBLN1	1	14.22561745
225996_at	LONRF2	1	15.82264447
227478_at	SETBP1	1	16.35197347
1553102_a_at	CCDC69	1	16.3557941
224663_s_at	CFL2	1	17.41022216
213714_at	CACNB2	1	16.46736791
228406_at	SMYD1	1	12.07782333
207957_s_at	PRKCB	1	16.24262361
232113_at	0	1	15.75022179
229024_at	0	1	19.43519735
210170_at	PDLIM3	1	16.96844476
209894_at	LEPR	1	16.56841034
204749_at	NAP1L3	1	16.30341899
238919_at	0	1	14.55451213
229530_at	GUCY1A3	1	17.10001406
212915_at	PDZRN3	1	15.60396867
226824_at	CPXM2	1	18.46904766
243140_at	ACTA2	1	17.339861
203881_s_at	DMD	1	14.84507268
217966_s_at	FAM129A	1	18.44766707
213974_at	ADAMTSL3	1	19.39081417
238481_at	MGP	1	13.82801975
227526_at	CDON	1	18.85820455
243864_at	CCDC80	1	16.94220778
227705_at	TCEAL7	1	16.82670399
225328_at	0	1	15.80267749
212554_at	CAP2	1	15.50150426
201645_at	TNC	1	11.83511503
204457_s_at	GAS1	1	11.00456938
209821_at	IL33	1	11.08433878
228827_at	0	1	15.48412251
224396_s_at	ASPN	1	11.27617577
213071_at	DPT	1	13.08265599
213436_at	CNR1	1	13.32871058
231067_s_at	0	1	17.37211468
205529_s_at	RUNX1T1	1	15.67315998
203697_at	FRZB	1	14.1708839
212423_at	ZCCHC24	1	19.97662902
225442_at	DDR2	1	16.75338201
225207_at	PDK4	1	11.00955681
1554547_at	FAM13C1	1	16.79433281
209209_s_at	FERMT2	1	18.16108217
224823_at	MYLK	1	15.27313999
228186_s_at	RSPO3	1	11.2410189
212764_at	ZEB1	1	18.28808246

227719_at	SMAD9	1	13.95975126
235489_at	RHOJ	1	17.24186828
238478_at	BNC2	1	18.71520108
226047_at	MRVI1	1	18.99110192
219737_s_at	PCDH9	1	14.21066585
223121_s_at	SFRP2	1	9.340537005
212886_at	CCDC69	1	17.35708259
219647_at	POPDC2	1	14.40341681
227530_at	AKAP12	1	16.27370931
226084_at	MAP1B	1	17.9669234
209897_s_at	SLIT2	1	16.70219856
222924_at	SLMAP	1	15.62215928
241789_at	0	1	22.06540722
228228_at	DACT3	1	19.32597009
211737_x_at	PTN	1	16.4499363
205933_at	SETBP1	1	17.53054297
230214_at	MRVI1	1	13.56560167
228507_at	0	1	17.72097736
206638_at	HTR2B	1	11.36787867
210875_s_at	ZEB1	1	18.84164036
212233_at	MAP1B	1	18.53702035
1555724_s_at	TAGLN	1	14.87942278
209469_at	GPM6A	1	14.16036831
231098_at	0	1	14.67225207
200930_s_at	VCL	1	15.9068054
227235_at	GUCY1A3	1	15.62428581
209436_at	SPON1	1	14.65442835
227915_at	ASB2	1	15.25709341
203698_s_at	FRZB	1	13.99483864
235182_at	ISM1	1	12.42125212
205330_at	MN1	1	15.90408179
1560359_at	PELO	1	17.64695289
227006_at	PPP1R14A	1	13.64222765
227561_at	DDR2	1	17.13682323
228850_s_at	0	1	18.1921761
226322_at	TMTCT1	1	18.95539589
204753_s_at	HLF	1	15.14778203
205392_s_at	CCL14 /// CCL15	1	15.67967536
203305_at	F13A1	1	13.20507819
230722_at	BNC2	1	18.34957939
204422_s_at	FGF2	1	20.39384959
207876_s_at	FLNC	1	16.737192
201615_x_at	CALD1	1	16.18538685
213992_at	COL4A6	1	11.28961747
221942_s_at	GUCY1A3	1	15.58712743
204223_at	PRELP	1	17.42156908
219654_at	PTPLA	1	11.77393379
212758_s_at	ZEB1	1	17.39547644
205547_s_at	TAGLN	1	14.37951466
223519_at	ZAK	1	17.51373348

1552848_a_at	PTCHD1	1	11.69144911
201616_s_at	CALD1	1	18.06045244
207317_s_at	CASQ2	1	14.14025272
213110_s_at	COL4A5	1	11.30259176
209465_x_at	PTN	1	15.78918453
230109_at	PDE7B	1	20.67020199
225241_at	CCDC80	1	14.98367282
204797_s_at	EML1	1	17.14912754
238441_at	PRKAA2	1	11.55155989
227971_at	NRK	1	13.91546392
200795_at	SPARCL1	1	17.29236451
225968_at	PRICKLE2	1	19.29845209
219845_at	BARX1	1	16.52127928
226523_at	TAGLN	1	16.50216659
205528_s_at	RUNX1T1	1	16.24377619
208096_s_at	COL21A1	1	16.17548492
204069_at	MEIS1	1	17.3497172
221019_s_at	COLEC12	1	13.64055145
213746_s_at	FLNA	1	16.36582725
232712_at	0	1	15.29180005
209243_s_at	PEG3 /// ZIM2	1	17.39812833
214348_at	TACR2	1	13.03145403
206227_at	CILP	1	11.03142646
204754_at	HLF	1	17.81754738
209210_s_at	FERMT2	1	18.86052015
221974_at	IPW	1	15.12699461
212419_at	ZCCHC24	1	21.20313441
201842_s_at	EFEMP1	1	12.34111258
203680_at	PRKAR2B	1	12.34177907
213306_at	MPDZ	1	22.3012521
202965_s_at	CAPN6	1	9.88321038
226931_at	TMTC1	1	17.66482504
235173_at	hCG_1806964	1	16.67199532
213933_at	PTGER3	1	16.40861268
1554741_s_at	FGF7 /// KGFLP1 /// KGFLP2	1	13.48525866
227618_at	0	1	19.90925371
208396_s_at	PDE1A	1	16.08787301
1553194_at	NEGR1	1	20.03771445
229578_at	JPH2	1	14.92556884
213904_at	0	1	15.32605347
205883_at	ZBTB16	1	16.81317851
228766_at	CD36	1	10.20360653
225345_s_at	0	1	14.52563535
236300_at	0	1	16.24397597
203498_at	RCAN2	1	14.89262279
224184_s_at	BOC	1	24.80325738
225662_at	ZAK	1	17.14288148
209542_x_at	IGF1	1	15.0192947
233857_s_at	ASB2	1	15.098782
227297_at	ITGA9	1	16.65120087

212992_at	AHNAK2	1	10.73235313
231213_at	PDE1A	1	16.62541661
212551_at	CAP2	1	14.69752159
1554007_at	0	1	15.29050836
214212_x_at	FERMT2	1	18.5089729
1556427_s_at	LRRN4CL	1	17.70543265
227762_at	0	1	16.95430898
227623_at	0	1	12.16560853
225665_at	ZAK	1	17.65251772
213451_x_at	TNXA /// TNXB	1	16.53743011
209470_s_at	GPM6A	1	13.25861433
239468_at	MKX	1	13.08017236
218418_s_at	KANK2	1	22.5643204
209505_at	NR2F1	1	13.61580615
201430_s_at	DPYSL3	1	13.79288815
209292_at	ID4	1	14.74808253
203065_s_at	CAV1	1	15.50306201
206104_at	ISL1	1	11.81488401
205478_at	PPP1R1A	1	11.52116245
218820_at	C14orf132	1	17.17866467
219902_at	BHMT2	1	17.9922771
218468_s_at	GREM1	1	7.926407937
209663_s_at	ITGA7	1	17.63400382
201117_s_at	CPE	1	11.2764924
230958_s_at	0	1	16.36578984
224149_x_at	SLMAP	1	14.16510383
223475_at	CRISPLD1	1	10.99795908
219213_at	JAM2	1	17.46326675
241255_at	0	1	12.22671442
225946_at	RASSF8	1	16.8847393
242348_at	FAM19A4	1	10.88763901
230730_at	SGCD	1	15.6932353
227657_at	RNF150	1	20.30070075
1553243_at	ITIH5	1	17.88932746
210072_at	CCL19	1	9.437096821
209335_at	DCN	1	12.31011881
212288_at	FNBP1	1	17.06861743
241879_at	0	1	14.96025213
211577_s_at	IGF1	1	14.50826663
209427_at	SMTN	1	16.48056512
210517_s_at	AKAP12	1	15.71345473
217897_at	FXVD6	1	16.91338219
227236_at	TSPAN2	1	12.48975648
216333_x_at	TNXA /// TNXB	1	16.30309251
227088_at	PDE5A	1	17.73817045
229975_at	BMPR1B	1	10.90509705
238458_at	EFHA2	1	18.66230901
236144_at	CPXM2	1	19.12309285
236936_at	0	1	18.34131114
209651_at	TGFB1I1	1	17.0811629

202566_s_at	SVIL	1	16.79735268
235649_at	ADAMTS8	1	14.05727623
231166_at	GPR155	1	13.14117289
216331_at	ITGA7	1	18.97695056
228783_at	BVES	1	14.81580964
239580_at	GUCY1A3	1	17.52227308
205612_at	MMRN1	1	11.73009981
209286_at	CDC42EP3	1	14.63965382
223843_at	SCARA3	1	15.23934233
235004_at	RBM24	1	13.3707249
243041_s_at	0	1	23.44771427
238906_s_at	RHOJ	1	18.19219207
214071_at	MPPE1	1	15.44903306
239708_at	0	1	17.37626786
219368_at	NAP1L2	1	16.41764466
225987_at	STEAP4	1	10.86096604
232067_at	C6orf168	1	10.73068829
209074_s_at	FAM107A	1	14.47242291
228218_at	0	1	14.66560017
206093_x_at	TNXA /// TNXB	1	16.4999307
216887_s_at	LDB3	1	14.3498993
219087_at	ASPN	1	10.87232739
201617_x_at	CALD1	1	17.10795784
225728_at	SORBS2	1	10.52685864
227892_at	PRKAA2	1	10.93721501
227265_at	FGL2	1	12.98213459
220955_x_at	RAB23	1	14.47661902
226587_at	SNRPN	1	15.37445854
225685_at	0	1	14.60070727
225915_at	CAB39L	1	16.58904415
218469_at	GREM1	1	7.658037936
204557_s_at	DZIP1	1	16.381683
202565_s_at	SVIL	1	17.09285921
235000_at	0	1	15.93639813
215440_s_at	BEX4	1	13.0618527
226439_s_at	NBEA	1	13.92067017
205168_at	DDR2	1	16.73069218
203295_s_at	ATP1A2	1	15.75812585
214752_x_at	FLNA	1	16.48911319
214761_at	ZNF423	1	16.80534661
206157_at	PTX3	1	10.06275257
226932_at	SSPN	1	14.38176825
209406_at	BAG2	1	12.01178053
229116_at	CNKS2	1	15.15562721
233364_s_at	0	1	18.11900477
209822_s_at	VLDLR	1	12.77183282
204731_at	TGFBR3	1	14.47369325
220751_s_at	C5orf4	1	17.72963486
238613_at	ZAK	1	15.53429186
206510_at	SIX2	1	11.39487285

209466_x_at	PTN	1	15.88080556
219728_at	MYOT	1	14.10627363
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205803_s_at	TRPC1	1	18.94802068
52837_at	LL22NC03-75B3.6	1	12.80520075
228082_at	ASAM	1	15.28407427
228602_at	SGCD	1	15.81069394
200859_x_at	FLNA	1	16.55491241
215039_at	HS2ST1	1	17.5539031
227198_at	AFF3	1	12.05487
236029_at	FAT3	1	12.36449539
204755_x_at	HLF	1	15.81222743
203088_at	FBLN5	1	15.56502943
204570_at	COX7A1	1	18.73518673
211734_s_at	FCER1A	1	11.33550291
205407_at	RECK	1	16.55308223
212097_at	CAV1	1	15.80312989
218974_at	SOBP	1	12.72957368
244370_at	KIAA2022	1	14.1663768
228080_at	LAYN	1	16.23776143
205382_s_at	CFD	1	10.29548449
226225_at	MCC	1	14.00094391
205384_at	FXD1	1	19.91886973
202157_s_at	CUGBP2	1	16.53435883
205952_at	KCNK3	1	10.86805554
228776_at	GJC1	1	13.86647736
238151_at	0	1	21.44951812
225688_s_at	PHLDB2	1	15.09044906
204963_at	SSPN	1	14.36309621
220765_s_at	LIMS2	1	18.02482056
224550_s_at	MRVI1	1	14.68416547
228724_at	0	1	14.32795104
1559477_s_at	MEIS1	1	17.71864439
230933_at	DSTN	1	15.80469219
208792_s_at	CLU	1	10.29103812
232267_at	GPR133	1	14.20025617
209737_at	MAGI2	1	15.12660017
211006_s_at	KCNB1	1	14.36617501
205200_at	CLEC3B	1	12.17020075
203562_at	FEZ1	1	17.42783826
227183_at	LOC728264	1	16.86640697
218694_at	ARMCX1	1	15.64294016
219064_at	ITIH5	1	16.57056591
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222918_at	RAB9B	1	14.60603432
228554_at	PGR	1	17.69386859
227209_at	CNTN1	1	14.34393835
213764_s_at	MFAP5	1	8.285063372
203723_at	ITPKB	1	18.77755973
1555233_at	RHOJ	1	17.32423318

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206116_s_at	TPM1	1	15.22850252
242033_at	RNF180	1	21.04812958
238484_s_at	0	1	19.46112884
215303_at	DCLK1	1	18.00188079
207453_s_at	DNAJB5	1	14.86638961
235562_at	C3orf70	1	12.15074203
209685_s_at	PRKCB	1	13.68985008
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235616_at	TSHZ2	1	15.51713063
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214369_s_at	RASGRP2	1	15.36660301
205893_at	NLGN1	1	11.98360021
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217889_s_at	CYBRD1	1	10.19640335
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227449_at	EPHA4	1	10.38383971
228592_at	MS4A1	1	5.445614255
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229485_x_at	SHISA3	1	8.111777875
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230968_at	0	1	11.13220544
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206852_at	EPHA7	1	9.139508425
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235497_at	LOC643837	1	14.07523007
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208789_at	PTRF	1	15.12873463
214321_at	NOV	1	9.645151999
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212675_s_at	CEP68	1	18.68109652
238778_at	MPP7	1	7.764127297
216693_x_at	HDGFRP3	1	11.18880421
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229084_at	CNTN4	1	10.46857446
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203001_s_at	STMN2	1	6.708231761
238451_at	MPP7	1	8.363934119

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231859_at	C14orf132 /// LOC100132684	1	17.38076917
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229225_at	NRP2	1	12.5736844
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238865_at	PABPC4L	1	14.23762077
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212670_at	ELN	1	11.56690598
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235836_at	MXRA7	1	16.72794434
238636_at	CACNA1C	1	13.22025173
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242358_at	0	1	16.14234378
232568_at	MGC24103	1	13.41578865
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219777_at	GIMAP6	1	11.18687714
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228962_at	PDE4D	1	11.96401926
216321_s_at	NR3C1	1	14.39894537
216235_s_at	EDNRA	1	13.09063073
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223599_at	TRIM6	1	11.4392126
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235264_at	HCFC2	1	16.58386282
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205265_s_at	SPEG	1	14.74825936
224901_at	SCD5	1	10.18910124
228882_at	TUB	1	12.1850946
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226382_at	LOC283070	1	11.04328831
226695_at	PRRX1	1	7.891511562
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228399_at	OSR1	1	9.475744978
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234936_s_at	CC2D2A	1	17.42601957
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226607_at	C20orf194	1	14.40804594
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223842_s_at	SCARA3	1	14.3100906
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228372_at	C10orf128	1	11.02066471
203372_s_at	SOCS2	1	9.771609996
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219106_s_at	KBTBD10	1	9.449074444
218717_s_at	LEPREL1	1	7.876628365

214040_s_at	GSN	1	13.09287593
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239336_at	THBS1	1	9.410477089
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203323_at	CAV2	1	8.23189749
218870_at	ARHGAP15	1	10.48837406
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231579_s_at	TIMP2	1	11.40394295
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242985_x_at	RNF180	1	15.86637732
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230142_s_at	CIRBP	1	16.67531198

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225185_at	MRAS	1	14.8123465
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230943_at	SOX17	1	11.61847231
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229092_at	NR2F2	1	12.04485253
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223854_at	PCDHB10	1	8.828520255
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228471_at	0	1	9.777408284
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229531_at	0	1	15.42746436
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238429_at	TMEM71	1	9.184226387
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228461_at	SH3RF3	1	13.29853152
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229317_at	KPNA5	1	11.64487312
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234989_at	NCRNA00084	1	7.535120972
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225093_at	UTRN	1	11.38893957
226002_at	GAB1	1	14.69849439
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1553962_s_at	RHOB	1	11.54770671

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228948_at	EPHA4	1	10.12929227
223008_s_at	C9orf5	1	13.97173915
227138_at	CRTAP	1	13.26066976
222291_at	FAM149A	1	11.31275589
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235737_at	TSLP	1	9.792717062
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226656_at	CRTAP	1	15.6325974
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225921_at	NIN	1	12.83693608
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212667_at	SPARC	1	9.79875755
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222494_at	FOXN3	1	16.73591954
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213922_at	TTBK2	1	15.11130897
231887_s_at	KIAA1274	1	11.67682525
216866_s_at	COL14A1	1	14.66099405
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213194_at	ROBO1	1	9.548220711
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224604_at	C4orf3	1	16.56710506
203324_s_at	CAV2	1	6.842105666
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209747_at	TGFB3	1	13.32423082
206826_at	PMP2	1	9.620974104
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224937_at	PTGFRN	1	13.10170474
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243946_at	SMOC2	1	11.15547913
1559287_at	0	1	11.68702965
204451_at	FZD1	1	10.82308872
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244040_at	0	1	10.7201771
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212158_at	SDC2	1	10.73568911
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1554012_at	RSPO2	1	8.007233115
201009_s_at	TXNIP	1	10.08887547
214266_s_at	PDLIM7	1	10.82987524
1556209_at	CLEC2B	1	9.923540293
204462_s_at	SLC16A2	1	8.776641132
212119_at	RHOQ	1	13.83949641
225239_at	0	1	6.752819616
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235867_at	GSTM3	1	11.51362807
228772_at	HNMT	1	9.581611015
223588_at	THAP2	1	12.2694047
213067_at	MYH10	1	7.349607239
228448_at	MAP6	1	13.26559045
216060_s_at	DAAM1	1	12.70507215
225048_at	PHF10	1	13.83525087
244313_at	CR1	1	7.315924253
213689_x_at	FAM69A	1	11.41794064
228194_s_at	SORCS1	1	10.24818251
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220117_at	ZNF385D	1	12.28859879

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219738_s_at	PCDH9		1	10.62427254
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230008_at	THSD7A		1	9.477700656
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230175_s_at		0	1	8.281816679
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228030_at		0	1	9.4453506
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241681_at		0	1	8.39696746
236277_at		0	1	8.338998494
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227728_at	PPM1A		1	14.09270889
229844_at		0	1	13.81440158
227923_at	SHANK3		1	10.85191185
215972_at		0	1	9.967811734
240317_at	PCDHB4		1	13.24863324
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1557169_x_at	HCG11		1	11.36981408
212157_at	SDC2		1	12.57768977
235978_at	FABP4		1	6.199899823
219134_at	ELTD1		1	9.018482959
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212385_at	TCF4		1	11.18420479
228584_at	SGCB		1	11.905146
201151_s_at	MBNL1		1	12.2868323
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238029_s_at	SLC16A14		1	6.848297466
214449_s_at	RHOQ		1	13.27083792

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235046_at	0	1	8.131547248
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214844_s_at	DOK5	1	9.192176049
238081_at	C4orf12	1	12.54967578
205279_s_at	GLRB	1	11.16725336
223422_s_at	ARHGAP24	1	11.9469761
217820_s_at	ENAH	1	10.31931619
202825_at	SLC25A4	1	9.914216971
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213422_s_at	MXRA8	1	10.07498007
221618_s_at	LOC728198 /// TAF9B	1	9.191997857
208983_s_at	PECAM1	1	9.604354159
224219_s_at	TRPC4	1	9.594844507
204604_at	PFTK1	1	8.667665194
209357_at	CITED2	1	8.760631494
227404_s_at	EGR1	1	7.469084
221213_s_at	ZNF280D	1	13.18509134
218573_at	MAGEH1	1	10.11820828
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229310_at	KLHL29	1	8.371283944
1566482_at	0	1	12.79174705
221740_x_at	LRRC37A2	1	14.19245963
208670_s_at	EID1	1	12.69472058
201792_at	AEBP1	1	7.317216716
212606_at	WDFY3	1	15.14914325
226352_at	JMY	1	14.0049651
216264_s_at	LAMB2	1	10.95202567
239710_at	FIGN	1	9.514072118
212240_s_at	PIK3R1	1	11.208902
223629_at	PCDHB5	1	6.403245019
206289_at	HOXA4	1	13.40485569
244419_at	FRZB	1	12.42197283
214318_s_at	FRY	1	10.90813237
228716_at	THRB	1	6.516791786
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235028_at	0	1	8.501263483
244289_at	LOC134466	1	12.19704917
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226722_at	FAM20C	1	10.75102124
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223006_s_at	C9orf5	1	13.37360407
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230433_at	LOC729970	1	11.71198742

227934_at	KPNA5	1	11.08010546
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231795_at	STON1	1	13.58284108
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207980_s_at	CITED2	1	8.477249982
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213737_x_at	GOLGA9P	1	13.7202287
210702_s_at	PTGIS	1	10.3957693
223119_s_at	USP47	1	13.69678298
227022_at	GNPDA2	1	13.23627881
213010_at	PRKCDBP	1	9.786743196
204368_at	SLCO2A1	1	8.032504235
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219432_at	EVC	1	13.50944883
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229890_at	PRRT1	1	15.56023143
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202976_s_at	RHOBTB3	1	6.827169394
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244130_at	0	1	12.30721519
224694_at	ANTXR1	1	7.151258574
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228973_at	DLG2	1	11.89799837
224772_at	NAV1	1	10.76883074
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210133_at	CCL11	1	4.531384325
225278_at	PRKAB2	1	9.710893539
240214_at	0	1	13.93106191
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208981_at	PECAM1	1	10.0628255
219506_at	C1orf54	1	11.91967824
244433_at	0	1	11.36706115
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228233_at	FREM1	1	11.2152232
221905_at	CYLD	1	13.85684978
228501_at	GALNTL2	1	7.059583092
222664_at	KCTD15	1	9.140791054

206542_s_at	SMARCA2	1	11.48045759
210786_s_at	FLI1	1	10.77185233
1555997_s_at	IGFBP5	1	9.502935986
230454_at	ICA1L	1	11.34814966
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221527_s_at	PARD3	1	11.21904123
225056_at	SIPA1L2	1	8.933567497
207233_s_at	MITF	1	10.49115761
221104_s_at	NIPSNAP3B	1	12.54952444
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213222_at	PLCB1	1	6.896445054
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204864_s_at	IL6ST	1	10.994164
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235079_at		0	6.751866032
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213479_at	NPTX2	1	6.256437498
231726_at	PCDHB14	1	8.039943192
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232176_at	SLITRK6	1	5.914139506
229809_at		0	17.84056828
216005_at	TNC	1	7.466643165
236635_at	ZNF667	1	15.09797794
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222820_at	TNRC6C	1	11.30145289
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201162_at	IGFBP7	1	14.42535455
212566_at	MAP4	1	14.46760863
220145_at	MAP9	1	7.466848064
204677_at	CDH5	1	9.026962967
214091_s_at	GPX3	1	6.003700515
221881_s_at	CLIC4	1	10.34355206
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240044_x_at	TNRC6B	1	12.79031024
204150_at	STAB1	1	11.80589065
226197_at		0	12.83544083
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235626_at	CAMK1D	1	9.217502306
200931_s_at	VCL	1	11.70962212
41577_at	PPP1R16B	1	7.953406116
210990_s_at	LAMA4	1	11.78552131

210479_s_at	RORA	1	9.936694263
211966_at	COL4A2	1	9.864519043
219243_at	GIMAP4	1	8.573974019
227276_at	PLXDC2	1	8.498950349
213940_s_at	FNBP1	1	11.40084486
213326_at	VAMP1	1	10.66515312
213236_at	SASH1	1	13.2710532
212706_at	LOC100132214 /// LOC100133005 /// LOC100134722 /// RASA4	1	7.810142595
202432_at	PPP3CB	1	14.92320504
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228007_at	C6orf204	1	10.92993582
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214620_x_at	PAM	1	12.74590029
234192_s_at	GKAP1	1	7.802407999
211160_x_at	ACTN1	1	11.56396444
212822_at	HEG1	1	12.28147209
219478_at	WFDC1	1	5.678037289
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225763_at	RCSD1	1	8.404841782
229459_at	FAM19A5	1	6.564559542
226688_at	C3orf23	1	11.55041435
238461_at	EIF4E3	1	9.557717674
223204_at	C4orf18	1	9.709646256
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238115_at	0	1	14.18977059
65718_at	GPR124	1	15.161703
203874_s_at	SMARCA1	1	6.816864376
221031_s_at	APOLD1	1	7.927069587
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231738_at	PCDHB7	1	8.459314191
211958_at	IGFBP5	1	8.716460783
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235879_at	MBNL1	1	8.067156735
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204732_s_at	TRIM23	1	14.25764671
239848_at	0	1	10.89174789
242845_at	0	1	14.1009032
213684_s_at	PDLIM5	1	11.16828486
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229178_at	LOC145786	1	9.935037345
211986_at	AHNAK	1	11.28578879
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228919_at		0	1	7.076207897
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233825_s_at	CD99L2		1	13.86482412
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215271_at	TNN		1	7.586337312
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227243_s_at	EBF3		1	9.376926367
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229430_at	C8orf46		1	9.269041032
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236153_at		0	1	13.26718262

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228562_at	0	1	5.598028902
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204612_at	PKIA	1	6.954491393
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232098_at	DST	1	8.333495399
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225930_at	NKIRAS1	1	12.98820276
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242172_at	MEIS1	1	14.800694
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226440_at	DUSP22 /// LOC100134371	1	15.29427585
216831_s_at	RUNX1T1	1	11.79417491
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204468_s_at	TIE1	1	8.617855243
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214602_at	COL4A4	1	6.586868956
213293_s_at	TRIM22	1	7.027874063
205923_at	RELN	1	8.75053722
205582_s_at	GGT5	1	12.13125852
203657_s_at	CTSF	1	12.89451822
240172_at	ERGIC2	1	13.38920945
219532_at	ELOVL4	1	10.3732872
211616_s_at	HTR2A	1	12.17205959
230849_at	KCNA1	1	9.097472947
209101_at	CTGF	1	7.851224816
209311_at	BCL2L2	1	13.9708998
235360_at	PLEKHM3	1	13.44428196
228582_x_at	0	1	9.108464169
218675_at	SLC22A17	1	11.57648142
1554464_a_at	CRTAP	1	12.48673099

229344_x_at	RIMKLB	1	8.883535539
227058_at	C13orf33	1	5.651202493
227448_at	ARGLU1	1	11.16956852
227909_at	CXorf48 /// NCRNA00086	1	7.81726412
200952_s_at	CCND2	1	6.652867469
243976_at	0	1	11.74175747
1598_g_at	GAS6 /// LOC100133684	1	11.47907027
244740_at	MGC9913	1	12.14915691
229802_at	0	1	5.406219809
38487_at	STAB1	1	11.82608719
41644_at	SASH1	1	12.96626509
204310_s_at	NPR2	1	16.23843748
235352_at	0	1	9.309974619
235030_at	FAM55C	1	9.240210814
208454_s_at	PGCP	1	10.90750776
226558_at	LOC653071	1	5.206906615
228826_at	0	1	11.94051876
209866_s_at	LPHN3	1	5.784448033
230146_s_at	FREQ	1	10.46747965
201693_s_at	EGR1	1	5.976831861
212647_at	RRAS	1	9.68020495
201234_at	ILK	1	13.27370003
229544_at	0	1	8.397186196
228843_at	0	1	9.370416498
229670_at	0	1	9.608738463
203549_s_at	LPL	1	5.451383408
215785_s_at	CYFIP2	1	8.007769619
214279_s_at	NDRG2	1	7.3702704
203249_at	EZH1	1	16.77040339
206115_at	EGR3	1	4.806245308
240432_x_at	0	1	11.02306834
213005_s_at	KANK1	1	9.368004085
211467_s_at	NFIB	1	10.74713614
1555894_s_at	MTSS1L	1	11.48647288
225941_at	EIF4E3	1	8.644131252
1552760_at	HDAC9	1	8.18456974
236330_at	0	1	11.68815149
201060_x_at	STOM	1	10.53059512
214829_at	AASS	1	9.979143063
225735_at	ANKRD50	1	12.01696859
228863_at	PCDH17	1	8.37452955
221030_s_at	ARHGAP24	1	15.05315403
206726_at	PGDS	1	8.533131376
203254_s_at	TLN1	1	11.5355686
210330_at	SGCD	1	11.34554666
211602_s_at	TRPC1	1	14.07904456
229319_at	0	1	12.41164323
228618_at	PEAR1	1	12.71076107
209946_at	VEGFC	1	9.518142207
206389_s_at	PDE3A	1	12.72451044

205610_at	MYOM1	1	10.78329777
215199_at	CALD1	1	12.10996128
227131_at	MAP3K3	1	17.04021718
37408_at	MRC2	1	9.507830595
238688_at	TPM1	1	11.08959817
219317_at	POLI	1	10.83688582
226612_at	FLJ25076	1	5.653539221
209304_x_at	GADD45B	1	9.544837996
200810_s_at	CIRBP	1	15.61808425
230305_at	0	1	8.764483729
203570_at	LOXL1	1	7.888868675
219501_at	ENOX1	1	12.07477691
226841_at	MPEG1	1	7.341687584
225283_at	ARRDC4	1	7.690212002
212253_x_at	DST	1	11.90581184
212117_at	RHOQ	1	12.98947277
206929_s_at	NFIC	1	11.94945087
219607_s_at	MS4A4A	1	5.455746526
242907_at	0	1	6.958279302
58780_s_at	FLJ10357	1	11.46438231
205419_at	GPR183	1	7.433394796
244026_at	0	1	7.167910054
226828_s_at	HEYL	1	9.050262501
207557_s_at	RYR2	1	8.913155499
217721_at	0	1	12.75790481
236079_at	DKFZp667E0512	1	14.01679364
219892_at	TM6SF1	1	8.268793746
220182_at	SLC25A23	1	9.637948565
236583_at	0	1	11.93551563
239270_at	PLCXD3	1	8.23380617
201426_s_at	VIM	1	11.3782978
205991_s_at	PRRX1	1	6.671432068
1556306_at	0	1	12.00223833
235606_at	LOC344595	1	12.34463681
205150_s_at	KIAA0644	1	7.762981794
205234_at	SLC16A4	1	6.295598392
236361_at	GALNTL2	1	6.675159177
203006_at	INPP5A	1	11.50114647
203340_s_at	SLC25A12	1	10.05609746
203888_at	THBD	1	8.777379991
229464_at	MYEF2	1	6.367961519
202861_at	PER1	1	10.58168971
231925_at	0	1	8.355819627
212757_s_at	CAMK2G	1	10.50292092
225269_s_at	C2orf12	1	9.084335197
224893_at	ATL3	1	14.91330585
1552754_a_at	CADM2	1	6.848452928
205404_at	HSD11B1	1	5.711649184
206243_at	TIMP4	1	6.189120816
229674_at	SERTAD4	1	6.684600867

213489_at	MAPRE2	1	13.52121149
212308_at	CLASP2	1	12.87605715
209795_at	CD69	1	4.99969624
228438_at	LOC100132891	1	7.973002339
209228_x_at	TUSC3	1	6.453545969
224817_at	SH3PXD2A	1	12.44109866
208206_s_at	RASGRP2	1	14.04694596
235976_at	SLITRK6	1	5.333037687
230180_at	0	1	8.772278176
1555154_a_at	QKI	1	11.62953356
210426_x_at	RORA	1	9.20950272
241835_at	0	1	7.194319236
1561180_at	0	1	9.450045456
213388_at	PDE4DIP	1	9.556844912
203424_s_at	IGFBP5	1	6.896511915
214596_at	CHRM3	1	5.741873744
244111_at	KRT222P	1	9.239742647
227041_at	SESTD1	1	10.17761605
227087_at	INPP4A	1	13.01554276
1559584_a_at	C16orf54 /// hCG_1644884	1	4.953632774
207749_s_at	PPP2R3A	1	9.8134631
211066_x_at	PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	1	11.97519032
212549_at	STAT5B	1	15.11711348
232205_at	0	1	8.110847774
217707_x_at	SMARCA2	1	11.37832694
236046_at	FLJ44896	1	10.95678777
223734_at	C4orf49	1	10.76470015
209392_at	ENPP2	1	5.835022363
207968_s_at	MEF2C	1	14.35950197
200811_at	CIRBP	1	14.68207884
1558142_at	TNRC6B	1	13.58210572
202238_s_at	NNMT	1	5.631836633
226773_at	0	1	10.4325917
205326_at	RAMP3	1	10.39727746
203845_at	KAT2B	1	8.994273603
242789_at	PDE1A	1	12.22888245
233442_at	0	1	12.30907076
230913_at	0	1	9.552991164
225098_at	ABI2	1	12.16959278
1558934_a_at	0	1	11.64483474
244294_at	0	1	12.46253288

226040_at		0	1	10.81658965
225613_at	LOC100128443 /// MAST4		1	10.43740464
209305_s_at	GADD45B		1	8.896522952
213358_at	KIAA0802		1	5.85168195
223316_at	CCDC3		1	10.15597259
235593_at	LOC100128821 /// ZEB2		1	8.883366039
225935_at		0	1	12.05362238
1553960_at	SNX21		1	11.88520867
230644_at	LRFN5		1	10.78756819
203264_s_at	ARHGEF9		1	10.12159567
218805_at	GIMAP5		1	9.713569958
235094_at		0	1	8.384094544
204844_at	ENPEP		1	6.739603517
239548_at	NEGR1		1	12.76320306
214043_at	PTPRD		1	5.747382087
214725_at	C8orf84		1	7.585212349
204671_s_at	ANKRD6		1	6.781114431
233249_at	LOC730200		1	13.18923008
226112_at	SGCB		1	13.21180264
207172_s_at	CDH11		1	7.464338822
230228_at	LOC284297		1	14.58945135
226395_at	HOOK3		1	10.98473125
236656_s_at	LOC100130506		1	8.654589665
229881_at	KLF12		1	12.29251596
235848_x_at	ATL2		1	9.186759937
213908_at	LOC652637 /// WHDC1L1		1	13.73400091
236335_at		0	1	7.464790544
228793_at	JMJD1C		1	8.425875227
213925_at	C1orf95		1	9.647510327
39582_at	CYLD		1	15.00301276
228121_at	TGFB2		1	7.417247896
205082_s_at	AOX1		1	8.62267812
202440_s_at	ST5		1	11.81685412
205968_at	KCNS3		1	6.393354296
209473_at	ENTPD1		1	11.46820731
229951_x_at		0	1	10.83072566
224358_s_at	MS4A7		1	7.659447494
219867_at	CHODL		1	7.156258455
228722_at	PRMT2		1	10.71947089
208070_s_at	REV3L		1	13.27873497
202973_x_at	FAM13A1		1	7.670093653
209576_at	GNAI1		1	6.62549458
218224_at	PNMA1		1	9.588307823
231899_at	ZC3H12C		1	6.351830285
235061_at	PPM1K		1	8.350634143
228297_at		0	1	9.839110357
200600_at	MSN		1	10.43043815
214632_at	NRP2		1	9.159746104
210815_s_at	CALCRL		1	7.692512948
212427_at	KIAA0368		1	9.367329454

218236_s_at	PRKD3	1	8.727785475
238647_at	C14orf28	1	12.81787595
	PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 ///		
215836_s_at	PCDHGC4 /// PCDHGC5	1	12.15602594
218266_s_at	FREQ	1	10.30629604
226909_at	ZNF518B	1	6.366711469
228006_at	0	1	13.02060055
213135_at	TIAM1	1	7.081860622
225273_at	WWC3	1	9.233079346
228723_at	0	1	10.57989762
229529_at	TCF21	1	11.40858045
218589_at	P2RY5	1	9.152645625
204442_x_at	LTBP4	1	9.615310748
206114_at	EPHA4	1	8.93804531
213652_at	PCSK5	1	7.174939854
237719_x_at	RGS7BP	1	8.766144189
225509_at	SAP30L	1	13.70889735
241722_x_at	0	1	8.359943437
231991_at	C20orf160	1	11.47114799
242590_at	0	1	13.32809739
235334_at	ST6GALNAC3	1	8.513000651
206363_at	MAF	1	8.202928056
227325_at	LOC255783	1	13.49086471
220146_at	TLR7	1	6.622021298
225809_at	DKFZP564O0823	1	4.750285339
219855_at	NUDT11	1	9.586255548
205858_at	NGFR	1	11.34651599
225940_at	EIF4E3	1	10.1921297
223487_x_at	GNB4	1	11.62446767
235735_at	0	1	7.34528436
	LOC652637 /// WHDC1L1 ///		
1557261_at	WHDC1L2	1	13.68096814
214175_x_at	PDLIM4	1	10.13227247
213348_at	CDKN1C	1	5.427421915
239277_at	0	1	10.66081107
201236_s_at	BTG2	1	8.000388779
201591_s_at	NISCH	1	16.79059188
204273_at	EDNRB	1	5.539233305
217066_s_at	DMPK	1	12.64076764
226969_at	MTR	1	12.10301326
230560_at	STXBP6	1	4.675712744
230903_s_at	C8orf42	1	10.09860333

243606_at	FAM55C	1	9.835792825
231867_at	ODZ2	1	7.126539341
228620_at	0	1	9.594923404
214894_x_at	MACF1	1	13.77294152
204993_at	GNAZ	1	9.971814728
219469_at	DYNC2H1	1	11.01896451
218691_s_at	PDLIM4	1	9.973680027
218259_at	MKL2	1	13.24943673
213316_at	KIAA1462	1	8.378769021
212558_at	SPRY1	1	9.904732925
203604_at	ZNF516	1	11.33578575
204530_s_at	TOX	1	9.619863506
210889_s_at	FCGR2B	1	5.533640974
241986_at	BMPER	1	10.59654436
230519_at	FAM124A	1	13.06109498
227069_at	0	1	11.3505445
1554726_at	ZNF655	1	7.954101469
229222_at	ACSS3	1	6.622412752
227167_s_at	0	1	10.71828404
217540_at	FAM55C	1	9.289888626
201841_s_at	HSPB1	1	8.220029727
230490_x_at	RSU1	1	13.67733535
225157_at	MLXIP	1	11.93352004
1553696_s_at	ZNF569	1	9.925159899
225914_s_at	CAB39L	1	8.779560234
202237_at	NNMT	1	5.75563902
218196_at	OSTM1	1	12.28112951
225687_at	FAM83D	1	5.086918191
225558_at	GIT2	1	15.24079935
226415_at	VAT1L	1	7.554521945
204334_at	KLF7	1	9.22424286
233868_x_at	ADAM33	1	13.68826913
211985_s_at	CALM1 /// CALM2 /// CALM3	1	11.62741267
48031_r_at	C5orf4	1	15.11127668
203748_x_at	RBMS1	1	8.554708251
229947_at	PI15	1	3.555011292
206453_s_at	NDRG2	1	8.225359245
211984_at	CALM1 /// CALM2 /// CALM3	1	12.22859019
218648_at	CRTC3	1	15.27503408
228630_at	ZNF84	1	9.460014196
202768_at	FOSB	1	4.065177606
215813_s_at	PTGS1	1	7.260099996
37022_at	PRELP	1	13.43581482
208850_s_at	THY1	1	7.845907928
234996_at	CALCRL	1	8.54661631
226818_at	MPEG1	1	6.289232007
225937_at	0	1	10.72235045
204249_s_at	LMO2	1	9.449555013
238740_at	AARSD1	1	8.789534968
235764_at	0	1	10.99650065

1555594_a_at	MBNL1	1	9.363194462
227169_at	DNAJC18	1	12.60544549
206314_at	ZNF167	1	8.7042764
228698_at	SOX7	1	5.753123425
233036_at	0	1	11.26569685
235121_at	ZNF542	1	8.845579733
202909_at	EPM2AIP1	1	8.183798667
211929_at	HNRNPA3	1	11.86803547
241808_at	0	1	8.609316674
228456_s_at	LOC149832	1	12.531245
224911_s_at	DCBLD2	1	6.470414343
1563466_at	MYLK	1	9.428757769
228452_at	C17orf39	1	12.65865708
219295_s_at	PCOLCE2	1	4.515124739
230292_at	LOC100131993	1	11.33471518
235803_at	0	1	8.977787144
238558_at	0	1	8.683555963
207547_s_at	FAM107A	1	12.31071826
210356_x_at	MS4A1	1	4.587844541
232382_s_at	PCMTD1	1	7.441937665
236331_at	CDKL2	1	9.193359224
202616_s_at	MECP2	1	15.69323061
242471_at	0	1	8.485779238
1562139_a_at	FOXP2	1	10.49117304
1556329_a_at	0	1	8.083238557
1569150_x_at	PDLIM7	1	11.06680749
208788_at	ELOVL5	1	7.713382434
212226_s_at	PPAP2B	1	9.955769076
215198_s_at	CALD1	1	11.49100752
211776_s_at	EPB41L3	1	6.585324404
207358_x_at	MACF1	1	14.43080984
201867_s_at	TBL1X	1	7.014905487
224356_x_at	MS4A6A	1	6.361634101
213040_s_at	NPTXR	1	8.477500039
204560_at	FKBP5	1	7.169648901
228709_at	TPR	1	11.79485614
228831_s_at	GNX7	1	12.48847831
235240_at	ATXN3	1	13.90521682
231262_at	0	1	12.40953499
209543_s_at	CD34	1	10.69445678
203140_at	BCL6	1	9.083889326
221834_at	LONP2	1	13.31306884
201152_s_at	MBNL1	1	15.29337017
202630_at	APPBP2	1	11.98550515
226244_at	CLEC14A	1	10.95835879
208965_s_at	IFI16	1	6.667822237
240041_at	PTCHD1	1	9.790863372
227300_at	TMEM119	1	5.584696851
219626_at	MAP7D3	1	15.70517956
211105_s_at	NFATC1	1	9.853691163

212177_at	SFRS18	1	8.883979558
1555793_a_at	ZFP82	1	8.008881543
218330_s_at	NAV2	1	6.787227477
209278_s_at	TFPI2	1	3.609748213
1556402_at	0	1	10.16781566
224568_x_at	MALAT1	1	6.969652186
226692_at	SERF2	1	12.24579061
226282_at	0	1	10.91693933
201506_at	TGFBI	1	7.502793556
235443_at	LOC100131067	1	11.9565823
213566_at	RNASE6	1	6.328344421
1568609_s_at	FAM91A2 /// FLJ39739 /// LOC728855 /// LOC728875	1	7.840524942
223504_at	DNAJC27	1	14.08858428
216184_s_at	RIMS1	1	5.949320433
238463_at	0	1	14.34866762
244677_at	0	1	10.66722811
219576_at	MAP7D3	1	12.30742557
228718_at	ZNF44	1	13.07747043
238569_at	GABBR1	1	12.04897831
213901_x_at	RBM9	1	11.67308129
215222_x_at	MACF1	1	13.38508783
207266_x_at	RBMS1	1	8.395236122
210997_at	HGF	1	7.999636496
226056_at	CDGAP	1	11.21993928
221045_s_at	PER3	1	7.578228323
219666_at	MS4A6A	1	6.818562544
222016_s_at	ZNF323	1	7.692476302
200762_at	DPYSL2	1	11.87274397
230779_at	TNRC6B	1	10.64840882
236666_s_at	0	1	8.097602769
235427_at	0	1	10.0199609
241484_x_at	0	1	10.82614657
235782_at	0	1	11.34065479
1556047_s_at	MAGEE1	1	10.76742962
229159_at	THSD7A	1	8.570125648
227576_at	0	1	9.199479861
201105_at	LGALS1	1	9.853153744
223672_at	SGIP1	1	10.71614569
243225_at	LOC283481	1	8.923430002
207120_at	ZNF667	1	13.25293384
225406_at	TWSG1	1	9.749216747
228745_at	SGTB	1	10.65486372
227847_at	EPM2AIP1	1	8.545114824
213656_s_at	KLC1	1	17.19140253
205262_at	KCNH2	1	8.089945512
225704_at	KIAA1545	1	11.22936214
209842_at	SOX10	1	12.2322321
243438_at	PDE7B	1	13.35637871
205121_at	SGCB	1	10.03255458

218338_at	PHC1 /// PHC1B	1	12.10720086
215127_s_at	RBMS1	1	8.646050719
228496_s_at	CRIM1	1	9.858844603
222409_at	CORO1C	1	11.2457622
1560296_at	0	1	13.01577981
225016_at	APCDD1	1	4.626009854
	PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	1	11.72405897
212565_at	STK38L	1	9.4005361
213400_s_at	TBL1X	1	7.585397367
211772_x_at	CHRNA3	1	10.01783366
205992_s_at	IL15	1	7.84962834
226164_x_at	RIMKLB	1	8.255458048
227559_at	0	1	9.404161847
223253_at	EPDR1	1	5.321610875
205872_x_at	PDE4DIP	1	7.730400171
203083_at	THBS2	1	4.059150608
201148_s_at	TIMP3	1	8.706900774
221564_at	PRMT2	1	14.00492098
212848_s_at	C9orf3	1	9.60886787
238468_at	TNRC6B	1	13.46262158
204992_s_at	PFN2	1	5.341462495
212985_at	APBB2	1	9.122469923
208633_s_at	MACF1	1	12.50273886
214177_s_at	PBXIP1	1	12.99552946
232099_at	PCDHB16	1	6.407699454
204912_at	IL10RA	1	7.036645696
213298_at	NFIC	1	10.61738437
205726_at	DIAPH2	1	9.447201651
211473_s_at	COL4A6	1	10.55724606
206762_at	KCNA5	1	10.78970755
213227_at	PGRMC2	1	12.68819117
209648_x_at	SOCS5	1	12.84261429
1569512_at	0	1	9.801781488
206331_at	CALCRL	1	7.68361362
223366_at	0	1	6.624516864
230147_at	F2RL2	1	4.552134286
208127_s_at	SOCS5	1	13.31010336
1560271_at	0	1	11.9759851
202877_s_at	CD93	1	8.000820622
212473_s_at	MICAL2	1	8.280054243
244463_at	ADAM23	1	11.21969752

220173_at	C14orf45	1	10.29777503
232628_at	0	1	8.319453825
238476_at	C5orf41	1	10.53804887
229716_at	0	1	8.339621168
212398_at	RDX	1	7.147477266
237071_at	0	1	12.45091343
212190_at	SERPINE2	1	4.846159602
212937_s_at	COL6A1	1	9.56307226
231789_at	PCDHB15	1	10.15411343
223344_s_at	MS4A7	1	6.475665172
1553275_s_at	0	1	11.66921619
236831_at	CCDC50	1	10.03157502
212791_at	C1orf216	1	11.89130213
223280_x_at	MS4A6A	1	6.574199779
244506_at	TMTC1	1	13.90968584
224747_at	UBE2Q2	1	10.61172473
201554_x_at	GYG1	1	10.28528201
210716_s_at	CLIP1	1	9.550684284
233882_s_at	SEMA6D	1	8.924007021
1569566_at	TBC1D1	1	9.397332061
1559901_s_at	C21orf34	1	15.39225235
228365_at	CPNE8	1	6.519806215
239741_at	LOC283658	1	11.20747742
235388_at	CHD9	1	12.61652955
219204_s_at	SRR	1	10.75415295
212518_at	PIP5K1C	1	14.386116
212646_at	RFTN1	1	8.5043516
227401_at	IL17D	1	9.673211553
231292_at	EID3	1	11.16786296
1565681_s_at	DIP2C	1	10.68610773
222426_at	MAPKAP1	1	11.63361261
212265_at	QKI	1	8.667318079
212739_s_at	NME4	1	8.796195519
220244_at	LOH3CR2A	1	9.014332124
226037_s_at	LOC728198 /// TAF9B	1	10.3003347
218983_at	C1RL	1	9.410916728
227771_at	LIFR	1	6.80437548
213578_at	BMPR1A	1	10.88989365
209264_s_at	TSPAN4	1	9.356726516
213817_at	IRAK3	1	5.037548616
238716_at	FAM85A	1	10.6837154
231950_at	ZNF658	1	8.300617241
211709_s_at	CLEC11A	1	7.4676856
241925_x_at	0	1	7.642590311
57715_at	CALHM2	1	10.87872727
244149_at	0	1	10.31603305
222156_x_at	CCPG1	1	10.13048585
1555363_s_at	0	1	12.30020046
203638_s_at	FGFR2	1	4.394439635
213125_at	OLFML2B	1	7.005076976

202401_s_at	SRF	1	12.1400616
227722_at	RPS23	1	10.2563447
202362_at	RAP1A	1	12.30992639
211592_s_at	CACNA1C	1	9.886919714
238454_at	ZNF540	1	13.36287817
210839_s_at	ENPP2	1	5.504363586
219935_at	ADAMTS5	1	5.978128811
209869_at	ADRA2A	1	3.862069055
232064_at		0 1	11.43934168
212855_at	DCUN1D4	1	11.41536376
237413_at		0 1	14.23653823
230174_at	LYPLAL1	1	9.995481662
213328_at	NEK1	1	12.63931192
227860_at	CPXM1	1	4.92632565
219205_at	SRR	1	13.07276065
201828_x_at	FAM127A	1	9.742147603
202982_s_at	ACOT1 /// ACOT2	1	9.613012415
209220_at	GPC3	1	3.786810001
243591_at		0 1	8.403169467
210683_at	NRTN	1	6.204698221
218559_s_at	MAFB	1	6.547464798
235639_at		0 1	10.28069258
228104_at	PLXNA4	1	10.98585749
244163_at	SEMA3A	1	6.759433817
207978_s_at	NR4A3	1	5.59243675
222454_s_at	PARVA	1	10.61953619
225611_at	LOC100128443 /// MAST4	1	10.50223954
1556658_a_at		0 1	8.628063151
226575_at	ZNF462	1	6.948003538
219992_at	TAC3	1	6.759876532
212747_at	ANKS1A	1	12.85877145
214030_at	CRYBG3	1	11.42643568
212154_at	SDC2	1	7.091955772
1557353_at		0 1	12.78481168
210075_at	MARCH2	1	12.14690105
229004_at		0 1	6.286950175
223449_at	SEMA6A	1	6.049527481
210407_at	PPM1A	1	11.57587797
244680_at	GLRB	1	12.15472366
224861_at	GNAQ	1	11.37068726
203104_at	CSF1R	1	9.036310195
238964_at	FIGN	1	8.740211022
204851_s_at	DCX	1	6.074875683
201107_s_at	THBS1	1	8.269762457
229027_at	PPM1A	1	10.73417498
1569149_at	PDLIM7	1	10.79784372
229585_at	ADAMTSL1	1	9.777696307
227047_x_at	ZBTB4	1	15.56636431
227188_at	C21orf63	1	6.455679239
227210_at		0 1	7.716139517

228492_at	LOC100130216 /// USP9Y	1	3.964285996
201141_at	GPNMB	1	4.915398782
217047_s_at	FAM13A1	1	7.223354955
1552347_at	CRYZL1	1	12.52537864
1555630_a_at	RAB34	1	6.399879073
235344_at	PPM1A	1	11.0090984
205752_s_at	GSTM5	1	14.30409464
225998_at	GAB1	1	13.56041719
228967_at	EIF1	1	7.981026643
244572_at	KY	1	8.843363867
238204_at	0	1	11.55106703
227976_at	LOC644538	1	11.33560314
210222_s_at	RTN1	1	6.226560328
215561_s_at	IL1R1	1	9.19737216
223095_at	MARVELD1	1	10.72058542
222911_s_at	CXorf36	1	10.08075021
202663_at	WIPF1	1	7.387851245
210305_at	PDE4DIP	1	6.997625984
235534_at	0	1	9.823635437
244428_at	DNMT3A	1	11.93667927
216048_s_at	RHOBTB3	1	6.122633352
203973_s_at	CEBPD	1	11.17344428
217783_s_at	YPEL5	1	14.32250834
210794_s_at	MEG3	1	11.10495526
211421_s_at	RET	1	7.182760563
226793_at	LOC283267	1	9.604671269
205961_s_at	PSIP1	1	9.686714139
225516_at	SLC7A2	1	5.114852719
228045_at	0	1	7.989380176
203504_s_at	ABCA1	1	8.172945797
231215_at	0	1	11.91372586
225055_at	0	1	10.38812792
227062_at	NCRNA00084	1	5.43764537
213434_at	STX2	1	12.17732445
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225913_at	SGK269	1	14.3168947
223276_at	MST150	1	7.93883312
229323_at	LOC387723	1	8.697698834
213808_at	0	1	12.32583642
217418_x_at	MS4A1	1	4.299122773
203868_s_at	VCAM1	1	5.459228788
227917_at	FAM85A	1	9.452801622
228642_at	0	1	7.315245282

	PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 ///		
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218528_s_at	RNF38	1	12.96920816
236764_at	0	1	14.08068335
228904_at	HOXB3	1	6.241239076
229586_at	CHD9	1	12.49056112
235108_at	0	1	9.468364158
221833_at	LONP2	1	10.65220079
212488_at	COL5A1	1	5.452058398
212887_at	SEC23A	1	9.63193872
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211965_at	ZFP36L1	1	6.792777573
213218_at	ZNF187	1	11.72875816
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226846_at	PHYHD1	1	12.80427256
205755_at	ITIH3	1	7.125318692
209307_at	SWAP70	1	9.920475397
214722_at	NOTCH2NL	1	9.970521283
231137_at	0	1	12.80200839
228540_at	QKI	1	15.47319611
221768_at	SFPQ	1	9.178614802
212408_at	TOR1AIP1	1	14.76818094
224941_at	PAPPA	1	5.401547476
214743_at	CUX1	1	9.815779134
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233536_at	ASXL3	1	8.955546482
204156_at	KIAA0999	1	12.41756486
226397_s_at	0	1	8.214504272
235657_at	0	1	10.94978475
228055_at	NAPSB	1	5.49026672
1556121_at	0	1	9.249898788
206584_at	LY96	1	5.392661775
203791_at	DMXL1	1	10.77685769
231980_at	0	1	12.94357681
205201_at	GLI3	1	12.75041057
211892_s_at	PTGIS	1	8.93667812
221565_s_at	CALHM2	1	10.36657828
238992_at	POLI	1	11.44184531
235834_at	CALD1	1	11.12368112
224229_s_at	AKT3	1	10.36125712
215606_s_at	ERC1	1	8.952710834

215046_at	C2orf67	1	8.641111075
227013_at	LATS2	1	8.557712906
229705_at	0	1	10.38864858
210432_s_at	SCN3A	1	4.864375681
225624_at	SNX29	1	14.15162851
55872_at	ZNF512B	1	6.263389543
225342_at	AK3L1 /// AK3L2	1	4.620805597
236698_at	0	1	8.816883769
209183_s_at	C10orf10	1	5.864988091
217627_at	ZNF573	1	8.354285948
212819_at	ASB1	1	12.58815584
210674_s_at	PCDHA11 /// PCDHA12 /// PCDHA13 /// PCDHA2 /// PCDHA3 /// PCDHA4 /// PCDHA5 /// PCDHA6 /// PCDHA7 /// PCDHA8 /// PCDHA9 /// PCDHAC1 /// PCDHAC2	1	4.387424168
228751_at	CLK4	1	10.1053196
1558686_at	0	1	6.881780277
204619_s_at	VCAN	1	5.666240886
225112_at	ABI2	1	12.21325409
1558964_at	FAT3	1	8.320430215
1555889_a_at	CRTAP	1	12.78713167
227370_at	FAM171B	1	6.240138929
226581_at	ZFYVE20	1	13.22513097
233587_s_at	SIPA1L2	1	7.234543704
1559965_at	LOC100192378	1	6.305769901
225999_at	RIMKLB	1	6.926641648
201866_s_at	NR3C1	1	9.050088286
206423_at	ANGPTL7	1	9.590554393
212982_at	ZDHHC17	1	13.42787247
241138_at	0	1	9.914286904
228278_at	NFIX	1	15.10849898
207053_at	SLC8A1	1	10.73645263
230791_at	0	1	6.814947481
242321_at	0	1	9.769348079
225167_at	FRMD4A	1	8.876743894
212741_at	MAOA	1	5.112676799
226985_at	FGD5	1	9.413267783
238990_x_at	TRIM61	1	13.79008628
229281_at	NPAS3	1	7.232995986
1558027_s_at	PRKAB2	1	8.434182127
225021_at	ZNF532	1	9.131029939
214913_at	ADAMTS3	1	8.111677107
201153_s_at	MBNL1	1	15.15746296
242766_at	0	1	8.706943258
212104_s_at	RBM9	1	12.47688558
211874_s_at	MYST4	1	11.37698577
1559425_at	0	1	9.15942709
201294_s_at	WSB1	1	7.832440175

213375_s_at	N4BP2L1	1	6.820542138
228770_at	GPR146	1	10.75202363
205656_at	PCDH17	1	7.462621139
230158_at	DPY19L2	1	9.223119608
209198_s_at	SYT11	1	7.574549678
204192_at	CD37	1	5.124286126
202172_at	VEZF1	1	13.63482213
227251_at	WDR22	1	13.12815645
222433_at	ENAH	1	8.451931428
201809_s_at	ENG	1	8.652981124
217943_s_at	MAP7D1	1	11.7068482
235302_at	0	1	11.18343344
228457_at	0	1	7.841813036
226933_s_at	ID4	1	7.197505278
232124_at	LOC729085	1	9.012375825
213688_at	CALM1 /// CALM2 /// CALM3	1	9.770078294
32625_at	NPR1	1	10.53750909
238472_at	FBXO9	1	9.457509997
1554757_a_at	INPP5A	1	8.12564343
227193_at	0	1	10.73619027
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225219_at	SMAD5	1	10.38959561
222444_at	ARMCX3	1	8.487319797
217367_s_at	ZHX3	1	14.29112637
225265_at	RBMS1	1	6.762831921
235747_at	SLC25A16	1	10.37774009
223730_at	GPC6	1	6.725564293
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229172_at	HSPA12B	1	10.22428477
40837_at	TLE2	1	8.714858258
221003_s_at	CAB39L	1	10.56986152
1552315_at	GIMAP1	1	9.853082292
206375_s_at	HSPB3	1	5.970201861
212409_s_at	TOR1AIP1	1	11.72292609
204552_at	INPP4A	1	11.1144112
209826_at	PPT2	1	12.65616202
200788_s_at	PEA15	1	14.58162746
222235_s_at	CSGALNACT2	1	10.25050539
215775_at	THBS1	1	8.0042449
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1560741_at	SNRPN	1	11.61800623
228532_at	C1orf162	1	6.163816674

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219552_at	SVEP1	1	12.72676883
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205128_x_at	PTGS1	1	7.294601303
204763_s_at	GNAO1	1	11.09408532
226756_at	0	1	7.093768405
203645_s_at	CD163	1	5.544158438
212257_s_at	SMARCA2	1	9.509738806
224860_at	C9orf123	1	8.790318824
209106_at	NCOA1	1	12.53375943
228416_at	ACVR2A	1	8.624533292
226528_at	MTX3	1	9.974036966
225755_at	KLHDC8B	1	10.06236479
213761_at	MDM1	1	8.625659235
218175_at	CCDC92	1	10.35648351
239409_at	0	1	9.124040427
212616_at	CHD9	1	13.90574193
239571_at	0	1	9.695197126
209004_s_at	FBXL5	1	14.17108348
238178_at	0	1	8.746152248
213715_s_at	KANK3	1	11.00976632
244286_at	0	1	12.18673022
223690_at	LTBP2	1	6.731371561
226211_at	MEG3	1	7.741150045
219520_s_at	WWC3	1	9.016189019
225225_at	LOC729082	1	14.93959776
215049_x_at	CD163	1	5.440035934
223641_at	0	1	10.29392074
209834_at	CHST3	1	10.32916482
242467_at	0	1	8.239733499
210172_at	SF1	1	8.223161524
226113_at	ZNF436	1	13.18713351
244043_at	0	1	8.00862339
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227873_at	TXNDC15	1	13.0744869
242856_at	0	1	9.140208787
227115_at	0	1	10.63233081
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202125_s_at	TRAK2	1	14.20625798
200808_s_at	ZYX	1	9.148710125
219767_s_at	CRYZL1	1	11.00985881
214510_at	GPR20	1	9.635681607
222357_at	ZBTB20	1	8.950139507
228243_at	0	1	10.5840023
230424_at	C5orf13	1	10.11597548
216442_x_at	FN1	1	5.468365771
219534_x_at	CDKN1C	1	4.917039495
221234_s_at	BACH2	1	7.184222794

229384_at		0	1	15.01614631
227610_at	TSPAN11		1	9.756842353
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212940_at	COL6A1		1	9.60179922
242605_at		0	1	9.207140701
213910_at	IGFBP7		1	13.4813695
212462_at	MYST4		1	11.64243863
212624_s_at	CHN1		1	7.997460158
236488_s_at		0	1	8.662423673
201801_s_at	SLC29A1		1	9.29240275
227584_at	NAV1		1	11.66365532
226119_at	PCMTD1		1	13.59436183
206337_at	CCR7		1	3.974121011
219922_s_at	LTBP3		1	7.851452743
212464_s_at	FN1		1	5.333450912
229278_at		0	1	9.815550537
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228523_at	NANOS1	1	3.967532532
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236610_at	0	1	7.684367427
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226981_at	MLL	1	11.29843537
1559296_at	LOC730057	1	14.00176996
231234_at	CTSC	1	8.120730502
228737_at	TOX2	1	4.863923882
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240433_x_at	0	1	6.169681201
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230068_s_at	PEG3	1	10.04076526
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213556_at	LOC390940	1	7.462528988
227821_at	LG14	1	11.90951349
241401_at	C4orf12	1	10.23302818
223494_at	MGEA5	1	7.616084641
234300_s_at	ZFP28	1	8.724142577

