

Supplemental Table-1: **Differentially Expressed Genes**
Significant Probe Sets for monotonic trend using Bonferroni corrected p-value

Significant Prob	Affy ID	Symbol	Unigene	Chromosome	Map	Normal Donor	Kid Normal	Allograft	CAN	trend
22914	205821_at	KLRK1	Hs.387787	12	12p13.2-p1	5.304		6.582	7.867	0.87
445347	211144_x	TARP	Hs.534032	7	7p15-p14	5.391		6.36	7.435	0.87
5644	213193_x	PRSS1	Hs.511522	7	7q32-qter					
					7q34	5.626		6.905	9.135	0.87
5733	210375_at	PTGER3	Hs.445000	1	1p31.2	7.931		5.967	4.76	-0.87
914	205831_at	CD2	Hs.523500	1	1p13	5.175		6.889	8.522	0.87
2841	210279_at	GPR18	Hs.631765	13	13q32	3.863		4.202	5.405	0.87
10154	213241_at	PLXNC1	Hs.584845	12	12q23.3	5.576		7.122	8.646	0.87
6402	204563_at	SELL	Hs.82848	1	1q23-q25	4.537		5.274	7.693	0.87
53829	220005_at	P2RY13	Hs.546396	3	3q24	4.188		5.056	6.326	0.87
915	213539_at	CD3D	Hs.504048	11	11q23	5.926		7.291	8.954	0.86
6964	217143_s	TRD@	Hs.74647	14	14q11.2	4.39		4.978	6.044	0.87
291	202825_at	SLC25A4	Hs.246506	4	4q35	8.44		7.779	6.793	-0.86
6352	1405_i_at	CCL5	Hs.514821	17	17q11.2-q1	4.277		6.907	8.762	0.86
3676	205884_at	ITGA4	Hs.440955	2	2q31.3	3.855		4.049	5.736	0.86
11119	209770_at	BTN3A1	Hs.191510	6	6p22.1	6.276		7.565	7.961	0.86
2124	211742_s	EVI2B	Hs.5509	17	17q11.2	5.121		7.697	9.632	0.86
51316	219014_at	PLAC8	Hs.546392	4	4q21.22	4.568		6.328	7.392	0.86
5788	212588_at	PTPRC	Hs.192039	1	1q31-q32	5.642		9.055	10.353	0.86
6967	215806_x	TRGC2	Hs.534032	7	7p14	4.693		5.921	7.125	0.86
5733	210831_s	PTGER3	Hs.445000	1	1p31.2	7.43		6.763	5.741	-0.86
10384	204820_s	BTN3A3	Hs.167741	6	6p21.3	7.75		10.017	10.384	0.86
10384	204821_at	BTN3A3	Hs.167741	6	6p21.3	5.378		7.247	7.851	0.86
26191	206060_s	PTPN22	Hs.535276	1	1p13.3-p13	3.941		4.742	5.768	0.86
55843	218870_at	ARHGAP15	Hs.171011	2	2q22.2	5.644		6.833	8.298	0.86
387751	220577_at	GVIN1	Hs.494757	11	11p15.4	4.655		5.204	5.882	0.86
3561	204116_at	IL2RG	Hs.84	X	Xq13.1	5.966		7.194	8.769	0.86
5788	207238_s	PTPRC	Hs.192039	1	1q31-q32	5.176		7.809	9.512	0.86
2999	210321_at	GZMH	Hs.348264	14	14q11.2	4.988		5.673	6.58	0.86
55619	219279_at	DOCK10	Hs.46578							
			Hs.603220	2	2q36.2	4.39		5.497	6.891	0.85
518	207508_at	ATP5G3	Hs.429	2	2q31.1	10.944		10.537	9.689	-0.86
2805	208813_at	GOT1	Hs.500756	10	10q24.1-q2	9.702		9.011	7.351	-0.85
5733	210374_x	PTGER3	Hs.445000	1	1p31.2	7.411		6.655	5.555	-0.85
6352	204655_at	CCL5	Hs.514821	17	17q11.2-q1	4.567		6.507	8.979	0.85
