Supplemental Table S2 : List of multiple myeloma spike genes

Probe sets	Gene name	Chromosome band	Spike score	spike category	Number of patients with spike expression signal
204379_s_at	FGFR3	4p16.3	10,08031818	1	21
216365_x_at	IGL@	22q11.22	7,24760147	1	11
209875_s_at	SPP1	4q22.1	6,98771197	1	11
223122_s_at	SFRP2	4q31.3	6,96995831	1	5
1553599_a_at	SYCP3	12q23.2	6,52455419	1	5
220179_at	DPEP3	16q22.1	6,37630256	1	4
227361_at	HS3ST3B1	17p12	6,32359243	1	7
234792_x_at	IGHA1	14q32.33	6,28453496	1	9
216853_x_at	IGLV3-19	22q11.22	6,25593837	1	16
207918_s_at	LOC728395	Yp11.2	6,25452053	1	13
240915_at	IGHG1	14q32.33	6,06653281	1	8
207638_at	PRSS7	21q21.1	6,03040808	1	5
201839_s_at	EPCAM	2p21	5,91803055	1	26
201131_s_at	CDH1	16q22.1	5,80995772	1	13
215621_s_at	IGHD	14q32.33	5,80200149	1	10
214254_at	MAGEA4	Xq28	5,75489320	1	3
203854_at	CFI	4q25	5,69062247	1	23
1569469_a_at	LHX8	1p31.1	5,67912332	1	10
221796_at	NTRK2	9q21.33	5,64802711	1	8
205404_at	HSD11B1	1q32.2	5,63642267	1	6
209167_at	GPM6B	Xp22.2	5,54051051	1	3
1556096_s_at	UNC13C	15q21.3	5,52911702	1	4
219702_at	PLAC1	Xq26.3	5,50877087	1	7
224480_s_at	AGPAT9	4q21.23	5,50444052	1	3
1556037_s_at	HHIP	4q31.21	5,43836057	1	8
223906_s_at	TEX101	19q13.31	5,40266367	1	3
221658_s_at	IL21R	16p12.1	5,39983692	1	7
209270_at	LAMB3	1q32.2	5,39802226	1	5
236739_at	LOC150622	2p25.2	5,36948545	1	3
207912_s_at	DAZ1	Yq11.223	5,34953267	1	7
213800_at	CFH	1q31.3	5,34318990	1	7
219837_s_at	CYTL1	4p16.2	5,33944986	1	4
216063_at	HBBP1	11p15.4	5,31317545	1	8
205076_s_at	MTMR11	1q21.2	5,31235401	1	3
210130_s_at	TM7SF2	11q13.1	5,29215882	1	3
214023_x_at	TUBB2B	6p25.2	5,25850898	1	18
229485_x_at	SHISA3	4p13	5,25828357	1	4
222162_s_at	ADAMTS1	21q21.3	5,24661116	1	6
207768_at	EGR4	2p13.1	5,23899197	1	4
223949_at	TMPRSS3	21q22.3	5,22858253	1	21
225275_at	EDIL3	5q14.3	5,21974732	1	13
227006_at	PPP1R14A	19q13.2	5,21801217	1	7
206023_at	NMU	4q12	5,21061647	1	6
210546_x_at	CTAG1A	Xq28	5,20214075	1	18
205363_at	BBOX1	11p14.2	5,17026059	1	23
224650_at	MAL2	8q24.12	5,16653168	1	13
231993_at	ITGBL1	13q33.1	5,15502773	1	3
214651_s_at	HOXA9	7p15.2	5,13656813	1	5
214218_s_at	XIST	Xq13.2	5,13136238	1	32
209656_s_at	TMEM47	Xp21.1	5,12847871	1	19

228737_at	TOX2	20q13.12	5,11694743	1	10
228592_at	MS4A1	11q12.2	5,09989897	1	31
206633_at	CHRNA1	2q31.1	5,09825930	1	3
242128_at	OTX2	14q22.3	5,09622457	1	3
208235_x_at	GAGE12F	Xp11.23	5,05475738	1	13
1553296_at	GPR128	3q12.2	5,04647575	1	4
1552386_at	GAPT	5q11.2	5,04567434	1	6
234764_x_at	IGLV1-44	22q11.22	5,02080902	1	25
206640_x_at	GAGE12C	Xp11.23	4,97433002	1	12
206691_s_at	PDIA2	16p13.3	4,96525390	1	7
203875_at	SMARCA1	Xq25	4,95127198	1	5
206185_at	CRYBB1	22q12.1	4,91969466	1	3
1554485_s_at	TMEM37	2q14.2	4,88556413	1	3
207739_s_at	GAGE1	Xp11.23	4,88010542	1	14
226769_at	FIBIN	11p14.2	4,87401086	1	16
205862_at	GREB1	2p25.1	4,87226007	1	7
1561225_at	LOC338579	10q11.21	4,86915169	1	4
211635_x_at	IGH@	14q32.33	4,84979580	1	15
206172_at	IL13RA2	Xq23	4,81332228	1	5
214768_x_at	FAM20B	1q25.2	4,81256811	1	20
219295_s_at	PCOLCE2	3q23	4,80312182	1	7
215733_x_at	CTAG2	Xq28	4,79633548	1	17
241224_x_at	DSCR8	21q22.13	4,77998653	1	10
207191_s_at	ISLR	15q24.1	4,76429937	1	12
205528_s_at	RUNX1T1	8q21.3	4,76205614	1	3
232068_s_at	TLR4	9q33.1	4,72127742	1	3
211074_at	FOLR1	11q13.4	4,71893066	1	5
207426_s_at	TNFSF4	1q25.1	4,70693966	1	4
214450_at	CTSW	11q13.1	4,68726038	1	22
209120_at	NR2F2	15q26.2	4,68296385	1	3
244080_at	LOC100287039	1q32.3	4,66906201	1	6
232765_x_at	LOC146429	16q24.3	4,66748058	1	13
244740_at	MGC9913	19q13.43	4,66605008	1	9
205433_at	BCHE	3q26.1	4,64398946	1	32
219310_at	TMEM90B	20p11.21	4,63852344	1	4
211642_at	C12orf32	14q32.33	4,63835581	1	6
204679_at	KCNK1	1q42.2	4,63465640	1	3
210016_at	MYT1L	2p25.3	4,62849596	1	3
204424_s_at	LMO3	12p12.3	4,62803508	1	14
204137_at	GPR137B	1q42.3	4,62469244	1	4
228038_at	SOX2	3q26.33	4,62238759	1	3
212328_at	LIMCH1	4p13	4,62029522	1	6
201667_at	GJA1	6q22.31	4,61937573	1	3
204575_s_at	MMP19	12q13.2	4,59758024	1	4
208711_s_at	CCND1	11q13.3	4,59521563	1	33
215025_at	NTRK3	15q25.3	4,59067279	1	6
211634_x_at	IGHM	14q32.33	4,59003911	1	17
229352_at	SPESP1	15q23	4,58930719	1	4
222777_s_at	WHSC1	4p16.3	4,58842528	1	27
209348_s_at	MAF	16q23.2	4,58744412	1	17
209822_s_at	VLDLR	9p24.2	4,58502723	1	12
229782_at	RMST	12q23.1	4,58336912	1	6
206897_at	PAGE1	Xp11.23	4,56950444	1	17
206394_at	MYBPC2	19q13.33	4,56688386	1	16

205826_at	MYOM2	8p23.3	4,55214476	1	9
203423_at	RBP1	3q23	4,54211575	1	7
203130_s_at	KIF5C	2q23.1	4,52165689	1	3
235557_at	GPAT2	2q11.2	4,51500542	1	44
220532_s_at	TMEM176B	7q36.1	4,51317011	1	20
204823_at	NAV3	12q21.2	4,50936657	1	4
204776_at	THBS4	5q14.1	4,50790565	1	6
229975_at	BMPR1B	4q22.3	4,50063073	1	20
227688_at	LRCH2	Xq23	4,49206761	1	3
203438_at	STC2	5q35.1	4,49066407	1	5
227194_at	FAM3B	21q22.3	4,47695758	1	5
227949_at	PHACTR3	20q13.32	4,46744865	1	21
1569323_at	PTPRG	3p14.2	4,46524193	1	3
220068_at	VPREB3	22q11.23	4,46038582	1	24
222939_s_at	SLC16A10	6q21	4,45264662	1	10
238846_at	TNFRSF11A	18q21.33	4,44025111	1	7
205728_at	ODZ1	Xq25	4,43987989	1	4
213094_at	GPR126	6q24.1	4,43977702	1	17
211643_x_at	IGK@	2p11.2	4,43968098	1	24
209728_at	HLA-DRB4	6p21.3	4,43467447	1	14
1554079_at	GALNTL4	11p15.3	4,42725413	1	3
219274_at	TSPAN12	7q31.31	4,42176569	1	20
221667_s_at	HSPB8	12q24.23	4,42016181	1	6
204589_at	NUAK1	12q23.3	4,41954106	1	10
207802_at	CRISP3	6p12.3	4,41712396	1	5
202403_s_at	COL1A2	7q21.3	4,41278889	1	26
215777_at	IGLV4-60	22q11.22	4,41123670	1	8
219578_s_at	CPEB1	15q25.2	4,40933479	1	3
222116_s_at	TBC1D16	17q25.3	4,40471700	1	8
209550_at	NDN	15q11.2	4,39795063	1	15
51158_at	FAM174B	15q26.1	4,39299418	1	18
204780_s_at	FAS	10q23.31	4,38469698	1	11
209307_at	SWAP70	11p15.4	4,37516871	1	5
214844_s_at	DOK5	20q13.2	4,37032374	1	14
209209_s_at	FERMT2	14q22.1	4,37015910	1	3
205943_at	TDO2	4q32.1	4,35628666	1	15
204030_s_at	SCHIP1	3q25.32	4,35523497	1	4
203559_s_at	ABP1	7q36.1	4,34802458	1	13
202668_at	EFNB2	13q33.3	4,34624869	1	3
210258_at	RGS13	1q31.2	4,32880781	1	30
205898_at	CX3CR1	3p22.2	4,29690202	1	26
200762_at	DPYSL2	8p21.2	4,29518524	1	22
224022_x_at	WNT16	7q31.31	4,28020808	1	4
232010_at	FSTL5	4q32.2	4,26715392	1	24
221035_s_at	TEX14	17q22	4,25890841	1	9
238878_at	ARX	Xp21.3	4,25840346	1	23
1560225_at	CNR1	6q15	4,25700575	1	26
1552754_a_at	CADM2	3p11.1	4,25697366	1	7
209392_at	ENPP2	8q24.12	4,25436425	1	15
206204_at	GRB14	2q24.3	4,25383488	1	7
231186_at	FLJ43390	14q23.2	4,24316659	1	4
212190_at	SERPINE2	2q36.1	4,23933652	1	36
203962_s_at	NEBL	10p12.31	4,22379040	1	16
223930_at	TOR1AIP1	1q25.2	4,21518438	1	7

205888_s_at	JAKMIP2	5q32	4,21236257	1	3
219892_at	TM6SF1	15q25.2	4,20889093	1	7
212646_at	RFTN1	Yp11.2	4,19163722	1	18
1557132_at	WDR17	4q34.2	4,19158175	1	4
202833_s_at	SERPINA1	14q32.13	4,18458633	1	6
223170_at	TMEM98	17q11.2	4,17789363	1	3
214636_at	CALCB	11p15.2	4,17723922	1	23
215035_at	IGLV6-57	22q11.2	4,17518923	1	21
201324_at	EMP1	12p13.1	4,17452829	1	14
203889_at	SCG5	15q13.3	4,16935180	1	6
220431_at	TMPRSS11E	4q13.2	4,16809850	1	15
230288_at	FGF14	13q33.1	4,16408694	1	16
1556839_s_at	SPTBN5	15q15.1	4,15653488	1	10
44790_s_at	C13orf18	13q14.13	4,15220617	1	7
210146_x_at	LILRB2	19q13.42	4,15030504	1	5
207663_x_at	GAGE3	Xp11.23	4,14696932	1	11
216027_at	TMX4	20p12.3	4,14323792	1	5
214603_at	MAGEA2	Xq28	4,14192856	1	7
221097_s_at	KCNMB2	3q26.32	4,13852575	1	20
214761_at	ZNF423	16q12.1	4,13768676	1	8
202295_s_at	CTSH	15q25.1	4,13495220	1	27
203820_s_at	IGF2BP3	7p15.3	4,13137309	1	4
241791_at	TTN	2q31.2	4,13050546	1	4
220051_at	PRSS21	16p13.3	4,12469392	1	12
205769_at	SLC27A2	15q21.2	4,11965673	1	5
217771_at	GOLM1	9q21.33	4,11957968	1	20
214971_s_at	ST6GAL1	3q27.3	4,11667743	1	4
207314_x_at	KIR3DL2	19q13.42	4,10916033	1	3
232054_at	PCDH20	13q21.2	4,10745524	1	3
242064_at	SDK2	17q25.1	4,10466755	1	4
208178_x_at	TRIO	5p15.2	4,10196830	1	3
211357_s_at	ALDOB	9q31.1	4,10014361	1	3
235458_at	HAVCR2	5q33.3	4,08838267	1	5
230195_at	LOC100131138	12q24.11	4,08790829	1	5
227812_at	TNFRSF19	13q12.12	4,07019411	1	10
205291_at	IL2RB	22q12.3	4,06664523	1	3
217320_at	LOC100293211	14q32.33	4,06315200	1	5
214228_x_at	TNFRSF4	1p36.33	4,05806557	1	3
207850_at	CXCL3	4q13.3	4,05117499	1	6
225911_at	NPNT	4q24	4,04599376	1	5
1553197_at	DCAF4L2	8q21.3	4,04547873	1	3
206595_at	CST6	11q13.1	4,03804757	1	21
214957_at	ACTL8	1p36.13	4,03309448	1	6
244407_at	CYP39A1	6p12.3	4,03215466	1	6
203908_at	SLC4A4	4q13.3	4,02727518	1	3
231265_at	COX7B2	4p12	4,02585338	1	9
243621_at	SPACA3	17q11.2	4,02360807	1	12
209847_at	CDH17	8q22.1	4,01883122	1	8
228915_at	DACH1	13q21.33	4,01869239	1	4
211560_s_at	ALAS2	Xp11.21	4,01776004	1	10
229778_at	C12orf39	12p12.1	4,01727561	1	3
211548_s_at	HPGD	4q34.1	4,01227979	1	3
211881_x_at	IGLJ3	22q11.1	4,00618914	1	8
219480_at	SNAI1	20q13.13	3,99672817	1	3

218086_at	NPDC1	9q34.3	3,98769613	1	7
201631_s_at	IER3	6p21.33	3,98509363	1	16
242301_at	CBLN2	18q22.3	3,97735464	1	4
203973_s_at	CEBPD	8q11.21	3,97622625	1	11
221698_s_at	CLEC7A	12p13.2	3,97620275	1	16
218623_at	HMP19	5q35.2	3,97166837	1	9
201162_at	IGFBP7	4q12	3,96861885	1	5
236040_at	XAGE3	Xp11.22	3,96810067	1	4
210321_at	GZMH	14q12	3,95851633	1	8
218974_at	SOBP	6q21	3,95139012	1	4
211796_s_at	TRBC1	7q34	3,94868665	1	5
231735_s_at	MALAT1	11q13.1	3,94813615	1	10
220313_at	GPR88	1p21.2	3,94737620	1	3
224583_at	COTL1	16q24.1	3,94350011	1	16
227174_at	WDR72	15q21.3	3,94284416	1	4
37145_at	GNLY	2p11.2	3,94265809	1	6
232985_s_at	DPPA4	3q13.13	3,94226464	1	4
209368_at	EPHX2	8p21.2	3,93817722	1	14
230496_at	FAM123A	13q12.13	3,93448291	1	4
209699_x_at	AKR1C2	10p15.1	3,93435120	1	5
209795_at	CD69	12p13.31	3,93277904	1	20
204114_at	NID2	14q22.1	3,92676709	1	18
203510_at	MET	7q31.2	3,92266899	1	4
231771_at	GJB6	13q12.11	3,92060142	1	3
206498_at	OCA2	15q13.1	3,90509599	1	4
206404_at	FGF9	13q12.11	3,90465349	1	4
241535_at	LOC100292909	2p25.3	3,90139745	1	12
223169_s_at	RHOU	1q42.13	3,89544375	1	3
1569290_s_at	GRIA3	Xq25	3,88965655	1	3
207264_at	KDELR3	22q13.1	3,88803303	1	3
209289_at	NFIB	9p22.3	3,88477833	1	18
220351_at	CCRL1	3q22.1	3,88234709	1	4
229870_at	LOC644656	11p15.4	3,88076836	1	10
231303_at	NCRNA00158	21q21.3	3,87710343	1	3
219772_s_at	SMPX	Xp22.12	3,87484241	1	4
1555745_a_at	LYZ	12q15	3,85954260	1	10
220231_at	C7orf16	7p14.3	3,85850106	1	11
223629_at	PCDHB5	5q31.3	3,85601420	1	5
237322_at	MIAT	22q12.1	3,84641299	1	13
209173_at	AGR2	7p21.1	3,83782440	1	18
206012_at	LEFTY2	1q42.12	3,83299869	1	10
227265_at	FGL2	7q11.23	3,83196601	1	9
213418_at	HSPA6	1q23.3	3,83134755	1	12
206310_at	SPINK2	4q12	3,82811546	1	9
221538_s_at	PLXNA1	3q21.3	3,82447685	1	4
207714_s_at	SERPINH1	11q13.5	3,82217407	1	4
208894_at	HLA-DRA	6p21.3	3,82131854	1	12
204803_s_at	RRAD	16q22.1	3,82109269	1	6
225242_s_at	CCDC80	3q13.2	3,82087389	1	4
218332_at	BEX1	Xq22.1	3,81956985	1	9
203394_s_at	HES1	3q29	3,81927158	1	15
201215_at	PLS3	Xq23	3,81420445	1	15
230081_at	PLCXD3	5p13.1	3,81397389	1	3
210587_at	INHBE	12q13.3	3,81341091	1	19

204971_at	CSTA	3q21.1	3,81315829	1	13
223836_at	FGFBP2	4p15.32	3,80313884	1	5
208524_at	GPR15	3q11.2	3,80205140	1	3
216594_x_at	AKR1C1	10p15.1	3,80186282	1	4
229900_at	CD109	6q13	3,80056532	1	7
230722_at	BNC2	9p22.2	3,79975593	1	7
204159_at	CDKN2C	1p32.3	3,79786214	1	11
209829_at	FAM65B	6p22.3	3,79721384	1	16
213992_at	COL4A6	Xq22.3	3,79501985	1	22
222068_s_at	LRRC50	16q23.3	3,79275015	1	7
230158_at	DPY19L2	7q22.1	3,79259616	1	3
226841_at	MPEG1	11q12.1	3,79234010	1	21
219213_at	JAM2	21q21.3	3,79177793	1	10
217165_x_at	MT1F	16q12.2	3,79124610	1	6
205844_at	VNN1	6q23.2	3,78995038	1	14
214079_at	DHRS2	14q11.2	3,78739574	1	8
228708_at	RAB27B	18q21.2	3,77723725	1	4
239657_x_at	FOXO6	1p34.2	3,77268189	1	7
227342_s_at	MYEOV	11q13.3	3,77130152	1	9
205173_x_at	CD58	1p13.1	3,77129579	1	6
226582_at	LOC400043	12q13.13	3,77048383	1	6
223640_at	HCST	19q13.12	3,77029232	1	7
203946_s_at	ARG2	14q24.1	3,76758186	1	3
206760_s_at	FCER2	19p13.2	3,76716208	1	8
209474_s_at	ENTPD1	10q24.1	3,76496457	1	10
40665_at	FMO3	1q24.3	3,76317289	1	4
214053_at	ERBB4	2q34	3,76191163	1	10
206218_at	MAGEB2	Xp21.2	3,75926763	1	10
205739_x_at	ZNF107	7q11.21	3,75619415	1	4
219000_s_at	DSCC1	8q24.12	3,75585649	1	3
203892_at	WFDC2	20q13.12	3,75452830	1	7
227947_at	PHACTR2	6q24.2	3,75188700	1	13
224762_at	SERINC2	1p35.2	3,74884926	1	4
212077_at	CALD1	7q33	3,74588791	1	3
201596_x_at	KRT18	12q13.13	3,74455098	1	12
229309_at	ADRB1	10q25.3	3,74244355	1	3
204439_at	IFI44L	1p31.1	3,74233808	1	19
209309_at	AZGP1	7q22.1	3,74118181	1	33
213831_at	HLA-DQA1	6p21.3	3,73981556	1	15
213056_at	FRMD4B	3p14.1	3,73684473	1	5
226303_at	PGM5	9q21.11	3,73539715	1	5
225822_at	TMEM125	1p34.2	3,73255928	1	6
204237_at	GULP1	2q32.1	3,73034563	1	22
214612_x_at	MAGEA6	Xq28	3,72968419	1	25
201445_at	CNN3	1p21.3	3,72959615	1	6
207706_at	USH2A	1q41	3,72949169	1	5
201012_at	ANXA1	9q21.13	3,72900933	1	15
218589_at	LPAR6	13q14.2	3,72671317	1	29
220234_at	CA8	8q12.1	3,72463096	1	6
1558216_at	LOC84740	4p16.1	3,72015305	1	4
209160_at	AKR1C3	10p15.1	3,71992753	1	12
244565_at	HMX2	10q26.13	3,71757555	1	3
217148_x_at	LOC100293440	22q11.22	3,71594652	1	18
205237_at	FCN1	9q34.3	3,71486190	1	14