230141_at	ARID4A	1	11.26386117
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227242_s_at	EBF3	1	6.012292049
230311_s_at	PRDM6	1	7.632585522
223618_at	FMN2	1	4.517936669
225820_at	PHF17	1	6.083817032
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203002_at	AMOTL2	1	6.529523666
235567_at	RORA	1	9.040161622
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232182_at	LOC286272	1	9.915343378
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238923_at	SPOP	1	7.708151334
209994_s_at	ABCB1 /// ABCB4	1	5.235989142
221606_s_at	NSBP1	1	4.167476509
219487_at	BBS10	1	6.174511784
215784_at	CD1E	1	4.203331766
219834_at	ALS2CR8	1	9.760474179
223712_at	PCBD2	1	9.020030691
205507_at	ARHGEF15	1	9.565091772
233814_at	EFNA5	1	4.391497593
227613_at	ZNF331	1	4.58276351
214870_x_at	LOC339047	1	9.690145543
227930_at	EIF2C4	1	7.497954631
237094_at	FAM19A5	1	5.666464917
205730_s_at	ABLIM3	1	7.258767626
211742_s_at	EVI2B	1	4.287614791
220512_at	DLC1	1	6.582956451
225223_at	SMAD5	1	9.176588776
217863_at	PIAS1	1	11.66781245
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212587_s_at	PTPRC	1	4.259972937
216997_x_at	TLE4	1	9.796411892
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237444_at	0	1	8.458035549
221727_at	SUB1	1	7.7683359

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223824_at	C10orf59	1	7.934733482
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228758_at	BCL6	1	6.44886661
239466_at	LOC344595	1	10.21871637
236862_at	GOPC	1	8.620292524
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220326_s_at	FLJ10357	1	9.643849048
207703_at	NLGN4Y	1	5.317360772
210976_s_at	PFKM	1	8.456896398
235938_at	0	1	9.114515026
238823_at	FMNL3	1	9.886943094
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204456_s_at	GAS1	1	6.200640895
205122_at	TMEFF1	1	4.516456304
223886_s_at	RNF146	1	10.60097884
235926_at	0	1	5.873853464
242277_at	0	1	5.091471257
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227319_at	0	1	12.38798438
240557_at	0	1	8.263993022
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233748_x_at	PRKAG2	1	8.405672487
212672_at	ATM	1	9.474240346
229285_at	RNASEL	1	7.169542985
241442_at	0	1	12.70472885
229352_at	NOX5 /// SPESP1	1	5.227769179
242920_at	0	1	7.428072748
212796_s_at	TBC1D2B	1	10.33840039
205845_at	CACNA1H	1	10.2271131
225350_s_at	ZYG11B	1	10.78447882
228042_at	ADPRH	1	8.71093127
224365_s_at	TIGD7	1	5.650410701
1556190_s_at	PRNP	1	5.32946219
226219_at	ARHGAP30	1	4.855735922
213243_at	VPS13B	1	10.0903218
224929_at	TMEM173	1	7.535892161
219939_s_at	CSDE1	1	13.5056377
227654_at	FAM65C	1	4.099336845
235592_at	0	1	4.731923066
210347_s_at	BCL11A	1	4.370301803

223444_at	SENP7		1	8.691891643
228968_at	ZNF449		1	10.45460292
239058_at		0	1	7.156705632
216894_x_at	CDKN1C		1	4.392052657
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243046_at		0	1	7.725867842
217371_s_at	IL15		1	6.543525501
235962_at		0	1	11.0044829
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226632_at	CYGB		1	5.863194748
229822_at		0	1	9.209369426
1569129_s_at	C3orf38		1	7.96842999
232889_at		0	1	5.822152597
242607_at		0	1	8.162272658
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232317_at	PLXNA4		1	7.251223558
212660_at	PHF15		1	7.430704957
229537_at	LMO4		1	5.612503255
227485_at	DDX26B		1	6.7269616
224704_at	TNRC6A		1	10.71489354
203890_s_at	DAPK3		1	8.069950034
219269_at	HMBOX1		1	8.856294257
214823_at	ZNF204		1	5.427056428
203636_at	MID1		1	5.755813973
226633_at	RAB8B		1	7.827597042
214151_s_at	CCPG1		1	8.461813128
234937_x_at	ZFP28		1	8.53656658
229898_at		0	1	12.99450039
204546_at	KIAA0513		1	8.232288891
1556138_a_at		0	1	9.9081398
203773_x_at	BLVRA		1	6.246531342
203049_s_at	TTC37		1	8.439121158
228097_at	MYLIP		1	7.045219126
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230161_at		0	1	9.422490902
223510_at	NRP2		1	8.976496662
211621_at	AR		1	10.30103398
220952_s_at	PLEKHA5		1	7.096995838
219114_at	C3orf18		1	13.52136431
238940_at	KLF12		1	11.35500789
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231862_at	CBX5		1	5.994326523
232429_at		0	1	10.81961096
212357_at	FAM168A		1	11.81949601
213998_s_at	DDX17		1	6.077529595
237351_at		0	1	5.646164881

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212294_at	GNG12	1	8.922042954
204904_at	GJA4	1	8.198224798
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221885_at	DENND2A	1	8.029336306
225180_at	TTC14	1	6.359736545
218692_at	GOLSYN	1	4.211680045
217552_x_at	CR1	1	5.31553739
236166_at	LOC285147	1	8.905559565
227351_at	C16orf52	1	10.01472545
205131_x_at	CLEC11A	1	6.769770849
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1558702_at	TEX10	1	9.67836997
235728_at	ZFP3	1	5.262611237
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224566_at	NCRNA00084	1	4.610488215
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213195_at	LOC201229	1	10.58630425
1559882_at	SAMHD1	1	6.303092738
204344_s_at	SEC23A	1	8.680951013
238782_at	0	1	8.199359849
231842_at	KIAA1462	1	6.017401366
233223_at	0	1	5.765912184
213488_at	SNED1	1	6.608031406
224341_x_at	TLR4	1	5.279891828
209827_s_at	IL16	1	6.226700814
207238_s_at	PTPRC	1	3.828673832
1555929_s_at	0	1	7.326707384
212650_at	EHBP1	1	6.918794419
220190_s_at	GTF2A1L /// STON1 /// STON1-	1	6.947853958
208656_s_at	CCNI	1	16.49509938
224844_at	SLAIN2	1	11.68479654
233329_s_at	KRCC1	1	6.41546896
219291_at	DTWD1	1	10.59780324
224916_at	TMEM173	1	6.525294954
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205584_at	ALG13	1	9.316245765
239286_at	CDH11	1	6.663886514
225856_at	0	1	10.36408412
224518_s_at	ZNF559	1	6.070643841
201681_s_at	DLG5	1	7.408569711
225627_s_at	CACHD1	1	4.39789103
238723_at	ATXN3	1	8.827680579
219342_at	CASD1	1	8.195016344
222161_at	NAALAD2	1	7.008665877
214683_s_at	CLK1	1	8.149719377

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238883_at		0	1	7.336433493
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227266_s_at	FYB		1	3.691778836
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221899_at	N4BP2L2		1	5.167632768
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228506_at	NSMCE4A		1	6.387762795
235725_at	SMAD4		1	8.177343072
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225331_at	CCDC50		1	8.455263465
208873_s_at	REEP5		1	8.641295864
219044_at	THNSL2		1	6.037261164
204038_s_at	LPAR1		1	8.86724213
1555897_at	AOF2		1	11.13820521
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233648_at		0	1	7.326908033
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210166_at	TLR5		1	7.09371745
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212977_at	CXCR7		1	4.92680412
207704_s_at	GAS7		1	8.582754838
225553_at		0	1	8.770892016
227204_at	PARD6G		1	7.797595844
208859_s_at	ATRX		1	7.645053708
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219645_at	CASQ1		1	8.299920043
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232724_at	MS4A6A		1	11.06281098
227246_at	PLRG1		1	8.19389731
227397_at	TPM2		1	10.16264595
203426_s_at	IGFBP5		1	9.253305194
206574_s_at	LOC100131062 /// PTP4A3		1	4.960974199
236264_at	LPHN3		1	4.568468674
225816_at	PHF17		1	6.651189321
35776_at	ITSN1		1	11.50062068
229710_at		0	1	8.967074519
232865_at	AFF4		1	7.311923715
217317_s_at	HERC2P2 /// HERC2P3 ///		1	9.048083274
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231879_at	COL12A1		1	3.602694253
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242500_at		0	1	7.89778298
228839_s_at	LOC439994 /// LOC642361		1	9.286155035

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228346_at	ZNF844		1	7.32783591
209075_s_at	ISCU		1	14.9648228
209019_s_at	PINK1		1	10.53547516
225018_at	SPIRE1		1	4.841728545
227918_s_at	ZYG11B		1	7.932869929
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211864_s_at	MYOF		1	4.383322613
203425_s_at	IGFBP5		1	8.617136838
239984_at		0	1	8.667013139
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218537_at	HCFC1R1		1	10.90331603
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207326_at	BTC		1	6.688091245
232882_at		0	1	6.940781124
203423_at	RBP1		1	3.693609163
228720_at	SORCS2		1	10.50369493
228446_at	KIAA2026		1	10.79792113
212350_at	TBC1D1		1	8.477168715
221725_at		0	1	12.05694612
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226464_at	C3orf58		1	8.830057907
222423_at	NDFIP1		1	9.841825604
218373_at	AKTIP		1	11.11863099
228519_x_at	CIRBP		1	12.86759364
228375_at	IGSF11		1	5.929293722
1552509_a_at	CD300LG		1	5.004768837
228537_at	GLI2		1	10.99245144
228469_at	PPID		1	5.107052789
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231042_s_at		0	1	5.373786716
1559942_at	MDFIC		1	7.507252111
238752_at		0	1	7.820771167
235281_x_at	AHNAK		1	8.000563671
229828_at		0	1	10.14654798
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1559412_at	C21orf34		1	14.92057551
227536_at	ZC3H13		1	9.115035994
215513_at	HYMAI		1	8.816647943
214035_x_at	LOC399491		1	9.746948346
209901_x_at	AIF1		1	5.41051955
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212765_at	CAMSAP1L1		1	9.673833358
238656_at		0	1	9.219299871
229434_at		0	1	6.661742089
229009_at	SIX5		1	8.754128101

242865_at		0	1	6.802885193
211626_x_at	ERG		1	11.49756831
212163_at	KIDINS220		1	7.90737353
221330_at	CHRM2		1	8.337928184
1558881_at	LOC145820		1	9.110914865
230917_at		0	1	5.229334113
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222760_at	ZNF703		1	5.199485033
230822_at	TMEM61		1	5.457087861
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218552_at	ECHDC2		1	6.229302696
205789_at	CD1D		1	5.457407863
1554029_a_at	TTC37		1	5.959270291
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235009_at	FAM44A		1	7.158727977
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214711_at	GATC	2	-6.864975459
217124_at	IQCE	2	-6.408934026
231269_at	ASCC3	2	-6.747556093
223165_s_at	IP6K2	2	-5.949863148
224407_s_at	RP6-213H19.1	2	-4.506803775
213807_x_at	MET	2	-5.00440157
230666_at	HOXA11AS	2	-5.394382955
218893_at	ISOC2	2	-8.160358323
210457_x_at	HMGAI	2	-10.06062186
225598_at	SLC45A4	2	-6.399476857
215195_at	PRKCA	2	-6.097172812
206467_x_at	RTSL1 /// TNFRSF6B	2	-3.907689802
218511_s_at	PNPO	2	-7.906424978
210876_at	ANXA2P1	2	-7.303470986
1559072_a_at	ELFN2	2	-4.807508838
212800_at	STX6	2	-8.403500821
225463_x_at	GPR89A /// GPR89B /// GPR89C	2	-8.487774146
224716_at	SLC35B2	2	-8.099615032
231667_at	SLC39A5	2	-5.502106972
1487_at	ESRRA	2	-8.877617136
222981_s_at	RAB10	2	-10.00736749
209804_at	DCLRE1A	2	-9.535663111
212075_s_at	CSNK2A1	2	-7.917326641
213427_at	RPP40	2	-5.883896893
208647_at	FDFT1	2	-5.484335453
239818_x_at	TRIB1	2	-4.060046454
233829_at	C20orf118	2	-7.229132604
215594_at	0	2	-5.196246833
203313_s_at	TGIF1	2	-6.82886176
212110_at	SLC39A14	2	-5.331485628
201886_at	WDR23	2	-11.15951308
201764_at	TMEM106C	2	-6.595372418
222537_s_at	CDC42SE1	2	-9.250320475
221754_s_at	CORO1B	2	-8.820866881
233334_x_at	GIYD1 /// GIYD2 /// SULT1A3 /// SULT1A4	2	-8.862109672
200054_at	ZNF259	2	-9.573244226
222216_s_at	MRPL17	2	-11.40652835
205372_at	PLAG1	2	-4.461197793
236983_at	TMC5	2	-6.712438825
218728_s_at	CNIH4	2	-9.775501207
224674_at	TTYH3	2	-8.391686504
202193_at	LIMK2	2	-6.219127857
203715_at	TBCE	2	-7.508520459
205429_s_at	MPP6	2	-4.077352966
202416_at	DNAJC7	2	-8.674991257
218887_at	MRPL2	2	-8.949968674
236347_at	MMAA	2	-7.542824892

1556166_x_at	0	2	-4.661928984
202595_s_at	LEPROTL1	2	-7.67855978
218533_s_at	UCKL1	2	-8.798376812
211971_s_at	LRPPRC	2	-9.458350458
218834_s_at	TMEM132A	2	-7.336694058
203007_x_at	LYPLA1	2	-8.533111148
205759_s_at	SULT2B1	2	-6.235015133
203126_at	IMPA2	2	-4.874628147
203405_at	PSMG1	2	-7.086015071
218477_at	TMEM14A	2	-7.461673923
212611_at	DTX4	2	-5.631256168
224742_at	ABHD12	2	-10.93991883
220104_at	ZC3HAV1	2	-6.151311832
200738_s_at	PGK1	2	-10.3545864
203415_at	PDCD6	2	-8.39910529
219099_at	C12orf5	2	-6.869428724
211363_s_at	MTAP	2	-5.486485748
200820_at	PSMD8	2	-8.592423725
229933_at	C1orf74	2	-9.247601554
218499_at	RP6-213H19.1	2	-4.338540413
1554472_a_at	PHF20L1	2	-6.263515429
208693_s_at	GARS	2	-10.13373843
230871_at	DHX30	2	-8.175812925
212898_at	KIAA0406	2	-8.133174717
234927_s_at	MAGIX	2	-8.691363314
210048_at	NAPG	2	-6.954578215
210092_at	MAGOH	2	-8.955058034
201476_s_at	RRM1	2	-7.828807316
244593_at	C17orf28	2	-7.707749256
216841_s_at	SOD2	2	-4.448790996
232331_at	0	2	-5.549485535
1559322_at	LOC727916	2	-5.15608728
1553690_at	SGOL1	2	-10.14523818
234291_s_at	SLC6A20	2	-3.862239946
214827_at	PAR6B	2	-5.046496564
213937_s_at	FTSJ1	2	-11.71713184
212321_at	SGPL1	2	-7.606290894
204947_at	E2F1	2	-12.26307631
225468_at	PATL1	2	-7.160579787
211494_s_at	SLC4A4	2	-3.962428745
219108_x_at	DDX27	2	-8.172287485
219622_at	RAB20	2	-7.36090161
241466_at	0	2	-10.28181671
220934_s_at	MGC3196	2	-7.810271282
226499_at	NRARP	2	-5.036385397
224707_at	C5orf32	2	-4.078229074
238807_at	ANKRD46	2	-5.794079805
221704_s_at	VPS37B	2	-6.572720986
227737_at	SRPRB	2	-8.113735988
224675_at	MESDC2	2	-9.986493015

226459_at	PIK3AP1	2	-4.80352329
225663_at	ACBD5	2	-7.190428334
223531_x_at	GPR89A /// GPR89B /// GPR89C	2	-9.72078367
203806_s_at	FANCA	2	-10.83325045
223017_at	TXNDC12	2	-12.37320965
204883_s_at	HUS1	2	-9.796804146
214963_at	NUP160	2	-7.322118895
219283_at	C1GALT1C1	2	-8.71588513
219556_at	C16orf59	2	-13.15402947
215215_s_at	LOC81691	2	-8.996137461
222735_at	TMEM38B	2	-5.958813677
224221_s_at	VAV3	2	-3.731946402
208881_x_at	IDI1	2	-7.756664703
203714_s_at	TBCE	2	-8.033354689
218382_s_at	U2AF2	2	-9.799532869
226488_at	RCCD1	2	-7.620659726
202793_at	LPCAT3	2	-7.042469681
226390_at	STARD4	2	-5.505194503
214264_s_at	C14orf143	2	-7.184267946
230406_at	0	2	-4.567531125
212656_at	TSFM	2	-10.97830292
206724_at	CBX4	2	-7.268997093
203433_at	MTHFS	2	-9.22844403
226650_at	ZFAND2A	2	-6.400997567
209600_s_at	ACOX1	2	-6.634569285
214708_at	SNTB1	2	-4.857677162
211851_x_at	BRCA1	2	-11.06587742
215438_x_at	GSPT1	2	-9.36474084
206410_at	NR0B2	2	-4.23099156
203165_s_at	SLC33A1	2	-7.749962478
233550_s_at	SLC4A11	2	-7.491146003
213435_at	SATB2	2	-3.862828485
228286_at	GEN1	2	-7.545912758
221780_s_at	DDX27	2	-8.154347248
201771_at	SCAMP3	2	-11.11935014
200616_s_at	MLEC	2	-8.162041858
1555487_a_at	ACTR3B /// LOC100133409	2	-9.175574604
229208_at	CEP27	2	-8.90328229
203918_at	PCDH1	2	-7.735206178
216316_x_at	GK /// GK3P	2	-7.592452385
209262_s_at	NR2F6	2	-8.78230581
220602_s_at	FLJ22795 /// LOC388152 /// LOC388161 /// LOC727751 /// LOC727849 /// LOC727994 /// LOC728125 /// LOC729353	2	-8.850865451
1552575_a_at	C6orf141	2	-3.83649671
205906_at	FOXJ1	2	-6.203979282
205281_s_at	PIGA	2	-7.274336287
204434_at	SPATA2	2	-7.493185097
208726_s_at	EIF2S2	2	-11.58171972

222931_s_at	THNSL1	2	-6.378594592
229068_at	CCT5	2	-6.06314874
227606_s_at	STAMBPL1	2	-5.327522712
208029_s_at	LAPTM4B	2	-4.714085002
1552472_a_at	ACAP2	2	-6.836089667
203119_at	CCDC86	2	-8.671289992
200638_s_at	YWHAZ	2	-8.6222467
223582_at	GPR98	2	-5.267320186
226241_s_at	MRPL52	2	-11.29274391
221696_s_at	STYK1	2	-4.655129627
239134_at	0	2	-9.316754405
235253_at	RAD1	2	-6.510361518
205519_at	WDR76	2	-7.363640955
204408_at	APEX2	2	-11.57764663
208854_s_at	STK24	2	-8.94720067
238804_at	LOC100131701	2	-4.53126278
219117_s_at	FKBP11	2	-4.447610628
1552884_at	NKX6-3	2	-5.435438434
202185_at	PLOD3	2	-7.291072214
232155_at	KIAA1618	2	-5.063695611
1554508_at	PIK3AP1	2	-5.364135778
223791_at	FAM27A /// LOC100132948	2	-6.255395383
218737_at	SBNO1	2	-7.1665003
203125_x_at	SLC11A2	2	-7.993575717
211754_s_at	SLC25A17	2	-8.658055445
229232_at	LRRC57	2	-8.624455127
232861_at	PDP2	2	-6.874029612
203647_s_at	FDX1	2	-7.796873814
227033_at	PDIA3	2	-8.373661439
1566472_s_at	RETSAT	2	-5.189152398
201416_at	SOX4	2	-4.52171341
219212_at	HSPA14	2	-7.520576143
224617_at	ROD1	2	-8.924675536
213112_s_at	SQSTM1	2	-6.371832729
206696_at	GPR143	2	-5.006473336
235239_at	QSOX2	2	-10.98952709
211747_s_at	LSM5	2	-10.456768
219131_at	UBIAD1	2	-9.612211059
229901_at	ZNF488	2	-5.879924821
200807_s_at	HSPD1	2	-11.23603269
203942_s_at	MARK2	2	-8.631438652
200750_s_at	RAN	2	-9.60798972
205217_at	TIMM8A	2	-8.637423053
204905_s_at	EEF1E1	2	-7.571009858
206034_at	SERPINB8	2	-6.718876386
227123_at	RAB3B	2	-4.409407025
232922_s_at	C20orf59	2	-6.778730571
208612_at	PDIA3	2	-10.69455799
40020_at	CELSR3 /// SLC26A6	2	-5.991246705
228671_at	TMEM201	2	-8.436831736

228450_at	PLEKHA7	2	-6.374648495
205812_s_at	TMED9	2	-10.6901554
212685_s_at	TBL2	2	-8.919421765
217790_s_at	SSR3	2	-7.196813557
219890_at	CLEC5A	2	-3.740028118
201946_s_at	CCT2	2	-7.083545022
204455_at	DST	2	-4.137529519
213622_at	COL9A2	2	-5.433162317
231875_at	KIF21A	2	-6.135611007
225887_at	C13orf23	2	-7.502059656
221738_at	KIAA1219	2	-10.6507411
212766_s_at	ISG20L2	2	-8.878181197
206153_at	CYP4F11	2	-5.420978434
205232_s_at	PAFAH2	2	-8.611163137
212290_at	SLC7A1	2	-7.034591697
209222_s_at	OSBPL2	2	-8.200646898
215458_s_at	SMURF1	2	-6.61559858
216606_x_at	LYPLA2P1	2	-14.48564107
226566_at	TRIM11	2	-10.62159239
224521_s_at	CCDC77	2	-7.680812629
227609_at	EPSTI1	2	-3.908540785
203557_s_at	PCBD1	2	-7.237173282
211150_s_at	DLAT	2	-7.943073162
228366_at	0	2	-8.382926416
207279_s_at	NEBL	2	-6.373862933
212619_at	TMEM194A	2	-6.109408128
205238_at	TRMT2B	2	-7.203105467
225944_at	NLN	2	-6.318468594
205351_at	GGCX	2	-6.640341466
216602_s_at	FARSA	2	-8.52718751
1553031_at	GPR115	2	-6.158869244
208937_s_at	ID1	2	-3.663605201
222993_at	MRPL37	2	-11.78998953
217094_s_at	ITCH	2	-9.246818614
232827_at	0	2	-8.041387632
218010_x_at	C20orf149	2	-7.171634473
226294_x_at	FAM91A1	2	-9.888899902
218340_s_at	UBA6	2	-5.144603114
219360_s_at	TRPM4	2	-5.432604675
239054_at	0	2	-8.421850529
220238_s_at	KLHL7	2	-6.046174408
210497_x_at	LOC100130648 /// SSX2 /// SSX2B	2	-5.134981319
213600_at	SIPA1L3	2	-8.921463409
205260_s_at	ACYP1	2	-6.953875292
223245_at	STRBP	2	-8.256763804
228876_at	BAIAP2L2	2	-7.734031768
242196_at	0	2	-6.0142258
204942_s_at	ALDH3B2	2	-5.114665508
214501_s_at	H2AFY	2	-10.32251101
204588_s_at	SLC7A7	2	-5.005933727

209744_x_at	ITCH	2	-8.676128434
221627_at	TRIM10	2	-11.31719086
223159_s_at	NEK6	2	-6.272615191
221998_s_at	VRK3	2	-8.677403713
218046_s_at	MRPS16	2	-9.014191871
202929_s_at	DDT	2	-8.404880251
230971_x_at	GLTPD2	2	-7.935914585
1558329_at	NFKBIL2	2	-10.10822308
212694_s_at	PCCB	2	-7.239960164
217080_s_at	HOMER2	2	-4.240697381
218898_at	FAM57A	2	-6.421697558
219324_at	NOL12 /// TRIOBP	2	-11.79917581
232530_at	PLD1	2	-3.679017165
219809_at	WDR55	2	-8.933692447
218163_at	MCTS1	2	-9.277324372
211810_s_at	GALC	2	-5.259380454
220013_at	ABHD9	2	-3.939646536
229273_at	SALL1	2	-5.526506149
1555606_a_at	GDPD1	2	-7.597496664
229678_at	LOC728431	2	-6.611756463
200640_at	YWHAZ	2	-10.61831637
219066_at	PPCDC	2	-9.46546995
237086_at	FOXA1	2	-5.786510478
202857_at	CNPY2	2	-8.823593127
201377_at	UBAP2L	2	-9.450280676
229661_at	SALL4	2	-3.998489204
227268_at	RNFT1	2	-6.766915921
202195_s_at	TMED5	2	-8.338940026
227578_at	LOC100128191	2	-8.704770493
227560_at	SFXN2	2	-7.395000321
230105_at	HOXB13	2	-7.669782306
205704_s_at	ATP6VOA2	2	-8.867767431
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223586_at	ARNTL2	2	-5.564189575
222416_at	ALDH18A1	2	-8.03135916
223639_s_at	ZNRD1	2	-10.71039879
219653_at	LSM14B	2	-8.610475111
219076_s_at	PXMP2	2	-7.085009179
1554466_a_at	C16orf13	2	-8.87443619
203462_x_at	EIF3B	2	-9.179605769
201942_s_at	CPD	2	-5.742397029
1554915_a_at	PDE12	2	-7.529328626
230481_at	ACY3	2	-5.002890956
211116_at	SLC9A2	2	-4.923697392
231938_at	SGOL1	2	-8.381613625
217794_at	PRR13	2	-8.462967909
33814_at	PAK4	2	-11.55920766
203118_at	PCSK7	2	-8.505696418
209233_at	EMG1	2	-9.69492516
233982_x_at	STYXL1	2	-7.306306077

222405_at	PTPLAD1	2	-9.368099511
222590_s_at	NLK	2	-9.840402474
200875_s_at	NOP56	2	-7.312658277
225694_at	CRKRS	2	-9.186939758
225723_at	C6orf129	2	-9.014287774
205191_at	RP2	2	-6.824542796
218159_at	DDRKG1	2	-9.367499032
202626_s_at	LYN	2	-6.129483951
201772_at	AZIN1	2	-8.33555245
208337_s_at	NR5A2	2	-4.775175851
222837_s_at	NARG1	2	-7.050290147
218590_at	C10orf2	2	-7.97922729
214542_x_at	HIST1H2AG /// HIST1H2AH /// HIST1H2AI /// HIST1H2AJ /// HIST1H2AK /// HIST1H2AL /// HIST1H2AM	2	-11.35537889
213509_x_at	CES2	2	-3.585680051
1558330_x_at	NFKBIL2	2	-10.14765456
228892_at	SH3RF2	2	-6.258615527
1569555_at	GDA	2	-7.807083983
222269_at	APOOL	2	-6.433838972
217871_s_at	LOC284889 /// MIF	2	-8.68978017
206606_at	LIPC	2	-3.598068868
201381_x_at	CACYBP	2	-10.41172764
221572_s_at	SLC26A6	2	-7.36822282
208767_s_at	LAPTM4B	2	-4.873180422
236381_s_at	WDR8	2	-8.264351691
1552682_a_at	CASC5	2	-9.015249289
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204478_s_at	RABIF	2	-12.37632347
201298_s_at	MOBK1B	2	-8.385722799
219080_s_at	CTPS2	2	-7.14673541
234635_at	KRTAP4-1	2	-4.978083355
200973_s_at	TSPAN3	2	-6.45118773
205479_s_at	PLAU	2	-4.201432552
200929_at	TMED10	2	-9.067954777
225036_at	SHB /// TOMM5	2	-9.738659931
223151_at	DCUN1D5	2	-8.147284913
212072_s_at	CSNK2A1	2	-9.803111804
223156_at	MRPS23	2	-9.542868188
204267_x_at	PKMYT1	2	-13.05296071
232116_at	GRHL3	2	-5.373893377
203524_s_at	MPST	2	-7.432250367
225037_at	SLC35C2	2	-10.29109048
226350_at	CHML	2	-6.726193349
209796_s_at	CNPY2	2	-8.39340078
225520_at	MTHFD1L	2	-6.348943775
227374_at	EARS2	2	-8.863234704
206103_at	RAC3	2	-7.416448272
219564_at	KCNJ16	2	-3.785295971

204172_at	CPOX	2	-7.543517849
1555976_s_at	0	2	-6.150455167
201633_s_at	CYB5B	2	-7.064502025
1563792_at	0	2	-4.473148874
219275_at	PDCD5	2	-6.844810783
228454_at	LCOR	2	-7.083200292
213078_x_at	LPCAT4	2	-5.267609621
204107_at	NFYA	2	-9.260319844
1554556_a_at	ATP11B	2	-10.7394979
1554063_at	C8orf76	2	-8.58595064
225652_at	0	2	-9.092963842
215631_s_at	BRMS1	2	-8.901114786
202072_at	HNRNPL	2	-6.25608028
223299_at	SEC11C	2	-6.00145953
212556_at	SCRIB	2	-9.072346432
205233_s_at	PAFAH2	2	-8.260569898
223209_s_at	SELS	2	-8.444467913
204279_at	PSMB9	2	-4.784149039
216698_x_at	LOC441453 /// OR7E18P /// OR7E35P /// OR7E37P ///	2	-10.5044284
209393_s_at	EIF4E2	2	-11.82774713
230263_s_at	DOCK5	2	-4.774961635
243862_at	0	2	-6.213478953
208921_s_at	SRI	2	-6.997868157
223355_at	ALG1	2	-9.218933192
218140_x_at	SRPRB	2	-9.164722675
225736_at	FBXO22	2	-9.394194987
207740_s_at	NUP62	2	-9.290977752
214991_s_at	PIGO	2	-10.10853348
204247_s_at	CDK5	2	-8.911964151
205633_s_at	ALAS1	2	-9.143251951
201091_s_at	CBX3 /// LOC653972	2	-9.355684494
228726_at	0	2	-4.951487193
219517_at	ELL3	2	-5.534442715
237439_at	USP43	2	-11.40366288
207515_s_at	POLR1C	2	-8.490683016
225765_at	TNPO1	2	-11.3996381
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211885_x_at	FUT6	2	-4.780930582
201399_s_at	TRAM1	2	-7.609931189
238084_at	PCGF3	2	-10.09405948
214205_x_at	GLRX3	2	-10.20300302
225737_s_at	FBXO22	2	-8.275986087
233252_s_at	STRBP	2	-8.196393721
237690_at	GPR115	2	-5.266081288
220312_at	FAM83E	2	-6.176445275
241433_at	RCOR3	2	-9.322783305
210639_s_at	ATG5	2	-8.167019023
204727_at	WDHD1	2	-7.853998663
207011_s_at	PTK7	2	-5.961718596

1557754_at	LOC401068	2	-7.352448783
203739_at	ZNF217	2	-5.701895899
220137_at	FLJ20674	2	-6.226091392
210396_s_at	BOLA2 /// LOC440354 ///	2	-6.968321997
228181_at	SLC30A1	2	-6.306910209
205074_at	SLC22A5	2	-6.88464801
227569_at	LNK2	2	-8.763935853
220966_x_at	ARPC5L	2	-12.68119753
220486_x_at	LOC100130886 /// TMEM164	2	-6.158588533
222443_s_at	RBM8A	2	-10.94278503
221345_at	FFAR2	2	-4.218790547
230626_at	TSPAN12	2	-4.73569293
212815_at	ASCC3	2	-9.245435688
212285_s_at	AGRN	2	-7.040994615
213330_s_at	STIP1	2	-11.39769796
219075_at	YIPF2	2	-10.18569695
1553338_at	C1orf55	2	-8.772292505
214214_s_at	C1QBP	2	-8.636896353
226423_at	PAQR8	2	-4.939722053
218961_s_at	PNKP	2	-9.133831886
223651_x_at	CDC23	2	-7.283437394
224232_s_at	PRELID1	2	-9.727015442
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222977_at	SURF4	2	-10.42198093
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204034_at	ETHE1	2	-5.31028921
222500_at	PPIL1	2	-7.000482851
208688_x_at	EIF3B	2	-9.818010671
221739_at	C19orf10	2	-8.894332856
239596_at	SLC30A7	2	-9.660678226
216652_s_at	DR1	2	-9.364475701
208583_x_at	HIST1H2AG /// HIST1H2AH /// HIST1H2AI /// HIST1H2AJ /// HIST1H2AK /// HIST1H2AL /// HIST1H2AM	2	-11.76886065
205640_at	ALDH3B1	2	-4.712513082
217499_x_at	OR7E37P	2	-8.108171802
217909_s_at	MLX	2	-8.072189569
224654_at	DDX21	2	-8.560013805
212812_at	0	2	-6.191942854
208972_s_at	ATP5G1	2	-8.737368328
217419_x_at	AGRN	2	-7.717658297
202418_at	YIF1A	2	-9.184740745
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229522_at	SDR42E1	2	-6.611954474
212973_at	RPIA	2	-8.407030989
236140_at	GCLM	2	-6.511699103
225726_s_at	PLEKHH1	2	-5.233174045
224583_at	COTL1	2	-5.236903146
214924_s_at	TRAK1	2	-5.705143598

213843_x_at	SLC6A8	2	-4.264918431
223076_s_at	NSUN2	2	-9.804290581
202562_s_at	C14orf1	2	-10.73776327
219904_at	ZSCAN5A	2	-8.316200948
239169_at	RDM1	2	-9.910798116
224870_at	KIAA0114	2	-5.67517938
224443_at	C1orf97	2	-6.26555615
222976_s_at	TPM3	2	-11.2994091
221680_s_at	ETV7	2	-6.692316212
225779_at	SLC27A4	2	-8.75641956
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230633_at	TMEM102	2	-10.54200285
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202223_at	STT3A	2	-8.323803621
202610_s_at	MED14	2	-9.558893039
223364_s_at	DHX37	2	-10.92108122
204799_at	ZBED4	2	-8.462836975
204252_at	CDK2	2	-8.641113355
209585_s_at	MINPP1	2	-7.13339375
220192_x_at	SPDEF	2	-4.583461458
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217916_s_at	FAM49B	2	-9.299675741
204017_at	KDELRL3	2	-4.258417967
218321_x_at	STYXL1	2	-7.653756765
212449_s_at	LYPLA1	2	-9.5321805
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236001_at	LOC400573	2	-3.705740075
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239492_at	SEC14L4	2	-3.682284376
222878_s_at	OTUB2	2	-7.719644523
218719_s_at	GIN5	2	-9.646944714
212127_at	RANGAP1	2	-13.17168181
218389_s_at	APH1A	2	-10.53346594
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222398_s_at	EFTUD2	2	-12.36042442
235707_at	LOC221710	2	-8.210399328
223506_at	ZC3H8	2	-8.670311083
204514_at	DPH2	2	-10.70647844
205161_s_at	PEX11A	2	-6.268670073
222234_s_at	DBNDD1	2	-8.559406092
205135_s_at	NUFIP1	2	-8.514874909
202115_s_at	NOC2L	2	-12.55368809
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229104_s_at	GPR39	2	-9.192396569
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1557257_at	BCL10	2	-5.298314451

1552304_at	ALG10	2	-8.669891038
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212340_at	YIPF6	2	-9.118045698
205077_s_at	PIGF	2	-9.167996929
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1558152_at	LOC100131262	2	-4.871904796
225527_at	CEBPG	2	-6.781778223
235095_at	CCDC64B	2	-7.397284105
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1552696_at	NIPA1	2	-7.987031135
228485_s_at	SLC44A1	2	-6.179459496
225707_at	ARL6IP6	2	-9.168017196
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202199_s_at	SRPK1	2	-8.584203585
213011_s_at	TPI1	2	-12.2806939
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222979_s_at	SURF4	2	-10.15690489
202459_s_at	LPIN2	2	-6.508919289
243508_at	C20orf196	2	-8.694150704
219864_s_at	RCAN3	2	-9.726852795
207852_at	CXCL5	2	-4.187267118
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205829_at	HSD17B1	2	-4.870498696
225879_at	TSEN54	2	-12.51789001
203394_s_at	HES1	2	-5.259980197
219031_s_at	NIP7	2	-9.168522456
205289_at	BMP2	2	-3.63083403
212038_s_at	VDAC1	2	-8.548009697
213889_at	PIGL	2	-7.363991497
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218593_at	RBM28	2	-11.04050615
226886_at	GFPT1	2	-6.129108783
211574_s_at	CD46	2	-7.277002411
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201662_s_at	ACSL3	2	-7.941535324
221922_at	GPSM2	2	-6.436436066
218894_s_at	MAGOHB	2	-9.124870937
224779_s_at	FAM96A	2	-9.731229894
212767_at	MTG1	2	-11.1879319
206877_at	MXD1	2	-6.252509352
38766_at	SRCAP	2	-8.529390289
226574_at	PSPC1	2	-8.400356873
207254_at	SLC15A1	2	-3.813571041
220642_x_at	GPR89A /// GPR89B /// GPR89C	2	-10.36928566
205263_at	BCL10	2	-8.421020662
205628_at	LOC100134172 /// PRIM2	2	-8.238626403
219219_at	TMEM160	2	-9.577035164

201923_at	PRDX4	2	-7.999886654
205264_at	CD3EAP	2	-9.633129575
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225119_at	CHMP4B	2	-6.820641947
216913_s_at	RRP12	2	-8.513921206
202295_s_at	CTSH	2	-4.759338391
1558164_s_at	PEX13	2	-8.061392993
1558304_s_at	TSEN54	2	-12.01707059
225154_at	SYAP1	2	-7.974558181
201203_s_at	RRBP1	2	-7.422793867
201411_s_at	PLEKHB2	2	-9.766613768
235346_at	FUNDCl	2	-6.830067683
208343_s_at	NR5A2	2	-3.672919476
230966_at	IL4I1	2	-5.12538959
222507_s_at	TMEM9B	2	-7.528998408
228544_s_at	CSRP2BP	2	-9.017272402
202475_at	TMEM147	2	-10.34588477
1555785_a_at	XRNI	2	-6.743448979
202937_x_at	RRP7A	2	-8.880615947
217992_s_at	EFHD2	2	-7.129893741
203350_at	AP1G1	2	-11.51501767
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201709_s_at	NIPSNAP1	2	-9.306489728
236037_at	LOC202451	2	-6.533225484
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221693_s_at	MRPS18A	2	-9.85962803
214463_x_at	HIST1H4J	2	-7.79216956
231769_at	FBXO6	2	-5.668376388
210399_x_at	FUT6	2	-4.799996183
219177_at	BXDC2	2	-7.818707947
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228705_at	CAPN12	2	-5.824450995
1557103_a_at	LMTK3	2	-7.317161194
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224783_at	FAM100B	2	-8.774008095
227180_at	ELOVL7	2	-3.887138036
1553219_a_at	AMMECR1	2	-7.096439385
1558045_a_at	LOC441528	2	-6.976939959
235329_at	NOXO1	2	-5.01874039
205102_at	TMPRSS2	2	-8.326862677
225872_at	SLC35F5	2	-6.869459117
213582_at	ATP11A	2	-8.406175157
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204212_at	ACOT8	2	-9.862450342
217140_s_at	LOC100133724 /// VDACC1	2	-8.153255039
233092_s_at	DKFZP434B061	2	-3.828630443
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225126_at	MRRF	2	-8.142550336
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228524_at	ADCK5	2	-8.674729504
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223201_s_at	LOC100130886 /// TMEM164	2	-5.917492181
213822_s_at	UBE3B	2	-8.303213696
218156_s_at	TSR1	2	-8.234912648
230487_at	C6orf99 /// LOC100130967	2	-10.04736974
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229638_at	IRX3	2	-3.837748845
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222140_s_at	GPR89A /// GPR89B /// GPR89C	2	-9.896704598
212048_s_at	YARS	2	-9.935465852
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227021_at	AOF1	2	-7.351852264
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223575_at	KIAA1549	2	-5.823546943
213897_s_at	MRPL23	2	-9.431089902
203176_s_at	TFAM	2	-8.663747234
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218866_s_at	POLR3K	2	-8.318378518
218027_at	MRPL15	2	-8.610619908
224444_s_at	C1orf97	2	-5.843216027
210950_s_at	FDFT1	2	-5.631405084
207549_x_at	CD46	2	-7.297124693
1555501_s_at	RSRC1	2	-8.968566511
204341_at	TRIM16	2	-4.97740315
204305_at	MIPEP	2	-8.137102953
238012_at	DPP7	2	-6.141710763
224437_s_at	VTA1	2	-10.57703264
233492_s_at	LOC728377 /// OR2A4 /// OR2A7	2	-6.683042566
231200_at	LSM14B	2	-9.026018466
213449_at	POP1	2	-8.586363059
223109_at	TRUB2	2	-12.21155218
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224225_s_at	ETV7	2	-6.003955144
227332_at	LOC100129022	2	-8.091568654
200910_at	CCT3	2	-11.17822883
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205531_s_at	GLS2	2	-5.604252947
229616_s_at	GRAMD2	2	-5.499975719
231936_at	HOXC9	2	-5.88640972
230301_at	0	2	-5.547214891
205648_at	WNT2	2	-3.79383059
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229648_at	0	2	-5.836693125
226943_at	C12orf73	2	-7.490904929
229534_at	ACOT4	2	-6.274292915

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231232_at	0	2	-6.79560232
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236760_at	AMMECR1	2	-7.707956371
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214895_s_at	ADAM10	2	-7.52605476
218188_s_at	TIMM13	2	-8.870069597
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209171_at	ITPA	2	-11.11216915
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216969_s_at	KIF22	2	-11.22961591
207181_s_at	CASP7	2	-6.503158959
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208318_s_at	XYLB	2	-10.00493004
205761_s_at	DUS4L	2	-6.758202241
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230954_at	C20orf112	2	-8.599471199
220525_s_at	AUP1	2	-13.5328062
226320_at	THOC4	2	-9.642118843
230782_at	SORD	2	-4.751108252
219270_at	CHAC1	2	-6.707026571
1553991_s_at	FLJ20674	2	-7.345865609
219819_s_at	MRPS28	2	-8.522313421
227429_at	EFCAB4A	2	-6.519892843
226565_at	TMEM99	2	-5.285351277
223120_at	FUCA2	2	-9.907775646
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216032_s_at	LOC727849	2	-10.07480474
227944_at	ERGIC3	2	-8.857064743
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209678_s_at	PRKCI	2	-5.895892358
219217_at	NARS2	2	-9.05168735
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225237_s_at	MSI2	2	-5.662175107
230005_at	SVIP	2	-7.694375638
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221810_at	RAB15	2	-5.38631395
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1554417_s_at	APH1A	2	-8.770819904
229304_s_at	MLF1IP	2	-7.781278118
237030_at	ACPP	2	-5.851663205
57540_at	RBKS	2	-7.166729288
227437_at	0	2	-11.20290885

208901_s_at	TOP1	2	-11.66569722
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204990_s_at	ITGB4	2	-4.654162219
225802_at	TOP1MT	2	-7.140423641
1564706_s_at	GLS2	2	-6.133443561
59697_at	RAB15	2	-5.423229478
206675_s_at	SKIL	2	-6.14337782
239078_at	C1orf58	2	-5.611960558
203342_at	TIMM17B	2	-10.7302099
220174_at	LRRC8E	2	-6.17320278
242218_at	PPARD	2	-10.30769
218096_at	AGPAT5	2	-6.382832439
210816_s_at	CYB561	2	-9.222311601
227920_at	BEND3	2	-10.81159575
223057_s_at	XPO5	2	-8.903632293
1563272_at	TBC1D8B	2	-7.71194021
243582_at	SH3RF2	2	-3.742840033
212541_at	FLAD1	2	-10.30134378
215812_s_at	LOC653562 /// SLC6A10P ///	2	-6.013337746
204858_s_at	TYMP	2	-5.657277139
239595_at	GPX2	2	-6.394794699
225492_at	TMEM33	2	-11.09276554
202874_s_at	ATP6V1C1	2	-8.292725225
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223478_at	TIMM8B	2	-9.695912403
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200641_s_at	YWHAZ	2	-7.917708394
233328_x_at	C20orf59	2	-7.954297836
226915_s_at	ARPC5L	2	-12.08064921
213499_at	CLCN2	2	-10.27153009
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235389_at	PHF20	2	-7.99571944
239647_at	CHST13	2	-4.454663598
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206249_at	MAP3K13	2	-5.959727943
228490_at	ABHD2	2	-4.748440521

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219716_at	APOL6	2	-6.809787798
209992_at	PFKFB2	2	-6.062743445
218070_s_at	GMPPA	2	-10.62741098
239253_at	0	2	-5.752834984
238662_at	ATPBD4	2	-8.742248434
219428_s_at	PXMP4	2	-11.02742717
212680_x_at	PPP1R14B	2	-9.730400614
229715_at	0	2	-4.208549697
219016_at	FASTKD5	2	-10.04425694
203974_at	HDHD1A	2	-6.202794184
228053_s_at	TOMM5	2	-9.992442682
236967_at	LOC645249	2	-7.677747576
201410_at	PLEKHB2	2	-12.53462261
200658_s_at	PHB	2	-10.20331746
239825_at	0	2	-7.921110794
1554036_at	ZBTB24	2	-6.558101035
205477_s_at	AMBP	2	-4.539483136
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1554077_a_at	TMEM53	2	-9.491363154
226431_at	FAM117B	2	-6.665593974
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1552281_at	SLC39A5	2	-5.071974912
225519_at	PPP4R2	2	-10.70357754
202138_x_at	JTV1	2	-10.36586233
201420_s_at	WDR77	2	-9.164775
219491_at	LRFN4	2	-8.036245006
218239_s_at	GTPBP4	2	-8.773644756
213324_at	SRC	2	-9.169597393
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238821_at	CSTF2	2	-8.091494461
1564220_a_at	0	2	-3.613901833
212330_at	TFDP1	2	-10.07918222
243840_at	0	2	-11.86864604
203564_at	FANCG	2	-8.768966017
233588_x_at	PFDN6	2	-10.30369524
218725_at	SLC25A22	2	-13.28891985
214581_x_at	TNFRSF21	2	-5.520668521
216483_s_at	C19orf10	2	-9.017920353
218967_s_at	PTER	2	-6.007037995
201943_s_at	CPD	2	-6.461377191
204420_at	FOSL1	2	-4.109336285
207747_s_at	DOK4	2	-8.182700727
1559591_s_at	CHDH	2	-8.088188748
243507_s_at	C20orf196	2	-8.268872341
210243_s_at	B4GALT3	2	-11.05535326
204108_at	NFYA	2	-9.308599472
218326_s_at	LGR4	2	-4.727935808
238673_at	SAMD12	2	-4.377235443
211002_s_at	TRIM29	2	-4.497161814

232654_s_at	UGT1A6	2	-4.349206345
220386_s_at	EML4	2	-7.632691315
201691_s_at	TPD52	2	-4.550014091
226609_at	DCBLD1	2	-7.174043722
52285_f_at	CEP76	2	-6.770575253
206218_at	MAGEB2	2	-3.57982223
208680_at	PRDX1	2	-11.92610831
236616_at	0	2	-6.771135237
210854_x_at	SLC6A8	2	-4.868478442
213726_x_at	TUBB2C	2	-10.06047791
221291_at	ULBP2	2	-6.294444342
204775_at	CHAF1B	2	-11.57075903
218557_at	NIT2	2	-9.334646291
1559382_at	C19orf42	2	-10.61006545
231018_at	PALM3	2	-6.325196146
231994_at	CHDH	2	-9.249157691
1552641_s_at	ATAD3A /// ATAD3B /// ATAD3C /// LOC732419	2	-11.08814753
208580_x_at	HIST1H4C /// HIST1H4D /// HIST1H4E /// HIST1H4F /// HIST1H4H /// HIST1H4I /// HIST1H4J /// HIST1H4K /// HIST1H4L /// HIST2H4A /// HIST2H4B /// HIST4H4	2	-9.017976257
202296_s_at	RER1	2	-10.22835386
222029_x_at	PFDN6	2	-10.35719178
215923_s_at	PSD4	2	-8.047780268
201271_s_at	RALY	2	-12.60076406
217167_x_at	GK	2	-7.065240665
208910_s_at	C1QBP	2	-8.879105601
200868_s_at	RNF114	2	-8.302055846
218273_s_at	PPM2C	2	-6.670362893
1568598_at	KAZALD1	2	-7.816735241
216251_s_at	TTLL12	2	-8.678982315
223681_s_at	INADL	2	-6.41080709
208600_s_at	GPR39	2	-7.552951187
223632_s_at	BCAN	2	-7.110211049
235089_at	FBXL20	2	-5.51991151
219545_at	KCTD14	2	-4.955683077
223239_at	C14orf129	2	-6.439845756
1553186_x_at	RASEF	2	-4.737353965
208968_s_at	CIAPIN1	2	-11.81124865
235965_at	0	2	-5.122759805
223158_s_at	NEK6	2	-7.420562131
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208107_s_at	LOC81691	2	-9.354265694
218756_s_at	DHRS11	2	-3.722389718
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222147_s_at	ACTR5	2	-9.531988993
223069_s_at	EML4	2	-9.138886392

205180_s_at	ADAM8	2	-6.454151263
209998_at	PIGO	2	-9.945179998
215728_s_at	ACOT7	2	-8.113041634
208675_s_at	DDOST	2	-11.24582908
229835_s_at	0	2	-6.808842375
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206536_s_at	XIAP	2	-8.535910185
209545_s_at	RIPK2	2	-7.518597242
223078_s_at	TMOD3	2	-7.863422337
209971_x_at	JTV1	2	-10.53643496
212339_at	EPB41L1	2	-5.505166493
203779_s_at	MPZL2	2	-5.811980608
200656_s_at	P4HB	2	-9.295397339
214431_at	GMPS	2	-11.19849802
1554679_a_at	LAPTM4B	2	-4.760078905
223202_s_at	LOC100130886 /// TMEM164	2	-7.678731923
207264_at	KDELR3	2	-6.42911749
205449_at	SAC3D1	2	-7.726720706
202706_s_at	UMPS	2	-10.99685721
209294_x_at	TNFRSF10B	2	-7.306360607
213571_s_at	EIF4E2	2	-12.0284014
203015_s_at	SSX2IP	2	-6.991219516
215150_at	YOD1	2	-7.297873183
215223_s_at	SOD2	2	-4.441152944
237810_at	CLDN6	2	-4.506797253
228302_x_at	CAMK2N1	2	-4.171733422
232893_at	LMBRD2	2	-8.045216627
1554628_at	ZNF57	2	-6.429731249
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237324_s_at	HKDC1	2	-7.692026059
221811_at	PERLD1	2	-5.042916924
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214073_at	CTTN	2	-6.043310652
224454_at	ETNK1	2	-6.851945593
229400_at	HOXD10	2	-4.192259006
202486_at	AFG3L2	2	-9.578156575
231148_at	IGFL2	2	-5.453934051
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225849_s_at	SFT2D1	2	-9.43659836
205248_at	DOPEY2	2	-6.933838735
204109_s_at	NFYA	2	-8.173130738
205483_s_at	ISG15	2	-5.022944567
221732_at	CANT1	2	-7.183912923
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218317_x_at	GIYD1 /// GIYD2	2	-8.414671361
242996_at	MTRF1	2	-7.039227136
223628_at	TMEM191A	2	-8.114318372
219311_at	CEP76	2	-8.042314264
220087_at	BCMO1	2	-5.305266533
204147_s_at	TFDP1	2	-9.789860526
227349_at	HELLS	2	-7.468785787
218702_at	SARS2	2	-9.107292101
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219462_at	TMEM53	2	-10.53225553
237323_at	HKDC1	2	-8.266081146
238598_s_at	0	2	-7.666679026
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236937_at	VPS8	2	-7.270785394
230556_at	IMMP1L	2	-7.303277371
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223545_at	FANCD2	2	-10.51430205
230792_at	FAAH2	2	-6.607834827
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238578_at	TMEM182	2	-9.010590896
210112_at	HPS1	2	-9.457951165
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242224_at	GPATCH2	2	-7.684754898
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221987_s_at	TSR1	2	-8.949583489
202415_s_at	HSPBP1	2	-11.62926399
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205770_at	GSR	2	-6.478072394
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231880_at	FAM40B	2	-6.233006119
236028_at	IBSP	2	-5.665283621
204712_at	WIF1	2	-3.780578612
227477_at	ZMYND19	2	-9.539129941
231775_at	TNFRSF10A	2	-5.467236283
33307_at	RRP7A	2	-9.722343536
1553185_at	RASEF	2	-4.796016255
227829_at	GYLTL1B	2	-7.13888548
236491_at	BCL2L10	2	-5.697671065
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239697_x_at	C3orf67	2	-4.875309065
204561_x_at	APOC2 /// APOC4	2	-5.413358254
227008_at	HDDC3	2	-9.895368552
240069_at	0	2	-6.995093701
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210386_s_at	MTX1	2	-12.64381171

235245_at	TMEM92	2	-6.860210071
202314_at	CYP51A1	2	-5.907500239
217942_at	MRPS35	2	-8.547661989
227015_at	ASPHD2	2	-5.79975768
217749_at	COPG	2	-8.776275062
1559590_at	CHDH	2	-6.69203079
227828_s_at	FAM176A	2	-4.864681967
210413_x_at	SERPINB3 /// SERPINB4	2	-3.945674196
206259_at	PROC	2	-6.001712072
205129_at	NPM3	2	-7.521472396
201930_at	MCM6	2	-10.25636548
228607_at	OAS2	2	-5.216553673
223549_s_at	ESPN	2	-8.169128569
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212218_s_at	FASN	2	-7.886196552
219161_s_at	CKLF	2	-8.021796564
235026_at	C12orf66	2	-7.619267378
223296_at	SLC25A33	2	-7.179909868
209482_at	POP7	2	-10.62462059
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231399_at	RAB3IP	2	-5.634944344
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202647_s_at	NRAS	2	-7.428633736
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209190_s_at	DIAPH1	2	-9.038028643
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209509_s_at	DPAGT1	2	-10.56641556
218385_at	MRPS18A	2	-9.883473619
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225766_s_at	TNPO1	2	-10.75586941
226242_at	C1orf131	2	-9.567855046
218622_at	NUP37	2	-10.1844456
213043_s_at	MED24	2	-6.083989782
210627_s_at	GCS1	2	-11.21021358
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1554885_a_at	PRIM2	2	-7.880465629
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218689_at	FANCF	2	-8.297981558
204398_s_at	EML2	2	-10.3350494
223458_at	LOC652900 /// SEZ6L2	2	-7.613131826
217834_s_at	SYNCRIP	2	-9.87359141
242799_at	0	2	-4.973431544

1554594_at	ARHGAP27 /// LOC201175	2	-7.632607664
217984_at	RNASET2	2	-7.100300847
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228550_at	RTN4R	2	-10.01231497
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219118_at	FKBP11	2	-4.905833942
210663_s_at	KYNU	2	-4.17149893
225947_at	MYO19	2	-9.343902243
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242998_at	RDH12	2	-5.00361408
227921_at	0	2	-5.602631968
229440_at	RBM47	2	-8.586770828
205466_s_at	HS3ST1	2	-3.741844114
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217185_s_at	LOC442240 /// ZNF259	2	-9.641735661
212475_at	AVL9	2	-11.37508811
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231871_at	GPR180	2	-8.407784159
238518_x_at	GLYCTK	2	-8.772667542
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1554533_at	C2	2	-5.888413717
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207456_at	HNF4G	2	-5.108340816
218817_at	SPCS3	2	-7.926550873
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216484_x_at	0	2	-12.34887904
201853_s_at	CDC25B	2	-6.865829154
205627_at	CDA	2	-3.972443228
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204441_s_at	POLA2	2	-9.056718411
208639_x_at	PDIA6	2	-11.59430439
230096_at	0	2	-7.871831392
231104_at	TDRD5	2	-6.439020575
230398_at	TNS4	2	-4.462169799
212009_s_at	STIP1	2	-8.605600209
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231953_at	BPTF	2	-9.434398744
223249_at	CLDN12	2	-6.512390449
208436_s_at	IRF7	2	-6.107441601
222250_s_at	INTS7	2	-10.87336616
204401_at	KCNN4	2	-3.693543088
201252_at	PSMC4	2	-10.06971193
204330_s_at	MRPS12	2	-8.987268615
218849_s_at	PPP1R13L	2	-7.256155823
226483_at	TMEM68	2	-9.240572253
209387_s_at	TM4SF1	2	-4.18128174
229983_at	TIGD2	2	-10.17846588
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226264_at	SUSD1	2	-8.560504991
205290_s_at	BMP2	2	-3.666151499
213198_at	ACVR1B	2	-7.930917799
215033_at	TM4SF1	2	-5.72048111
223491_at	COMMD2	2	-10.59068141
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219649_at	ALG6	2	-10.56549032
1554110_at	CDCP1	2	-8.589772096
204133_at	RRP9	2	-11.02392745
238164_at	USP6NL	2	-8.111053424
222583_s_at	NUP50	2	-8.46000707
203422_at	POLD1	2	-13.12557228
210791_s_at	RICS	2	-6.685509196
202904_s_at	LSM5	2	-9.438754166
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226550_at	0	2	-5.226572761
216627_s_at	B4GALT1	2	-6.234722019
219559_at	C20orf59	2	-6.794987689
204385_at	KYNU	2	-5.234319646
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235738_at	0	2	-8.0165745
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224608_s_at	VPS25	2	-12.87767698
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1553715_s_at	C16orf14	2	-7.423207024
212125_at	RANGAP1	2	-11.32543032
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229290_at	DAPL1	2	-3.876347453
238853_at	RAB3IP	2	-5.961211534
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209108_at	TSPAN6	2	-5.200940349
225548_at	SHROOM3	2	-4.839870647
238699_s_at	CASK	2	-6.576247102
218647_s_at	YRDC	2	-9.99073366
239087_at	ANKS4B	2	-7.539782566
203816_at	DGUOK	2	-11.07217718
205296_at	RBL1	2	-10.07061093
226686_at	CISD2	2	-10.34433319
208932_at	PPP4C	2	-13.55967603
232594_at	LOC440498	2	-8.242883962

211070_x_at	DBI	2	-11.82290362
208429_x_at	HNFA4	2	-10.39446027
218069_at	DCTPP1	2	-9.384161643
219026_s_at	RASAL2	2	-8.149591934
221620_s_at	APOO	2	-9.239699855
239853_at	KLC3	2	-7.294211909
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222645_s_at	KCTD5	2	-9.46109883
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219447_s_at	SLC35C2	2	-12.57395601
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225578_at	C13orf37	2	-8.634586771
226882_x_at	WDR4	2	-8.463842934
1555751_a_at	GEMIN7	2	-10.89136923
214614_at	MNX1	2	-11.90126344
229886_at	C5orf34	2	-7.017742541
1555908_at	FAM120A	2	-9.149516623
220009_at	LONRF3	2	-6.779089693
229099_at	C11orf83	2	-10.28789535
203927_at	NFKBIE	2	-7.656896037
209800_at	KRT16	2	-4.539234255
1555829_at	FAM62B	2	-7.132402725
225316_at	MFSD2	2	-6.29617643
211668_s_at	PLAU	2	-4.744844503
205517_at	GATA4	2	-3.7320732
217752_s_at	CNDP2	2	-8.724891432
203431_s_at	RICS	2	-5.82837479
219301_s_at	CNTNAP2	2	-5.273608774
201003_x_at	RNPEP /// TMEM189 /// TMEM189-UBE2V1 /// UBE2V1 ///	2	-9.275070504
225638_at	C1orf31	2	-11.6514211
208270_s_at	RNPEP	2	-9.287386554
224392_s_at	OPN3	2	-5.851199289
214681_at	GK	2	-6.654983832
215947_s_at	FAM136A	2	-12.90995528
223361_at	C6orf115	2	-6.571817459
213237_at	C16orf88	2	-8.384901831
214898_x_at	MUC3B	2	-4.594278949
207517_at	LAMC2	2	-5.310376775
212378_at	GART	2	-10.39092477
211599_x_at	MET	2	-6.266849272
219320_at	MYO19	2	-11.44779906
218448_at	C20orf11	2	-10.45438713
230532_at	CXorf38	2	-8.880937535
227996_at	FARP1	2	-6.47707775
225375_at	TMEM199	2	-12.06845329
223984_s_at	NUPL1	2	-8.108667549
1563900_at	FAM83B	2	-6.587267139

210405_x_at	TNFRSF10B	2	-7.475029081
206976_s_at	HSPH1	2	-8.97642708
216488_s_at	ATP11A	2	-10.59041995
213370_s_at	SFMBT1	2	-10.24058573
224785_at	FAM100B	2	-9.885850101
202655_at	ARMET	2	-11.11848004
227224_at	RALGPS2	2	-6.893081634
229555_at	GALNT5	2	-5.848292049
222768_s_at	TRMT6	2	-9.529422939
228543_at	CSRP2BP	2	-8.245657599
218619_s_at	SUV39H1	2	-12.60482997
58696_at	EXOSC4	2	-10.41537266
212902_at	SEC24A	2	-7.146467638
226375_at	0	2	-8.010283417
235113_at	PPIL5	2	-9.915239481
229289_at	FAM71E1	2	-6.169542044
1554575_a_at	BPNT1	2	-10.19070507
1559132_at	TMEM80	2	-8.422836835
218966_at	MYO5C	2	-5.919468679
234973_at	SLC38A5	2	-3.958244107
235546_at	SPINT1	2	-9.198740986
234983_at	0	2	-8.06951072
203201_at	PMM2	2	-8.266001049
202872_at	ATP6V1C1	2	-9.129465331
236225_at	GGT6	2	-3.948743956
202868_s_at	POP4	2	-6.803671576
224483_s_at	MFSD9	2	-9.831150051
214583_at	RSC1A1	2	-9.825516637
225861_at	C16orf14	2	-7.889980794
209421_at	MSH2	2	-7.53265433
222206_s_at	NCLN	2	-7.438041338
235363_at	0	2	-5.846296162
217289_s_at	SLC37A4	2	-8.644334816
215672_s_at	AHCYL2	2	-5.336037492
201231_s_at	ENO1	2	-11.69776298
1555895_at	DNM2	2	-8.756490976
200831_s_at	SCD	2	-6.130276199
209040_s_at	PSMB8	2	-7.389504253
225142_at	JHDM1D	2	-7.709856652
229812_at	USP48	2	-7.772641831
217772_s_at	MTCH2	2	-10.81832379
204224_s_at	GCH1	2	-6.215187425
203177_x_at	TFAM	2	-7.747318075
208744_x_at	HSPH1	2	-8.51718243
243754_at	0	2	-7.285455053
238498_at	0	2	-7.16206928
222812_s_at	RHOF	2	-6.529834912
1556009_at	PEX13	2	-9.315509017
208540_x_at	S100A11 /// S100A11P	2	-9.608683884
226473_at	CBX2	2	-5.218642893