3932	204891_s	LCK	Hs.470627	1	1p34.3	4.65		6.213	7.938	0.85
834	206011_at	CASP1	Hs.2490	11	11q23	4.526		5.575	7.324	0.85
3003	206666_at	GZMK	Hs.277937	5	5q11-q12	4.881		5.848	8.545	0.85
5644	210915_x	PRSS1	Hs.511522	7	7q32-qter					

				7q34	4.797	6.571	9.16	0.85
57823	219159_s	SLAMF7	Hs.517265	1 1q23.1-q24	5.142	5.633	7.641	0.85
51411	219191_s	BIN2	Hs.14770	12 12q13	6.125	6.994	7.811	0.86
916	205456_at	CD3E	Hs.3003	11 11q23	5.002	5.677	6.751	0.86
6375	206366_x	XCL1	Hs.546295	1 1q23	4.89	6.165	7.27	0.85
3683	213475_s	ITGAL	Hs.174103	16 16p11.2	4.994	5.419	6.024	0.85
5502	205478_at	PPP1R1A	Hs.505662	12 12q13.2	9.228	7.935	6.231	-0.85
	217329_x	NA	NA	NA	9.288	8.798	8.525	-0.85
60489	204205_at	APOBEC3C	Hs.441124	22 22q13.1-q1	5.631	7.85	8.982	0.85
6001	204319_s	RGS10	Hs.501200	10 10q25	5.722	7.302	8.484	0.85
925	205758_at	CD8A	Hs.85258	2 2p12	5.045	7.27	7.943	0.86
6983	209813_x	TRGV9	Hs.534032	7 7p14	5.273	6.362	7.533	0.85
5644	211796_s	PRSS1	Hs.511522	7 7q32-qter				
				7q34	5.415	7.254	9.742	0.85
445347	216920_s	TARP	Hs.534032	7 7p15-p14	5.215	6.419	7.725	0.85
55303	219243_at	GIMAP4	Hs.438823	7 7q36.1	7.028	8.274	9.105	0.85
9452	202747_s	ITM2A	Hs.17109 X	Xq13.3-Xq2	7.515	8.059	9.209	0.85
3932	204890_s	LCK	Hs.470627	1 1p34.3	4.968	5.557	6.672	0.85
54440	204923_at	CXorf9	Hs.61469 X	Xq26	5.381	6.198	7.271	0.85
9459	209539_at	ARHGEF6	Hs.522795 X	Xq26	5.853	6.657	8.016	0.85
7456	202664_at	WASPIP	Hs.591641	2 2q31.1	6.115	7.489	8.601	0.85
399	204951_at	RHOH	Hs.160673	4 4p13	4.727	5.096	6.461	0.85
3702	211339_s	ITK	Hs.558348	5 5q31-q32	4.48	4.928	6.693	0.85
10346	213293_s	TRIM22	Hs.501778					
				11 11p15	7.169	9.32	9.939	0.85
1043	34210_at	CD52	Hs.276770	1 1p36	4.835	6.765	9.445	0.85
10768	200849_s	AHCYL1	Hs.485365					
				1 1p13.2	9.216	8.505	7.784	-0.85
4128	204389_at	MAOA	Hs.183109 X	Xp11.3	7.646	7.041	4.694	-0.85
6351	204103_at	CCL4	Hs.75703	17 17q12	5.46	7.388	8.176	0.85
951	204192_at	CD37	Hs.166556	19 19q13.3	4.245	5.576	6.958	0.84
3127	204670_x	HLA-DRB5	Hs.534322	6 6p21.3	10.084	11.475	12.007	0.85
9934	206637_at	P2RY14	Hs.2465	3 3q21-q25	4.508	5.33	6.268	0.84
29909	207651_at	GPR171	Hs.549152	3 3q25.1	4.046	5.311	6.783	0.85
389840	200980_s	MAP3K15	Hs.471144 X	Xp22.12	9.243	8.89	8.07	-0.84
1647	203725_at	GADD45A	Hs.80409	1 1p31.2-p31	10.01	8.655	7.814	-0.85
7386	208909_at	UQCRFS1	Hs.170107	19 19q12-q13.	10.675	10.384	9.574	-0.84
51660	218024_at	BRP44L	Hs.172755	6 6q27	10.849	9.884	9.236	-0.85