1569003_at	TMEM49	17q23.1	3,71392258	1	16
205066_s_at	ENPP1	6q23.2	3,70967386	1	5
239726_at	ANK3	10q21.2	3,70928826	1	4
1565162_s_at	MGST1	12p12.3	3,70856946	1	5
1554676_at	SRGN	10q22.1	3,70810197	1	8
212778_at	PACS2	14q32.33	3,70802630	1	4
213050_at	COBL	7p12.1	3,70789053	1	8
211835_at	IGKC	2p11.2	3,70621472	1	4
220115_s_at	CDH10	5p14.1	3,70588620	1	4
237956_s_at	LOC133874	5q35.1	3,70554070	1	3
204688_at	SGCE	7q21.3	3,70448075	1	34
219812_at	PVRIG	7q22.1	3,70440463	1	10
203705_s_at	FZD7	2q33.1	3,70280050	1	10
228997_at	TRNAU1AP	1p35.3	3,70276824	1	4
205081_at	CRIP1	14q32.33	3,70268834	1	19
203508_at	TNFRSF1B	1p36.22	3,70230364	1	7
209993_at	ABCB1	7q21.12	3,70047798	1	4
214146_s_at	PPBP	4q13.3	3,69782925	1	14
231093_at	FCRL3	1q23.1	3,69714272	1	13
1568796_at	CCDC157	22q12.2	3,69393700	1	4
242712_x_at	RANBP2	2q12.3	3,69112480	1	10
219263_at	RNF128	Xq22.3	3,69034659	1	4
209242_at	PEG3	19q13.43	3,68905976	1	9
227266_s_at	FYB	5p13.1	3,68802959	1	3
210164_at	GZMB	14q12	3,68769455	1	14
223557_s_at	TMEFF2	2q32.3	3,68693029	1	6
214617_at	PRF1	10q22.1	3,67622561	1	10
214395_x_at	EEF1D	8q24.3	3,67615225	1	5
228260_at	ELAVL2	9p21.3	3,67302297	1	3
226084_at	MAP1B	5q13.2	3,67131161	1	19
1405_i_at	CCL5	17q12	3,67127855	1	10
203304_at	BAMBI	10p12.1	3,66706318	1	13
214369_s_at	RASGRP2	11q13.1	3,66634146	1	3
207325_x_at	MAGEA1	Xq28	3,66320754	1	13
204416_x_at	APOC1	19q13.32	3,66224053	1	15
231954_at	DKFZP434I0714	4q31.3	3,65803650	1	10
243194_at	ZNF551	19q13.43	3,65704135	1	7
218345_at	TMEM176A	7q36.1	3,65640849	1	18
200800_s_at	HSPA1A	6p21.33	3,65172691	1	23
1556820_a_at	DLEU2	13q14.2	3,64835392	1	3
227646_at	EBF1	5q33.3	3,64657884	1	4
227059_at	GPC6	13q31.3	3,64360575	1	20
204798_at	MYB	6q23.3	3,64359794	1	11
217143_s_at	TRA@	14q11.2	3,64234101	1	3
214464_at	CDC42BPA	1q42.13	3,64192273	1	6
213974_at	ADAMTSL3	15q25.2	3,64182867	1	7
220146_at	TLR7	Xp22.2	3,64170502	1	21
210140_at	CST7	20p11.21	3,64099257	1	6
203435_s_at	MME	3q25.2	3,64036708	1	3
205021_s_at	FOXN3	14q32.11	3,63798672	1	7
204900_x_at	SAP30	4q34.1	3,63488912	1	3
202018_s_at	LTF	3p21.31	3,63320567	1	15
207113_s_at	TNF	6p21.33	3,63237292	1	7
202458_at	PRSS23	11q14.2	3,62986733	1	7

229560_at	TLR8	Xp22.2	3,62974360	1	9
219508_at	GCNT3	15q22.2	3,62636490	1	4
225895_at	SYNPO2	4q26	3,62458026	1	3
208438_s_at	FGR	1p36.11	3,62095736	1	15
220423_at	PLA2G2D	1p36.12	3,61891392	1	7
213832_at	KCND3	1p13.2	3,61335867	1	3
202523_s_at	SPOCK2	10q22.1	3,60842220	1	6
223395_at	ABI3BP	3q12.2	3,60794110	1	16
203603_s_at	ZEB2	2q22.3	3,60785269	1	3
226625_at	TGFBR3	1p22.1	3,60642898	1	8
218687_s_at	MUC13	3q21.2	3,60413445	1	5
212070_at	GPR56	16q21	3,60315648	1	9
211071_s_at	MLLT11	1q21.3	3,60240379	1	10
228523_at	NANOS1	10q26.11	3,59926931	1	23
223204_at	C4orf18	4q32.1	3,59474970	1	6
206355_at	GNAL	18p11.21	3,59266167	1	13
218888_s_at	NETO2	16q12.1	3,59211621	1	3
214059_at	IFI44	1p31.1	3,59108085	1	12
205612_at	MMRN1	4q22.1	3,59080001	1	8
227984_at	LOC650392	16p13.3	3,58707973	1	5
204560_at	FKBP5	6p21.31	3,58392312	1	8
233500_x_at	CLEC2D	12p13.31	3,58368146	1	6
204103_at	CCL4	17q12	3,58225704	1	19
231930_at	ELMOD1	11q22.3	3,57779309	1	24
232388_at	CNTNAP4	16q23.1	3,57414443	1	4
212686_at	PPM1H	12q14.2	3,57372090	1	4
206843_at	CRYBA4	22q12.1	3,57263912	1	4
211913_s_at	MERTK	2q13	3,57136968	1	11
238488_at	IPO11	5q12.1	3,56987840	1	3
214068_at	BEAN	16q21	3,56935277	1	7
203821_at	HBEGF	5q31.3	3,56534255	1	3
206039_at	RAB33A	Xq26.1	3,56497076	1	15
238546_at	SLC8A1	2p22.1	3,56197085	1	11
219271_at	GALNT14	2p23.1	3,55847458	1	10
227449_at	EPHA4	2q36.1	3,55638672	1	8
228152_s_at	DDX60L	4q32.3	3,55445548	1	4
225105_at	C12orf75	12q23.3	3,55289905	1	14
213325_at	PVRL3	3q13.13	3,55164547	1	6
211709_s_at	CLEC11A	19q13.33	3,54994597	1	13
242135_at	LOC100289097	9q13	3,54786908	1	4
212148_at	PBX1	1q23.3	3,54684506	1	4
214777_at	IGKV4-1	2p11.2	3,54469668	1	21
227336_at	DTX1	12q24.13	3,54225284	1	6
204121_at	GADD45G	9q22.2	3,53983750	1	5
241763_s_at	FBXO32	8q24.13	3,53812280	1	9
213256_at	MARCH3	5q23.2	3,53090146	1	4
1553530_a_at	ITGB1	10p11.22	3,52959167	1	5
203313_s_at	TGIF1	18p11.31	3,52815217	1	23
206541_at	KLKB1	4q35.2	3,52767166	1	3
215346_at	CD40	20q13.12	3,52696063	1	4
235871_at	LIPH	3q27.2	3,52669059	1	4
209781_s_at	KHDRBS3	8q24.23	3,52650252	1	10
203949_at	MPO	17q22	3,52572289	1	19
205419_at	GPR183	13q32.3	3,52128610	1	5

1568957_x_at	SRGAP2P1	1q32.1	3,51873240	1	4
206715_at	TFEC	7q31.2	3,51726772	1	9
218454_at	PLBD1	12p13.1	3,51595376	1	12
224209_s_at	GDA	9q21.13	3,51571902	1	6
227803_at	ENPP5	6p21.1	3,51182414	1	4
228636_at	BHLHE22	8q12.3	3,50221178	1	3
206163_at	MAB21L1	13q13.3	3,50163495	1	11
235753_at	HOXA7	7p15.2	3,49915157	1	18
205269_at	LCP2	5q35.1	3,49427780	1	10
209803_s_at	PHLDA2	11p15.4	3,49361221	1	21
220266_s_at	KLF4	9q31.2	3,49199364	1	17
244023_at	SYK	9q22.2	3,49143175	1	13
217520_x_at	LOC100293306	15q13.1	3,48397593	1	4
218788_s_at	SMYD3	1q44	3,48267513	1	12
209901_x_at	AIF1	6p21.33	3,47862106	1	12
204105_s_at	NRCAM	7q31.1	3,47714095	1	8
1554600_s_at	LMNA	1q22	3,47706851	1	9
206390_x_at	PF4	4q13.3	3,47554767	1	12
1559618_at	LOC100129447	12q24.13	3,47436447	1	3
223832_s_at	CAPNS2	16q12.2	3,47399363	1	5
221088_s_at	PPP1R9A	7q21.3	3,47342272	1	3
229800_at	DCLK1	13q13.3	3,47089089	1	19
212762_s_at	TCF7L2	10q25.2	3,46961888	1	8
228060_at	SLC35F1	6q22.1	3,46394207	1	10
1555349_a_at	ITGB2	21q22.3	3,46305422	1	10
1553043_a_at	CD300LF	17q25.1	3,46304176	1	5
205033_s_at	DEFA1	8p23.1	3,46274396	1	30
223196_s_at	SESN2	1p35.3	3,46271220	1	9
210394_x_at	SSX4	Xp11.23	3,46089798	1	10
218995_s_at	EDN1	6p24.1	3,46038649	1	10
226436_at	RASSF4	10q11.21	3,45701818	1	9
205393_s_at	CHEK1	11q24.2	3,45606387	1	3
209785_s_at	PLA2G4C	19q13.33	3,45573126	1	10
224839_s_at	GPT2	16q11.2	3,45395505	1	3
217867_x_at	BACE2	21q22.2	3,45147563	1	20
221584_s_at	KCNMA1	10q22.3	3,44701461	1	20
227434_at	WBSCR17	7q11.22	3,44692114	1	4
209870_s_at	APBA2	15q13.1	3,44671733	1	7
209774_x_at	CXCL2	4q13.3	3,44588910	1	9
213197_at	ASTN1	1q25.2	3,44554057	1	4
235644_at	CCDC138	2q12.3	3,44531907	1	3
207392_x_at	UGT2B15	4q13.2	3,44059759	1	3
230364_at	CHPT1	12q23.2	3,43970614	1	3
201497_x_at	MYH11	16p13.11	3,43796441	1	7
209942_x_at	MAGEA3	Xq28	3,43662274	1	22
41660_at	CELSR1	22q13.31	3,43605354	1	5
219926_at	POPDC3	6q21	3,43327701	1	19
236088_at	NTNG1	1p13.3	3,43314537	1	6
210660_at	LILRA1	19q13.42	3,43304074	1	6
33323_r_at	SFN	1p36.11	3,43201005	1	8
235802_at	PLD4	14q32.33	3,42766977	1	16
212730_at	SYNM	15q26.3	3,42724923	1	5
238762_at	MTHFD2L	4q13.3	3,42223604	1	8
204747_at	IFIT3	10q23.31	3,42111945	1	8

209008_x_at	KRT8	12q13.13	3,41984122	1	4
221832_s_at	LUZP1	1p36.12	3,41963720	1	5
223903_at	TLR9	3p21.2	3,41956144	1	3
207445_s_at	CCR9	3p21.31	3,41560415	1	3
203225_s_at	RFK	9q21.13	3,41547821	1	5
204072_s_at	FRY	13q13.1	3,41282877	1	3
206398_s_at	CD19	16p11.2	3,41010955	1	23
221491_x_at	HLA-DRB1	6p21.32	3,40998501	1	4
213906_at	MYBL1	8q13.1	3,40912667	1	17
203954_x_at	CLDN3	7q11.23	3,40854042	1	5
214169_at	C7orf20	7p22.3	3,40853747	1	3
1558437_at	IGHE	14q32.33	3,40841671	1	8
1559502_s_at	LRRC25	19p13.11	3,40578267	1	14
218678_at	NES	1q23.1	3,40544480	1	24
242778_at	LPXN	11q12.1	3,40495079	1	4
234994_at	TMEM200A	6q23.1	3,40387124	1	5
211743_s_at	PRG2	11q12.1	3,40377325	1	20
205185_at	SPINK5	5q32	3,40268537	1	5
203562_at	FEZ1	11q24.2	3,40176729	1	3
221467_at	MC4R	18q21.32	3,40048513	1	16
225842_at	PHLDA1	12q21.2	3,39759342	1	16
204351_at	S100P	4p16.1	3,39656480	1	4
207874_s_at	CFHR4	1q31.3	3,39620134	1	6
209568_s_at	RGL1	1q25.3	3,39481292	1	14
201700_at	CCND3	6p21.1	3,39404305	1	6
218608_at	ATP13A2	1p36.13	3,39374392	1	3
242234_at	XAF1	17p13.1	3,39313839	1	3
206881_s_at	LILRA3	19q13.42	3,39296275	1	3
242931_at	LONRF3	Xq24	3,39171439	1	4
203936_s_at	MMP9	20q13.12	3,39093381	1	12
231046_at	LOC100289641	5q21.3	3,39055239	1	7
229313_at	ANO5	11p14.3	3,39051812	1	3
225478_at	MFHAS1	8p23.1	3,39020474	1	4
211658_at	PRDX2	19p13.2	3,38785425	1	3
205573_s_at	SNX7	1p21.3	3,38532243	1	8
227405_s_at	FZD8	10p11.21	3,38516108	1	6
212062_at	ATP9A	20q13.2	3,38511017	1	8
214370_at	S100A8	1q21.3	3,38506328	1	3
213385_at	CHN2	7p14.3	3,38229776	1	12
213915_at	NKG7	19q13.41	3,37981007	2	6
206632_s_at	APOBEC3B	22q13.1	3,37909695	2	4
219737_s_at	PCDH9	13q21.32	3,37893180	2	19
205863_at	S100A12	1q21.3	3,37848936	2	9
1552727_s_at	ADAMTS17	15q26.3	3,37655312	2	3
215633_x_at	LST1	6p21.3	3,37595143	2	4
212372_at	MYH10	17p13.1	3,37538635	2	4
206871_at	ELANE	19p13.3	3,37142639	2	8
213010_at	PRKCDBP	11p15.4	3,36756666	2	3
235490_at	TMEM107	17p13.1	3,36630547	2	3
232327_at	THSD7B	2q22.1	3,36566263	2	6
202687_s_at	TNFSF10	3q26.31	3,36372702	2	7
210152_at	LILRB4	19q13.42	3,36214419	2	10
209790_s_at	CASP6	4q25	3,36056522	2	5
231252_at	C2orf67	2q34	3,35951249	2	3

241716_at	HSPD1	5p14.3	3,35943495	2	6
217478_s_at	HLA-DMA	6p21.32	3,35932798	2	6
235568_at	C19orf59	19p13.2	3,35930461	2	9
221748_s_at	TNS1	2q35	3,35698076	2	4
205542_at	STEAP1	7q21.13	3,35554076	2	9
1554057_at	LOC645676	1q22	3,35482980	2	13
206115_at	EGR3	8p21.3	3,35417729	2	10
203535_at	S100A9	1q21.3	3,35399266	2	11
211276_at	TCEAL2	Xq22.1	3,35198698	2	14
216840_s_at	LAMA2	6q22.33	3,34637231	2	17
218839_at	HEY1	8q21.13	3,34465621	2	15
221958_s_at	GPR177	1p31.3	3,34391070	2	23
219440_at	RAI2	Xp22.13	3,34386588	2	4
227742_at	CLIC6	21q22.12	3,34366205	2	7
213693_s_at	MUC1	1q22	3,34362779	2	15
219414_at	CLSTN2	3q23	3,34347673	2	5
213797_at	RSAD2	2p25.2	3,34281891	2	13
220920_at	ATP10B	5q34	3,34079928	2	28
206525_at	GABRR1	6q15	3,34016788	2	7
218952_at	PCSK1N	Xp11.23	3,33942228	2	5
209924_at	CCL18	17q12	3,33931613	2	7
236033_at	ASB12	Xq11.2	3,33765796	2	3
212013_at	PXDN	2p25.3	3,33546359	2	20
1553994_at	NT5E	6q14.3	3,33491796	2	14
1553728_at	LRRC43	12q24.31	3,33311429	2	17
210467_x_at	MAGEA12	Xq28	3,33307399	2	13
214596_at	CHRM3	1q43	3,33277882	2	3
204419_x_at	HBG1	11p15.4	3,33046536	2	16
206683_at	ZNF165	6p22.1	3,33011380	2	12
1555355_a_at	ETS1	11q24.3	3,32982893	2	8
202411_at	IFI27	14q32.12	3,32822549	2	16
220062_s_at	MAGEC2	Xq27.2	3,32556340	2	12
205386_s_at	MDM2	12q15	3,32384014	2	4
203104_at	CSF1R	5q32	3,32364765	2	8
1563209_a_at	MACROD2	20p12.1	3,32263298	2	13
200606_at	DSP	6p24.3	3,32118985	2	6
204440_at	CD83	6p23	3,32110749	2	9
244780_at	SGPP2	2q36.1	3,32076250	2	5
227649_s_at	SRGAP2	1q32.1	3,32010504	2	5
218400_at	OAS3	12q24.13	3,31874910	2	4
231203_at	LOC100129633	9q32	3,31708517	2	4
201719_s_at	EPB41L2	6q23.2	3,31683239	2	5
211379_x_at	B3GALNT1	3q26.1	3,31566412	2	9
214041_x_at	RPL37A	2q35	3,31352514	2	16
215049_x_at	CD163	12p13.31	3,31083897	2	18
209101_at	CTGF	6q23.2	3,31019556	2	20
218638_s_at	SPON2	4p16.3	3,30952512	2	7
226136_at	GLIPR1	12q21.2	3,30806408	2	7
207269_at	DEFA4	8p23.1	3,30773862	2	22
212793_at	DAAM2	6p21.2	3,30718658	2	6
204256_at	ELOVL6	4q25	3,30652544	2	5
202014_at	PPP1R15A	19q13.33	3,30642945	2	4
225589_at	SH3RF1	4q33	3,30331285	2	10
205286_at	TFAP2C	20q13.31	3,30294313	2	14

229437_at	MIR155HG	21q21.3	3,30273754	2	9
206907_at	TNFSF9	19p13.3	3,30203638	2	4
209470_s_at	GPM6A	4q34.2	3,30112041	2	15
232045_at	PHACTR1	6p24.1	3,30083395	2	5
220161_s_at	EPB41L4B	9q31.3	3,30068233	2	4
210873_x_at	APOBEC3A	22q13.1	3,29915302	2	7
230143_at	RNF165	18q21.1	3,29876166	2	3
1552749_a_at	KLC3	19q13.32	3,29807837	2	5
230896_at	BEND4	4p13	3,29594556	2	3
206953_s_at	LPHN2	1p31.1	3,29230150	2	20
207238_s_at	PTPRC	1q31.3	3,28955766	2	16
230690_at	TUBB1	20q13.32	3,28918388	2	7
212573_at	ENDOD1	11q21	3,28769352	2	6
213059_at	CREB3L1	11p11.2	3,28705983	2	5
217646_at	SURF1	9q34.2	3,28621239	2	4
213249_at	FBXL7	5p15.1	3,28597828	2	11
203373_at	SOCS2	12q22	3,28575340	2	3
1552531_a_at	NLRP11	19q13.43	3,28549046	2	8
214945_at	FAM153A	5q35.3	3,28505171	2	3
1554201_at	CABP4	11q13.2	3,28371334	2	6
207666_x_at	SSX3	Xp11.23	3,28292314	2	8
239203_at	C7orf53	7q31.1	3,28245629	2	9
206858_s_at	HOXC6	12q13.13	3,28185550	2	3
207395_at	BTN1A1	6p22.2	3,28184540	2	8
216379_x_at	CD24	Yq11.222	3,27902709	2	4
205003_at	DOCK4	7q31.1	3,27884130	2	5
207104_x_at	LILRB1	19q13.42	3,27801587	2	8
202638_s_at	ICAM1	19p13.2	3,27788233	2	12
204959_at	MNDA	1q23.1	3,27679448	2	20
202898_at	SDC3	1p35.2	3,27625862	2	4
200952_s_at	CCND2	12p13.32	3,27565175	2	3
213524_s_at	G0S2	1q32.2	3,27361454	2	12
204466_s_at	SNCA	4q22.1	3,27336586	2	7
200664_s_at	DNAJB1	19p13.12	3,27182831	2	16
202095_s_at	BIRC5	17q25.3	3,27119756	2	4
213967_at	RALYL	8q21.2	3,27091398	2	24
207610_s_at	EMR2	19p13.12	3,27014917	2	4
225450_at	AMOTL1	11q21	3,27009388	2	11
201037_at	PFKP	10p15.2	3,26974151	2	9
220088_at	C5AR1	19q13.32	3,26938181	2	10
1556168_s_at	HEATR7B1	2q37.1	3,26925066	2	5
226587_at	SNRPN	15q11.2	3,26896421	2	5
206626_x_at	SSX1	Xp11.23	3,26844744	2	17
225702_at	C8orf76	8q24.13	3,26819924	2	3
227889_at	LPCAT2	16q12.2	3,26635178	2	9
235829_at	LOC100128405	6q26	3,26504484	2	4
203153_at	IFIT1	10q23.31	3,26422937	2	12
243968_x_at	FCRL1	1q23.1	3,26418019	2	4
232122_s_at	VEPH1	3q25.32	3,26381045	2	5
217384_x_at	IGHV3-23	14q32.33	3,26351140	2	14
207075_at	NLRP3	1q44	3,26305977	2	3
219211_at	USP18	22q11.21	3,26256504	2	3
200648_s_at	GLUL	1q25.3	3,25556871	2	5
1552388_at	FLJ30901	22q13.31	3,25542166	2	4