236113_at	0	2	-7.929255608
218257_s_at	UGCGL1	2	-13.29276323
211630_s_at	GSS	2	-11.58098327
211208_s_at	CASK	2	-8.34979686
201708_s_at	NIPSNAP1	2	-9.335247024
244561_at	0	2	-7.533713851
213083_at	SLC35D2	2	-9.909705846
243579_at	MSI2	2	-9.21023062
215380_s_at	GGCT	2	-10.86240811
210978_s_at	TAGLN2	2	-9.462222952
223403_s_at	POLR1B	2	-9.860138259
202483_s_at	RANBP1	2	-11.66784597
222821_s_at	GEMIN7	2	-11.55125821
230448_at	SLC38A10	2	-8.729971246
203828_s_at	IL32	2	-4.983024731
1552257_a_at	TTL12	2	-8.773339786
207717_s_at	PKP2	2	-4.426577778
219071_x_at	C8orf30A	2	-12.17564943
206604_at	OVOL1	2	-12.81148678
236055_at	DQX1	2	-6.228540469
1553423_a_at	SLFN13	2	-5.023459238
240382_at	LOC100131914	2	-6.866520297
207265_s_at	KDEL3	2	-5.277886178
222752_s_at	TMEM206	2	-9.073056248
203347_s_at	MTF2	2	-9.676163847
228230_at	PRIC285	2	-9.211755894
221081_s_at	DENND2D	2	-6.889648388
235013_at	SLC31A1	2	-10.43746641
221666_s_at	PYCARD	2	-5.962907906
219750_at	TMEM144	2	-5.525427669
227706_at	SPIRE2	2	-9.067590222
45633_at	GINS3	2	-8.73080263
208967_s_at	AK2	2	-12.2037822
236430_at	TMED6	2	-4.226998018
1553535_a_at	RANGAP1	2	-11.45567705
208864_s_at	TXN	2	-8.892370127
244385_at	JMJD2C	2	-7.214334136
222631_at	PI4K2B	2	-10.1094023
205078_at	PIGF	2	-7.275085343
203127_s_at	SPTLC2	2	-10.7277145
209720_s_at	SERPINB3	2	-3.605927136
58916_at	KCTD14	2	-4.649709789
201242_s_at	ATP1B1	2	-6.214799998
209367_at	STXBP2	2	-10.41474917
231882_at	FLJ39632 /// LOC100131139	2	-4.518303683
218543_s_at	PARP12	2	-7.951592126
1558292_s_at	PIGW	2	-8.817642918
214481_at	HIST1H2AM	2	-8.224692654
223246_s_at	STRBP	2	-10.16390694
200896_x_at	HDGF	2	-12.18718689

218911_at	YEATS4	2	-7.530256636
216212_s_at	DKC1	2	-11.10223529
206884_s_at	SCEL	2	-3.769386743
202883_s_at	PPP2R1B	2	-8.981782698
218474_s_at	KCTD5	2	-9.684361141
224613_s_at	DNAJC5	2	-11.37625779
201281_at	ADRM1	2	-11.60377008
232609_at	CRB3	2	-10.90348601
220948_s_at	ATP1A1	2	-8.958901562
224523_s_at	C3orf26	2	-9.400142766
205623_at	ALDH3A1	2	-3.593264082
204117_at	PREP	2	-8.651988993
202667_s_at	SLC39A7	2	-9.84254029
213572_s_at	SERPINB1	2	-5.952867128
244545_at	0	2	-7.110333271
207528_s_at	SLC7A11	2	-6.759694578
219735_s_at	TFCP2L1	2	-5.441793627
218984_at	PUS7	2	-7.962379394
214440_at	NAT1	2	-5.298996668
217736_s_at	EIF2AK1	2	-12.04909734
225841_at	C1orf59	2	-5.912749964
209668_x_at	CES2	2	-3.870255474
209615_s_at	PAK1	2	-8.51287952
201762_s_at	PSME2	2	-9.398271917
206173_x_at	GABPB1	2	-10.64278644
55616_at	PERLD1	2	-5.311880165
204415_at	IFI6	2	-5.072295018
203458_at	SPR	2	-10.44176358
216471_x_at	LOC100130648 /// SSX2 /// SSX2B	2	-5.26644809
206533_at	CHRNA5	2	-6.672444504
243594_x_at	SPIRE2	2	-8.380904217
228773_at	0	2	-9.431049549
212171_x_at	VEGFA	2	-7.410594923
228205_at	TKT	2	-9.518904896
209690_s_at	DOK4	2	-9.830292385
201755_at	MCM5	2	-10.00504058
214745_at	PLCH1	2	-7.230694308
208051_s_at	PAIP1	2	-7.261892272
205776_at	FMO5	2	-3.616868571
209665_at	CYB561D2	2	-9.108335504
46323_at	CANT1	2	-7.044298652
243529_at	MARS2	2	-9.952445823
226319_s_at	THOC4	2	-9.457801846
221194_s_at	RNFT1	2	-7.908035332
227143_s_at	BID	2	-10.41580366
205827_at	CCK	2	-4.403804433
211298_s_at	ALB	2	-3.707376705
203702_s_at	TTLL4	2	-9.047597016
213172_at	TTC9	2	-6.804567422
1556429_a_at	WDR67	2	-7.926011065

214763_at	ACOT11	2	-9.185159893
203252_at	CDK2AP2	2	-8.773465912
221845_s_at	CLPB	2	-12.27973789
203716_s_at	DPP4	2	-3.847698562
208712_at	CCND1	2	-5.443305313
213857_s_at	CD47	2	-8.394566747
214006_s_at	GGCX	2	-10.72925666
228560_at	0	2	-7.570935346
209391_at	DPM2	2	-12.06692591
1559052_s_at	PAK2	2	-10.5418978
212729_at	DLG3	2	-8.650952232
224695_at	C2orf29	2	-14.50649042
225320_at	CCDC109A	2	-6.426825625
214095_at	SHMT2	2	-8.604890782
240770_at	TMEM171	2	-6.048432286
217919_s_at	MRPL42	2	-10.21518539
203721_s_at	UTP18	2	-11.66045688
203219_s_at	APRT	2	-10.96600795
234488_s_at	GMCL1 /// GMCL1L	2	-8.350325563
208659_at	CLIC1	2	-12.17165569
226733_at	PFKFB2	2	-4.709591784
205848_at	GAS2	2	-4.004574279
203612_at	BYSL	2	-9.907784592
201953_at	CIB1	2	-8.40813437
225402_at	TP53RK	2	-9.794836588
213624_at	SMPDL3A	2	-5.887954662
219253_at	TMEM185B	2	-9.215317491
203696_s_at	RFC2	2	-11.03115281
201201_at	CSTB	2	-8.937163633
202961_s_at	ATP5J2	2	-11.95858148
220987_s_at	C11orf17 /// NUA2	2	-5.376338798
215044_s_at	STAM2	2	-11.28125219
202183_s_at	KIF22	2	-11.19745959
231779_at	IRAK2	2	-5.220355231
213399_x_at	RPN2	2	-14.00443769
229453_at	PDIA3	2	-8.466865633
230271_at	ONECUT2	2	-4.674266787
203626_s_at	SKP2	2	-8.288113771
238681_at	GDPD1	2	-5.307777876
204391_x_at	TRIM24	2	-7.423236403
203856_at	VRK1	2	-10.29206986
221637_s_at	C11orf48	2	-12.97310118
215017_s_at	FBNP1L	2	-8.288558381
208002_s_at	ACOT7	2	-8.413720601
219916_s_at	RNF39	2	-6.714884887
223397_s_at	NIP7	2	-10.69883983
201209_at	HDAC1	2	-10.7947119
218458_at	GMCL1	2	-9.427547157
235542_at	TET3	2	-8.76545262
222748_s_at	TXNL4B	2	-9.649825539

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212659_s_at	IL1RN	2	-7.443960391
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230710_at	0	2	-7.536401237
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211882_x_at	FUT6	2	-4.800156193
223308_s_at	WDR5	2	-10.60384374
210547_x_at	ICA1	2	-7.069604313
38340_at	HIP1R	2	-8.830058843
202200_s_at	SRPK1	2	-10.64790449
1553611_s_at	KLHL35	2	-6.495809326
243000_at	CDK6	2	-5.276524905
205185_at	SPINK5	2	-3.608251785
203040_s_at	HMBS	2	-11.1849282
1053_at	RFC2	2	-10.50335115
222939_s_at	SLC16A10	2	-4.430558801
227972_at	TOR2A	2	-10.85362551
206669_at	GAD1	2	-5.992932744
208928_at	POR	2	-9.64419382
218238_at	GTPBP4	2	-9.853913515
227916_x_at	EXOSC3	2	-11.47954717
205595_at	DSG3	2	-3.652398691
204853_at	ORC2L	2	-11.98789897
214355_x_at	CTAGE4 /// LOC100142659 /// LOC441294	2	-10.3369141
239202_at	0	2	-6.143130113
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227764_at	LYPD6	2	-5.380731663
222736_s_at	TMEM38B	2	-8.94735792
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213491_x_at	RPN2	2	-13.78274588
241950_at	0	2	-6.358082886
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217968_at	TSSC1	2	-12.49585575
218295_s_at	NUP50	2	-8.80918443

208009_s_at	ARHGEF16	2	-10.86718415
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201614_s_at	RUVBL1	2	-10.90078287
214347_s_at	DDC	2	-4.391984562
223055_s_at	XPO5	2	-10.13425762
232437_at	CPSF3L	2	-11.19076399
91684_g_at	EXOSC4	2	-10.54924932
229271_x_at	COL11A1	2	-4.222122852
204433_s_at	SPATA2	2	-9.882293302
227134_at	SYTL1	2	-4.603549725
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1558507_at	C1orf53	2	-11.12743505
210513_s_at	VEGFA	2	-7.843698867
213253_at	SMC2	2	-9.061124767
223298_s_at	NT5C3	2	-8.833413438
214698_at	ROD1	2	-11.08872869
1552648_a_at	TNFRSF10A	2	-7.174950266
1565358_at	RARA	2	-4.572763926
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212312_at	BCL2L1	2	-10.29338731
212474_at	AVL9	2	-10.54322659
221597_s_at	TMEM208	2	-12.96213242
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222989_s_at	UBQLN1	2	-11.90153567
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209094_at	DDAH1	2	-8.03299394
211416_x_at	GGTLC1	2	-7.237565584
207813_s_at	FDXR	2	-7.098735509
230467_at	TMEM52	2	-7.167707992
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222546_s_at	EPS8L2	2	-9.108802959
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227556_at	NME7	2	-4.750771653
205505_at	GCNT1	2	-4.468769516
210264_at	GPR35	2	-8.117580211
222569_at	UGCGL1	2	-13.58460622
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225201_s_at	MRPL14	2	-11.16773949

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36830_at	MIPEP	2	-8.357613777
236026_at	GPATCH2	2	-8.283875788
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223611_s_at	LNK1	2	-4.888487783
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203672_x_at	TPMT	2	-9.735616061
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227474_at	LOC654433	2	-4.173248816
205093_at	PLEKHA6	2	-9.486729502
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1555679_a_at	RTN4IP1	2	-8.345508021
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226060_at	RFT1	2	-12.76202273
230204_at	HAPLN1	2	-6.06218064
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220603_s_at	MCTP2	2	-7.403327573
1558217_at	SLFN13	2	-5.079578353
207628_s_at	WBSCR22	2	-11.63187806
203208_s_at	MTFR1	2	-10.54135903
230259_at	C10orf125	2	-7.888050549
229061_s_at	SLC25A13	2	-7.602060994
213789_at	0	2	-9.190727377
209052_s_at	WHSC1	2	-10.52159313
214522_x_at	HIST1H2AD /// HIST1H3D	2	-10.11450878
209317_at	POLR1C	2	-9.816962308
215747_s_at	RCC1 /// SNHG3-RCC1	2	-13.28912509
229566_at	LOC645638	2	-6.649333702
215227_x_at	ACP1	2	-11.30858914
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233589_x_at	C9orf167	2	-6.797792565
212115_at	HN1L	2	-10.14037494
227818_at	CCDC21	2	-11.89354565
212314_at	KIAA0746 /// SERINC2	2	-6.362985658

204989_s_at	ITGB4	2	-5.715114173
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210239_at	IRX5	2	-6.573234786
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228124_at	ABHD12	2	-7.717847846
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227212_s_at	PHF19	2	-9.073329533
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209208_at	MPDU1	2	-11.79371287
223723_at	MFI2	2	-5.900642286
1557128_at	FAM111B	2	-10.3680025
209691_s_at	DOK4	2	-7.987364004
218399_s_at	CDCA4	2	-11.42215813
201243_s_at	ATP1B1	2	-6.605063949
1555826_at	EPR1	2	-11.55977997
211833_s_at	BAX	2	-9.809970611
232195_at	GPR158	2	-4.876909343
206082_at	HCP5	2	-6.24578838
213143_at	C2orf72	2	-6.246940467
212479_s_at	RMND5A	2	-10.95724742
208837_at	TMED3	2	-9.745242931
223541_at	HAS3	2	-4.504923267
223530_at	TDRKH	2	-6.731071316

229671_s_at	C21orf45	2	-9.412639592
205891_at	ADORA2B	2	-5.236703866
218512_at	WDR12	2	-11.64584628
229845_at	MAPKAP1	2	-10.7335836
230641_at	0	2	-7.328550507
204934_s_at	HPN	2	-6.986608083
226150_at	PPAPDC1B	2	-7.990509327
201695_s_at	NP	2	-9.060132591
215977_x_at	GK	2	-8.322174073
218556_at	ORMDL2	2	-11.11081129
223100_s_at	NUDT5	2	-11.02188242
210885_s_at	TRIM15	2	-9.850648442
202830_s_at	SLC37A4	2	-9.746280494
203434_s_at	MME	2	-3.706593087
239433_at	LRRC8E	2	-7.783022207
204459_at	CSTF2	2	-12.69681302
200806_s_at	HSPD1	2	-10.82267259
224447_s_at	C17orf37	2	-6.406013371
227320_at	FAM101A	2	-4.649598008
217777_s_at	PTPLAD1	2	-9.969233554
209629_s_at	NXT2	2	-9.549417691
223490_s_at	EXOSC3	2	-10.77031292
209424_s_at	AMACR	2	-5.029952613
211162_x_at	SCD	2	-5.96060132
225612_s_at	B3GNT5	2	-7.136216095
236496_at	DEGS2	2	-5.918644339
220607_x_at	TH1L	2	-11.53849876
202071_at	SDC4	2	-7.255427175
210056_at	RND1	2	-7.256380411
232065_x_at	CENPL	2	-10.28495749
219934_s_at	SULT1E1	2	-3.577583701
213667_at	SRCAP	2	-8.41608536
219742_at	PRR7	2	-11.07806888
223241_at	SNX8	2	-10.08427408
214061_at	WDR67	2	-9.726288928
217809_at	BZW2	2	-11.29282074
220789_s_at	TBRG4	2	-13.83884026
212662_at	PVR	2	-9.008373466
220688_s_at	MRTO4	2	-11.85714463
200636_s_at	PTPRF	2	-9.639608408
1557448_a_at	0	2	-7.868497107
206994_at	CST4	2	-5.797465141
209507_at	RPA3	2	-11.46717874
209608_s_at	ACAT2	2	-10.81400918
200783_s_at	STMN1	2	-9.331542773
209186_at	ATP2A2	2	-11.35615628
210253_at	HTATIP2	2	-7.204542354
201489_at	PPIF	2	-10.61945862
201111_at	CSE1L	2	-9.346531915
242546_at	FLJ39632	2	-5.09741329

212322_at	SGPL1	2	-11.28273067
201478_s_at	DKC1	2	-11.93773777
214651_s_at	HOXA9	2	-3.634899886
206043_s_at	ATP2C2	2	-4.855581564
226907_at	PPP1R14C	2	-4.455009991
208527_x_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	2	-7.899416913
244261_at	IL28RA	2	-6.35637992
219211_at	USP18	2	-6.789530649
204649_at	TROAP	2	-12.71099177
226520_at	0	2	-9.419260533
201926_s_at	CD55	2	-4.64785121
204976_s_at	AMMECR1	2	-8.272508425
206055_s_at	SNRPA1	2	-13.98842178
1569582_at	LOC201651	2	-3.718522865
202726_at	LIG1	2	-12.9399475
214769_at	CLCN4	2	-5.602497344
209369_at	ANXA3	2	-4.480609144
202924_s_at	PLAGL2	2	-10.10387159
216202_s_at	SPTLC2	2	-9.955183861
201415_at	GSS	2	-12.78716129
209719_x_at	SERPINB3	2	-3.933236179
202581_at	HSPA1A /// HSPA1B	2	-6.527118276
219796_s_at	MUPCDH	2	-5.640210882
218867_s_at	C12orf49	2	-12.79134309
205778_at	KLK7	2	-4.010795138
207239_s_at	PCTK1	2	-11.80436671
220318_at	EPN3	2	-7.99095657
1552390_a_at	C8orf47	2	-3.934137996
207259_at	C17orf73	2	-3.663470358
222767_s_at	C12orf49	2	-13.30157958
203936_s_at	MMP9	2	-3.990626381
205302_at	IGFBP1	2	-3.673010924
204827_s_at	CCNF	2	-11.74789282
1554101_a_at	TMTC4	2	-7.832311542
219531_at	CEP72	2	-8.369056139
1555962_at	B3GNT7	2	-4.617825828
209426_s_at	AMACR	2	-5.224739186
218888_s_at	NETO2	2	-4.99924635
202533_s_at	DHFR	2	-8.697357507
209904_at	TNNC1	2	-4.665760916
218776_s_at	TMEM62	2	-10.99646323
222713_s_at	FANCF	2	-10.65261544
228923_at	S100A6	2	-6.213438122
210766_s_at	CSE1L	2	-11.66697844
227759_at	PCSK9	2	-6.377521447
209591_s_at	BMP7	2	-4.831785177
208824_x_at	PCTK1	2	-12.503758
234863_x_at	FBXO5	2	-10.3599724

1559827_at	LOC401074	2	-4.779894595
1552470_a_at	ABHD11	2	-7.804338021
227068_at	PGK1	2	-11.40608346
213518_at	PRKCI	2	-7.659012537
204130_at	HSD11B2	2	-6.093824396
206295_at	IL18	2	-4.907230787
205523_at	HAPLN1	2	-5.612231381
201195_s_at	SLC7A5	2	-6.156595143
219347_at	NUDT15	2	-10.9580611
230166_at	KIAA1958	2	-10.27271741
201188_s_at	ITPR3	2	-8.62032492
213088_s_at	DNAJC9	2	-11.52120572
209434_s_at	PPAT	2	-11.79906856
208613_s_at	FLNB	2	-8.572647816
212563_at	BOP1	2	-9.283660938
214465_at	ORM1 /// ORM2	2	-4.162256049
214096_s_at	SHMT2	2	-11.1389565
202307_s_at	TAP1	2	-8.332789406
1558549_s_at	VNN1	2	-4.04662438
205670_at	GAL3ST1	2	-9.76476157
218282_at	EDEM2	2	-12.37731209
225750_at	0	2	-9.186164393
201797_s_at	VAR5	2	-11.80262828
226013_at	TRAK1	2	-6.287612124
230318_at	SERPINA1	2	-5.117633758
1553810_a_at	KIAA1524	2	-9.742481974
201422_at	IFI30	2	-6.694535244
203961_at	NEBL	2	-3.576878019
206276_at	LY6D	2	-4.462418773
225829_at	PDZD8	2	-7.473002187
1552306_at	ALG10	2	-9.316318891
228708_at	RAB27B	2	-4.005086045
204836_at	GLDC	2	-6.117645433
204826_at	CCNF	2	-12.92439654
224204_x_at	ARNTL2	2	-8.575389386
211713_x_at	KIAA0101	2	-10.82162518
235937_at	0	2	-8.026721255
243292_at	FAM132A	2	-5.889615876
229927_at	LEMD1	2	-4.775108564
212175_s_at	AK2	2	-11.51154041
209754_s_at	TMPO	2	-8.569314907
211977_at	GPR107	2	-11.48160632
1555906_s_at	C3orf23	2	-10.05220872
225676_s_at	WDSOF1	2	-11.23344057
218928_s_at	SLC37A1	2	-8.327584668
217771_at	GOLM1	2	-4.882634689
209919_x_at	GGT1	2	-6.905429743
216010_x_at	FUT3	2	-4.847768337
228624_at	TMEM144	2	-6.867537883
204256_at	ELOVL6	2	-6.081273953

202674_s_at	LMO7	2	-7.125055462
201490_s_at	PPIF	2	-10.11567632
210732_s_at	LGALS8	2	-6.487359016
238742_x_at	0	2	-11.79046394
224468_s_at	C19orf48	2	-10.53001244
202540_s_at	HMGCR	2	-9.866753447
226121_at	DHRS13	2	-11.28623614
224467_s_at	PDCD2L	2	-9.557285234
210678_s_at	AGPAT2	2	-9.190185943
226446_at	HES6	2	-4.934846627
220812_s_at	HHLA2	2	-5.723146976
225991_at	TMEM41A	2	-11.82640542
201689_s_at	TPD52	2	-5.932730638
235463_s_at	LASS6	2	-7.661479329
211075_s_at	CD47	2	-8.921854692
200737_at	PGK1	2	-11.24623475
218681_s_at	SDF2L1	2	-10.4874351
206108_s_at	SFRS6	2	-4.251521416
220622_at	LRRC31	2	-3.850462397
224618_at	ROD1	2	-11.36510539
209109_s_at	TSPAN6	2	-6.510589408
204086_at	PRAME	2	-4.494912397
223452_s_at	ATL3	2	-7.756422963
222774_s_at	NETO2	2	-5.485922333
236009_at	0	2	-7.315798083
216977_x_at	SNRPA1	2	-14.10584759
218810_at	ZC3H12A	2	-6.740811111
234464_s_at	EME1	2	-12.2749687
229883_at	GRIN2D	2	-7.416223016
225711_at	ARL6IP6	2	-12.04494493
221827_at	RBCK1	2	-9.425538099
243894_at	SLC41A2	2	-7.241276433
226926_at	DMKN	2	-4.504474032
201819_at	SCARB1	2	-8.889910992
201189_s_at	ITPR3	2	-7.75859021
201774_s_at	NCAPD2	2	-12.26367718
236840_at	C12orf56	2	-4.795645617
202925_s_at	PLAGL2	2	-8.67268237
211318_s_at	RAE1	2	-11.78279509
202545_at	PRKCD	2	-10.98220827
1569190_at	SCLT1	2	-9.565335458
32837_at	AGPAT2	2	-8.948567745
234976_x_at	SLC4A5	2	-10.77309996
201013_s_at	PAICS	2	-10.85651766
204014_at	DUSP4	2	-4.548358038
225869_s_at	UNC93B1	2	-7.833989813
216952_s_at	LMNB2	2	-10.79532594
218275_at	SLC25A10	2	-12.17086912
222441_x_at	SLMO2	2	-12.4521415
235247_at	0	2	-9.302559466

226088_at	ZDHC12	2	-14.02336239
	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG ///		
208523_x_at	HIST1H2BI	2	-8.380511745
234672_s_at	TMEM48	2	-13.31521872
235177_at	FAM119A	2	-9.625583821
223649_s_at	SLC25A39	2	-13.96673342
200644_at	MARCKSL1	2	-9.768675684
207037_at	TNFRSF11A	2	-5.70488104
227647_at	KCNE3	2	-4.289652833
212623_at	TMEM41B	2	-11.46599123
226606_s_at	GTPBP5	2	-9.346031644
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214472_at	HIST1H3J	2	-9.159179574
218465_at	TMEM33	2	-13.58904574
216870_x_at	DLEU2	2	-7.887440912
	HGD /// LOC100132552 /// LOC727722		
214307_at		2	-6.395110223
209558_s_at	HIP1R	2	-9.16659301
203210_s_at	RFC5	2	-9.841117866
212311_at	KIAA0746 /// SERINC2	2	-7.184286908
208368_s_at	BRCA2	2	-10.86805999
231120_x_at	PKIB	2	-4.741573885
209774_x_at	CXCL2	2	-3.758607787
219045_at	RHOF	2	-6.514852432
206665_s_at	BCL2L1	2	-9.168576433
219258_at	TIPIN	2	-10.19089247
229801_at	C10orf47	2	-7.248229081
226064_s_at	DGAT2	2	-6.114260406
203360_s_at	MYCBP	2	-14.4212431
211056_s_at	SRD5A1	2	-8.532643797
222603_at	ERMP1	2	-8.834030692
224320_s_at	MCM8	2	-9.571632077
210845_s_at	PLAUR	2	-5.810054261
1552921_a_at	FIGNL1	2	-9.807899933
229526_at	AQP11	2	-8.502619058
203209_at	RFC5	2	-10.73703982
212978_at	LRRC8B	2	-11.66891698
226405_s_at	ARRDC1	2	-10.32160796
208689_s_at	RPN2	2	-14.77143588
222456_s_at	LIMA1	2	-6.003835051
215729_s_at	VGLL1	2	-3.802392093
206469_x_at	AKR7A3	2	-6.327156293
230655_at	0	2	-7.690898753
219466_s_at	APOA2	2	-3.595343733
226482_s_at	hCG_20857 /// RP11-544M22.4	2	-8.286341176
220123_at	SLC35F5	2	-9.043898901

1554095_at	RBM33	2	-10.52357324
211527_x_at	VEGFA	2	-7.766970419
225903_at	PIGU	2	-13.98580057
205807_s_at	TUFT1	2	-8.192493274
218826_at	SLC35F2	2	-6.866896457
210293_s_at	SEC23B	2	-12.4457484
242037_at	ASPH	2	-7.438358671
241547_at	0	2	-4.499644544
205977_s_at	EPHA1	2	-8.642297234
1568877_a_at	ACBD5	2	-9.840409409
203028_s_at	CYBA	2	-10.08576834
203124_s_at	SLC11A2	2	-9.354156837
1568593_a_at	NUDT16P	2	-7.819032243
229865_at	FNDC3B	2	-8.361681172
223772_s_at	TMEM87A	2	-9.383315428
205403_at	IL1R2	2	-3.903042183
204203_at	CEBPG	2	-8.887847061
205148_s_at	CLCN4	2	-7.261974997
204532_x_at	UGT1A1 /// UGT1A10 /// UGT1A4 /// UGT1A6 /// UGT1A8 ///	2	-4.081204961
220073_s_at	PLEKHG6	2	-10.31867286
212236_x_at	KRT17	2	-4.186208511
202411_at	IFI27	2	-6.131434333
205470_s_at	KLK11	2	-3.774625835
242787_at	0	2	-8.656638931
224623_at	LOC728554 /// THOC3	2	-12.56298608
214088_s_at	FUT3	2	-4.611928165
210437_at	MAGEA9 /// MAGEA9B	2	-4.484735953
231033_at	0	2	-6.189081632
1552256_a_at	SCARB1	2	-9.011158838
238689_at	GPR110	2	-4.421317202
204728_s_at	WDHD1	2	-10.77990354
211924_s_at	PLAUR	2	-6.035973824
218586_at	C20orf20	2	-11.44519906
218434_s_at	AACS	2	-11.01451878
224027_at	CCL28	2	-4.976843707
216548_x_at	HMG4L	2	-11.06733359
205043_at	CFTR	2	-3.618922996
225597_at	SLC45A4	2	-9.519421147
203925_at	GCLM	2	-10.96150231
220442_at	GALNT4 /// WDR51B	2	-6.180125197
205196_s_at	AP1S1	2	-11.6276437
208084_at	ITGB6	2	-6.409242201
225702_at	C8orf76	2	-12.0631185
215549_x_at	CTAGE4	2	-10.84204007
241371_at	0	2	-9.041739204
202671_s_at	PDXK	2	-9.45237418
1554539_a_at	RHOF	2	-7.131238565
231121_at	HPS3	2	-9.132137126
242283_at	C1orf67 /// DNAH14	2	-6.5438233

217979_at	TSPAN13	2	-8.540958166
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218151_x_at	GPR172A	2	-11.70829341
204485_s_at	TOM1L1	2	-7.395688347
221927_s_at	ABHD11	2	-8.941323461
204317_at	GTSE1	2	-12.77474329
226649_at	PANK1	2	-7.325308671
225447_at	GPD2	2	-11.31453264
1007_s_at	DDR1	2	-9.560772759
226707_at	NAPRT1	2	-7.489113461
218454_at	FLJ22662	2	-6.245754478
235783_at	MRT04	2	-11.31016705
210821_x_at	CENPA	2	-12.87083991
210959_s_at	SRD5A1	2	-8.067697066
1555963_x_at	B3GNT7	2	-4.625196889
243252_at	0	2	-6.969543167
228931_at	COQ4	2	-11.08462895
1560089_at	LOC286208	2	-7.077402696
211042_x_at	MCAM	2	-10.53268582
204233_s_at	CHKA	2	-8.871060082
218342_s_at	ERMP1	2	-10.93677474
222549_at	CLDN1	2	-3.882626972
219959_at	MOCOS	2	-5.453945007
238531_x_at	0	2	-5.354440377
201388_at	PSMD3	2	-9.150699022
227862_at	C1orf225	2	-4.783366233
218365_s_at	DARS2	2	-11.66677987
202145_at	LY6E	2	-7.739621484
236083_at	BCL2L15	2	-5.709840837
202847_at	PCK2	2	-9.275349219
219125_s_at	RAG1AP1	2	-12.73009414
218701_at	LACTB2	2	-7.12388728
223454_at	CXCL16	2	-7.224449599
205874_at	ITPKA	2	-8.629312475
216381_x_at	AKR7A3	2	-6.115658096
233110_s_at	BCL2L12	2	-12.31322718
230244_at	C2orf82	2	-5.770037734
220144_s_at	ANKRD5	2	-9.90187382
241224_x_at	DSCR8	2	-4.694966138
231894_at	0	2	-9.028042288
209163_at	CYB561	2	-10.00097918
1559051_s_at	C6orf150	2	-8.795398386
231784_s_at	WDSOF1	2	-10.40360509
210085_s_at	ANXA9	2	-8.751482818
202016_at	MEST	2	-5.494917855
209433_s_at	PPAT	2	-9.520479429
235117_at	CHAC2	2	-7.805903876
219189_at	FBXL6	2	-10.6058258
210008_s_at	MRPS12	2	-12.63956572
214106_s_at	GMDS	2	-5.614953155

209627_s_at	OSBPL3	2	-7.735875641
203593_at	CD2AP	2	-10.56131596
209753_s_at	TMPO	2	-9.575444367
221539_at	EIF4EBP1	2	-9.839394896
232510_s_at	DPP3	2	-11.95703239
238075_at	CHEK1	2	-8.809607987
207590_s_at	CENPI	2	-11.26201524
205199_at	CA9	2	-4.574545697
205660_at	OASL	2	-6.01371618
209836_x_at	BOLA2 /// BOLA2B	2	-13.29994889
213927_at	MAP3K9	2	-10.22511448
205286_at	TFAP2C	2	-5.352954068
208579_x_at	H2BFS	2	-6.867882342
227342_s_at	MYEOV	2	-5.965121724
1552364_s_at	MSI2	2	-11.00701957
230573_at	SGK2	2	-6.03483495
201704_at	ENTPD6	2	-11.5038321
201349_at	SLC9A3R1	2	-9.56493826
222940_at	SULT1E1	2	-3.718256826
208103_s_at	ANP32E	2	-11.20793098
219461_at	PAK6	2	-8.628762137
212268_at	SERPINB1	2	-7.174438822
217851_s_at	SLMO2	2	-11.21744481
235583_at	ILDR1	2	-6.988160816
214005_at	GGCX	2	-11.90204984
221610_s_at	STAP2	2	-7.299012445
204493_at	BID	2	-10.96489181
210007_s_at	GPD2	2	-10.70981367
221685_s_at	CCDC99	2	-11.68105654
208511_at	PTTG3	2	-14.43947794
203971_at	SLC31A1	2	-11.49861306
219004_s_at	C21orf45	2	-11.43010736
218400_at	OAS3	2	-8.090866403
229097_at	DIAPH3	2	-9.739282359
210793_s_at	NUP98	2	-10.85733969
215629_s_at	DLEU2 /// DLEU2L	2	-7.269303129
207620_s_at	CASK	2	-9.734188564
207223_s_at	ROD1	2	-10.61597147
225864_at	FAM84B	2	-8.364022428
218280_x_at	HIST2H2AA3 /// HIST2H2AA4	2	-8.15307028
227935_s_at	PCGF5	2	-11.58701944
243669_s_at	PRAP1	2	-4.029910981
219296_at	ZDHHC13	2	-10.02537677
221582_at	HIST3H2A	2	-7.85412163
208821_at	SNRPB	2	-12.01116452
219300_s_at	CNTNAP2	2	-5.368164431
222701_s_at	CHCHD7	2	-12.09688698
225418_at	PVRL2	2	-9.772585797
201870_at	TOMM34	2	-14.03638107
208916_at	SLC1A5	2	-10.95214148

242727_at	ARL5B	2	-8.747765352
200894_s_at	FKBP4	2	-10.65524415
202543_s_at	GMFB	2	-10.23374505
227296_at	MFSD3	2	-11.13108966
213816_s_at	MET	2	-5.708793402
232105_at	0	2	-7.321896494
227042_at	YDJC	2	-13.04447107
236312_at	0	2	-11.09341554
228955_at	0	2	-6.988870174
206626_x_at	SSX1	2	-5.275029581
218816_at	LRRC1	2	-9.663036873
219510_at	POLQ	2	-12.51206592
207018_s_at	RAB27B	2	-5.158670189
206670_s_at	GAD1	2	-6.235665345
204558_at	RAD54L	2	-13.43075157
205650_s_at	FGA	2	-4.810555501
207131_x_at	GGT1	2	-7.508844676
205942_s_at	ACSM3	2	-5.766037464
223551_at	PKIB	2	-4.142860131
208795_s_at	MCM7	2	-11.42452674
215037_s_at	BCL2L1	2	-9.027617175
236129_at	GALNT5	2	-4.778967535
222705_s_at	SLC25A15	2	-10.47789265
205073_at	CYP2J2	2	-6.576921213
233446_at	ONECUT2	2	-4.117218879
212070_at	GPR56	2	-9.252675224
226034_at	0	2	-5.184907123
203270_at	DTYMK /// LOC727761	2	-12.45692171
222675_s_at	BAIAP2L1	2	-7.540924811
221241_s_at	BCL2L14	2	-5.057934541
205220_at	GPR109B	2	-3.73481119
222750_s_at	SRD5A3	2	-8.930870382
209628_at	NXT2	2	-10.52215698
227801_at	TRIM59	2	-8.886201222
204331_s_at	MRPS12	2	-11.82406594
223798_at	SLC41A2	2	-7.1557641
240180_at	0	2	-7.107361104
210868_s_at	ELOVL6	2	-6.572965446
223540_at	PVRL4	2	-10.74748336
225362_at	FAM122B	2	-10.29449033
1553984_s_at	DTYMK /// LOC727761	2	-12.41732218
1555037_a_at	IDH1	2	-10.91375456
219502_at	NEIL3	2	-11.06408693
218875_s_at	FBXO5	2	-10.90519751
214235_at	CYP3A5	2	-4.417330078
209696_at	FBP1	2	-5.998415201
228597_at	C21orf45	2	-10.59639605
234970_at	TC2N	2	-6.885854293
203215_s_at	MYO6	2	-10.35036908
220085_at	HELLS	2	-8.358952953

231832_at	GALNT4	2	-5.207855523
225830_at	PDZD8	2	-7.7660375
207439_s_at	SLC35A2	2	-12.51660096
205067_at	IL1B	2	-4.830536091
200635_s_at	PTPRF	2	-10.66786965
221879_at	CALML4	2	-5.478775811
202869_at	OAS1	2	-6.417079029
209146_at	SC4MOL	2	-10.02437225
1554557_at	ATP11B	2	-9.645516811
209448_at	HTATIP2	2	-9.823864179
241726_at	0	2	-7.141836237
216228_s_at	WDHD1	2	-10.45831092
238846_at	TNFRSF11A	2	-4.415524647
207387_s_at	GK	2	-7.419640135
224746_at	KIAA1522	2	-11.06801425
204856_at	B3GNT3	2	-9.396056758
205053_at	PRIM1	2	-10.9050149
220951_s_at	A1CF	2	-6.000330334
201193_at	IDH1	2	-11.41772995
230294_at	0	2	-12.68964707
239911_at	ONECUT2	2	-4.018375381
230122_at	MLLT10	2	-10.57679011
230793_at	LRRC16A	2	-7.245042164
211372_s_at	IL1R2	2	-4.626387591
206558_at	SIM2	2	-8.795626618
214290_s_at	HIST2H2AA3 /// HIST2H2AA4	2	-8.026476103
230093_at	RSPH1	2	-6.926014928
236122_at	0	2	-8.279708233
201663_s_at	SMC4	2	-11.53542595
212471_at	AVL9	2	-13.21298456
213175_s_at	SNRPB	2	-12.63028394
242473_at	TRAF4	2	-11.87906302
219403_s_at	HPSE	2	-6.54220992
223874_at	ARP11	2	-8.6853555
222606_at	ZWILCH	2	-12.02756965
201301_s_at	ANXA4	2	-7.623689806
204927_at	RASSF7	2	-11.28547302
205676_at	CYP27B1	2	-8.412677392
229599_at	LOC440335	2	-8.70355123
219987_at	0	2	-6.017682515
214866_at	PLAUR	2	-7.108728437
214734_at	EXPH5	2	-7.073262506
214727_at	BRCA2	2	-11.2775658
223225_s_at	SEH1L	2	-10.74016764
218392_x_at	SFXN1	2	-12.04435186
221586_s_at	E2F5	2	-8.658798772
201629_s_at	ACP1	2	-11.7787193
225536_at	TMEM54	2	-8.4448781
210041_s_at	PGM3	2	-11.17202379

	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG ///		
208490_x_at	HIST1H2BI	2	-8.584907795
208691_at	TFRC	2	-11.80107727
235911_at	0	2	-6.155784314
227314_at	ITGA2	2	-6.104159914
222592_s_at	ACSL5	2	-5.793982235
214437_s_at	SHMT2	2	-11.11645851
205195_at	AP1S1	2	-12.12077612
218182_s_at	CLDN1	2	-5.293148028
	/// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9		
206094_x_at		2	-4.249092849
1554020_at	BICD1	2	-9.623430968
203775_at	SLC25A13	2	-9.715120705
209892_at	FUT4	2	-6.541968131
223274_at	TCF19	2	-10.95567047
219956_at	GALNT6	2	-5.311277899
201088_at	KPNA2 /// LOC728860	2	-14.51368776
219439_at	C1GALT1	2	-9.106660381
215243_s_at	GJB3	2	-6.581993787
221750_at	HMGCS1	2	-9.625541885
208433_s_at	LRP8	2	-9.571609439
204268_at	S100A2	2	-5.820236695
1554576_a_at	ETV4	2	-7.292195894
206400_at	LGALS7 /// LGALS7B	2	-5.886771445
	UGT1A1 /// UGT1A10 /// UGT1A4 /// UGT1A6 /// UGT1A8 ///		
207126_x_at		2	-4.224801891
216243_s_at	IL1RN	2	-7.567835663
218653_at	SLC25A15	2	-11.40091624
219000_s_at	DSCC1	2	-11.18687642
220106_at	NPC1L1	2	-6.005066035
204895_x_at	MUC4	2	-6.05520148
225762_x_at	LOC284801	2	-7.715280651
229215_at	ASCL2	2	-4.183981748
231855_at	KIAA1524	2	-10.5917846
204740_at	CNKSR1	2	-13.03001435
1555310_a_at	PAK6	2	-8.508064626
222843_at	FIGNL1	2	-10.84783787
221178_at	BAIAP2L2	2	-8.353051686
221256_s_at	HDHD3	2	-9.670937566
232682_at	MREG	2	-11.42456552
209680_s_at	KIFC1	2	-15.40453896
	GAGE1 /// GAGE12F /// GAGE12G /// GAGE12I /// GAGE12J /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2D /// GAGE2E /// GAGE3 /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7 /// GAGE8		
207739_s_at		2	-3.713238157
232083_at	KIF16B	2	-7.975453801

204973_at	GJB1	2	-7.275228999
218567_x_at	DPP3	2	-12.00611508
203878_s_at	MMP11	2	-5.519557427
201118_at	PGD	2	-10.62030323
209893_s_at	FUT4	2	-9.469736615
209950_s_at	VILL	2	-5.500671609
219573_at	LRRC16A	2	-10.66511528
205455_at	MST1R	2	-6.763292805
1568678_s_at	FGFR1OP	2	-13.64753233
214435_x_at	RALA	2	-13.14032549
242069_at	CBX5	2	-11.65356614
202546_at	VAMP8	2	-9.228509403
39402_at	IL1B	2	-4.757931236
209238_at	STX3	2	-9.934965109
223845_at	FLJ20674	2	-9.456907257
215145_s_at	CNTNAP2	2	-5.936767349
221122_at	HRASLS2	2	-4.782773743
209035_at	MDK	2	-8.222749264
228221_at	SLC44A3	2	-7.087711498
221677_s_at	DONSON	2	-11.08107061
226355_at	WDR51A	2	-14.40051858
228559_at	CENPN	2	-10.87612805
206125_s_at	KLK8	2	-4.481565873
33304_at	ISG20	2	-7.409527594
1554897_s_at	RHBDL2	2	-5.763204225
217835_x_at	C20orf24	2	-15.12314743
219615_s_at	KCNK5	2	-7.374402786
204734_at	KRT15	2	-7.774277036
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202023_at	EFNA1	2	-8.280649746
232277_at	0	2	-4.838298755
238755_at	0	2	-4.906724398
205774_at	F12	2	-7.018370349
210213_s_at	EIF6	2	-14.07275807
221923_s_at	NPM1	2	-11.83961016
207180_s_at	HTATIP2	2	-10.7350399
211048_s_at	PDIA4	2	-13.60060317
221655_x_at	EPS8L1	2	-9.109500961
226597_at	REEP6	2	-6.026771948
205588_s_at	FGFR1OP	2	-13.41144744
210117_at	SPAG1	2	-7.329305753
206600_s_at	LOC100133772 /// SLC16A5	2	-6.432563509
211767_at	GIN54	2	-11.73839989
244519_at	ASXL1	2	-10.47687836
219946_x_at	MYH14	2	-9.195203602
204698_at	ISG20	2	-7.228051834
218252_at	CKAP2	2	-11.04921959
203379_at	RPS6KA1	2	-9.504679107
209626_s_at	OSBPL3	2	-8.716301824
210029_at	IDO1	2	-4.078077671

237563_s_at	LOC440731	2	-9.936965327
213929_at	0	2	-6.851312605
221085_at	TNFSF15	2	-8.049293761
1554271_a_at	CENPL	2	-11.13175227
223880_x_at	C20orf24	2	-15.03909861
218308_at	TACC3	2	-12.77319206
225806_at	JUB	2	-6.624292283
219888_at	SPAG4	2	-7.564602243
205085_at	ORC1L	2	-12.72525346
208779_x_at	DDR1	2	-9.582221295
225601_at	HMGB3	2	-8.885170054
1554830_a_at	STEAP3	2	-11.29456705
210675_s_at	PTPRR	2	-5.391619525
242093_at	SYTL5	2	-4.491387414
222396_at	HN1	2	-9.929955057
242354_at	0	2	-8.908768712
209605_at	TST	2	-8.434829427
220075_s_at	MUPCDH	2	-5.355529201
235244_at	CCDC58	2	-8.684017141
202178_at	PRKCZ	2	-11.23981818
204798_at	MYB	2	-5.397214304
223785_at	FANCI	2	-9.846646748
232158_x_at	NPAL1	2	-9.535865433
201850_at	CAPG	2	-8.102957224
216493_s_at	IGF2BP3 /// LOC645468	2	-6.646096281
205309_at	SMPDL3B	2	-8.830309078
202504_at	TRIM29	2	-4.117916017
231311_at	0	2	-6.784590669
211237_s_at	FGFR4	2	-9.926416897
1553764_a_at	JUB	2	-7.145207192
242890_at	0	2	-9.628957084
222392_x_at	PERP	2	-9.330595211
212444_at	0	2	-4.441606057
228706_s_at	CLDN23	2	-4.964035587
222118_at	CENPN	2	-13.596989
201688_s_at	TPD52	2	-7.313177518
212445_s_at	NEDD4L	2	-9.726899789
205436_s_at	H2AFX	2	-12.97091223
205107_s_at	EFNA4	2	-9.561759536
218500_at	C8orf55	2	-9.373919171
226118_at	CENPO	2	-13.16503907
204015_s_at	DUSP4	2	-6.039091932
238632_at	0	2	-6.285995976
210177_at	TRIM15	2	-9.694288944
221591_s_at	FAM64A	2	-11.34694737
211848_s_at	CEACAM7	2	-5.771010653
209911_x_at	HIST1H2BD	2	-7.104863659
210319_x_at	MSX2	2	-6.33963762
223811_s_at	C7orf20	2	-12.71354732
214751_at	ZNF468	2	-10.04164479

228846_at	MXD1	2	-7.263132594
204717_s_at	SLC29A2	2	-10.50463939
228468_at	MASTL	2	-10.96385185
200903_s_at	AHCY	2	-13.04765682
229276_at	IGSF9	2	-9.416794079
223038_s_at	FAM60A	2	-9.919820317
222946_s_at	C1orf135	2	-13.98913169
201761_at	MTHFD2	2	-12.87483759
210567_s_at	SKP2	2	-9.099781337
234932_s_at	CDCP1	2	-11.15100328
228360_at	LYPD6B	2	-5.567287079
223172_s_at	MTP18	2	-13.32447782
219143_s_at	RPP25	2	-10.59985595
204817_at	ESPL1	2	-13.43073595
228191_at	0	2	-9.027795277
220147_s_at	FAM60A	2	-11.48976482
208126_s_at	CYP2C18	2	-3.932373815
235588_at	ESCO2	2	-12.21881949
231856_at	KIAA1244	2	-7.908206466
64408_s_at	CALML4	2	-5.588531884
227165_at	C13orf3	2	-13.69639794
207332_s_at	TFRC	2	-11.26503835
202856_s_at	SLC16A3	2	-7.814741187
231772_x_at	CENPH	2	-10.24674917
205282_at	LRP8	2	-9.811682269
235092_at	0	2	-8.451668364
229305_at	MLF1IP	2	-9.552791248
215103_at	CYP2C18	2	-4.190585209
225203_at	PPP1R16A	2	-9.549146965
202740_at	ACY1	2	-8.55132333
1557129_a_at	FAM111B	2	-9.979715352
243010_at	MSI2	2	-11.34373338
210983_s_at	MCM7	2	-11.45568337
239834_at	0	2	-8.148374506
220658_s_at	ARNTL2	2	-8.923701566
230051_at	C10orf47	2	-7.100730715
219014_at	PLAC8	2	-3.870054945
221909_at	RNFT2	2	-8.827486862
236514_at	ACOT8	2	-8.081560381
201583_s_at	SEC23B	2	-13.83689761
217590_s_at	TRPA1	2	-5.305991144
223895_s_at	EPN3	2	-7.932184844
1555733_s_at	AP1S3	2	-7.039082649
235153_at	RNF183	2	-7.418500707
203824_at	TSPAN8	2	-3.601361285
222642_s_at	TMEM33	2	-14.0632156
235266_at	ATAD2	2	-11.38986526
35148_at	TJP3	2	-9.213779348
202721_s_at	GFPT1	2	-11.37747774
204614_at	SERPINB2	2	-4.626271344

224376_s_at	C20orf24	2	-15.05570903
222922_at	KCNE3	2	-5.164765992
224802_at	NDFIP2	2	-11.09937737
204244_s_at	DBF4	2	-9.892903007
235269_at	FAM83F	2	-9.521186773
205490_x_at	GJB3	2	-6.868461342
241453_at	PTK2	2	-9.258958459
204608_at	ASL	2	-10.04585769
206084_at	PTPRR	2	-5.442074964
208450_at	LGALS2	2	-4.525747217
203911_at	RAP1GAP	2	-7.736659478
226287_at	CCDC34	2	-8.91850259
230238_at	ANKRD43	2	-4.864323059
214308_s_at	HGD /// LOC100132552 /// LOC727722	2	-7.487194835
235609_at	0	2	-9.858034611
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210749_x_at	DDR1	2	-9.728529554
204875_s_at	GMDS	2	-4.975481644
203510_at	MET	2	-7.468844884
219194_at	SEMA4G	2	-8.817946766
203876_s_at	MMP11	2	-6.165108913
1568596_a_at	TROAP	2	-13.07302935
208083_s_at	ITGB6	2	-5.446272575
209825_s_at	UCK2	2	-13.31764786
226936_at	C6orf173	2	-11.64414218
220239_at	KLHL7	2	-10.44824913
227046_at	SLC39A11	2	-10.17307212
201202_at	PCNA	2	-12.46118213
224715_at	WDR34	2	-13.03218838
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225177_at	RAB11FIP1	2	-7.837436941
1560916_a_at	DPY19L1	2	-11.11954023
218349_s_at	ZWILCH	2	-12.02605413
201644_at	TSTA3	2	-9.935955878
219650_at	ERCC6L	2	-13.67666047
232596_at	DIAPH3	2	-11.08617253
1552478_a_at	IRF6	2	-9.187547128
218704_at	RNF43	2	-8.098696046
236769_at	LOC158402	2	-9.135702765
217127_at	CTH	2	-7.446492262
213147_at	HOXA10	2	-7.478256905
204886_at	PLK4	2	-12.38351859
206010_at	HABP2	2	-5.857762914
219739_at	RNF186	2	-5.294976997
228401_at	ATAD2	2	-11.51890907
215779_s_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	2	-8.707222451
211708_s_at	SCD	2	-6.659887244

213647_at	DNA2	2	-11.33009436
226610_at	CENPV	2	-9.323875194
222077_s_at	RACGAP1	2	-12.63132546
228462_at	IRX2	2	-4.466093171
209398_at	HIST1H1C	2	-7.119743906
203499_at	EPHA2	2	-6.890585749
205194_at	PSPH	2	-9.652492445
218779_x_at	EPS8L1	2	-9.093723742
201014_s_at	PAICS	2	-11.80056977
229551_x_at	ZNF367	2	-9.730025617
222067_x_at	HIST1H2BD	2	-9.519542341
216985_s_at	STX3	2	-10.33178168
202855_s_at	SLC16A3	2	-8.350834972
242417_at	LOC283278	2	-9.764214254
212925_at	C19orf21	2	-6.97772451
231270_at	CA13	2	-6.075852292
236471_at	NFE2L3	2	-7.66955381
235456_at	0	2	-6.171245147
220056_at	IL22RA1	2	-7.752449026
223000_s_at	F11R	2	-10.02290912
226611_s_at	CENPV	2	-8.75765189
242939_at	TFDP1	2	-9.71191063
208596_s_at	/// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	2	-4.451410171
229500_at	SLC30A9	2	-10.56863809
204437_s_at	FOLR1	2	-5.138222551
226132_s_at	MANEAL	2	-6.709727123
1552797_s_at	PROM2	2	-4.611009124
202722_s_at	GFPT1	2	-10.55361392
237215_s_at	TFRC	2	-8.683758032
226988_s_at	MYH14	2	-8.983358099
225739_at	RAB11FIP4	2	-13.79603112
200637_s_at	PTPRF	2	-11.76230426
208546_x_at	HIST1H2BH	2	-9.619259612
210480_s_at	MYO6	2	-12.51278492
209969_s_at	STAT1	2	-7.564732751
229545_at	FERMT1	2	-8.736628906
1554006_a_at	LLGL2	2	-10.74366781
241898_at	0	2	-7.007969472
201577_at	NME1 /// NME2	2	-14.2457948
209832_s_at	CDT1	2	-13.15697371
207169_x_at	DDR1	2	-9.861438196
203726_s_at	LAMA3	2	-5.170405526
223666_at	SNX5	2	-12.79212342
219612_s_at	FGG	2	-3.914327417
205654_at	C4BPA	2	-4.76735139
219512_at	DSN1	2	-14.43751199
235099_at	CMTM8	2	-9.475451314
229223_at	0	2	-10.353941

213695_at	PON3	2	-4.554677659
226960_at	CXCL17	2	-3.752496996
204867_at	GCHFR	2	-11.14826604
208209_s_at	C4BPB	2	-5.699144232
241994_at	XDH	2	-5.552194084
242053_at	0	2	-11.26119846
203625_x_at	SKP2	2	-11.23267523
235515_at	C19orf46	2	-8.088952328
214804_at	CENPI	2	-11.596072
218180_s_at	EPS8L2	2	-11.55149136
202889_x_at	MAP7	2	-10.16015255
211762_s_at	KPNA2 /// LOC728860	2	-14.69064016
201468_s_at	NQO1	2	-5.682923374
220840_s_at	C1orf112	2	-11.14381408
239370_at	0	2	-4.070336923
223509_at	CLDN2	2	-4.419511544
232078_at	PVRL2	2	-9.445142201
219911_s_at	LOC100134295 /// SLCO4A1	2	-6.205090372
1555225_at	C1orf43	2	-9.399237994
1559361_at	MACC1	2	-7.912565726
208658_at	PDIA4	2	-12.32728462
38158_at	ESPL1	2	-13.68153633
226456_at	C16orf75	2	-10.58685454
211425_x_at	SSX4 /// SSX4B	2	-4.902658717
218424_s_at	STEAP3	2	-11.76893435
206499_s_at	RCC1 /// SNHG3-RCC1	2	-14.85100359
1562921_at	0	2	-5.83588284
225150_s_at	RTKN	2	-11.92939058
219529_at	CLIC3	2	-6.12826889
223385_at	CYP2S1	2	-6.541738758
228648_at	LRG1	2	-8.003815109
220082_at	PPP1R14D	2	-6.726520299
214697_s_at	ROD1	2	-12.12041797
1555905_a_at	C3orf23	2	-9.459350143
209679_s_at	LOC57228	2	-8.95677962
210390_s_at	CCL14 /// CCL15	2	-4.244848451
201582_at	SEC23B-	2	-12.45760637
201286_at	SDC1	2	-7.53025195
218720_x_at	LOC652900 /// SEZ6L2	2	-8.243393295
211725_s_at	BID	2	-13.54185766
241455_at	0	2	-8.493735474
1552502_s_at	RHBDL2	2	-5.441462861
202357_s_at	C2 /// CFB	2	-6.512993512
203954_x_at	CLDN3	2	-5.432362003
235425_at	SGOL2	2	-11.90488154
229070_at	C6orf105	2	-3.943336708
214469_at	HIST1H2AB /// HIST1H2AE	2	-8.282813926
224839_s_at	GPT2	2	-9.724580716
208623_s_at	EZR	2	-10.55763426
225300_at	C15orf23	2	-13.60829061

238750_at	0	2	-5.533533702
203216_s_at	MYO6	2	-11.99346332
205680_at	MMP10	2	-5.663964725
218498_s_at	ERO1L	2	-10.04727417
236098_at	hCG_1643808	2	-7.11883324
223839_s_at	SCD /// SCDOS	2	-8.299058063
204981_at	SLC22A18	2	-7.865549311
205733_at	BLM	2	-12.03897676
229634_at	TMEM139	2	-7.378965658
219513_s_at	SH2D3A	2	-9.064288195
232977_x_at	MYH14	2	-9.347923023
203432_at	TMPO	2	-10.86154631
242881_x_at	0	2	-5.01240182
219105_x_at	ORC6L	2	-13.85936531
228058_at	LOC124220	2	-4.257049225
213412_at	TJP3	2	-9.871726442
215471_s_at	MAP7	2	-10.38171384
213577_at	SQLE	2	-11.16104785
212686_at	PPM1H	2	-7.654228075
205157_s_at	KRT17	2	-4.640448482
231849_at	KRT80	2	-6.947692427
227103_s_at	ECE2	2	-14.07777812
214455_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	2	-7.302770963
203046_s_at	TIMELESS	2	-12.90415886
224799_at	NDFIP2	2	-11.99345676
232238_at	ASPM	2	-10.37871039
214254_at	MAGEA4	2	-4.557941717
204240_s_at	SMC2	2	-11.61092698
238956_at	0	2	-4.763973425
204653_at	TFAP2A	2	-6.06924432
232079_s_at	PVRL2	2	-9.761665242
205894_at	ARSE	2	-6.125017901
36936_at	TSTA3	2	-9.927079509
241031_at	FAM148A	2	-5.002255853
229954_at	0	2	-8.70055579
232322_x_at	STARD10	2	-9.157819315
217640_x_at	C18orf24	2	-12.23870145
225436_at	FAM108C1	2	-8.245385788
236058_at	C1orf172	2	-13.76629553
233337_s_at	LOC652900 /// SEZ6L2	2	-8.593904055
222155_s_at	GPR172A	2	-11.78372014
214157_at	GNAS	2	-7.161274959
220892_s_at	PSAT1	2	-8.912396868
235955_at	MARVELD2	2	-9.541694176
202240_at	PLK1	2	-15.2473275
223748_at	SLC4A11	2	-7.386124362
209309_at	AZGP1	2	-4.203207263
204695_at	CDC25A	2	-12.87380963

207291_at	PRRG4	2	-11.1018564
219017_at	ETNK1	2	-9.982648378
1553997_a_at	ASPHD1	2	-6.60604729
236741_at	WDR72	2	-5.599227699
1566766_a_at	MACC1	2	-7.130546684
234290_x_at	MYH14	2	-9.029411206
227133_at	CXorf39	2	-11.07811645
210394_x_at	SSX4 /// SSX4B	2	-5.01935112
222906_at	FLVCR1	2	-8.735147128
202488_s_at	FXD3	2	-9.074067972
204127_at	RFC3	2	-13.03423239
204675_at	SRD5A1	2	-8.679621222
1553132_a_at	TC2N	2	-7.424584175
239196_at	ANKRD22	2	-7.033902096
238805_at	C11orf52	2	-8.830732888
236957_at	CDCA2	2	-12.10923463
216074_x_at	WWC1	2	-12.24767578
229964_at	C9orf152	2	-4.311576186
229377_at	GRTP1	2	-7.862309687
209872_s_at	PKP3	2	-10.51896224
227747_at	MPZL3	2	-11.64980604
237159_x_at	AP1S3	2	-8.674090301
219681_s_at	RAB11FIP1	2	-8.187224792
1558508_a_at	C1orf53	2	-10.745062
201710_at	MYBL2	2	-13.73808764
227350_at	HELLS	2	-10.63600859
231022_at	0	2	-9.718343504
201287_s_at	SDC1	2	-7.847828015
228051_at	LOC202451	2	-7.502511834
201562_s_at	SORD	2	-12.07203335
239350_at	MARVELD3	2	-11.5669508
206110_at	0	2	-8.110015941
228707_at	CLDN23	2	-5.061025315
203022_at	RNASEH2A	2	-12.83004393
220865_s_at	PDSS1	2	-10.92817738
227928_at	C12orf48	2	-11.86796691
219727_at	DUOX2 -	2	-4.172300154
203276_at	LMNB1	2	-11.22584047
238028_at	LOC100128918	2	-8.687406408
218741_at	CENPM	2	-13.59557503
36742_at	TRIM15	2	-9.911233528
203453_at	SCNN1A	2	-4.168886022
223948_s_at	TMPRSS3	2	-8.108706685
211695_x_at	MUC1	2	-7.164594438
213285_at	TMEM30B	2	-7.498991952
224762_at	KIAA0746 /// SERINC2	2	-9.044375461
218959_at	HOXC10	2	-5.85578266
212142_at	MCM4	2	-11.5716574
203228_at	PAFAH1B3	2	-12.57168644
238022_at	hCG_1815491	2	-7.211154943

225777_at	C9orf140	2	-12.46735811
1566764_at	MACC1	2	-6.425346681
232361_s_at	EHF	2	-8.473673979
202735_at	EBP	2	-14.3389596
91826_at	EPS8L1	2	-9.29673365
204073_s_at	C11orf9	2	-8.052331683
203744_at	HMGB3	2	-11.36412842
211899_s_at	TRAF4	2	-13.79797463
228868_x_at	CDT1	2	-13.19284609
204887_s_at	PLK4	2	-13.15913256
203256_at	CDH3	2	-7.054675932
225105_at	OCC-1	2	-8.368620986
219588_s_at	NCAPG2	2	-14.31279217
217110_s_at	MUC4	2	-5.734101727
215942_s_at	GTSE1	2	-13.90313155
226553_at	TMPRSS2	2	-7.198859216
218792_s_at	BSPRY	2	-10.43385888
218847_at	IGF2BP2	2	-8.627822494
205221_at	HGD /// LOC100132552 /// LOC727722	2	-6.589600679
205552_s_at	OAS1	2	-8.249838447
229332_at	HPDL	2	-8.897369873
204679_at	KCNK1	2	-6.546910364
235871_at	LIPH	2	-6.651017992
206858_s_at	HOXC4 /// HOXC6	2	-6.231102082
203559_s_at	ABP1	2	-4.14294513
228281_at	C11orf82	2	-12.90721105
1555716_a_at	CXADR	2	-9.973321062
1568617_a_at	KIAA1543	2	-12.35301379
216238_s_at	FGB	2	-4.974611378
218872_at	TESC	2	-5.802342764
230831_at	FRMD5	2	-7.459357062
204767_s_at	FEN1	2	-15.29041345
216568_x_at	0	2	-10.56678935
202597_at	IRF6	2	-8.775525596
220445_s_at	CSAG2 /// CSAG3	2	-5.536005181
209172_s_at	CENPF -	2	-12.33612453
213693_s_at	MUC1	2	-6.170498264
225767_at	LOC284801	2	-7.460958141
211712_s_at	ANXA9	2	-7.820792384
215395_x_at	PRSS1 /// TRY6	2	-8.477534011
217744_s_at	PERP	2	-9.652803917
234944_s_at	FAM54A	2	-13.96417568
206429_at	F2RL1	2	-7.511700141
205137_x_at	USH1C	2	-7.824827132
226187_at	CDS1	2	-12.24217184
226622_at	MUC20	2	-4.791193514
206198_s_at	CEACAM7	2	-5.119213933
219648_at	MREG	2	-10.67300776
229538_s_at	IQGAP3	2	-11.11398682