4710	218226_s	NDUFB4	Hs.304613					
				3 3q13.33	11.531	10.996	10.598	-0.85
2908	201865_x	NR3C1	Hs.122926	5 5q31.3	8.078	8.561	9.111	0.84
9452	202746_at	ITM2A	Hs.17109 X	Xq13.3-Xq2	6.277	7.33	8.299	0.84
3635	203332_s	INPP5D	Hs.262886					

			Hs.601911	2	2q37.1	5.324	5.904	6.761	0.84
962	204118_at	CD48	Hs.243564	1	1q21.3-q22	5.298	6.823	8.6	0.84
28755	209670_at	TRAC	Hs.74647	14	14q11	6.268	7.561	8.617	0.84
3113	211991_s	HLA-DPA1	Hs.347270	6	6p21.3	8.307	11.071	11.644	0.85
10659	202157_s	CUGBP2	Hs.309288	10	10p13	6.094	7.452	8.994	0.84
3112	205671_s	HLA-DOB	Hs.1802	6	6p21.3	5.082	5.496	6.615	0.84
4064	206206_at	CD180	Hs.87205	5	5q12	5.852	6.031	7.233	0.84
834	209970_x	CASP1	Hs.2490	11	11q23	6.366	8.47	9.127	0.85
834	211366_x	CASP1	Hs.2490	11	11q23	6.62	8.445	9.247	0.85
10859	213975_s	LILRB1	Hs.67846	19	19q13.4	7.407	10.278	11.172	0.84
5121	205549_at	PCP4	Hs.80296	21	21q22.2	9.026	6.903	5.827	-0.84
2806	200708_at	GOT2	Hs.599470	16	16q21	9.384	9.042	8.326	-0.84
1950	206254_at	EGF	Hs.419815	4	4q25	8.169	5.597	4.703	-0.84
113	203741_s	ADCY7	Hs.513578	16	16q12-q13	4.135	5.201	6.588	0.84
1043	204661_at	CD52	Hs.276770	1	1p36	5.786	7.078	8.749	0.84
6039	213566_at	RNASE6	Hs.23262	14	14q11.2	5.554	8.416	9.067	0.85
6846	214567_s	XCL2	Hs.458346						
			Hs.546295	1	1q23-q25	4.68	5.856	6.928	0.84
54809	219691_at	SAMD9	Hs.65641	7	7q21.2	4.899	5.456	6.164	0.84
79958	221080_s	DENND1C	Hs.236449	19	19p13.3	5.981	6.38	6.685	0.84
3001	205488_at	GZMA	Hs.90708	5	5q11-q12	4.362	7.681	8.555	0.84
695	205504_at	BTK	Hs.159494 X		Xq21.33-q2	4.438	4.909	5.635	0.83
27299	206134_at	ADAMDEC	Hs.521459	8	8p21.2	3.803	5.316	8.429	0.84
3936	208885_at	LCP1	Hs.381099	13	13q14.3	6.786	9.192	10.076	0.85
9976	209732_at	CLEC2B	Hs.85201	12	12p13-p12	7.009	8.953	9.743	0.84
2908	211671_s	NR3C1	Hs.122926	5	5q31.3	7.712	8.388	8.794	0.83
3676	213416_at	ITGA4	Hs.440955	2	2q31.3	4.499	5.318	7.793	0.84
80342	213888_s	TRAF3IP3	Hs.147434	1	1q32.3-q41	4.475	4.948	6.986	0.84
23766	211458_s	GABARAPI	Hs.592014	15	15q26.1	10.695	9.811	8.801	-0.84
80183	219471_at	C13orf18	Hs.98117	13	13q14.12	4.817	5.209	6.062	0.84
518	207507_s	ATP5G3	Hs.429	2	2q31.1	10.674	10.189	9.415	-0.83
6775	206118_at	STAT4	Hs.80642	2	2q32.2-q32	4.915	5.723	6.786	0.83
939	206150_at	TNFRSF7	Hs.355307	12	12p13	5.157	5.577	7.213	0.83
80264	206829_x	ZNF430	Hs.466289	19	19p12	5.886	6.458	6.869	0.84
960	209835_x	CD44	Hs.502328	11	11p13	5.538	6.657	8.156	0.83