219607_s_at	MS4A4A	11q12.1	3,25503977	2	18
203146_s_at	GABBR1	6p22.1	3,25454262	2	3
1553297_a_at	CSF3R	1p34.3	3,25418354	2	3
1558688_at	LOC441461	9q31.1	3,25382323	2	7
205220_at	NIACR2	12q24.31	3,25198995	2	5
59697_at	RAB15	14q23.3	3,25162729	2	15
218502_s_at	TRPS1	8q23.3	3,25066828	2	3
219102_at	RCN3	19q13.33	3,24877516	2	5
206380_s_at	CFP	Xp11.23	3,24461031	2	7
210254_at	MS4A3	11q12.1	3,24456776	2	12
227424_x_at	C21orf119	21q22.11	3,24425919	2	4
221539_at	EIF4EBP1	8p11.23	3,24295890	2	6
212560_at	SORL1	11q24.1	3,24186667	2	15
202794_at	INPP1	2q32.2	3,24167121	2	3
215501_s_at	DUSP10	1q41	3,24081705	2	3
1557945_at	TCTE3	6q27	3,24042842	2	3
212543_at	AIM1	6q21	3,24034121	2	14
1559826_a_at	LOC401074	3p12.3	3,23913931	2	14
205967_at	HIST1H4C	6p22.2	3,23762933	2	15
228186_s_at	RSPO3	6q22.33	3,23640617	2	11
202357_s_at	C2	6p21.33	3,23637693	2	7
235199_at	RNF125	18q12.1	3,23583488	2	6
236835_at	LOC645431	14q23.3	3,23376048	2	6
217678_at	SLC7A11	4q28.3	3,23246900	2	9
1558920_at	LOC100128590	2p22.1	3,23094089	2	8
209909_s_at	TGFB2	1q41	3,22888756	2	21
203761_at	SLA	8q24.22	3,22839283	2	11
225191_at	CIRBP	19p13.3	3,22552304	2	3
64408_s_at	CALML4	15q23	3,22458025	2	6
202478_at	TRIB2	2p24.3	3,22424542	2	10
232311_at	B2M	15q21.1	3,22235971	2	3
201416_at	SOX4	6p22.3	3,22071921	2	13
1562648_at	CCDC88A	2p16.1	3,22070832	2	9
218346_s_at	SESN1	6q21	3,21976930	2	4
202953_at	C1QB	1p36.12	3,21953876	2	10
212022_s_at	MKI67	10q26.2	3,21895703	2	3
204112_s_at	HNMT	2q22.1	3,21747708	2	9
219403_s_at	HPSE	4q21.23	3,21687596	2	6
205141_at	ANG	14q11.2	3,21622169	2	14
206510_at	SIX2	2p21	3,21417921	2	10
216905_s_at	ST14	11q24.3	3,21382902	2	5
209480_at	HLA-DQB1	6p21.32	3,21257640	2	13
225757_s_at	CLMN	14q32.13	3,21192242	2	3
209037_s_at	EHD1	11q13.1	3,21034749	2	9
227320_at	FAM101A	12q24.31	3,21027697	2	4
203636_at	MID1	Xp22.2	3,21000110	2	4
209687_at	CXCL12	10q11.21	3,20962205	2	14
210001_s_at	SOCS1	16p13.13	3,20899241	2	6
222871_at	KLHDC8A	1q32.1	3,20714505	2	13
38671_at	PLXND1	3q22.1	3,20660846	2	5
1568815_a_at	DDX50	10q22.1	3,20628994	2	4
218720_x_at	SEZ6L2	16p11.2	3,20515905	2	8
204958_at	PLK3	1p34.1	3,20433583	2	5
210355_at	PTHLH	12p11.22	3,20353305	2	10

1555865_at	LOC255512	11p15.5	3,20296461	2	4
204454_at	LDOC1	Xq27.1	3,20082800	2	22
234381_at	IGLV4-3	22q11.22	3,20077426	2	6
201218_at	CTBP2	10q26.13	3,19953719	2	3
223582_at	GPR98	5q14.3	3,19912594	2	19
235148_at	KRTCAP3	2p23.3	3,19755426	2	11
213150_at	HOXA10	7p15.2	3,19715941	2	3
205119_s_at	FPR1	19q13.41	3,19632142	2	7
1553493_a_at	TDH	8p23.1	3,19620242	2	5
205034_at	CCNE2	8q22.1	3,19468432	2	9
214149_s_at	ATP6V0E1	5q35.1	3,19447288	2	9
206207_at	CLC	19q13.2	3,19253774	2	6
203665_at	HMOX1	22q12.3	3,19134687	2	16
212701_at	TLN2	15q22.2	3,19087292	2	3
230047_at	FLJ32810	11q22.1	3,18966233	2	3
221731_x_at	VCAN	5q14.2	3,18958121	2	11
204924_at	TLR2	4q31.3	3,18952346	2	4
204948_s_at	FST	5q11.2	3,18923247	2	3
205158_at	RNASE4	14q11.2	3,18684769	2	8
1558641_at	LOC202051	5q31.2	3,18356249	2	8
212094_at	PEG10	7q21.3	3,18289337	2	8
220358_at	BATF3	1q32.3	3,18225746	2	7
205453_at	HOXB2	17q21.32	3,18212980	2	17
204518_s_at	PPIC	5q23.2	3,18045321	2	3
218918_at	MAN1C1	1p36.11	3,17962067	2	3
205830_at	CLGN	4q31.1	3,17955158	2	11
1552398_a_at	CLEC12A	12p13.2	3,17914097	2	7
218297_at	FAM188A	10p13	3,17899686	2	4
1557122_s_at	GABRB2	5q34	3,17838932	2	6
217147_s_at	TRAT1	3q13.13	3,17786996	2	3
244353_s_at	SLC2A12	6q23.2	3,17715570	2	3
201939_at	PLK2	5q11.2	3,17704844	2	8
227868_at	LOC154761	7q35	3,17693582	2	4
205653_at	CTSG	14q12	3,17609091	2	6
236421_at	ANKRD45	1q25.1	3,17539972	2	9
209318_x_at	PLAGL1	6q24.2	3,17453918	2	13
242470_at	EID2B	19q13.2	3,17238886	2	5
203473_at	SLCO2B1	11q13.4	3,17085501	2	7
225972_at	TMEM64	8q21.3	3,17023566	2	6
240545_at	LOC286382	9q21.13	3,17018429	2	6
206214_at	PLA2G7	6p12.3	3,16991936	2	7
220129_at	SOHLH2	13q13.3	3,16966245	2	9
220122_at	MCTP1	5q15	3,16947952	2	4
205123_s_at	TMEFF1	9q31.1	3,16935483	2	14
204779_s_at	HOXB7	17q21.32	3,16886349	2	5
232231_at	RUNX2	6p21.1	3,16882627	2	21
237145_at	EIF2AK4	15q15.1	3,16757130	2	3
218501_at	ARHGEF3	3p14.3	3,16714231	2	7
1555112_a_at	C1orf114	1q24.2	3,16702603	2	13
211340_s_at	MCAM	11q23.3	3,16683943	2	8
210497_x_at	SSX2	Xp11.22	3,16629007	2	11
1555758_a_at	CDKN3	14q22.2	3,16529964	2	6
219360_s_at	TRPM4	19q13.33	3,16393876	2	7
1557366_at	CCDC144B	17p11.2	3,16307776	2	5

201341_at	ENC1	5q13.3	3,16250637	2	9
225207_at	PDK4	7q21.3	3,16194802	2	9
1566342_at	SOD2	6q25.3	3,16182033	2	5
224860_at	C9orf123	9p24.1	3,16096116	2	3
220016_at	AHNAK	11q12.3	3,15956325	2	3
231235_at	NKTR	3p22.1	3,15882132	2	3
206420_at	IGSF6	16p12.2	3,15783491	2	4
212473_s_at	MICAL2	11p15.3	3,15729377	2	5
225728_at	SORBS2	4q35.1	3,15644693	2	20
203037_s_at	MTSS1	8q24.13	3,15619056	2	12
209409_at	GRB10	7p12.1	3,15552139	2	3
226186_at	TMOD2	15q21.2	3,15531120	2	4
220496_at	CLEC1B	12p13.2	3,15384311	2	4
226322_at	TMTC1	12p11.22	3,15360599	2	13
225959_s_at	ZNRF1	16q23.1	3,15278487	2	6
1556606_at	NAV2	11p15.1	3,15165828	2	15
213924_at	MPPE1	18p11.21	3,15090776	2	14
219064_at	ITIH5	10p14	3,15088005	2	8
207857_at	LILRA2	19q13.42	3,15048092	2	7
230477_at	LOC100130522	18q23	3,15012409	2	6
208962_s_at	FADS1	11q12.2	3,14970294	2	8
238694_at	DGKE	17q22	3,14869508	2	4
220237_at	ATG3	3q13.2	3,14863193	2	5
201348_at	GPX3	5q33.1	3,14848371	2	12
212923_s_at	C6orf145	6p25.2	3,14792526	2	3
227961_at	CTSB	8p23.1	3,14782992	2	6
213030_s_at	PLXNA2	1q32.2	3,14761322	2	4
228820_at	XPNPEP3	22q13.2	3,14727640	2	3
203881_s_at	DMD	Xp21.1	3,14716715	2	3
227799_at	MYO1G	7p13	3,14701537	2	5
204642_at	S1PR1	1p21.2	3,14668114	2	18
221802_s_at	KIAA1598	10q25.3	3,14389687	2	10
218326_s_at	LGR4	11p14.1	3,14323839	2	12
223822_at	SUSD4	1q41	3,14297579	2	4
204249_s_at	LMO2	11p13	3,14287045	2	12
212884_x_at	APOE	19q13.32	3,14053381	2	3
209504_s_at	PLEKHB1	11q13.4	3,14049950	2	5
231688_at	MMP8	11q22.2	3,14012225	2	13
217741_s_at	ZFAND5	9q21.13	3,13995083	2	4
205347_s_at	TMSB15A	Xq22.1	3,13987121	2	11
212098_at	LOC151162	2q21.2	3,13822617	2	6
201461_s_at	MAPKAPK2	1q32.1	3,13740486	2	5
213435_at	SATB2	2q33.1	3,13709086	2	3
231442_at	ZPBP2	17q12	3,13681060	2	8
219010_at	C1orf106	1q32.1	3,13519399	2	7
202242_at	TSPAN7	Xp21.1	3,13508844	2	3
205681_at	BCL2A1	15q25.1	3,13500751	2	6
204451_at	FZD1	7q21.13	3,13492147	2	4
1566079_at	RPS16P5	6p12.1	3,13485645	2	6
206331_at	CALCRL	2q32.1	3,13451253	2	4
218872_at	TESC	12q24.22	3,13305238	2	3
205413_at	MPPED2	11p14.1	3,13136123	2	20
205207_at	IL6	7p15.3	3,12910785	2	11
213537_at	HLA-DPA1	6p21.32	3,12894874	2	5

210746_s_at	EPB42	15q15.2	3,12851442	2	4
210168_at	C6	5p13.1	3,12607275	2	4
225532_at	CABLES1	18q11.2	3,12536492	2	5
221185_s_at	IQCG	3q29	3,12494800	2	19
223194_s_at	SLC22A23	6p25.2	3,12447161	2	9
226810_at	OGFRL1	6q13	3,12356352	2	9
204849_at	TCFL5	20q13.33	3,12315993	2	3
200665_s_at	SPARC	5q33.1	3,12277347	2	3
225645_at	EHF	11p13	3,12272278	2	4
1554624_a_at	SIRPB1	20p13	3,12250066	2	6
227053_at	PACSIN1	6p21.31	3,12213987	2	12
221666_s_at	PYCARD	16p11.2	3,12141467	2	5
239343_at	LOC728705	12q23.3	3,12126959	2	3
230529_at	HECA	6q24.1	3,12093327	2	5
206864_s_at	HRK	12q24.22	3,12033669	2	10
1552807_a_at	SIGLEC10	19q13.41	3,12011852	2	4
227802_at	RUFY3	4q13.3	3,12001234	2	4
242201_at	PMS2L2	7q11.23	3,11946022	2	5
222527_s_at	RBM22	5q33.1	3,11932856	2	5
235749_at	UGGT2	13q32.1	3,11926358	2	3
239996_x_at	ATP2A2	12q24.11	3,11898816	2	8
227382_at	CYB5B	16q22.1	3,11861864	2	3
200885_at	RHOC	1p13.2	3,11799744	2	4
238013_at	PLEKHA2	8p11.22	3,11789383	2	3
202555_s_at	MYLK	3q21.1	3,11764567	2	20
228376_at	GGTA1	9q33.2	3,11614788	2	3
220057_at	XAGE1A	Xp11.22	3,11384137	2	8
208456_s_at	RRAS2	1p32.3	3,11269324	2	17
232342_at	MTMR14	3p25.3	3,11208305	2	3
205934_at	PLCL1	2q33.1	3,11193984	2	3
222037_at	MCM4	8q11.21	3,11181457	2	3
237291_at	NCRNA00117	2p16.1	3,11154618	2	4
1559078_at	BCL11A	2p16.1	3,11075071	2	9
211849_s_at	RNGTT	6q15	3,11074757	2	3
209631_s_at	GPR37	7q31.33	3,10953469	2	9
218986_s_at	DDX60	4q32.3	3,10905406	2	8
213849_s_at	PPP2R2B	5q32	3,10734082	2	6
200628_s_at	WARS	14q32.2	3,10542217	2	9
1557049_at	LOC149478	1p34.1	3,10510374	2	3
239552_at	VWDE	7p21.3	3,10479201	2	17
213248_at	LOC730101	6p12.2	3,10473702	2	7
218232_at	C1QA	1p36.12	3,10409800	2	14
217414_x_at	HBA1	16p13.3	3,10347134	2	11
202206_at	ARL4C	2q37.1	3,10328872	2	6
1554242_a_at	COCH	14q12	3,10136025	2	12
219230_at	TMEM100	17q22	3,10121945	2	4
1568604_a_at	CADPS	3p14.2	3,10113078	2	3
213733_at	MYO1F	19p13.2	3,10068890	2	9
213350_at	RPS11	19q13.33	3,10013345	2	14
209465_x_at	PTN	7q33	3,09942427	2	5
242352_at	NIPBL	5p13.2	3,09870518	2	15
1564277_a_at	LOC100133920	9q11	3,09763087	2	3
231148_at	IGFL2	19q13.32	3,09750876	2	3
237461_at	NLRP7	19q13.42	3,09641306	2	10

208146_s_at	CPVL	7p14.3	3,09583991	2	18
213138_at	ARID5A	2q11.2	3,09578278	2	12
1564310_a_at	PARP15	3q21.1	3,09566071	2	5
213599_at	OIP5	15q15.1	3,09547514	2	7
1557719_at	PIKFYVE	2q34	3,09504148	2	4
217901_at	DSG2	18q12.1	3,09457829	2	20
212192_at	KCTD12	13q22.3	3,09444583	2	12
223272_s_at	C1orf57	1q42.2	3,09322919	2	4
210314_x_at	TNFSF13	17p13.1	3,09304378	2	5
238737_at	C1orf83	1p32.3	3,09201766	2	3
201369_s_at	ZFP36L2	2p21	3,09104477	2	8
207339_s_at	LTB	6p21.33	3,09072321	2	7
228338_at	LOC120376	11q23.1	3,08986118	2	11
236295_s_at	NLRC3	16p13.3	3,08985312	2	6
223307_at	CDCA3	12p13.31	3,08934218	2	7
226425_at	CLIP4	2p23.2	3,08781458	2	4
231382_at	FGF18	5q35.1	3,08606040	2	8
218943_s_at	DDX58	9p21.1	3,08557212	2	4
219270_at	CHAC1	15q15.1	3,08407540	2	4
225283_at	ARRDC4	15q26.3	3,08299204	2	5
229391_s_at	FAM26F	6q22.1	3,08243485	2	10
212681_at	EPB41L3	18p11.31	3,08215934	2	4
227792_at	ITPRIPL2	16p12.3	3,08149109	2	18
201645_at	TNC	9q33.1	3,08119685	2	3
235956_at	KIAA1377	11q22.1	3,08039890	2	6
243376_at	TANK	2q24.2	3,07807128	2	15
232271_at	HNF4G	8q21.11	3,07772537	2	5
228531_at	SAMD9	7q21.2	3,07730533	2	6
214033_at	ABCC6	16p13.11	3,07689947	2	4
241396_at	NEDD4L	18q21.31	3,07664121	2	3
205098_at	CCR1	3p21.31	3,07619313	2	16
229552_at	LOC283454	12q24.23	3,07587053	2	6
205883_at	ZBTB16	11q23.2	3,07458401	2	10
221929_at	RBM12B	8q22.1	3,07376010	2	3
219619_at	DIRAS2	9q22.2	3,07327068	2	14
228094_at	AMICA1	11q23.3	3,07204159	2	3
227034_at	ANKRD57	2q13	3,07145287	2	6
215894_at	PTGDR	14q22.1	3,07125366	2	14
1556771_a_at	LOC415056	9p13.3	3,07021253	2	3
208018_s_at	HCK	20q11.21	3,07020405	2	10
240336_at	HBM	16p13.3	3,07001573	2	5
226896_at	CHCHD1	10q22.2	3,06984114	2	4
203400_s_at	TF	3q22.1	3,06874595	2	3
203764_at	DLGAP5	14q22.3	3,06872284	2	11
205718_at	ITGB7	12q13.13	3,06797731	2	12
1553226_at	NCRNA00052	15q25.3	3,06767648	2	5
203431_s_at	RICS	11q24.3	3,06715309	2	3
208079_s_at	AURKA	20q13.2	3,06476294	2	9
227645_at	PIK3R5	17p13.1	3,06418619	2	11
1556900_at	LOC149773	20q13.32	3,06322174	2	5
205168_at	DDR2	1q23.3	3,06250934	2	3
243981_at	STK4	20q13.12	3,06241504	2	12
202508_s_at	SNAP25	20p12.2	3,06218422	2	3
1554903_at	FRMD8	11q13.1	3,06214279	2	5

208580_x_at	HIST1H4J	6p22.1	3,06125474	2	3
214693_x_at	NBPF10	1q21.1	3,06078547	2	5
219127_at	ATAD4	17q21.32	3,05974143	2	6
222810_s_at	RASAL2	1q25.2	3,05740658	2	7
227372_s_at	BAIAP2L1	7q22.1	3,05725707	2	3
1558139_at	FLJ39632	14q11.2	3,05574818	2	3
205637_s_at	SH3GL3	15q25.2	3,05438556	2	5
224917_at	MIR21	17q23.1	3,05421032	2	9
202345_s_at	FABP5	11q12.1	3,05254178	2	10
1554594_at	SH3D20	17q21.31	3,05237294	2	4
204836_at	GLDC	9p24.1	3,05076770	2	11
228113_at	RAB37	17q25.1	3,04984323	2	6
219489_s_at	NXN	17p13.3	3,04907402	2	12
40016_g_at	MAST4	5q12.3	3,04829109	2	7
228496_s_at	CRIM1	2p22.3	3,04803820	2	12
203932_at	HLA-DMB	6p21.32	3,04790931	2	5
214433_s_at	SELENBP1	1q21.3	3,04770316	2	3
206337_at	CCR7	17q21.2	3,04768100	2	6
213736_at	COX5B	2q11.2	3,04733519	2	6
1554929_at	QSK	11q23.3	3,04685264	2	3
209351_at	KRT14	17q21.2	3,04594168	2	3
220543_at	C21orf62	21q22.11	3,04317779	2	3
228071_at	GIMAP7	7q36.1	3,04301436	2	9
223343_at	MS4A7	11q12.2	3,04299819	2	11
205559_s_at	PCSK5	9q21.13	3,04233088	2	6
236632_at	LOC646576	4q31.21	3,04184509	2	7
239468_at	MKX	10p12.1	3,03918260	2	6
208463_at	GABRA4	4p12	3,03841111	2	7
204201_s_at	PTPN13	4q21.3	3,03668218	2	3
220993_s_at	GPR63	6q16.1	3,03623524	2	10
235174_s_at	LOC100128822	7q36.1	3,03548022	2	7
1556316_s_at	LOC284889	22q11.23	3,03459539	2	4
217523_at	CD44	11p13	3,03299847	2	4
229050_s_at	SNHG7	9q34.3	3,03278079	2	8
1558147_a_at	FLJ90757	17q25.3	3,03251940	2	6
209960_at	HGF	7q21.11	3,03018408	2	3
227556_at	NME7	1q24.2	3,02930049	2	6
205249_at	EGR2	10q21.1	3,02887520	2	7
240159_at	SLC15A2	3q13.33	3,02707891	2	7
215047_at	TRIM58	1q44	3,02660628	2	6
204730_at	RIMS3	1p34.2	3,02613700	2	3
223800_s_at	LIMS3	2q13	3,02607620	2	3
206374_at	DUSP8	11p15.5	3,02505232	2	6
235638_at	RASSF6	4q13.3	3,02343913	2	13
227038_at	SGMS2	4q25	3,02302515	2	3
204777_s_at	MAL	2q11.1	3,02261504	2	25
206453_s_at	NDRG2	14q11.2	3,02094384	2	3
207307_at	HTR2C	Xq23	3,01904511	2	7
218368_s_at	TNFRSF12A	16p13.3	3,01755038	2	4
233814_at	EFNA5	5q21.3	3,01747671	2	14
205382_s_at	CFD	19p13.3	3,01712038	2	5
222357_at	ZBTB20	3q13.31	3,01703220	2	10
207826_s_at	ID3	1p36.12	3,01630154	2	9
206493_at	ITGA2B	17q21.31	3,01586831	2	3