218145_at	TRIB3	2	-7.210077038
	/// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	2	-4.143868341
215125_s_at	CD24	2	-6.545036188
242560_at	FANCD2	2	-12.86675522
1555383_a_at	POF1B	2	-5.935908246
202338_at	TK1	2	-12.97415365
224453_s_at	ETNK1	2	-9.875162449
205632_s_at	PIP5K1B	2	-6.248560046
226912_at	ZDHHC23	2	-11.13904815
221664_s_at	F11R	2	-12.05695679
205394_at	CHEK1	2	-10.08156444
223103_at	STARD10	2	-9.27226621
228969_at	AGR2	2	-4.514334139
201790_s_at	DHCR7	2	-13.63506146
202005_at	ST14	2	-10.0426919
212023_s_at	MKI67	2	-13.70002439
229490_s_at	0	2	-9.216038143
226403_at	TMC4	2	-8.670469888
211814_s_at	CCNE2	2	-10.10473003
216641_s_at	LAD1	2	-10.67133018
204320_at	COL11A1	2	-4.402022495
222262_s_at	ETNK1	2	-10.36928162
219233_s_at	GSDMB	2	-6.161945845
229644_at	PREP	2	-10.81006877
242013_at	BCL2L15	2	-7.093190333
204678_s_at	KCNK1	2	-7.345821669
238898_at	0	2	-8.822546381
234219_at	0	2	-7.482638199
233177_s_at	PNKD	2	-11.30561021
222039_at	KIF18B	2	-13.27141326
206074_s_at	HMGAI	2	-11.43341919
204128_s_at	RFC3	2	-12.51252378
220289_s_at	AIM1L	2	-10.01173217
236979_at	BCL2L15	2	-7.994059794
211889_x_at	CEACAM1	2	-9.326628186
208621_s_at	EZR	2	-10.36786226
206242_at	TM4SF5	2	-6.746437767
219544_at	C13orf34	2	-13.42665727
204768_s_at	FEN1	2	-15.17405741
208622_s_at	EZR	2	-10.6585354
218350_s_at	GMNN	2	-12.26854111
210103_s_at	FOXA2	2	-7.112229113
213680_at	KRT6B	2	-3.833831041
220060_s_at	C12orf48	2	-13.51546869
234992_x_at	ECT2	2	-12.38057028
204667_at	FOXA1	2	-8.661445004
226817_at	DSC2	2	-8.19211803
242722_at	LMO7	2	-8.449447789

204162_at	NDC80		2	-11.90434443
1554246_at	C1orf210		2	-9.585777062
212020_s_at	MKI67		2	-14.27906993
227919_at	UCA1		2	-5.241650291
205393_s_at	CHEK1		2	-10.60709923
224428_s_at	CDCA7		2	-7.786819504
231008_at	UNC5CL		2	-6.297124158
210761_s_at	GRB7		2	-8.853109039
231810_at	BRI3BP		2	-10.68624664
200832_s_at	SCD		2	-8.017114721
201791_s_at	DHCR7		2	-14.05801778
220030_at	STYK1		2	-6.408788048
225847_at	AADACL1		2	-8.867490349
205311_at	DDC		2	-4.897225018
203997_at	PTPN3		2	-13.00551083
209326_at	SLC35A2		2	-14.33849531
222848_at	CENPK		2	-9.961357959
225716_at		0	2	-10.75225661
216379_x_at	CD24		2	-6.60355904
209803_s_at	PHLDA2		2	-8.204540518
230165_at	SGOL2		2	-12.76397633
227985_at		0	2	-9.463217258
220011_at	C1orf135		2	-15.19264075
231941_s_at	MUC20		2	-4.734916188
220441_at	DNAJC22		2	-8.465116526
227055_at	METTL7B		2	-7.443384311
218115_at	ASF1B		2	-13.66089542
222962_s_at	MCM10		2	-12.20401334
219494_at	RAD54B		2	-11.93954903
218035_s_at	RBM47		2	-9.889667967
221577_x_at	GDF15		2	-5.240672883
1552680_a_at	CASC5		2	-12.67569129
1553986_at	RASEF		2	-7.016672778
203287_at	LAD1		2	-10.36101152
225299_at	MYO5B		2	-7.106580381
210074_at	CTSL2		2	-11.17653978
239002_at	ASPM		2	-12.14394937
217234_s_at	EZR		2	-10.75424288
202267_at	LAMC2		2	-7.072943418
205041_s_at	ORM1 /// ORM2		2	-4.348734652
65517_at	AP1M2		2	-11.56880781
205167_s_at	CDC25C		2	-13.17088089
204519_s_at	PLL		2	-7.355526743
201897_s_at	CKS1B		2	-13.7813045
218644_at	PLEK2		2	-8.993117812
204603_at	EXO1		2	-14.39977311
235229_at		0	2	-5.501883167
211883_x_at	CEACAM1		2	-8.942390205
219404_at	EPS8L3		2	-8.055913284
202871_at	TRAF4		2	-13.94088944

238513_at	PRRG4	2	-9.367845652
209529_at	PPAP2C	2	-8.073407579
212141_at	MCM4	2	-13.57881248
223423_at	GPR160	2	-6.492976141
205980_s_at	ARHGAP8 /// LOC553158 /// PRR5	2	-10.18688123
226213_at	ERBB3	2	-7.679607053
212657_s_at	IL1RN	2	-6.28724497
1554408_a_at	TK1	2	-12.71732084
208651_x_at	CD24	2	-6.746598415
232151_at	MACC1	2	-6.875547833
223700_at	MND1	2	-12.00176616
227614_at	HKDC1	2	-6.603480616
205024_s_at	RAD51	2	-14.44866564
209847_at	CDH17	2	-3.861411691
212021_s_at	MKI67	2	-12.96467208
210519_s_at	NQO1	2	-7.105220179
218073_s_at	TMEM48	2	-12.96122577
208300_at	PTPRH	2	-8.925769818
220161_s_at	EPB41L4B	2	-8.578860131
205538_at	CORO2A	2	-9.782383301
205016_at	TGFA	2	-7.893253296
206576_s_at	CEACAM1	2	-8.981764418
243018_at	0	2	-7.573785545
221521_s_at	GIN52	2	-12.01287379
218585_s_at	DTL	2	-12.17550298
204702_s_at	NFE2L3	2	-9.959997114
214079_at	DHRS2	2	-3.965501366
209173_at	AGR2	2	-4.276511346
209016_s_at	KRT7	2	-4.63373362
229105_at	GPR39	2	-10.43016187
205909_at	POLE2	2	-12.83798694
221665_s_at	EPS8L1	2	-10.1116023
202779_s_at	LOC731049 /// UBE2S	2	-12.67186203
235651_at	0	2	-8.290504913
221436_s_at	CDCA3	2	-16.56527596
209792_s_at	KLK10	2	-4.148873874
222930_s_at	AGMAT	2	-12.71845212
211184_s_at	USH1C	2	-7.79002277
210159_s_at	TRIM31	2	-7.254311441
266_s_at	CD24	2	-6.567699712
209873_s_at	PKP3	2	-11.7349747
205769_at	SLC27A2	2	-7.283220429
219388_at	GRHL2	2	-9.746011283
215509_s_at	BUB1	2	-13.64336132
220520_s_at	NUP62CL	2	-7.886189724
219411_at	ELMO3	2	-11.46825338
201250_s_at	SLC2A1	2	-9.59855212
219756_s_at	POF1B	2	-6.740650195
205822_s_at	HMGCS1	2	-10.40056984
238542_at	ULBP2	2	-7.671373082

221215_s_at	RIPK4	2	-12.5674895
206134_at	ADAMDEC1	2	-5.817856255
219215_s_at	SLC39A4	2	-9.71606354
230772_at	0	2	-9.314451073
224189_x_at	EHF	2	-8.207696279
210608_s_at	FUT2	2	-8.065617346
233565_s_at	SDCBP2	2	-8.567977051
240303_at	TMC5	2	-6.439408717
210387_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	2	-7.307313391
205239_at	AREG /// AREGB	2	-5.397236819
204259_at	MMP7	2	-4.073611602
213008_at	FANCI	2	-12.81042933
222830_at	GRHL1	2	-9.693845949
212279_at	TMEM97	2	-11.27324104
227753_at	TMEM139	2	-7.960215156
204272_at	LGALS4	2	-3.904354568
204315_s_at	GTSE1	2	-13.60700367
1553296_at	GPR128	2	-4.90255346
205046_at	CENPE	2	-14.5916201
1553830_s_at	MAGEA2 /// MAGEA2B	2	-4.942598797
229610_at	CKAP2L	2	-15.79036005
222036_s_at	MCM4	2	-13.49903685
207847_s_at	MUC1	2	-6.718505424
203108_at	GPRC5A	2	-5.838567127
202589_at	TYMS	2	-12.11482467
202528_at	GALE	2	-11.80814756
235545_at	DEPDC1	2	-12.55579527
208165_s_at	PRSS16	2	-8.898266911
239148_at	MARVELD3	2	-10.8279146
206482_at	PTK6	2	-7.442851497
203924_at	GSTA1	2	-4.605894479
202454_s_at	ERBB3	2	-7.920636425
213787_s_at	EBP	2	-14.65750436
223427_s_at	EPB41L4B	2	-8.839781592
231982_at	LOC284422	2	-5.426382169
226661_at	CDCA2	2	-11.79907347
227194_at	FAM3B	2	-4.292737027
209714_s_at	CDKN3	2	-11.4967881
236279_at	0	2	-9.965455563
202107_s_at	MCM2	2	-13.31920418
220468_at	ARL14	2	-4.755808965
209114_at	TSPAN1	2	-5.598235851
209644_x_at	CDKN2A	2	-8.540326598
238021_s_at	hCG_1815491	2	-6.872947185
204126_s_at	CDC45L	2	-14.77487389
235638_at	RASSF6	2	-6.979937952
202890_at	MAP7	2	-9.27984347
221520_s_at	CDCA8	2	-15.02405897

222740_at	ATAD2	2	-12.84883791
205402_x_at	PRSS2	2	-6.260560727
226067_at	C20orf114	2	-3.922605399
229396_at	OVOL1	2	-11.56287135
238567_at	SGPP2	2	-8.177420019
229372_at	GOLT1A	2	-8.898924306
212282_at	TMEM97	2	-10.9679036
208250_s_at	DMBT1	2	-4.550421479
37117_at	ARHGAP8 /// LOC553158 /// PRR5	2	-9.944520506
205768_s_at	SLC27A2	2	-7.316513488
222646_s_at	ERO1L	2	-11.22783878
201015_s_at	JUP	2	-10.33812568
210334_x_at	BIRC5	2	-15.17998128
206023_at	NMU	2	-5.350264298
223471_at	RAB3IP	2	-12.05531286
224361_s_at	IL17RB	2	-9.919606095
232202_at	0	2	-7.577557338
224753_at	CDCA5	2	-14.46979959
220295_x_at	DEPDC1	2	-13.27586056
208358_s_at	UGT8	2	-8.349538283
219493_at	SHCBP1	2	-12.80947338
205339_at	STIL	2	-13.63643905
215108_x_at	TOX3	2	-6.328886972
209212_s_at	KLF5	2	-7.578949887
219555_s_at	CENPN	2	-13.80321756
40284_at	FOXA2	2	-7.173661247
37892_at	COL11A1	2	-4.406023175
235924_at	0	2	-10.58945893
235141_at	MARVELD2	2	-9.933654745
213523_at	CCNE1	2	-9.184766136
226560_at	0	2	-6.998971915
1555772_a_at	CDC25A	2	-12.01024581
222496_s_at	RBM47	2	-11.12747465
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60474_at	FERMT1	2	-8.462721719
204470_at	CXCL1	2	-5.674490426
218451_at	CDCP1	2	-11.74559773
222746_s_at	BSPRY	2	-12.12355543
227177_at	CORO2A	2	-8.63632095
204988_at	FGB	2	-5.382729652
227163_at	GSTO2	2	-8.179167358
218796_at	FERMT1	2	-8.419912757
218261_at	AP1M2	2	-11.11881761
206632_s_at	APOBEC3B	2	-6.518148398
202712_s_at	CKMT1A /// CKMT1B /// LOC100133623	2	-7.728322439
224097_s_at	F11R	2	-13.38982432
223556_at	HELLS	2	-12.37790341
207850_at	CXCL3	2	-6.021443046
214642_x_at	MAGEA5	2	-5.531236809

238017_at	SDR16C5	2	-5.041305868
204750_s_at	DSC2	2	-8.940051961
203358_s_at	EZH2	2	-12.60755077
219474_at	C3orf52	2	-10.71682794
223278_at	GJB2	2	-6.912176106
229147_at	0	2	-6.474835259
227371_at	BAIAP2L1	2	-9.772727796
203713_s_at	LLGL2	2	-11.66793088
1555758_a_at	CDKN3	2	-11.57922031
235148_at	KRTCAP3	2	-9.45718258
218883_s_at	MLF1IP	2	-12.11063227
217755_at	HN1	2	-12.22776794
213007_at	FANCI	2	-12.94562917
219763_at	DENND1A	2	-11.9329287
201563_at	SORD	2	-12.55595263
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217678_at	SLC7A11	2	-7.958611337
214603_at	MAGEA2 /// MAGEA2B	2	-4.811824967
230914_at	HNF4A	2	-12.67805423
238439_at	ANKRD22	2	-6.573899491
205890_s_at	GABBR1 /// UBD	2	-6.284450417
225655_at	UHRF1	2	-12.18275294
218782_s_at	ATAD2	2	-13.16441322
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1554696_s_at	TYMS	2	-12.63844913
216623_x_at	TOX3	2	-6.140859967
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240304_s_at	TMC5	2	-5.650627857
1559258_a_at	CXorf61	2	-4.701520622
202094_at	BIRC5	2	-14.1668892
219787_s_at	ECT2	2	-13.00708976
223883_s_at	STK31	2	-7.834035224
219856_at	C1orf116	2	-9.473432405
206364_at	KIF14	2	-13.36613871
208025_s_at	HMGA2	2	-6.293226413
218726_at	HJURP	2	-14.3786372
213085_s_at	WWC1	2	-12.52420676
1555274_a_at	SEI	2	-13.98066194
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1555731_a_at	AP1S3	2	-8.701243996
228273_at	0	2	-12.08589558
226535_at	ITGB6	2	-5.61447191
219429_at	FA2H	2	-7.368291746
235350_at	C4orf19	2	-8.980399798
222680_s_at	DTL	2	-13.45793769
204818_at	HSD17B2	2	-5.123669149
204286_s_at	PMAIP1	2	-10.2932285
203145_at	SPAG5	2	-14.82942721

228463_at	FOXA3	2	-7.925056442
212022_s_at	MKI67	2	-12.81617036
209921_at	SLC7A11	2	-8.186584041
217109_at	MUC4	2	-5.665423965
211778_s_at	OVOL2	2	-10.18958869
244780_at	SGPP2	2	-7.447202819
212281_s_at	TMEM97	2	-11.19902397
214774_x_at	TOX3	2	-6.177581954
228912_at	VIL1	2	-7.725267255
221258_s_at	KIF18A	2	-13.098378
204579_at	FGFR4	2	-11.19089361
203304_at	BAMBI	2	-6.78042698
218755_at	KIF20A	2	-13.60952821
213226_at	CCNA2	2	-13.79653668
200606_at	DSP	2	-9.321818404
228323_at	CASC5	2	-12.90446593
213562_s_at	SQLE	2	-11.5947613
205513_at	TCN1	2	-4.336454755
219850_s_at	EHF	2	-8.085628391
211429_s_at	SERPINA1	2	-6.202764639
224156_x_at	IL17RB	2	-9.84605015
223062_s_at	PSAT1	2	-9.061175738
1552619_a_at	ANLN	2	-11.96108039
228565_at	KIAA1804	2	-10.80166307
219976_at	HOOK1	2	-14.80508831
222037_at	MCM4	2	-14.70198534
206683_at	ZNF165	2	-11.02794517
204285_s_at	PMAIP1	2	-10.72545996
210397_at	DEFB1	2	-6.415736328
232271_at	HNF4G	2	-7.328595765
1555203_s_at	SLC44A4	2	-6.961467745
209772_s_at	CD24	2	-7.722466566
227804_at	TLCD1	2	-12.06817426
219395_at	RBM35B	2	-12.06088715
203560_at	GGH	2	-8.891035326
223232_s_at	CGN	2	-9.725075047
215444_s_at	TRIM31	2	-7.156798532
219580_s_at	TMC5	2	-6.150035821
213150_at	HOXA10	2	-5.824562982
226961_at	PRR15	2	-8.490852935
220638_s_at	CBLC	2	-11.03303453
219255_x_at	IL17RB	2	-9.798189091
219306_at	KIF15	2	-13.59749729
204170_s_at	CKS2	2	-13.5242359
225301_s_at	MYO5B	2	-9.3620826
205780_at	BIK	2	-8.128828881
209260_at	SFN	2	-9.12830529
204733_at	KLK6	2	-5.6409495
204475_at	MMP1	2	-4.79103349
201596_x_at	KRT18	2	-8.80427391

220177_s_at	TMPRSS3	2	-6.318589444
235144_at	0	2	-7.188510474
219978_s_at	NUSAP1	2	-13.69484663
225822_at	TMEM125	2	-11.25224683
224209_s_at	GDA	2	-6.311311771
216470_x_at	PRSS1	2	-8.800076312
207178_s_at	FRK	2	-14.45417039
209218_at	SQLE	2	-12.03965179
33322_i_at	SFN	2	-8.375136974
226980_at	DEPDC1B	2	-11.6190751
215425_at	BTG3	2	-10.39096629
201130_s_at	CDH1	2	-9.532662909
208650_s_at	CD24	2	-7.072997702
223233_s_at	CGN	2	-10.96879008
223229_at	UBE2T	2	-14.67574584
226374_at	0	2	-9.831283893
230361_at	HEATR7A	2	-14.2955032
204146_at	RAD51AP1	2	-13.90846761
218960_at	TMPRSS4	2	-8.443939242
203397_s_at	GALNT3	2	-7.671833108
218662_s_at	NCAPG	2	-15.29062588
218039_at	NUSAP1	2	-13.42410317
210058_at	MAPK13	2	-12.28102632
204709_s_at	KIF23	2	-13.21348411
209464_at	AURKB	2	-14.38281738
227372_s_at	BAIAP2L1 /// LOC100128461	2	-9.135384089
217551_at	LOC441453	2	-10.41721994
209008_x_at	KRT8	2	-10.23656053
202826_at	SPINT1	2	-10.92285412
211519_s_at	KIF2C	2	-16.63581323
219450_at	C4orf19	2	-9.22500246
228865_at	C1orf116	2	-8.621071241
204379_s_at	FGFR3	2	-9.320552007
219476_at	C1orf116	2	-6.734194975
204444_at	KIF11	2	-12.55996184
203362_s_at	MAD2L1	2	-14.3239626
211080_s_at	NEK2	2	-13.94404784
218687_s_at	MUC13	2	-6.986362863
214974_x_at	CXCL5	2	-4.254513694
204033_at	TRIP13	2	-13.76048143
219990_at	E2F8	2	-11.58302166
227492_at	0	2	-9.414800137
202934_at	HK2	2	-11.61711171
201839_s_at	EPCAM	2	-6.858260633
222904_s_at	TMC5	2	-7.63715955
206224_at	CST1	2	-5.812598059
202859_x_at	IL8	2	-6.309617355
1554768_a_at	MAD2L1	2	-14.32850944
216905_s_at	ST14	2	-10.07141666
236641_at	KIF14	2	-13.92527347

204318_s_at	GTSE1	2	-14.20904673
213506_at	F2RL1	2	-7.292588335
223307_at	CDCA3	2	-16.28547788
226226_at	TMEM45B	2	-9.252568202
202580_x_at	FOXMI	2	-14.10488106
227452_at	0	2	-10.73032912
211689_s_at	TMPRSS2	2	-7.903180908
222608_s_at	ANLN	2	-11.837817
200862_at	DHCR24	2	-14.09011478
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217901_at	DSG2	2	-8.957842153
204351_at	S100P	2	-5.217518124
209408_at	KIF2C	2	-15.82348286
209498_at	CEACAM1	2	-9.402951798
219010_at	C1orf106	2	-8.302391419
210059_s_at	MAPK13	2	-12.13092549
202833_s_at	SERPINA1	2	-6.356782163
229842_at	ELF3	2	-8.58144992
210827_s_at	ELF3	2	-8.743972264
222958_s_at	DEPDC1	2	-13.40944366
203917_at	CXADR	2	-10.24595675
211506_s_at	IL8	2	-6.462109045
201510_at	ELF3	2	-8.176703128
219263_at	RNF128	2	-6.493320211
229777_at	CLRN3	2	-5.819621199
227475_at	FOXQ1	2	-6.603616002
209270_at	LAMB3	2	-10.65634882
204026_s_at	ZWINT	2	-13.76393918
203755_at	BUB1B	2	-13.63464993
226185_at	CDS1	2	-9.892887396
223484_at	C15orf48	2	-6.78637598
229292_at	EPB41L5	2	-12.97204618
208190_s_at	LSR	2	-11.93117514
230951_at	0	2	-13.67973711
222712_s_at	MUC13	2	-7.344077387
219508_at	GCNT3	2	-6.256724781
215101_s_at	CXCL5	2	-4.77443951
226129_at	FAM83H	2	-11.27304506
205709_s_at	CDS1	2	-10.75364808
210652_s_at	TTC39A	2	-10.54585874
223631_s_at	C19orf33	2	-6.903576533
218009_s_at	PRC1	2	-13.89754659
218677_at	S100A14	2	-8.746990955
218355_at	KIF4A	2	-14.26332344
33323_r_at	SFN	2	-7.742270112
213421_x_at	PRSS3	2	-9.324821173
206239_s_at	SPINK1	2	-4.906417996
209709_s_at	HMMR	2	-13.98091847
211657_at	CEACAM6	2	-5.136756518
227174_at	WDR72	2	-4.77546254

232278_s_at	DEPDC1	2	-13.94646909
202936_s_at	SOX9	2	-9.469228482
202503_s_at	KIAA0101	2	-12.48313209
205506_at	VIL1	2	-8.324558901
225834_at	FAM72A /// FAM72B /// GCUD2	2	-14.1206559
213599_at	OIP5	2	-13.3331623
210467_x_at	MAGEA12	2	-4.773248395
202935_s_at	SOX9	2	-8.823161587
204825_at	MELK	2	-14.62333967
203021_at	SLPI	2	-7.320835632
228956_at	UGT8	2	-7.321636063
205190_at	PLS1	2	-7.45651333
202525_at	PRSS8	2	-9.0366101
226803_at	CHMP4C	2	-9.813031805
1553105_s_at	DSG2	2	-9.152940208
203953_s_at	CLDN3	2	-5.553282002
218963_s_at	KRT23	2	-6.634783169
221648_s_at	0	2	-10.22523054
228033_at	E2F7	2	-14.10367516
239155_at	CXADRP1	2	-11.62105473
210715_s_at	SPINT2	2	-12.72726241
209925_at	OCLN	2	-10.55928184
204855_at	SERPINB5	2	-5.981205224
207165_at	HMMR	2	-12.75356536
202286_s_at	TACSTD2	2	-7.748032112
219127_at	ATAD4	2	-8.121820498
214710_s_at	CCNB1	2	-13.80825402
223949_at	TMPRSS3	2	-7.748899963
1552477_a_at	IRF6	2	-11.55890571
203819_s_at	IGF2BP3	2	-6.976860948
228729_at	CCNB1	2	-13.36083346
208170_s_at	TRIM31	2	-6.914727808
202095_s_at	BIRC5	2	-13.63508784
207463_x_at	PRSS3	2	-9.67969218
220651_s_at	MCM10	2	-13.6813524
219918_s_at	ASPM	2	-12.53574325
204962_s_at	CENPA	2	-13.13829811
201890_at	RRM2	2	-12.60800381
209773_s_at	RRM2	2	-13.10500767
202705_at	CCNB2	2	-14.28030579
219121_s_at	RBM35A	2	-10.26659816
202831_at	GPX2	2	-7.513943122
203968_s_at	CDC6	2	-14.74556093
203820_s_at	IGF2BP3	2	-7.464053928
203757_s_at	CEACAM6	2	-5.104879779
203418_at	CCNA2	2	-15.79869352
218663_at	NCAPG	2	-15.19864927
201884_at	CEACAM5	2	-4.920750981
244056_at	SFTA2	2	-6.78551989
202790_at	CLDN7	2	-11.1792992

1553589_a_at	PDZK1IP1	2	-7.437643344
203213_at	CDC2	2	-13.80807678
201428_at	CLDN4	2	-10.1437062
218542_at	CEP55	2	-12.58763188
228069_at	FAM54A	2	-14.09420064
203214_x_at	CDC2	2	-14.61183816
205597_at	SLC44A4	2	-7.367692948
225645_at	EHF	2	-7.560759385
206102_at	GIN51	2	-15.20943826
225846_at	RBM35A	2	-8.538112851
205828_at	MMP3	2	-6.058896312
218186_at	RAB25	2	-9.500224568
209891_at	SPC25	2	-15.91652732
235165_at	PAR6B	2	-12.54992015
202870_s_at	CDC20	2	-15.90935916
223381_at	NUF2	2	-13.35963214
210559_s_at	CDC2	2	-14.73442643
201131_s_at	CDH1	2	-7.78036641
203691_at	PI3	2	-6.922738768
219630_at	PDZK1IP1	2	-7.497325274
210052_s_at	TPX2	2	-16.14261732
202489_s_at	FXD3	2	-8.870280675
225792_at	HOOK1	2	-13.37342199
204092_s_at	AURKA	2	-16.11440706
201292_at	TOP2A	2	-14.10197164
219148_at	PBK	2	-12.54931729
219795_at	SLC6A14	2	-5.629262568
203764_at	DLGAP5	2	-14.47553579
201291_s_at	TOP2A	2	-13.77858106
41469_at	PI3	2	-7.079220093
203967_at	CDC6	2	-14.82202019
202954_at	UBE2C	2	-15.70472128
208079_s_at	AURKA	2	-15.80061866
204822_at	TTK	2	-13.93197246
224650_at	MAL2	2	-9.217181275
230323_s_at	TMEM45B	2	-8.829344251
206199_at	CEACAM7	2	-6.945654132
204641_at	NEK2	2	-13.19010607
209642_at	BUB1	2	-15.6436849
205476_at	CCL20	2	-7.88131056
227196_at	RHPN2	2	-11.08986419
214612_x_at	MAGEA2 /// MAGEA2B ///	2	-5.311533091
209942_x_at	MAGEA3 /// MAGEA6	2	-5.337269158
201650_at	JUP /// KRT19	2	-9.670354686
212531_at	LCN2	2	-7.603809258
204580_at	MMP12	2	-12.2456953

Figure 19**Invasive subtype vs Metabolic subtype**

probeset	GeneName	Inv1_Meta2	t
204938_s_at	PLN	1	14.09392689
212730_at	SYNM	1	13.80182378
228202_at	PLN	1	13.54517885
225894_at	SYNPO2	1	14.19717891
232298_at	hCG_1806964	1	15.83812021
201496_x_at	MYH11	1	12.59323124
220595_at	PDZRN4	1	16.39555707
202222_s_at	DES	1	11.86779117
222722_at	OGN	1	12.00665659
218730_s_at	OGN	1	13.27565917
204940_at	PLN	1	13.50225721
226303_at	PGM5	1	15.28825371
1556325_at	FILIP1	1	17.76083197
205433_at	BCHE	1	12.71901061
225381_at	LOC399959	1	17.33970616
228133_s_at	MYH11	1	12.98553483
205475_at	SCRG1	1	12.97207847
221276_s_at	SYNC	1	15.29752362
224396_s_at	ASPN	1	15.43157459
233496_s_at	CFL2	1	16.29506959
229649_at	NRXN3	1	13.33598854
235183_at		0	16.77297617
225895_at	SYNPO2	1	11.78908946
236141_at	NBLA00301	1	15.30249842
205357_s_at	AGTR1	1	15.51345588
243278_at	FOXP2	1	16.43774665
228504_at		0	16.7648113
210299_s_at	FHL1	1	12.7661302
244745_at	RERG	1	20.51637938
206201_s_at	MEOX2	1	17.87199538
204939_s_at	PLN	1	12.70951081
223623_at	C2orf40	1	10.85156567
231773_at	ANGPTL1	1	15.53679379
225720_at	SYNPO2	1	12.65386009
201058_s_at	MYL9	1	13.74350339
202992_at	C7	1	12.49635469
209406_at	BAG2	1	14.32723994
228750_at		0	12.55670777
203951_at	CNN1	1	12.98145269
218087_s_at	SORBS1	1	12.65306979
225782_at	MSRB3	1	14.36757515
203766_s_at	LMOD1	1	13.13542066
222877_at		0	16.85155362
230130_at		0	17.18499272
235759_at		0	16.32047278
219772_s_at	SMPX	1	10.10753275
203296_s_at	ATP1A2	1	14.35704531
229461_x_at	NEGR1	1	15.83797586
227827_at		0	9.874048299
202037_s_at	SFRP1	1	11.38140577
202274_at	ACTG2	1	10.8468411
227826_s_at		0	10.21314968

227662_at	SYNPO2	1	11.50846497
201539_s_at	FHL1	1	14.11953437
219791_s_at	NBLA00301	1	13.76240105
225328_at	0	1	16.09725265
225721_at	SYNPO2	1	13.19153022
212554_at	CAP2	1	16.52009514
220955_x_at	RAB23	1	15.75314442
204796_at	EML1	1	17.68073419
212806_at	PRUNE2	1	14.33138507
238533_at	EPHA7	1	12.22808648
227727_at	MRGPRF	1	14.78536521
235503_at	ASB5	1	10.18067332
223235_s_at	SMOC2	1	13.68165843
227061_at	0	1	12.06061029
227529_s_at	AKAP12	1	18.62434004
1570515_a_at	FILIP1	1	14.94308551
210298_x_at	FHL1	1	13.10804266
229504_at	0	1	14.25101421
223122_s_at	SFRP2	1	9.215388356
219685_at	TMEM35	1	15.13025541
204457_s_at	GAS1	1	15.38797911
224663_s_at	CFL2	1	14.45383836
223519_at	ZAK	1	17.16120355
1552309_a_at	NEXN	1	13.66840733
213791_at	PENK	1	9.945201242
224339_s_at	ANGPTL1	1	15.79763761
1554127_s_at	MSRB3	1	17.50035805
226103_at	NEXN	1	14.35188068
212805_at	PRUNE2	1	13.06018825
211276_at	TCEAL2	1	11.44207412
221584_s_at	KCNMA1	1	13.8165812
223475_at	CRISPLD1	1	13.76703542
206070_s_at	EPHA3	1	14.1367241
202363_at	SPOCK1	1	15.94143018
221667_s_at	HSPB8	1	13.88855276
204776_at	THBS4	1	12.48825186
206577_at	VIP	1	9.208780277
209209_s_at	FERMT2	1	16.08781898
229288_at	EPHA7	1	11.95341753
204083_s_at	TPM2	1	14.62244273
202555_s_at	MYLK	1	14.22076953
201617_x_at	CALD1	1	17.70377399
239183_at	ANGPTL1	1	14.80252738
206552_s_at	TAC1	1	9.768157874
1569956_at	MYLK	1	12.46483663
207390_s_at	SMTN	1	13.60978644
213413_at	STON1	1	17.44686219
227758_at	RERG	1	17.70856315
214505_s_at	FHL1	1	12.93742328
209763_at	CHRD1	1	11.01162297
201495_x_at	MYH11	1	12.20930535
209687_at	CXCL12	1	10.18021133
204749_at	NAP1L3	1	19.97413219
227526_at	CDON	1	18.13832247
209613_s_at	ADH1B	1	7.727501195
225790_at	MSRB3	1	16.53337309

225242_s_at	CCDC80	1	11.45218708
202036_s_at	SFRP1	1	11.30455123
237169_at	0	1	11.27976576
201645_at	TNC	1	11.75309572
235201_at	FOXP2	1	15.05110957
228107_at	LOC100127983	1	14.59083837
219778_at	ZFPM2	1	18.92298443
204463_s_at	EDNRA	1	16.58515007
201430_s_at	DPYSL3	1	16.95330615
215306_at	0	1	17.79125912
214724_at	DIXDC1	1	13.78484008
235182_at	ISM1	1	14.22561347
237206_at	MYOCD	1	10.59546946
238592_at	PDLIM3	1	16.44056944
223121_s_at	SFRP2	1	9.83630006
209242_at	PEG3	1	18.64916285
214027_x_at	DES /// FAM48A	1	10.99866577
228827_at	0	1	19.08753221
212865_s_at	COL14A1	1	11.72275283
226237_at	0	1	11.76133189
225662_at	ZAK	1	14.71950005
226834_at	0	1	15.02207998
201431_s_at	DPYSL3	1	15.9787065
225946_at	RASSF8	1	20.5913718
205907_s_at	OMD	1	11.87800697
229530_at	GUCY1A3	1	17.10143492
204464_s_at	EDNRA	1	15.17195641
227705_at	TCEAL7	1	15.99719124
219230_at	TMEM100	1	11.82540806
209210_s_at	FERMT2	1	13.51292587
204364_s_at	REEP1	1	12.68872752
222717_at	SDPR	1	13.80482443
228776_at	GJC1	1	15.99508784
204797_s_at	EML1	1	16.0863
228640_at	PCDH7	1	11.6725122
224352_s_at	CFL2	1	13.51499189
205795_at	NRXN3	1	11.17365185
242447_at	C3orf70	1	12.09043794
202566_s_at	SVIL	1	15.93462597
201616_s_at	CALD1	1	16.81056145
231067_s_at	0	1	17.42819986
212915_at	PDZRN3	1	14.82615361
210875_s_at	ZEB1	1	20.59872522
212992_at	AHNAK2	1	13.84695469
227006_at	PPP1R14A	1	14.05275453
211562_s_at	LMOD1	1	14.24922157
227197_at	SGEF	1	13.75755299
224149_x_at	SLMAP	1	13.00001703
218934_s_at	HSPB7	1	12.22853279
1555229_a_at	C1S	1	13.24234766
219087_at	ASPN	1	12.82007606
225665_at	ZAK	1	15.55740029
204793_at	GPRASP1	1	16.39287974
238481_at	MGP	1	14.02050733
217967_s_at	FAM129A	1	16.62786189
221747_at	TNS1	1	16.19842573

213371_at	LDB3		1	10.79029475
209621_s_at	PDLIM3		1	14.20397658
228885_at	MAMDC2		1	12.75369577
209283_at	CRYAB		1	14.21453217
202995_s_at	FBLN1		1	10.41780155
202920_at	ANK2		1	12.84670658
209170_s_at	GPM6B		1	11.61197199
203881_s_at	DMD		1	13.29305638
222924_at	SLMAP		1	12.60324719
239468_at	MKX		1	15.14675208
209612_s_at	ADH1B		1	7.545907639
204337_at	RGS4		1	14.24489431
226304_at	HSPB6		1	13.05588962
213714_at	CACNB2		1	14.81067383
210170_at	PDLIM3		1	16.73430685
232067_at	C6orf168		1	11.86928482
228507_at		0	1	19.24661289
230595_at	LOC572558		1	13.76616151
205782_at	FGF7		1	14.14106573
213746_s_at	FLNA		1	14.50816959
219654_at	PTPLA		1	10.69826622
213438_at	NFASC		1	14.09095056
201497_x_at	MYH11		1	11.41012427
206898_at	CDH19		1	11.0069586
221207_s_at	NBEA		1	15.65862542
201957_at	PPP1R12B		1	13.53893541
1557961_s_at	LOC100127983		1	15.44148543
226930_at	FNDC1		1	9.318772231
238478_at	BNC2		1	19.32771039
206116_s_at	TPM1		1	14.29144014
229800_at	DCLK1		1	12.80851051
214660_at	PELO		1	17.5626444
227997_at	IL17RD		1	18.36540459
224997_x_at	H19		1	10.42563206
232119_at	SYNPO2		1	13.01325126
212551_at	CAP2		1	14.28962823
225567_at		0	1	14.76558562
238751_at		0	1	9.269175897
221583_s_at	KCNMA1		1	10.69113873
209948_at	KCNMB1		1	11.47208299
224646_x_at	H19		1	8.40733358
204154_at	CDO1		1	13.52926245
204753_s_at	HLF		1	14.87784429
236038_at		0	1	17.93576304
209541_at	IGF1		1	9.661016101
209167_at	GPM6B		1	11.59093775
212764_at	ZEB1		1	15.62122588
225442_at	DDR2		1	15.5641688
1554547_at	FAM13C1		1	14.77749379
1558828_s_at	LOC728264		1	12.77693086
243140_at	ACTA2		1	13.51254915
205330_at	MN1		1	18.68345135
236300_at		0	1	19.99328164
204894_s_at	AOC3		1	13.97604459
227971_at	NRK		1	13.74647499
213994_s_at	SPON1		1	12.76130146

204284_at	PPP1R3C	1	11.50543342
208096_s_at	COL21A1	1	15.69675583
221748_s_at	TNS1	1	13.23564424
203065_s_at	CAV1	1	12.20474016
224823_at	MYLK	1	12.98267384
205399_at	DCLK1	1	15.21752924
205908_s_at	OMD	1	12.24605977
229024_at	0	1	17.37627365
204051_s_at	SFRP4	1	8.407007797
227561_at	DDR2	1	16.43762279
202291_s_at	MGP	1	11.86132559
212233_at	MAP1B	1	14.04520161
204030_s_at	SCHIP1	1	15.45449381
217966_s_at	FAM129A	1	15.96275381
209243_s_at	PEG3 /// ZIM2	1	15.87774586
213993_at	SPON1	1	14.17830014
241789_at	0	1	17.80185344
225481_at	FRMD6	1	15.08126805
202437_s_at	CYP1B1	1	10.33568744
1555724_s_at	TAGLN	1	11.84967366
205528_s_at	RUNX1T1	1	18.52632824
238613_at	ZAK	1	14.57168259
203698_s_at	FRZB	1	13.97599109
204719_at	ABCA8	1	8.629082683
1560359_at	PELO	1	14.90291984
205498_at	GHR	1	11.3544687
209540_at	IGF1	1	9.525926587
213306_at	MPDZ	1	18.95421419
202565_s_at	SVIL	1	14.31600466
204359_at	FLRT2	1	12.22069682
214761_at	ZNF423	1	16.47206254
1552848_a_at	PTCHD1	1	9.773959447
221942_s_at	GUCY1A3	1	15.04338214
201843_s_at	EFEMP1	1	10.78090744
235489_at	RHOJ	1	14.97384719
205529_s_at	RUNX1T1	1	16.1191639
201615_x_at	CALD1	1	14.59390521
222288_at	0	1	12.47829219
235004_at	RBM24	1	13.73568205
210198_s_at	PLP1	1	9.740396489
229802_at	0	1	13.51843892
239349_at	C1QTNF7	1	12.67585407
204052_s_at	SFRP4	1	8.144919215
243864_at	CCDC80	1	14.56109927
208131_s_at	PTGIS	1	12.6721798
226824_at	CPXM2	1	14.94002635
213974_at	ADAMTSL3	1	15.58711481
209897_s_at	SLIT2	1	15.4433758
230730_at	SGCD	1	16.32008035
225968_at	PRICKLE2	1	16.14894099
238455_at	0	1	16.72859887
235570_at	0	1	15.25799761
201559_s_at	CLIC4	1	16.51872714
210517_s_at	AKAP12	1	13.68059979
205547_s_at	TAGLN	1	11.308504
226545_at	CD109	1	14.6326485

227070_at	GLT8D2	1	14.17791485
231098_at	0	1	12.69329738
218468_s_at	GREM1	1	8.178779126
221019_s_at	COLEC12	1	12.85382673
209427_at	SMTN	1	13.27059536
225996_at	LONRF2	1	13.35586109
228406_at	SMYD1	1	8.517261751
238919_at	0	1	11.22275464
203688_at	PKD2	1	16.74944537
223463_at	RAB23	1	13.84246836
204688_at	SGCE	1	15.36088696
225685_at	0	1	13.65176256
212758_s_at	ZEB1	1	15.75914539
209288_s_at	CDC42EP3	1	14.13279115
228850_s_at	0	1	18.15791677
209286_at	CDC42EP3	1	13.63572387
206638_at	HTR2B	1	10.50123263
244108_at	SYNPO2	1	11.58336558
214212_x_at	FERMT2	1	15.59841786
204557_s_at	DZIP1	1	18.24569256
214752_x_at	FLNA	1	14.91874462
204834_at	FGL2	1	13.09419979
238441_at	PRKAA2	1	10.93479455
215440_s_at	BEX4	1	14.00687674
227236_at	TSPAN2	1	12.21760808
228224_at	PRELP	1	14.4000193
238906_s_at	RHOJ	1	16.35337382
202035_s_at	SFRP1	1	10.0664067
230179_at	LOC285812	1	16.25671276
204069_at	MEIS1	1	15.51764594
201540_at	FHL1	1	10.10908656
243357_at	NEGR1	1	15.2848
235000_at	0	1	14.6853557
227235_at	GUCY1A3	1	14.74578968
221618_s_at	LOC728198 /// TAF9B	1	17.78288378
218656_s_at	LHFP	1	13.74960199
223468_s_at	RGMA	1	13.26833409
229339_at	0	1	11.19739091
225801_at	0	1	13.30322841
227530_at	AKAP12	1	15.82766508
235518_at	SLC8A1	1	15.34045732
214767_s_at	HSPB6	1	12.31132374
204422_s_at	FGF2	1	16.34947877
222043_at	CLU	1	10.13337617
229994_at	LOC100190890	1	17.99843556
205226_at	PDGFRL	1	12.93317762
211737_x_at	PTN	1	13.94521569
228728_at	C7orf58	1	12.75412465
200859_x_at	FLNA	1	14.54385789
225345_s_at	0	1	12.66725101
227084_at	DTNA	1	11.36814361
213068_at	DPT	1	7.1435751
228802_at	RBPM52	1	12.02579028
220979_s_at	ST6GALNAC5	1	12.08155977
210221_at	CHRNA3	1	9.506072233
238447_at	RBMS3	1	12.71355574

205803_s_at	TRPC1	1	21.72548964
227088_at	PDE5A	1	15.48071594
208790_s_at	PTRF	1	15.50615812
218711_s_at	SDPR	1	15.12125832
225688_s_at	PHLDB2	1	12.17442419
228080_at	LAYN	1	16.2343511
235371_at	GLT8D4	1	11.96857641
213904_at	0	1	12.43894703
228228_at	DACT3	1	14.34608347
211538_s_at	HSPA2	1	11.747771
235723_at	BNC2	1	21.88278487
242245_at	0	1	12.40790444
226338_at	TMEM55A	1	18.34088072
209894_at	LEPR	1	9.503500197
1553102_a_at	CCDC69	1	12.46039381
229975_at	BMPR1B	1	9.245114821
204963_at	SSPN	1	17.36460294
225524_at	ANTXR2	1	16.13238012
229127_at	JAM2	1	13.63181498
218694_at	ARMCX1	1	15.14861365
203980_at	FABP4	1	6.145497015
205422_s_at	ITGBL1	1	8.504653821
200930_s_at	VCL	1	11.2636472
223987_at	CHRD12	1	8.542663739
226769_at	FIBIN	1	14.23096008
230722_at	BNC2	1	17.83459639
228854_at	0	1	9.426537896
227478_at	SETBP1	1	14.31946021
226084_at	MAP1B	1	14.19130568
204955_at	SRPX	1	9.252245255
209469_at	GPM6A	1	10.00811232
218162_at	OLFML3	1	13.98484139
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212636_at	QKI	1	16.40852337
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204754_at	HLF	1	12.53986437
226885_at	0	1	16.8352767
239708_at	0	1	13.17298525
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226677_at	ZNF521	1	12.18732086
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231726_at	PCDHB14		1	16.1455981
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226439_s_at	NBEA	1	13.42430475
205934_at	PLCL1	1	17.59856161
1558019_at	0	1	12.85695386
1553113_s_at	CDK8	1	10.26772976
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235631_at	DDR2	1	17.60792745
227326_at	MXRA7	1	16.3991896
229302_at	TMEM178	1	13.35198402
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221900_at	COL8A2	1	15.00491463
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211564_s_at	PDLIM4	1	13.08610698
222918_at	RAB9B	1	11.2612363
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209047_at	AQP1	1	11.57984185
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228218_at	0	1	12.10224182
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203706_s_at	FZD7	1	11.7786508
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232125_at		0	1
226142_at	GLIPR1	1	16.35576393
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235649_at	ADAMTS8	1	10.08178075
213364_s_at	SNX1	1	18.2889646
207808_s_at	PROS1	1	12.17291471
206710_s_at	EPB41L3	1	10.63277991

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213844_at	HXA5	1	12.62354052
222455_s_at	PARVA	1	14.33121883
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226591_at	SNRPN	1	11.54695186
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231384_at	GRIN2A	1	9.851189859
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204451_at	FZD1	1	12.31202853
242358_at	0	1	15.51515247
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213765_at	MFAP5	1	5.594444046
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213764_s_at	MFAP5	1	5.632267455
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205898_at	CX3CR1	1	8.349312258
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212099_at	RHOB	1	11.10054744
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231866_at	LNPEP	1	12.92046176
223614_at	MMP16	1	13.05714024
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228863_at	PCDH17	1	9.375418682
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229014_at	FLJ42709	1	15.79984172
229092_at	NR2F2	1	12.44841706
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235979_at	C7	1	7.560029518

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233543_s_at	FAM175A	1	13.59045076
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242137_at	0	1	13.81103197
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221039_s_at	ASAP1	1	14.23556868
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219829_at	ITGB1BP2	1	10.24842881
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235311_at	FKBP14	1	16.16397181
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222426_at	MAPKAP1	1	10.76870923
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220088_at	CSAR1	1	7.237942882
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242828_at	FIGN	1	10.15124438
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212535_at	MEF2A	1	12.8558278
226186_at	0	1	11.79701507
223041_at	CD99L2	1	16.72730505
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227107_at	0	1	12.80197496
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230744_at	0	1	11.82865493
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231842_at	KIAA1462	1	13.17194356
229067_at	SRGAP2P1	1	10.25908678
226694_at	AKAP2 /// PALM2 /// PALM2-AKAP2	1	10.71597279
203254_s_at	TLN1	1	12.77194971
209648_x_at	SOC5	1	12.78291409
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219979_s_at	C11orf73	1	11.71026041
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229613_at	0	1	8.912933341
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225921_at	NIN	1	12.32485764
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227860_at	CPXM1	1	5.671838809
205265_s_at	SPEG	1	9.73511567
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214632_at	NRP2	1	12.07379972
219935_at	ADAMTS5	1	6.679834956

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233825_s_at	CD99L2	1	16.34603826
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244008_at	0	1	11.5942909
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222433_at	ENAH	1	8.944090583
228399_at	OSR1	1	7.030091316
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226818_at	MPEG1	1	7.28275498
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226982_at	ELL2	1	6.871326633
210829_s_at	SSBP2	1	12.88581579
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1552789_at	SEC62	1	11.37062591
229130_at	LOC285535	1	12.99639947
219767_s_at	CRYZL1	1	11.93325576
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235210_s_at	C8orf84	1	4.609106807
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212706_at	LOC100132214 /// LOC100133005 /// LOC100134722 /// RASA4	1	8.820245171
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224995_at	SPIRE1	1	10.89496393
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229623_at	FLJ12993	1	8.400383354
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227550_at	LOC143381	1	9.402837808
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230351_at	LOC283481	1	10.18802767
225735_at	ANKRD50	1	12.59643069
1555756_a_at	CLEC7A	1	7.328236027
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209355_s_at	PPAP2B	1	8.042687465
212670_at	ELN	1	8.405830308
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224605_at	C4orf3	1	13.85452443
240214_at	0	1	13.16622389
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211379_x_at	B3GALNT1	1	7.744043946
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222772_at	MYEF2	1	9.130365273
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215813_s_at	PTGS1	1	6.149104773
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226615_at	XPR1	1	13.30430906
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228788_at	YPEL1	1	12.05759808
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229464_at	MYEF2	1	6.987245332
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221898_at	PDPN	1	6.766920915
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244294_at		0	9.801301809
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213218_at	ZNF187	1	11.89290413
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205381_at	LRRC17	1	5.012476654
235767_x_at	0	1	9.530501376
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227339_at	RGMB	1	7.766641667
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235443_at	LOC100131067	1	12.76545836
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235956_at	KIAA1377	1	8.807661596
224311_s_at	CAB39	1	8.792289711

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235976_at	SLITRK6		1	5.321401335
221858_at	TBC1D12		1	11.26497758
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231789_at	PCDHB15		1	12.43555685
225313_at	C20orf177		1	8.707810922
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229512_at	FAM120C		1	11.77405987
222605_at	RCOR3		1	8.5126139
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228916_at	CWF19L2		1	9.971398282
216033_s_at	FYN		1	8.10791203
219743_at	HEY2		1	8.104977488
241370_at	LOC286052		1	8.180701057
228771_at	ADRBK2		1	7.40424681
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225953_at	RPRD1A		1	8.326009514
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241689_at		0	1	11.56971067
232591_s_at	TMEM30A		1	7.480587358
231292_at	EID3		1	10.47251313
238794_at	C10orf78		1	7.710687459
213376_at	ZBTB1		1	10.28853554
226164_x_at	RIMKLB		1	8.560439767
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224602_at	C4orf3		1	11.69192366
241780_at		0	1	10.09530724
239888_at		0	1	11.480555
227780_s_at	ECSM2		1	7.141672369
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222273_at	PAPOLG		1	11.04023996
228280_at	ZC3HAV1L		1	10.09679721
231907_at	ABL2		1	7.450162221
204159_at	CDKN2C		1	7.783202551
212538_at	DOCK9		1	10.18989805
202056_at	KPNA1		1	11.85684774
214736_s_at	ADD1		1	13.45653545
218870_at	ARHGAP15		1	6.342439218
226122_at	PLEKHG1		1	7.33599497
212223_at	IDS		1	9.428171049
227836_at		0	1	9.090591829
238115_at		0	1	11.20626574
1556389_at	CNPY3		1	9.700222102
214336_s_at	COPA		1	8.059104797
200755_s_at	CALU		1	10.31587506

204173_at	MYL6B	1	10.82335754
203032_s_at	FH	1	7.189019777
226542_at	0	1	9.473988007
212328_at	LIMCH1	1	5.644926695
1553108_at	C5orf24	1	11.35422316
213327_s_at	USP12	1	8.965594942
217886_at	EPS15	1	11.13139098
1552754_a_at	CADM2	1	5.566961956
208055_s_at	HERC4	1	10.01543343
243225_at	LOC283481	1	8.1972596
241342_at	TMEM65	1	6.912826546
218311_at	MAP4K3	1	6.583070124
235390_at	SFRS12IP1	1	9.457542585
232164_s_at	EPPK1	1	4.462195317
223316_at	CCDC3	1	7.628910672
234994_at	TMEM200A	1	4.029290611
238700_at	0	1	10.14871147
1567107_s_at	TPM4	1	7.624743471
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212294_at	GNG12	1	9.301885822
221260_s_at	CSRNP2	1	14.12645799
208776_at	PSMD11	1	12.73295178
213304_at	FAM179B	1	10.14113691
215836_s_at	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	1	9.346457506
201963_at	ACSL1	1	5.092917514
216831_s_at	RUNX1T1	1	8.313592336
212481_s_at	TPM4	1	9.513010974
230265_at	SEL1L	1	7.973625386
214895_s_at	ADAM10	1	7.232066104
222624_s_at	ZNF639	1	9.820013425
204984_at	GPC4	1	7.200181954
229393_at	L3MBTL3	1	11.94744991
1560271_at	0	1	9.935144111
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227191_at	0	1	9.829303511
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223271_s_at	CTDSPL2	1	11.30441306
236035_at	0	1	11.17981608
1558378_a_at	AHNAK2	1	4.584485562
202749_at	WRB	1	9.602516575
228386_s_at	DDX59	1	13.39637171
226109_at	C21orf91	1	9.179238861
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232327_at	THSD7B	1	7.120793487
233849_s_at	ARHGAP5	1	6.674317038

225926_at	VTI1B	1	8.159706201
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227249_at	NDE1	1	7.862518595
212244_at	GCOM1 /// GRINL1A	1	14.90816283
229342_at	0	1	11.57186532
218935_at	EHD3	1	9.530151597
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210449_x_at	MAPK14	1	10.80996561
213033_s_at	NFIB	1	9.35772825
214829_at	AASS	1	7.317630855
1552344_s_at	CNOT7	1	8.527661897
210084_x_at	TPSAB1	1	4.184274428
221104_s_at	NIPSNAP3B	1	7.378687789
230508_at	DKK3	1	10.02540254
209362_at	MED21	1	9.098202367
1555106_a_at	CTDSPL2	1	10.62345008
202293_at	STAG1	1	11.44093891
206067_s_at	WT1	1	3.635347513
226458_at	0	1	8.434190124
224844_at	SLAIN2	1	9.438778563
226464_at	C3orf58	1	10.99078706
226889_at	WDR35	1	12.06015065
226747_at	TXNDC16	1	7.800651204
227004_at	0	1	7.251094588
214279_s_at	NDRG2	1	7.452848737
225572_at	CREB1	1	13.35336352
205917_at	ZNF264	1	9.123314272
226532_at	0	1	7.19959904
203700_s_at	DIO2	1	4.01515941
225971_at	DDHD1	1	11.72787026
1552733_at	KLHDC1	1	9.601447775
207719_x_at	CEP170	1	10.79157589
230679_at	WDR32	1	12.74727114
226408_at	TEAD2	1	10.2811287
225086_at	FAM98B	1	10.95566149
1563498_s_at	SLC25A45	1	11.76163692
221047_s_at	MARK1	1	8.657664158
225167_at	FRMD4A	1	8.162004917
216894_x_at	CDKN1C	1	7.716319088
209662_at	CETN3	1	8.845793555
239952_at	ZEB1	1	11.56753279
226071_at	ADAMTSL4	1	6.458470263
226347_at	0	1	11.06430088
212650_at	EHBP1	1	7.135872177
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227978_s_at	ZADH2	1	8.335780293
202250_s_at	WDR42A	1	8.990468481
205440_s_at	NPY1R	1	4.655280957
210004_at	OLR1	1	4.731076743
213173_at	PCNX	1	15.1931651
235803_at	0	1	8.297487277
211892_s_at	PTGIS	1	7.104382025
205084_at	BCAP29	1	10.66554425
238937_at	ZNF420	1	8.815751822

213725_x_at	XYLT1		1	6.785649277
229803_s_at		0	1	13.26364768
213447_at	IPW		1	8.829405528
205063_at	SIP1		1	8.506970082
231955_s_at	HIBADH		1	7.219530691
201798_s_at	MYOF		1	8.577393888
224791_at	ASAP1		1	9.988294967
229281_at	NPAS3		1	8.729159648
241763_s_at	FBXO32		1	9.036778503
221763_at	JMJD1C		1	9.45397238
226093_at	DCP1B		1	10.70858755
209721_s_at	IFFO1		1	15.97718555
239548_at	NEGR1		1	8.729335572
1554414_a_at	OSGIN2		1	10.52415698
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1552790_a_at	SEC62		1	7.368779258
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204863_s_at	IL6ST		1	8.771196331
204358_s_at	FLRT2		1	7.925539489
209236_at	SLC23A2		1	11.07915056
208748_s_at	FLOT1		1	10.78337846
238990_x_at	TRIM61		1	10.60671718
225159_s_at		0	1	10.36363037
224724_at	SULF2		1	7.025310277
225585_at	RAP2A		1	10.63628788
222654_at	IMPAD1		1	7.604714115
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206715_at	TFEC		1	5.106171407
244040_at		0	1	6.34214767
223341_s_at	SCOC		1	6.391770378
225579_at	PQLC3		1	8.666590483
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210872_x_at	GAS7		1	11.16438783
210465_s_at	SNAPC3		1	12.36206879
227169_at	DNAJC18		1	11.1415492
229297_at		0	1	12.38435595
230389_at	FNBP1		1	7.981609295
237094_at	FAM19A5		1	7.584384155
222698_s_at	IMPACT		1	7.179131347
222557_at	STMN3		1	6.833481977
240467_at		0	1	10.96722638
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1553055_a_at	SLFN5		1	9.178169042
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238551_at	FUT11		1	11.59444162
229734_at	LOC283174		1	6.128753591
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218839_at	HEY1		1	8.853776763
1554479_a_at	CARD8		1	8.160984086
225342_at	AK3L1 /// AK3L2		1	4.914092427

214196_s_at	TPP1	1	11.29633329
217047_s_at	FAM13A1	1	6.624126555
222656_at	UBE2W	1	12.56843029
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235179_at	ZNF641	1	12.89128473
209321_s_at	ADCY3	1	7.991353987
206978_at	CCR2 /// FLJ78302	1	5.937711263
212967_x_at	NAP1L1	1	11.51006449
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226251_at	ASXL2	1	13.31644117
231152_at	INO80D	1	9.294724672
239154_at	0	1	8.879538867
229704_at	0	1	6.751379064
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218166_s_at	RSF1	1	9.036899975
1569150_x_at	PDLIM7	1	8.377545665
225677_at	BCAP29	1	11.91098576
213317_at	CLIC5	1	4.323586605
219151_s_at	RABL2A /// RABL2B	1	11.55846211
205854_at	TULP3	1	12.01428977
203883_s_at	RAB11FIP2	1	6.148789609
1562139_a_at	FOXP2	1	7.592364125
224820_at	FAM36A	1	8.383003999
209741_x_at	SCAPER	1	10.95414584
235394_at	PLAA	1	10.34986417
217788_s_at	GALNT2	1	11.13213728
32541_at	PPP3CC	1	10.14393687
224314_s_at	EGLN1	1	10.22394756
207978_s_at	NR4A3	1	4.50598926
229430_at	C8orf46	1	5.864400069
226056_at	CDGAP	1	10.44400168
214045_at	LIAS	1	8.121080794
207749_s_at	PPP2R3A	1	7.337049352
235918_x_at	CEP97	1	8.890022655
242172_at	MEIS1	1	9.316658667
219137_s_at	MFF	1	8.537891833
236656_s_at	LOC100130506	1	8.440176897
210756_s_at	NOTCH2	1	13.76432972
210479_s_at	RORA	1	7.70451164
205006_s_at	NMT2	1	7.649604793
226447_at	ASH1L	1	9.833785765
213186_at	DZIP3	1	8.26417768
207231_at	DZIP3	1	10.06230412
224397_s_at	TMTTC1	1	9.355087876
223349_s_at	BOK	1	8.590567456
217863_at	PIAS1	1	10.7148424
240557_at	0	1	11.06477775
210145_at	PLA2G4A	1	5.792557745
229285_at	RNASEL	1	6.85417866
226821_at	0	1	10.29514108
204528_s_at	NAP1L1	1	11.57965889
222850_s_at	DNAJB14	1	8.593983623

225469_at	LYRM5		1	6.157315461
223380_s_at	LATS2		1	9.222294808
210260_s_at	TNFAIP8		1	6.945910904
227630_at		0	1	8.821713203
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211998_at	H3F3A /// H3F3B /// LOC440926		1	8.777395447
233233_at		0	1	8.161473653
203989_x_at	F2R		1	6.09064859
227976_at	LOC644538		1	11.33379259
227697_at	SOCS3		1	4.289686233
213269_at	ZNF248		1	10.53976266
201153_s_at	MBNL1		1	14.40152915
212299_at	NEK9		1	15.57639986
225892_at	IREB2		1	8.476928813
207864_at	SCN7A		1	7.072953364
221596_s_at	C7orf64		1	6.755011827
237968_at	ATL2		1	8.204678777
208982_at	PECAM1		1	5.801662815
224984_at	NFAT5		1	11.05089227
224600_at	CGGBP1		1	11.46887198
212364_at	MYO1B		1	6.770555862
212877_at	KLC1		1	11.18019156
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223181_at	C18orf55		1	9.4044559
201370_s_at	CUL3		1	8.115589109
225267_at	KPNA4		1	12.42718206
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239533_at	GPR155		1	4.068683874
224778_s_at		0	1	13.48370748
203683_s_at	VEGFB		1	9.748621084
1557950_at	SDCCAG1		1	10.57161736
235893_at		0	1	11.74551729
202744_at	SLC20A2		1	10.74428135
211084_x_at	PRKD3		1	13.00970699
230538_at	SHC4		1	8.148860925
202393_s_at	KLF10		1	9.062317974
201988_s_at	CREBL2		1	11.3722307
202973_x_at	FAM13A1		1	6.146381657
219279_at	DOCK10		1	6.74027079
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217858_s_at	ARMCX3		1	6.644218082
210892_s_at	GTF2I		1	8.43064639
209920_at	BMPR2		1	12.40336146
206742_at	FIGF		1	3.604965128
232935_at		0	1	6.464520442
1558700_s_at	ZNF260		1	7.746934994
212853_at	DCUN1D4		1	10.86201988
220005_at	P2RY13		1	6.619255901
212514_x_at	DDX3X		1	8.649668803
210257_x_at	CUL4B		1	11.47530058
202351_at	ITGAV		1	10.33072644
239024_at	ZNF148		1	12.66830411
201163_s_at	IGFBP7		1	9.868480892
206098_at	ZBTB6		1	9.165913368
222623_s_at	ZNF639		1	11.3238686