5788	212587_s	PTPRC	Hs.192039	1	1q31-q32	4.535	7.569	8.852	0.84
55196	218614_at	C12orf35	Hs.445129	12	12p11.21	6.721	7.429	8.699	0.83
4719	203039_s	NDUFS1	Hs.471207	2	2q33-q34	9.028	8.243	7.498	-0.84
3373	210619_s	HYAL1	Hs.75619						
			Hs.129910	3	3p21.3-p21	8.579	7.928	6.487	-0.83
5733	213933_at	PTGER3	Hs.445000	1	1p31.2	8.388	6.713	5.296	-0.84
10110	220357_s	SGK2	Hs.472793	20	20q13.2	8.124	7.708	7.094	-0.83
9848	205442_at	MFAP3L	Hs.178121						

			Hs.593942	4	4q32.3	9.154	8.542	6.658	-0.82
4707	206790_s	NDUFB1	Hs.183435	14	14q32.12	11.322	10.595	10.314	-0.84
3094	208826_x	HINT1	Hs.483305	5	5q31.2	11.142	10.986	10.601	-0.83
9848	210493_s	MFAP3L	Hs.178121						
			Hs.593942	4	4q32.3	4.669	4.481	4.28	-0.83
5733	210832_x	PTGER3	Hs.445000	1	1p31.2	6.82	6.111	4.972	-0.83
3115	201137_s	HLA-DPB1	Hs.485130	6	6p21.3	8.72	11.396	11.983	0.84
10123	202207_at	ARL4C	Hs.111554	2	2q37.1	4.885	7.086	8.76	0.83
864	204197_s	RUNX3	Hs.170019	1	1p36	4.428	4.717	5.396	0.83
2123	204774_at	EVI2A	Hs.591198	17	17q11.2	4.813	7.217	8.543	0.83
9750	206707_x	C6orf32	Hs.559459	6	6p22.3-p21	4.967	5.191	5.852	0.83
9595	209606_at	PSCDBP	Hs.270	2	2q11.2	5.215	6.291	8.464	0.83
8530	210140_at	CST7	Hs.143212	20	20p11.21	5.897	6.377	7.598	0.83
834	211368_s	CASP1	Hs.2490	11	11q23	5.568	8.15	9.015	0.84
26986	215823_x	PABPC1	Hs.387804	8	8q22.2-q23	9.714	10.034	10.299	0.83
50856	221724_s	CLEC4A	Hs.504657	12	12p13	4.944	5.539	6.262	0.83
5341	203471_s	PLEK	Hs.468840	2	2p14	5.227	8.233	8.606	0.84
5293	203879_at	PIK3CD	Hs.518451	1	1p36.2	6.043	6.59	7.131	0.83
960	204489_s	CD44	Hs.502328	11	11p13	6.123	6.983	8.358	0.83
10863	205997_at	ADAM28	Hs.174030	8	8p21.2	5.059	5.475	7.685	0.83
11126	207840_at	CD160	Hs.488237	1	1q21.1	4.326	4.502	5.095	0.83
5579	209685_s	PRKCB1	Hs.460355	16	16p11.2	4.961	5.875	7.48	0.83
834	211367_s	CASP1	Hs.2490	11	11q23	5.106	7.295	7.829	0.84
7940	211581_x	LST1	Hs.436066	6	6p21.3	6.145	7.203	8.015	0.83
1794	213160_at	DOCK2	Hs.586174	5	5q35.1	5.162	5.99	7.494	0.83
50852	217147_s	TRAT1	Hs.138701	3	3q13	3.747	3.859	5.263	0.83
9377	203663_s	COX5A	Hs.401903	15	15q25	10.768	10.225	9.6	-0.83
4128	204388_s	MAOA	Hs.183109 X		Xp11.3	9.824	9.149	5.944	-0.83
516	208972_s	ATP5G1	Hs.80986	17	17q21.32	8.702	8.202	7.655	-0.83
91	213198_at	ACVR1B	Hs.438918						
			Hs.638696	12	12q13	9.226	8.827	8.003	-0.83
11163	212181_s	NUDT4	Hs.591008	12	12q21	9.694	9.011	8.303	-0.83