244656_at	RASL10B	17q12	3,01543024	2	3
204007_at	FCGR3B	1q23.3	3,01447198	2	8
224861_at	GNAQ	9q21.2	3,01369079	2	11
203299_s_at	AP1S2	Xp22.2	3,01358797	2	11
235377_at	C6orf142	14q11.2	3,01319405	2	26
241938_at	QKI	6q26	3,01292804	2	9
235343_at	VASH2	1q32.3	3,01187797	2	17
205488_at	GZMA	5q11.2	3,01176503	2	4
203695_s_at	DFNA5	7p15.3	3,01108369	2	3
204787_at	VSIG4	Xq12	3,01080571	2	9
1553039_a_at	ASB10	7q36.1	3,00985862	2	3
241347_at	KIAA1618	17q25.3	3,00879943	2	4
231395_at	ATP8A2	13q12.13	3,00752281	2	5
209499_x_at	NFSF12-TNFSF1	17p13.1	3,00692808	2	3
241973_x_at	DPP7	9q34.3	3,00682782	2	3
204232_at	FCER1G	1q23.3	3,00599168	2	7
213324_at	SRC	20q11.23	3,00553289	2	6
223502_s_at	TNFSF13B	13q33.3	3,00506461	2	7
233512_at	SH3RF3	2q12.3	3,00501151	2	4
227067_x_at	NOTCH2NL	1q21.1	3,00500257	2	11
236565_s_at	LARP6	15q23	3,00495391	2	12
206851_at	RNASE3	14q11.2	3,00449077	2	16
232692_at	TDRD6	6p12.3	3,00281982	2	3
226423_at	PAQR8	6p12.2	3,00251134	2	5
207838_x_at	PBXIP1	1q21.3	3,00233190	2	13
208636_at	ACTN1	14q24.1	3,00214646	2	7
219833_s_at	EFHC1	6p12.2	3,00187960	2	3
213007_at	FANCI	15q26.1	3,00149246	2	4
237786_at	MAGI2	7q21.11	3,00144904	2	5
215175_at	PCNX	14q24.2	3,00139487	2	10
206676_at	CEACAM8	19q13.2	3,00118593	2	11
225990_at	BOC	3q13.2	3,00050993	2	4
210052_s_at	TPX2	20q11.21	2,99944912	2	4
200636_s_at	PTPRF	1p34.2	2,99824286	2	5
204411_at	KIF21B	1q32.1	2,99779819	2	10
229678_at	LOC728431	1p34.3	2,99749746	2	3
1560199_x_at	LOC728153	5q12.1	2,99578829	2	4
220952_s_at	PLEKHA5	12p12.3	2,99516809	2	5
201506_at	TGFBI	5q31.1	2,99488149	2	16
1554053_at	SPTLC1	9q22.31	2,99470541	2	3
220005_at	P2RY13	3q25.1	2,99443535	2	4
211657_at	CEACAM6	19q13.2	2,99239015	2	4
222843_at	FIGNL1	7p12.1	2,99152713	2	7
204465_s_at	INA	10q24.33	2,98998355	2	6
224443_at	C1orf97	1q32.3	2,98997584	2	5
219777_at	GIMAP6	7q36.1	2,98993652	2	4
216452_at	TRPM3	9q21.13	2,98989171	2	12
1559022_at	KIAA0494	1p33	2,98948061	2	7
231951_at	GNAO1	16q12.2	2,98913655	2	3
203030_s_at	PTPRN2	7q36.3	2,98872760	2	3
212813_at	JAM3	11q25	2,98824263	2	13
209529_at	PPAP2C	19p13.3	2,98774654	2	6
225285_at	BCAT1	12p12.1	2,98766572	2	11
39402_at	IL1B	2q13	2,98740192	2	12

210151_s_at	DYRK3	1q32.1	2,98716083	2	3
224745_x_at	OTUD5	Xp11.23	2,98615262	2	3
234980_at	TMEM56	1p21.3	2,98578292	2	3
215506_s_at	DIRAS3	1p31.3	2,98572980	2	24
1564603_at	C15orf55	15q14	2,98376415	2	3
204638_at	ACP5	19p13.2	2,98375241	2	5
226726_at	MBOAT2	2p25.1	2,98332491	2	3
225496_s_at	SYTL2	11q14.1	2,98307589	2	3
1552915_at	IL28A	19q13.2	2,98278838	2	3
225839_at	RBM33	7q36.3	2,98239223	2	5
222071_s_at	SLCO4C1	5q21.1	2,98232483	2	6
233609_at	PTPRK	6q22.33	2,98212577	2	3
205936_s_at	HK3	5q35.2	2,98197676	2	6
1559072_a_at	ELFN2	22q13.1	2,98160823	2	13
202761_s_at	SYNE2	14q23.2	2,98158592	2	3
207194_s_at	ICAM4	19p13.2	2,98019833	2	4
238669_at	PTGS1	9q33.2	2,97997416	3	4
222529_at	SLC25A37	8p21.2	2,97920544	3	7
210145_at	PLA2G4A	1q31.1	2,97914806	3	4
243977_at	LOC541472	7p15.3	2,97901067	3	3
228532_at	C1orf162	1p13.2	2,97886104	3	13
219312_s_at	ZBTB10	8q21.13	2,97882659	3	10
210033_s_at	SPAG6	10p12.2	2,97858965	3	9
201481_s_at	PYGB	20p11.21	2,97796034	3	7
241918_at	ANO7	2q37.3	2,97718664	3	10
209182_s_at	C10orf10	10q11.21	2,97679867	3	3
210399_x_at	FUT6	19p13.3	2,97636325	3	4
220232_at	SCD5	4q21.22	2,97556980	3	4
219983_at	HRASLS	3q29	2,97553876	3	6
1554997_a_at	PTGS2	1q31.1	2,97548959	3	12
206085_s_at	CTH	1p31.1	2,97406562	3	7
224193_s_at	FCRL2	1q23.1	2,97368437	3	10
209118_s_at	TUBA1A	12q13.12	2,97346164	3	12
209191_at	TUBB6	18p11.21	2,97336963	3	22
227376_at	GLI3	7p14.1	2,97290841	3	7
231997_at	TBCEL	11q23.3	2,97281287	3	6
202733_at	P4HA2	5q31.1	2,97146287	3	7
1553810_a_at	KIAA1524	3q13.13	2,97065775	3	3
210517_s_at	AKAP12	6q25.1	2,97065476	3	9
204966_at	BAI2	1p35.2	2,97042564	3	3
223391_at	SGPP1	14q23.2	2,96969496	3	8
202705_at	CCNB2	15q22.2	2,96894345	3	9
204469_at	PTPRZ1	7q31.32	2,96846054	3	22
231411_at	LHFP	13q14.11	2,96816152	3	3
1554910_at	PRKD3	2p22.2	2,96732756	3	9
229228_at	CREB5	7p15.1	2,96650822	3	7
206737_at	WNT11	11q13.5	2,96588857	3	4
235014_at	LOC147727	19p13.2	2,96516551	3	3
237737_at	LOC100289026	1q21.1	2,96478113	3	14
233177_s_at	PNKD	2q35	2,96442529	3	3
221582_at	HIST3H2A	1q42.13	2,96220026	3	14
207902_at	IL5RA	3p26.2	2,96202323	3	3
221602_s_at	FAIM3	1q32.1	2,96031121	3	11
223701_s_at	USP47	11p15.3	2,95852047	3	5

1561396_at	EPHA6	3q11.2	2,95849846	3	3
205919_at	HBE1	11p15.4	2,95708455	3	14
227692_at	GNAI1	7q21.11	2,95536588	3	8
211596_s_at	LRIG1	3p14.1	2,95529760	3	10
226757_at	IFIT2	10q23.31	2,95476989	3	7
221520_s_at	CDCA8	1p34.3	2,95453054	3	4
221565_s_at	CALHM2	10q24.33	2,95449234	3	8
230036_at	SAMD9L	7q21.2	2,95445146	3	3
1556721_at	LOC284805	20q11.21	2,95427072	3	23
206545_at	CD28	2q33.2	2,95398961	3	18
204994_at	MX2	21q22.3	2,95359196	3	3
211341_at	POU4F1	13q31.1	2,95352539	3	4
221122_at	HRASLS2	11q12.3	2,95296602	3	14
226388_at	TCEA3	1p36.12	2,95284478	3	23
220817_at	TRPC4	13q13.3	2,95213721	3	3
1559490_at	LRCH3	3q29	2,95159136	3	5
1560426_at	C12orf55	12q23.1	2,95156735	3	10
226185_at	CDS1	4q21.23	2,95081537	3	6
208886_at	H1F0	22q13.1	2,95002738	3	10
238893_at	LOC338758	12q21.33	2,94901432	3	6
206213_at	WNT10B	12q13.12	2,94822297	3	14
225775_at	TSPAN33	7q32.1	2,94798930	3	5
230090_at	LOC100287032	5p13.2	2,94734712	3	7
231969_at	STOX2	4q35.1	2,94732114	3	14
59644_at	BMP2K	4q21.21	2,94650286	3	4
201883_s_at	B4GALT1	9p21.1	2,94639437	3	8
238447_at	RBMS3	3p24.1	2,94560316	3	9
217378_x_at	LOC100130100	2q13	2,94554048	3	9
217685_at	SLC16A3	17q25.3	2,94436066	3	3
219690_at	TMEM149	19q13.12	2,94408231	3	7
230493_at	SHISA2	13q12.13	2,94362831	3	7
228877_at	RGL3	19p13.2	2,94334474	3	4
204472_at	GEM	8q22.1	2,94299013	3	10
205786_s_at	ITGAM	16p11.2	2,94262342	3	10
219090_at	SLC24A3	20p11.23	2,94201759	3	17
242268_at	CUGBP2	10p14	2,94188289	3	10
203542_s_at	KLF9	9q21.12	2,94116855	3	4
200965_s_at	ABLIM1	10q25.3	2,94105742	3	3
218223_s_at	PLEKHO1	1q21.2	2,94052990	3	7
203233_at	IL4R	16p12.1	2,94048477	3	3
203305_at	F13A1	6p25.1	2,94043063	3	8
211168_s_at	UPF1	19p13.11	2,93922547	3	5
241819_at	TNFSF8	9q32	2,93900410	3	10
204122_at	TYROBP	19q13.12	2,93742432	3	7
208210_at	MAS1	6q25.3	2,93566023	3	9
219304_s_at	PDGFD	11q22.3	2,93550803	3	12
223806_s_at	NAPSA	19q13.33	2,93390691	3	4
203186_s_at	S100A4	1q21.3	2,93268912	3	8
238902_at	PCMTD1	8q11.23	2,93223663	3	5
230349_at	XKRX	Xq22.1	2,93201289	3	5
238452_at	FCRLB	1q23.3	2,93188676	3	10
231996_at	N4BP2	4p14	2,93181336	3	3
217419_x_at	AGRN	1p36.33	2,93064441	3	3
204319_s_at	RGS10	10q26.11	2,93038326	3	11

224955_at	TEAD1	11p15.3	2,93034179	3	14
223217_s_at	NFKBIZ	3q12.3	2,92996316	3	6
229764_at	TPRG1	3q28	2,92920141	3	5
228758_at	BCL6	3q27.3	2,92773442	3	4
204563_at	SELL	1q24.2	2,92765195	3	16
208606_s_at	WNT4	1p36.12	2,92712995	3	9
204014_at	DUSP4	8p12	2,92634766	3	9
205929_at	GPA33	1q24.1	2,92491230	3	4
232240_at	DNHD1	11p15.4	2,92486159	3	5
210432_s_at	SCN3A	2q24.3	2,92280191	3	12
221273_s_at	RNF208	9q34.3	2,92241143	3	3
219243_at	GIMAP4	7q36.1	2,92220356	3	3
210220_at	FZD2	17q21.31	2,92195562	3	9
220250_at	ZNF286A	17p12	2,92151703	3	4
206181_at	SLAMF1	1q23.3	2,92091477	3	3
227188_at	C21orf63	21q22.11	2,92070036	3	8
1569652_at	MLLT3	9p21.3	2,92008064	3	11
205947_s_at	VIPR2	7q36.3	2,92001873	3	5
203196_at	ABCC4	13q32.1	2,91950755	3	3
232550_at	ABHD1	2p23.3	2,91884129	3	3
241972_at	LOC401588	Xp11.23	2,91855144	3	5
235925_at	TCF12	15q21.3	2,91806765	3	15
212531_at	LCN2	9q34.11	2,91709706	3	5
205983_at	DPEP1	16q24.3	2,91618737	3	10
201566_x_at	ID2	2p25.1	2,91588212	3	9
1565483_at	EGFR	7p11.2	2,91503789	3	6
203147_s_at	TRIM14	9q22.33	2,91500689	3	5
232977_x_at	MYH14	19q13.33	2,91493518	3	3
228097_at	MYLIP	6p22.3	2,91488049	3	3
202203_s_at	AMFR	16q12.2	2,91461495	3	4
1559593_a_at	MED26	19p13.11	2,91412432	3	4
205543_at	HSPA4L	4q28.1	2,91386010	3	5
223381_at	NUF2	1q23.3	2,91340284	3	9
229604_at	CMAH	6p22.2	2,91316590	3	8
218694_at	ARMCX1	Xq22.1	2,91255858	3	21
228400_at	SHROOM3	4q21.1	2,91141747	3	15
242029_at	FNDC3B	3q26.31	2,90934110	3	14
215336_at	AKAP11	13q14.11	2,90830474	3	4
206086_x_at	HFE	6p22.2	2,90746880	3	3
225353_s_at	C1QC	1p36.12	2,90690260	3	9
229585_at	ADAMTSL1	9p22.2	2,90659157	3	3
202672_s_at	ATF3	1q32.3	2,90622189	3	9
218935_at	EHD3	2p23.1	2,90614808	3	11
207031_at	NKX3-2	4p15.33	2,90605625	3	7
214157_at	GNAS	20q13.32	2,90542589	3	4
203680_at	PRKAR2B	7q22.3	2,90536362	3	7
203185_at	RASSF2	20p13	2,90482367	3	5
228868_x_at	CDT1	16q24.3	2,90400304	3	3
201710_at	MYBL2	20q13.12	2,90366365	3	7
214153_at	ELOVL5	6p12.1	2,90178939	3	5
202481_at	DHRS3	1p36.22	2,90109085	3	3
213326_at	VAMP1	12p13.31	2,90053225	3	3
219733_s_at	SLC27A5	19q13.43	2,89921224	3	6
227867_at	LOC129293	2p11.2	2,89828047	3	6

200675_at	CD81	11p15.5	2,89707137	3	17
236688_at	FRMPD3	Xq22.3	2,89686173	3	10
223126_s_at	C1orf21	1q25.3	2,89506825	3	4
1569867_at	EME2	16p13.3	2,89459630	3	11
1552863_a_at	CACNG6	19q13.42	2,89430148	3	3
1560014_s_at	PDXDC1	16p13.11	2,89413770	3	3
238462_at	UBASH3B	11q24.1	2,89399303	3	6
205505_at	GCNT1	9q21.13	2,89399063	3	3
205330_at	MN1	22q12.1	2,89376686	3	7
203868_s_at	VCAM1	1p21.2	2,89197123	3	12
219373_at	DPM3	1q22	2,89120517	3	7
232099_at	PCDHB16	5q31.3	2,89106918	3	7
1555779_a_at	CD79A	19q13.2	2,89087266	3	11
204033_at	TRIP13	5p15.33	2,89065797	3	3
233827_s_at	SUPT16H	14q11.2	2,88950480	3	4
204794_at	DUSP2	2q11.2	2,88884962	3	12
1553998_at	DMRTC1	Xq13.2	2,88862880	3	3
214710_s_at	CCNB1	5q13.2	2,88831937	3	9
223503_at	TMEM163	2q21.3	2,88717004	3	6
1554689_a_at	NLGN4X	Xp22.31	2,88681005	3	3
206369_s_at	PIK3CG	7q22.3	2,88660840	3	3
217497_at	TYMP	22q13.33	2,88512834	3	4
212107_s_at	DHX9	1q25.3	2,88362538	3	5
230245_s_at	LOC283663	15q21.3	2,88220446	3	3
213534_s_at	PASK	2q37.3	2,88168903	3	8
239304_at	MFSD4	1q32.1	2,88118029	3	4
214057_at	MCL1	1q21.3	2,88058380	3	5
220712_at	C8orf60	8q24.3	2,88032374	3	5
202510_s_at	TNFAIP2	14q32.32	2,88005802	3	7
204141_at	TUBB2A	6p25.2	2,87943137	3	14
219427_at	FAT4	4q28.1	2,87931255	3	9
214472_at	HIST1H2AD	6p22.2	2,87929042	3	10
225286_at	ARSD	Xp22.33	2,87928497	3	4
222453_at	CYBRD1	2q31.1	2,87921274	3	17
227062_at	NEAT1	11q13.1	2,87868536	3	8
223280_x_at	MS4A6A	11q12.1	2,87846883	3	19
225782_at	MSRB3	12q14.3	2,87813993	3	5
238513_at	PRRG4	11p13	2,87791979	3	11
219452_at	DPEP2	16q22.1	2,87787840	3	5
205859_at	LY86	6p25.1	2,87634693	3	8
206506_s_at	SUPT3H	6p21.1	2,87592817	3	5
205747_at	CBLN1	16q12.1	2,87560137	3	3
210387_at	HIST1H2BG	6p22.2	2,87548661	3	10
227461_at	STON2	14q31.1	2,87350701	3	5
215599_at	LOC653188	5q13.2	2,87293107	3	10
227613_at	ZNF331	19q13.42	2,87291928	3	9
237591_at	NCRNA00173	12q24.22	2,87105384	3	4
228033_at	E2F7	12q21.2	2,87037182	3	12
34408_at	RTN2	19q13.32	2,87018957	3	4
225402_at	TP53RK	20q13.12	2,87001869	3	7
212599_at	AUTS2	7q11.22	2,86908693	3	4
213283_s_at	SALL2	14q11.2	2,86879383	3	6
238534_at	LRRFIP1	2q37.3	2,86745215	3	4
225175_s_at	SLC44A2	19p13.2	2,86695603	3	8

219959_at	MOCOS	18q12.2	2,86575106	3	13
205027_s_at	MAP3K8	10p11.23	2,86496579	3	11
226999_at	RNPC3	1p21.1	2,86379765	3	3
214455_at	HIST1H2BC	6p22.2	2,86341920	3	7
238605_at	NOL4	18q12.1	2,86336793	3	11
230546_at	VASH1	14q24.3	2,86199085	3	3
238851_at	ANKRD13A	12q24.11	2,86139948	3	4
202861_at	PER1	17p13.1	2,86125645	3	4
200897_s_at	PALLD	4q32.3	2,86042032	3	11
212067_s_at	C1R	12p13.31	2,85971753	3	5
220316_at	NPAS3	14q13.1	2,85957340	3	3
223044_at	SLC40A1	2q32.2	2,85920722	3	9
1558796_a_at	LOC728052	6q12	2,85808553	3	13
202686_s_at	AXL	19q13.2	2,85761062	3	10
202068_s_at	LDLR	19p13.2	2,85703378	3	3
203213_at	CDC2	10q21.2	2,85616839	3	8
1555630_a_at	RAB34	17q11.2	2,85499191	3	3
207447_s_at	MGAT4C	12q21.31	2,85489193	3	9
1553718_at	ZNF548	19q13.43	2,85487451	3	4
201841_s_at	HSPB1	7q11.23	2,85478191	3	6
1564281_at	LOC285708	5q21.2	2,85451185	3	8
232720_at	LINGO2	9p21.1	2,85348731	3	3
205922_at	VNN2	6q23.2	2,85177702	3	9
235545_at	DEPDC1	1p31.2	2,85167876	3	3
218640_s_at	PLEKHF2	8q22.1	2,85110885	3	4
204526_s_at	TBC1D8	2q11.2	2,84888642	3	4
230875_s_at	ATP11A	13q34	2,84829428	3	3
206120_at	CD33	19q13.41	2,84805822	3	14
213605_s_at	LOC100272216	5p13.2	2,84727767	3	13
220338_at	RALGPS2	1q25.2	2,84512634	3	12
235597_s_at	RGPD1	2p11.2	2,84493890	3	3
214438_at	HLX	1q41	2,84376755	3	4
242121_at	NCRNA00182	Xq13.2	2,84363680	3	6
1569508_at	PRDM5	4q27	2,84362798	3	3
222670_s_at	MAFB	20q12	2,84292115	3	4
1555763_x_at	MKL1	22q13.2	2,84274297	3	13
228547_at	NRXN1	2p16.3	2,84230950	3	11
235310_at	GCET2	3q13.2	2,84100803	3	9
211622_s_at	ARF3	12q13.12	2,84043806	3	3
1558569_at	UNQ6228	11q21	2,84003269	3	5
215012_at	ZNF451	6p12.1	2,83954780	3	3
227236_at	TSPAN2	1p13.2	2,83869698	3	5
1559964_at	FLJ38717	6p21.1	2,83864528	3	7
223027_at	SNX9	6q25.3	2,83861880	3	14
222027_at	NUCKS1	1q32.1	2,83833492	3	7
210716_s_at	CLIP1	12q24.31	2,83821759	3	4
221656_s_at	ARHGEF10L	1p36.13	2,83820432	3	4
203922_s_at	CYBB	Xp11.4	2,83810507	3	6
224461_s_at	AIFM2	10q22.1	2,83728769	3	3
204066_s_at	AGAP1	2q37.2	2,83630292	3	22
204116_at	IL2RG	Xq13.1	2,83603663	3	4
229070_at	C6orf105	6p24.1	2,83581125	3	8
208373_s_at	P2RY6	11q13.4	2,83549004	3	13
214815_at	TRIM33	1p13.2	2,83440647	3	3