223418_x_at	ANKRD13C	1	7.990787861
227242_s_at	EBF3	1	7.412100424
223093_at	ANKH	1	7.778506041
230258_at	GLIS3	1	6.358601803
207079_s_at	MED6	1	8.361099741
205097_at	SLC26A2	1	6.452748864
207134_x_at	TPSB2	1	4.032734445
210895_s_at	CD86	1	5.632357412
222844_s_at	SRR	1	10.32322658
1553960_at	SNX21	1	10.58905187
228791_at	LOC100129502	1	13.02121128
213817_at	IRAK3	1	4.67282546
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224883_at	PLDN	1	10.49450359
238468_at	TNRC6B	1	9.227724334
204645_at	CCNT2	1	7.910368563
213694_at	RSBN1	1	10.28852731
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213698_at	LOC100130633 /// ZMYM6	1	8.151521466
219400_at	CNTNAP1	1	8.474804668
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222201_s_at	CASP8AP2	1	9.043672527
200835_s_at	MAP4	1	9.58442351
226000_at	CTTNBP2NL	1	11.31510573
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228725_x_at	PRMT2	1	12.04914518
238907_at	0	1	11.86770486
229119_s_at	ZSWIM7	1	7.167726643
219239_s_at	ZNF654	1	8.514935219
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230319_at	0	1	4.315937345
202165_at	PPP1R2	1	10.94552027
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226910_at	0	1	12.16562973
225928_at	VTI1B	1	9.672038522
212970_at	APBB2	1	10.8545397
230298_at	LOC153364	1	11.87643585
1555889_a_at	CRTAP	1	10.91846914
201044_x_at	DUSP1	1	5.372242032
208456_s_at	RRAS2	1	6.644456256
242943_at	ST8SIA4	1	6.605266313
221127_s_at	RIG	1	11.28916542
220330_s_at	SAMSN1	1	5.104955309
202362_at	RAP1A	1	8.354961724
219576_at	MAP7D3	1	9.639501837
204589_at	NUAK1	1	8.073580567
212402_at	ZC3H13	1	11.21251057
211965_at	ZFP36L1	1	5.66541776
233020_at	0	1	8.612079973
204249_s_at	LMO2	1	6.842612328
228471_at	0	1	6.19832994
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229371_at	0	1	10.35210104
203408_s_at	SATB1	1	7.217582336
228233_at	FREM1	1	7.974408563
225785_at	REEP3	1	9.289270112
211592_s_at	CACNA1C	1	7.81308527
238026_at	RPL35A	1	10.93632439
228240_at	0	1	8.833017194
234985_at	LDLRAD3	1	8.912872026
230643_at	WNT9A	1	10.39714327
242845_at	0	1	10.73092803
229090_at	LOC220930	1	9.863161035
227095_at	0	1	7.683758031
227843_at	NDE1	1	5.416455573
203424_s_at	IGFBP5	1	5.471610127
202116_at	DPF2	1	12.71016474
225231_at	CBL	1	13.10121606
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212586_at	CAST	1	10.75823188

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200799_at	HSPA1A /// HSPA1B	1	6.531197239
234998_at	0	1	5.761922017
PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5			
205717_x_at		1	8.289898267
212205_at	H2AFV	1	11.69072711
227567_at	AMZ2	1	7.99165481
202228_s_at	NPTN	1	9.764888058
212567_s_at	MAP4	1	12.99648633
1555609_a_at	ZMAT3	1	9.452545106
227489_at	SMURF2	1	12.73921227
227031_at	SNX13	1	6.931041741
209006_s_at	C1orf63	1	5.964570032
1552417_a_at	NEDD1	1	10.65093025
242605_at	0	1	8.539574589
1567214_a_at	PNN	1	8.638739303
226829_at	AFAP1L2	1	7.818989348
204489_s_at	CD44	1	6.875602472
203420_at	FAM8A1	1	9.499686459
212775_at	OBSL1	1	6.034356787
201580_s_at	TXNDC13	1	8.138654245
231991_at	C20orf160	1	8.29898984
228415_at	AP1S2	1	5.568121481
204513_s_at	ELMO1	1	8.801087938
227188_at	C21orf63	1	6.306931241
218395_at	ACTR6	1	10.01571662
232087_at	CXorf23	1	7.3994306
202988_s_at	RGS1	1	3.86454413
1554167_a_at	GOLGA7	1	10.81395791

226837_at	SPRED1	1	5.817566169
211255_x_at	DEDD	1	11.15168649
223024_at	AP1M1	1	12.98511738
226429_at	KIAA1704	1	8.583590122
1558512_at	0	1	10.10831269
224641_at	FYTTD1	1	10.99657394
44783_s_at	HEY1	1	7.000744175
230815_at	LOC389765	1	9.200825018
240041_at	PTCHD1	1	6.53309947
225763_at	RCSD1	1	5.188026487
224728_at	ATPAF1	1	7.052110169
213882_at	TM2D1	1	8.984686204
225399_at	TSEN15	1	8.550011362
212017_at	FAM168B	1	11.29862623
212579_at	SMCHD1	1	7.873193087
209901_x_at	AIF1	1	7.055026256
236369_at	0	1	11.42796669
204334_at	KLF7	1	9.758448974
206113_s_at	RAB5A	1	9.39460627
219497_s_at	BCL11A	1	4.418220267
207001_x_at	TSC22D3	1	7.264020983
234915_s_at	DENR	1	8.58561182
208092_s_at	FAM49A	1	8.540583339
202877_s_at	CD93	1	6.13333149
218970_s_at	CUTC	1	7.883992564
212499_s_at	FCF1 /// MAPK1IP1L	1	8.070007317
1557227_s_at	TPR	1	7.683287076
217902_s_at	HERC2	1	9.70785389
225229_at	AFF4	1	8.461146627
226990_at	CAPRIN1	1	8.641719611
242006_at	LCA5	1	13.4448075
204314_s_at	CREB1	1	10.74600015
231725_at	PGDHB2	1	7.279340278
1569149_at	PDLIM7	1	7.724170895
216866_s_at	COL14A1	1	7.556179704
202259_s_at	N4BP2L2	1	6.916766057
208667_s_at	ST13	1	10.37195593
203356_at	CAPN7	1	9.247243624
222662_at	PPP1R3B	1	6.435094387
202305_s_at	FEZ2	1	9.763102359
228606_at	TCTEX1D2 /// TM4SF19	1	8.622159121
225643_at	MAPK1IP1L	1	9.62117536
224908_s_at	TTL	1	12.0937802
210561_s_at	WSB1	1	8.401573409
225279_s_at	C3orf17	1	10.49321987
230502_s_at	LOC149832	1	10.62466071
224831_at	CPEB4	1	6.16940729
1563321_s_at	MLLT10	1	7.448421497
223046_at	EGLN1	1	9.459126738
200770_s_at	LAMC1	1	8.783959448
202646_s_at	CSDE1	1	10.05785457
213294_at	EIF2AK2	1	9.276324875
213312_at	C6orf162	1	8.220509589
212912_at	RPS6KA2	1	6.207443149
226049_at	ERC1	1	13.96470279
1554241_at	COCH	1	7.304229123

235103_at	MAN2A1	1	6.144201446
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227179_at	STAU2	1	9.986760182
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226976_at	KPNA6	1	10.68299697
206958_s_at	UPF3A	1	8.508307825
203186_s_at	S100A4	1	5.703425828
221139_s_at	CSAD	1	7.211247001
219229_at	SLCO3A1	1	7.841983534
231969_at	STOX2	1	5.518010603
203497_at	MED1	1	8.454940715
202034_x_at	RB1CC1	1	14.03873438
238007_at	ZNF271	1	9.288731921
223557_s_at	TMEFF2	1	6.310346024
212585_at	OSBPL8	1	9.621331614
225147_at	CYTH3	1	10.1889192
235207_at	0	1	7.205274265
223652_at	AS3MT	1	8.317649562
212253_x_at	DST	1	8.760333338
228785_at	ZNF281	1	8.038260534
213872_at	0	1	5.886657489
226085_at	CBX5	1	7.913155735
222562_s_at	TNKS2	1	9.403212652
225811_at	0	1	8.213028846
221014_s_at	RAB33B	1	7.993607396
226436_at	RASSF4	1	7.261541421
238013_at	PLEKHA2	1	7.155615292
244313_at	CR1	1	3.95177666
37433_at	PIAS2	1	11.58546971
213019_at	RANBP6	1	8.384375269
225526_at	MKLN1	1	9.50547461
226040_at	0	1	10.37122833
1553994_at	NT5E	1	6.901493645
230821_at	ZNF148	1	9.759008499
244704_at	NFYB	1	11.68314204
204851_s_at	DCX	1	5.30208342
225923_at	0	1	8.918287538
220173_at	C14orf45	1	10.24871554
224919_at	MRPS6	1	9.520928056
207724_s_at	SPAST	1	7.626545682
228968_at	ZNF449	1	8.734690679
226627_at	SEPT8	1	8.700162026
227166_at	DNAJC18	1	11.15756588
208965_s_at	IFI16	1	6.502826748
213623_at	KIF3A	1	9.763639119
207233_s_at	MITF	1	8.382229212
216620_s_at	ARHGEF10	1	10.55382631
203319_s_at	ZNF148	1	9.702782885
222116_s_at	TBC1D16	1	8.712887659
230183_at	EXT1	1	9.574921055
208740_at	SAP18	1	8.363277366
200810_s_at	CIRBP	1	8.836310018
219467_at	GIN1	1	9.200716736
219221_at	ZBTB38	1	9.034776417
229689_s_at	0	1	8.687114448
203531_at	CUL5	1	8.968173324

218626_at	EIF4ENIF1	1	11.38205374
227889_at	LPCAT2	1	5.356242386
227846_at	GPR176	1	8.443166617
235996_at	RASSF8	1	9.530367193
212917_x_at	RECQL	1	9.595647371
222574_s_at	DHX40	1	11.92293006
201466_s_at	JUN	1	5.226288628
212271_at	MAPK1	1	7.867336464
230158_at	DPY19L2	1	9.427566209
203538_at	CAMLG	1	11.10300328
228306_at	CNIH4	1	10.8528524
202467_s_at	COPS2	1	11.93930358
230893_at	DNAJC21	1	7.109135732
1554918_a_at	ABCC4	1	8.030892624
218450_at	HEBP1	1	7.326039131
201236_s_at	BTG2	1	6.303434168
205786_s_at	ITGAM	1	7.117608973
224368_s_at	NDRG3	1	8.865951242
1554341_a_at	HEL308	1	11.29192948
235331_x_at	PCGF5	1	6.816827155
223125_s_at	C1orf21	1	7.434347331
211772_x_at	CHRNA3	1	6.556933345
1565577_s_at		0	10.56928284
230063_at	ZNF264	1	10.60709343
218032_at	SNN	1	8.268452255
206826_at	PMP2	1	4.863636773
200796_s_at	MCL1	1	4.906672359
208990_s_at	HNRNPH3	1	10.65028686
212480_at	CYTA	1	13.50438155
226399_at		0	7.45177925
229699_at	LOC100129550	1	10.0233978
217722_s_at	NGRN	1	9.879071504
238963_at		0	6.968171578
228941_at	ALG10B	1	7.628909129
232156_at		0	9.348792338
216125_s_at	RANBP9	1	12.45752757
212184_s_at	MAP3K7IP2	1	9.18384659
1560296_at		0	8.483648644
222839_s_at	PAPOLG	1	10.21882442
242648_at	KLHL8	1	7.317898419
236383_at		0	4.712623085
208290_s_at	EIF5	1	8.054786589
226094_at	PIK3C2A	1	8.704009638
1555349_a_at	ITGB2	1	5.381505463
208964_s_at	FADS1	1	6.723248857
214452_at	BCAT1	1	5.615780029
243948_at		0	9.96940733
201578_at	PODXL	1	7.01925516
201485_s_at	RCN2	1	10.12384205
221510_s_at	GLS	1	7.760655515
225838_at	EPC2	1	11.3307636
202011_at	TJP1	1	9.709648001
209993_at	ABCB1	1	5.286057307
201666_at	TIMP1	1	6.771483042
226734_at	EIF4E2	1	10.94935716
203566_s_at	AGL	1	6.478523075

220936_s_at	H2AFJ	1	9.83226063
220775_s_at	UEVLD	1	6.520752604
229912_at	SDK1	1	5.551602218
221264_s_at	LOC100128223 /// TARDBP	1	10.84766803
1552798_a_at	TLR4	1	8.833394824
220943_s_at	C2orf56	1	13.85528742
217948_at	FAM127B	1	10.24491154
204186_s_at	PPID	1	7.910765472
209314_s_at	HBS1L	1	6.168562082
209304_x_at	GADD45B	1	6.270792962
202006_at	PTPN12	1	11.22939214
219801_at	ZNF34	1	10.75379222
204021_s_at	PURA	1	7.047364119
221425_s_at	ISCA1	1	10.60549593
204308_s_at	KIAA0329	1	11.73792363
229007_at	LOC283788	1	5.55508337
227539_at	0	1	9.063521601
1555167_s_at	NAMPT	1	4.749090502
205159_at	CSF2RB	1	4.598128097
223320_s_at	ABCB10	1	7.369944282
225639_at	SKAP2	1	8.558457705
226876_at	FAM101B	1	7.317047525
226409_at	TBC1D20	1	10.30690437
210251_s_at	RUFY3	1	9.912744001
239960_x_at	LYRM7	1	10.07483734
33850_at	MAP4	1	12.20887403
1566603_s_at	RPUSD3	1	10.19073967
238015_at	C4orf46	1	10.02260253
238050_at	0	1	9.620757307
201365_at	OAZ2	1	13.70504724
235159_at	0	1	11.81593754
222533_at	CRBN	1	10.71502339
208861_s_at	ATRX	1	9.431105065
225886_at	DDX5	1	9.037988157
230250_at	PTPRB	1	5.40197219
201230_s_at	ARIH2	1	10.87877871
241710_at	hCG_1645220	1	8.671949953
242738_s_at	ZFXH3	1	10.02363142
220116_at	KCNN2	1	5.57768381
217880_at	CDC27	1	10.02961595
222548_s_at	MAP4K4	1	8.68232647
209067_s_at	HNRPD1	1	10.23084898
203620_s_at	FCHSD2	1	8.115858219
211380_s_at	PRKG1	1	8.34584142
200993_at	IPO7	1	10.89052026
229809_at	0	1	9.923208703
208810_at	DNAJB6	1	7.882068297
209481_at	SNRK	1	9.718073294
37384_at	PPM1F	1	11.49899362
209194_at	CETN2	1	9.276025504
226939_at	CPEB2	1	6.016955049
224729_s_at	ATPAF1	1	8.342453456
221486_at	ENSA	1	8.610103695
225768_at	NR1D2	1	5.574162393
220419_s_at	USP25	1	11.26634232
36554_at	ASMTL	1	10.12716537

201881_s_at	ARIH1	1	11.1008516
227658_s_at	PLEKHA3	1	10.28428092
201215_at	PLS3	1	8.882857229
211616_s_at	HTR2A	1	7.276177651
212450_at	KIAA0256	1	6.740964895
232088_x_at	0	1	9.872198919
202134_s_at	WWTR1	1	8.13370634
1563466_at	MYLK	1	5.936626259
218613_at	PSD3	1	6.820346236
205277_at	PRDM2	1	13.46596668
234977_at	ZADH2	1	7.947462499
201628_s_at	RRAGA	1	11.21124617
238360_s_at	0	1	7.142725939
228695_at	C8orf46	1	5.973680348
202519_at	MLXIP	1	8.44739332
226658_at	PDPN	1	7.022984677
224492_s_at	ZNF627	1	8.847804473
205352_at	SERPINI1	1	5.520272735
232124_at	LOC729085	1	8.055310891
203628_at	IGF1R	1	6.32958137
230561_s_at	C2orf67	1	8.290280862
227536_at	ZC3H13	1	10.28790266
221078_s_at	CCDC88A	1	11.49429303
202983_at	HLTF	1	8.152016312
214051_at	MGC39900 /// TMSB15A	1	10.0530866
226753_at	FAM76B	1	7.181326279
202530_at	MAPK14	1	10.05883462
218823_s_at	KCTD9	1	8.041677576
207304_at	ZNF45	1	13.44009062
225033_at	ST3GAL1	1	5.779892051
202657_s_at	SERTAD2	1	6.538877337
238436_s_at	ZNF805	1	9.666201989
202717_s_at	CDC16	1	7.866636801
220076_at	ANKH	1	9.050083977
213564_x_at	LDHB	1	6.593507459
230278_at	0	1	8.278903487
242338_at	TMEM64	1	7.588074357
203870_at	USP46	1	7.99515732
222868_s_at	IL18BP	1	6.087570314
225910_at	HELZ	1	10.63058251
211086_x_at	NEK1	1	10.94675398
208460_at	GJC1	1	7.127080525
203595_s_at	IFIT5	1	8.383627434
219156_at	SYNJ2BP	1	6.824207218
227351_at	C16orf52	1	8.755233369
227144_at	C22orf9	1	13.00373909
203486_s_at	ARMC8	1	9.958217514
219939_s_at	CSDE1	1	11.47289205
45714_at	HCFC1R1	1	9.426629949
223287_s_at	FOXP1	1	9.362217593
230630_at	AK3L1 /// AK3L2	1	4.998257497
226463_at	ATP6V1C1	1	9.809900379
222760_at	ZNF703	1	7.11346411
1557905_s_at	CD44	1	6.810301089
41644_at	SASH1	1	7.813530999
227525_at	GLCCI1	1	6.110670027

202641_at	ARL3	1	9.529302652
224996_at	ASPH	1	6.115232603
205128_x_at	PTGS1	1	5.733497553
203173_s_at	C16orf62	1	9.141405022
227639_at	PIGK	1	8.274848343
225679_at	NAT12	1	8.264181535
221497_x_at	EGLN1	1	8.045184415
218521_s_at	UBE2W	1	8.665046721
226038_at	LONRF1	1	8.459872531
206030_at	ASPA	1	4.236916729
213227_at	PGRMC2	1	6.992105231
227917_at	FAM85A	1	7.463532637
218348_s_at	ZC3H7A	1	12.29668097
235612_at	0	1	8.83616902
1553218_a_at	ZNF512	1	14.03508085
1554080_at	RQCD1	1	7.830492702
207334_s_at	TGFB2	1	7.776738411
225057_at	SLC15A4	1	9.698694456
231921_at	C2orf37	1	8.288631134
1553725_s_at	ZNF644	1	12.03146304
200613_at	AP2M1	1	11.99551547
222420_s_at	UBE2H	1	9.916392733
236738_at	LOC401097	1	6.296784973
235653_s_at	THAP6	1	5.651445117
229580_at	0	1	5.003457928
212776_s_at	OBSL1	1	6.952236612
228963_at	RSBN1L	1	9.589654638
238077_at	KCTD6	1	10.70811189
218729_at	LXN	1	4.531807557
201029_s_at	CD99	1	10.75691194
204214_s_at	RAB32	1	9.136797202
211561_x_at	MAPK14	1	9.748497427
212214_at	OPA1	1	8.001153057
228608_at	NALCN	1	5.582836064
1552277_a_at	C9orf30 /// TMEFF1	1	8.954381004
223129_x_at	MYLIP	1	11.03377297
1553175_s_at	PDE5A	1	7.526561609
203282_at	GBE1	1	8.239078583
227086_at	C22orf39	1	10.62477241
208920_at	SRI	1	6.597131379
200742_s_at	TPP1	1	7.984287093
225742_at	MDM4	1	10.25212947
211681_s_at	PDLIM5	1	6.301793954
1556190_s_at	PRNP	1	6.344918889
224780_at	RBM17	1	8.262645416
226343_at	0	1	11.17546165
226897_s_at	ZC3H7A	1	11.50157505
223300_s_at	CCDC82	1	11.77454015
225661_at	IFNAR1	1	10.55841825
217955_at	BCL2L13	1	6.678131766
223591_at	RNF135	1	9.27525167
241685_x_at	0	1	8.609979983
221834_at	LONP2	1	8.580686626
223618_at	FMN2	1	6.173919265
201294_s_at	WSB1	1	7.021424712
222644_s_at	GLT25D1	1	10.99308276

229312_s_at	GKAP1		1	7.116916041
219421_at	TTC33		1	7.047869259
231822_at	CTTNBP2NL		1	11.53514657
214177_s_at	PBXIP1		1	7.799690542
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213111_at	PIP5K3		1	9.968595081
207842_s_at	CASC3		1	11.09938432
226329_s_at	MITD1		1	8.134132878
213224_s_at	NCRNA00081		1	8.172364233
212796_s_at	TBC1D2B		1	10.16796118
209112_at	CDKN1B		1	10.79080932
229299_at	C5orf33		1	6.006513554
1555705_a_at	CMTM3		1	9.602819371
226995_at	C21orf86		1	7.61110786
212615_at	CHD9		1	6.978285484
216804_s_at	PDLIM5		1	8.887020476
212687_at	LIMS1		1	12.68277253
238723_at	ATXN3		1	9.787476896
225420_at	GPAM		1	4.481358742
228835_at		0	1	11.25866486
209009_at	ESD		1	9.491746611
225198_at	VAPA		1	7.655341815
213341_at	FEM1C		1	6.686710914
229881_at	KLF12		1	9.654602067
239866_at		0	1	12.68838035
234989_at	NCRNA00084		1	5.372101749
240344_x_at	LYRM7		1	8.261678509
227809_at	ZC3H6		1	8.265062685
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76897_s_at	FKBP15		1	9.284600226
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38892_at	KIAA0240		1	8.465283158
226254_s_at	KIAA1430		1	10.93195251
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242289_at		0	1	9.834394999
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223042_s_at	FUNDC2		1	8.498448616
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1553672_at	ENAH		1	7.77567148
203197_s_at	C1orf123		1	13.33326114
205805_s_at	ROR1		1	7.290450797
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205369_x_at	DBT		1	6.843087002
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239415_at	MAP9		1	8.471830814
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226820_at	ZNF362		1	11.60811298
49452_at	ACACB		1	5.086502735
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212199_at	MRFAP1L1		1	9.250602154
237413_at		0	1	9.83069284

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214560_at	FPR3	1	5.898486196
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243521_at	0	1	8.917078341
212580_at	ERAP1	1	9.65883453
214820_at	BRWD1	1	8.844984863
222520_s_at	IFT57	1	8.487562174
229635_at	0	1	6.378173464
218637_at	IMPACT	1	8.196927947
226297_at	0	1	9.410808774
226443_at	FAM122A	1	10.9336034
36553_at	ASMTL	1	9.031219459
225624_at	SNX29	1	11.36886609
226233_at	B3GALNT2	1	8.458413784
235554_x_at	PACRGL	1	10.75940087
201780_s_at	RNF13	1	9.301517463
227726_at	RNF166	1	6.900727148
200749_at	RAN	1	9.435541674
238463_at	0	1	9.063368189
219174_at	IFT74	1	7.388320058
229019_at	ZNF385B	1	3.709565896
201816_s_at	GBAS	1	7.565310578
219077_s_at	WVOX	1	6.095279667
226816_s_at	KIAA1143	1	10.846807
212671_s_at	HLA-DQA1 /// HLA-DQA2	1	3.691150654
225084_at	EXOC5	1	9.543303225
205151_s_at	KIAA0644	1	6.316660983
226468_at	0	1	10.08087075
235032_at	DNAJC21	1	7.991837827
209079_x_at	PCDHGA1 /// PCDHGA10 /// PCDHGA11 /// PCDHGA12 /// PCDHGA2 /// PCDHGA3 /// PCDHGA4 /// PCDHGA5 /// PCDHGA6 /// PCDHGA7 /// PCDHGA8 /// PCDHGA9 /// PCDHGB1 /// PCDHGB2 /// PCDHGB3 /// PCDHGB4 /// PCDHGB5 /// PCDHGB6 /// PCDHGB7 /// PCDHGC3 /// PCDHGC4 /// PCDHGC5	1	7.87938273
219260_s_at	C17orf81	1	5.902177313
221211_s_at	C21orf7	1	6.239774386
204113_at	CUGBP1	1	10.08882451
230519_at	FAM124A	1	8.260942737
235056_at	ETV6	1	9.02852336
209882_at	RIT1	1	8.239932607
215116_s_at	DNM1	1	6.258862767
218496_at	RNASEH1	1	11.47234867
225178_at	TTC14	1	6.756619061
228378_at	C12orf29	1	8.551647536

228092_at	CREM	1	5.832358113
238073_at	ELAVL4	1	5.622018942
235890_at	0	1	9.069064672
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208971_at	UROD	1	12.57806691
227961_at	CTSB	1	6.859163292
225698_at	C5orf26	1	7.736251562
202660_at	ITPR2	1	6.621335728
211945_s_at	ITGB1	1	11.70811613
211797_s_at	NFYC	1	10.26228502
243816_at	ZNF70	1	9.793030963
213128_s_at	UBE3A	1	7.371939334
221477_s_at	SOD2	1	6.716687366
229359_at	0	1	12.50037771
201566_x_at	ID2	1	8.268454732
227480_at	SUSD2	1	6.246996439
225902_at	0	1	9.163233354
227065_at	RNF216	1	10.30496519
201565_s_at	ID2	1	8.635144684
204829_s_at	FOLR2	1	6.454484864
235260_s_at	PACRGL	1	8.344012145
203586_s_at	ARL4D	1	8.941364209
238844_s_at	NPHP1	1	7.534941342
205579_at	HRH1	1	5.942147019
222815_at	RNF12	1	7.704875454
1556069_s_at	HIF3A	1	6.555690247
207000_s_at	PPP3CC	1	9.679987988
212300_at	TXLNA	1	9.666358748
225845_at	ZBTB44	1	9.366299134
206833_s_at	ACYP2	1	8.945369139
225390_s_at	KLF13	1	9.119493692
225992_at	MLLT10	1	10.07319405
1555326_a_at	ADAM9	1	4.939866178
213526_s_at	LIN37	1	9.652074644
224435_at	C10orf57 /// C10orf58	1	5.706015312
225962_at	ZNRF1	1	8.020060746
238020_at	PSMC2	1	6.933731439
223099_s_at	LONP2	1	8.353981874
212241_at	GCOM1 /// GRINL1A	1	10.96428476
209293_x_at	ID4	1	6.607948675
226116_at	0	1	10.49912167
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225335_at	ZNF496	1	11.45275123
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239768_x_at	0	1	9.863984779
212589_at	RRAS2	1	5.547308728
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235670_at	STX11	1	5.863623655

217976_s_at	DYNC1L1	1	10.39990147
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218165_at	C1orf149	1	9.871134523
224938_at	NUFIP2	1	8.475619163
235202_x_at	IKIP	1	9.753628753
210374_x_at	PTGER3	1	6.959865005
1558487_a_at	TMED4	1	11.11934624
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229244_at	0	1	7.928594171
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227221_at	0	1	10.5031342
205903_s_at	KCNN3	1	6.081075972
224900_at	ANKFY1	1	10.17654111
213225_at	PPM1B	1	8.084975155
201888_s_at	IL13RA1	1	6.522775361
212797_at	SORT1	1	8.336656567
204007_at	FCGR3B	1	4.052381859
203333_at	KIFAP3	1	9.214974054
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208703_s_at	APLP2	1	8.477258251
222026_at	RBM3	1	11.55222382
203249_at	EZH1	1	10.89553649
201010_s_at	TXNIP	1	7.998321012
213797_at	RSAD2	1	4.169475208
217842_at	LUC7L2	1	9.364187137
228289_at	0	1	8.453726915
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202497_x_at	SLC2A3	1	5.440349653
227548_at	ORMDL1	1	7.129059056
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228190_at	ATG4C /// CTR9	1	8.187496701
225093_at	UTRN	1	6.619182489
202557_at	HSPA13	1	7.761155055
219843_at	IPP	1	9.358290863
226285_at	CAPRIN1	1	9.396970023
222765_x_at	ESF1	1	6.44953034
218665_at	FZD4	1	7.683031735
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230621_at	IAH1	1	7.475852516
209815_at	PTCH1	1	3.645130487
241470_x_at	0	1	9.148681186
203368_at	CRELD1	1	10.23677977
225889_at	AEBP2	1	9.623027388
235961_at	GPR161	1	8.333098849
218513_at	C4orf43	1	9.732466584
222580_at	ZNF644	1	11.65561498

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236224_at	RIT1		1	8.161180498
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39582_at	CYLD		1	8.92593418
227993_at	METAP2		1	10.42915898
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221045_s_at	PER3		1	4.673087964
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208447_s_at	PRPS1		1	8.179099206
217759_at	TRIM44		1	8.13164421
238768_at	C2orf68		1	8.498412708
226534_at	KITLG		1	6.13709022
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209250_at	DEGS1		1	9.654175377
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228561_at	CDC37L1		1	8.284217364
222595_s_at	DIDO1		1	9.993521621
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49111_at		0	1	10.95326068
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244439_at	SPRED1	1	8.173657052
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218292_s_at	PRKAG2	1	7.578666743
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224660_at	PIGY	1	10.03772819
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1554433_a_at	ZNF146	1	9.89238758
217816_s_at	PCNP	1	14.99912404
1555831_s_at	LRRC41	1	8.902919494
226124_at	ZFP90	1	10.24861936
235567_at	RORA	1	9.29808013
1559633_a_at	CHRM3	1	4.342751672
219863_at	HERC5	1	6.833207617
221699_s_at	DDX50	1	10.89732406
229334_at	RUFY3	1	9.393853224
1557113_at	LOC283588	1	7.610610299
240239_at	ZNF566	1	11.05939014
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225856_at	0	1	7.3277566
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205684_s_at	DENND4C	1	5.651027887
229618_at	SNX16	1	8.440544932
235620_x_at	ZMYM5	1	8.771252211
214709_s_at	KTN1	1	10.40280867
213208_at	KIAA0240	1	10.94074439
227947_at	PHACTR2	1	7.490646072
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1554089_s_at	SBDS /// SBDSP	1	7.368418935
226985_at	FGD5	1	7.033468566
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208178_x_at	TRIO	1	10.11894433
236235_at	ITCH	1	7.022397009
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215884_s_at	UBQLN2	1	9.419726989
219386_s_at	SLAMF8	1	5.140024067
223446_s_at	DTNBP1	1	10.58893746
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225949_at	NRBP2	1	10.64533732
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210645_s_at	TTC3	1	7.218695054
230903_s_at	C8orf42	1	8.161742849
202552_s_at	CRIM1	1	8.122849258
231798_at	NOG	1	7.044187341
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225108_at	AGPS		1	8.56151472
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244552_at	ZNF788		1	9.153609423
230326_s_at	C11orf73		1	9.144093515
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203756_at	ARHGEF17	1	12.0592402
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237252_at	THBD	1	5.965336215
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211930_at	HNRNPA3	1	9.936414505
227111_at	ZBTB34	1	8.494422522
221897_at	TRIM52	1	7.358776888
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217915_s_at	C15orf15	1	8.487658825
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1552664_at	FLCN	1	9.411637216
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228046_at	ZNF827	1	5.748486518
226358_at	LOC145842	1	9.248493573
238688_at	TPM1	1	6.560644161
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209042_s_at	UBE2G2	1	8.083919612
209765_at	ADAM19	1	7.412238601
227572_at	USP30	1	8.255110315
236994_at	0	1	6.808657205
212060_at	SR140	1	7.308617768
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221786_at	C6orf120	1	6.283271422
202909_at	EPM2AIP1	1	6.637508605
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227624_at	TET2	1	6.80596197
228937_at	C13orf31	1	5.794441741
224794_s_at	CERCAM	1	6.259119291
212820_at	DMXL2	1	6.502514036
228305_at	ZNF565	1	8.425077046
212632_at	STX7	1	10.56737649

222619_at	ZNF281	1	7.852960343
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219094_at	ARMC8	1	8.551114779
209561_at	THBS3	1	9.577998935
235532_at	PIGM	1	8.822476931
226760_at	MBTPS2	1	6.297015712
226895_at	NFIC	1	6.6221762
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222613_at	C12orf4	1	10.09046709
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212518_at	PIP5K1C	1	8.778869736
201179_s_at	GNAI3	1	8.694588437
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223542_at	ANKRD32	1	7.655016108
212245_at	MCFD2	1	7.803522599
238793_at	TIGD7	1	10.58352024
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223135_s_at	BBX	1	11.95477266
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214794_at	PA2G4	1	8.751254084
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242706_s_at	MED23	1	6.678656222
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222565_s_at	PRKD3		1	8.110259074
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226178_at	SOCS4		1	6.216624606
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218570_at	KBTBD4 /// PTPMT1		1	7.275385565
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235834_at	CALD1		1	7.003567143
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222150_s_at	PION		1	6.480941736
229723_at	TAGAP		1	3.594024324
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221755_at	EHBP111		1	7.667065092
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217952_x_at	PHF3		1	9.167591241
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229034_at	SOBP		1	7.081677587
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210665_at	TFPI		1	4.280606691
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218713_at	NARG2	1	8.188067054
230379_x_at	C2orf56	1	7.914319369
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213754_s_at	PAIP1	1	7.816823836
228433_at	NFYA	1	7.168537418
225479_at	LRRC58	1	10.24423028
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227601_at	KIAA1627	1	8.175357551
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231819_at	0	1	7.275579019
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238597_at	ANKRD13C	1	10.56070619
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217808_s_at	MAPKAP1	1	8.31882849
213093_at	PRKCA	1	6.424062067
217118_s_at	C22orf9	1	8.768641904
212068_s_at	BAT2L	1	11.33098019
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220797_at	METT10D	1	10.41020288
219961_s_at	NCRNA00153	1	5.217844273
225900_at	EXOC6B	1	8.587830445
217299_s_at	NBN	1	6.876985724

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229391_s_at	FAM26F		1	3.558147757
213282_at	APOOL		1	7.703629347
223424_s_at	ZSCAN21		1	7.778475408
213677_s_at	PMS1		1	9.046331313
222389_s_at	WAC		1	10.18918131
212557_at	ZNF451		1	7.416825714
230644_at	LRFN5		1	5.528127768
208781_x_at	SNX3		1	10.67784135
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212733_at	KIAA0226		1	10.79900518
235589_s_at	MDM4		1	5.668201916
226249_at	SNX30		1	7.131848949
210871_x_at	SSX2IP		1	6.832912342
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210779_x_at	SIP1		1	9.613720976
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224704_at	TNRC6A		1	7.430952039
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218051_s_at	NT5DC2		1	5.502892788
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232429_at		0	1	8.828385022
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243013_at		0	1	8.746696485
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224703_at	WDR22	1	10.0952421
228153_at	RNF144B	1	5.392898779
227280_s_at	CCNYL1	1	6.007918248
226221_at	KIAA1432	1	11.97976274
206142_at	ZNF135	1	10.02124291
230738_at	LOC730631	1	6.727130163
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203584_at	TTC35	1	8.125537619
1553192_at	ZNF441	1	11.02027136
204405_x_at	DIMT1L	1	10.05733372
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235252_at	KSR1	1	6.178603856
232902_s_at	RARS2	1	7.438472694
227798_at	SMAD1	1	5.981173453
208866_at	CSNK1A1	1	6.669350503
238315_s_at	ZNF567	1	9.306154263
236561_at	TGFBR1	1	4.382688248
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224939_at	NUFIP2	1	8.730801979
210389_x_at	TUBD1	1	8.388041014
226893_at	ABL2	1	6.406618019
221825_at	ANGEL2	1	5.89571453
211587_x_at	CHRNA3	1	6.001985535
223984_s_at	NUPL1	1	5.618692387
239100_x_at	PCNX	1	10.20092255
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244498_x_at	LOC440302	1	11.61855939
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235071_at	WDR92	1	9.181845812
214683_s_at	CLK1	1	6.193506326
221878_at	C2orf68	1	10.22852681
232751_at	RBBP9	1	8.524328962
229953_x_at	LCA5	1	11.41728714
215286_s_at	PHTF2	1	8.927064619
201707_at	PEX19	1	8.554038879
207838_x_at	PBXIP1	1	7.842297634
227020_at	YPEL2	1	6.252260407
226571_s_at	PTPRS	1	6.463877993
204353_s_at	POT1	1	7.205584254
238504_at	C6orf57	1	6.561698984
239135_at	FLJ11151	1	8.187788428
212648_at	DHX29	1	8.722533408
225994_at	CPSF2	1	6.70520334
241393_at	IPP	1	8.12978855

206383_s_at	G3BP2	1	7.873616117
213075_at	OLFML2A	1	5.589122305
203283_s_at	HS2ST1	1	7.026552371
237025_at	0	1	9.243805138
228933_at	NHS	1	5.151396519
1552315_at	GIMAP1	1	7.179354489
210105_s_at	FYN	1	6.635023288
225989_at	HERC4	1	6.521233882
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212847_at	FUBP1	1	6.873071636
233442_at	0	1	6.027274027
235108_at	0	1	5.726148804
238562_at	0	1	9.84052027
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224013_s_at	SOX7	1	4.652311893
218179_s_at	C4orf41	1	8.273353051
218526_s_at	RANGRF	1	8.95526609
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219157_at	KLHL2	1	6.718352912
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202536_at	CHMP2B	1	5.65749007
223260_s_at	POLK	1	9.564679589
205082_s_at	AOX1	1	4.571777474
1555929_s_at	0	1	6.158559816
218187_s_at	C8orf33	1	6.638689246
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242569_at	STAM2	1	6.82792939
236577_at	0	1	5.56418036
202967_at	GSTA4	1	4.697982216
202405_at	TIAL1	1	9.519365865
215708_s_at	PRIM2	1	6.263651796
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222465_at	C15orf15	1	8.359152197
221517_s_at	MED17	1	7.375851229
221606_s_at	NSBP1	1	4.865862975
224940_s_at	PAPPA	1	4.347857117
226778_at	C8orf42	1	6.78464871
1556306_at	0	1	6.651438819
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208663_s_at	TTC3	1	7.375023347
225871_at	STEAP2	1	5.980256966
222437_s_at	VPS24	1	7.588183652
225297_at	CCDC5	1	7.149242012
204436_at	PLEKHO2	1	9.626143189
232600_at	0	1	5.967195023
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225821_s_at	FAM44A	1	9.636686277
200975_at	PPT1	1	9.381471055
229673_at	0	1	12.61164109
233748_x_at	PRKAG2	1	7.351706966
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242422_at	G3BP1	1	8.709760372

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227354_at	PAG1		1	5.531755372
208384_s_at	MID2		1	8.737824754
227081_at	DNALI1		1	4.924107825
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226925_at	ACPL2		1	5.494496664
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227304_at	SMCR8		1	8.865010297
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227844_at	FMNL3		1	10.02452982
235962_at		0	1	9.481160346
217833_at	SYNCRIP		1	7.776779697
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226277_at	COL4A3BP		1	7.471209052
225530_at	MOBK2A		1	8.173810991
211087_x_at	MAPK14		1	9.202874675
222157_s_at	WDR48		1	10.881294
205427_at	ZNF354A		1	9.128534578
237062_at		0	1	9.517407447
236764_at		0	1	8.399135006
239891_x_at	RAB12		1	6.702274797
222279_at	RP3-377H14.5		1	9.633642488
236453_at	LOC100132161		1	7.07982383
214376_at		0	1	7.374308373
223043_at	TMEM85		1	7.528661817
209185_s_at	IRS2		1	4.592589009

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212061_at	SR140	1	7.666209203
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226642_s_at	NUDCD2	1	7.110657107
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224621_at	MAPK1	1	8.400592529
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225669_at	IFNAR1	1	8.207352316
205237_at	FCN1	1	3.925457891
218094_s_at	DBNDD2 /// SYS1-DBNDD2	1	5.660772974
225827_at	EIF2C2	1	6.583096751
238523_at	KLHL36	1	6.549317974
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211749_s_at	VAMP3	1	8.615725097
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202480_s_at	DEDD	1	9.850680436
226831_at	SLC25A46	1	5.860992364
214438_at	HLX	1	5.937378721
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224790_at	ASAP1	1	9.504196583
227822_at	ZNF605	1	6.331390421
222243_s_at	TOB2	1	6.444640782
210734_x_at	MAX	1	7.599312709
232909_s_at	BPTF	1	7.854169827
204850_s_at	DCX	1	4.251158777
212343_at	YIPF6	1	6.929493365
226398_s_at	C10orf4	1	8.065358154
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223422_s_at	ARHGAP24	1	6.348810311
226775_at	ENY2	1	7.333625859
224335_s_at	BACE1	1	10.61355191
225646_at	CTSC	1	5.540760835
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220939_s_at	DPP8	1	7.257793656
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211763_s_at	UBE2B	1	6.527424011
219594_at	NINJ2	1	6.207925486
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217294_s_at	ENO1	1	5.851301403
227873_at	TXNDC15	1	9.967804985
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210425_x_at	GOLGA8A /// GOLGA8B	1	5.935695067
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205443_at	SNAPC1	1	7.185357196
209255_at	KLHDC10	1	5.170010507
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229890_at	PRRT1	1	6.447484706
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227361_at	HS3ST3B1	1	3.950045949
204049_s_at	PHACTR2	1	7.188212696
210564_x_at	CFLAR	1	7.335430029
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226472_at	PPIL4	1	6.444396856
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222816_s_at	ZCCHC2	1	6.441832467
202359_s_at	SNX19	1	7.893872721

205945_at	IL6R		1	4.236512787
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227620_at	SLC44A1		1	7.490869373
227195_at	ZNF503		1	4.22411914
229710_at		0	1	7.615547696
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238649_at	PITPNC1		1	7.584334131
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224647_at	CCNY		1	8.932634162
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222789_at	RSBN1		1	8.874029998
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212987_at	FBXO9		1	6.345320188
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213206_at	GOSR2		1	7.793609968
220637_at	FAM124B		1	7.956777538
218572_at	CHMP4A		1	6.757564387
226015_at	ZNF12		1	9.276750758
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230781_at		0	1	4.820222954
227955_s_at	EFNA5		1	4.689698065
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218374_s_at	C12orf4		1	9.623641013
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231909_x_at	ODF2L		1	11.14866971
210276_s_at	TRIOBP		1	6.711771191
210783_x_at	CLEC11A		1	7.436833257
224463_s_at	C11orf70		1	5.512696374
205687_at	UBFD1		1	6.835738994
201781_s_at	AIP		1	8.161470764
201235_s_at	BTG2		1	5.453737571
223716_s_at	ZRANB2		1	10.91364034
204772_s_at	TTF1		1	9.729972358
208763_s_at	TSC22D3		1	4.804262419

217819_at	GOLGA7		1	10.71486389
213239_at	PIBF1		1	5.639170153
235155_at	BDH2		1	5.913493741
203582_s_at	RAB4A		1	5.560157508
244170_at		0	1	6.926812636
220606_s_at	C17orf48		1	7.02324554
51228_at	RBM12B		1	7.431831269
225904_at	C1orf96		1	7.399127838
221090_s_at	OGFOD1		1	8.907557741
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201802_at	SLC29A1		1	8.233726145
211339_s_at	ITK		1	3.519798449
202816_s_at	SS18		1	7.186345946
225573_at	ACAD11 /// NPHP3		1	7.563293447
223735_at	ARL6		1	10.03666679
223412_at	KBTBD7		1	4.943263357
202872_at	ATP6V1C1		1	5.714740102
233827_s_at	SUPT16H		1	6.622066178
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207112_s_at	GAB1		1	9.324391681
208655_at		0	1	9.353158178
230411_at		0	1	8.899656361
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204068_at	STK3		1	7.676469944
230592_at	NSL1		1	8.400493702
202318_s_at	SENP6		1	6.592475974
228588_s_at	UBE2B		1	5.748899801
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207127_s_at	HNRNPH3		1	11.08828819
203440_at	CDH2		1	5.392303806
209876_at	GIT2		1	13.29594183
210878_s_at	JMJD1B		1	8.620638867
228446_at	KIAA2026		1	6.245966571
235278_at	MACROD2		1	3.703566143
208423_s_at	MSR1		1	5.130010441
221916_at	NEFL		1	5.708228814
242984_at	MKLN1		1	7.946764888
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227161_at	NOM1		1	8.432357663
227485_at	DDX26B		1	6.542464485
212824_at	FUBP3		1	8.501052613
224974_at	SUDS3		1	7.11396877
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238561_s_at		0	1	9.462810478
221483_s_at	ARPP-19		1	9.947894253
235409_at	MGA		1	6.56771695
202623_at	EAPP		1	6.675054229
222519_s_at	IFT57		1	6.496697621
221983_at	FAM134A		1	7.14655933
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219603_s_at	ZNF226		1	5.412698685
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243084_at	CALD1		1	9.248556775

218247_s_at	MEX3C	1	6.792056723
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241698_at	RFTN2	1	9.787670838
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203037_s_at	MTSS1	1	4.424119815
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233461_x_at	ZNF226	1	7.63990373
1554470_s_at	ZBTB44	1	9.101576283
229614_at	ZNF320	1	5.237231186
1557100_s_at	HECTD1	1	5.799889849
226510_at	HEATR5A	1	5.021717843
241699_at	0	1	9.366048189
222204_s_at	RRN3	1	6.830515634
230657_at	0	1	8.188520207
214016_s_at	SFPQ	1	6.12860026
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219351_at	SEDLP /// TRAPPC2 /// ZNF547	1	5.78244298
221563_at	DUSP10	1	6.340496536
203846_at	TRIM32	1	8.212194104
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230069_at	SFXN1	1	6.927280227
225633_at	DPY19L3	1	6.566914372
201737_s_at	MARCH6	1	6.233526606
222787_s_at	TMEM106B	1	5.499802914
1552486_s_at	LACTB	1	5.519707703
218561_s_at	LYRM4	1	6.796133317
219598_s_at	RWDD1	1	9.618531027
218306_s_at	HERC1	1	8.960806876
229908_s_at	UNKL	1	10.98432528
239133_at	0	1	9.932823365
228943_at	MAP6	1	10.15884699
203438_at	STC2	1	6.822100203
210191_s_at	PHTF1	1	6.604413185
216593_s_at	PIGC	1	6.45783924
1554093_a_at	SNAPC5	1	8.154667572
208664_s_at	TTC3	1	8.482639329
214693_x_at	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 ///	1	7.101960012
217202_s_at	GLUL	1	3.851774385
225289_at	STAT3	1	10.30998744
213686_at	0	1	6.181792762
210460_s_at	PSMD4	1	9.519019035
231016_s_at	0	1	8.957549354
219013_at	GALNT11	1	6.21657426
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1555803_a_at	C11orf57	1	8.505580024
205119_s_at	FPR1	1	3.911520374
225213_at	PPTC7	1	8.018725663
223228_at	LDLOC1L	1	9.803092629
219983_at	HRASLS	1	6.115689837

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216997_x_at	TLE4	1	7.731968062
238879_at	0	1	7.006858045
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205401_at	AGPS	1	6.823577878
227003_at	RAB28	1	7.313371005
201885_s_at	CYB5R3	1	10.82400292
223117_s_at	USP47	1	7.155934206
211612_s_at	IL13RA1	1	5.466137304
1559535_s_at	0	1	9.746343481
208073_x_at	TTC3	1	6.854239979
219789_at	NPR3	1	5.190236052
204715_at	PANX1	1	6.943529234
225244_at	SNAP47	1	10.97604813
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218775_s_at	WWC2	1	7.954820596
221986_s_at	KLHL24	1	6.400196154
202434_s_at	CYP1B1	1	4.903240721
221502_at	KPNA3	1	8.328267074
203852_s_at	SMN1 /// SMN2	1	6.552686878
221193_s_at	ZCCHC10	1	6.144931094
225136_at	PLEKHA2	1	8.387495409
213009_s_at	TRIM37	1	8.80730917
218761_at	RNF111	1	6.701451889
1558136_s_at	TAF11	1	7.587202641
220254_at	LRP12	1	10.8266889
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235658_at	0	1	10.15592802
206989_s_at	SFRS2IP	1	9.078415452
204518_s_at	PPIC	1	5.850260577
211473_s_at	COL4A6	1	5.338365682
204112_s_at	HNMT	1	6.859179943
223983_s_at	C19orf12	1	8.54694486
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210933_s_at	FSCN1	1	4.774272953
209046_s_at	GABARAPL2	1	8.126647509
203906_at	IQSEC1	1	9.149082565
204800_s_at	DHRS12	1	8.087281308
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226498_at	0	1	4.090291044
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209332_s_at	MAX	1	10.25062974
223538_at	SERF1A /// SERF1B	1	6.391476729
231997_at	TBCEL	1	8.912385388
203843_at	RPS6KA3	1	7.661464604

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215501_s_at	DUSP10		1	7.271107925
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206129_s_at	ARSB		1	7.750790408
207153_s_at	GLMN		1	7.797591867
227308_x_at	LTBP3		1	11.34895661
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231577_s_at	GBP1		1	4.347698346
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244030_at	STYX		1	8.029843228
241706_at	CPNE8		1	7.735302843
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224524_s_at	ASB3		1	9.766099378
235365_at	DFNB59		1	10.02309653
238465_at	C5orf35		1	3.795385103
226230_at	SMEK2		1	6.56782839
213221_s_at	SIK2		1	5.139330025
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205868_s_at	PTPN11		1	6.731292643
227856_at	C4orf32		1	3.549977308
227119_at	CNOT6L		1	5.903741397
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204840_s_at	EEA1		1	7.69341901
223331_s_at	DDX20		1	9.08868536
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225262_at	FOSL2		1	4.79724746
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235938_at	0	1	7.334701668
226372_at	CHST11	1	6.7464813
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59644_at	BMP2K	1	5.863120645
217552_x_at	CR1	1	4.011395877
244752_at	ZNF438	1	9.632310725
214221_at	ALMS1	1	9.50773173
225919_s_at	C9orf72	1	5.53060644
225352_at	SEC62	1	6.535491265
205686_s_at	CD86	1	5.390397803

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204426_at	TMED2	1	5.851234729
227787_s_at	MED30	1	6.985808209
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229585_at	ADAMTSL1	1	4.662863029
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235439_at	RBMS2	1	8.3338709
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223677_at	ATG10	1	7.534992617
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226215_s_at	FBXL10	1	8.996249283
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223796_at	CNTNAP3 /// CNTNAP3B /// LOC643827 /// LOC653355 /// RP11- 138L21.1	1	4.298184435
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225813_at	RC3H2	1	7.939144556
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225504_at	0	1	9.321286119
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236401_at	0	1	6.841308163
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233866_at	KLHL5	1	6.823448094
232086_at	0	1	10.31656
203830_at	C17orf75	1	7.071564149
227595_at	ZMYM6	1	8.196292282
222876_s_at	ADAP2	1	7.497964575
213573_at	0	1	9.084543841

238781_at		0	1	10.22106379
212203_x_at	IFITM3		1	9.3970566
219266_at	ZNF350		1	8.200424434
225230_at	TMEM77		1	4.817582463
209532_at	PLAA		1	10.40970025
212438_at	SNRNP27		1	8.810731792
215028_at	SEMA6A		1	4.780281864
200878_at	EPAS1		1	5.508827463
202653_s_at	MARCH7		1	7.714408966
203556_at	ZHX2		1	6.258743124
1554352_s_at	DENND4A		1	9.181671503
1566557_at	FLI90757		1	6.706759167
236533_at	ASAP1		1	7.985701972
219321_at	MPP5		1	5.526227203
1552705_at	DUSP19		1	5.410535604
222761_at	BIVM		1	6.276705612
210154_at	ME2		1	5.080083324
201103_x_at	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF12 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// RP11-94I2.2		1	7.615719791
1555471_a_at	FMN2		1	6.389140609
212893_at	ZZZ3		1	8.98862193
212997_s_at	TLK2		1	8.256212942
238604_at		0	1	7.16201341
232023_at	TMEM67		1	10.18568862
215784_at	CD1E		1	3.577517361
217975_at	WBP5		1	3.885506229
201804_x_at	TBCB		1	11.25205911
226503_at	RIF1		1	6.913937914
222916_s_at	HDLBP		1	7.629937138
211569_s_at	HADH		1	3.985904807
210573_s_at	POLR3C		1	9.183216774
233268_s_at	CHURC1		1	8.698246076
223257_at	KIAA1333		1	5.773545629
222436_s_at	VPS24		1	6.975486059
236132_at	TLN1		1	7.113895919
226244_at	CLEC14A		1	6.208766549
226774_at	FAM120B		1	8.653450312
235381_at		0	1	7.700360915
225032_at	FNDC3B		1	6.9702697
226673_at	SH2D3C		1	6.692874726
230865_at	LIX1		1	4.527100492
207040_s_at	ST13		1	9.996651819
212880_at	WDR7		1	7.941361663
212854_x_at	NBPF10		1	8.910671677
235421_at	MAP3K8		1	5.201097232
209553_at	VPS8		1	9.492330729
244407_at	CYP39A1		1	4.762699611
223351_at	C17orf80		1	9.096997015
212676_at	NF1		1	7.696090712
212744_at	BBS4		1	8.435677018
222637_at	COMMD10		1	5.363696195
227501_at		0	1	6.649953704

228061_at	CCDC126	1	6.246753095
243735_at	0	1	9.712166797
214880_x_at	CALD1	1	7.924437757
203301_s_at	DMTF1	1	6.97765377
201383_s_at	LOC100133166 /// NBR1	1	8.501042763
202147_s_at	IFRD1	1	6.68101983
204520_x_at	BRD1	1	5.909006782
230407_at	0	1	8.639426321
219054_at	C5orf23	1	5.449806196
225422_at	CDC26 /// LOC729948 /// LOC730314	1	7.876280329
202019_s_at	LANCL1	1	7.578255675
204149_s_at	GSTM4	1	4.383262665
209840_s_at	LRRN3	1	5.411106307
212944_at	SLC5A3	1	6.483014239
217799_x_at	UBE2H	1	9.155614486
239184_at	0	1	7.899217222
1569594_a_at	SDCCAG1	1	5.309571807
236977_at	LOC646588	1	4.725328423
218945_at	C16orf68	1	10.09891627
212066_s_at	USP34	1	9.903871105
218712_at	C1orf109	1	8.693289263
202214_s_at	CUL4B	1	8.724536808
229804_x_at	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6	1	6.353270486
213620_s_at	ICAM2	1	4.103188261
226740_x_at	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// RP11-9412.2	1	7.947540676
227466_at	LOC285550	1	7.172561753
206917_at	GNA13	1	6.557255903
218603_at	HECA	1	8.090957668
215175_at	PCNX	1	5.780923178
1558697_a_at	KIAA0430	1	7.793899256
212598_at	WDFY3	1	10.25327322
244171_at	MKLN1	1	8.666444451
232905_at	0	1	9.842269279
219284_at	HSPBAP1	1	7.608345869
222065_s_at	FLII	1	8.686701706
228571_at	RBAK	1	7.970371269
225088_at	C16orf63	1	5.526747956
220150_s_at	FAM184A	1	6.596613093
1569003_at	TMEM49	1	4.725187551
213274_s_at	CTSB	1	4.67017078
227636_at	THAP5	1	6.170614182
200718_s_at	SKP1	1	10.83038874
213073_at	ZFYVE26	1	10.60424864
205594_at	ZNF652	1	6.608577336
203690_at	TUBGCP3	1	6.974476166
230360_at	GLDN	1	3.731789926
208839_s_at	CAND1	1	6.757329601
225816_at	PHF17	1	5.741094865
204490_s_at	CD44	1	4.913874018

218917_s_at	ARID1A	1	7.122625893
204024_at	OSGIN2	1	9.853060543
226908_at	LRIG3	1	4.472936216
239984_at	0	1	5.906542059
214753_at	N4BP2L2	1	5.493128796
213176_s_at	LTBP4	1	5.478340216
228328_at	KLHL28	1	6.889045094
207704_s_at	GAS7	1	5.898726004
218379_at	RBM7	1	8.435408987
226074_at	PPM1M	1	8.731544278
218343_s_at	GTF3C3	1	7.737007182
1560023_x_at	0	1	8.662288084
239147_at	ARSK	1	7.017620006
238489_at	PRKAA2	1	7.538111985
225760_at	MYSM1	1	6.024090274
218297_at	C10orf97	1	7.201173686
212082_s_at	MYL6 /// MYL6B	1	10.6214705
201080_at	PIP4K2B	1	9.145421406
226602_s_at	BCR /// FLJ42953 /// LOC100133163 /// LOC644079 /// LOC644165 /// LOC728468	1	6.455854791
244422_at	0	1	6.532964132
1554339_a_at	COG3	1	5.650170122
235189_at	NARG2	1	8.391062532
215832_x_at	PICALM	1	8.088641729
208498_s_at	AMY1A /// AMY1B /// AMY1C /// AMY2A /// AMY2B	1	3.961892647
209157_at	DNAJA2	1	6.768552306
226148_at	ZBTB44	1	6.696027306
227132_at	ZNF706	1	5.498603355
227115_at	0	1	5.843735711
221861_at	0	1	8.338550928
233665_x_at	MTO1	1	7.70254981
37965_at	PARVB	1	7.36620255
210849_s_at	VPS41	1	7.313997568
1558517_s_at	LRRRC8C	1	5.986846102
212881_at	PIAS4	1	7.978008859
206158_s_at	CNBP	1	9.79428299
229009_at	SIX5	1	7.386416575
231927_at	ATF6	1	7.066266937
210092_at	MAGOH	1	6.583842997
225936_at	EID2	1	8.03760718
225005_at	PHF13	1	9.803577698
226406_at	C18orf25	1	7.098589158
227313_at	CNPY4	1	10.09417673
209860_s_at	ANXA7	1	8.744316308
214666_x_at	IREB2	1	7.363963043
222912_at	ARRB1	1	5.213942681
223513_at	CENPJ	1	7.092433523
200880_at	DNAJA1	1	9.367567047
225409_at	C2orf64	1	6.1650454
219581_at	TSEN2	1	8.067656787
202407_s_at	PRPF31	1	9.440251104
202918_s_at	MOBK13	1	7.119855296

204809_at	CLPX		1	6.929358159
205253_at	PBX1		1	6.883346334
223066_at	SNAPIN		1	11.52049542
223708_at	C1QTNF4		1	8.387008061
224325_at	FZD8		1	4.777772612
203223_at	RABEP1		1	10.05813315
228172_at		0	1	6.700063389
227187_at	CBLL1		1	7.8897041
227415_at	LOC283508		1	5.969894114
226202_at	ZNF398		1	8.442806081
225012_at	HDLBP		1	5.455087081
201132_at	HNRNPH2		1	6.77009309
1558956_s_at	IFT80		1	4.556549168
214487_s_at	RAP2A /// RAP2B		1	7.691760363
210110_x_at	HNRNPH3		1	13.02206978
225236_at	RBM18		1	7.8088254
213848_at		0	1	7.15598119
204396_s_at	GRK5		1	4.277502319
201713_s_at	RANBP2		1	8.626586032
223254_s_at	KIAA1333		1	5.404245629
228574_at	TMTC2		1	5.893929277
212170_at	CPNE1 /// RBM12		1	10.74321451
202829_s_at	VAMP7		1	6.995075741
204354_at	POT1		1	6.529401901
202800_at	SLC1A3		1	4.746877906
213984_at	PDS5A		1	6.541796196
222683_at	RNF20		1	8.54222807
226660_at	RPS6KB1		1	7.323720427
202514_at	DLG1		1	5.285007921
201817_at	UBE3C		1	7.078261671
221833_at	LONP2		1	6.086061622
242787_at		0	1	5.525642484
239046_at		0	1	6.86840394
225988_at	HERC4		1	6.086087693
226046_at	MAPK8		1	7.535149306
229511_at	SMARCE1		1	6.266515941
212800_at	STX6		1	5.806111987
202622_s_at	ATXN2		1	8.322673379
238762_at	MTHFD2L		1	4.259154987
226819_at		0	1	8.735088846
201125_s_at	ITGB5		1	7.560061097
212704_at	ZCCHC11		1	8.33101091
226801_s_at	AIDA		1	11.002219
235014_at	LOC147727		1	6.407973002
201111_at	CSE1L		1	5.799964143
235492_at	RNF217		1	8.04622612
215460_x_at	BRD1		1	6.212319765
207294_at	AGTR2		1	5.237553946
214659_x_at	YLP1M1		1	9.957757706
227467_at	RDH10		1	5.214731559
221570_s_at	METTL5		1	6.842453927
225139_at		0	1	10.21464369
200751_s_at	HNRNPC		1	7.680691297
226696_at	RBBP9		1	6.758079704
219457_s_at	RIN3		1	9.202257511
227777_at	C10orf18		1	7.047736794

227524_at		0	1	5.333420697
211700_s_at	TRO		1	7.262933782
212932_at	RAB3GAP1		1	10.9630814
225932_s_at	HNRNPA2B1		1	7.230192872
229815_at		0	1	7.254882927
225948_at	C14orf153		1	7.64861921
228537_at	GLI2		1	9.242488048
211987_at	TOP2B		1	10.04269195
231727_s_at	MIF4GD		1	9.782121925
201607_at	PWP1		1	9.527843738
213861_s_at	FAM119B		1	6.798532213
206555_s_at	THUMPD1		1	6.111546382
227810_at	ZNF558		1	8.2987557
202927_at	PIN1		1	10.81081219
241366_at	RBAK		1	9.687931981
205841_at	JAK2		1	4.767320924
203188_at	B3GNT1		1	7.420607297
203492_x_at	CEP57		1	9.578188593
212266_s_at	SFRS5		1	7.758613058
234929_s_at	SPATA7		1	10.29557949
242760_x_at	PIGB		1	7.555839901
201574_at	ETF1		1	9.27911017
222804_x_at	WDR32		1	7.102383887
203045_at	NINJ1		1	10.31363053
205326_at	RAMP3		1	5.392532545
211721_s_at	ZNF551		1	5.971521172
229731_at	FOXS1		1	5.230696301
212301_at	RTF1		1	10.15611001
221838_at	KLHL22		1	7.805920833
206240_s_at	ZNF136		1	7.510939694
232182_at	LOC286272		1	8.409383033
40837_at	TLE2		1	6.199309652
218569_s_at	KBTBD4		1	8.206310328
203465_at	MRPL19		1	6.232728187
236402_at		0	1	6.376200166
204502_at	SAMHD1		1	6.917251629
215698_at	JARID1A		1	7.13803177
1558881_at	LOC145820		1	6.669900869
212014_x_at	CD44		1	4.355765145
236350_at		0	1	10.52698674
225963_at	KLHDC5		1	7.730606473
205361_s_at	PFDN4		1	7.718563233
203062_s_at	MDC1		1	9.445222419
203139_at	DAPK1		1	4.970580542
219067_s_at	NSMCE4A		1	5.046677394
228737_at	TOX2		1	3.897852213
56919_at	WDR48		1	10.45184061
221622_s_at	TMEM126B		1	6.546607268
203375_s_at	TPP2		1	6.696673063
210320_s_at	DDX52		1	6.561870126
221012_s_at	TRIM8		1	7.597802909
221326_s_at	TUBD1		1	7.936369699
213133_s_at	GCSH /// LOC730107		1	7.24056745
32042_at	ENOX2		1	8.302949774
200090_at	FNTA		1	10.62267643
224718_at	YY1		1	8.280624449