4332	204959_at	MNDA	Hs.153837	1	1q22	4.798	6.82	8.4	0.83
9450	205859_at	LY86	Hs.544738	6	6p25.1	5.664	7.249	8.068	0.84
56253	206914_at	CRTAM	Hs.159523	11	11q22-q23	4.047	4.388	5.447	0.83
919	210031_at	CD247	Hs.156445	1	1q22-q23	4.704	5.327	6.062	0.83
7940	211582_x	LST1	Hs.436066	6	6p21.3	6.123	7.421	8.123	0.83
11118	212613_at	BTN3A2	Hs.376046	6	6p22.1	5.511	7.17	7.562	0.84
9404	216250_s	LPXN	Hs.125474	11	11q12.1	5.767	6.92	8.373	0.83
6955	209671_x	TRA@	Hs.74647	14	14q11.2	5.499	6.365	7.406	0.83
969	209795_at	CD69	Hs.208854	12	12p13-p12	4.381	4.856	7.597	0.82
960	210916_s	CD44	Hs.502328	11	11p13	4.685	5.145	6.003	0.83
6955	211902_x	TRA@	Hs.74647	14	14q11.2	6.065	6.608	7.775	0.83

5880	213603_s	RAC2	Hs.517601	22	22q13.1	5.916	8.285	9.158	0.83
4603	213906_at	MYBL1	Hs.445898	8	8q22	3.957	4.355	4.826	0.83
3134	221978_at	HLA-F	Hs.519972	6	6p21.3	4.881	5.497	6.072	0.83
1773	210165_at	DNASE1	Hs.30345						
			Hs.629638	16	16p13.3	5.721	4.845	4.465	-0.83
9531	217911_s	BAG3	Hs.643507	10	10q25.2-q2	8.386	7.796	6.845	-0.82
4046	203523_at	LSP1	Hs.56729	11	11p15.5	5.251	5.648	6.896	0.81
9535	204220_at	GMFG	Hs.5210	19	19q13.2	6.257	7.847	8.712	0.83
10875	204834_at	FGL2	Hs.520989	7	7q11.23	6.906	8.871	9.093	0.84
9262	205214_at	STK17B	Hs.88297	2	2q32.3	3.938	4.22	5.177	0.82
3937	205270_s	LCP2	Hs.304475	5	5q33.1-qter	5.521	7.892	8.546	0.83
11151	209083_at	CORO1A	Hs.415067	16	16p11.2	5.589	7.175	8.552	0.82
3002	210164_at	GZMB	Hs.1051	14	14q11.2	4.194	6.187	7.364	0.84
5142	211302_s	PDE4B	Hs.198072	1	1p31	4.719	5.206	6.289	0.83
	212385_at	NA	NA		NA	4.642	5.011	6.127	0.82
3117	212671_s	HLA-DQA1	Hs.387679	6	6p21.3	6.885	10.933	11.325	0.84
53827	218084_x	FXD5	Hs.333418	19	19q12-q13.	5.962	6.467	7.832	0.82
10384	38241_at	BTN3A3	Hs.167741	6	6p21.3	4.424	6.738	6.937	0.84
1652	202929_s	DDT	Hs.632781	22	22q11.23	8.65	7.963	7.163	-0.82
283	205141_at	ANG	Hs.283749	14	14q11.1-q1	7.774	6.939	6.357	-0.82
54205	208905_at	CYCS	Hs.437060						
			Hs.617193	7	7p15.2	11.595	10.938	10.439	-0.82
11163	212183_at	NUDT4	Hs.591008	12	12q21	8.32	6.759	6.011	-0.81
51078	220417_s	THAP4	Hs.435759						
			Hs.600486	2	2q37.3	8.253	7.795	7.35	-0.82
4154	201152_s	MBNL1	Hs.478000						
			Hs.558914	3	3q25	8.631	9.164	9.949	0.82
3560	205291_at	IL2RB	Hs.474787	22	22q13				
					22q13.1	5.426	6.156	6.804	0.82
29969	211675_s	MDFIC	Hs.427236	7	7q31.1-q31	7.183	7.768	8.764	0.82
7940	214574_x	LST1	Hs.436066	6	6p21.3	6.078	7.554	8.145	0.83