200872_at	S100A10	1q21.3	2,83366013	3	11
206756_at	CHST7	Xp11.23	2,83251999	3	4
204438_at	MRC1	10p12.33	2,83247602	3	4
203744_at	HMGB3	Xq28	2,83214218	3	11
206111_at	RNASE2	14q11.2	2,83121252	3	12
206478_at	KIAA0125	14q32.33	2,83115694	3	17
200832_s_at	SCD	10q24.31	2,83115507	3	10
226505_x_at	USP32	17q23.2	2,83072077	3	4
237094_at	FAM19A5	22q13.32	2,82984961	3	5
201212_at	LGMN	14q32.12	2,82982856	3	5
226980_at	DEPDC1B	5q12.1	2,82982673	3	6
206424_at	CYP26A1	10q23.33	2,82946128	3	3
204829_s_at	FOLR2	11q13.4	2,82855535	3	3
1552365_at	SCIN	7p21.3	2,82845595	3	7
232762_at	KIAA1217	10p12.2	2,82830300	3	7
222024_s_at	AKAP13	15q25.3	2,82802210	3	10
219670_at	BEND5	1p33	2,82783545	3	10
229994_at	NFIA	1p31.3	2,82731264	3	5
209732_at	CLEC2B	12p13.31	2,82710977	3	9
226038_at	LONRF1	8p23.1	2,82696523	3	3
205110_s_at	FGF13	Xq27.1	2,82672659	3	5
47571_at	ZNF236	18q23	2,82624837	3	21
1556474_a_at	FLJ38379	2q37.3	2,82576163	3	3
238914_at	DCC	18q21.2	2,82347187	3	3
213293_s_at	TRIM22	11p15.4	2,82324747	3	9
226763_at	SESTD1	2q31.2	2,82307925	3	6
228477_at	ARGLU1	13q33.3	2,82281251	3	4
209324_s_at	RGS16	1q25.3	2,82276445	3	5
201693_s_at	EGR1	5q31.2	2,82215630	3	10
222696_at	AXIN2	17q24.1	2,82151715	3	5
202609_at	EPS8	12p12.3	2,82085815	3	7
219998_at	HSPC159	2p14	2,82006228	3	6
238303_at	STT3B	3p23	2,81949885	3	12
236696_at	SR140	3q23	2,81917111	3	5
201760_s_at	WSB2	12q24.23	2,81870430	3	4
206486_at	LAG3	12p13.31	2,81856398	3	12
217911_s_at	BAG3	10q26.11	2,81818704	3	6
222912_at	ARRB1	11q13.4	2,81813672	3	3
236442_at	DPF3	14q24.2	2,81785696	3	3
1569906_s_at	PHF20	20q11.22	2,81767598	3	4
242131_at	LOC100288418	1p36.33	2,81664078	3	5
231577_s_at	GBP1	1p22.2	2,81635015	3	3
217593_at	ZSCAN18	19q13.43	2,81549516	3	3
204749_at	NAP1L3	Xq21.32	2,81539906	3	3
236478_at	IFNAR1	21q22.11	2,81387866	3	7
225354_s_at	SH3BGRL2	6q14.1	2,81339953	3	4
244804_at	SQSTM1	5q35.3	2,81275445	3	11
208237_x_at	ADAM22	7q21.12	2,81153164	3	3
214156_at	MYRIP	3p22.1	2,81100500	3	16
234006_s_at	C1orf91	1p35.1	2,81070612	3	3
225662_at	ZAK	2q31.1	2,81050766	3	3
213998_s_at	DDX17	22q13.1	2,81022837	3	5
210225_x_at	LILRA6	19q13.42	2,81002028	3	3
206680_at	CD5L	1q23.1	2,80948509	3	12

219051_x_at	METRN	16p13.3	2,80913839	3	4
219918_s_at	ASPM	1q31.3	2,80875605	3	6
220771_at	LOC51152	1q21.1	2,80873961	3	3
1553185_at	RASEF	9q21.32	2,80838062	3	14
202323_s_at	ACBD3	1q42.12	2,80828825	3	6
205164_at	GCAT	22q13.1	2,80818067	3	6
244619_at	LOC646626	1p22.3	2,80733029	3	6
202499_s_at	SLC2A3	12p13.31	2,80676786	3	5
210105_s_at	FYN	6q21	2,80668119	3	9
221011_s_at	LBH	2p23.1	2,80667852	3	9
214467_at	GPR65	14q31.3	2,80651777	3	5
203773_x_at	BLVRA	7p13	2,80617514	3	5
212859_x_at	MT1E	16q12.2	2,80617333	3	3
202430_s_at	PLSCR1	3q24	2,80604361	3	4
202260_s_at	STXBP1	9q34.11	2,80587201	3	14
213938_at	ERC2	3p14.3	2,80570542	3	12
217551_at	LOC441453	11p15.1	2,80570267	3	9
218625_at	NRN1	6p25.1	2,80365912	3	11
218726_at	HJURP	2q37.1	2,80360642	3	3
230332_at	ZCCHC7	9p13.2	2,80261341	3	16
217892_s_at	LIMA1	12q13.12	2,80190310	3	3
206105_at	AFF2	Xq28	2,80179781	3	5
220323_at	CNTD2	19q13.2	2,80166809	3	5
225017_at	CCDC14	3q21.1	2,80136940	3	3
215541_s_at	DIAPH1	5q31.3	2,80057448	3	8
238076_at	GATAD2B	1q21.3	2,80051794	3	5
236966_at	ARMC8	3q22.3	2,79977978	3	9
1570239_a_at	CLNK	4p16.1	2,79839796	3	5
204567_s_at	ABCG1	21q22.3	2,79535945	3	12
227735_s_at	C10orf99	10q23.1	2,79532922	3	4
220158_at	LGALS14	19q13.2	2,79492428	3	5
228377_at	KLHL14	18q12.1	2,79465414	3	8
242814_at	SERPINB9	6p25.2	2,79427743	3	12
229399_at	C10orf118	10q25.3	2,79380208	3	14
201906_s_at	CTDSPL	3p22.2	2,79328632	3	3
207354_at	CCL16	17q12	2,79319361	3	4
230560_at	STXBP6	14q12	2,79294176	3	8
220123_at	SLC35F5	2q14.1	2,79293601	3	6
203927_at	NFKBIE	6p21.1	2,79231114	3	3
207717_s_at	PKP2	12p11.21	2,79204393	3	22
235863_at	JSRP1	19p13.3	2,79155438	3	5
209369_at	ANXA3	4q21.21	2,79067565	3	13
1552280_at	TIMD4	5q33.3	2,79060724	3	11
207746_at	POLQ	3q13.33	2,79006950	3	4
204529_s_at	TOX	8q12.1	2,78992668	3	6
225441_x_at	LSMD1	17p13.1	2,78964635	3	6
232235_at	DSEL	18q22.1	2,78947380	3	14
223625_at	FAM126A	7p15.3	2,78944061	3	3
233555_s_at	SULF2	20q13.13	2,78917178	3	4
201798_s_at	MYOF	10q23.33	2,78914174	3	4
218113_at	TMEM2	9q21.13	2,78876295	3	4
203413_at	NELL2	12q12	2,78854002	3	7
229264_at	LOC100292701	1q21.2	2,78843756	3	5
228976_at	ICOSLG	21q22.3	2,78823515	3	3

219168_s_at	ARHGAP8	22q13.31	2,78720779	3	7
202340_x_at	NR4A1	12q13.13	2,78614486	3	5
237180_at	PSME4	2p16.2	2,78565497	3	8
211258_s_at	TGFA	2p13.3	2,78525320	3	6
232160_s_at	TNIP2	4p16.3	2,78457039	3	4
209066_x_at	UQCRB	8q22.1	2,78455087	3	11
209555_s_at	CD36	7q21.11	2,78452865	3	5
204641_at	NEK2	1q32.3	2,78441515	3	11
205552_s_at	OAS1	12q24.13	2,78415664	3	7
230000_at	RNF213	17q25.3	2,78388874	3	3
235400_at	FCRLA	1q23.3	2,78365321	3	6
222343_at	BCL2L11	2q13	2,78342127	3	6
206631_at	PTGER2	14q22.1	2,78338345	3	4
235498_at	LRRIQ3	1p31.1	2,78337306	3	3
213566_at	RNASE6	14q11.2	2,78314621	3	13
209378_s_at	FAM190B	10q23.1	2,78304892	3	5
218901_at	PLSCR4	3q24	2,78243885	3	9
200923_at	LGALS3BP	17q25.3	2,78174471	3	13
202107_s_at	MCM2	3q21.3	2,78142797	3	7
209283_at	CRYAB	11q23.1	2,78137619	3	4
203755_at	BUB1B	15q15.1	2,78067399	3	7
202580_x_at	FOXM1	12p13.33	2,78065702	3	6
244546_at	CYCS	7p15.3	2,78030638	3	6
214020_x_at	ITGB5	3q21.2	2,78020340	3	9
201242_s_at	ATP1B1	1q24.2	2,78009590	3	6
203657_s_at	CTSF	11q13.2	2,77976758	3	7
204491_at	PDE4D	5q12.1	2,77862166	3	4
220448_at	KCNK12	2p21	2,77829972	3	9
235130_at	PANK2	20p13	2,77744839	3	3
244632_at	CNTN5	11q22.1	2,77703757	3	6
200730_s_at	PTP4A1	6q12	2,77668553	3	9
238118_s_at	PPOX	1q23.3	2,77539120	3	4
206834_at	HBD	11p15.4	2,77498119	3	8
202145_at	LY6E	8q24.3	2,77496342	3	5
205937_at	CGREF1	2p23.3	2,77483552	3	5
201695_s_at	NP	14q11.2	2,77479491	3	7
212897_at	CDC2L6	6q21	2,77447930	3	3
240062_at	FAM3C	7q31.31	2,77320662	3	3
202990_at	PYGL	14q22.1	2,77221549	3	7
227235_at	GUCY1A3	4q32.1	2,77181976	3	14
208890_s_at	PLXNB2	22q13.33	2,77144596	3	7
209627_s_at	OSBPL3	7p15.3	2,77136219	3	3
217388_s_at	KYNU	2q22.2	2,77109480	3	11
214594_x_at	ATP8B1	18q21.31	2,77040580	3	4
1555847_a_at	LOC284454	19p13.13	2,76987728	3	5
212977_at	CXCR7	2q37.3	2,76930414	3	16
203767_s_at	STS	Xp22.31	2,76848817	3	7
236609_at	LOC100129592	2q32.2	2,76832611	3	7
1569608_x_at	LOC643187	1q12	2,76830250	3	4
209298_s_at	ITSN1	21q22.11	2,76768745	3	6
223697_x_at	C9orf64	9q21.32	2,76758580	3	12
234475_x_at	CCKBR	11p15.4	2,76735429	3	4
213069_at	HEG1	3q21.2	2,76692371	3	11
209958_s_at	BBS9	7p14.3	2,76668880	3	4

239297_at	C8orf79	8p22	2,76616413	3	4
235306_at	GIMAP8	7q36.1	2,76570838	3	6
214131_at	CYorf15B	Yq11.223	2,76521991	3	10
204055_s_at	CTAGE5	14q21.1	2,76487968	3	4
1557185_at	TPCN1	12q24.13	2,76454897	3	3
227212_s_at	PHF19	9q33.2	2,76445795	3	13
221943_x_at	RPL38	17q25.1	2,76419460	3	10
219951_s_at	C20orf12	20p11.23	2,76403664	3	3
225681_at	CTHRC1	8q22.3	2,76330429	3	4
207819_s_at	ABCB4	7q21.12	2,76292654	3	8
227410_at	FAM43A	3q29	2,76237725	3	3
229719_s_at	DERL3	22q11.23	2,76135490	3	6
205551_at	SV2B	15q26.1	2,76082020	3	11
1552822_at	TMX3	18q22.1	2,76062689	3	5
218542_at	CEP55	10q23.33	2,76036637	3	6
218459_at	TOR3A	1q25.2	2,75993979	3	4
1565867_a_at	ZC3H11A	1q32.1	2,75992751	3	5
201397_at	PHGDH	1p12	2,75943687	3	7
211924_s_at	PLAUR	19q13.31	2,75807965	3	3
230494_at	SLC20A1	2q13	2,75804180	3	3
220377_at	FAM30A	14q32.33	2,75780337	3	12
230075_at	RAB39B	Xq28	2,75561819	3	3
234485_at	LOC340947	10p11.1	2,75552788	3	7
204042_at	WASF3	13q12.13	2,75506124	3	4
204784_s_at	MLF1	3q25.32	2,75458524	3	3
1556929_at	PAPOLG	2p16.1	2,75424219	3	14
214715_x_at	ZNF160	19q13.41	2,75394319	3	6
217239_x_at	LOC100132941	14q32.33	2,75345489	3	10
227616_at	BCL9L	11q23.3	2,75320399	3	13
203507_at	CD68	17p13	2,75314448	3	3
1554679_a_at	LAPTM4B	8q22.1	2,75300777	3	6
237044_s_at	C10orf41	10q22.2	2,75299335	3	5
206429_at	F2RL1	5q13.3	2,75173808	3	3
240770_at	TMEM171	5q13.2	2,75165846	3	9
209731_at	NTHL1	16p13.3	2,75115236	3	6
219522_at	FJX1	11p13	2,75076486	3	5
218854_at	DSE	6q22.1	2,75041055	3	7
205309_at	SMPDL3B	1p35.3	2,75005097	3	4
211530_x_at	HLA-G	6p22.1	2,74923390	3	6
230363_s_at	INPP5F	10q26.11	2,74813942	3	3
225564_at	C1QTNF9	13q12.12	2,74786141	3	7
202565_s_at	SVIL	10p11.23	2,74758571	3	5
214930_at	SLITRK5	13q31.2	2,74751494	3	7
203879_at	PIK3CD	1p36.22	2,74715010	3	6
217963_s_at	NGFRAP1	Xq22.2	2,74674509	3	15
209906_at	C3AR1	12p13.31	2,74668710	3	9
201137_s_at	HLA-DPB1	6p21.32	2,74587285	3	9
232552_at	DAAM1	14q23.1	2,74562523	3	9
242109_at	SYTL3	6q25.3	2,74283038	3	6
228471_at	ANKRD44	2q33.1	2,74119858	3	3
221047_s_at	MARK1	1q41	2,74083755	3	6
232034_at	LOC203274	9q21.11	2,74052904	3	4
203952_at	ATF6	1q23.3	2,73988822	3	8
201785_at	RNASE1	14q11.2	2,73974781	3	3

209949_at	NCF2	1q25.3	2,73946675	3	9
200986_at	SERPING1	11q12.1	2,73921607	3	3
227846_at	GPR176	15q15.1	2,73914107	3	8
221558_s_at	LEF1	4q25	2,73883934	3	9
206571_s_at	MAP4K4	2q11.2	2,73818871	3	3
235562_at	C3orf70	3q27.2	2,73780888	3	3
230265_at	SEL1L	14q31.1	2,73773444	3	9
1557996_at	LOC100132832	7p13	2,73749798	3	3
208578_at	SCN10A	3p22.2	2,73636363	3	3
202766_s_at	FBN1	15q21.1	2,73602599	3	6
209680_s_at	KIFC1	6p21.32	2,73568795	3	3
228450_at	PLEKHA7	11p15.1	2,73562493	3	6
203126_at	IMPA2	18p11.21	2,73526453	3	6
238725_at	IRF1	5q31.1	2,73469272	3	6
228263_at	GRASP	12q13.13	2,73442459	3	4
201830_s_at	NET1	10p15.1	2,73405867	3	6
205531_s_at	GLS2	12q13.3	2,73344107	3	4
1555638_a_at	SAMSN1	21q11.2	2,73278553	3	3
1558747_at	SMCHD1	18p11.32	2,73261979	3	4
1558185_at	CLLU1	12q22	2,73244530	3	5
221119_at	FLJ20184	4q24	2,73243530	3	3
1556026_at	LOC100131434	Xq28	2,73234925	3	3
1555392_at	LOC100128868	7q31.2	2,73208471	3	7
202464_s_at	PFKFB3	10p15.1	2,73204924	3	10
236915_at	C4orf47	4q35.1	2,73168377	3	4
224991_at	CMIP	16q23.2	2,73041094	3	6
1560503_a_at	LOC100130275	6p24.3	2,72962463	3	5
205809_s_at	WASL	7q31.32	2,72906611	3	4
202651_at	LPGAT1	1q32.3	2,72830790	3	5
205774_at	F12	5q35.3	2,72740208	3	6
222868_s_at	IL18BP	11q13.4	2,72697398	3	9
202554_s_at	GSTM3	1p13.3	2,72671340	3	9
206674_at	FLT3	13q12.2	2,72654255	3	8
208820_at	PTK2	8q24.3	2,72653439	3	5
203215_s_at	MYO6	6q14.1	2,72649717	3	5
218500_at	C8orf55	8q24.3	2,72572501	3	3
209136_s_at	USP10	22q11.1	2,72570478	3	12
201292_at	TOP2A	17q21.2	2,72486139	3	11
203470_s_at	PLEK	2p14	2,72480735	3	6
205694_at	TYRP1	9p23	2,72461373	3	11
244419_at	FRZB	2q32.1	2,72456820	3	11
232767_at	CADM1	11q23.3	2,72418916	3	6
230637_at	SFXN4	10q26.11	2,72392521	3	4
204361_s_at	SKAP2	7p15.2	2,72380568	3	4
203060_s_at	PAPSS2	10q23.2	2,72341905	3	9
235328_at	PLXNC1	12q22	2,72296788	3	4
204182_s_at	ZBTB43	9q33.3	2,72207182	3	3
202878_s_at	CD93	20p11.21	2,72193270	3	5
203505_at	ABCA1	9q31.1	2,72167568	3	6
218644_at	PLEK2	14q23.3	2,72165146	3	3
229584_at	LRRK2	12q12	2,72109929	3	7
226076_s_at	MBD6	12q13.3	2,72098203	3	5
34210_at	CD52	1p36.11	2,72097686	3	9
1559966_a_at	LOC100192378	8q21.11	2,72094111	3	5

226430_at	RELL1	4p14	2,72061874	3	3
216392_s_at	SEC23IP	10q26.11	2,71985855	4	5
215992_s_at	RAPGEF2	4q32.1	2,71966009	4	7
230389_at	FNBP1	9q34.11	2,71936320	4	7
201792_at	AEBP1	7p13	2,71795829	4	8
215978_x_at	LOC152719	4p16.3	2,71790362	4	8
226189_at	ITGB8	7p21.1	2,71750086	4	7
202969_at	DYRK2	12q15	2,71745355	4	5
215490_at	C1orf69	1q42.13	2,71729110	4	3
213155_at	WSCD1	17p13.2	2,71616188	4	11
225595_at	CREBZF	11q14.1	2,71469642	4	3
1567213_at	PNN	14q21.1	2,71468061	4	3
218660_at	DYSF	2p13.2	2,71411858	4	3
231538_at	C11orf1	11q23.1	2,71358908	4	6
218554_s_at	ASH1L	1q22	2,71281756	4	3
219602_s_at	FAM38B	18p11.22	2,71250217	4	3
214038_at	CCL8	17q12	2,71031992	4	6
221581_s_at	LAT2	7q11.23	2,70943880	4	3
229693_at	TMEM220	17p13.1	2,70880676	4	4
211900_x_at	CD6	11q12.2	2,70822687	4	3
226218_at	IL7R	5p13.2	2,70802871	4	5
201743_at	CD14	5q31.3	2,70745009	4	13
225834_at	FAM72A	1q32.1	2,70732837	4	11
225955_at	METRNL	17q25.3	2,70691913	4	5
211590_x_at	TBXA2R	19p13.3	2,70609894	4	3
218066_at	SLC12A7	5p15.33	2,70501993	4	3
208937_s_at	ID1	20q11.21	2,70498203	4	3
203547_at	CD4	12p13.31	2,70490802	4	5
239012_at	RNF144B	6p22.3	2,70394587	4	17
32094_at	CHST3	10q22.1	2,70348988	4	3
206697_s_at	HP	16q22.2	2,70293736	4	4
210644_s_at	LAIR1	19q13.42	2,70265291	4	6
220646_s_at	KLRF1	12p13.31	2,70231711	4	13
242243_at	TMF1	3p14.1	2,70173630	4	3
216293_at	CLTA	9p13.3	2,70166838	4	3
217763_s_at	RAB31	18p11.22	2,70166729	4	3
242781_at	CXorf39	Xq22.2	2,70047384	4	3
210493_s_at	MFAP3L	4q33	2,70036621	4	8
208885_at	LCP1	13q14.13	2,70028912	4	6
204273_at	EDNRB	13q22.3	2,70007707	4	21
218700_s_at	RAB7L1	1q32.1	2,69988923	4	6
219882_at	TTLL7	1p31.1	2,69978139	4	4
219014_at	PLAC8	4q21.22	2,69950295	4	5
212829_at	PIP4K2A	10p12.2	2,69944017	4	8
227697_at	SOCS3	17q25.3	2,69913594	4	11
208511_at	PTTG3P	8q13.1	2,69738395	4	5
219895_at	FAM70A	Xq24	2,69710334	4	11
226707_at	NAPRT1	8q24.3	2,69709880	4	4
219954_s_at	GBA3	4p15.2	2,69665323	4	7
214469_at	HIST1H2AE	6p22.2	2,69593865	4	5
1555785_a_at	XRN1	3q23	2,69569721	4	5
212488_at	COL5A1	9q34.3	2,69546673	4	3
219855_at	NUDT11	Xp11.22	2,69533531	4	8
205638_at	BAI3	6q12	2,69532388	4	8