222809_x_at	C14orf65	1	5.100170867
228453_at	KIAA1632	1	6.494182705
224873_s_at	MRPS25	1	8.031347384
204554_at	PPP1R3D	1	5.203081395
205347_s_at	MGC39900 /// TMSB15A	1	4.849420567
202170_s_at	AASDHPPT	1	7.798252399
218042_at	COPS4	1	6.684430292
205117_at	FGF1	1	7.070459181
225232_at	MTMR12	1	6.106375262
223595_at	TMEM133	1	4.131183188
230185_at	THAP9	1	6.384680257
214510_at	GPR20	1	5.05675914
235639_at	0	1	5.199221201
212818_s_at	ASB1	1	9.032982078
233085_s_at	OBFC2A	1	3.989181219
202946_s_at	BTBD3	1	4.048809822
225367_at	PGM2	1	7.774647261
222696_at	AXIN2	1	3.818711332
1558775_s_at	NSMAF	1	9.688314311
1554456_a_at	LINS1	1	7.677302849
226073_at	TMEM218	1	5.587019212
218845_at	DUSP22	1	8.486675693
1552557_a_at	ZDHHC15	1	10.30373228
235106_at	MAML2	1	9.860113611
1564339_a_at	CHRM3	1	5.675303205
1557260_a_at	ZNF382	1	9.378944557
211938_at	EIF4B	1	9.311520387
225140_at	KLF3	1	4.013491796
204001_at	SNAPC3	1	8.417316694
235009_at	FAM44A	1	4.839357243
212371_at	FAM152A	1	6.319223542
213095_x_at	AIF1	1	6.187494932
220591_s_at	EFHC2	1	3.883584616
230176_at	0	1	7.231286288
200785_s_at	LOC100134190 /// LRP1	1	6.462639478
236918_s_at	LRRC34	1	6.141934129
231864_at	ZNF33A	1	7.058283362
235321_at	0	1	7.126985493
202845_s_at	RALBP1	1	6.935740213
241666_at	C3orf23	1	6.444158129
225043_at	SLC15A4	1	8.465014575
238174_at	0	1	8.337214394
228662_at	SOC57	1	5.779978042
1555638_a_at	SAMSN1	1	4.298876225
215038_s_at	SETD2	1	8.791007499
228580_at	HTRA3	1	7.633044129
228391_at	CYP4V2	1	4.131824039
223180_s_at	C18orf55	1	7.447265408
223940_x_at	MALAT1	1	4.682483553
213887_s_at	POLR2E	1	9.123655971
205511_at	FLJ10038	1	5.063386384
232013_at	C9orf102	1	8.457671247
218616_at	INTS12	1	6.924520459
203909_at	SLC9A6	1	6.994604247
1554769_at	ZNF785	1	8.176231502
244354_at	0	1	7.351579403

225385_s_at	HNRPLL		1	7.576112251
212709_at	NUP160		1	6.446578957
1552263_at	MAPK1		1	5.838773775
225693_s_at	CAMTA1		1	7.454992758
212124_at	ZMIZ1		1	7.260232571
1565867_a_at	LOC100131402		1	5.946111802
1554082_a_at	NOL9		1	8.449812146
214960_at	API5		1	6.76208371
213113_s_at	SLC43A3		1	5.474429129
218172_s_at	DERL1		1	5.953723915
218716_x_at	MT01		1	7.110258551
202365_at	UNC119B		1	7.964011878
238438_at	CNOT6L		1	6.704898442
226754_at	ZNF251		1	9.123569677
204155_s_at	KIAA0999		1	8.350615541
211376_s_at	NSMCE4A		1	5.170696529
217738_at	NAMPT		1	3.806683335
243927_x_at	KIAA1429		1	9.784322955
230072_at		0	1	6.991055479
236648_at		0	1	8.138427903
200866_s_at	PSAP		1	7.160396532
212484_at	FAM89B		1	12.62076221
207821_s_at	PTK2		1	8.013359952
209835_x_at	CD44		1	4.437381973
228736_at	HEL308		1	7.994849948
235729_at	ZNF514		1	7.636171641
220992_s_at	C1orf25		1	5.621846256
238782_at		0	1	6.107596705
202382_s_at	GNPDA1		1	7.456891676
223721_s_at	DNAJC12		1	4.395497562
202998_s_at	ENTPD4 /// LOXL2		1	3.842843676
222629_at	REV1		1	6.868877014
226697_at	FAM114A1		1	5.199425989
1556059_s_at	SPEN		1	8.325297682
206170_at	ADRB2		1	3.705730061
229442_at	C18orf54		1	7.573502659
221432_s_at	SLC25A28		1	10.08248681
235735_at		0	1	3.665083389
235689_at	MTFMT		1	7.437067624
228393_s_at	ZNF302		1	4.443298976
1560648_s_at	TSPYL1		1	9.511542603
238646_at		0	1	6.407277509
212712_at	CAMSAP1		1	8.93240988
206474_at	PCTK2		1	8.131765625
208963_x_at	FADS1		1	5.972676695
220346_at	MTHFD2L		1	8.250860491
242434_at		0	1	10.07290794
238320_at	NCRNA00084		1	5.099387283
239432_at	FLJ31306		1	6.310420478
217946_s_at	SAE1		1	7.681297237
232667_at		0	1	7.954110243
210658_s_at	GGA2		1	6.073376857
238122_at	RBM12B		1	6.749296815
212213_x_at	OPA1		1	8.328062178
222164_at	FGFR1		1	7.233472206
236834_at	SCFD2		1	7.196696577

216591_s_at	hCG_1776980 /// SDHC	1	6.156064992
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236634_at	C8orf48	1	8.135877571
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220471_s_at	MYCT1	1	7.383854911
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229664_at	MAPK8	1	9.524504508
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238454_at	ZNF540	1	6.786700257
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219974_x_at	ECHDC1	1	5.710457617
1554606_at	CEP120	1	10.14368073
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229670_at		0	4.252328332
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229822_at		0	7.464046332
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226033_at	USP31	1	7.509924139
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241859_at	PLCL1	1	8.79269939
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220818_s_at	TRPC4	1	4.335209111
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215788_at	C1orf222	2	-9.776029793
200644_at	MARCKSL1	2	-5.692945991
232593_at	LINCR	2	-5.603376998
230191_at	TTBK1	2	-10.13810338
1564164_at	DENND1B	2	-5.138917523
210325_at	CD1A	2	-8.878792063
240076_at	0	2	-8.928601362
237307_at	0	2	-9.210112254
241202_at	0	2	-11.6046336
216243_s_at	IL1RN	2	-4.908268543
206640_x_at	GAGE12B /// GAGE12C /// GAGE12D /// GAGE12E /// GAGE12F /// GAGE12G /// GAGE12H /// GAGE12I /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2E /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7	2	-4.737949153
1558324_a_at	TMEM72	2	-7.487352064
237497_at	0	2	-7.415040792
223755_at	KIRREL2	2	-7.654181302
204636_at	COL17A1	2	-4.832021169
228673_s_at	EML4	2	-10.17733008
234008_s_at	CES3	2	-9.653715372
216374_at	LOC728137 /// LOC728395 /// LOC728412 /// TSPY1	2	-7.305246083
224032_x_at	SPANXA1 /// SPANXA2 /// SPANXC	2	-8.351529753
217200_x_at	CYB561	2	-11.32778498

	GAGE1 /// GAGE12B /// GAGE12C /// GAGE12D /// GAGE12E /// GAGE12F /// GAGE12G /// GAGE12H /// GAGE12I /// GAGE12J /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2D /// GAGE2E /// GAGE4 /// GAGE5 /// GAGE6 /// GAGE7 /// GAGE8		
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228139_at	RIPK3	2	-8.726219503
204997_at	GPD1	2	-4.478240441
229524_at	KIAA0494	2	-6.094106337
202338_at	TK1	2	-5.172574874
219707_at	CPNE7	2	-11.53737093
223874_at	ARP11	2	-6.289927821
228323_at	CASC5	2	-3.694655368
1563405_at	ATP4B	2	-9.363169937
229330_at		0	2 -6.747709826
232554_at	LRRCS6	2	-13.02046955
226599_at	FHDC1	2	-8.382741107
237266_at	LOC100133686	2	-8.951623067
231044_at	C1orf194	2	-7.663699611
220679_s_at	CDH7	2	-6.889789167
205297_s_at	CD79B	2	-4.268099091
206998_x_at	PRB3	2	-10.06358833
1559915_at		0	2 -10.14318297
230982_at	SOX1	2	-7.691341502
215184_at	DAPK2	2	-9.176117006
203435_s_at	MME	2	-3.815934248
220396_at		0	2 -9.482275004
220234_at	CA8	2	-4.448961482
219883_at	C11orf20	2	-10.1768816
232367_x_at	ZNF598	2	-9.950235865
207380_x_at	NOX1	2	-7.047801249
241045_at	JMJD5	2	-7.732166321
1552915_at	IL28A	2	-7.870845598
210060_at	PDE6G	2	-9.062395344
202674_s_at	LMO7	2	-5.516400425
210761_s_at	GRB7	2	-5.345927561
1566550_at		0	2 -8.106475818
239869_at		0	2 -10.35615245
232542_at	COL9A2	2	-10.81219755
1552833_at	B3GNT6	2	-5.918957643
220515_at	DUSP21	2	-7.714375266
221232_s_at	ANKRD2	2	-7.858543535
224001_at	FAM135B	2	-9.114181436
208606_s_at	WNT4	2	-5.051951175
221173_at	USH1C	2	-6.262012446
214750_at	PLAC4	2	-8.72474484
235892_at		0	2 -4.198174287
225757_s_at	CLMN	2	-11.03164371
237763_at		0	2 -11.19364745
213042_s_at	ATP2A3	2	-5.627818101
229690_at	FAM109A	2	-11.94259314
201250_s_at	SLC2A1	2	-4.809090586

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243018_at		0	2	-3.561758234
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222901_s_at	KCNJ16		2	-9.855244964
239341_at		0	2	-7.774386889
1569579_at		0	2	-8.026799482
235741_at	PPIA		2	-11.15105889
1553566_at	C12orf53		2	-7.862617857
1569127_at		0	2	-9.266954062
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219573_at	LRRC16A		2	-5.801924859
220584_at	FLJ22184		2	-8.686726728
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212314_at	KIAA0746 /// SERINC2		2	-4.220775312
218317_x_at	GIYD1 /// GIYD2		2	-7.050514645
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209373_at	MALL		2	-3.73752865
209992_at	PFKFB2		2	-7.062654507
204558_at	RAD54L		2	-7.34362737
236041_at		0	2	-8.229912516
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1570430_at		0	2	-10.07285517
236286_at	PROCA1		2	-11.88432818
230096_at		0	2	-8.250038487
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211434_s_at	CCRL2 /// LOC727811		2	-5.294953213
229245_at	PLEKHA6		2	-4.341892618
240672_at		0	2	-9.159661509
1557651_x_at	GALE		2	-12.65846406
215066_at	PTPRF		2	-8.966795331
216119_s_at	SPEF1		2	-8.545303295
214798_at	ATP2C2		2	-6.921642101
236857_at		0	2	-8.362899506
1558327_at	ZDHHC18		2	-8.630046884
227996_at	FARP1		2	-5.759145596
1563587_at	CDH4		2	-7.526405726
1558329_at	NFKBIL2		2	-6.076990332
202735_at	EBP		2	-5.964644316
230006_s_at	SVIP		2	-4.63225893
242497_at	TRAFD1		2	-7.636417405
243603_at		0	2	-11.52849738
1552819_at	C21orf86		2	-7.414305344
208072_s_at	DGKD		2	-8.843297576
244385_at	JMJD2C		2	-8.557726932
217117_x_at	MUC3A		2	-7.710273771
226667_x_at	EPN1		2	-13.72981986
233741_at	FTCD		2	-6.372550693
1561355_at	LOC692247		2	-8.424712203
1560513_at	LOC400568		2	-8.74453006
241371_at		0	2	-7.561860844
1554222_at	MGC45922		2	-7.577340955
234285_at	SYNGAP1		2	-8.265070479
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211484_s_at	DSCAM		2	-8.977681607

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227240_at	NGEF		2	-4.815426002
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242733_at		0	2	-8.227627937
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238837_at	PHF8		2	-7.689330234
223870_at	FBXW10		2	-8.870088192
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234834_at		0	2	-11.40874861
210951_x_at	RAB27A		2	-4.35138188
244612_at		0	2	-6.141240094
219753_at	STAG3		2	-8.783638796
219439_at	C1GALT1		2	-5.105449461
217752_s_at	CNDP2		2	-6.496732283
220377_at	FAM30A		2	-7.713065775
215672_s_at	AHCYL2		2	-5.148115901
1553123_at	WDR62		2	-7.600957222
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51158_at	FAM174B		2	-5.496140623
220303_at	PDZD3		2	-11.31134384
1559638_at	C1orf200		2	-8.516640723
233895_at	ANKRD24		2	-9.571214912
1553727_at	B4GALNT3		2	-12.58535431
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212020_s_at	MKI67		2	-5.74564714
1552857_a_at	HTR6		2	-7.894076379
212814_at	AHCYL2		2	-4.501165984
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229469_at	CTD-2267G17.3 /// XAGE2		2	-9.895805376
221436_s_at	CDCA3		2	-6.196965826
238645_at		0	2	-11.66078995
205914_s_at	GRIN1		2	-7.657277417
201704_at	ENTPD6		2	-6.726458272
238113_at		0	2	-9.178688446
203838_s_at	TNK2		2	-6.789213783
242350_s_at	LOC100128098		2	-4.616751248
208389_s_at	SLC1A2		2	-11.10722472
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223695_s_at	ARSD		2	-4.573527925
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229424_s_at	ARHGAP27		2	-8.526539412
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237212_at		0	2	-8.836003694
214440_at	NAT1		2	-4.009922954
1563808_at	MCF2L		2	-8.838808249
231978_at	TPCN2		2	-3.673284317
223239_at	C14orf129		2	-5.930854687
223990_at	C4orf17		2	-9.4856501
229771_at		0	2	-9.769380019
1554539_a_at	RHOF		2	-5.301381712
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1555616_at		0	2	-7.887305096
241439_at		0	2	-5.565203598
228428_at	FAM102A		2	-6.573193007
222025_s_at	OPLAH		2	-6.095350193
243010_at	MSI2		2	-9.107084855
244409_at	CCDC154		2	-13.4434938
206276_at	LY6D		2	-4.302906587
1552749_a_at	KLC3		2	-10.85643966
221404_at	IL1F6		2	-9.319075063
235383_at	MYO7B		2	-7.445102649
229396_at	OVOL1		2	-4.405991887
234882_at		0	2	-10.1746797
205563_at	KISS1		2	-8.864892183
209844_at	HOXB13		2	-5.541731395
221859_at	SYT13		2	-7.246253675
208157_at	SIM2		2	-7.09334179
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219835_at	PRDM8		2	-7.562286526
219517_at	ELL3		2	-6.329915805
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232828_at		0	2	-7.636052826
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228898_s_at	SMARCB1		2	-6.946823847
225513_at	SCRN2		2	-11.01009565
232654_s_at	UGT1A6		2	-4.787012967
238884_at		0	2	-5.108561973
238366_at	NCRNA00082		2	-9.513405468
231457_at		0	2	-11.32745262
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222878_s_at	OTUB2		2	-9.021288481
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231025_at		0	2	-7.407623367
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215328_at	EFR3B		2	-10.03820495
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221000_s_at	KAZALD1		2	-9.754418171
222457_s_at	LIMA1		2	-5.389687864

244341_at		0	2	-4.534892345
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225418_at	PVRL2		2	-8.472335114
1553115_at	NKD1		2	-7.360456479
1563074_at	LOC255654		2	-9.305501168
236580_at		0	2	-9.527613998
205950_s_at	CA1		2	-5.862691951
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213078_x_at	LPCAT4		2	-5.644990246
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77508_r_at	LOC100133585 /// RABEP2		2	-11.79579307
221750_at	HMGCS1		2	-4.981817718
238333_s_at	SPRN		2	-9.603768687
209367_at	STXBP2		2	-7.784505422
220087_at	BCMO1		2	-5.270918836
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1552872_at	NCRNA00105		2	-5.909450885
217149_x_at	TNK1		2	-14.72052764
210922_at		0	2	-10.04262466
221668_s_at	DNAI2		2	-6.308404121
212268_at	SERPINB1		2	-4.593433276
211298_s_at	ALB		2	-4.675634413
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229721_x_at	DERL3		2	-4.682442887
219215_s_at	SLC39A4		2	-4.320291068
1554183_s_at	TRIM73 /// TRIM74		2	-8.916187864
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1566630_at	LOC100134089		2	-11.68385453
237019_at		0	2	-7.086319073
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221521_s_at	GIN52		2	-4.756656914
205670_at	GAL3ST1		2	-8.469269447
218951_s_at	PLCXD1		2	-5.156679995
222587_s_at	GALNT7		2	-4.571267391
204231_s_at	FAAH		2	-9.634617442
220922_s_at	SPANXA1 /// SPANXA2 /// SPANXB1 /// SPANXB2 /// SPANXC /// SPANXF1		2	-8.303705216
234092_s_at	HAPLN4 /// TM6SF2		2	-4.663506078
1556340_at	MAPK12		2	-9.211344478
206737_at	WNT11		2	-7.387568297
203673_at	TG		2	-9.160553589
231401_s_at		0	2	-7.974023553
211738_x_at	ELA3A		2	-4.709153707
236736_at		0	2	-11.06694474

229104_s_at	GPR39	2	-11.0216823
224079_at	IL17C	2	-12.50546468
211848_s_at	CEACAM7	2	-4.147703007
1569200_at	0	2	-8.362303192
208235_x_at	GAGE12F /// GAGE12G /// GAGE12I /// GAGE2A /// GAGE2B /// GAGE2C /// GAGE2E /// GAGE4 /// GAGE7	2	-5.078627352
208216_at	DLX4	2	-9.630400219
225548_at	SHROOM3	2	-4.497357844
1553542_at	CCDC125	2	-6.684318918
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218797_s_at	SIRT7	2	-7.598562432
1554616_at	SERPINB8	2	-9.513164902
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1564281_at	LOC285708	2	-8.461806698
1566643_a_at	0	2	-7.01827217
1555374_at	0	2	-12.70168873
227706_at	SPIRE2	2	-7.921804057
222333_at	ALS2CL	2	-12.45079149
203474_at	IQGAP2	2	-4.364734984
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235633_at	0	2	-8.090226526
240069_at	0	2	-7.247632925
210025_s_at	CARD10	2	-11.58089066
1561171_a_at	FLJ36131 /// LOC100131452 /// LOC100132025 /// LOC100132566 /// LOC100132727 /// LOC729272	2	-9.968616524
206513_at	AIM2	2	-3.879794207
244600_at	0	2	-6.619661886
228403_at	ENHO	2	-13.85309988
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1553734_at	AK7	2	-8.5351144
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204740_at	CNKSRI	2	-7.5232651
1555763_x_at	MKL1	2	-5.19271949
90265_at	ADAP1	2	-6.386667765
220871_at	0	2	-9.543694054
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226121_at	DHRS13	2	-9.765069203
40472_at	LPCAT4	2	-5.753838458
228818_at	0	2	-7.868681493
46323_at	CANT1	2	-5.328815713
232642_at	VWA5B2	2	-11.25567413
203236_s_at	LGALS9	2	-7.028815495
1557129_a_at	FAM111B	2	-6.246885797
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1554517_x_at	LOC203274	2	-7.622762187
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233658_at	0	2	-7.154145987
230487_at	C6orf99 /// LOC100130967	2	-10.80007729
243653_at	SHROOM3	2	-8.486111157

220344_at	C11orf16		2	-9.741145796
1552623_at	HSH2D		2	-8.693622757
230093_at	RSPH1		2	-5.192160897
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201283_s_at	TRAK1		2	-6.532292268
230131_x_at	ARSD		2	-5.877909651
229720_at	BAG1		2	-4.207813553
218726_at	HJURP		2	-5.111480032
219768_at	VTCN1		2	-6.038463212
238072_at		0	2	-13.2739616
242649_x_at	C15orf21		2	-6.071014864
225354_s_at	SH3BGRL2		2	-5.203102859
219739_at	RNF186		2	-3.66396357
210791_s_at	RICS		2	-6.463291974
232378_at	SLC5A9		2	-7.829399219
1559702_at		0	2	-6.846833361
206082_at	HCP5		2	-5.830050107
241855_s_at		0	2	-8.632964213
242885_at		0	2	-11.46562204
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225966_at	C17orf89 /// LOC100133328		2	-8.946398172
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229292_at	EPB41L5	2	-5.781962354
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239156_at	0	2	-11.19576865
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218963_s_at	KRT23	2	-5.157853285
223509_at	CLDN2	2	-3.798193536
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221610_s_at	STAP2	2	-6.827823267

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231832_at	GALNT4	2	-5.435294066
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244056_at	SFTA2	2	-3.649958139
225726_s_at	PLEKHH1	2	-5.926150262
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219756_s_at	POF1B	2	-4.629825251
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230573_at	SGK2	2	-6.911078767
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238028_at	LOC100128918	2	-7.971964939
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209919_x_at	GGT1		2	-10.66287199
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242773_at	SLC5A1		2	-6.063312847
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238846_at	TNFRSF11A		2	-5.127476085
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207131_x_at	GGT1	2	-10.68521264
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224707_at	C5orf32	2	-7.621635103
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236129_at	GALNT5	2	-5.403237689
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226622_at	MUC20	2	-4.320668778
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225792_at	HOOK1	2	-5.065963747
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227985_at	0	2	-7.538405516
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235955_at	MARVELD2	2	-7.560079477
242417_at	LOC283278	2	-9.52028713
1556554_at	TRIM50	2	-7.649007802
213085_s_at	WWC1	2	-7.359894957
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237466_s_at	HHIP	2	-6.691429624
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219194_at	SEMA4G	2	-9.912095929
238385_at	C6orf58	2	-5.666620223
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224189_x_at	EHF	2	-5.68215976
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223427_s_at	EPB41L4B	2	-5.847458986
218002_s_at	CXCL14	2	-4.394483764
206242_at	TM4SF5	2	-6.489900665
204981_at	SLC22A18	2	-7.164749609
237654_at	C14orf50	2	-10.38135652
221655_x_at	EPS8L1	2	-11.57363876
218872_at	TESC	2	-5.436087918
229599_at	LOC440335	2	-9.600534992
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214421_x_at	CYP2C9	2	-8.251098516
203287_at	LAD1	2	-8.127232146
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210058_at	MAPK13	2	-7.059861751
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210119_at	KCNJ15	2	-5.479252036
232322_x_at	STARD10	2	-7.840760873
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210390_s_at	CCL14 /// CCL15	2	-4.39877224
206576_s_at	CEACAM1	2	-8.761445747
206000_at	MEP1A	2	-3.717077313
205929_at	GPA33	2	-4.676596521
232977_x_at	MYH14	2	-9.724797528
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65517_at	AP1M2	2	-8.948225717
210059_s_at	MAPK13	2	-6.786305928
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234290_x_at	MYH14	2	-9.123765943

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232321_at	MUC17	2	-3.736584869
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215118_s_at	IGHG1	2	-4.872034174
1553105_s_at	DSG2	2	-5.549303057
202488_s_at	FXD3	2	-9.102720312
227452_at	0	2	-5.816756242
236118_at	LOC100128893 /// LOC728473	2	-7.165855846
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214106_s_at	GMDS	2	-8.494357596
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222675_s_at	BAIAP2L1	2	-9.62221525
227371_at	BAIAP2L1	2	-6.977146364
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220017_x_at	CYP2C9	2	-8.129872237
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205660_at	OASL	2	-7.818228994
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226817_at	DSC2	2	-6.445365729
219962_at	ACE2	2	-4.253677308
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205267_at	POU2AF1	2	-4.476223476
222484_s_at	CXCL14	2	-4.784312014
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211184_s_at	USH1C	2	-6.791825691
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225165_at	PPP1R1B	2	-5.637319149
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228806_at	RORC	2	-9.98299316
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229105_at	GPR39	2	-8.922802343
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213412_at	TJP3	2	-10.39904104
231008_at	UNC5CL	2	-5.730011125
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236083_at	BCL2L15	2	-8.100452755
206094_x_at	UGT1A1 /// UGT1A10 /// UGT1A3 /// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	2	-5.897167988
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222245_s_at	FER1L4	2	-11.25163613
234709_at	CAPN13	2	-6.073333896
236225_at	GGT6	2	-7.678433067
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232083_at	KIF16B	2	-9.914162545
228707_at	CLDN23	2	-4.546288615
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216470_x_at	PRSS1	2	-6.578586823
209008_x_at	KRT8	2	-6.752482343
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227163_at	GSTO2	2	-6.849558998
211778_s_at	OVOL2	2	-7.047021462
215108_x_at	TOX3	2	-5.103978923
228051_at	LOC202451	2	-7.972231435
226129_at	FAM83H	2	-6.710936585
226403_at	TMC4	2	-7.541580003
218796_at	FERMT1	2	-6.397297195
239155_at	CXADRP1	2	-6.696996002
242013_at	BCL2L15	2	-7.638261643
219411_at	ELMO3	2	-9.64580055
223949_at	TMPSRSS3	2	-4.98313072
227742_at	CLIC6	2	-4.804127403
210107_at	CLCA1	2	-4.097412963
204679_at	KCNK1	2	-6.581256774
205476_at	CCL20	2	-3.802958351
202712_s_at	CKMT1A /// CKMT1B /// LOC100133623	2	-6.243225911
204919_at	PRR4	2	-5.035165256
215444_s_at	TRIM31	2	-5.80970258
238017_at	SDR16C5	2	-4.097175498
217590_s_at	TRPA1	2	-6.732216337
214465_at	ORM1 /// ORM2	2	-6.099768991
207601_at	SULT1B1	2	-7.753412308
209211_at	KLF5	2	-5.659321043
228462_at	IRX2	2	-5.993352143
217110_s_at	MUC4	2	-6.671110194
219856_at	C1orf116	2	-7.533823791
209966_x_at	ESRRG	2	-5.713064405
221874_at	KIAA1324	2	-4.912466414

202286_s_at	TACSTD2	2	-5.19888692
209270_at	LAMB3	2	-7.445987787
202833_s_at	SERPINA1	2	-4.292776119
213874_at	SERPINA4	2	-9.421004597
229254_at	MFSD4	2	-4.948787534
209498_at	CEACAM1	2	-6.447900878
220421_at	BTNL8 /// LOC653117	2	-6.270151575
230238_at	ANKRD43	2	-6.125192551
215129_at	PIK3C2G	2	-5.839221642
238197_at	GATA5	2	-8.200990512
209260_at	SFN	2	-7.518582239
210608_s_at	FUT2	2	-7.152645478
206262_at	ADH1C	2	-3.801109463
223385_at	CYP2S1	2	-7.493885047
226226_at	TMEM45B	2	-6.945654021
226803_at	CHMP4C	2	-5.702600817
228956_at	UGT8	2	-5.047983184
221241_s_at	BCL2L14	2	-6.892459445
202936_s_at	SOX9	2	-5.534753534
210381_s_at	CCKBR	2	-6.895107208
222257_s_at	ACE2	2	-5.372024129
241994_at	XDH	2	-6.101561932
217901_at	DSG2	2	-6.409424777
208170_s_at	TRIM31	2	-5.014903619
207158_at	APOBEC1	2	-7.231771237
207981_s_at	ESRRG	2	-4.638560021
216381_x_at	AKR7A3	2	-8.593553096
216905_s_at	ST14	2	-6.868194335
227492_at	0	2	-6.330437039
209212_s_at	KLF5	2	-6.61587141
218035_s_at	RBM47	2	-8.214544045
204304_s_at	PROM1	2	-4.660900299
243582_at	SH3RF2	2	-8.251112054
229369_at	VSIG2	2	-7.167370785
204875_s_at	GMDS	2	-7.123075209
201467_s_at	NQO1	2	-6.870682915
214774_x_at	TOX3	2	-5.028207657
216623_x_at	TOX3	2	-5.146688131
230772_at	0	2	-8.920589837
219233_s_at	GSDMB	2	-7.478903651
244780_at	SGPP2	2	-6.371618142
208300_at	PTPRH	2	-8.659991482
227320_at	FAM101A	2	-7.400488637
211695_x_at	MUC1	2	-8.238022728
202826_at	SPINT1	2	-7.408538821
203824_at	TSPAN8	2	-4.668565074
205221_at	HGD /// LOC100132552 /// LOC727722	2	-7.428020777
206681_x_at	GP2	2	-6.561590235
212657_s_at	IL1RN	2	-6.484010776
213285_at	TMEM30B	2	-7.134488368
1552834_at	B3GNT6	2	-9.058635765
219850_s_at	EHF	2	-5.754423066
227177_at	CORO2A	2	-7.617956471
218211_s_at	MLPH	2	-7.155430922
235871_at	LIPH	2	-8.202749953

201839_s_at	EPCAM	2	-4.836250742
91826_at	EPS8L1	2	-11.75146829
226560_at	0	2	-6.295958324
221665_s_at	EPS8L1	2	-10.94931951
240303_at	TMC5	2	-6.15613512
208165_s_at	PRSS16	2	-8.211104418
33322_i_at	SFN	2	-6.630023082
210397_at	DEFB1	2	-6.452528528
204475_at	MMP1	2	-3.579157885
219404_at	EPS8L3	2	-8.143547726
239196_at	ANKRD22	2	-8.882090416
229223_at	0	2	-11.92223906
205402_x_at	PRSS2	2	-6.267268138
202528_at	GALE	2	-9.222758145
205969_at	AADAC	2	-4.740739283
222904_s_at	TMC5	2	-5.904175063
209921_at	SLC7A11	2	-6.724407809
213421_x_at	PRSS3	2	-7.336877219
209772_s_at	CD24	2	-6.87738481
223232_s_at	CGN	2	-8.172235782
230615_at	DUOXA2	2	-8.868757736
238103_at	0	2	-4.864084822
207463_x_at	PRSS3	2	-7.31533704
219014_at	PLAC8	2	-5.409741875
231211_s_at	LOC541469	2	-10.20009137
236098_at	hCG_1643808	2	-8.669646242
210519_s_at	NQO1	2	-7.578123085
225299_at	MYO5B	2	-6.872742687
205632_s_at	PIP5K1B	2	-7.179128021
228708_at	RAB27B	2	-6.2031229
41469_at	PI3	2	-4.954047046
227725_at	ST6GALNAC1	2	-6.241181387
208651_x_at	CD24	2	-6.599399653
218677_at	S100A14	2	-6.450397106
228360_at	LYPD6B	2	-7.924551609
225301_s_at	MYO5B	2	-7.357971861
209771_x_at	CD24	2	-6.847788806
222712_s_at	MUC13	2	-5.919687472
235141_at	MARVELD2	2	-8.227133932
235651_at	0	2	-7.498546102
227306_at	0	2	-6.480006566
236279_at	0	2	-8.856944705
220161_s_at	EPB41L4B	2	-7.692162745
213456_at	SOSTDC1	2	-4.889429866
226961_at	PRR15	2	-7.26571724
206691_s_at	PDIA2	2	-7.748778915
207222_at	PLA2G10	2	-6.26105171
203917_at	CXADR	2	-7.12236373
1564333_a_at	PSAPL1	2	-11.14715005
223862_at	GHRL	2	-5.897614724
208250_s_at	DMBT1	2	-4.701102711
204437_s_at	FOLR1	2	-7.311430646
235591_at	SSTR1	2	-5.516935068
218960_at	TMPRSS4	2	-6.785907856
236430_at	TMED6	2	-5.4365895
209950_s_at	VILL	2	-8.552908008

1553296_at	GPR128	2	-5.44235858
204073_s_at	C11orf9	2	-9.891758167
206212_at	CPA2	2	-7.391328712
216379_x_at	CD24	2	-7.015051246
218687_s_at	MUC13	2	-6.188789523
220030_at	STYK1	2	-6.895561248
229964_at	C9orf152	2	-6.233149227
226374_at	0	2	-7.315849601
202935_s_at	SOX9	2	-6.022295176
219010_at	C1orf106	2	-6.496535598
226535_at	ITGB6	2	-5.137223255
228303_at	GALNT6	2	-8.572734908
266_s_at	CD24	2	-6.636727861
225822_at	TMEM125	2	-8.430956021
205470_s_at	KLK11	2	-7.857203948
229777_at	CLRN3	2	-5.051406797
1552797_s_at	PROM2	2	-6.611028326
233565_s_at	SDCBP2	2	-9.884026428
204855_at	SERPINB5	2	-5.047052758
215125_s_at	UGT1A1 /// UGT1A10 /// UGT1A3 /// UGT1A4 /// UGT1A5 /// UGT1A6 /// UGT1A7 /// UGT1A8 /// UGT1A9	2	-5.3743622
210827_s_at	ELF3	2	-7.083689208
225846_at	RBM35A	2	-5.501507559
206199_at	CEACAM7	2	-5.152154219
213506_at	F2RL1	2	-5.850260108
211372_s_at	IL1R2	2	-7.22984064
219508_at	GCNT3	2	-5.702666991
229842_at	ELF3	2	-7.233986506
204580_at	MMP12	2	-4.763217991
238750_at	0	2	-8.136265909
220639_at	TM4SF20	2	-4.600170804
226185_at	CDS1	2	-7.072837232
224650_at	MAL2	2	-5.254812069
205403_at	IL1R2	2	-6.056668388
210064_s_at	UPK1B	2	-6.028437617
218186_at	RAB25	2	-6.411777695
204750_s_at	DSC2	2	-8.829970136
213693_s_at	MUC1	2	-8.39041078
207847_s_at	MUC1	2	-7.851952398
208650_s_at	CD24	2	-6.17264512
209114_at	TSPAN1	2	-6.27542096
210065_s_at	UPK1B	2	-5.572206025
204378_at	BCAS1	2	-6.916963996
238439_at	ANKRD22	2	-6.670678197
203021_at	SLPI	2	-6.553607192
1553589_a_at	PDZK1IP1	2	-6.037028521
205190_at	PLS1	2	-5.400852098
205892_s_at	FABP1	2	-3.772315329
235144_at	0	2	-6.561200272
209847_at	CDH17	2	-4.577068792
216687_x_at	UGT2B15	2	-8.598659236
213921_at	SST	2	-4.732523955
204818_at	HSD17B2	2	-5.118072852

201468_s_at	NQO1	2	-8.608197794
221132_at	CLDN18	2	-4.837396056
226553_at	TMPRSS2	2	-9.631341985
201510_at	ELF3	2	-7.063661074
211657_at	CEACAM6	2	-4.491672956
205041_s_at	ORM1 /// ORM2	2	-5.469376632
219395_at	RBM35B	2	-11.04966636
219450_at	C4orf19	2	-8.596803648
204519_s_at	PLL	2	-8.976173929
223895_s_at	EPN3	2	-13.82859555
40284_at	FOXA2	2	-7.489004042
228004_at	C20orf56	2	-6.648605305
203397_s_at	GALNT3	2	-6.905125668
235350_at	C4orf19	2	-9.357334922
228463_at	FOXA3	2	-7.615741616
205709_s_at	CDS1	2	-7.94693607
224209_s_at	GDA	2	-7.118398698
211689_s_at	TMPRSS2	2	-7.040789553
210103_s_at	FOXA2	2	-9.647888056
203559_s_at	ABP1	2	-5.793663324
209301_at	CA2	2	-4.848205011
227196_at	RHPN2	2	-6.696179158
221122_at	HRASLS2	2	-7.79376054
242093_at	SYTL5	2	-6.742669604
223484_at	C15orf48	2	-5.904368067
203757_s_at	CEACAM6	2	-4.514908688
207249_s_at	SLC28A2	2	-5.513146447
210641_at	CAPN9	2	-8.173428916
204705_x_at	ALDOB	2	-5.872704338
227676_at	FAM3D	2	-7.659912916
209173_at	AGR2	2	-5.341202841
208473_s_at	GP2	2	-6.439810443
236001_at	LOC400573	2	-10.7593829
219630_at	PDZK1IP1	2	-6.310768217
228865_at	C1orf116	2	-8.16928232
214070_s_at	ATP10B	2	-8.085026548
210652_s_at	TTC39A	2	-8.382762571
217109_at	MUC4	2	-6.608556401
219127_at	ATAD4	2	-6.925302133
202489_s_at	FXD3	2	-6.685117311
215103_at	CYP2C18	2	-6.790145666
219956_at	GALNT6	2	-7.777506048
242271_at	SLC26A9	2	-9.267677293
205623_at	ALDH3A1	2	-8.454275907
206664_at	SI	2	-3.756596101
231982_at	LOC284422	2	-6.578228256
219564_at	KCNJ16	2	-8.059312108
223631_s_at	C19orf33	2	-6.754973264
225645_at	EHF	2	-5.695496735
211357_s_at	ALDOB	2	-5.002145269
219263_at	RNF128	2	-5.979520395
205199_at	CA9	2	-9.303553047
1553986_at	RASEF	2	-9.0647199
214234_s_at	CYP3A5	2	-7.200635473
214324_at	GP2	2	-6.715333726
201131_s_at	CDH1	2	-6.182703885

228241_at	AGR3	2	-4.857896973
221133_s_at	CLDN18	2	-5.361306476
217238_s_at	ALDOB	2	-4.844148619
209309_at	AZGP1	2	-6.887474606
220177_s_at	TMPRSS3	2	-7.115422675
201650_at	JUP /// KRT19	2	-5.837181992
230323_s_at	TMEM45B	2	-6.743847125
219429_at	FA2H	2	-8.154426563
235638_at	RASSF6	2	-7.346372216
227475_at	FOXQ1	2	-6.293974717
226248_s_at	KIAA1324	2	-6.482463592
228232_s_at	VSIG2	2	-6.691685008
212768_s_at	OLFM4	2	-3.512554795
229147_at	0	2	-7.052202517
205597_at	SLC44A4	2	-6.928313718
33323_r_at	SFN	2	-7.579954662
204272_at	LGALS4	2	-5.77010657
221095_s_at	KCNE2	2	-8.178846675
219580_s_at	TMC5	2	-7.172446974
207392_x_at	UGT2B15	2	-7.565110243
203453_at	SCNN1A	2	-6.763653502
219476_at	C1orf116	2	-7.455212404
207912_s_at	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4 /// LOC732447	2	-3.678404663
203924_at	GSTA1	2	-6.148676176
239370_at	0	2	-7.976560405
214046_at	FUT9	2	-5.609235891
229659_s_at	0	2	-5.941007728
228058_at	LOC124220	2	-7.812350984
208126_s_at	CYP2C18	2	-7.7557406
205765_at	CYP3A5	2	-6.501023777
219727_at	DUOX2	2	-7.607402098
202525_at	PRSS8	2	-8.304269636
202018_s_at	LTF	2	-5.606794894
210297_s_at	MSMB	2	-4.603108872
208063_s_at	CAPN9	2	-9.720255418
217187_at	MUC5AC	2	-10.63060237
214133_at	LOC100133432 /// MUC6	2	-8.856977131
205979_at	SCGB2A1	2	-6.490146248
205927_s_at	CTSE	2	-5.594437438
219795_at	SLC6A14	2	-6.060041781
229070_at	C6orf105	2	-6.722431963
220468_at	ARL14	2	-6.571721781
240304_s_at	TMC5	2	-7.06933424
202831_at	GPX2	2	-7.628654172
1565666_s_at	LOC100133432 /// LOC100133761 /// MUC6	2	-6.280369913
229030_at	CAPN8	2	-8.582163809
214135_at	CLDN18	2	-6.138987144
234370_at	VSIG1	2	-8.377292745
214235_at	CYP3A5	2	-9.906812807
228969_at	AGR2	2	-7.750283312
207430_s_at	MSMB	2	-4.70668249
204351_at	S100P	2	-7.083182814
209752_at	REG1A	2	-4.460752205
227194_at	FAM3B	2	-6.263456333

206239_s_at	SPINK1	2	-6.202460363
232578_at	CLDN18	2	-5.138506568
205343_at	SULT1C2	2	-7.393552304
205815_at	REG3A	2	-4.40132199
205342_s_at	SULT1C2	2	-6.85890834
213953_at	KRT20	2	-5.087902505
201884_at	CEACAM5	2	-5.888552995
203240_at	FCGBP /// LOC100133944	2	-7.85443595
205513_at	TCN1	2	-6.298401466
211470_s_at	SULT1C2	2	-7.045220894
207139_at	ATP4A	2	-7.72285773
226147_s_at	PIGR	2	-6.360002342
226067_at	C20orf114	2	-6.656082943
210143_at	ANXA10	2	-6.001730156
205009_at	TFF1	2	-5.953806308
212531_at	LCN2	2	-7.465927659
206561_s_at	AKR1B10	2	-6.234653656
241137_at	DPCR1	2	-7.500570594
243764_at	VSIG1	2	-7.15222623
231646_at	DPCR1	2	-7.417026724
205261_at	PGC	2	-5.851980475
226960_at	CXCL17	2	-8.902864553
205319_at	PSCA	2	-7.702430558
238383_at	C6orf58	2	-6.426541767
214303_x_at	MUC5AC	2	-9.568217007
214476_at	TFF2	2	-7.658511922
207546_at	ATP4B	2	-7.215802801
1555236_a_at	PGC	2	-5.81446978
214385_s_at	MUC5AC	2	-8.301981334
207033_at	GIF	2	-6.969294166
213265_at	PGA3 /// PGA4 /// PGA5	2	-6.799243904
206334_at	LIPF	2	-6.573529133
238222_at	GKN2	2	-7.658369049
220191_at	GKN1	2	-7.041732932

Figure 20

Proliferative subtype vs Metabolic subtype

probeset	GeneName	Pro1	Meta2	t
203820_s_at	IGF2BP3		1	7.581779073
209942_x_at	MAGEA3		1	4.186209781
214612_x_at	MAGEA2 /// MAGEA2B /// MAGEA3 /// MAGEA6		1	4.178889548
224646_x_at	H19		1	5.986113293
211506_s_at	IL8		1	7.432131539
217428_s_at	COL10A1		1	6.012800962
203819_s_at	IGF2BP3		1	6.673363133
37892_at	COL11A1		1	5.471087316
222608_s_at	ANLN		1	12.34057324
224997_x_at	H19		1	6.080201078
209642_at	BUB1		1	14.77876238
1552619_a_at	ANLN		1	14.37776743
1554768_a_at	MAD2L1		1	14.07386396
204709_s_at	KIF23		1	14.44737269
204006_s_at	FCGR3A /// FCGR3B		1	8.643163982
203967_at	CDC6		1	10.96057595
1554679_a_at	LAPTM4B		1	9.539207398
1553764_a_at	JUB		1	10.92351503
236641_at	KIF14		1	13.89414512
223381_at	NUF2		1	10.8550844
225806_at	JUB		1	9.662775663
209875_s_at	SPP1		1	5.38500818
205394_at	CHEK1		1	12.31334758
203214_x_at	CDC2		1	13.25327417
206224_at	CST1		1	5.477192289
203968_s_at	CDC6		1	11.41546832
204580_at	MMP12		1	5.931063326
202859_x_at	IL8		1	5.901814372
220651_s_at	MCM10		1	12.76611217
232278_s_at	DEPDC1		1	13.12180511
211080_s_at	NEK2		1	12.95308963
204128_s_at	RFC3		1	13.55404696
213599_at	OIP5		1	11.98668929
218782_s_at	ATAD2		1	13.19296399
204822_at	TTK		1	10.10358542
210559_s_at	CDC2		1	13.03256946
206858_s_at	HOXC4 /// HOXC6		1	7.607244634
1555731_a_at	AP1S3		1	9.323686532
204602_at	DKK1		1	3.953159711
227140_at		0	1	6.607730907
213562_s_at	SQLE		1	10.73378003
219148_at	PBK		1	9.327985458
1554899_s_at	FCER1G		1	8.682049642
214895_s_at	ADAM10		1	14.42783788
202311_s_at	COL1A1		1	6.488368163
222740_at	ATAD2		1	12.27480425
228033_at	E2F7		1	11.24949481
231879_at	COL12A1		1	7.857633766
218542_at	CEP55		1	10.17352811
210511_s_at	INHBA		1	6.76393768

242787_at		0	1	13.93746224
228729_at	CCNB1		1	10.82993402
209891_at	SPC25		1	12.51607515
211122_s_at	CXCL11		1	4.559492229
221258_s_at	KIF18A		1	12.19721079
204962_s_at	CENPA		1	11.25909583
202779_s_at	LOC731049 /// UBE2S		1	12.09417209
205393_s_at	CHEK1		1	11.59264852
218009_s_at	PRC1		1	12.22139879
201292_at	TOP2A		1	9.763571358
231766_s_at	COL12A1		1	6.848216282
204641_at	NEK2		1	9.691486791
203560_at	GGH		1	7.422074043
235088_at	C4orf46		1	12.84894168
225834_at	FAM72A /// FAM72B /// GCUD2		1	10.51987161
203213_at	CDC2		1	11.56094144
217294_s_at	ENO1		1	13.86746161
219918_s_at	ASPM		1	10.86107769
1564053_a_at	YTHDF3		1	10.4579554
201111_at	CSE1L		1	11.86728489
206364_at	KIF14		1	12.81332828
214603_at	MAGEA2 /// MAGEA2B		1	4.003057716
204320_at	COL11A1		1	4.503363966
220238_s_at	KLHL7		1	14.16465051
204162_at	NDC80		1	11.09286099
229128_s_at		0	1	8.478060607
229802_at		0	1	6.425166129
215708_s_at	PRIM2		1	13.28668705
210567_s_at	SKP2		1	11.65162343
214845_s_at	CALU		1	12.73451527
226980_at	DEPDC1B		1	11.52126449
210004_at	OLR1		1	6.527034274
225681_at	CTHRC1		1	6.202895077
220239_at	KLHL7		1	12.42027903
209218_at	SQLE		1	7.806917641
203764_at	DLGAP5		1	10.70936916
237215_s_at	TFRC		1	10.2681223
205220_at	GPR109B		1	5.708569285
52285_f_at	CEP76		1	10.95761115
227566_at	HNT		1	6.014675069
202954_at	UBE2C		1	10.71394271
202089_s_at	SLC39A6		1	13.45151988
204092_s_at	AURKA		1	11.52199837
208079_s_at	AURKA		1	10.69633837
203418_at	CCNA2		1	11.76744613
222611_s_at	PSPC1		1	11.69041437
226537_at	HINT3		1	10.42400384
210052_s_at	TPX2		1	11.32277663
215629_s_at	DLEU2 /// DLEU2L		1	8.795141616
230831_at	FRMD5		1	7.328651461
223984_s_at	NUPL1		1	11.644864
1554918_a_at	ABCC4		1	9.186235133
204146_at	RAD51AP1		1	12.1043826
220840_s_at	C1orf112		1	12.97543619
208025_s_at	HMGGA2		1	5.199172824

218355_at	KIF4A	1	10.42482016
214642_x_at	MAGEA5	1	4.408934994
205941_s_at	COL10A1	1	4.382378953
210691_s_at	CACYBP	1	14.69099881
223700_at	MND1	1	10.96910035
219493_at	SHCBP1	1	11.02148493
202872_at	ATP6V1C1	1	13.10635385
1555758_a_at	CDKN3	1	9.812246702
201291_s_at	TOP2A	1	8.508006763
214710_s_at	CCNB1	1	10.47015879
205122_at	TMEFF1	1	8.534413953
218073_s_at	TMEM48	1	12.55389482
1554018_at	GPNMB	1	6.514099483
209408_at	KIF2C	1	12.68376644
238542_at	ULBP2	1	6.29313587
228468_at	MASTL	1	12.87471367
235016_at	REEP3	1	8.289058091
211450_s_at	MSH6	1	12.73059188
234915_s_at	DENR	1	14.17079846
206632_s_at	APOBEC3B	1	5.588925335
222037_at	MCM4	1	11.6397311
210148_at	HIPK3	1	10.61579465
209421_at	MSH2	1	11.82735159
218156_s_at	TSR1	1	13.51871203
202874_s_at	ATP6V1C1	1	14.05604429
222958_s_at	DEPDC1	1	10.54285802
218755_at	KIF20A	1	11.40102945
223530_at	TDRKH	1	9.971335474
205206_at	KAL1	1	6.470651908
204286_s_at	PMAIP1	1	8.55666027
1553113_s_at	CDK8	1	9.057560814
211814_s_at	CCNE2	1	9.522468415
212105_s_at	DHX9	1	11.14275919
1553830_s_at	MAGEA2 /// MAGEA2B	1	4.049772758
226930_at	FNDC1	1	4.551809702
205063_at	SIP1	1	12.37415212
205321_at	EIF2S3	1	8.645502652
206667_s_at	SCAMP1	1	9.678961457
222646_s_at	ERO1L	1	8.817822452
223490_s_at	EXOSC3	1	12.37775214
1554333_at	DNAJA4	1	9.254018911
203417_at	MFAP2	1	7.497221618
221268_s_at	SGPP1	1	9.641828007
225295_at	SLC39A10	1	9.931492543
225687_at	FAM83D	1	8.44806304
218748_s_at	EXOC5	1	10.89311189
203304_at	BAMBI	1	4.927283295
204240_s_at	SMC2	1	10.62992168
223079_s_at	GLS	1	7.52000697
204444_at	KIF11	1	11.00697924
1554414_a_at	OSGIN2	1	14.65289948
1555460_a_at	SLC39A6	1	12.42373979

223229_at	UBE2T	1	11.35592561
207724_s_at	SPAST	1	13.98631962
213226_at	CCNA2	1	9.760917937
218663_at	NCAPG	1	10.19253559
210387_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	1	6.329102021
201014_s_at	PAICS	1	11.8650964
241342_at	TMEM65	1	9.104630111
235089_at	FBXL20	1	8.875517379
207165_at	HMMR	1	9.483462489
205194_at	PSPH	1	9.125037603
1555274_a_at	SELI	1	9.93686184
222680_s_at	DTL	1	10.30553955
201896_s_at	PSRC1	1	10.52105635
207079_s_at	MED6	1	12.72510231
222036_s_at	MCM4	1	11.75158106
229610_at	CKAP2L	1	12.21572172
218145_at	TRIB3	1	6.643004532
230165_at	SGOL2	1	11.46132679
218349_s_at	ZWILCH	1	13.53062449
1552921_a_at	FIGNL1	1	12.3177584
203032_s_at	FH	1	11.2780169
230399_at	0	1	10.10527857
204748_at	PTGS2	1	4.25739267
214590_s_at	UBE2D1	1	11.47570973
203362_s_at	MAD2L1	1	9.959450524
219312_s_at	ZBTB10	1	5.615811655
1563111_a_at	PIGX	1	12.25753126
210074_at	CTSL2	1	8.960551588
227801_at	TRIM59	1	10.28912326
1552485_at	LACTB	1	11.45434464
242881_x_at	0	1	4.695220759
212353_at	SULF1	1	4.713473743
201897_s_at	CKS1B	1	12.53693103
209955_s_at	FAP	1	6.059280618
231784_s_at	WDSOF1	1	10.25523286
212009_s_at	STIP1	1	13.35199336
229067_at	SRGAP2P1	1	9.344708558
218238_at	GTPBP4	1	13.19410656
231772_x_at	CENPH	1	10.6530014
202870_s_at	CDC20	1	10.13855799
223038_s_at	FAM60A	1	11.12597647
228597_at	C21orf45	1	10.60664288
211519_s_at	KIF2C	1	12.48792047
206102_at	GIN51	1	9.511718159
91816_f_at	MEX3D	1	10.54200395
227928_at	C12orf48	1	10.65577992
1552312_a_at	MFAP3	1	12.19485538
207039_at	CDKN2A	1	5.166480764
223879_s_at	OXR1	1	11.97164447
209709_s_at	HMMR	1	10.27899751
231819_at	0	1	13.45661109
204005_s_at	PAWR	1	10.12441637

1555326_a_at	ADAM9	1	7.4827925
223556_at	HELLS	1	10.142141
202823_at	TCEB1	1	14.00316585
1566764_at	MACC1	1	6.191565252
238623_at	0	1	4.947940846
227926_s_at	KIAA1245 /// NBPF1 /// NBPF10 /// NBPF11 /// NBPF14 /// NBPF16 /// NBPF20 /// NBPF8 /// NBPF9 /// RP11-9412.2	1	13.50766307
202580_x_at	FOXN1	1	10.33194707
221618_s_at	LOC728198 /// TAF9B	1	9.150955915
219253_at	TMEM185B	1	11.20913218
213007_at	FANCI	1	10.83463618
1553678_a_at	ITGB1	1	10.94518593
220800_s_at	TMOD3	1	11.25002983
221729_at	COL5A2	1	6.71022294
1555830_s_at	FAM62B	1	10.92463012
203755_at	BUB1B	1	10.21275831
215646_s_at	VCAN	1	5.974152651
230422_at	FPR3	1	7.363642435
206302_s_at	NUDT4 /// NUDT4P1	1	9.86949536
220295_x_at	DEPDC1	1	9.884825973
206025_s_at	TNFAIP6	1	5.423787286
233878_s_at	XRN2	1	12.15271073
223225_s_at	SEH1L	1	11.06442822
1555772_a_at	CDC25A	1	8.404662068
1554878_a_at	ABCD3	1	8.599576065
214975_s_at	MTMR1	1	11.10025485
230556_at	IMMP1L	1	11.08591114
226311_at	0	1	6.281330685
1555756_a_at	CLEC7A	1	6.759720755
1554696_s_at	TYMS	1	10.60621671
219494_at	RAD54B	1	9.704514988
204033_at	TRIP13	1	9.411845423
201308_s_at	SEPT11	1	11.89100219
205114_s_at	CCL3 /// CCL3L1 /// CCL3L3 /// LOC728830	1	5.736160125
205909_at	POLE2	1	10.47329669
214697_s_at	ROD1	1	11.14108902
203209_at	RFC5	1	11.60285094
226608_at	C16orf87	1	12.08652878
221730_at	COL5A2	1	6.508873971
218401_s_at	ZNF281	1	9.917829935
1554271_a_at	CENPL	1	12.27870859
1555137_a_at	FGD6	1	8.802536602
202581_at	HSPA1A /// HSPA1B	1	7.788008925
219787_s_at	ECT2	1	9.825771129
231973_s_at	ANAPC1	1	13.94460809
202817_s_at	SS18	1	10.31286751
225717_at	KIAA1715	1	12.07047955
226237_at	0	1	4.187119037
203284_s_at	HS2ST1	1	12.60602298
219901_at	FGD6	1	8.544768512
226777_at	0	1	5.596520456
211708_s_at	SCD	1	7.629060551

1554020_at	BICD1	1	10.04145554
212942_s_at	KIAA1199	1	4.589074179
202107_s_at	MCM2	1	11.33567284
209406_at	BAG2	1	5.649774937
219479_at	KDELC1	1	10.02982868
222846_at	RAB8B	1	8.404158224
224725_at	MIB1	1	10.52510142
219311_at	CEP76	1	11.81394418
233899_x_at	ZBTB10	1	5.531855667
1552486_s_at	LACTB	1	10.88882547
219306_at	KIF15	1	9.392652043
216100_s_at	TOR1AIP1	1	10.56814065
203561_at	FCGR2A	1	7.602424384
225647_s_at	CTSC	1	7.795159637
1555278_a_at	CKAP5	1	14.38702712
203878_s_at	MMP11	1	5.535327362
210830_s_at	PON2	1	7.581283075
209172_s_at	CENPF	1	9.420178242
238015_at	C4orf46	1	12.30186987
1553530_a_at	ITGB1	1	11.38754881
204533_at	CXCL10	1	4.736278354
210092_at	MAGOH	1	13.6350136
214804_at	CENPI	1	10.87978761
219454_at	EGFL6	1	5.508256646
204114_at	NID2	1	7.327644577
222654_at	IMPAD1	1	10.83812275
220643_s_at	FAIM	1	8.8644959
212800_at	STX6	1	13.33059452
215223_s_at	SOD2	1	7.236800218
1558508_a_at	C1orf53	1	8.450616912
1554572_a_at	SUV39H2	1	10.88690468
1559883_s_at	SAMHD1	1	7.453146435
202604_x_at	ADAM10	1	13.44862173
213470_s_at	HNRNPH1	1	8.979921998
228273_at	0	1	8.851813475
209464_at	AURKB	1	10.92765288
213310_at	EIF2C2	1	9.687168651
205157_s_at	KRT17	1	4.282255887
222678_s_at	DCUN1D1	1	12.43771976
219512_at	DSN1	1	12.29008731
212354_at	SULF1	1	4.860791652
219819_s_at	MRPS28	1	12.24588077
205046_at	CENPE	1	10.71263793
1553106_at	C5orf24	1	10.55071539
218252_at	CKAP2	1	9.917964291
1557910_at	HSP90AB1	1	12.53943727
238075_at	CHEK1	1	10.2001869
226483_at	TMEM68	1	11.0993327
238856_s_at	PANK2	1	13.39232654
214038_at	CCL8	1	4.847242961
238010_at	C1orf174	1	12.89317683
204427_s_at	TMED2	1	11.85290616
212464_s_at	FN1	1	6.011291151
227268_at	RNFT1	1	8.763808651
208103_s_at	ANP32E	1	11.48949875
204470_at	CXCL1	1	4.136071436

219607_s_at	MS4A4A	1	5.103113831
202058_s_at	KPNA1	1	13.74388123
214336_s_at	COPA	1	10.63598853
1558254_s_at	SRPK2	1	11.17647239
1555905_a_at	C3orf23	1	7.811376659
225737_s_at	FBXO22	1	13.34761238
205729_at	OSMR	1	6.461599927
212142_at	MCM4	1	10.34026618
1555225_at	C1orf43	1	8.524832316
219399_at	LIN7C	1	10.29213764
204298_s_at	LOX	1	6.31649384
222962_s_at	MCM10	1	10.4897208
202705_at	CCNB2	1	10.08463383
228281_at	C11orf82	1	11.4135062
228069_at	FAM54A	1	7.708866383
205174_s_at	QPCT	1	4.893605508
208447_s_at	PRPS1	1	10.66925836
210320_s_at	DDX52	1	12.25271714
235545_at	DEPDC1	1	9.353375905
201663_s_at	SMC4	1	12.18647183
221428_s_at	TBL1XR1	1	12.75096468
202195_s_at	TMED5	1	9.78564311
211681_s_at	PDLIM5	1	10.50444126
219979_s_at	C11orf73	1	10.38513115
213741_s_at	KPNA1	1	12.52057587
210904_s_at	IL13RA1	1	8.463639777
215509_s_at	BUB1	1	10.29701714
208097_s_at	TXNDC1	1	10.70206712
200806_s_at	HSPD1	1	13.63610291
238794_at	C10orf78	1	8.633585809
216841_s_at	SOD2	1	7.868232213
1557455_s_at	MOSPD1	1	10.56500941
216493_s_at	IGF2BP3 /// LOC645468	1	6.84273358
211762_s_at	KPNA2 /// LOC728860	1	12.448778
211571_s_at	VCAN	1	6.018116221
203987_at	FZD6	1	7.751492449
219303_at	RNF219	1	9.348780393
232591_s_at	TMEM30A	1	9.494723554
204825_at	MELK	1	10.42734507
210935_s_at	WDR1	1	10.35479112
204507_s_at	PPP3R1 /// WDR92	1	11.95154753
202363_at	SPOCK1	1	4.731057723
222118_at	CENPN	1	12.50704702
218772_x_at	TMEM38B	1	8.442806626
208811_s_at	DNAJB6	1	12.70585628
1554351_a_at	TIPRL	1	11.86562327
210959_s_at	SRD5A1	1	8.241539595
201476_s_at	RRM1	1	12.43177537
214240_at	GAL	1	4.039152208
204186_s_at	PPID	1	11.54256137
227787_s_at	MED30	1	11.17387651
202016_at	MEST	1	6.175389776
222830_at	GRHL1	1	7.631821443
1558014_s_at	FAR1	1	7.278555918
227812_at	TNFRSF19	1	4.370918493
200730_s_at	PTP4A1	1	8.523958609

205687_at	UBFD1	1	11.25727052
1558152_at	LOC100131262	1	7.565544277
234488_s_at	GMCL1 /// GMCL1L	1	10.52611256
216088_s_at	PSMA7	1	12.1560046
203465_at	MRPL19	1	12.36349356
221586_s_at	E2F5	1	8.82299703
206173_x_at	GABPB1	1	15.56104818
202095_s_at	BIRC5	1	9.38245259
231955_s_at	HIBADH	1	9.046322379
243042_at	FAM73A	1	10.81716228
211563_s_at	C19orf2	1	8.565225823
219403_s_at	HPSE	1	7.297763281
203210_s_at	RFC5	1	11.41314368
219294_at	CENPQ	1	12.35530153
241343_at	RNASEH1	1	12.24809674
204113_at	CUGBP1	1	15.38572632
219588_s_at	NCAPG2	1	11.39726515
1556009_at	PEX13	1	10.93764532
222765_x_at	ESF1	1	9.557572383
228378_at	C12orf29	1	10.88656215
227936_at	TMEM68	1	11.11059939
205339_at	STIL	1	9.640458743
226350_at	CHML	1	8.477125746
214544_s_at	SNAP23	1	10.69323947
225686_at	FAM33A	1	10.68411372
226946_at	C5orf33	1	9.380995829
217640_x_at	C18orf24	1	10.33363712
205618_at	PRRG1	1	6.660373203
41037_at	TEAD4	1	9.853463765
223271_s_at	CTDSPL2	1	13.71049355
210732_s_at	LGALS8	1	7.813744479
204426_at	TMED2	1	12.17446956
203744_at	HMGB3	1	9.427894859
221677_s_at	DONSON	1	10.48501341
225702_at	C8orf76	1	11.56346028
214727_at	BRCA2	1	11.0683946
220892_s_at	PSAT1	1	7.261245432
206026_s_at	TNFAIP6	1	5.065957819
225664_at	COL12A1	1	5.184346202
204463_s_at	EDNRA	1	6.862133258
204887_s_at	PLK4	1	10.5768208
215037_s_at	BCL2L1	1	8.914571012
1554451_s_at	DNAJC14	1	13.618973
214452_at	BCAT1	1	7.335345022
235509_at	C8orf38	1	10.91126139
222309_at	C6orf62	1	9.00294871
1554433_a_at	ZNF146	1	11.40765202
206550_s_at	NUP155	1	10.89708039
1555281_x_at	ARMC8	1	11.4691267
209653_at	KPNA4	1	11.21395738
218728_s_at	CNIH4	1	10.80711637
210334_x_at	BIRC5	1	10.50535351
223452_s_at	ATL3	1	8.317931648
208047_s_at	NAB1	1	10.1652634
208767_s_at	LAPTM4B	1	7.568643333
230951_at		0	8.363869085