63901	218248_at	FAM111A	Hs.150651	11	11q12.1	7.168	7.701	7.921	0.83
9938	38149_at	ARHGAP25	Hs.531807	2	2p14	5.439	6.307	7.115	0.82
55340	64064_at	GIMAP5	Hs.438823	7	7q36.1	6.732	7.501	8.269	0.82
7001	211658_at	PRDX2	Hs.631612	19	19p13.2	7.067	6.778	6.371	-0.81
2014	203729_at	EMP3	Hs.9999	19	19q13.3	6.682	7.574	8.796	0.82
9938	204882_at	ARHGAP25	Hs.531807	2	2p14	5.486	6.764	7.429	0.83
10320	205038_at	ZNFN1A1	Hs.435949	7	7p13-p11.1	4.517	4.712	5.133	0.82
51379	205474_at	CRLF3	Hs.370168	17	17q11.2	6.554	7.186	8.082	0.82
11064	205642_at	CEP110	Hs.643601	9	9q33-q34	4.768	5.108	5.439	0.82
2213	210889_s	FCGR2B	Hs.352642	1	1q23	5.129	5.641	7.772	0.82
10663	211469_s	CXCR6	Hs.34526	3	3p21	4.712	5.38	6.148	0.82
4818	213915_at	NKG7	Hs.10306	19	19q13.33	4.514	5.63	6.302	0.83

931	217418_x	MS4A1	Hs.438040	11	11q12	4.152	4.295	5.733	0.82
55340	218805_at	GIMAP5	Hs.438823	7	7q36.1	6.829	7.727	8.634	0.82
79630	219506_at	C1orf54	Hs.91283	1	1q21.2	7.511	8.664	8.811	0.84
29121	220132_s	CLEC2D	Hs.268326	12	12p13	4.003	4.442	5.269	0.82
4720	201966_at	NDUFS2	Hs.173611	1	1q23	9.647	9.28	8.677	-0.82
4700	202001_s	NDUFA6	Hs.274416	22	22q13.2-q1	10.614	9.977	9.567	-0.82
1329	202343_x	COX5B	Hs.1342	2	2cen-q13	10.655	10.304	9.679	-0.82
183	202834_at	AGT	Hs.19383	1	1q42-q43	10.256	9.556	5.947	-0.82
4128	212741_at	MAOA	Hs.183109 X		Xp11.3	10.268	9.837	7.28	-0.82
10123	202206_at	ARL4C	Hs.111554	2	2q37.1	5.128	6.419	7.227	0.83
10287	204336_s	RGS19	Hs.422336	20	20q13.3	6.675	7.235	7.955	0.82
3937	205269_at	LCP2	Hs.304475	5	5q33.1-qter	4.152	7.098	7.873	0.83
9447	206513_at	AIM2	Hs.281898	1	1q22	4.518	6.681	6.77	0.84
1234	206991_s	CCR5	Hs.450802						
			Hs.536735	3	3p21	5.937	6.339	7.847	0.82
199	209901_x	AIF1	Hs.76364	6	6p21.3	7.725	9.633	10.269	0.83
960	212063_at	CD44	Hs.502328	11	11p13	7.16	8.604	10.268	0.82
9881	213261_at	LBA1	Hs.170999	3	3p22.2	5.036	5.598	6.137	0.82
11103	214085_x	KRR1	Hs.205558	12	12q21.2	5.828	7.515	8.426	0.82
79668	219033_at	PARP8	Hs.369581	5	5q11.1	5.804	6.343	7.171	0.82
1349	202110_at	COX7B	Hs.522699 X		Xq21.1	11.435	10.869	10.35	-0.81
522	202325_s	ATP5J	Hs.246310	21	21q21.1	11.199	10.589	10.202	-0.81
2571	205278_at	GAD1	Hs.420036	2	2q31	4.416	4.045	3.937	-0.82
1329	211025_x	COX5B	Hs.1342	2	2cen-q13	10.665	10.252	9.664	-0.81
301	201012_at	ANXA1	Hs.494173	9	9q12-q21.2	8.076	9.517	10.441	0.82
10225	206761_at	CD96	Hs.142023	3	3q13.13-q1	3.977	4.084	4.706	0.81
11118	209846_s	BTN3A2	Hs.376046	6	6p22.1	5.621	8.409	8.594	0.83