201670_s_at	MARCKS	6q21	2,69453598	4	3
221835_at	DTX3	12q13.3	2,69415949	4	4
213725_x_at	XYLT1	16p12.3	2,69385623	4	3
207828_s_at	CENPF	1q41	2,69340272	4	5
222304_x_at	OR7E47P	12q13.13	2,69326998	4	4
244165_at	C10orf18	10p15.1	2,69286349	4	7
212451_at	SECISBP2L	15q21.1	2,69264469	4	12
226702_at	CMPK2	2p25.2	2,69249643	4	3
36711_at	MAFF	22q13.1	2,69243998	4	8
222541_at	RSF1	11q14.1	2,69206685	4	4
215888_at	PDS5B	13q13.1	2,69203520	4	8
200917_s_at	SRPR	11q24.2	2,69195368	4	11
202859_x_at	IL8	4q13.3	2,69142874	4	12
209211_at	KLF5	13q22.1	2,69039911	4	6
228323_at	CASC5	15q15.1	2,69015126	4	7
203418_at	CCNA2	4q27	2,69002810	4	3
244443_at	CHD2	15q26.1	2,68993912	4	5
213900_at	FAM189A2	9q21.12	2,68991955	4	3
218692_at	GOLSYN	8q23.2	2,68803726	4	5
203585_at	ZNF185	Xq28	2,68731310	4	6
223229_at	UBE2T	1q32.1	2,68727405	4	6
204908_s_at	BCL3	19q13.32	2,68626685	4	6
202147_s_at	IFRD1	7q31.1	2,68574171	4	3
217234_s_at	EZR	6q25.3	2,68547834	4	6
222279_at	RP3-377H14.5	6p22.1	2,68533130	4	3
227016_at	ERICH1	8p23.3	2,68521643	4	3
214608_s_at	EYA1	8q13.3	2,68465005	4	5
219040_at	CORO7	16p13.3	2,68381898	4	6
217602_at	PPIA	7p13	2,68352856	4	3
1563808_at	MCF2L	13q34	2,68274800	4	5
216086_at	SV2C	5q13.3	2,68203835	4	11
208322_s_at	ST3GAL1	8q24.22	2,68182739	4	7
226644_at	MIB2	1p36.33	2,68150036	4	3
227202_at	CNTN1	12q12	2,68092501	4	11
238935_at	RPS27L	15q22.2	2,68090486	4	4
204686_at	IRS1	2q36.3	2,68052623	4	7
209773_s_at	RRM2	2p25.1	2,68048843	4	5
1560916_a_at	DPY19L1	7p14.2	2,67970716	4	4
1552306_at	ALG10	12p11.1	2,67963856	4	7
232897_at	FLJ20444	9q21.11	2,67924914	4	5
202643_s_at	TNFAIP3	6q23.3	2,67908283	4	9
205557_at	BPI	20q11.23	2,67806539	4	12
207703_at	NLGN4Y	Yq11.221	2,67671306	4	3
227145_at	LOXL4	10q24.2	2,67649527	4	6
210325_at	CD1A	1q23.1	2,67649299	4	4
216779_at	CYLC1	Xq21.1	2,67577077	4	4
219990_at	E2F8	11p15.1	2,67475873	4	3
243534_at	CC2D2B	10q24.1	2,67436009	4	5
1556499_s_at	COL1A1	17q21.33	2,67405921	4	5
222077_s_at	RACGAP1	12q13.12	2,67398585	4	6
210450_at	LOC90925	14q32.33	2,67387714	4	6
208268_at	ADAM28	8p21.2	2,67383974	4	7
214958_s_at	TMC6	17q25.3	2,67379450	4	10
228943_at	MAP6	11q13.5	2,67309595	4	6

203749_s_at	RARA	17q21.2	2,67146158	4	9
237230_at	GPHA2	11q13.1	2,67107444	4	4
242292_at	CXorf50B	Xq13.2	2,66988986	4	5
218880_at	FOSL2	2p23.2	2,66911712	4	4
204146_at	RAD51AP1	12p13.32	2,66827933	4	7
229396_at	OVOL1	11q13.1	2,66729450	4	7
225846_at	ESRP1	8q22.1	2,66726365	4	18
228284_at	TLE1	9q21.32	2,66644108	4	5
223278_at	GJB2	13q12.11	2,66628316	4	6
228593_at	MTMR9L	1p35.1	2,66622381	4	3
219327_s_at	GPRC5C	17q25.1	2,66619010	4	4
212820_at	DMXL2	15q21.2	2,66514904	4	6
209459_s_at	ABAT	16p13.2	2,66460804	4	3
241844_x_at	TMEM156	4p14	2,66425568	4	4
204962_s_at	CENPA	2p23.3	2,66420068	4	8
201259_s_at	SYPL1	7q22.3	2,66411536	4	5
236561_at	TGFBR1	9q22.33	2,66395154	4	8
217559_at	RPL10L	14q21.2	2,66387447	4	3
225337_at	ABHD2	15q26.1	2,66364136	4	9
228407_at	SCUBE3	6p21.31	2,66297436	4	4
223950_s_at	FLYWCH1	16p13.3	2,66185092	4	3
242916_at	CEP110	9q33.2	2,66035581	4	3
1558759_s_at	CLASP2	3p22.3	2,66033704	4	8
230052_s_at	NFKBID	19q13.12	2,66006525	4	7
205082_s_at	AOX1	2q33.1	2,66000599	4	3
227834_at	TXLNB	6q24.1	2,65940740	4	7
210641_at	CAPN9	1q42.2	2,65923682	4	3
220421_at	BTNL8	5q35.3	2,65877273	4	8
202619_s_at	PLOD2	3q24	2,65805907	4	4
223740_at	C6orf59	6q26	2,65799283	4	3
242765_at	MOBP	3p22.1	2,65784682	4	3
213280_at	GARNL4	17p13.3	2,65783089	4	3
41386_i_at	KDM6B	17p13.1	2,65751774	4	10
219947_at	CLEC4A	12p13.31	2,65709864	4	6
236463_at	ADAD2	16q24.1	2,65699615	4	3
206762_at	KCNA5	12p13.32	2,65683750	4	12
204999_s_at	ATF5	19q13.33	2,65673222	4	5
231779_at	IRAK2	3p25.3	2,65494434	4	5
225688_s_at	PHLDB2	3q13.2	2,65452139	4	9
203959_s_at	ZBTB40	1p36.12	2,65435054	4	6
206991_s_at	CCR5	3p21.31	2,65411904	4	20
210180_s_at	TRA2B	3q27.2	2,65328401	4	5
212993_at	NACC2	9q34.3	2,65325531	4	7
219566_at	PLEKHF1	19q12	2,65240810	4	3
1569132_s_at	ARSK	5q15	2,64947213	4	7
206805_at	SEMA3A	7q21.11	2,64945197	4	4
221690_s_at	NLRP2	19q13.42	2,64917218	4	8
243198_at	TEX9	15q21.3	2,64916444	4	7
242918_at	NASP	1p34.1	2,64884460	4	5
221087_s_at	APOL3	22q12.3	2,64796563	4	5
226499_at	NRARP	9q34.3	2,64713956	4	4
239533_at	GPR155	2q31.1	2,64644082	4	3
232352_at	ISL2	15q24.3	2,64532177	4	4
242282_at	ZFPM1	16q24.2	2,64512919	4	4

209621_s_at	PDLIM3	4q35.1	2,64324695	4	9
204760_s_at	NR1D1	17q21.1	2,64275054	4	6
226403_at	TMC4	19q13.42	2,64272031	4	6
204115_at	GNG11	7q21.3	2,64232231	4	17
238063_at	TMEM154	4q31.3	2,64176526	4	6
216804_s_at	PDLIM5	4q22.3	2,64111115	4	3
31874_at	GAS2L1	22q12.2	2,64108238	4	5
216401_x_at	LOC652493	2p11.2	2,64018120	4	15
244166_at	APLN	Xq26.1	2,64002526	4	5
224973_at	FAM46A	6q14.1	2,63950408	4	5
219352_at	HERC6	4q22.1	2,63905433	4	4
220615_s_at	FAR2	12p11.22	2,63897860	4	3
1554212_s_at	KCNS2	8q22.2	2,63890754	4	3
225102_at	MGLL	3q21.3	2,63857604	4	7
242903_at	IFNGR1	6q23.3	2,63855359	4	9
225380_at	SGK493	2p21	2,63850848	4	3
206928_at	ZNF124	1q44	2,63816121	4	11
215767_at	ZNF804A	2q32.1	2,63713396	4	4
206160_at	APOBEC2	6p21.1	2,63708276	4	4
202704_at	TOB1	17q21.33	2,63672902	4	8
213358_at	KIAA0802	18p11.22	2,63623410	4	8
213407_at	PHLPP2	16q22.2	2,63603009	4	8
215203_at	GOLGA4	3p22.2	2,63460231	4	12
235009_at	BOD1L	4p15.33	2,63369275	4	5
201843_s_at	EFEMP1	2p16.1	2,63359905	4	17
219697_at	HS3ST2	16p12.2	2,63260735	4	4
1569020_at	NEDD9	6p24.2	2,63215148	4	3
210978_s_at	TAGLN2	1q23.2	2,63213018	4	7
1557078_at	SLFN5	17q12	2,63199330	4	3
205456_at	CD3E	11q23.3	2,63187678	4	4
1559975_at	BTG1	12q21.33	2,63147914	4	11
205120_s_at	SGCB	4q12	2,63046286	4	16
203998_s_at	SYT1	12q21.2	2,63024216	4	8
202075_s_at	PLTP	20q13.12	2,62987379	4	8
1559127_x_at	RRP12	10q24.1	2,62958779	4	6
204897_at	PTGER4	5p13.1	2,62923385	4	4
232395_x_at	AGBL3	7q33	2,62918687	4	6
1557450_s_at	WHAMML2	15q11.2	2,62707872	4	3
37462_i_at	SF3A2	19p13.3	2,62642726	4	3
237654_at	C14orf50	14q23.3	2,62547412	4	4
207980_s_at	CITED2	6q24.1	2,62464862	4	5
218717_s_at	LEPREL1	3q28	2,62427650	4	7
218417_s_at	SLC48A1	12q13.11	2,62382690	4	3
206985_at	HSD17B3	9q22.32	2,62378163	4	3
214239_x_at	PCGF2	17q12	2,62376050	4	3
232542_at	COL9A2	1p34.2	2,62370596	4	4
215342_s_at	RABGAP1L	1q25.1	2,62358296	4	6
206954_at	WIT1	11p13	2,62271675	4	3
226433_at	RNF157	17q25.1	2,62221422	4	6
204612_at	PKIA	8q21.12	2,62220449	4	7
209696_at	FBP1	9q22.32	2,62126950	4	6
203441_s_at	CDH2	18q12.1	2,62089108	4	5
219820_at	SLC6A16	19q13.33	2,62078211	4	4
200878_at	EPAS1	2p21	2,62053742	4	4

232597_x_at	SFRS2IP	12q12	2,61983538	4	16
228898_s_at	SMARCB1	22q11.23	2,61895332	4	7
1560921_at	ZNF169	9q22.32	2,61864717	4	6
236621_at	RPS27	1q32.1	2,61778851	4	6
1552316_a_at	GIMAP1	7q36.1	2,61717366	4	8
227281_at	SLC29A4	7p22.1	2,61654992	4	3
214097_at	RPS21	20q13.33	2,61512756	4	5
1561403_at	SOHLH1	9q34.3	2,61475267	4	9
228245_s_at	OVOS	12p11.21	2,61452520	4	10
220918_at	C21orf96	21q22.12	2,61448181	4	6
238908_at	CALU	7q32.1	2,61445281	4	5
225792_at	HOOK1	1p32.1	2,61427317	4	3
205072_s_at	XRCC4	5q14.2	2,61413791	4	10
224374_s_at	EMILIN2	18p11.32	2,61378990	4	6
1558220_at	MUC20	3q29	2,61269370	4	3
229872_s_at	LOC100132999	1q21.1	2,61235700	4	11
215518_at	STXBP5L	3q13.33	2,61183935	4	3
228401_at	ATAD2	8q24.13	2,61164547	4	5
1569935_at	ZNF664	12q24.31	2,61143546	4	3
48030_i_at	C5orf4	5q33.2	2,61122890	4	6
212750_at	PPP1R16B	20q11.23	2,61122124	4	3
212561_at	DENND5A	11p15.4	2,61047778	4	3
212187_x_at	PTGDS	9q34.3	2,61030294	4	3
214767_s_at	HSPB6	19q13.12	2,60935115	4	4
207165_at	HMMR	5q34	2,60920298	4	7
218718_at	PDGFC	4q32.1	2,60894322	4	8
205871_at	PLGLA	2q12.2	2,60820719	4	3
231931_at	PRDM15	21q22.3	2,60811730	4	5
1569642_at	F2R	5q13.3	2,60798729	4	4
241233_x_at	C21orf81	21q11.2	2,60784524	4	4
204545_at	PEX6	6p21.1	2,60762098	4	3
219377_at	FAM59A	18q12.1	2,60757641	4	5
203386_at	TBC1D4	13q22.2	2,60743172	4	3
205124_at	OC729991-MEF2	19p13.11	2,60742727	4	8
235590_at	FAM178A	10q24.31	2,60696650	4	3
215176_x_at	LOC100291464	2p11.2	2,60653086	4	3
221606_s_at	NSBP1	Xq21.1	2,60540606	4	3
205464_at	SCNN1B	16p12.2	2,60515671	4	4
204239_s_at	NNAT	20q11.23	2,60377321	4	4
217264_s_at	SCNN1A	12p13.31	2,60357735	4	3
215771_x_at	RET	10q11.21	2,60317642	4	3
219330_at	VANGL1	1p13.1	2,60280278	4	3
220727_at	KCNK10	14q31.3	2,60279036	4	3
225540_at	MAP2	2q34	2,60266929	4	4
219622_at	RAB20	13q34	2,60248193	4	7
238787_at	DENND1B	1q31.3	2,60209758	4	6
216535_at	CADM3	1q23.2	2,60189568	4	4
203496_s_at	MED1	17q12	2,60176910	4	4
214642_x_at	MAGEA5	Xq28	2,60073386	4	10
202503_s_at	KIAA0101	15q22.31	2,59961904	4	7
232475_at	C15orf42	15q26.1	2,59921829	4	3
221680_s_at	ETV7	6p21.31	2,59921303	4	5
227217_at	WNK2	9q22.31	2,59904043	4	3
219593_at	SLC15A3	11q12.2	2,59902374	4	3

234496_x_at	NYX	Xp11.4	2,59809458	4	5
235358_at	LOC728485	19q13.12	2,59793929	4	4
236957_at	CDCA2	8p21.2	2,59790174	4	5
1553241_at	NKAIN3	8q12.3	2,59747720	4	6
1555868_at	LOC729070	6q24.1	2,59720324	4	3
226438_at	SNTB1	8q24.12	2,59606140	4	7
1557056_at	C5orf47	5q35.2	2,59594829	4	3
238593_at	C11orf80	11q13.2	2,59519738	4	7
229628_s_at	KIAA1529	9q22.33	2,59481757	4	4
60794_f_at	ZNF814	19q13.43	2,59467100	4	3
235879_at	MBNL1	3q25.1	2,59348392	4	7
208003_s_at	NFAT5	16q22.1	2,59189017	4	7
229570_at	LAMA5	20q13.33	2,59149052	4	5
223794_at	ARMC4	10p12.1	2,59115876	4	9
226349_at	C12orf45	12q23.3	2,58984903	4	6
229707_at	ZNF606	19q13.43	2,58969061	4	3
211597_s_at	HOPX	4q12	2,58948524	4	14
217757_at	A2M	12p13.31	2,58945628	4	7
224002_s_at	FKBP7	2q31.2	2,58874845	4	8
219555_s_at	CENPN	16q23.2	2,58829720	4	4
213716_s_at	SECTM1	17q25.3	2,58790206	4	7
230559_x_at	FGD4	12p11.21	2,58694019	4	12
218355_at	KIF4A	Xq13.1	2,58678512	4	4
1562403_a_at	SLC8A3	14q24.2	2,58664655	4	4
201170_s_at	BHLHE40	3p26.1	2,58608571	4	8
215554_at	GPLD1	6p22.3	2,58603280	4	3
1562778_at	FAM166A	9q34.3	2,58506768	4	5
210298_x_at	FHL1	Xq26.3	2,58347921	4	3
241601_at	WIPF3	7p14.3	2,58327941	4	7
210925_at	CIITA	16p13.13	2,58309825	4	6
215017_s_at	FNBP1L	1p22.1	2,58278972	4	3
206178_at	PLA2G5	1p36.13	2,58268328	4	3
204724_s_at	COL9A3	20q13.33	2,58208959	4	6
206150_at	CD27	12p13.31	2,58202133	4	6
242517_at	KISS1R	19p13.3	2,58163266	4	10
1552872_at	NCRNA00105	Xp22.33	2,58154843	4	3
228360_at	LYPD6B	2q23.1	2,58127096	4	4
226809_at	LOC100216479	2q21.1	2,58093272	4	8
209109_s_at	TSPAN6	Xq22.1	2,58058243	4	5
204444_at	KIF11	10q23.33	2,58043631	4	5
211499_s_at	MAPK11	22q13.33	2,58036013	4	7
209305_s_at	GADD45B	19p13.3	2,58017914	4	9
207111_at	EMR1	19p13.3	2,58007697	4	4
203865_s_at	ADARB1	21q22.3	2,58000741	4	3
222746_s_at	BSPRY	9q32	2,57986949	4	4
235469_at	FAM133B	2q24.1	2,57956648	4	4
219195_at	PPARGC1A	4p15.2	2,57865387	4	4
223514_at	CARD11	7p22.2	2,57804207	4	6
235461_at	TET2	4q24	2,57798243	4	7
212122_at	RHOQ	2p21	2,57764048	4	5
1553114_a_at	PTK6	20q13.33	2,57613455	4	8
228645_at	SNHG9	16p13.3	2,57593286	4	3
234917_at	MARVELD1	10q24.2	2,57449970	4	7
206271_at	TLR3	4q35.1	2,57335875	4	7

1553972_a_at	CBS	21q22.3	2,57296890	4	3
223709_s_at	WNT10A	2q35	2,57252958	4	5
205352_at	SERPINI1	3q26.1	2,57149606	4	6
204168_at	MGST2	4q31.1	2,57049900	4	6
1570571_at	CCDC91	12p11.22	2,56972378	4	8
212446_s_at	LASS6	2q24.3	2,56903242	4	3
201927_s_at	PKP4	2q24.1	2,56898311	4	3
212186_at	ACACA	17q12	2,56838469	4	3
206102_at	GINS1	20p11.21	2,56836040	4	7
204058_at	ME1	6q14.2	2,56831610	4	7
217738_at	NAMPT	10p11.21	2,56802384	4	5
230673_at	PKHD1L1	8q23.1	2,56787581	4	3
214814_at	YTHDC1	4q13.2	2,56717535	4	5
205483_s_at	ISG15	1p36.33	2,56688397	4	11
1569679_at	CDH22	20q13.12	2,56679534	4	5
244700_at	SEC61B	9q22.33	2,56675853	4	8
221908_at	RNFT2	12q24.22	2,56611350	4	5
202440_s_at	ST5	11p15.4	2,56545843	4	6
200935_at	CALR	19p13.2	2,56532995	4	5
224847_at	CDK6	7q21.2	2,56527992	4	6
209897_s_at	SLIT2	4p15.31	2,56495202	4	7
1562731_s_at	MDS2	1p36.11	2,56491760	4	4
230788_at	GCNT2	6p24.3	2,56471902	4	9
204766_s_at	NUDT1	7p22.3	2,56413776	4	3
215887_at	ZNF277	7q31.1	2,56409537	4	6
224916_at	TMEM173	5q31.2	2,56361949	4	3
238811_at	ATP11B	3q26.33	2,56343593	4	7
202870_s_at	CDC20	1p34.2	2,56329688	4	5
218546_at	C1orf115	1q41	2,56305464	4	3
217027_x_at	KPNB1	17q21.32	2,56169689	4	4
1563497_at	USP25	21q21.1	2,56137804	4	12
239743_at	SP8	7p21.1	2,56119104	4	3
204032_at	BCAR3	1p22.1	2,56057033	4	3
201195_s_at	SLC7A5	16q24.2	2,56039753	4	7
222848_at	CENPK	5q12.3	2,55997493	4	7
237367_x_at	CFLAR	2q33.1	2,55883434	4	9
222309_at	C6orf62	6p22.3	2,55761218	4	3
213348_at	CDKN1C	11p15.4	2,55698764	4	5
239720_at	GLP-1	19p13.2	2,55679793	4	3
227909_at	NCRNA00086	Xq26.3	2,55595182	4	6
235228_at	CCDC85A	2p16.1	2,55497645	4	5
203498_at	RCAN2	6p12.3	2,55472262	4	3
1553205_at	C20orf200	20q13.33	2,55405659	4	4
232098_at	DST	6p12.1	2,55347882	4	4
219667_s_at	BANK1	4q24	2,55142314	4	3
213742_at	SFRS11	1p31.1	2,55101600	4	3
207957_s_at	PRKCB	16p12.2	2,55056163	4	3
206229_x_at	PAX2	10q24.31	2,55021009	4	3
235160_at	ATF7	12q13.13	2,54966244	4	4
201028_s_at	CD99	Xp22.33	2,54867776	4	8
231874_at	FAM126B	2q33.1	2,54841848	4	3
1559587_at	SYMPK	19q13.32	2,54822045	4	12
209642_at	BUB1	2q13	2,54817931	4	8
222380_s_at	PDCD6	5p15.33	2,54780190	4	3