218458_at	GMCL1	1	10.93497761
215997_s_at	CUL4B	1	12.97648005
216950_s_at	FCGR1A /// FCGR1C	1	6.578225821
1553956_at	ALS2CR4	1	12.11976368
218209_s_at	RPRD1A	1	8.752590572
202638_s_at	ICAM1	1	6.319359868
1555501_s_at	RSRC1	1	11.73012268
201529_s_at	RPA1	1	13.49534061
210779_x_at	SIP1	1	14.72085203
218875_s_at	FBXO5	1	9.636046643
216870_x_at	DLEU2	1	7.888485473
1554885_a_at	PRIM2	1	12.17567389
212141_at	MCM4	1	10.62562548
227451_s_at	CCDC90A	1	7.647247631
207223_s_at	ROD1	1	11.00003986
226145_s_at	FRAS1	1	4.209482996
204127_at	RFC3	1	9.487082668
218602_s_at	FAM29A	1	10.72308547
221194_s_at	RNFT1	1	10.17860636
224396_s_at	ASPN	1	4.074575119
210317_s_at	YWHAE	1	9.705250003
239346_at	0	1	10.56253898
226997_at	ADAMTS12	1	6.621724171
232164_s_at	EPPK1	1	5.823487569
202145_at	LY6E	1	7.61424183
205246_at	PEX13	1	12.23166982
202404_s_at	COL1A2	1	5.836527917
1554997_a_at	PTGS2	1	4.346482368
204285_s_at	PMAIP1	1	6.702939511
204299_at	FUSIP1 /// LOC642558	1	13.7509354
203283_s_at	HS2ST1	1	11.0557831
225285_at	BCAT1	1	6.323697444
211090_s_at	PRPF4B	1	9.561635328
214511_x_at	FCGR1B	1	5.873300628
201971_s_at	ATP6V1A	1	12.1138923
213984_at	PDS5A	1	10.13250161
203285_s_at	HS2ST1	1	10.91119725
202647_s_at	NRAS	1	8.870835361
218894_s_at	MAGOHB	1	10.79526245
210495_x_at	FN1	1	5.766599658
224368_s_at	NDRG3	1	11.98747088
202213_s_at	CUL4B	1	11.40979633
222752_s_at	TMEM206	1	10.96712449
214061_at	WDR67	1	10.992424
210664_s_at	TFPI	1	5.038350038
229479_at	0	1	5.06822941
219390_at	FKBP14	1	9.842534062
224314_s_at	EGLN1	1	12.0960912
218842_at	RPAP3	1	12.60574458
225601_at	HMGB3	1	8.282605683
209387_s_at	TM4SF1	1	5.168465241
1555733_s_at	AP1S3	1	6.937387813
211212_s_at	ORC5L	1	11.55862991
204407_at	TTF2	1	11.74734981
1558214_s_at	CTNNA1	1	7.443702654
224582_s_at	NUCKS1	1	10.31396975

1568609_s_at	FAM91A2 /// FLJ39739 /// LOC728855 /// LOC728875	1	7.369050912
205169_at	RBBP5	1	12.10778493
221685_s_at	CCDC99	1	10.85587476
201946_s_at	CCT2	1	11.07238428
234986_at	0	1	9.158331034
215446_s_at	LOX	1	4.840970814
207387_s_at	GK	1	7.340460048
216593_s_at	PIGC	1	11.37575953
211703_s_at	TM2D1	1	10.17020297
32128_at	CCL18	1	4.129807878
209035_at	MDK	1	7.462521194
229560_at	TLR8	1	5.408193362
209131_s_at	SNAP23	1	9.458976142
223062_s_at	PSAT1	1	5.099164675
224320_s_at	MCM8	1	9.14567517
238562_at	0	1	10.30566551
223307_at	CDCA3	1	9.870679761
205401_at	AGPS	1	12.00083502
208029_s_at	LAPTM4B	1	7.221128494
209754_s_at	TMPO	1	10.08701621
219275_at	PDCD5	1	10.09433763
234992_x_at	ECT2	1	10.07601848
224247_s_at	MRPS10	1	10.56840152
217356_s_at	PGK1	1	11.28901921
222837_s_at	NARG1	1	11.39482154
221039_s_at	ASAP1	1	10.02442073
208875_s_at	PAK2	1	11.7514864
205053_at	PRIM1	1	10.66817993
203830_at	C17orf75	1	11.0007465
1552660_a_at	C5orf22	1	11.17859256
218172_s_at	DERL1	1	11.63394703
228401_at	ATAD2	1	9.318852904
200737_at	PGK1	1	11.0785732
204807_at	TMEM5	1	8.183141391
216442_x_at	FN1	1	5.652299997
209598_at	PNMA2	1	4.454048305
218783_at	INTS7	1	9.955456905
1558015_s_at	ACTR2	1	9.469684699
203145_at	SPAG5	1	9.40081922
208456_s_at	RRA52	1	5.87557854
224753_at	CDCA5	1	10.753311
218239_s_at	GTPBP4	1	10.99357641
220060_s_at	C12orf48	1	9.815877411
211668_s_at	PLAU	1	6.541437107
208910_s_at	C1QBP	1	11.1881575
225195_at	DPH3	1	9.038871711
211115_x_at	SIP1	1	13.17396095
200604_s_at	PRKAR1A	1	9.364791765
228810_at	CCNYL1	1	10.50089207
205048_s_at	PSPH	1	4.033476479
202533_s_at	DHFR	1	10.02831006
230875_s_at	ATP11A	1	8.039498665
201428_at	CLDN4	1	5.922515204
217100_s_at	UBXN7	1	12.48935417

214583_at	RSC1A1	1	11.88297803
203087_s_at	KIF2A	1	10.69292683
235296_at	EIF5A2	1	6.055967799
218051_s_at	NT5DC2	1	7.718682394
214290_s_at	HIST2H2AA3 /// HIST2H2AA4	1	7.796345129
203381_s_at	APOE	1	5.012778317
205302_at	IGFBP1	1	4.208446072
1555106_a_at	CTDSPL2	1	11.38905153
233655_s_at	FAM29A	1	10.88089868
226517_at	BCAT1	1	5.270376575
230793_at	LRRCL16A	1	6.853028995
214830_at	SLC38A6	1	8.814164453
231227_at	0	1	6.508226275
210793_s_at	NUP98	1	9.50685365
227650_at	HSPA14	1	9.644680489
1554883_a_at	ERCC8	1	11.0494871
1554080_at	RQCD1	1	10.42957891
235625_at	VPS41	1	10.24494781
218187_s_at	C8orf33	1	9.446134825
201821_s_at	TIMM17A	1	10.83650067
217785_s_at	YKT6	1	10.71456603
225904_at	C1orf96	1	10.38959178
204521_at	C12orf24	1	7.183060397
223078_s_at	TMOD3	1	11.22371605
219773_at	NOX4	1	6.172521769
1555167_s_at	NAMPT	1	7.419848949
229676_at	PAPD1	1	9.999902169
1558279_a_at	KDSR	1	8.420486509
221381_s_at	MORF4 /// MORF4L1	1	10.96831847
1558233_s_at	ATF1	1	9.542591833
211016_x_at	HSPA4	1	11.46526036
211719_x_at	FN1	1	5.611206899
210892_s_at	GTF2I	1	9.399989862
209424_s_at	AMACR	1	5.407735007
218352_at	RCBTB1	1	8.197171452
212877_at	KLC1	1	9.383156198
212619_at	TMEM194A	1	10.19881712
205429_s_at	MPP6	1	6.818242596
222547_at	MAP4K4	1	9.660720714
205990_s_at	WNT5A	1	5.25235702
222714_s_at	LACTB2	1	6.878911131
218340_s_at	UBA6	1	7.482766277
227350_at	HELLS	1	8.877308416
220477_s_at	C20orf30	1	11.27506123
213523_at	CCNE1	1	5.64652066
209949_at	NCF2	1	6.148892988
201647_s_at	SCARB2	1	9.327965773
219553_at	NME7	1	10.58395132
205260_s_at	ACYP1	1	9.70712721
1560916_a_at	DPY19L1	1	9.600330054
204831_at	CDK8	1	8.195127687
225884_s_at	GZF1	1	10.36776831
241453_at	PTK2	1	7.445548653
223854_at	PCDHB10	1	6.540844795
219908_at	DKK2	1	5.697004945

216591_s_at	hCG_1776980 /// SDHC	1	11.61444245
224173_s_at	MRPL30	1	11.97806297
1553603_s_at	ATL2	1	10.83618693
210665_at	TFPI	1	4.51397488
212335_at	GNS	1	8.086697054
202190_at	CSTF1	1	13.07038232
229666_s_at	CSTF3	1	8.834905229
221520_s_at	CDCA8	1	9.930815728
225088_at	C16orf63	1	10.32849584
1557411_s_at	SLC25A43	1	7.116247009
206613_s_at	TAF1A	1	9.349198379
217188_s_at	C14orf1	1	10.52367375
1552417_a_at	NEDD1	1	12.24880865
222906_at	FLVCR1	1	6.506805309
1563646_a_at	TMEM67	1	10.8978319
218343_s_at	GTF3C3	1	13.95823338
203207_s_at	MTFR1	1	9.746083843
203695_s_at	DFNA5	1	5.470336749
1558093_s_at	MATR3	1	11.2395961
225676_s_at	WDSOF1	1	11.3260221
223542_at	ANKRD32	1	10.28731153
203714_s_at	TBCE	1	10.86005389
205822_s_at	HMGCS1	1	6.63033084
225438_at	NUDCD1	1	10.85088173
209714_s_at	CDKN3	1	7.677571578
206204_at	GRB14	1	6.047383122
212344_at	SULF1	1	4.648651148
206134_at	ADAMDEC1	1	4.525176113
208055_s_at	HERC4	1	10.78105625
205034_at	CCNE2	1	7.139044506
220865_s_at	PDSS1	1	8.425189347
231855_at	KIAA1524	1	8.164123259
212092_at	PEG10	1	4.479673462
209629_s_at	NXT2	1	9.93309499
225521_at	ANAPC7	1	9.246319668
226329_s_at	MITD1	1	10.53051272
238699_s_at	CASK	1	8.922040437
203664_s_at	POLR2D	1	13.13719596
1558028_x_at	0	1	9.031703368
211071_s_at	MLLT11	1	5.167818037
200665_s_at	SPARC	1	7.137583433
217196_s_at	CAMSAP1L1	1	9.67572172
204510_at	CDC7	1	7.944199572
219763_at	DENND1A	1	6.703017253
204232_at	FCER1G	1	6.483510427
207543_s_at	P4HA1	1	8.341820047
218039_at	NUSAP1	1	10.20588717
208310_s_at	C7orf28A /// C7orf28B	1	12.96508073
218911_at	YEATS4	1	8.836591914
202855_s_at	SLC16A3	1	7.163749729
242224_at	GPATCH2	1	9.448149568
236044_at	PPAPDC1A	1	4.912740412
235456_at	0	1	4.725157405
223651_x_at	CDC23	1	9.62318833
225836_s_at	C12orf32	1	10.31298151
205282_at	LRP8	1	8.042170781

202543_s_at	GMFB	1	8.153849019
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208180_s_at	HIST2H4B /// HIST4H4	1	6.748725512
1555780_a_at	RHEB	1	11.20400234
231121_at	HPS3	1	9.254445735
212949_at	NCAPH	1	10.15526441
221220_s_at	SCYL2	1	9.368714019
1555279_at	ARMC8	1	11.38308577
206392_s_at	RARRES1	1	3.927464565
235033_at	NPEPL1	1	9.869258811
202953_at	C1QB	1	5.523352453
1555193_a_at	ZNF277	1	7.949060353
206303_s_at	NUDT4 /// NUDT4P1	1	9.785140951
223772_s_at	TMEM87A	1	9.750965854
225994_at	CPSF2	1	11.37396558
214359_s_at	HSP90AB1	1	12.47833576
219947_at	CLEC4A	1	6.248723885
225402_at	TP53RK	1	10.14448407
213372_at	PAQR3	1	8.142765843
219978_s_at	NUSAP1	1	9.71584357
201504_s_at	TSN	1	12.79872779
204331_s_at	MRPS12	1	10.50778506
226615_at	XPR1	1	9.28191121
201112_s_at	CSE1L	1	12.07536349
211015_s_at	HSPA4	1	12.53751339
221210_s_at	NPL	1	6.186326872
211379_x_at	B3GALNT1	1	5.622288437
206683_at	ZNF165	1	6.072083696
231841_s_at	KIAA1462	1	7.057189517
228061_at	CCDC126	1	9.501268711
220955_x_at	RAB23	1	7.145081504
235114_x_at	HOOK3	1	10.37566657
211797_s_at	NFYC	1	14.86885951
213461_at	NUDT21	1	9.233566634
235165_at	PARD6B	1	6.93278444
227786_at	MED30	1	10.2679828
219555_s_at	CENPN	1	8.524250084
211363_s_at	MTAP	1	8.700372243
212154_at	SDC2	1	5.884404581
1554339_a_at	COG3	1	9.573027911
228485_s_at	SLC44A1	1	8.758248874
206715_at	TFEC	1	5.002199397
222685_at	FAM29A	1	7.702196043
215236_s_at	PICALM	1	9.290430101
209363_s_at	MED21	1	10.01958697
235918_x_at	CEP97	1	9.148636221
222108_at	AMIGO2	1	4.280730834
208698_s_at	NONO	1	11.87320143
200641_s_at	YWHAZ	1	11.00920316

202906_s_at	NBN	1	9.355333631
225439_at	NUDCD1	1	11.1895166
218331_s_at	C10orf18	1	11.86269307
222642_s_at	TMEM33	1	10.1695359
226437_at	YIF1B	1	11.05730915
205042_at	GNE	1	5.663010607
209882_at	RIT1	1	11.29627236
224416_s_at	MED28	1	10.33882828
208290_s_at	EIF5	1	10.25516371
223254_s_at	KIAA1333	1	9.314906509
222402_at	POMP	1	8.649538984
238686_at	FBXO3	1	8.929896474
209677_at	PRKCI	1	8.146964932
205167_s_at	CDC25C	1	9.527689546
219858_s_at	MFSD6	1	8.074179452
209657_s_at	HSF2	1	9.959573495
225161_at	GFM1	1	11.62478261
214770_at	MSR1	1	5.867323008
218182_s_at	CLDN1	1	5.078565882
222989_s_at	UBQLN1	1	10.70603557
209314_s_at	HBS1L	1	7.210225517
222843_at	FIGNL1	1	8.316528965
1555736_a_at	AGTRAP	1	11.01259816
235260_s_at	PACRGL	1	9.438276677
239818_x_at	TRIB1	1	6.664963459
238762_at	MTHFD2L	1	6.602992219
1555618_s_at	SAE1	1	10.82578465
211953_s_at	IPO5	1	8.915067523
1555728_a_at	MS4A4A	1	6.088554969
219026_s_at	RASAL2	1	9.965821887
211150_s_at	DLAT	1	11.08838575
218853_s_at	MOSPD1	1	8.015421747
220199_s_at	AIDA	1	11.79048043
225892_at	IREB2	1	9.275618707
205543_at	HSPA4L	1	4.694016594
223176_at	KCTD20	1	10.9775999
228280_at	ZC3HAV1L	1	8.170723671
212514_x_at	DDX3X	1	10.38287397
213647_at	DNA2	1	8.655892805
236249_at	IKIP	1	10.99859502
201634_s_at	CYB5B	1	8.204753439
203715_at	TBC1	1	10.60103288
242618_at	HCG18	1	10.88452524
214157_at	GNAS	1	5.131044223
1558943_x_at	ZNF765	1	9.306645866
222697_s_at	ABHD10	1	10.64375868
235694_at	TCFL5	1	8.915217143
219166_at	C14orf104	1	9.17508779
218129_s_at	NFYB	1	11.43235413
202691_at	SNRPD1	1	12.21020811
205425_at	HIP1	1	8.102305457
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216902_s_at	RRN3	1	7.317398969
204172_at	CPOX	1	9.748696263
205763_s_at	DDX18	1	11.96084245
244563_at	QSER1	1	9.198500731

214155_s_at	LARP4	1	8.178562154
221561_at	SOAT1	1	6.112220262
212621_at	TMEM194A	1	9.742182576
210543_s_at	PRKDC	1	12.20778464
222825_at	OTUD6B	1	9.103638441
213548_s_at	CDV3	1	9.180967052
223320_s_at	ABCB10	1	9.25224749
216228_s_at	WDHD1	1	9.227844357
210337_s_at	ACLY	1	10.66626242
221922_at	GPSM2	1	7.427305607
201211_s_at	DDX3X	1	10.78124222
205661_s_at	FLAD1	1	11.97491136
201629_s_at	ACP1	1	11.16508459
210156_s_at	PCMT1	1	12.78916352
211981_at	COL4A1	1	7.14940224
218111_s_at	CMAS	1	8.316767058
208694_at	PRKDC	1	10.39140636
221987_s_at	TSR1	1	10.856423
227921_at	0	1	6.976076574
1555202_a_at	RPRD1A	1	9.370823244
220520_s_at	NUP62CL	1	5.155174117
205479_s_at	PLAU	1	5.946384383
228654_at	SPIN4	1	5.528915003
227545_at	0	1	10.8741183
230361_at	HEATR7A	1	7.228269813
209935_at	ATP2C1	1	9.479547344
211547_s_at	PAFAH1B1	1	8.927667465
205191_at	RP2	1	8.806041785
218662_s_at	NCAPG	1	8.396137484
206098_at	ZBTB6	1	11.1098874
231726_at	PCDHB14	1	6.502304712
211833_s_at	BAX	1	9.106261
200712_s_at	MAPRE1	1	11.32248992
204023_at	RFC4	1	10.76207286
200832_s_at	SCD	1	5.367366688
206075_s_at	CSNK2A1	1	10.97856798
212364_at	MYO1B	1	7.468909745
214005_at	GGCX	1	10.02359115
202498_s_at	SLC2A3	1	5.778082365
231849_at	KRT80	1	5.123381414
238756_at	GAS2L3	1	6.133679349
213872_at	0	1	6.956349808
201399_s_at	TRAM1	1	10.49618291
218888_s_at	NETO2	1	5.064435333
225792_at	HOOK1	1	7.777975374
211672_s_at	ARPC4 /// TTL3	1	10.13378974
215931_s_at	ARFGEF2	1	12.00173203
206943_at	TGFBR1	1	10.06695665
229181_s_at	CEP27	1	12.42389857
235177_at	FAM119A	1	9.378540752
225158_at	GFM1	1	10.60999737
208478_s_at	BAX	1	8.906911452
212489_at	COL5A1	1	4.954275217
233656_s_at	VP54	1	9.944365968
207439_s_at	SLC35A2	1	11.30005159
218119_at	TIMM23 /// TIMM23B	1	11.54371891

219972_s_at	C14orf135 /// LOC100130173	1	9.485672152
214437_s_at	SHMT2	1	10.20955666
242019_at	LASS6	1	7.320162486
1552472_a_at	ACAP2	1	10.47767538
225520_at	MTHFD1L	1	9.367206309
209925_at	OCLN	1	6.179726336
221638_s_at	STX16	1	8.642653483
242706_s_at	MED23	1	8.693674024
1553694_a_at	PIK3C2A	1	9.309236869
218984_at	PUS7	1	9.230958319
208840_s_at	G3BP2	1	9.020515259
225644_at	CCDC117	1	10.60183404
222549_at	CLDN1	1	3.587906242
207178_s_at	FRK	1	7.115786222
220329_s_at	RMND1	1	10.16652464
228323_at	CASC5	1	8.186655665
230795_at	0	1	5.081777599
219470_x_at	CCNJ	1	8.34455025
205732_s_at	NCOA2	1	9.104064389
204252_at	CDK2	1	11.04188902
240983_s_at	CARS	1	9.350174357
232149_s_at	NSMAF	1	11.13381392
214769_at	CLCN4	1	5.676830008
200800_s_at	HSPA1A /// HSPA1B	1	7.274561938
225114_at	AGPS	1	8.641131853
212766_s_at	ISG20L2	1	11.32362937
215739_s_at	TUBGCP3	1	10.58586881
204933_s_at	TNFRSF11B	1	3.569930969
235463_s_at	LASS6	1	7.105145831
208343_s_at	NR5A2	1	4.985780713
201123_s_at	EIF5A	1	4.36990213
211725_s_at	BID	1	10.30278188
203358_s_at	EZH2	1	8.055806477
209704_at	MTF2	1	9.936203355
219410_at	TMEM45A	1	4.488094215
207620_s_at	CASK	1	8.807232194
201939_at	PLK2	1	6.484350356
201890_at	RRM2	1	7.558469983
204464_s_at	EDNRA	1	5.689869499
1554441_a_at	WAPAL	1	11.39417149
200894_s_at	FKBP4	1	9.119159957
204126_s_at	CDC45L	1	10.18680438
201043_s_at	ANP32A /// LOC100128146	1	11.21774392
227220_at	NFXL1	1	10.5845042
235295_at	0	1	11.55489045
203832_at	SNRPF	1	12.08713862
222698_s_at	IMPACT	1	6.96155742
201614_s_at	RUVBL1	1	11.91434668
210041_s_at	PGM3	1	8.690240773
1557094_at	LOC653110	1	5.365877826
211559_s_at	CCNG2	1	8.991006526
206205_at	MPHOSPH9	1	10.61350792
218959_at	HOXC10	1	4.130661443
213067_at	MYH10	1	5.472104628

224311_s_at	CAB39	1	9.005885161
243495_s_at	0	1	5.683453094
225424_at	GPAM	1	7.690367325
1053_at	RFC2	1	10.62512671
214751_at	ZNF468	1	7.847537849
225237_s_at	MSI2	1	7.67637693
211977_at	GPR107	1	10.06831871
219376_at	ZNF322B	1	9.274811067
207590_s_at	CENPI	1	9.700396579
210458_s_at	TANK	1	10.03008383
235207_at	0	1	8.151589964
213404_s_at	RHEB	1	10.77756417
212590_at	RRAS2	1	5.263942511
201337_s_at	VAMP3	1	9.115715687
200910_at	CCT3	1	12.87845334
211804_s_at	CDK2	1	11.71981874
201888_s_at	IL13RA1	1	7.620617497
218273_s_at	PPM2C	1	7.598544453
202223_at	STT3A	1	11.32230025
235911_at	0	1	5.265528286
215779_s_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	1	7.387551914
238455_at	0	1	4.934975389
209096_at	UBE2V2	1	10.85221625
223403_s_at	POLR1B	1	10.01965368
235783_at	MRT04	1	10.18129412
223296_at	SLC25A33	1	8.681724544
228977_at	LOC729680	1	5.637826453
203497_at	MED1	1	8.684405637
1553689_s_at	METTL6	1	11.25422923
203228_at	PAFAH1B3	1	9.162714021
210983_s_at	MCM7	1	8.991662414
218737_at	SBNO1	1	10.54209956
216266_s_at	ARFGEF1	1	9.114136912
1558699_a_at	HERPUD2	1	9.612378237
208821_at	SNRPB	1	10.26778311
214959_s_at	API5	1	9.976167472
227105_at	CSPP1	1	8.256789796
227247_at	PLEKHA8	1	8.619634221
212398_at	RDX	1	6.1426015
209027_s_at	ABI1	1	10.50141738
202196_s_at	DKK3	1	5.664454565
223566_s_at	BCOR	1	9.741047111
222506_at	LMBR1	1	10.00777114
212720_at	PAPOLA	1	9.803718738
203313_s_at	TGIF1	1	9.61780814
242560_at	FANCD2	1	8.331154531
203357_s_at	CAPN7	1	9.713302345
202310_s_at	COL1A1	1	4.446727935
206091_at	MATN3	1	5.598100429
229271_x_at	COL11A1	1	4.876882252
226269_at	GDAP1	1	4.586851543
223005_s_at	C9orf5	1	9.384924016

205980_s_at	ARHGAP8 /// LOC553158 /// PRR5	1	7.145719479
228050_at	UTP15	1	10.51658704
1559190_s_at	RDH13	1	7.105294837
203377_s_at	CDC40	1	10.9007233
212709_at	NUP160	1	10.83031985
202094_at	BIRC5	1	7.733216242
226952_at	EAF1	1	9.582200623
216194_s_at	TBCB	1	9.7856627
201048_x_at	RAB6A	1	10.37321358
1554513_s_at	CCDC123	1	9.167594204
221781_s_at	DNAJC10	1	8.513012994
221596_s_at	C7orf64	1	6.530166239
209799_at	PRKAA1	1	9.773631893
203428_s_at	ASF1A	1	9.02650281
218585_s_at	DTL	1	7.851522655
205091_x_at	RECQL	1	10.1562774
214484_s_at	SIGMAR1	1	9.109343325
203946_s_at	ARG2	1	5.803494327
224200_s_at	RAD18	1	9.287314317
203245_s_at	NCRNA00094	1	9.59207635
219031_s_at	NIP7	1	9.207843271
1555639_a_at	RBM14	1	10.63921745
224467_s_at	PDCD2L	1	8.824968899
224453_s_at	ETNK1	1	6.030040658
1559361_at	MACC1	1	6.337990167
209520_s_at	NCBP1	1	10.99944979
224484_s_at	BRMS1L	1	12.59546259
239138_at		0	8.825839698
213139_at	SNAI2	1	5.229952924
201633_s_at	CYB5B	1	8.745127202
204768_s_at	FEN1	1	10.66620266
229091_s_at	CCNJ	1	7.967332509
219258_at	TIPIN	1	8.48294555
36830_at	MIPEP	1	8.272905853
204361_s_at	SKAP2	1	7.641931923
222088_s_at	SLC2A14 /// SLC2A3	1	5.305226373
213391_at	DPY19L4	1	8.296118017
211075_s_at	CD47	1	8.490079851
1552789_at	SEC62	1	7.119242128
233970_s_at	TRMT6	1	8.510487645
223785_at	FANCI	1	8.54876731
201179_s_at	GNAI3	1	11.42792401
205767_at	EREG	1	3.777228349
202407_s_at	PRPF31	1	12.11625966
220038_at	C8orf44 /// SGK3	1	6.410970744
234942_s_at	DNTTIP1	1	9.697717022
223454_at	CXCL16	1	6.995516449
210449_x_at	MAPK14	1	10.8458549
215780_s_at	hCG_1644608 /// SET	1	7.830440337
209015_s_at	DNAJB6	1	9.555986109
203177_x_at	TFAM	1	8.62876166
1554807_a_at	SPIRE1	1	7.339618543
222815_at	RNF12	1	9.409422095
218049_s_at	MRPL13	1	10.50472189
226478_at		0	7.213351575

1552344_s_at	CNOT7	1	8.331721469
202717_s_at	CDC16	1	9.443408093
216652_s_at	DR1	1	8.68059466
206110_at	0	1	5.675508634
207845_s_at	ANAPC10	1	10.73045302
238443_at	0	1	9.603736891
209896_s_at	PTPN11	1	10.07666026
219037_at	RRP15	1	9.312615566
203347_s_at	MTF2	1	10.01330391
222555_s_at	MRPL44	1	10.95784533
202868_s_at	POP4	1	7.744240564
231311_at	0	1	5.703931184
1555785_a_at	XRN1	1	8.282134586
202690_s_at	SNRPD1	1	11.5184271
221079_s_at	METTL2A /// METTL2B	1	9.898564165
202613_at	CTPS	1	10.15640523
238465_at	C5orf35	1	5.656904911
222393_s_at	NAT13	1	9.548105424
201772_at	AZIN1	1	10.90977523
228955_at	0	1	5.974043181
205628_at	LOC100134172 /// PRIM2	1	10.17242577
208876_s_at	PAK2	1	11.69085867
239010_at	FLJ39632	1	5.984490488
1558692_at	C1orf85	1	7.968128266
220172_at	C2orf37	1	10.96450846
214527_s_at	PQBP1	1	10.03296529
201577_at	NME1 /// NME2	1	10.46363669
228418_at	EXOC5	1	9.441250556
213346_at	C13orf27	1	8.268735004
209676_at	TFPI	1	4.518686017
219000_s_at	DSCC1	1	8.191237852
225827_at	EIF2C2	1	9.177482581
202516_s_at	DLG1	1	8.877024542
235147_at	0	1	5.027876928
208810_at	DNAJB6	1	9.365498708
214701_s_at	FN1	1	5.850718849
1552478_a_at	IRF6	1	7.116799062
222458_s_at	AKIRIN1	1	8.547200927
222719_s_at	PDGFC	1	6.170715191
200769_s_at	MAT2A	1	8.407098099
217919_s_at	MRPL42	1	10.9886046
203276_at	LMNB1	1	8.377180199
209825_s_at	UCK2	1	11.23106957
222590_s_at	NLK	1	12.40819618
204956_at	MTAP	1	7.453854385
225456_at	MED1	1	8.599429614
227021_at	AOF1	1	8.212584864
203925_at	GCLM	1	9.466016792
201823_s_at	RNF14	1	8.6322445
203046_s_at	TIMELESS	1	9.87881734
91684_g_at	EXOSC4	1	11.30017014
204767_s_at	FEN1	1	10.12322933
204007_at	FCGR3B	1	5.797969516
212460_at	C14orf147	1	7.054886558
235026_at	C12orf66	1	8.746789005

200889_s_at	SSR1	1	9.907158163
204728_s_at	WDHD1	1	9.389549164
211337_s_at	TUBGCP4	1	11.54651863
226003_at	KIF21A	1	6.906008194
202129_s_at	RIOK3	1	6.925644916
242890_at	0	1	7.83460344
1553528_a_at	TAF5	1	10.18442442
205572_at	ANGPT2	1	6.402698014
209433_s_at	PPAT	1	7.856369729
200052_s_at	ILF2	1	12.24988496
227295_at	IKIP	1	7.820628953
203153_at	IFIT1	1	4.032280067
201267_s_at	PSMC3	1	12.51819724
212373_at	FEM1B	1	10.00651323
202635_s_at	POLR2K	1	11.87849862
219181_at	LIPG	1	4.645313126
221497_x_at	EGLN1	1	9.676214179
201309_x_at	C5orf13	1	6.520885484
242586_at	FSD1L	1	6.129465337
223089_at	VEZT	1	7.370450511
1554678_s_at	HNRPD1	1	9.700370178
1554334_a_at	DNAJA4	1	7.169638306
209257_s_at	SMC3	1	10.42961013
210716_s_at	CLIP1	1	9.943011915
220658_s_at	ARNTL2	1	6.75776555
208116_s_at	MAN1A1	1	5.59318708
204809_at	CLPX	1	10.60687849
225047_at	NUPL1	1	9.729828014
228181_at	SLC30A1	1	8.036369357
225113_at	AGPS	1	10.01837765
204992_s_at	PFN2	1	4.413710487
214173_x_at	C19orf2	1	7.06596289
201456_s_at	BUB3	1	11.03262977
1552767_a_at	HS6ST2	1	4.098120668
239106_at	CASBL	1	7.853729653
226158_at	KLHL24	1	7.639462167
244187_at	0	1	6.737002688
215286_s_at	PHTF2	1	9.712401217
207156_at	HIST1H2AG /// HIST1H2AH /// HIST1H2AI /// HIST1H2AJ /// HIST1H2AK /// HIST1H2AL /// HIST1H2AM	1	6.200224803
218701_at	LACTB2	1	5.8891316
209080_x_at	GLRX3	1	11.50393023
220088_at	C5AR1	1	5.519184008
219683_at	FZD3	1	6.544370975
208926_at	NEU1	1	4.868000947
212298_at	NRP1	1	6.787090478
202589_at	TYMS	1	8.17993639
218360_at	RAB22A	1	9.99273412
204369_at	PIK3CA	1	9.92297258
234304_s_at	IPO11	1	9.076066008
203696_s_at	RFC2	1	11.16844543

1553112_s_at	CDK8	1	7.598818756
202790_at	CLDN7	1	5.990014958
205351_at	GGCX	1	9.242957654
243786_at	ZDHHC20	1	9.011303364
1555882_at	SPIN3	1	6.521357271
204932_at	TNFRSF11B	1	3.67532521
1555229_a_at	C1S	1	3.859813677
213125_at	OLFML2B	1	6.334467161
214130_s_at	PDE4DIP	1	6.852899694
226132_s_at	MANEAL	1	4.855833129
205347_s_at	MGC39900 /// TMSB15A	1	4.225112034
243661_at	ZNF273	1	7.737774942
201521_s_at	NCBP2	1	11.55635351
218854_at	DSE	1	5.739830186
210371_s_at	RBBP4	1	10.23611165
225150_s_at	RTKN	1	8.573495866
242140_at	0	1	7.084958606
203598_s_at	WBP4	1	8.856930338
225366_at	PGM2	1	9.206615885
1552978_a_at	SCAMP1	1	7.612234298
222442_s_at	ARL8B	1	9.40854804
205442_at	MFAP3L	1	4.107542744
221020_s_at	SLC25A32	1	10.03633205
222039_at	KIF18B	1	9.229647163
221826_at	ANGEL2	1	10.44587654
211760_s_at	VAMP4	1	8.099134256
205296_at	RBL1	1	10.2425869
218395_at	ACTR6	1	10.91205104
217299_s_at	NBN	1	8.284524361
211721_s_at	ZNF551	1	7.02923346
226600_at	TMTC3	1	9.756293771
202706_s_at	UMPS	1	11.89124223
203676_at	GNS	1	8.954314699
218304_s_at	OSBPL11	1	9.998301177
204715_at	PANX1	1	9.695315276
205891_at	ADORA2B	1	5.019067292
202952_s_at	ADAM12	1	5.503201219
203705_s_at	FZD7	1	5.199487678
221517_s_at	MED17	1	10.31414168
226421_at	AMMECR1	1	6.932679946
207714_s_at	SERPINH1	1	8.209174107
224410_s_at	LMBR1	1	8.865393153
200868_s_at	RNF114	1	9.177530148
203414_at	MMD	1	7.978148571
235949_at	0	1	9.925435937
214700_x_at	RIF1	1	11.19824467
1565717_s_at	FUS	1	8.693570771
201013_s_at	PAICS	1	9.717001267
222606_at	ZWILCH	1	10.20865105
216899_s_at	SKAP2	1	7.792651728
213568_at	OSR2	1	4.899653861
225300_at	C15orf23	1	9.439899291
209743_s_at	ITCH	1	10.01402335
222726_s_at	EXOC5	1	11.5392386
1554915_a_at	PDE12	1	8.33719799

201742_x_at	SFRS1	1	11.22262934
224523_s_at	C3orf26	1	9.64085234
207828_s_at	CENPF	1	7.581204789
235253_at	RAD1	1	8.488839537
	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG ///		
214455_at	HIST1H2BI	1	4.943783791
225841_at	C1orf59	1	6.358009481
223263_s_at	FGFR1OP2	1	8.659352445
210568_s_at	RECQL	1	9.354638435
232155_at	KIAA1618	1	6.78100135
226661_at	CDCA2	1	6.824904239
215936_s_at	KIAA1033	1	11.23993709
212636_at	QKI	1	6.236889266
213253_at	SMC2	1	8.243732961
213262_at	SACS	1	5.857850579
221510_s_at	GLS	1	6.869966955
203432_at	TMPO	1	8.870392879
203165_s_at	SLC33A1	1	8.096953816
208546_x_at	HIST1H2BH	1	7.410296004
223491_at	COMMD2	1	9.258942059
201297_s_at	MOBK1B	1	9.918322254
226936_at	C6orf173	1	7.504259534
211255_x_at	DEDD	1	12.38927414
226631_at	METTL10	1	8.954717742
226503_at	RIF1	1	10.35497643
232296_s_at	GFM1	1	12.78128006
218498_s_at	ERO1L	1	6.67204919
216521_s_at	BRCC3	1	8.733869958
207740_s_at	NUP62	1	11.64435124
205133_s_at	HSPE1	1	11.05320931
225901_at	PTPMT1	1	10.74474417
201444_s_at	ATP6AP2	1	11.35521678
229551_x_at	ZNF367	1	6.684943482
218757_s_at	UPF3B	1	7.518333602
213118_at	UHRF1BP1L	1	9.634461057
212397_at	RDX	1	5.129412358
226524_at	C3orf38	1	10.18856974
219330_at	VANGL1	1	9.423582543
222572_at	PPM2C	1	7.403204285
204147_s_at	TFDP1	1	11.39930158
203557_s_at	PCBD1	1	9.461956517
203645_s_at	CD163	1	4.937896705
212365_at	MYO1B	1	7.671674826
225847_at	AADA1L1	1	5.296583303
218726_at	HJURP	1	8.850447053
223330_s_at	SUGT1	1	9.995787045
201559_s_at	CLIC4	1	6.465047788
212499_s_at	FCF1 /// MAPK1IP1L	1	9.866805314
225774_at	RSPRY1	1	8.046166119
222558_at	RPRD1A	1	8.278456265
229865_at	FNDC3B	1	7.484519818
227124_at	LOC221710	1	7.620576368
236192_at	HOOK3	1	9.279148592

222881_at	HPSE	1	7.413628707
206470_at	PLXNC1	1	6.937028423
200751_s_at	HNRNPC	1	12.73719867
206445_s_at	PRMT1	1	11.94461418
227399_at	VGLL3	1	3.852780599
238907_at	0	1	8.867149164
224308_s_at	INTS2	1	9.107740763
226366_at	SHPRH	1	7.670889799
242727_at	ARL5B	1	7.117290757
226046_at	MAPK8	1	9.298244762
206247_at	MICB	1	5.488689947
226628_at	THOC2	1	7.715571308
223374_s_at	B3GALNT1	1	4.988907814
207124_s_at	GNB5	1	7.749021233
212815_at	ASCC3	1	9.666718665
219434_at	TREM1	1	5.114138177
212132_at	LSM14A	1	10.01442379
204866_at	PHF16	1	7.344268557
1555996_s_at	EIF4A2	1	8.480155033
229812_at	USP48	1	7.919957365
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222701_s_at	CHCHD7	1	10.01770281
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232751_at	RBBP9	1	10.18008421

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217445_s_at	GART	1	8.788989848
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210005_at	GART	1	8.32308992
210104_at	MED6	1	11.26921424
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235022_at	C18orf19	1	9.076172924
226800_at	EFCAB7	1	8.511545263
1554464_a_at	CRTAP	1	6.623534629
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222848_at	CENPK	1	6.588992286
236622_at	PIGM	1	8.778841601
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225455_at	TADA1L	1	8.708843625
210460_s_at	PSMD4	1	14.61151668
212479_s_at	RMND5A	1	9.452590087
236741_at	WDR72	1	3.733653751
215794_x_at	GLUD2	1	8.952067097
206536_s_at	XIAP	1	9.299380042
212523_s_at	KIAA0146	1	10.16692028
217457_s_at	RAP1GDS1	1	9.245934882
201088_at	KPNA2 /// LOC728860	1	10.13606547
218595_s_at	HEATR1	1	10.298814
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220011_at	C1orf135	1	9.556324743
220083_x_at	UCHL5	1	10.67919097
206383_s_at	G3BP2	1	11.07877846
238561_s_at	0	1	10.24455232
37117_at	ARHGAP8 /// LOC553158 /// PRR5	1	6.47154209

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220123_at	SLC35F5	1	7.838268147
241666_at	C3orf23	1	8.7603862
205024_s_at	RAD51	1	9.412572186
223898_at	ZNF670	1	8.517396299
213425_at	WNT5A	1	4.207554407
214764_at	RRP15	1	6.958555115
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211114_x_at	SIP1	1	12.32442664
238662_at	ATPBD4	1	8.376785758
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226668_at	WDSUB1	1	8.887782778
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225694_at	CRKRS	1	9.972853909
210639_s_at	ATG5	1	8.695681872
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204315_s_at	GTSE1	1	7.632310671
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223400_s_at	PBRM1	1	10.18914715
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227836_at	0	1	8.347435623
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227161_at	NOM1	1	10.16652397
202170_s_at	AASDHPPT	1	9.929337067
219633_at	TTPAL	1	9.493033346
225106_s_at	OGFOD1	1	11.1665181
227068_at	PGK1	1	9.010728544
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221482_s_at	ARPP-19	1	10.03910047
214193_s_at	C1orf107	1	8.176736283
1554761_a_at	HEATR2	1	10.74979294
209666_s_at	CHUK	1	8.623730201
202491_s_at	IKBKAP	1	9.542674439
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218513_at	C4orf43	1	8.968944211
37079_at	YDD19	1	11.40894507

225807_at	JUB	1	7.228926279
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202666_s_at	ACTL6A	1	9.414671672
235521_at	HOXA3	1	5.46651221
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223511_at	C1orf124	1	8.801969008
218280_x_at	HIST2H2AA3 /// HIST2H2AA4	1	6.665750318
241682_at	KLHL23	1	7.012591684
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224744_at	IMPAD1	1	11.10097375
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226943_at	C12orf73	1	8.778006237
219003_s_at	MANEA	1	6.54006684
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76897_s_at	FKBP15	1	8.482493917
225217_s_at	BRPF3	1	8.592217027
222693_at	FNDC3B	1	6.043538846
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223151_at	DCUN1D5	1	9.291564095
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220775_s_at	UEVLD	1	7.927075595
218185_s_at	ARMC1	1	12.54666728
223021_x_at	VTA1	1	9.835141256
212898_at	KIAA0406	1	8.795636576
211759_x_at	TBCB	1	9.061917582
235198_at	OSTM1	1	7.997439529
230278_at	0	1	7.997477466
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238617_at	0	1	5.339190929
218507_at	HIG2	1	6.028815189
212321_at	SGPL1	1	9.888582475
225890_at	C20orf72	1	9.32267056
205761_s_at	DUS4L	1	7.819199885
204165_at	WASF1	1	5.378670794
244439_at	SPRED1	1	8.33873149
204716_at	CCDC6	1	7.472694845
219703_at	MNS1	1	6.139031104
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210813_s_at	XRCC4	1	6.89569888
204725_s_at	NCK1	1	9.828713731
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209662_at	CETN3	1	8.417274627
219260_s_at	C17orf81	1	6.494719396
204645_at	CCNT2	1	8.485429272
201714_at	TUBG1	1	8.950531955
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220386_s_at	EML4	1	8.636865985
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213289_at	APOOL	1	8.800383323
45633_at	GIN5	1	8.773519842
204886_at	PLK4	1	9.856381659
204068_at	STK3	1	8.826832964
213175_s_at	SNRPB	1	9.567898343
204122_at	TYROBP	1	5.340542877
224913_s_at	TIMM50	1	9.542168473
1553111_a_at	KBTBD6	1	8.520661335
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220607_x_at	TH1L	1	9.499867452
226319_s_at	THOC4	1	9.344802837
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228785_at	ZNF281	1	8.088825209
201797_s_at	VAR5	1	9.280528109
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211612_s_at	IL13RA1	1	6.945516502
226501_at	XPNPEP3	1	8.831044028
211810_s_at	GALC	1	6.571150378
203077_s_at	SMAD2	1	8.041884103
204353_s_at	POT1	1	9.310850675
206788_s_at	CBFB	1	9.829056598
226479_at	KBTBD6	1	6.820134012
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235266_at	ATAD2	1	7.328047223
218582_at	MARCH5	1	9.91073458
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231769_at	FBXO6	1	6.16948941
218622_at	NUP37	1	10.30678156
223983_s_at	C19orf12	1	6.183141787
214545_s_at	PROSC	1	7.519923481
205240_at	GP5M2	1	7.927586919
220253_s_at	LRP12	1	7.831513534
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1554321_a_at	NFS1	1	9.992382806
233827_s_at	SUPT16H	1	8.80030902
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214666_x_at	IREB2	1	10.27833789

219631_at	LRP12	1	7.519522279
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219502_at	NEIL3	1	8.798270354
222583_s_at	NUP50	1	9.530248634
211085_s_at	STK4	1	8.363327233
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235744_at	PPTC7	1	10.3445513
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228851_s_at	ENSA	1	10.15332292
222703_s_at	YRDC	1	10.33666736
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218932_at	ZNHIT6	1	10.25445904
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226513_at	LOC145758	1	9.958605091
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209122_at	ADFP	1	5.04654035
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203203_s_at	KRR1	1	8.627151965
210087_s_at	MPZL1	1	9.102465018
218404_at	SNX10	1	5.077852977
218295_s_at	NUP50	1	9.152083078
218398_at	MRPS30	1	8.713600978
214581_x_at	TNFRSF21	1	5.565744484
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222614_at	RWDD2B	1	6.520047091
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205366_s_at	HOXB6	1	4.818833572
216985_s_at	STX3	1	6.989294392
221523_s_at	RRAGD	1	5.059256028
235609_at	0	1	7.103632893
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225375_at	TMEM199	1	11.60541424
214649_s_at	MTMR2	1	10.12701008
214553_s_at	ARPP-19	1	11.57662806
214264_s_at	C14orf143	1	7.804225821
222946_s_at	C1orf135	1	9.745140614
223156_at	MRPS23	1	9.699015619
227103_s_at	ECE2	1	9.718013649
209751_s_at	SEDLP /// TRAPPC2 /// ZNF547	1	8.020996412
201231_s_at	ENO1	1	12.05278021

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209927_s_at	C1orf77	1	12.57958696
217185_s_at	LOC442240 /// ZNF259	1	9.973450344
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232596_at	DIAPH3	1	7.528134544
209628_at	NXT2	1	7.377072909
221514_at	UTP14A	1	8.661196441
37577_at	ARHGAP19	1	10.35680615
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203109_at	UBE2M	1	9.277555423
223258_s_at	KIAA1333	1	8.269054585
202918_s_at	MOBK13	1	11.74236572
241370_at	LOC286052	1	6.00068391
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216915_s_at	PTPN12	1	6.373913056
216574_s_at	hCG_2024410 /// RPE	1	11.15370855
1554740_a_at	IPP	1	9.948489716
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219178_at	QTRTD1	1	10.46603673
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244519_at	ASXL1	1	7.784372617
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1555831_s_at	LRRC41	1	10.40315024
213274_s_at	CTSB	1	5.788205207
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207791_s_at	RAB1A	1	8.707221743
213610_s_at	KLHL23	1	6.379728849
214741_at	ZNF131	1	7.302504777
218700_s_at	RAB7L1	1	6.016832269
223275_at	PRMT6	1	5.298707422
220985_s_at	RNF170	1	7.284169939
235648_at	ZNF567	1	5.954555125
204702_s_at	NFE2L3	1	6.395922737
227256_at	USP31	1	8.653065899
1552617_a_at	RFWD2	1	9.816924433

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225537_at	TRAPPC6B	1	8.356902646
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222839_s_at	PAPOLG	1	10.37614949
204653_at	TFAP2A	1	4.095604015
219161_s_at	CKLF	1	7.660336059
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225580_at	MRPL50	1	8.185826263
208925_at	CLDND1	1	9.46893294
222713_s_at	FANCF	1	9.181188754
227804_at	TLCD1	1	6.557708414
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218884_s_at	GUF1	1	7.778891411
210470_x_at	NONO	1	10.48992741
201881_s_at	ARIH1	1	10.97392509
201804_x_at	TBCB	1	8.860152885
223397_s_at	NIP7	1	8.74578935
206918_s_at	CPNE1	1	6.724630636
202619_s_at	PLOD2	1	5.288709194
222443_s_at	RBM8A	1	12.05738359
218605_at	TFB2M	1	9.284174386
1555427_s_at	SYNCRIP	1	9.902416438
215034_s_at	TM4SF1	1	3.896284706
225367_at	PGM2	1	11.48547492
225837_at	C12orf32	1	8.593687707
202043_s_at	SMS	1	7.837605197
218229_s_at	POGK	1	9.358644158
210389_x_at	TUBD1	1	8.561338864
1554424_at	FIP1L1	1	11.28413872
224361_s_at	IL17RB	1	5.553645358
218336_at	PFDN2	1	11.08391331
231921_at	C2orf37	1	9.849183078
205085_at	ORC1L	1	9.179572438
221676_s_at	CORO1C	1	9.493516986
207098_s_at	MFN1	1	8.26416937
219558_at	ATP13A3	1	10.47742334
1554868_s_at	PCNP	1	11.3631616
203743_s_at	TDG	1	8.820659168
212271_at	MAPK1	1	8.858012826

203625_x_at	SKP2	1	6.714682777
225291_at	PNPT1	1	10.52149353
209512_at	HSDL2	1	5.201389519
214960_at	API5	1	9.02260635
232682_at	MREG	1	8.733814118
204492_at	ARHGAP11A	1	9.170640236
222849_s_at	SCRN3	1	6.341809854
227689_at	ZNF227	1	7.050980367
206451_at	TBCCD1	1	8.658264527
203105_s_at	DNM1L	1	11.65251697
200658_s_at	PHB	1	10.30817965
202382_s_at	GNPDA1	1	9.94672587
1556064_at	LOC284926	1	8.030260349
203654_s_at	COIL	1	9.526686607
222574_s_at	DHX40	1	10.23258614
225060_at	LRP11	1	7.725377075
1552470_a_at	ABHD11	1	6.775513015
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231513_at		0	4.467443928
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232194_at	METTL4	1	8.945902806
1553725_s_at	ZNF644	1	9.76798955
228606_at	TCTEX1D2 /// TM4SF19	1	6.348470708
229635_at		0	6.128284147
227212_s_at	PHF19	1	7.330488413
242905_at	PNO1	1	10.21167961
203535_at	S100A9	1	3.801450293
207855_s_at	CLCC1	1	7.301253478
211124_s_at	KITLG	1	6.924222487
219929_s_at	ZFYVE21	1	8.066184645
225617_at	ODF2	1	9.699617604
209231_s_at	DCTN5	1	7.118653871
222250_s_at	INTS7	1	10.57410351
203741_s_at	ADCY7	1	5.61855277
229671_s_at	C21orf45	1	8.472981229
235387_at	GSTCD	1	9.261396657
224694_at	ANTXR1	1	4.094417196
222624_s_at	ZNF639	1	8.251797281
229700_at	ZNF738	1	5.408393736
1554767_s_at	CRYZL1	1	8.90942015
224787_s_at	RAB18	1	8.942765266
229846_s_at	MAPKAP1	1	11.34553079
219372_at	IFT81	1	8.554635901
222155_s_at	GPR172A	1	8.033337839
201457_x_at	BUB3	1	7.957095097
236312_at		0	8.404851408
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201196_s_at	AMD1	1	8.866567903
235057_at	ITCH	1	6.205851556
202904_s_at	LSM5	1	7.755188456
243999_at	SLFN5	1	6.38916617
225869_s_at	UNC93B1	1	7.218282303
208748_s_at	FLOT1	1	9.263189303
220176_at	NUBPL	1	7.683540682

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217970_s_at	CNOT6	1	10.56732699
225599_s_at	C8orf83	1	6.104926511
203721_s_at	UTP18	1	10.37632026
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1556021_at	0	1	8.042263146
214949_at	0	1	8.099535227
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225297_at	CCDC5	1	8.081549076
232023_at	TMEM67	1	9.184521165
202654_x_at	MARCH7	1	9.089287405
218538_s_at	MRS2	1	7.938668398
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211594_s_at	MRPL9	1	12.3525912
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202670_at	MAP2K1	1	10.71678113
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224830_at	NUDT21	1	8.575838747
242283_at	C1orf67 /// DNAH14	1	5.036845351
205519_at	WDR76	1	9.314559618
231918_s_at	GFM2	1	8.064169062
218724_s_at	TGIF2	1	7.357883227
218712_at	C1orf109	1	10.76990689
242887_at	KCMF1	1	10.05527531
215049_x_at	CD163	1	4.52075248
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200903_s_at	AHCY	1	9.912683252
213133_s_at	GCSH /// LOC730107	1	9.495116141
226089_at	RABL3	1	9.00516237
226837_at	SPRED1	1	6.234005234
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219060_at	WDYHV1	1	8.062318731
221786_at	C6orf120	1	7.699827047
1554397_s_at	UEVLD	1	8.357729931
219038_at	MORC4	1	6.05097585
226881_at	GRPEL2	1	8.363238126
218013_x_at	DCTN4	1	9.163069144
221550_at	COX15	1	8.174810247
212591_at	RBM34	1	9.387929497
215165_x_at	UMPS	1	10.76793036
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221505_at	ANP32E	1	10.82295618
222201_s_at	CASP8AP2	1	8.665846602
235554_x_at	PACRGL	1	9.720797657
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215570_s_at	ZNF780A /// ZNF780B	1	9.176840256
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235025_at	WDR89	1	10.00929445
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223241_at	SNX8	1	8.499358234
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235202_x_at	IKIP	1	10.56382311
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201743_at	CD14	1	5.580885114
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229442_at	C18orf54	1	8.569225671
212612_at	RCOR1	1	7.321203503
207426_s_at	TNFSF4	1	5.06645009
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213352_at	TMCC1	1	6.852884867
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215030_at	GRSF1	1	6.564790321
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221085_at	TNFSF15	1	5.282682319
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218566_s_at	CHORDC1	1	7.967716202
213518_at	PRKCI	1	6.056071164
236026_at	GPATCH2	1	8.085332515
209647_s_at	SOCSS	1	7.591040298
242546_at	FLJ39632	1	4.502288768
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235003_at	UHMK1	1	7.889898751
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224896_s_at	TTL	1	9.69903467
242753_x_at	C4orf16	1	9.589179067
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223043_at	TMEM85	1	10.46203092
223723_at	MFI2	1	4.934750413
216976_s_at	RYK	1	10.57958669
227942_s_at	CRIP1	1	9.487109481
210154_at	ME2	1	7.045320368
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1554450_s_at	MIER3	1	6.911501335
235180_at	STYX	1	8.736889362
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221531_at	WDR61	1	7.944808878
209474_s_at	ENTPD1	1	6.17378744
224996_at	ASPH	1	5.853397855
201005_at	CD9	1	7.481613429
219793_at	SNX16	1	7.664628237
219544_at	C13orf34	1	7.084977982

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235006_at	CDKN2AIPNL	1	9.961727121
214214_s_at	C1QBP	1	9.81767863
224642_at	FYTTD1	1	9.677662543
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203605_at	SRP54	1	8.910749992
218883_s_at	MLF1IP	1	5.835585705
228996_at	RC3H1	1	8.229269909
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229292_at	EPB41L5	1	6.770580987
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225099_at	FBXO45	1	9.996658475
226962_at	ZBTB41	1	7.437830379
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212887_at	SEC23A	1	6.515770164
226545_at	CD109	1	4.28370582
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227918_s_at	ZYG11B	1	9.459582719
221487_s_at	ENSA	1	8.647815382
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221437_s_at	MRPS15	1	11.25743735
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225399_at	TSEN15	1	8.224930298
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226360_at	ZNRF3	1	4.991712306
222736_s_at	TMEM38B	1	8.240736413
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204603_at	EXO1	1	7.557599639
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215966_x_at	GK3P	1	6.78478892
221803_s_at	NRBF2	1	8.737900066
226760_at	MBTPS2	1	6.828078371
221770_at	RPE	1	10.34572358
217043_s_at	MFN1	1	9.549734631
217871_s_at	LOC284889 /// MIF	1	9.811082597
212470_at	SPAG9	1	9.318957762
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219433_at	BCOR	1	7.578887115
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213092_x_at	DNAJC9	1	7.013711149
209109_s_at	TSPAN6	1	4.695961322
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219255_x_at	IL17RB	1	4.854880082
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219922_s_at	LTBP3	1	5.973116839
229236_s_at	SFXN4	1	8.518609503
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214875_x_at	APLP2	1	8.179416666
225485_at	TSGA14	1	6.035543119
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217924_at	C6orf106	1	11.76244499
200838_at	CTSB	1	6.943116935
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209434_s_at	PPAT	1	9.713559764
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218909_at	RPS6KC1	1	7.838388294
219177_at	BXDC2	1	7.965410181
202272_s_at	FBXO28	1	9.481560521
209198_s_at	SYT11	1	6.276033569
209585_s_at	MINPP1	1	6.73190329
210802_s_at	DIMT1L	1	8.622196422
204493_at	BID	1	8.35092443
231975_s_at	MIER3	1	6.546213546
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227077_at	ZNF286A	1	9.076732759
1553928_at	ELMOD2	1	6.237860734
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233110_s_at	BCL2L12	1	9.691216303
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52731_at	AMBRA1	1	8.319862662
225021_at	ZNF532	1	7.107489833
212515_s_at	DDX3X	1	9.251902513
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215425_at	BTG3	1	4.95082472
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224914_s_at	CIP29	1	10.10676424
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212180_at	CRKL	1	8.056268947
212653_s_at	EHBP1	1	8.167990216
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235707_at	LOC221710	1	9.132570665
219015_s_at	ALG13	1	6.908663192
212060_at	SR140	1	7.817164425
226395_at	HOOK3	1	7.207976184
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228386_s_at	DDX59	1	10.8699056
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231779_at	IRAK2	1	5.176554317
222702_x_at	CRIP1	1	9.329461314
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222705_s_at	SLC25A15	1	7.685386767
218576_s_at	DUSP12	1	10.96487053
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232902_s_at	RARS2	1	9.251320919
212918_at	RECQL	1	9.438103558
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1554052_at	CNOT1	1	8.920899501
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202979_s_at	CREBZF	1	6.429117178
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221452_s_at	TMEM14B	1	8.230591977
228275_at	0	1	5.631076835
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243252_at	0	1	5.068133839
214006_s_at	GGCX	1	10.19916617
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224799_at	NDFIP2	1	6.583686034
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226912_at	ZDHHC23	1	7.368202936
206316_s_at	KNTC1	1	8.615079025
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1553679_s_at	VKORC111	1	9.477084133
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221326_s_at	TUBD1	1	9.011246218
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205369_x_at	DBT	1	8.028921735
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243299_at	0	1	7.304833739
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227257_s_at	C10orf46	1	9.826685903
234405_s_at	PHAX	1	8.821724838
227905_s_at	AZI2	1	9.679700272
235848_x_at	ATL2	1	7.155571866
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221082_s_at	NDRG3	1	10.51550225
212250_at	MTDH	1	10.08611206
218448_at	C20orf11	1	9.425592183
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213312_at	C6orf162	1	7.839728202
1554466_a_at	C16orf13	1	9.181528515
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230027_s_at	MRPL43	1	10.00810603
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218617_at	TRIT1	1	9.909436318
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227880_s_at	LOC100132969 /// TMEM185A	1	8.506914223
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215723_s_at	PLD1	1	5.297006155
222522_x_at	MRPS10	1	8.981192298
213376_at	ZBTB1	1	8.395710103
201872_s_at	ABCE1	1	10.06789011
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212502_at	ADO	1	10.24009107
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214507_s_at	EXOSC2	1	10.75651573
232079_s_at	PVRL2	1	5.700786688
231725_at	PCDHB2	1	4.166460372
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205395_s_at	MRE11A	1	6.907815195

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214720_x_at	SEPT10	1	7.406251753
209744_x_at	ITCH	1	9.318445871
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238420_at	0	1	10.39497649
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235331_x_at	PCGF5	1	6.168301466
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219872_at	C4orf18	1	5.105321189
225736_at	FBXO22	1	10.90692733
230763_at	SPATA17	1	4.715319992
235241_at	SLC38A9	1	8.316400014
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218027_at	MRPL15	1	8.981854235
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229614_at	ZNF320	1	4.961389096
200713_s_at	MAPRE1	1	10.86910322
235907_at	TMEM33	1	8.140657444
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219004_s_at	C21orf45	1	8.095174848
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226775_at	ENY2	1	6.844475008
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203198_at	CDK9	1	11.44220358
210284_s_at	MAP3K7IP2	1	9.442423063
229884_s_at	MRPL2	1	8.430454175
225400_at	TSEN15	1	8.877376427
235341_at	DNAJC3	1	7.234886647
228201_at	ARL13B	1	6.917477367
222548_s_at	MAP4K4	1	8.176632999
235311_at	FKBP14	1	8.099092346
223513_at	CENPJ	1	8.101183997

210236_at	PPFIA1	1	7.871877309
212792_at	DPY19L1	1	7.097041453
225830_at	PDZD8	1	5.690406237
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225850_at	SFT2D1	1	7.222464969
212871_at	MAPKAPK5	1	10.53590241
241734_at	SRFBP1	1	9.17080928
221582_at	HIST3H2A	1	5.731831886
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225129_at	CPNE2	1	7.764005027
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213021_at	GOSR1	1	8.544699296
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226287_at	CCDC34	1	6.676388964
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233558_s_at	C4orf41	1	7.185614294
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215722_s_at	SNRPA1	1	9.465159867
201275_at	FDPS	1	9.632721663
209026_x_at	TUBB	1	10.51498369
225135_at	SIN3A	1	9.991482622
235223_at	C6orf153	1	9.782728015
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212372_at	MYH10	1	4.291857475
214310_s_at	ZFPL1	1	9.617876274
229533_x_at	ZNF680	1	7.439815729
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238879_at	0	1	8.605864724
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223341_s_at	SCOC	1	5.062464921
224150_s_at	CEP70	1	6.458071671
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217430_x_at	COL1A1	1	5.505589332

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234863_x_at	FBXO5	1	7.871463958
235103_at	MAN2A1	1	5.95315734
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217959_s_at	TRAPPC4	1	7.575126435
217944_at	POMGNT1	1	7.930890038
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208839_s_at	CAND1	1	8.753352568
211300_s_at	TP53	1	6.184526169
1554417_s_at	APH1A	1	9.515839553
236235_at	ITCH	1	6.597534591
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238513_at	PRRG4	1	4.72409429
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236840_at	C12orf56	1	3.878740105
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239647_at	CHST13	1	4.736722811
222851_at	ZNF654	1	8.707916603
227133_at	CXorf39	1	6.027468541
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209576_at	GNAI1	1	4.297817226
203208_s_at	MTFR1	1	8.630485268
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224824_at	FAM36A	1	8.053948602
225200_at	DPH3	1	6.571947022
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212667_at	SPARC	1	4.615290856
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212488_at	COL5A1	1	4.064336219
224496_s_at	TMEM107	1	6.281553067
219043_s_at	LOC285359 /// PDCL3	1	10.8247249
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211395_x_at	FCGR2C	1	5.769525176
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238578_at	TMEM182	1	8.771386515
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205808_at	ASPH	1	6.612151574
209566_at	INSIG2	1	6.393248966
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223993_s_at	CNIH4	1	9.254858884
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228505_s_at	TMEM170A	1	8.470047881
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225519_at	PPP4R2	1	9.275463845
223308_s_at	WDR5	1	8.689673069
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212438_at	SNRNP27	1	11.4212334
241937_s_at	WDR4	1	6.911074054
226552_at	IER5L	1	6.278419734
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229333_at	0	1	7.547765247
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235425_at	SGOL2	1	6.290815987
216237_s_at	MCM5	1	8.433291437
218438_s_at	MED28	1	8.413564805
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213549_at	0	1	5.208294747