4688	209949_at	NCF2	Hs.587558	1	1q25	4.817	7.645	7.542	0.83
960	212014_x	CD44	Hs.502328	11	11p13	5.789	6.431	7.858	0.81
84986	212738_at	ARHGAP19	Hs.80305	10	10q24.1	5.821	6.093	6.298	0.82
199	213095_x	AIF1	Hs.76364	6	6p21.3	7.715	9.961	10.206	0.83
2534	216033_s	FYN	Hs.390567	6	6q21	6.033	6.723	7.11	0.83
864	204198_s	RUNX3	Hs.170019	1	1p36	4.629	5.165	6.51	0.81
63940	204265_s	GPSM3	Hs.520046	6	6p21.3	6.528	7.07	7.93	0.81
5551	214617_at	PRF1	Hs.2200	10	10q22	5.546	7.117	7.887	0.83
5516	201375_s	PPP2CB	Hs.491440	8	8p12	10.516	10.21	9.801	-0.81
64284	218931_at	RAB17	Hs.44278	2	2q37.3	7.262	6.848	5.596	-0.82
3676	205885_s	ITGA4	Hs.440955	2	2q31.3	3.988	4.197	5.29	0.81
3428	206332_s	IFI16	Hs.380250	1	1q22	7.801	8.571	9.926	0.81
917	206804_at	CD3G	Hs.2259	11	11q23	4.431	4.593	5.114	0.81
1438	207085_x	CSF2RA	Hs.520937 X						
			Y		Xp22.32 an	4.005	4.708	5.351	0.82
5579	207957_s	PRKCB1	Hs.460355	16	16p11.2	4.042	4.369	5.763	0.81

4208	209199_s	MEF2C	Hs.444409	5	5q14	6.237	7.319	8.139	0.81
3824	210606_x	KLRD1	Hs.562457	12	12p13	4.767	6.383	6.444	0.83
81794	213733_at	ADAMTS10	Hs.465818	19	19p13.3-p1	5.406	6.65	7.037	0.82
3820	214470_at	KLRB1	Hs.169824	12	12p13	4.894	5.325	7.039	0.82
3123	215193_x	HLA-DRB1	Hs.534322	6	6p21.3	9.596	11.531	11.687	0.82
7849	221990_at	PAX8	Hs.469728	2	2q12-q14	7.2	6.827	6.367	-0.8
10577	200701_at	NPC2	Hs.433222	14	14q24.3	9.977	10.353	10.629	0.81
9770	203185_at	RASSF2	Hs.631504	20	20pter-p12.	5.067	5.856	7.219	0.81
963	203416_at	CD53	Hs.443057	1	1p13	7.515	10.049	10.735	0.82
80342	205804_s	TRAF3IP3	Hs.147434	1	1q32.3-q41	4.991	5.207	6.032	0.81
55603	221766_s	FAM46A	Hs.10784	6	6q14	6.622	6.934	7.659	0.81
10891	219195_at	PPARGC1A	Hs.527078	4	4p15.1	7.58	7.133	6.001	-0.81
2908	201866_s	NR3C1	Hs.122926	5	5q31.3	6.427	6.664	7.188	0.8
3119	212998_x	HLA-DQB1	Hs.409934						
			Hs.534322	6	6p21.3	6.727	9.978	10.192	0.82
26986	215157_x	PABPC1	Hs.387804	8	8q22.2-q23	9.923	10.342	10.702	0.81
1537	201066_at	CYC1	Hs.289271	8	8q24.3	9.459	9.177	8.369	-0.81
506	201322_at	ATP5B	Hs.406510	12	12q13.13	11.376	11.223	10.395	-0.81
316	205083_at	AOX1	Hs.406238	2	2q33	9.789	7.719	6.447	-0.81
8825	206440_at	LIN7A	Hs.144333	12	12q21	4.76	4.525	4.232	-0.8
7417	211662_s	VDAC2	Hs.355927						
			Hs.568267	10	10q22	10.658	10.364	10.022	-0.8
642502	215088_s	LOC642501	Hs.632231	17	17p13.3	9.274	8.898	8.303	-0.8
3109	203932_at	HLA-DMB	Hs.351279	6	6p21.3	7.636	9.639	9.891	0.82