228749_at	ZDBF2	2q33.3	2,54717175	4	7
205194_at	PSPH	7p11.2	2,54695576	4	4
240280_at	UFSP1	7q22.1	2,54675397	4	3
1552426_a_at	TM2D3	15q26.3	2,54668830	4	4
243759_at	SFRS15	21q22.11	2,54616962	4	3
236645_at	HBP1	7q22.3	2,54601122	4	5
230465_at	HS2ST1	1p22.3	2,54568141	4	6
219493_at	SHCBP1	16q11.2	2,54519171	4	5
232489_at	CCDC76	1p21.2	2,54516792	4	5
1562772_a_at	DAND5	19p13.2	2,54447026	4	6
208944_at	TGFBR2	3p24.1	2,54441390	4	3
226875_at	DOCK11	Xq24	2,54441021	4	3
226846_at	PHYHD1	9q34.11	2,54435178	4	12
203045_at	NINJ1	9q22.31	2,54379238	4	4
224553_s_at	TNFRSF18	1p36.33	2,54344868	4	4
243589_at	KIAA1267	17q21.31	2,54343817	4	9
220565_at	CCR10	17q21.2	2,54341830	4	14
232865_at	AFF4	5q31.1	2,54341601	4	9
235763_at	SLC44A5	1p31.1	2,54240168	4	5
205225_at	ESR1	6q25.1	2,54198654	4	8
214290_s_at	HIST2H2AA3	1q21.2	2,54054555	4	5
229597_s_at	WDFY4	10q11.23	2,54050220	4	4
225701_at	AKNA	9q32	2,54011145	4	4
219545_at	KCTD14	11q14.1	2,54007695	4	18
203302_at	DCK	4q13.3	2,53987526	4	5
233595_at	USP34	2p15	2,53987037	4	11
207992_s_at	AMPD3	11p15.4	2,53982274	4	4
227715_at	LOC100132288	Yq11.21	2,53974881	4	3
1556608_a_at	EHD4	15q15.1	2,53956918	4	6
209383_at	DDIT3	12q13.3	2,53821240	4	7
1553708_at	MGC16075	7p12.3	2,53808064	4	3
226404_at	LOC643167	20q11.22	2,53781294	4	4
205051_s_at	KIT	4q12	2,53660143	4	6
224972_at	ROMO1	20q11.22	2,53647693	4	8
1553288_a_at	C7orf51	7q22.1	2,53618988	4	3
227353_at	TMC8	17q25.3	2,53572775	4	12
205236_x_at	SOD3	4p15.2	2,53482807	4	3
230425_at	EPHB1	3q22.2	2,53428408	4	10
205909_at	POLE2	14q21.3	2,53381354	4	4
222873_s_at	EHMT1	9q34.3	2,53339153	4	5
208700_s_at	TKT	3p21.1	2,53316500	4	6
1554999_at	RASGEF1B	4q21.21	2,53268157	4	4
1556277_a_at	PAPD4	5q14.1	2,53205661	4	8
218862_at	ASB13	10p15.1	2,53156873	4	6
204817_at	ESPL1	12q13.13	2,53140397	4	4
224767_at	RPL37	5p13.1	2,53128017	4	4
204822_at	TTK	6q14.1	2,53069195	4	4
239757_at	ZFAND6	9p13.3	2,53054629	4	14
228678_at	FAM116B	22q13.33	2,52859203	4	3
205902_at	KCNN3	1q21.3	2,52840572	4	4
201795_at	LBR	1q42.12	2,52812274	4	6
221555_x_at	CDC14B	9q22.33	2,52791526	4	4
227684_at	S1PR2	19p13.2	2,52720679	4	6
217207_s_at	BTNL3	5q35.3	2,52711113	4	4

1567069_at	OR4D1	17q22	2,52680715	4	5
240375_at	PIGV	1p36.11	2,52628856	4	4
229787_s_at	OGT	Xq13.1	2,52611458	4	3
201278_at	DAB2	5p13.1	2,52569725	4	10
1556291_at	POM121L12	7p12.1	2,52557138	4	9
1557458_s_at	SHB	9p13.1	2,52550833	4	4
226837_at	SPRED1	15q14	2,52471304	4	8
223704_s_at	DMRT2	9p24.3	2,52438057	4	13
1560762_at	LOC285972	7q36.1	2,52422843	4	3
1558345_a_at	LOC439911	10q11.21	2,52327402	4	4
227743_at	MYO15B	17q25.1	2,52240454	4	6
1554117_at	CCDC60	12q24.23	2,52237016	4	4
210577_at	CASR	3q21.1	2,52187250	4	3
242280_x_at	CPEB4	5q35.2	2,52096339	4	7
212611_at	DTX4	11q12.1	2,52036388	4	3
236009_at	PERP	6q23.3	2,51984840	4	3
235128_at	SYNPO	5q33.1	2,51909595	4	8
213587_s_at	ATP6V0E2	7q36.1	2,51895258	4	5
200632_s_at	NDRG1	8q24.22	2,51850886	4	5
206170_at	ADRB2	5q32	2,51833712	4	5
214481_at	HIST1H2AM	6p22	2,51785543	4	7
1555697_at	KLK4	19q13.41	2,51728337	4	3
1552657_a_at	TXNDC2	18p11.22	2,51707015	4	3
232551_at	SLC26A6	3p21.31	2,51698825	4	5
234829_at	C20orf57	20q11.21	2,51679770	4	4
203324_s_at	CAV2	7q31.2	2,51665052	4	4
232138_at	MBNL2	13q32.1	2,51661474	4	4
219474_at	C3orf52	3q13.2	2,51603786	4	7
229389_at	ATG16L2	11q13.4	2,51589260	4	6
218755_at	KIF20A	5q31.2	2,51556025	4	3
222680_s_at	DTL	1q32.3	2,51441169	4	7
235471_at	C10orf72	10q11.23	2,51415651	4	3
229082_at	CCDC125	5q13.2	2,51412070	4	3
244120_at	LOC340178	6q27	2,51380425	4	3
1564229_at	LOC729173	11q23.3	2,51375286	4	4
205222_at	EHHADH	3q27.2	2,51339075	4	4
206609_at	MAGEC1	Xq27.2	2,51328380	4	4
213061_s_at	NTAN1	16p13.11	2,51269404	4	7
222347_at	LOC644450	21q11.1	2,51236570	4	3
224355_s_at	MS4A8B	11q12.2	2,51143223	4	7
215789_s_at	AJAP1	1p36.32	2,51135256	4	5
1553166_at	CDH24	14q11.2	2,51071038	4	4
201897_s_at	CKS1B	1q21.2	2,51064009	4	6
1554762_a_at	WWC2	4q35.1	2,51015140	4	3
203397_s_at	GALNT3	2q24.3	2,50977519	4	4
58780_s_at	FLJ10357	14q11.2	2,50971337	4	5
202967_at	GSTA4	6p12.2	2,50925566	4	3
217078_s_at	CD300A	17q25.1	2,50837700	4	9
220520_s_at	NUP62CL	Xq22.3	2,50825491	4	3
215565_at	LOC100289053	2p23.3	2,50798940	4	4
226991_at	NFATC2	20q13.2	2,50787971	4	4
210908_s_at	PFDN5	12q13.13	2,50776831	4	6
222293_at	CADM4	19q13.31	2,50770482	4	3
211962_s_at	ZFP36L1	14q24.1	2,50767401	4	4

207509_s_at	LAIR2	19q13.42	2,50745188	4	3
225698_at	C5orf26	5q22.1	2,50691132	4	4
202890_at	MAP7	6q23.3	2,50674515	4	3
204368_at	SLCO2A1	3q22.2	2,50567542	4	4
214750_at	PLAC4	21q22.2	2,50566018	4	12
234775_at	OR51B5	11p15.4	2,50546833	4	5
222608_s_at	ANLN	7p14.2	2,50477660	4	5
243835_at	ZDHHC21	9p22.3	2,50426853	4	4
209184_s_at	IRS2	13q34	2,50304719	4	5
208180_s_at	HIST1H4H	6p22.2	2,50282543	4	10
204647_at	HOMER3	19p13.11	2,50263774	4	3
1557239_at	BBX	3q13.12	2,50255442	4	7
239481_at	FAM133A	Xq21.32	2,50191296	4	3
225189_s_at	RAPH1	2q33.2	2,50129547	4	6
201141_at	GPNMB	7p15.3	2,50000217	4	7
1557867_s_at	C9orf117	9q34.11	2,49999954	4	4
202589_at	TYMS	18p11.32	2,49945222	4	5
221765_at	UGCG	9q31.3	2,49930993	4	5
204352_at	TRAF5	1q32.2	2,49928914	4	4
205821_at	KLRK1	12p13.2	2,49727760	4	6
202086_at	MX1	21q22.3	2,49657086	4	3
230848_s_at	MGA	15q15.1	2,49652559	4	3
231210_at	C11orf85	11q13.1	2,49633745	4	4
219464_at	CA14	1q21.2	2,49552828	4	3
244110_at	MLL	11q23.3	2,49526147	4	3
200934_at	DEK	6p22.3	2,49524073	4	6
218789_s_at	C11orf71	11q23.2	2,49510263	4	7
218810_at	ZC3H12A	1p34.3	2,49499423	4	7
218224_at	PNMA1	14q24.3	2,49322871	4	4
1557756_a_at	C14orf145	14q31.1	2,49283463	4	6
1562892_at	CHCHD5	2q13	2,49222114	4	4
201203_s_at	RRBP1	20p12.1	2,49162473	4	6
211518_s_at	BMP4	14q22.2	2,49150607	4	7
229581_at	ELFN1	7p22.3	2,49134734	4	4
228372_at	C10orf128	10q11.23	2,49134118	4	10
1557166_at	PDCD4	10q25.2	2,49132818	4	8
206225_at	ZNF507	19q13.11	2,49122996	4	3
212338_at	MYO1D	17q11.2	2,48955978	5	5
231548_at	FOXO3	6q21	2,48908272	5	5
220575_at	FAM106A	17p11.2	2,48908172	5	7
207184_at	SLC6A13	12p13.33	2,48905072	5	3
1560278_at	LOC221122	11p11.2	2,48891628	5	4
224964_s_at	GNG2	14q22.1	2,48755404	5	7
231119_at	RFC3	13q13.2	2,48624027	5	4
205975_s_at	HOXD1	2q31.1	2,48566936	5	5
208893_s_at	DUSP6	12q21.33	2,48492865	5	3
208158_s_at	OSBPL1A	18q11.2	2,48395046	5	9
239742_at	TULP4	6q25.3	2,48330225	5	8
231866_at	LNPEP	5q15	2,48284178	5	6
206461_x_at	MT1H	16q13	2,48096688	5	9
236007_at	AKAP10	17p11.2	2,48089911	5	3
205259_at	NR3C2	4q31.23	2,48025808	5	3
202247_s_at	MTA1	14q32.33	2,47956901	5	6
220304_s_at	CNGB3	8q21.3	2,47857633	5	4

214713_at	YLPM1	14q24.3	2,47748432	5	4
242828_at	FIGN	2q24.3	2,47744059	5	10
219429_at	FA2H	16q23.1	2,47678944	5	5
205156_s_at	ACCN2	12q13.12	2,47625530	5	9
212179_at	SFRS18	6q16.2	2,47606300	5	3
201465_s_at	JUN	1p32.1	2,47599237	5	7
235154_at	TAF3	10p14	2,47522289	5	5
235048_at	FAM169A	5q13.3	2,47521201	5	7
228790_at	FAM110B	8q12.1	2,47416571	5	3
226961_at	PRR15	7p14.3	2,47404619	5	3
221979_at	LOC100129250	9p21.1	2,47371557	5	5
225904_at	C1orf96	1q42.13	2,47361149	5	10
208782_at	FSTL1	3q13.33	2,47315976	5	3
216383_at	RPL18A	19p13.11	2,47211343	5	4
210136_at	MBP	18q23	2,47182267	5	7
202338_at	TK1	17q25.3	2,47157890	5	5
229019_at	ZNF385B	2q31.3	2,47107489	5	8
1555870_at	RNF207	1p36.31	2,47034143	5	4
236930_at	NUMB	14q24.3	2,46961270	5	4
223809_at	RGS18	1q31.2	2,46860161	5	7
219306_at	KIF15	3p21.31	2,46835196	5	5
230236_at	TDRG1	6p21.2	2,46813480	5	6
1558327_at	ZDHHC18	1p36.11	2,46763471	5	4
221024_s_at	SLC2A10	20q13.12	2,46747721	5	10
1552899_at	RP4-662A9.2	6q23.2	2,46691397	5	6
228646_at	PPP1R1C	2q31.3	2,46610033	5	3
224560_at	TIMP2	17q25.3	2,46570512	5	6
213556_at	LOC390940	19q13.31	2,46567898	5	4
208498_s_at	AMY1A	1p21.1	2,46491265	5	3
236026_at	GPATCH2	1q41	2,46410281	5	4
217080_s_at	HOMER2	15q25.2	2,46300378	5	4
210109_at	C7orf54	7q32.1	2,46227629	5	6
203710_at	ITPR1	3p26.1	2,46050375	5	8
1558855_at	FARP2	2q37.3	2,46010260	5	4
230608_at	C1orf182	1q22	2,45951948	5	4
209880_s_at	SELPLG	12q24.11	2,45937855	5	3
234562_x_at	LOC728678	3p22.3	2,45923979	5	4
208439_s_at	FCN2	9q34.3	2,45886273	5	3
212044_s_at	RPL27A	6q25.2	2,45745041	5	11
234956_at	LOC93444	15q22.32	2,45660670	5	4
228781_at	OBFC1	10q24.33	2,45656561	5	3
214354_x_at	SFTPB	2p11.2	2,45616881	5	5
205514_at	ZNF415	19q13.42	2,45596433	5	5
223355_at	ALG1	16p13.3	2,45582122	5	7
213222_at	PLCB1	20p12.3	2,45576321	5	13
208092_s_at	FAM49A	2p24.2	2,45561408	5	7
214313_s_at	EIF5B	2q11.2	2,45492030	5	6
238732_at	COL24A1	1p22.3	2,45475698	5	3
227396_at	PTPRJ	11p11.2	2,45413687	5	7
209946_at	VEGFC	4q34.3	2,45373827	5	6
1558120_at	DDX3X	Xp11.4	2,45292558	5	8
214753_at	N4BP2L2	13q13.1	2,45258949	5	8
240890_at	LOC643733	11q22.3	2,45183598	5	5
210983_s_at	MCM7	7q22.1	2,45160967	5	5

231004_s_at	H1FX	3q21.3	2,45143741	5	9
210475_at	POU3F1	1p34.3	2,45129908	5	3
203151_at	MAP1A	15q15.3	2,45126529	5	3
238239_at	WDR27	6q27	2,45126035	5	4
202786_at	STK39	2q24.3	2,45123785	5	3
209959_at	NR4A3	9q22.33	2,45120947	5	11
220850_at	MORC1	3q13.13	2,45111559	5	3
225738_at	RAPGEF1	9q34.13	2,45110315	5	7
223513_at	CENPJ	13q12.12	2,45077266	5	3
223655_at	CD163L1	12p13.31	2,45063171	5	7
1554003_at	RGNEF	5q13.2	2,44973905	5	3
210244_at	CAMP	3p21.31	2,44933089	5	10
204415_at	IFI6	1p36.11	2,44916521	5	4
1552719_at	CASC4	15q15.3	2,44878847	5	5
229499_at	CAPN13	2p23.1	2,44873599	5	3
222831_at	SAP30L	5q33.2	2,44624096	5	4
221756_at	PIK3IP1	22q12.2	2,44612146	5	4
231904_at	U2AF1	21q22.3	2,44596744	5	7
212845_at	SAMD4A	14q22.2	2,44592011	5	4
1562002_at	MYOZ3	5q33.1	2,44542316	5	8
232531_at	EMX2OS	10q26.11	2,44504780	5	4
210040_at	SLC12A5	20q13.12	2,44486553	5	4
227350_at	HELLS	10q23.33	2,44480517	5	6
232181_at	LOC153346	5q32	2,44367655	5	5
209735_at	ABCG2	4q22.1	2,44328054	5	3
204790_at	SMAD7	18q21.1	2,44261308	5	10
227186_s_at	MRPL41	9q34.3	2,44260932	5	4
204621_s_at	NR4A2	2q24.1	2,44188613	5	6
200908_s_at	RPLP2	11p15.5	2,44071428	5	8
205590_at	RASGRP1	15q14	2,44058029	5	9
225786_at	NCRNA00201	1q44	2,44056232	5	5
213758_at	COX4I1	16q24.1	2,43968076	5	3
1553656_at	TECTB	10q25.2	2,43957920	5	4
1552611_a_at	JAK1	1p31.3	2,43952440	5	6
225710_at	GNB4	3q26.33	2,43902930	5	5
205968_at	KCNS3	2p24.2	2,43755236	5	6
230443_at	NHP2L1	22q13.2	2,43752340	5	3
226419_s_at	FLJ44342	17q22	2,43658586	5	3
219150_s_at	ADAP1	7p22.3	2,43640097	5	4
243709_at	SLC38A9	5q11.2	2,43619953	5	3
224952_at	TANC2	17q23.2	2,43546827	5	4
238741_at	FAM83A	8q24.13	2,43535674	5	3
221560_at	MARK4	19q13.32	2,43480333	5	3
204162_at	NDC80	18p11.32	2,43300010	5	9
1568249_at	LOC388796	20q11.23	2,43282087	5	7
220668_s_at	DNMT3B	20q11.21	2,43280675	5	4
227660_at	ANTXR1	2p13.3	2,43234618	5	5
213135_at	TIAM1	21q22.11	2,43166991	5	5
226288_s_at	NLGN2	17p13.1	2,43156848	5	5
203979_at	CYP27A1	2q35	2,43058967	5	3
217480_x_at	LOC100287723	2p11.1	2,42963617	5	12
209507_at	RPA3	7p21.3	2,42897489	5	11
1559227_s_at	VHL	3p25.3	2,42846816	5	3
225575_at	LIFR	5p13.1	2,42819082	5	3

219779_at	ZFHX4	8q21.11	2,42460236	5	5
205313_at	HNF1B	17q12	2,42377384	5	3
202096_s_at	TSPO	22q13.2	2,42352539	5	9
220004_at	DDX43	6q13	2,42330040	5	24
242417_at	LOC283278	11p15.1	2,42202369	5	3
232030_at	KIAA1632	18q21.1	2,42157287	5	12
215111_s_at	TSC22D1	13q14.11	2,42102923	5	5
204429_s_at	SLC2A5	1p36.23	2,42064389	5	3
202708_s_at	HIST2H2BE	1q21.2	2,42024457	5	6
224818_at	SORT1	1p13.3	2,41981876	5	3
207996_s_at	C18orf1	18p11.21	2,41968768	5	3
1554229_at	C5orf41	5q35.1	2,41932736	5	4
234210_x_at	ACTR2	2p14	2,41844485	5	5
230563_at	RASGEF1A	10q11.21	2,41786909	5	8
209843_s_at	SOX10	22q13.1	2,41769041	5	5
213264_at	PCBP2	12q13.13	2,41767055	5	6
219155_at	PITPNC1	17q24.2	2,41720292	5	6
1562267_s_at	ZNF709	19p13.2	2,41705216	5	6
227522_at	CMBL	5p15.2	2,41673357	5	6
214723_x_at	ANKRD36	2q11.2	2,41661871	5	4
237257_at	RAB4B	19q13.2	2,41612470	5	4
209437_s_at	SPON1	11p15.2	2,41470516	5	3
227602_at	RAB7A	3q21.3	2,41385760	5	4
1553153_at	ATP6V0D2	8q21.3	2,41323508	5	6
201963_at	ACSL1	4q35.1	2,41204589	5	7
210666_at	IDS	Xq28	2,41200330	5	4
236605_at	EIF3K	19q13.2	2,41057507	5	3
223952_x_at	DHRS9	2q31.1	2,40972934	5	12
1569291_at	CROCCL1	1p36.13	2,40931710	5	10
219288_at	C3orf14	3p14.2	2,40835364	5	3
1561258_at	TMEM151B	6p21.1	2,40739660	5	3
226184_at	FMNL2	2q23.3	2,40703190	5	6
223159_s_at	NEK6	9q33.3	2,40693841	5	6
228837_at	TCF4	18q21.2	2,40677832	5	4
219132_at	PELI2	14q22.3	2,40645595	5	4
219333_s_at	CAPN10	2q37.3	2,40636737	5	4
227537_s_at	SP3	2q31.1	2,40484483	5	4
228249_at	C11orf74	11p12	2,40369388	5	4
1553961_s_at	SNX21	20q13.12	2,40262527	5	6
213169_at	SEMA5A	5p15.31	2,40209468	5	5
214639_s_at	HOXA1	7p15.2	2,40080508	5	5
220128_s_at	NIPAL2	8q22.2	2,40018592	5	4
230229_at	DLG1	3q29	2,40007111	5	7
235140_at	SHROOM1	5q31.1	2,40002070	5	3
216563_at	ANKRD12	18p11.22	2,39811838	5	3
217591_at	SKIL	3q26.2	2,39776473	5	7
239196_at	ANKRD22	10q23.31	2,39726537	5	3
227196_at	RHPN2	19q13.11	2,39724711	5	4
226439_s_at	NBEA	13q13.3	2,39712370	5	7
222165_x_at	C9orf16	9q34.11	2,39551188	5	5
225961_at	KLHDC5	12p11.22	2,39426205	5	4
232304_at	PELI1	2p14	2,39384763	5	7
229513_at	STRBP	9q33.3	2,39334491	5	5
224920_x_at	MYADM	19q13.42	2,39261654	5	8