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33646_g_at	GM2A	1	7.133392361
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214512_s_at	SUB1	1	8.681921072
208424_s_at	CIAPIN1	1	9.347680882
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221634_at	RPL23AP7	1	9.122145125
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207108_s_at	NIPBL	1	8.133186177
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204185_x_at	PPID	1	9.091676854
226271_at	GDAP1	1	4.832136067
221276_s_at	SYNC	1	3.820302277
209796_s_at	CNPY2	1	9.691629237
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211089_s_at	NEK3	1	5.429650806
219624_at	BAG4	1	7.253890016
223158_s_at	NEK6	1	7.019999398
211955_at	IPO5	1	8.299110648
213582_at	ATP11A	1	8.086618587
205565_s_at	FXN	1	6.93740727
232861_at	PDP2	1	7.408529835
227164_at	SFRS1	1	7.69362736
207304_at	ZNF45	1	7.964894781
202684_s_at	RNMT	1	8.699436534
212676_at	NF1	1	8.177723973
204109_s_at	NFYA	1	7.405155014
208788_at	ELOVL5	1	4.252962802
214045_at	LIAS	1	6.159193741

205071_x_at	XRCC4	1	6.089585327
210418_s_at	IDH3B	1	8.095512534
222763_s_at	WDR33	1	7.255756584
218118_s_at	TIMM23	1	9.33198891
1553940_a_at	LRRC28	1	7.781775401
240549_at	0	1	5.544363188
204772_s_at	TTF1	1	11.51239747
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223002_s_at	XRN2	1	9.334136506
202627_s_at	SERPINE1	1	3.761846879
224177_s_at	CXorf26	1	6.055346832
204238_s_at	C6orf108	1	6.29339665
213128_s_at	UBE3A	1	7.327607484
1553959_a_at	B3GALT6	1	7.743394025
232033_at	USP37	1	9.585226506
209627_s_at	OSBPL3	1	6.076585315
200613_at	AP2M1	1	10.72753913
221881_s_at	CLIC4	1	6.014758267
238421_at	RC3H2	1	9.725844783
209020_at	C20orf111	1	7.341054689
227335_at	DIDO1	1	5.60310042
204432_at	SOX12	1	6.296484016
226797_at	MBTD1	1	7.14589746
231948_s_at	UBE2F	1	8.686030984
209317_at	POLR1C	1	7.970941826
215285_s_at	PHTF1	1	7.674800514
233085_s_at	OBFC2A	1	4.854808895
225024_at	RPRD1B	1	9.774167056
1554667_s_at	METTL8	1	8.009897363
221935_s_at	C3orf64	1	5.516772065
211205_x_at	PIP5K1A	1	8.78521459
208973_at	ERI3	1	9.150484389
219208_at	FBXO11	1	8.878323422
201969_at	NASP	1	6.641251748
227245_at	C12orf30	1	8.662235853
221962_s_at	UBE2H	1	7.449918963
201653_at	CNIH	1	8.872499772
221528_s_at	ELMO2	1	8.491361189
209545_s_at	RIPK2	1	6.633897352
210759_s_at	PSMA1	1	10.35255733
1554415_at	TAF5L	1	7.311934568
210048_at	NAPG	1	7.798319595
225777_at	C9orf140	1	6.633495252
202675_at	SDHB	1	8.955992981
208743_s_at	YWHAB	1	8.738719463
217818_s_at	ARPC4 /// TTLL3	1	9.963713976
223894_s_at	AKTIP	1	8.894189766
204313_s_at	CREB1	1	9.039105414
212789_at	NCAPD3	1	8.35022832
1555467_a_at	CUGBP1	1	9.065987002
225543_at	0	1	7.775467944
201128_s_at	ACLY	1	7.476098862
226910_at	0	1	9.315362321
218558_s_at	MRPL39	1	6.900575092
203693_s_at	E2F3	1	7.18088778
209157_at	DNAJA2	1	8.024257168

1557918_s_at	SLC16A1	1	5.103007415
224898_at	WDR26	1	7.992071009
204857_at	MAD1L1	1	6.20943753
234295_at	DBR1	1	4.723891315
202829_s_at	VAMP7	1	8.193741507
1553535_a_at	RANGAP1	1	10.4857069
202980_s_at	SIAH1	1	8.464869188
204827_s_at	CCNF	1	8.273868923
1555788_a_at	TRIB3	1	6.302468771
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210319_x_at	MSX2	1	3.955304168
200778_s_at	SEPT2	1	7.952241242
208152_s_at	DDX21	1	8.326405615
204675_at	SRD5A1	1	4.355979961
223478_at	TIMM8B	1	8.453092961
219229_at	SLCO3A1	1	5.057015941
228523_at	NANOS1	1	4.347829552
203023_at	NOP16	1	7.446912353
227943_at	0	1	6.46640093
208817_at	COMT	1	7.525324107
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208394_x_at	ESM1	1	5.175064663
226330_s_at	FAM48A	1	7.599653458
217916_s_at	FAM49B	1	9.621720756
229885_at	0	1	6.615273512
212804_s_at	GAPVD1	1	10.66632519
230192_at	TRIM13	1	5.674060545
210761_s_at	GRB7	1	4.200825705
205226_at	PDGFRL	1	3.970046255
212966_at	HIC2	1	4.327648879
214698_at	ROD1	1	9.893234109
1568877_a_at	ACBD5	1	6.716704782
214962_s_at	NUP160	1	8.359821278
219715_s_at	TDP1	1	9.635905284
225267_at	KPNA4	1	10.36089962
214681_at	GK	1	5.206514477
1552613_s_at	CDC42SE2	1	6.229164685
1554390_s_at	ACTR2	1	8.341626068
211574_s_at	CD46	1	6.942220524
221931_s_at	SEH1L	1	7.164776009
223538_at	SERF1A /// SERF1B	1	7.124981759
223457_at	COPG2	1	6.835695193
202370_s_at	CBFB	1	8.833403345
218323_at	RHOT1	1	7.477313826
222569_at	UGCGL1	1	11.00351454
219402_s_at	DERL1	1	8.515817837
37793_r_at	RAD51L3	1	8.097263502
218479_s_at	XPO4	1	7.714047623
204620_s_at	VCAN	1	4.002859793
1552364_s_at	MSI2	1	7.145988813
235532_at	PIGM	1	5.813045519
209899_s_at	PUF60	1	10.19187625
218866_s_at	POLR3K	1	7.594824061
219212_at	HSPA14	1	8.411537002

216607_s_at	CYP51A1	1	5.126657693
201554_x_at	GYG1	1	8.281397814
218465_at	TMEM33	1	7.442388958
202052_s_at	RAI14	1	5.991861361
201652_at	COP55	1	8.336952064
202206_at	ARL4C	1	4.58992533
238191_at	0	1	5.823641043
206061_s_at	DICER1	1	6.367459179
203502_at	BPGM	1	6.340301353
224387_at	COMMD5	1	9.079575024
210178_x_at	FUSIP1 /// LOC642558	1	11.26247957
212673_at	METAP1	1	10.22759792
231842_at	KIAA1462	1	6.150350523
213301_x_at	TRIM24	1	5.93674408
226947_at	GUSBL2 /// LOC728411	1	8.107654436
218218_at	APPL2	1	6.526325372
218721_s_at	C1orf27	1	7.108749811
224570_s_at	IRF2BP2	1	8.214910201
210733_at	TRAM1	1	8.285612157
205930_at	GTF2E1	1	9.335134935
224479_s_at	MRPL45	1	7.922134872
208822_s_at	DAP3	1	12.1427161
212183_at	NUDT4 /// NUDT4P1	1	5.43565144
219653_at	LSM14B	1	8.281854109
221538_s_at	PLXNA1	1	7.890374418
239775_at	LOC100131512	1	5.906023729
209832_s_at	CDT1	1	8.157710183
201177_s_at	UBA2	1	8.35272662
214992_s_at	DNASE2	1	8.701768347
208795_s_at	MCM7	1	7.38056741
219913_s_at	CRNKL1	1	7.093335393
224452_s_at	MGC12966	1	9.05240602
1555241_at	C8orf59	1	7.113716322
225614_at	SAAL1	1	8.298198824
219105_x_at	ORC6L	1	6.970803182
233555_s_at	SULF2	1	4.619107104
218774_at	DCPS	1	8.488693341
206188_at	ZNF623	1	7.301676261
206752_s_at	DFFB	1	7.102843063
235168_at	PIGM	1	6.10495638
209063_x_at	PAIP1	1	7.213912979
216262_s_at	TGIF2	1	8.029039584
204727_at	WDHD1	1	8.141937756
200900_s_at	M6PR	1	8.969173472
230676_s_at	TMEM19	1	7.458441913
220104_at	ZC3HAV1	1	6.375729945
226364_at	HIP1	1	6.249509785
209330_s_at	HNRNPD	1	8.570902831
210338_s_at	HSPA8	1	9.482546971
200812_at	CCT7	1	12.33210168
231852_at	ERI1	1	7.372888032
224684_at	SNX12	1	8.110253558
242648_at	KLHL8	1	6.086307646
204085_s_at	CLN5	1	5.402145942
226749_at	MRPS9	1	10.08433536
201761_at	MTHFD2	1	8.595522438

223339_at	ATPIF1	1	5.177181827
201558_at	RAE1	1	7.861745329
239697_x_at	C3orf67	1	4.546657055
223675_s_at	VEZT	1	7.392147597
225863_s_at	C19orf12	1	4.695053836
211871_x_at	GNB5	1	7.885789168
201310_s_at	C5orf13	1	4.155018102
203972_s_at	PEX3	1	7.231114468
225105_at	OCC-1	1	4.633145709
210008_s_at	MRPS12	1	8.410989605
222603_at	ERMP1	1	5.45133569
212501_at	CEBPB	1	7.424273567
204222_s_at	GLIPR1	1	4.368427483
202165_at	PPP1R2	1	8.736576166
201486_at	RCN2	1	9.100728334
205691_at	SYNGR3	1	3.577631126
228700_at	0	1	6.449435517
1554145_a_at	KLRAQ1	1	8.06850976
208696_at	CCT5	1	8.769053595
211623_s_at	FBL	1	8.223984043
211162_x_at	SCD	1	5.256574123
219165_at	PDLIM2	1	5.88495811
204030_s_at	SCHIP1	1	4.644605609
216488_s_at	ATP11A	1	9.009017134
201298_s_at	MOBK1B	1	8.358173489
203242_s_at	PDLIM5	1	7.332035017
225712_at	GEMIN5	1	9.565446669
219257_s_at	SPHK1	1	5.246520351
201381_x_at	CACYBP	1	9.923089499
220147_s_at	FAM60A	1	7.910756766
218919_at	ZFAND1	1	6.988003168
233496_s_at	CFL2	1	4.039438849
201323_at	EBNA1BP2	1	8.521539647
203337_x_at	ITGB1BP1	1	5.777838777
234926_s_at	C20orf43	1	10.00498727
1554053_at	SPTLC1	1	8.263753508
226630_at	C14orf106	1	6.9317998
212449_s_at	LYPLA1	1	9.747994756
234660_s_at	DIS3	1	7.243707205
228283_at	CMC1	1	7.918393867
224895_at	YAP1	1	5.051896229
213951_s_at	PSMC3IP	1	7.684492732
202925_s_at	PLAGL2	1	5.817527688
201198_s_at	PSMD1	1	10.05983985
227370_at	FAM171B	1	4.08389995
224156_x_at	IL17RB	1	4.302649505
226521_s_at	FAM175A	1	6.527275131
217857_s_at	RBM8A	1	9.887513476
230416_at	0	1	4.909133023
223765_s_at	KBTBD4	1	9.078105734
218356_at	FTSJ2	1	9.028106427
208527_x_at	HIST1H2BC /// HIST1H2BE /// HIST1H2BF /// HIST1H2BG /// HIST1H2BI	1	6.002989062

209362_at	MED21	1	7.088616731
201351_s_at	YME1L1	1	9.543225956
1569472_s_at	TTC3	1	6.304375603
210009_s_at	GOSR2	1	8.685128228
205746_s_at	ADAM17	1	6.427358465
1554757_a_at	INPP5A	1	6.771904542
202438_x_at	IDS	1	7.593454189
204618_s_at	GABPB1	1	9.681071797
223451_s_at	CKLF	1	6.409604754
206653_at	POLR3G	1	5.158280053
208675_s_at	DDOST	1	9.500688952
218147_s_at	GLT8D1	1	6.65606261
207338_s_at	ZNF200	1	7.68888107
209861_s_at	METAP2	1	9.10696917
226995_at	C21orf86	1	5.988592639
213790_at	ADAM12	1	4.088362377
205010_at	GNL3L	1	9.235834915
213623_at	KIF3A	1	7.820175182
226386_at	C7orf30	1	10.03111101
227653_at	TRMT5	1	8.104433559
221752_at	SSH1	1	8.81573388
213429_at	0	1	3.735903444
201259_s_at	SYPL1	1	5.895083978
213358_at	KIAA0802	1	3.823285951
242273_at	0	1	5.668720509
228824_s_at	PTGR1	1	3.656200855
218556_at	ORMDL2	1	7.518279545
210685_s_at	UBE4B	1	8.73824971
1553587_a_at	POLE4	1	7.040513282
218570_at	KBTBD4 /// PTPMT1	1	7.159963699
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213526_s_at	LIN37	1	7.327402423
210278_s_at	AP4S1	1	9.015102043
226743_at	SLFN11	1	4.427028141
1558201_s_at	SLC4A1AP	1	11.45035238
209527_at	EXOSC2	1	8.939203073
218152_at	HMG20A	1	7.931319536
214500_at	H2AFY	1	7.063292349
1568597_at	LOC646762	1	7.088362433
224437_s_at	VTA1	1	7.259878854
202998_s_at	ENTPD4 /// LOXL2	1	4.176719239
202446_s_at	PLSCR1	1	5.963163428
218823_s_at	KCTD9	1	6.1780976
201233_at	PSMD13	1	11.79491263
205084_at	BCAP29	1	7.346547702
227111_at	ZBTB34	1	7.245751704
208941_s_at	SEPHS1	1	7.816558132
1554588_a_at	TTC30B	1	5.361563824
219239_s_at	ZNF654	1	7.03694914
224463_s_at	C11orf70	1	3.639103742
209105_at	NCOA1	1	6.632058843
238448_at	MRPL19	1	8.883068056
227382_at	CY5B	1	5.872022115
211864_s_at	MYOF	1	3.78826967
230122_at	MLLT10	1	6.438903624
220202_s_at	RC3H2	1	10.57607762

225086_at	FAM98B	1	9.420466053
209162_s_at	PRPF4	1	9.784449986
201725_at	CDC123	1	9.409199329
205932_s_at	MSX1	1	4.540794454
220121_at	LINS1	1	7.831749164
204844_at	ENPEP	1	4.338931287
225045_at	CCDC88A	1	4.995836877
209608_s_at	ACAT2	1	7.144954215
212020_s_at	MKI67	1	7.016657766
1555565_s_at	TAPBP	1	7.192775815
212008_at	UBXN4	1	8.887980881
212453_at	KIAA1279	1	7.404392764
220007_at	METTL8	1	8.518226395
201727_s_at	ELAVL1	1	9.867180696
202984_s_at	BAG5	1	6.91878795
225376_at	C20orf11	1	7.708368149
1553719_s_at	ZNF548	1	6.415391895
201469_s_at	SHC1	1	9.780417515
224129_s_at	DPY30	1	9.923490992
201604_s_at	PPP1R12A	1	9.085543579
208700_s_at	TKT	1	8.380987474
242149_at	C18orf19	1	8.587835217
222562_s_at	TNKS2	1	7.865264589
203870_at	USP46	1	7.308691263
232078_at	PVRL2	1	5.09922294
221900_at	COL8A2	1	4.193053931
221504_s_at	ATP6V1H	1	8.866150128
205769_at	SLC27A2	1	3.562766236
205704_s_at	ATP6VOA2	1	6.82697033
219890_at	CLEC5A	1	4.126106654
231853_at	TUBD1	1	6.495745186
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201624_at	DARS	1	8.057589984
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222875_at	DHX33	1	8.382091931
227828_s_at	FAM176A	1	4.298553671
53202_at	C7orf25	1	8.379504463
212342_at	YIPF6	1	7.783305172
201108_s_at	THBS1	1	3.83399909
218647_s_at	YRDC	1	8.260824276
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212985_at	APBB2	1	5.473400707
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204333_s_at	AGA	1	4.308126681
204593_s_at	SMCR7L	1	9.963791121
234976_x_at	SLC4A5	1	7.650373985
201222_s_at	RAD23B	1	9.718565547
220668_s_at	DNMT3B	1	5.48053857
1564381_s_at	0	1	9.134380582
203545_at	ALG8	1	7.252058141
225898_at	WDR54	1	5.926353818
1554456_a_at	LINS1	1	7.595387684
215416_s_at	STOML2	1	8.361172667

208896_at	DDX18	1	8.006026774
227017_at	ERICH1	1	6.921948668
222212_s_at	LASS2	1	8.210538421
217831_s_at	NSFL1C	1	10.07831967
224392_s_at	OPN3	1	4.886804436
224455_s_at	ADPGK	1	11.56989372
229891_x_at	KIAA1704	1	5.898259067
1568838_at	hCG_1742852 /// LOC100132169	1	4.46172675
203577_at	GTF2H4	1	9.659102851
1553994_at	NT5E	1	4.179149882
217813_s_at	SPIN1	1	7.687055418
202420_s_at	DHX9	1	14.29456894
222794_x_at	MTPAP	1	7.239953298
212367_at	FEM1B	1	6.888193869
203120_at	TP53BP2	1	8.718265258
206796_at	WISP1	1	5.485674944
206958_s_at	UPF3A	1	6.714648685
224894_at	YAP1	1	4.926502418
224560_at	TIMP2	1	4.008838033
223506_at	ZC3H8	1	8.735218775
203360_s_at	MYCBP	1	8.7411355
225997_at	MOBK1A	1	7.573265405
229549_at	0	1	6.954031231
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207127_s_at	HNRNPH3	1	10.10469924
222595_s_at	DIDO1	1	7.374570294
203634_s_at	CPT1A	1	6.028915097
222699_s_at	PLEKHF2	1	6.739913801
204976_s_at	AMMECR1	1	5.387953687
203356_at	CAPN7	1	7.241453828
213088_s_at	DNAJC9	1	7.436382412
211237_s_at	FGFR4	1	5.911714614
213152_s_at	SFRS2B	1	8.130257118
232095_at	0	1	7.1221218
224618_at	ROD1	1	8.133398271
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225448_at	NAPG	1	5.530601059
218649_x_at	SDCCAG1	1	7.118710925
1564520_s_at	PRMT5	1	7.766996094
204588_s_at	SLCZA7	1	5.18390045
1554478_a_at	HEATR3	1	8.96337127
219443_at	TASP1	1	7.391687563
218455_at	NFS1	1	7.394115597
201576_s_at	GLB1	1	7.969661592
201001_s_at	TMEM189-UBE2V1 /// UBE2V1	1	8.922533648
218291_at	ROBLD3	1	9.053837059
210174_at	NR5A2	1	3.57171084
204120_s_at	ADK	1	5.821288197
218586_at	C20orf20	1	7.003324164
207431_s_at	DEGS1	1	6.722544927
242943_at	ST8SIA4	1	4.910315694
205148_s_at	CLCN4	1	4.699704461
230026_at	MRPL43	1	4.170824677
48808_at	DHFR	1	6.906507631

203960_s_at	HSPB11	1	7.189725479
223666_at	SNX5	1	6.515051486
221579_s_at	NUDT3	1	9.414274444
224872_at	DIP2B	1	8.183124675
215136_s_at	EXOSC8	1	7.372357135
209974_s_at	BUB3	1	9.194461365
202591_s_at	SSBP1	1	9.579549821
204699_s_at	C1orf107	1	9.135154326
225642_at	KTI12	1	9.404378691
227897_at	0	1	5.31589748
212944_at	SLC5A3	1	6.760653649
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223378_at	GLIS2	1	5.012665701
218195_at	C6orf211	1	6.867090474
222417_s_at	SNX5	1	8.339063168
203612_at	BYSL	1	8.101309647
230051_at	C10orf47	1	4.013880747
229010_at	CBL	1	5.994789402
225964_at	ZXDC	1	10.63487615
218397_at	FANCL	1	6.828598685
210992_x_at	FCGR2C	1	6.215179259
221434_s_at	C14orf156	1	8.928095491
223570_at	MCM10	1	7.978058723
203016_s_at	SSX2IP	1	6.066352601
226835_s_at	C20orf199	1	6.91261695
224671_at	MRPL10	1	9.28149686
201774_s_at	NCAPD2	1	8.088431562
204812_at	ZW10	1	10.76892337
203094_at	MAD2L1BP	1	7.62394141
205089_at	ZNF7	1	8.377180764
218930_s_at	TMEM106B	1	6.770688988
203584_at	TTC35	1	7.612360204
224883_at	PLDN	1	8.371904452
209511_at	POLR2F	1	10.38693969
219688_at	BBS7	1	8.270116886
235159_at	0	1	8.21702655
215984_s_at	ARFRP1 /// IGLJ3	1	9.680442566
203626_s_at	SKP2	1	6.871025949
211564_s_at	PDLIM4	1	4.673379806
201400_at	PSMB3	1	9.18136111
211537_x_at	MAP3K7	1	10.60544955
213552_at	GLCE	1	5.215408926
225164_s_at	EIF2AK4	1	6.251296818
201377_at	UBAP2L	1	8.48562664
228106_at	C4orf30	1	6.883647202
205188_s_at	SMAD5	1	7.59754935
1553167_a_at	SEPSECS	1	5.360020976
212628_at	PKN2	1	7.049817298
210588_x_at	HNRNPH3	1	10.34666482
222877_at	0	1	4.129582184
202497_x_at	SLC2A3	1	4.506466147
226215_s_at	FBXL10	1	8.610309073
223839_s_at	SCD /// SCDOS	1	4.437225376
228452_at	C17orf39	1	7.752998307
210933_s_at	FSCN1	1	4.665040134
202721_s_at	GFPT1	1	6.473314177

212568_s_at	DLAT	1	6.631045169
236957_at	CDCA2	1	5.593171432
217763_s_at	RAB31	1	4.374889896
226604_at	TMTC3	1	5.886888948
225991_at	TMEM41A	1	7.682688068
221425_s_at	ISCA1	1	8.18352569
227748_at	CCBL2	1	7.000922118
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1552691_at	ARL11	1	4.290613479
228053_s_at	TOMM5	1	8.370149487
221423_s_at	YIPF5	1	7.056635639
203775_at	SLC25A13	1	5.544856349
200873_s_at	CCT8	1	9.56472524
212485_at	GPATCH8	1	8.786408783
227314_at	ITGA2	1	3.699879284
211980_at	COL4A1	1	5.15096124
221986_s_at	KLHL24	1	6.407681496
218224_at	PNMA1	1	5.777687307
222872_x_at	OBFC2A	1	4.537146258
228425_at	LOC654433	1	3.587303188
219016_at	FASTKD5	1	8.297052689
218699_at	RAB7L1	1	5.59026686
207769_s_at	PQBP1	1	9.368969441
222824_at	0	1	4.996189254
212371_at	FAM152A	1	7.418539487
201261_x_at	BGN	1	4.1768473
220943_s_at	C2orf56	1	10.71537428
209279_s_at	NSDHL	1	7.149052386
200753_x_at	SFRS2	1	11.56010616
201238_s_at	CAPZA2	1	6.949387199
202321_at	GGPS1	1	6.443994588
208985_s_at	EIF3J	1	8.790575428
219032_x_at	OPN3	1	4.674049251
219485_s_at	PSMD10	1	8.309344904
225711_at	ARL6IP6	1	6.730822724
225829_at	PDZD8	1	5.478495005
213134_x_at	BTG3	1	6.002732568
231984_at	MTAP	1	5.737614238
207396_s_at	ALG3	1	9.737978915
206085_s_at	CTH	1	5.016330588
228334_x_at	KIAA1712	1	6.769939831
223575_at	KIAA1549	1	5.580282179
205991_s_at	PRRX1	1	4.375843958
204283_at	FARS2	1	7.47394497
227044_at	0	1	6.876907274
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202892_at	CDC23	1	9.794913643
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224878_at	UBFD1	1	9.521359251
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235275_at	BMP8B	1	7.427444141
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201376_s_at	HNRNPF	1	10.02202215
217851_s_at	SLMO2	1	7.632507067
204666_s_at	RP5-1000E10.4	1	9.033661604
218104_at	TEX10	1	9.033540913
225754_at	AP1G1	1	7.84390464
213410_at	C10orf137	1	6.083429412
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238768_at	C2orf68	1	6.685875575
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225261_x_at	TH1L	1	8.011932125
207610_s_at	EMR2	1	5.085048162
202899_s_at	SFRS3	1	11.52777106
214531_s_at	SNX1	1	8.731303013
207319_s_at	CDC2L5	1	10.09313203
222793_at	DDX58	1	5.263987713
1558105_a_at	0	1	4.093425805
220925_at	MAK10	1	7.989376075
214119_s_at	FKBP1A	1	8.076412065
37433_at	PIAS2	1	7.673052617
222553_x_at	OXR1	1	6.33593806
208127_s_at	SOC55	1	6.364834638
205461_at	RAB35	1	8.479113185
220230_s_at	CYB5R2	1	4.689521943
230741_at	0	1	4.601406684
213387_at	ATAD2B	1	8.506408833
202306_at	POLR2G	1	9.858104117
222270_at	SMEK2	1	6.555318549
207821_s_at	PTK2	1	8.444191674
225149_at	PCID2	1	8.697141521
228149_at	C7orf60	1	7.488678663
223220_s_at	PARP9	1	5.651675598
200608_s_at	RAD21	1	9.62541321
203552_at	MAP4K5	1	6.365050971
232661_s_at	C7orf64	1	6.676050564
226033_at	USP31	1	7.89784069
229064_s_at	RCAN3	1	7.237555803
208996_s_at	POLR2C	1	8.653084001
203125_x_at	SLC11A2	1	6.867285678
204634_at	NEK4	1	7.50520069
222505_at	LMBR1	1	8.238401742
233632_s_at	XRN1	1	7.1562891
205499_at	SRPX2	1	4.203354355
219644_at	CCDC41	1	6.580812471
226750_at	LARP2	1	5.26811282
224430_s_at	MTO1	1	8.691814637
220494_s_at	0	1	5.666264609
242139_s_at	0	1	6.876870103
229305_at	MLF1IP	1	5.420218647
221580_s_at	TAF1D	1	7.286851985
238462_at	UBASH3B	1	4.291698208
231202_at	ALDH1L2	1	4.157517523
208680_at	PRDX1	1	10.5300972
204787_at	VSIG4	1	4.070741341
222916_s_at	HDLBP	1	7.279635946

242923_at	ZNF678	1	6.823814667
228123_s_at	ABHD12	1	7.106661834
222470_s_at	UQCC	1	7.729022836
216241_s_at	TCEA1	1	8.841230352
210849_s_at	VPS41	1	8.573465204
212037_at	PNN	1	6.721974317
224334_s_at	MRPL51 /// SPTLC1	1	11.05103632
220092_s_at	ANTXR1	1	5.524449923
1555814_a_at	RHOA	1	7.970423844
1555247_a_at	RAPGEF6	1	6.801116687
231907_at	ABL2	1	6.731713845
219030_at	TPRKB	1	8.239110706
1552928_s_at	MAP3K7IP3	1	7.629480155
235136_at	ORMDL3	1	4.84695626
211769_x_at	SERINC3	1	6.807850979
1553219_a_at	AMMECR1	1	7.094947798
232432_s_at	SLC30A5	1	7.153435284
218643_s_at	CRIP1	1	7.395716311
228559_at	CENPN	1	6.143385829
213889_at	PIGL	1	6.687125981
218768_at	NUP107	1	6.538588384
216548_x_at	HMG4L	1	7.409268251
219384_s_at	ADAT1	1	7.08528068
222000_at	C1orf174	1	8.59905157
242245_at	0	1	4.050495434
219366_at	AVEN	1	8.98171288
1555450_a_at	NARG1L	1	7.887184567
223441_at	SLC17A5	1	4.663959178
226807_at	ZFP1	1	8.186603352
220241_at	TMCO3	1	7.690018835
1554105_at	TMEM185A	1	10.10897286
212409_s_at	TOR1AIP1	1	7.572577078
210286_s_at	SLC4A7	1	6.45720422
212478_at	RMND5A	1	8.988567037
230621_at	IAH1	1	5.37664755
202034_x_at	RB1CC1	1	9.913219675
222503_s_at	WDR41	1	7.552511093
212731_at	ANKRD46	1	5.492723653
201970_s_at	NASP	1	10.42436027
202679_at	NPC1	1	5.363692835
243026_x_at	XIAP	1	6.740762754
202296_s_at	RER1	1	7.670498717
212680_x_at	PPP1R14B	1	8.310820731
229704_at	0	1	4.249349715
222735_at	TMEM38B	1	5.018582082
203732_at	TRIP4	1	8.053718851
206920_s_at	GLE1	1	8.950727551
51228_at	RBM12B	1	7.533711986
1554627_a_at	ASCC1	1	8.4385139
1555803_a_at	C11orf57	1	8.33199438
205126_at	VRK2	1	6.516818885
225803_at	FBXO32	1	4.845550368
203068_at	KLHL21	1	7.339280682
202164_s_at	CNOT8	1	6.871623306
218948_at	QRSL1	1	4.98959152
202251_at	PRPF3	1	8.550441781

218715_at	UTP6	1	10.15453666
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208776_at	PSMD11	1	6.833181839
200992_at	IPO7	1	9.003457895
225950_at	0	1	6.590455182
227693_at	WDR20	1	7.167139072
204835_at	POLA1	1	6.995962273
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208762_at	SUMO1	1	8.702119343
1556121_at	0	1	6.40255713
235011_at	MAP3K2	1	10.34988536
223090_x_at	VEZT	1	6.725292824
200722_s_at	CAPRIN1	1	8.430050747
229742_at	C1orf61	1	7.256775454
219557_s_at	NRIP3	1	6.110745284
223273_at	C14orf142	1	5.748138342
207980_s_at	CITED2	1	4.280068248
224793_s_at	TGFBR1	1	6.107635983
204461_x_at	RAD1	1	6.332084777
219356_s_at	CHMP5	1	8.617768626
235197_s_at	OSTM1	1	8.171334634
1556178_x_at	TAF8	1	8.67709414
202784_s_at	NNT	1	4.612749851
202338_at	TK1	1	6.673680904
234000_s_at	PTPLAD1	1	6.764316796
223328_at	ARMC10	1	7.64308764
201232_s_at	PSMD13	1	9.661957963
205796_at	TCP11L1	1	6.020962395
222502_s_at	UFM1	1	7.202487319
215071_s_at	HIST1H2AC	1	4.317214744
218282_at	EDEM2	1	8.289450189
219698_s_at	METTL4	1	7.535361917
210845_s_at	PLAUR	1	4.107214812
204341_at	TRIM16	1	4.139628868
223585_x_at	KBTBD2	1	8.266093872
201501_s_at	GRSF1	1	7.338911839
203517_at	MTX2	1	9.359752419
214578_s_at	ROCK1	1	8.433579467
200975_at	PPT1	1	9.095559284
205003_at	DOCK4	1	5.330716822
1556551_s_at	SLC39A6	1	8.289454389
200828_s_at	ZNF207	1	12.38412919
1552330_at	MGC16385	1	5.104903989
208778_s_at	TCP1	1	8.884974093
210296_s_at	PXMP3	1	6.129299958
213696_s_at	MED8	1	10.39841734
226606_s_at	GTPBP5	1	6.02559962
223804_s_at	THUMPD3	1	8.813139404
1553698_a_at	C1orf96	1	7.171070363
238844_s_at	NPHP1	1	5.929750996
213899_at	METAP2	1	7.050174887
212740_at	PIK3R4	1	8.988884387
210621_s_at	RASA1	1	6.240478928
1552612_at	CDC42SE2	1	5.190909414
211899_s_at	TRAF4	1	7.11148293
226784_at	TWISTNB	1	7.743127448

209572_s_at	EED	1	7.697623804
217774_s_at	HSPC152	1	9.86360903
218128_at	NFYB	1	7.007963227
209149_s_at	TM9SF1	1	6.845676756
234311_s_at	GTPBP10	1	6.441674599
224574_at	C17orf49 /// RNASEK	1	9.553234746
220085_at	HELLS	1	5.224568048
218197_s_at	OXR1	1	5.875502849
203489_at	SIVA1	1	7.585944585
203492_x_at	CEP57	1	9.793998081
214499_s_at	BCLAF1	1	9.017242845
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222634_s_at	TBL1XR1	1	8.346491371
202475_at	TMEM147	1	8.703898424
202346_at	UBE2K	1	6.3349611
225752_at	NIPA1	1	7.224106711
227455_at	C6orf136	1	5.978076477
223300_s_at	CCDC82	1	9.848571126
217976_s_at	DYNC1LI1	1	8.517724019
214647_s_at	HFE	1	6.40746809
224654_at	DDX21	1	9.010356236
204176_at	KLHL20	1	6.861581971
202303_x_at	SMARCA5	1	10.9011324
202113_s_at	SNX2	1	6.380353109
202593_s_at	GDE1	1	6.280096312
242594_at	FAM44A	1	6.006207773
223416_at	SF3B14	1	9.809119933
211094_s_at	NF1	1	7.495189212
218497_s_at	RNASEH1	1	9.43281233
216503_s_at	MLLT10	1	7.371779066
222029_x_at	PFDN6	1	9.133246728
220617_s_at	ZNF532	1	6.957935094
208639_x_at	PDIA6	1	9.076819421
242116_x_at	0	1	7.380139705
235520_at	ZNF280C	1	6.932687343
201930_at	MCM6	1	8.216904749
202226_s_at	CRK	1	8.767030091
203114_at	LYPLA1 /// SSSCA1	1	8.676726649
203484_at	SEC61G	1	8.654123789
228916_at	CWF19L2	1	6.853025015
1555609_a_at	ZMAT3	1	7.559571428
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1555973_at	0	1	7.164352777
221185_s_at	IQCG	1	5.095313649
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1555419_a_at	ASAH1	1	5.961666993
211764_s_at	UBE2D1	1	8.467181484
200008_s_at	GDI2	1	7.994619333
211081_s_at	MAP4K5	1	8.617934945
205097_at	SLC26A2	1	4.246135288
221096_s_at	TMCO6	1	7.758425197
201619_at	PRDX3	1	9.063106533
201514_s_at	G3BP1	1	8.496594896
222551_s_at	C8orf33	1	7.318982843
218653_at	SLC25A15	1	6.092556396
222044_at	PCIF1	1	6.664282844

218579_s_at	DHX35	1	7.745912722
224726_at	MIB1	1	6.422293038
226782_at	SLC25A30	1	7.933499476
218400_at	OAS3	1	5.026908006
1555735_a_at	BAP1	1	8.668261902
203971_at	SLC31A1	1	6.678669361
229500_at	SLC30A9	1	4.753477207
209338_at	TFCP2	1	9.988445456
205648_at	WNT2	1	3.765025641
206141_at	MOC53	1	7.812551388
225210_s_at	FAM103A1	1	6.53616171
212468_at	SPAG9	1	6.474891863
227034_at	ANKRD57	1	4.56121895
219675_s_at	UXS1	1	8.139678564
208935_s_at	LGALS8	1	6.385676938
223649_s_at	SLC25A39	1	8.982016118
202934_at	HK2	1	4.795795213
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212072_s_at	CSNK2A1	1	8.264599504
213913_s_at	TBC1D30	1	4.391594587
221536_s_at	LSG1	1	7.874244095
243413_at	TTC30B	1	5.692021635
228108_at	0	1	3.592615454
1567458_s_at	RAC1	1	8.487569134
225057_at	SLC15A4	1	7.855423082
235573_at	0	1	5.838935627
239153_at	HOTAIR	1	4.302652882
201697_s_at	DNMT1	1	9.306438721
235007_at	BBS7	1	6.89633744
214097_at	RPS21	1	4.844890564
218132_s_at	TSEN34	1	9.030284042
215537_x_at	DDAH2	1	6.295111571
238122_at	RBM12B	1	7.145647983
201096_s_at	ARF4	1	7.392952034
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218085_at	CHMP5	1	6.685372094
235230_at	PLCXD2	1	5.192052757
202932_at	YES1	1	5.804706351
237435_at	0	1	3.575627744
224602_at	C4orf3	1	7.742740442
218370_s_at	S100PBP	1	7.837799794
220770_s_at	LOC63920	1	5.412732649
218829_s_at	CHD7	1	5.4615614
213476_x_at	TUBB3	1	7.994490576
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243507_s_at	C20orf196	1	7.149979262
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224974_at	SUDS3	1	6.983409447
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229886_at	C5orf34	1	5.129340596
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218163_at	MCTS1	1	6.617275477
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223978_s_at	CRLS1	1	5.880624823
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222427_s_at	LARS	1	7.794590032
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239078_at	C1orf58	1	4.810806333
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223360_at	C21orf56	1	5.664960669
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226327_at	ZNF507	1	5.29694868
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224587_at	SUB1	1	5.893358288
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227520_at	CXorf15	1	5.415966827
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224315_at	DDX20	1	7.855421179
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225716_at		0	5.657026235
222192_s_at	C2orf43	1	5.902367712
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227304_at	SMCR8	1	7.824164003
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228734_at		0	6.614791701
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219200_at	FASTKD3	1	6.34388797
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239888_at		0	1	7.164415479
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224561_s_at	MORF4L1	1	7.066882164
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243372_at	HSPD1 /// HSPD1P4	1	5.38755732
208436_s_at	IRF7	1	4.850062672
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87100_at	ABHD2	1	3.721485452
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1554093_a_at	SNAPC5	1	7.287013701
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218420_s_at	C13orf23	1	6.708921932
225600_at	C8orf83	1	5.635158665
222857_s_at	KCNMB4	1	4.360796655
218500_at	C8orf55	1	5.23325552
206116_s_at	TPM1	1	4.563655384
220206_at	ZMYM1	1	7.640755466
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222645_s_at	KCTD5	1	7.215986875
218115_at	ASF1B	1	6.558871602
222759_at	SUV420H1	1	5.945755105
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222269_at	APOOL	1	5.848994863
219953_s_at	C11orf17	1	8.993972016
209181_s_at	RABGGTB	1	7.318343868
222233_s_at	DCLRE1C	1	5.761178811
225547_at	SNHG6	1	7.362429313
239314_at	NHLRC3	1	7.819603493
222715_s_at	AP1GBP1	1	6.603156025
209599_s_at	PRUNE	1	6.554516075
223256_at	KIAA1333	1	5.725333646
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219449_s_at	TMEM70	1	7.453733235
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226181_at	TUBE1	1	5.492828924
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214765_s_at	NAAA	1	5.118516533
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213239_at	PIBF1	1	5.084625743
228299_at	KCTD20	1	9.233009721
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213616_at	C18orf10	1	6.292934457
202147_s_at	IFRD1	1	5.566528434
223094_s_at	ANKH	1	4.803798729
226408_at	TEAD2	1	4.887151753
236268_at	SEC22C	1	5.641239864
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206656_s_at	C2orf3	1	7.234156927
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213047_x_at	SET	1	9.503699702
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227110_at	HNRNPC	1	5.72938371
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217915_s_at	C15orf15	1	7.241473499
242422_at	G3BP1	1	6.953074801
222263_at	SLC35E1	1	6.056262295
218816_at	LRRC1	1	5.531521651
229983_at	TIGD2	1	6.797344243
225889_at	AEBP2	1	6.703482457
208827_at	PSMB6	1	9.058477237
1552618_at	STX6	1	10.16742017
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201483_s_at	SUPT4H1	1	7.97919123
226159_at	C5orf51	1	7.963163543
225581_s_at	MRPL50	1	6.783458203
214443_at	PVR	1	7.887913937
223488_s_at	GNB4	1	7.931508632
208555_x_at	CST2	1	4.124756975
234977_at	ZADH2	1	5.511037473
218028_at	ELOVL1	1	7.155766495
202209_at	LSM3	1	8.072670269
217988_at	CCNB1IP1	1	6.254544372
203564_at	FANCG	1	6.473014332
221673_s_at	CSNK1G1	1	10.1159022
226431_at	FAM117B	1	5.102957156
205924_at	RAB3B	1	4.034929087
1555543_a_at	CLCC1	1	7.411102033
229804_x_at	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6	1	6.811161198
228357_at	UNK	1	4.153298599
209188_x_at	DR1	1	6.771236886
218826_at	SLC35F2	1	4.016028405
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231822_at	CTTNBP2NL	1	7.174459715
226048_at	MAPK8	1	6.256277436
234726_s_at	TMEM168	1	4.726544578
211615_s_at	LRPPRC	1	6.702790892
214196_s_at	TPP1	1	5.924771907
212377_s_at	NOTCH2	1	5.73136811
224756_s_at	BAT5	1	7.311524423
215078_at	SOD2	1	3.975274923
224713_at	MKI67IP	1	8.767580693

224908_s_at	TTL	1	8.058802473
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204928_s_at	SLC10A3	1	7.091690097
207809_s_at	ATP6AP1	1	7.667530575
202846_s_at	PIGC	1	7.434219521
212163_at	KIDINS220	1	5.416890797
238614_x_at	ZNF430	1	6.91550578
229665_at	CSTF3	1	5.596014595
218374_s_at	C12orf4	1	8.190586967
224330_s_at	MRPL27	1	7.746895794
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204867_at	GCHFR	1	5.111175793
217722_s_at	NGRN	1	7.225591935
224509_s_at	RTN4IP1	1	5.870348622
219056_at	RNASEH2B	1	5.577141602
219575_s_at	COG8 /// PDF	1	7.807119281
213292_s_at	SNX13	1	6.053375925
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220305_at	VISA	1	5.510231137
225075_at	PDRG1	1	7.766267846
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213761_at	MDM1	1	5.652865153
204528_s_at	NAP1L1	1	5.949505268
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209860_s_at	ANXA7	1	7.840325649
1554533_at	C2	1	4.403662784
218996_at	TFPT	1	6.685922672
238056_at	SDHC	1	6.522793245
208801_at	SRP72	1	8.075151455
215424_s_at	SNW1	1	10.16183411
222067_x_at	HIST1H2BD	1	4.928693934
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234975_at	GSPT1	1	5.53454223
244177_at	0	1	6.272311717
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204496_at	STRN3	1	5.775217588
221291_at	ULBP2	1	4.903837984
224888_at	SELI	1	7.584806535
218165_at	C1orf149	1	7.670003734
211575_s_at	UBE3A	1	9.087857116
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203017_s_at	SSX2IP	1	5.254260802
222747_s_at	SCML1	1	4.605842662
208021_s_at	RFC1	1	7.440910936
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235191_at	LOC148189	1	4.921046559
1554345_a_at	GIN1	1	7.437120014
203871_at	SENP3	1	9.942821685
224728_at	ATPAF1	1	5.003709358
233842_x_at	C20orf43	1	9.263386277
226060_at	RFT1	1	8.60209385
233421_s_at	NUP133	1	9.323212649
201608_s_at	PWP1	1	9.905328565
228124_at	ABHD12	1	5.194953936
227246_at	PLRG1	1	6.361637741
203338_at	PPP2R5E	1	8.868223438

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213471_at	NPHP4	1	6.42077012
230789_at	ZNF280B	1	3.722538636
208939_at	SEPHS1	1	6.287309051
236477_at	PRPF40A	1	10.05149196
212529_at	LSM12	1	7.009597183
209161_at	PRPF4	1	8.409473474
202216_x_at	NFYC	1	11.31398778
212820_at	DMXL2	1	4.71277488
207785_s_at	RBPJ	1	5.953215616
203589_s_at	TFDP2	1	6.21889961
223098_s_at	LONP2	1	6.275482127
230261_at	ST8SIA4	1	4.414365181
208846_s_at	VDAC3	1	6.510469372
236514_at	ACOT8	1	3.979317089
217948_at	FAM127B	1	4.504696689
219510_at	POLQ	1	7.082396131
201207_at	TNFAIP1	1	6.80547628
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223113_at	TMEM138	1	8.743197041
213313_at	RABGAP1	1	7.5457368
203511_s_at	TRAPPC3	1	9.332779127
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221158_at	C21orf66	1	7.55285341
227162_at	ZBTB26	1	6.701122158
226263_at	SNRNP48	1	6.619035542
237289_at	CREB1	1	10.27982512
219495_s_at	ZNF180	1	5.769041498
243405_at	0	1	5.791636305
213090_s_at	TAF4	1	6.402686658
228231_at	0	1	7.703836309
203044_at	CHSY1	1	5.734782669
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238917_s_at	DENND5B	1	7.175251396
233341_s_at	POLR1B	1	7.313669031
207686_s_at	CASP8	1	6.642985092
213124_at	ZNF473	1	6.263591074
208842_s_at	GORASP2	1	10.53925839
201585_s_at	SFPQ	1	10.33207262
202950_at	CRYZ	1	4.614309982
203460_s_at	PSEN1	1	5.294292637
201681_s_at	DLG5	1	5.375862873
202567_at	SNRPD3	1	9.231253653
218981_at	ACN9	1	4.482757268
220356_at	CORIN	1	3.94523703
218640_s_at	PLEKHF2	1	5.131351071
210734_x_at	MAX	1	6.686519989
230482_at	ST6GALNAC5	1	4.213954726
227640_s_at	RP9 /// RP9P	1	8.88652795
236381_s_at	WDR8	1	6.687745392
209544_at	RIPK2	1	6.466658515

205573_s_at	SNX7	1	6.468918635
234672_s_at	TMEM48	1	8.226520911
214766_s_at	AHCTF1	1	7.052621401
225043_at	SLC15A4	1	7.357483599
221972_s_at	SDF4	1	6.773908373
203588_s_at	TFDP2	1	5.546729161
217094_s_at	ITCH	1	7.862669979
203302_at	DCK	1	5.498654611
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229946_at	FAM168B	1	8.026150125
202946_s_at	BTBD3	1	3.773055982
210612_s_at	SYNJ2	1	5.064129745
1555240_s_at	GNG12	1	5.438848775
203880_at	COX17	1	7.497488026
217744_s_at	PERP	1	4.329785776
202309_at	MTHFD1	1	6.830605358
200887_s_at	STAT1	1	4.652559771
219217_at	NARS2	1	6.384744418
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239376_at		0	6.311570651
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242214_at	RPS27A /// UBB /// UBC	1	6.909606763
203415_at	PDCD6	1	7.044557165
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218641_at	MGC3032	1	5.02320341
222690_s_at	TMEM39A	1	7.178885458
229359_at		0	7.288829383
221705_s_at	RP5-1000E10.4	1	7.504238341
219231_at	TGS1	1	8.893570798
201795_at	LBR	1	6.243879278
226794_at	STXBP5	1	5.543249377
223055_s_at	XPO5	1	6.388006196
202003_s_at	ACAA2	1	4.356863444
209141_at	UBE2G1	1	8.111628505
225082_at	CPSF3	1	8.408909143
227200_at		0	5.687583441
242909_at		0	3.859961166
223560_s_at	C2orf56	1	8.566453417
218166_s_at	RSF1	1	5.887790266
207842_s_at	CASC3	1	4.717680799
209934_s_at	ATP2C1	1	6.362580054
212421_at	C22orf9	1	7.280387744
202633_at	TOPBP1	1	7.742793964
210405_x_at	TNFRSF10B	1	5.411991134
223215_s_at	C14orf100	1	6.203540183

219316_s_at	FLVCR2	1	4.533186226
228031_at	TTPAL	1	6.639076123
218342_s_at	ERMP1	1	5.794660615
225351_at	FAM45A /// FAM45B	1	6.107764796
221702_s_at	TM2D3	1	7.191319632
230201_at	0	1	7.393470873
213864_s_at	NAP1L1	1	5.80709666
221040_at	CAPN10	1	4.658395409
211152_s_at	HTRA2	1	9.149340182
239834_at	0	1	4.030840183
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208114_s_at	ISG20L2	1	7.792713825
210563_x_at	CFLAR	1	5.675992947
217956_s_at	ENOPH1	1	8.171031148
200827_at	PLOD1	1	6.47741617
200815_s_at	PAFAH1B1	1	7.956408134
1558249_s_at	STX16	1	6.84850181
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218669_at	RAP2C	1	6.141720346
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225073_at	PPHLN1	1	7.268666749
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217821_s_at	WBP11	1	9.329019276
212243_at	GCOM1 /// GRINL1A	1	8.565303669
203579_s_at	SLC7A6	1	6.064944783
36499_at	CELSR2	1	5.555538252
217788_s_at	GALNT2	1	7.113081641
218411_s_at	MBIP	1	5.210295362
219024_at	PLEKHA1	1	5.163696945
225398_at	RPUSD4	1	7.203085121
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1555751_a_at	GEMIN7	1	7.443068154
239843_at	RIT1	1	7.459338827
212582_at	OSBPL8	1	5.075275007
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202897_at	SIRPA	1	4.652070718
236193_at	HIST1H2BC	1	3.580841801
218646_at	C4orf27	1	7.033250841
212385_at	TCF4	1	4.443366349
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217829_s_at	USP39	1	11.17183864

226747_at	TXNDC16	1	4.000254531
208860_s_at	ATRX	1	5.897350703
218314_s_at	C11orf57	1	8.109375644
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242181_at	0	1	4.635531441
228415_at	AP1S2	1	3.937619316
200669_s_at	UBE2D3	1	8.104654153
221060_s_at	TLR4	1	5.274835209
216048_s_at	RHOBTB3	1	3.768069111
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236388_at	0	1	7.780772143
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218836_at	RPP21 /// TRIM39R	1	8.060102591
226565_at	TMEM99	1	4.013300921
1553565_s_at	DDAH1	1	6.582884834
218511_s_at	PNPO	1	6.34016129
202162_s_at	CNOT8	1	8.057049083
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213246_at	C14orf109	1	5.758070187
228620_at	0	1	5.316285082
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226414_s_at	ANAPC11 /// LOC100131844	1	7.945621678
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232287_at	PGBD3	1	8.065766916
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202261_at	VPS72	1	8.133331364
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229905_at	RAP1GDS1	1	5.741607268
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221898_at	PDPN	1	3.607599772
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223480_s_at	MRPL47	1	9.097292719
239824_s_at	TMEM107	1	6.716114966
228087_at	CCDC126	1	5.66891137
203531_at	CUL5	1	6.544233603
218732_at	PTRH2	1	7.414365207
218344_s_at	RCOR3	1	5.774663973
218526_s_at	RANGRF	1	7.401011446
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221668_s_at	DNAI2	2	-6.424283361
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243827_at	0	2	-6.135525165
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215123_at	LOC23117 /// LOC642799 /// LOC729602	2	-4.540045916
1556507_at	0	2	-9.054363784
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227915_at	ASB2	2	-4.611897839
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217251_x_at	IVD	2	-7.250732843
222278_at	0	2	-13.11109853
231463_at	CNTD1	2	-5.722871358
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232174_at	0	2	-3.820578338
241488_at	0	2	-10.76457783
224707_at	C5orf32	2	-3.861467104
243933_at	0	2	-8.641596127
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215863_at	TFR2	2	-8.921034503
217715_x_at	0	2	-8.540041576
221419_s_at	0	2	-8.967821437
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232121_at	TRDMT1	2	-11.50914876
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241223_x_at	0	2	-7.127453601
242578_x_at	SLC22A3	2	-7.68203179
219610_at	RGNEF	2	-7.951867624
222372_at	0	2	-7.691999545
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241486_at	0	2	-8.326700468
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224258_at	ELP1P	2	-8.464874367
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215538_at	LARGE	2	-7.220365879
235811_at	0	2	-9.352023775
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46142_at	LMF1	2	-5.561051718
213158_at	0	2	-4.341363823
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232814_x_at	KLC1	2	-8.117363149
234540_at	GCNT7	2	-6.628040641
233741_at	FTCD	2	-7.09026764
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231245_s_at	0	2	-8.220699437
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232726_at	0	2	-7.12474701
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243618_s_at	ZNF827	2	-5.155559055
227984_at	LOC650392	2	-4.658376335
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237662_at	LOC646522	2	-8.494267829
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224451_x_at	ARHGAP9	2	-4.782585228
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214131_at	CYorf15B		2	-4.013008702

231554_at	TPD52L3		2	-9.696384682
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226895_at	NFIC		2	-5.798470279
231644_at		0	2	-4.586101473
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222310_at	SFRS15		2	-6.289392159
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231015_at	KLF15		2	-8.662076416
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226903_s_at	SLC6A10P /// SLC6A8		2	-11.17113469
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228409_at	KIAA1881	2	-7.776669104
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35974_at	LRMP		2	-4.348613642
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233658_at		0	2	-8.572687496
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242874_at		0	2	-5.039333353
237104_at		0	2	-7.947413822
208072_s_at	DGKD		2	-9.291644629
241161_at		0	2	-8.886611305
1558678_s_at	MALAT1		2	-7.865456982
229483_at		0	2	-5.313937563
213611_at	AQP5		2	-3.639110465
240304_s_at	TMC5		2	-3.55108501
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235525_at		0	2	-10.77154577
235084_x_at		0	2	-9.226267814
1556797_at	LOC386597		2	-9.977404364
1555786_s_at	CUEDC1		2	-5.776249802
244358_at		0	2	-6.677911088
237475_x_at	CCDC152		2	-7.692129667
1558784_at		0	2	-10.89984714
1552383_at	FAM71A		2	-9.630124772
1556340_at	MAPK12		2	-11.35569796
1569001_at	BMP1		2	-10.67557773
240262_at		0	2	-6.965843728
232245_at	SLC25A34		2	-9.12088597
228984_at	ATPGD1		2	-9.12706805
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230682_x_at	ABCC3		2	-10.53662607
232169_x_at	NDUFS8		2	-7.622235591
221601_s_at	FAIM3		2	-4.556255434
213813_x_at		0	2	-8.460007298
225239_at		0	2	-4.013935653
207356_at	DEFB4		2	-4.219347302
236114_at		0	2	-7.735310661
1557658_at		0	2	-6.362516847
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213036_x_at	ATP2A3		2	-4.367474468
233036_at		0	2	-9.063446009
213059_at	CREB3L1		2	-3.961007606
242022_at		0	2	-12.68345614
214372_x_at	ERN2		2	-7.138299036
232500_at	C20orf74		2	-6.852484812

231275_at	LOC100129346	2	-10.88023505
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205295_at	CKMT2	2	-5.446708009
233908_x_at	0	2	-11.78551329
232867_at	0	2	-13.55673786
216025_x_at	CYP2C9	2	-5.620570417
205971_s_at	CTRB1 /// CTRB2	2	-4.27187628
215385_at	0	2	-7.81316771
203029_s_at	PTPRN2	2	-3.766526699
1554516_at	LOC203274	2	-7.616353514
238619_at	0	2	-7.23360731
1553071_a_at	MYOZ3	2	-8.384984165
242068_at	0	2	-5.803240495
204674_at	LRMP	2	-5.87396367
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34210_at	CD52	2	-3.789369874
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231647_s_at	FCRL5	2	-4.040733879
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226304_at	HSPB6	2	-4.584511655
240971_x_at	0	2	-5.946666307
244678_at	0	2	-7.135353453
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206119_at	BHMT	2	-5.869236945
239576_at	MTUS1	2	-9.46623017
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227384_s_at	LOC727820	2	-6.13810601
231093_at	FCRL3	2	-4.355612568
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1564444_at	LOC100130264	2	-7.502239692
218211_s_at	MLPH	2	-3.772220405
243233_at	0	2	-7.184778626
242239_at	0	2	-6.634858178
208109_s_at	C15orf5	2	-6.861491391
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222073_at	COL4A3	2	-4.571106137
206170_at	ADRB2	2	-6.114976829
1566957_at	0	2	-8.601683947
231496_at	FCAMR	2	-5.260563346
204581_at	CD22	2	-9.520229739
228518_at	IGH@ /// IGHG1 /// IGHM	2	-5.676332698
238884_at	0	2	-6.698051758
232528_at	0	2	-6.750477057
231580_at	0	2	-7.326757134
223895_s_at	EPN3	2	-5.927673777
207899_at	GIP	2	-5.181027413
1556510_at	0	2	-7.306817591

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227946_at	OSBPL7	2	-5.57303968
241769_at	0	2	-7.557969692
244197_x_at	0	2	-6.517259976
243768_at	0	2	-3.868835709
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235661_at	0	2	-5.916855395
243981_at	STK4	2	-8.746369815
242071_x_at	ITGA8	2	-6.05381655
230087_at	PRIMA1	2	-8.374604134
244548_at	0	2	-7.406097885
1561044_at	0	2	-10.31991601
206539_s_at	CYP4F12	2	-11.08743113
221928_at	ACACB	2	-5.810845252
244753_at	0	2	-6.167402038
228528_at	0	2	-4.065704712
230615_at	DUOXA2	2	-5.235490264
242110_at	0	2	-5.198919921
204368_at	SLCO2A1	2	-6.176620226
227717_at	FLJ41603	2	-8.71383748
215588_x_at	RIOK3	2	
40016_g_at	LOC100128443 /// MAST4	2	-9.526586422
1552872_at	NCRNA00105	2	-8.466215743
226675_s_at	MALAT1	2	-5.685868206
211996_s_at	LOC100132247 /// LOC23117 /// LOC613037	2	-6.842543924
228806_at	RORC	2	-5.394987231
239533_at	GPR155	2	-4.218902634
205757_at	ENTPD5	2	-8.360487775
1555779_a_at	CD79A	2	-5.738029455
1555653_at	HNRNPA3	2	-10.31393166
1553396_a_at	CCDC13	2	-7.932250079
212187_x_at	PTGDS	2	-3.87616483
229909_at	B4GALNT3	2	-7.452807297
216910_at	XPNPEP2	2	-5.500826945
237654_at	C14orf50	2	-6.657091148
229740_at	LOC643008	2	-9.653012798
1564069_at	0	2	-7.803509814
244875_at	0	2	-9.508106859
214723_x_at	ANKRD36	2	-5.443479621
225491_at	SLC1A2	2	-5.967565615

234756_at	CACNG8	2	-8.223343992
239673_at	0	2	-7.891477358
205883_at	ZBTB16	2	-5.796418832
1559436_x_at	0	2	-8.668829119
220609_at	LOC202181	2	-8.412306681
1561079_at	ANKRD28	2	-7.702733326
243582_at	SH3RF2	2	-4.842575227
214265_at	ITGA8	2	-5.239351405
238543_x_at	MDGA1	2	-11.16712742
225496_s_at	SYTL2	2	-5.443553883
1566848_x_at	0	2	-7.525724347
205392_s_at	CCL14 /// CCL15	2	-5.619137049
205509_at	CPB1	2	-3.807061782
214156_at	MYRIP	2	-4.015157965
236118_at	LOC100128893 /// LOC728473	2	-5.07447387
226856_at	MUSTN1	2	-6.058245869
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1566887_x_at	0	2	-8.639548825
229467_at	PCBP2	2	-10.28905279
241897_at	0	2	-6.994573997
230180_at	0	2	-7.218516415
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230292_at	LOC100131993	2	-11.18759671
1553808_a_at	NKX2-3	2	-6.607773302
205999_x_at	CYP3A4	2	-4.919824659
244357_at	0	2	-9.097874399
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240200_at	SULT1C2	2	-8.938562205
211748_x_at	PTGDS	2	-4.091170884
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206093_x_at	TNXA /// TNXB	2	-7.053652042
206988_at	CCL25	2	-4.748845072
216333_x_at	TNXA /// TNXB	2	-6.832775822
227062_at	NCRNA00084	2	-5.15106547
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238751_at	0	2	-4.032887352
220059_at	STAP1	2	-4.991027743
241640_at	BCAP29	2	-12.86854736
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201785_at	RNASE1	2	-4.4982133
244387_at	0	2	-8.154961666
242055_at	0	2	-8.105531094
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228303_at	GALNT6	2	-5.3913013
228599_at	MS4A1	2	-5.410747678
221122_at	HRASLS2	2	-3.57221615
235666_at	0	2	-4.938348988
220017_x_at	CYP2C9	2	-5.853745827
227198_at	AFF3	2	-4.576853885
210119_at	KCNJ15	2	-4.105064664
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204697_s_at	CHGA		2	-3.912210964
238942_at		0	2	-10.71585516
213674_x_at	IGHD		2	-4.603392795
228854_at		0	2	-4.057752449
231278_at		0	2	-6.36830088
233463_at	RASSF6		2	-6.793262463
205200_at	CLEC3B		2	-5.313154519
205671_s_at	HLA-DOB		2	-6.284524346
49452_at	ACACB		2	-7.259499607
1556336_at	CCBL2 /// LOC100131735 /// RBMX		2	-8.568316237
243149_at		0	2	-7.447876575
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233152_x_at		0	2	-9.502827785
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229369_at	VSIG2		2	-4.963353708
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239832_at		0	2	-7.571968118
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223395_at	ABI3BP		2	-3.740240208
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239597_at		0	2	-7.310348836
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229150_at		0	2	-6.857267602

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234723_x_at	0	2	-8.535451975
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219667_s_at	BANK1	2	-5.167603108
217546_at	MT1M	2	-3.662928204
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1556554_at	TRIM50	2	-8.74630792
222915_s_at	BANK1	2	-8.950551627
231211_s_at	LOC541469	2	-8.690721723
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228232_s_at	VSIG2	2	-4.465054474
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227676_at	FAM3D	2	-5.393343628
229254_at	MFSD4	2	-5.094874422
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214046_at	FUT9	2	-4.413107404
217187_at	MUC5AC	2	-6.947695047
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205267_at	POU2AF1	2	-5.544345328
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213953_at	KRT20	2	-3.951789294
221095_s_at	KCNE2	2	-7.713361642
229177_at	C16orf89	2	-9.657075527
207912_s_at	DAZ1 /// DAZ2 /// DAZ3 /// DAZ4 /// LOC732447	2	-3.564525305
210143_at	ANXA10	2	-4.356808118
226960_at	CXCL17	2	-5.788297467
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214476_at	TFF2	2	-4.941091434
241137_at	DPCR1	2	-5.020704235

229152_at	C4orf7	2	-6.472570435
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243764_at	VSIG1	2	-4.823877725
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231646_at	DPCR1	2	-4.994147958
226147_s_at	PIGR	2	-5.090968363
203240_at	FCGBP /// LOC100133944	2	-6.970618495
228592_at	MS4A1	2	-7.165183582
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238383_at	C6orf58	2	-6.262209532
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206334_at	LIPF	2	-5.604911448
238222_at	GKN2	2	-6.847335127
220191_at	GKN1	2	-6.478140643