239214_at	LOC100130458	9p13.2	2,39235207	5	4
1552504_a_at	BRSK1	19q13.42	2,39180284	5	4
203786_s_at	TPD52L1	6q22.31	2,39157621	5	3
224995_at	SPIRE1	18p11.21	2,39137337	5	5
220645_at	FAM55D	11q23.2	2,39123667	5	6
241905_at	PIK3C2A	11p15.1	2,39105050	5	4
219906_at	FLJ10213	3p13	2,39085354	5	4
202728_s_at	LTBP1	2p22.3	2,39023856	5	4
236175_at	TRIM55	8q13.1	2,38986664	5	5
223275_at	PRMT6	1p13.3	2,38956228	5	3
204825_at	MELK	9p13.2	2,38934775	5	5
1569320_at	GPBP1L1	1p34.1	2,38926655	5	4
236782_at	SAMD3	6q23.1	2,38888331	5	4
224838_at	FOXP1	3p13	2,38880236	5	3
221911_at	ETV1	7p21.2	2,38819896	5	7
1561391_at	LOC100128126	8q21.11	2,38590496	5	4
228855_at	NUDT7	16q23.1	2,38558017	5	6
205691_at	SYNGR3	16p13.3	2,38450496	5	5
213110_s_at	COL4A5	Xq22.3	2,38424594	5	7
228384_s_at	PYROXD2	10q24.2	2,38409254	5	4
235221_at	CBLN3	14q12	2,38286425	5	6
232229_at	SETX	9q34.13	2,38272631	5	3
208950_s_at	ALDH7A1	5q23.2	2,38217093	5	3
203408_s_at	SATB1	3p24.3	2,38204153	5	3
206994_at	CST4	20p11.21	2,38184917	5	4
218706_s_at	GRAMD3	5q23.2	2,38120395	5	6
226651_at	HOMER1	5q14.1	2,38102242	5	6
1552735_at	PCDHGA4	5q31	2,38081072	5	5
201739_at	SGK1	6q23.2	2,38037947	5	3
206059_at	ZNF91	19p12	2,37992560	5	4
1559413_at	TCP11L2	12q23.3	2,37893510	5	4
227084_at	DTNA	18q12.1	2,37869009	5	16
1554253_a_at	LASS3	15q26.3	2,37766351	5	9
223313_s_at	MAGED4	Xp11.22	2,37743090	5	5
219550_at	ROBO3	11q24.2	2,37517666	5	3
227899_at	VIT	2p22.2	2,37495042	5	3
225245_x_at	H2AFJ	12p12.3	2,37431723	5	5
212099_at	RHOB	2p24.1	2,37408271	5	5
1563117_at	LOC388456	18p11.32	2,37240473	5	3
202431_s_at	MYC	8q24.21	2,37010765	5	3
202436_s_at	CYP1B1	2p22.2	2,37005462	5	5
1561820_at	SCN8A	12q13.13	2,36894347	5	3
213649_at	SFRS7	2p22.1	2,36879060	5	3
226456_at	C16orf75	16p13.13	2,36772944	5	3
239654_at	CHD9	16q12.2	2,36704209	5	6
210992_x_at	FCGR2C	1q23.3	2,36572285	5	8
206408_at	LRRTM2	5q31.2	2,36468906	5	4
228361_at	E2F2	1p36.12	2,36452533	5	8
1553279_at	BTNL9	5q35.3	2,36303536	5	9
208397_x_at	KCNJ5	11q24.3	2,36250612	5	7
227747_at	MPZL3	11q23.3	2,36166726	5	3
1564333_a_at	PSAPL1	4p16.1	2,36166091	5	12
230188_at	NIPAL4	5q33.3	2,36161919	5	7
205592_at	SLC4A1	17q21.31	2,36109226	5	6

217966_s_at	FAM129A	1q25.3	2,36097725	5	5
210282_at	ZMYM2	13q12.11	2,36038023	5	3
206399_x_at	CACNA1A	19p13.2	2,35999121	5	6
229435_at	GLIS3	9p24.2	2,35985333	5	5
221763_at	JMJD1C	10q21.3	2,35701822	5	4
223961_s_at	CISH	3p21.2	2,35666470	5	3
228365_at	CPNE8	12q12	2,35490594	5	4
225308_s_at	TANC1	2q24.2	2,35452379	5	7
219148_at	PBK	8p21.1	2,35323032	5	6
207865_s_at	BMP8B	1p34.2	2,35211086	5	8
207480_s_at	MEIS2	15q14	2,35185688	5	5
225524_at	ANTXR2	4q21.21	2,35177068	5	8
1560818_at	LOC387895	12q24.32	2,35036918	5	3
221521_s_at	GINS2	16q24.1	2,34983263	5	4
236717_at	FAM179A	2p23.2	2,34974201	5	3
1552348_at	PRSS33	16p13.3	2,34959168	5	3
219677_at	SPSB1	1p36.22	2,34917064	5	4
201422_at	IFI30	19p13.11	2,34890952	5	9
205050_s_at	MAPK8IP2	22q13.33	2,34796001	5	5
208198_x_at	KIR2DS1	19q13.42	2,34687522	5	4
40020_at	CELSR3	3p21.31	2,34605616	5	6
206314_at	ZNF167	3p21.31	2,34408328	5	4
217019_at	RPS4P6	20q13.31	2,34335119	5	6
210056_at	RND1	12q13.12	2,34216454	5	6
236707_at	DAPP1	4q23	2,34195585	5	4
207794_at	CCR2	3p21.31	2,34054054	5	3
204286_s_at	PMAIP1	18q21.32	2,33862275	5	3
242930_at	OSGEP	14q11.2	2,33781274	5	4
229656_s_at	EML6	2p16.2	2,33775255	5	4
204457_s_at	GAS1	9q21.33	2,33771611	5	5
207951_at	CSN2	4q13.3	2,33660466	5	10
226876_at	FAM101B	17p13.3	2,33626011	5	3
212745_s_at	BBS4	15q24.1	2,33580540	5	3
228476_at	KIAA1407	3q13.31	2,33432584	5	7
225655_at	UHRF1	19p13.3	2,33336664	5	5
241403_at	CLK4	5q35.3	2,33288886	5	9
205239_at	AREG	4q13.3	2,33264926	5	3
1552912_a_at	IL23R	1p31.3	2,33259659	5	4
230972_at	ANKRD9	14q32.31	2,33064861	5	3
212504_at	DIP2C	10p15.3	2,33048352	5	6
201469_s_at	SHC1	1q21.3	2,33038974	5	6
225214_at	LOC100129034	9q33.3	2,33014211	5	3
1560128_x_at	LOC441108	5q31.1	2,32931968	5	7
1562257_x_at	NLRP1	17p13.2	2,32907360	5	5
226733_at	PFKFB2	1q32.2	2,32867780	5	4
207076_s_at	ASS1	9q34.11	2,32847014	5	5
219194_at	SEMA4G	10q24.31	2,32829794	5	4
1564029_at	USP49	6p21.1	2,32701996	5	3
211032_at	COBLL1	2q24.3	2,32616858	5	5
241174_at	AP4E1	15q21.2	2,32594694	5	3
1569607_s_at	ANKRD20A1	2q11.1	2,32499670	5	3
223748_at	SLC4A11	20p13	2,32464964	5	3
203723_at	ITPKB	1q42.12	2,32397197	5	5
226663_at	ANKRD10	13q34	2,32388640	5	3

219122_s_at	THG1L	5q33.3	2,32363332	5	5
202600_s_at	NRIP1	21q21.1	2,32275501	5	7
217728_at	S100A6	1q21.3	2,32255616	5	6
204057_at	IRF8	16q24.1	2,32254654	5	5
39763_at	HPX	11p15.4	2,32165532	5	6
221413_at	KCNAB3	17p13.1	2,32163608	5	3
228396_at	PRKG1	10q11.23	2,32123797	5	4
210426_x_at	RORA	15q22.2	2,32084405	5	6
228157_at	ZNF207	17q11.2	2,32015703	5	4
203490_at	ELF4	Xq26.1	2,32001325	5	3
224273_at	C3orf20	3p25.1	2,31996077	5	3
228422_at	LHFPL4	3p25.3	2,31955284	5	3
222799_at	WDR91	7q33	2,31914731	5	3
217362_x_at	HLA-DRB6	6p21.32	2,31843010	5	4
218051_s_at	NT5DC2	3p21.1	2,31821529	5	3
215926_x_at	SNAPC4	9q34.3	2,31814704	5	5
213888_s_at	TRAF3IP3	1q32.2	2,31778205	5	5
202597_at	IRF6	1q32.2	2,31734598	5	4
218953_s_at	PCYOX1L	5q32	2,31653175	5	4
244050_at	PTPLAD2	9p21.3	2,31566498	5	3
233077_at	FLJ13439	11p15.1	2,31557300	5	8
1562664_at	tcag7.929	7q31.2	2,31304213	5	4
230008_at	THSD7A	7p21.3	2,31275175	5	5
206410_at	NR0B2	1p36.11	2,31156093	5	7
204793_at	GPRASP1	Xq22.1	2,31023340	5	8
208960_s_at	KLF6	10p15.1	2,30947945	5	3
209258_s_at	SMC3	10q25.2	2,30887252	5	9
227988_s_at	VPS13A	9q21.2	2,30815590	5	6
201015_s_at	JUP	17q21.2	2,30800292	5	5
202826_at	SPINT1	15q15.1	2,30728697	5	5
209193_at	PIM1	6p21.2	2,30621884	5	5
237266_at	LOC100133686	10q24.32	2,30614024	5	4
235023_at	VPS13C	15q22.2	2,30611866	5	9
201601_x_at	IFITM1	11p15.5	2,30592498	5	3
235897_at	COPZ2	17q21.32	2,30556401	5	4
223318_s_at	ALKBH7	19p13.3	2,30519582	5	4
223253_at	EPDR1	7p14.1	2,30408170	5	5
209035_at	MDK	11p11.2	2,30372864	5	4
1558784_at	LOC100133089	10q11.23	2,30142459	5	4
213194_at	ROBO1	3p12.2	2,29985849	5	7
230388_s_at	LOC644246	17q21.31	2,29940230	5	6
1555673_at	hCG_1749898	17q21.2	2,29873582	5	5
233254_x_at	PTEN	10q23.31	2,29796325	5	5
223058_at	FAM107B	10p13	2,29754359	5	3
232745_x_at	SPEF2	5p13.2	2,29719517	5	9
205651_x_at	RAPGEF4	2q31.1	2,29457282	5	3
242021_at	XBP1	22q12.1	2,29414847	5	3
206011_at	CASP1	11q22.3	2,29025721	5	7
201951_at	ALCAM	3q13.11	2,29004165	5	4
244453_at	ANKRD53	2p13.3	2,29000753	5	6
1557669_at	LOC100132005	6p21.2	2,28918988	5	4
209604_s_at	GATA3	10p14	2,28893937	5	7
1557105_a_at	ZNF397OS	18q12.2	2,28801192	5	4
225622_at	PAG1	8q21.13	2,28707045	5	3

216998_s_at	ADAM5P	8p11.22	2,28666184	5	4
238921_at	LOC644794	7q11.21	2,28644088	5	4
235670_at	STX11	6q24.2	2,28596075	5	5
226101_at	PRKCE	2p21	2,28419010	5	5
208344_x_at	IFNA1	9p21.3	2,28369680	5	5
213913_s_at	TBC1D30	12q14.3	2,28290768	5	3
219032_x_at	OPN3	1q43	2,28259390	5	3
219431_at	ARHGAP10	4q31.23	2,28256461	5	4
220737_at	RPS6KA6	Xq21.1	2,28227400	5	8
222900_at	NRIP3	11p15.4	2,28172907	5	3
215946_x_at	IGLL3	22q11.23	2,28166428	5	4
1559864_at	LCN6	9q34.3	2,28160554	5	3
209116_x_at	HBB	11p15.4	2,28133220	5	5
212607_at	AKT3	1q44	2,28000783	5	3
218741_at	CENPM	22q13.2	2,27916826	5	3
219138_at	RPL14	12q14.2	2,27810691	5	5
238022_at	CRNDE	16q12.2	2,27735749	5	4
219883_at	C11orf20	11q13.1	2,27664061	5	7
224925_at	PREX1	20q13.13	2,27660956	5	3
236140_at	GCLM	1p22.1	2,27539515	5	4
227806_at	C16orf74	16q24.1	2,27237630	5	3
202831_at	GPX2	14q23.3	2,27183380	5	3
227058_at	C13orf33	13q12.3	2,27041245	5	4
214052_x_at	BAT2D1	1q24.3	2,26971833	5	6
212203_x_at	IFITM3	11p15.5	2,26928248	5	3
239415_at	MAP9	4q32.1	2,26838324	5	5
201666_at	TIMP1	Xp11.23	2,26765904	5	3
1559471_s_at	D21S2088E	21q21.2	2,26760266	5	6
201387_s_at	UCHL1	4p13	2,26709936	5	3
1560897_a_at	KRTAP10-11	21q22.3	2,26503269	5	5
226001_at	KLHL5	4p14	2,26461150	5	5
209498_at	CEACAM1	19q13.2	2,26428816	5	3
228397_at	TUG1	22q12.2	2,26386675	5	4
220340_at	KIAA1772	18q11.1	2,26325640	5	4
1559291_at	NCRNA00032	9p21.2	2,26303995	5	4
205306_x_at	KMO	1q43	2,26202751	5	4
210613_s_at	SYNGR1	22q13.1	2,26185673	5	3
235030_at	FAM55C	3q12.3	2,25900583	5	8
208744_x_at	HSPH1	13q12.3	2,25835340	5	3
1555944_at	FAM120A	9q22.31	2,25629901	5	4
219563_at	C14orf139	14q32.13	2,25543718	5	6
206534_at	GRIN2A	16p13.2	2,25485593	5	13
227218_at	RLTPR	16q22.1	2,25461540	5	3
208610_s_at	SRRM2	16p13.3	2,25413236	5	8
219629_at	FAM118A	22q13.31	2,25327505	5	4
211066_x_at	PCDHGA1	5q31.3	2,25272512	5	5
217187_at	MUC5AC	11p15.5	2,24984031	5	3
219669_at	CD177	19q13.31	2,24708599	5	3
202762_at	ROCK2	2p25.1	2,24678431	5	3
207051_at	SLC17A4	6p22.2	2,24659875	5	4
207106_s_at	LTK	15q15.1	2,24626356	5	4
209355_s_at	PPAP2B	1p32.2	2,24445235	5	5
1552656_s_at	UHMK1	1q23.3	2,24417807	5	3
49452_at	ACACB	12q24.11	2,24378026	5	3

206255_at	BLK	8p23.1	2,24304716	5	5
223614_at	MMP16	8q21.3	2,24041000	5	3
1554396_at	UEVLD	11p15.1	2,24004377	5	5
222876_s_at	ADAP2	17q11.2	2,23526727	5	3
1568377_x_at	DEFB124	20q11.21	2,23291165	5	3
35974_at	LRMP	12p12.1	2,23266881	5	3
227275_at	MEX3C	18q21.2	2,23213555	5	4
224207_x_at	MMP28	17q12	2,23143579	5	3
216570_x_at	RPL29	3p22.2	2,23090065	5	5
225065_x_at	NCRNA00188	17p11.2	2,22897851	5	3
205923_at	RELN	7q22.1	2,22735023	5	6
225464_at	FRMD6	14q22.1	2,22572864	5	8
206034_at	SERPINB8	18q22.1	2,22529624	5	3
207309_at	NOS1	12q24.22	2,22479348	5	3
222866_s_at	FLVCR2	14q24.3	2,22462423	5	3
1570243_at	LOC440731	1q42.2	2,22413464	5	5
1569484_s_at	MDN1	6q15	2,22404368	5	3
203886_s_at	FBLN2	3p25.1	2,22346658	5	5
220595_at	PDZRN4	12q12	2,22227716	5	5
243109_at	MCTP2	15q26.2	2,22062918	5	4
239487_at	FAM98A	2p22.3	2,21787196	5	3
231011_at	LARP2	4q28.2	2,21682969	5	5
212706_at	LOC100286937	7p13	2,21246794	5	5
1555009_a_at	SYNJ2	6q25.3	2,20788620	5	3
205544_s_at	CR2	1q32.2	2,20770999	5	3
1552542_s_at	TAGAP	6q25.3	2,20532135	5	5
214357_at	C1orf105	1q24.3	2,20500812	5	5
228728_at	C7orf58	7q31.31	2,20443304	5	3
1555554_at	RP11-49G10.8	20q11.21	2,20315013	5	3
231899_at	ZC3H12C	11q22.3	2,20040491	5	5
223481_s_at	MRPL47	3q26.33	2,19998192	5	4
204462_s_at	SLC16A2	Xq13.2	2,19934449	5	3
223812_at	FAM178B	2q11.2	2,19930668	5	3
207601_at	SULT1B1	4q13.3	2,19735259	5	4
1557723_at	LOC285847	6p21.31	2,19715244	5	3
207505_at	PRKG2	4q21.21	2,19706310	5	7
235645_at	ESCO1	18q11.2	2,19557070	5	6
1564112_at	FAM71A	1q32.3	2,19505488	5	3
202988_s_at	RGS1	1q31.2	2,19453522	5	4
1553637_s_at	TMCO5A	15q14	2,19249729	5	6
1561671_at	LOC286121	8q24.3	2,19221862	5	4
228783_at	BVES	6q21	2,19073978	5	3
218805_at	GIMAP5	7q36.1	2,18766670	5	3
206372_at	MYF6	12q21.31	2,18715880	5	3
216604_s_at	SLC7A8	14q11.2	2,18503253	5	3
219681_s_at	RAB11FIP1	8p11.23	2,18331754	5	4
212724_at	RND3	2q23.3	2,18308335	5	7
209582_s_at	CD200	3q13.2	2,17679924	5	6
1553586_at	NCRNA00095	16p11.2	2,17491152	5	7
213624_at	SMPDL3A	6q22.31	2,16518569	5	3
210336_x_at	MZF1	19q13.43	2,16337031	5	3
234999_at	C19orf47	19q13.2	2,16309494	5	3
202308_at	SREBF1	17p11.2	2,16168320	5	3
240452_at	GSPT1	16p13.13	2,16166608	5	4

205624_at	CPA3	3q24	2,15898479	5	6
221234_s_at	BACH2	6q15	2,15826307	5	7
228492_at	USP9Y	Yq11.221	2,15762300	5	4
232055_at	SFXN1	5q35.2	2,15322023	5	5
204610_s_at	CCDC85B	11q13.1	2,15289839	5	6
241376_at	LOC100130097	1q44	2,15226142	5	6
205965_at	BATF	14q24.3	2,15073899	5	4
217998_at	LOC100289208	12q21.2	2,14969447	5	5
203817_at	GUCY1B3	4q32.1	2,14733681	5	3
1555464_at	IFIH1	2q24.2	2,14288706	5	5
221960_s_at	RAB2A	8q12.1	2,13916398	5	5
211909_x_at	PTGER3	1p31.1	2,13503570	5	3
1553453_at	ASB14	3p14.3	2,13413869	5	4
219736_at	TRIM36	5q22.3	2,13252128	5	3
201720_s_at	LAPTM5	1p35.2	2,12822280	5	3
212319_at	SGSM2	17p13.3	2,12746162	5	3
1557212_at	FLJ33065	3p22.1	2,12551373	5	3
1553555_at	TAS2R38	7q34	2,12221740	5	3
214599_at	IVL	1q21.3	2,11613902	5	4
1567623_at	ABLIM2	4p16.1	2,11505503	5	5
233229_at	SCFD1	14q12	2,11485366	5	4
224506_s_at	PPAPDC3	9q34.13	2,11422771	5	3
228825_at	PTGR1	9q31.3	2,11277198	5	3
209889_at	SEC31B	10q24.31	2,11258614	5	4
224414_s_at	CARD6	5p13.1	2,11176715	5	6
230179_at	LOC285812	6p23	2,10513384	5	3
1555510_at	ZNF215	11p15.4	2,10495715	5	4
1560370_x_at	ANKH	5p15.2	2,09690100	5	5
214752_x_at	FLNA	Xq28	2,09221949	5	3
224961_at	SCYL2	12q23.1	2,09172091	5	3
239930_at	GALNT2	1q42.13	2,08627498	5	3
218981_at	ACN9	7q21.3	2,08297567	5	4
231726_at	PCDHB14	5q31.3	2,08110952	5	3
238886_at	TMED10	14q24.3	2,08083933	5	7
215172_at	PTPN20A	10q11.22	2,07980636	5	3
220017_x_at	CYP2C9	10q23.33	2,07853771	5	4
207095_at	SLC10A2	13q33.1	2,07721046	5	3
208121_s_at	PTPRO	12p12.3	2,07456603	5	4
208930_s_at	ILF3	19p13.2	2,06762685	5	6
243437_at	GCC1	7q32.1	2,06415150	5	3
210039_s_at	PRKCQ	10p14	2,06295409	5	3
227919_at	UCA1	19p13.12	2,06273179	5	7
212332_at	RBL2	16q12.2	2,04386998	5	3
212509_s_at	MXRA7	17q25.1	2,04271189	5	3
210538_s_at	BIRC3	11q22.2	2,04235904	5	4
236539_at	PTPN22	1p13.2	2,04040522	5	3
230609_at	CLINT1	5q33.3	2,03341948	5	3
230097_at	GART	21q22.11	2,02733124	5	3
224741_x_at	GAS5	1q25.1	2,01338250	5	4
204602_at	DKK1	10q21.1	2,01172730	5	3
210601_at	CDH6	5p13.3	2,00124851	5	4
1553749_at	FAM76B	11q21	1,91435613	5	4
200989_at	HIF1A	14q23.2	1,85709063	5	4