11010	204222_s	GLIPR1	Hs.205558						
			Hs.591034	12	12q21.2	5.346	6.857	7.957	0.81
3587	204912_at	IL10RA	Hs.504035	11	11q23	4.831	6.881	8.197	0.81
942	205686_s	CD86	Hs.171182	3	3q21	4.234	5.888	6.372	0.82
5880	207419_s	RAC2	Hs.517601	22	22q13.1	4.791	5.964	7.488	0.81
3824	207795_s	KLRD1	Hs.562457	12	12p13	4.623	6	6.045	0.83
3126	208306_x	HLA-DRB4	Hs.534322						
			Hs.612586	6	6p21.3	10.12	11.8	11.973	0.82
3428	208966_x	IFI16	Hs.380250	1	1q22	7.418	8.329	9.496	0.81
7940	214181_x	LST1	Hs.436066	6	6p21.3	6.066	7.742	8.267	0.82
2359	214560_at	FPRL2	Hs.445466	19	19q13.3-q1	4.545	6.24	6.536	0.82
3535	216984_x	IGL@	Hs.449585	22	22q11.1-q1	5.745	6.016	10.426	0.81
3535	217148_x	IGL@	Hs.449585	22	22q11.1-q1	6.999	7.624	12.134	0.81
3125	221491_x	HLA-DRB3	Hs.534322	6	6p21.3	6.116	6.744	7.981	0.8
2180	201963_at	ACSL1	Hs.406678	4	4q34-q35	10.815	10.446	9.237	-0.8
1346	204570_at	COX7A1	Hs.421621						
			Hs.631480	19	19q13.1	8.705	8.055	7.283	-0.8
1160	205295_at	CKMT2	Hs.80691	5	5q13.3	6.446	5.942	5.285	-0.81
9093	205963_s	DNAJA3	Hs.459779	16	16p13.3	8.039	7.681	7.202	-0.8

5733	210833_at	PTGER3	Hs.445000	1	1p31.2	4.637	4.243	3.958	-0.8
3394	204057_at	IRF8	Hs.137427	16	16q24.1	6.381	8.012	8.841	0.8
960	204490_s	CD44	Hs.502328	11	11p13	5.58	6.236	7.775	0.81
1806	204646_at	DPYD	Hs.335034	1	1p22	7.476	8.76	8.985	0.81
4939	204972_at	OAS2	Hs.414332	12	12q24.2	4.495	6.268	6.354	0.82
10010	207616_s	TANK	Hs.556496	2	2q24-q31	7.966	8.326	8.66	0.8
3123	209312_x	HLA-DRB1	Hs.534322	6	6p21.3	10.011	11.963	11.997	0.82
7852	211919_s	CXCR4	Hs.421986	2	2q21	5.588	6.171	9.242	0.8
8477	214467_at	GPR65	Hs.513440	14	14q31-q32.	4.929	7.21	7.698	0.81
50856	219947_at	CLEC4A	Hs.504657	12	12p13	4.227	4.982	6.124	0.81
1540	221903_s	CYLD	Hs.578973	16	16q12.1	6.229	6.966	7.759	0.81
7384	201903_at	UQCRC1	Hs.119251	3	3p21.3	9.908	9.636	9.094	-0.79
5162	211023_at	PDHB	Hs.161357	3	3p21.1-p14	10.005	9.428	9.211	-0.8
3945	213564_x	LDHB	Hs.446149	12	12p12.2-p1	12.606	12.266	11.477	-0.8
1350	217491_x	COX7C	Hs.430075	5	5q14	11.559	11.138	10.86	-0.8
4600	204994_at	MX2	Hs.926	21	21q22.3	5.141	5.778	6.595	0.8
8832	205988_at	CD84	Hs.398093	1	1q24	4.953	6.252	6.259	0.82
5042	208113_x	PABPC3	Hs.458280	13	13q12-q13	9.861	10.087	10.344	0.8
3620	210029_at	INDO	Hs.840	8	8p12-p11	4.876	9.326	8.279	0.83
3119	211656_x	HLA-DQB1	Hs.409934						
			Hs.534322	6	6p21.3	6.723	9.122	9.572	0.81
1462	215646_s	CSPG2	Hs.443681	5	5q14.3	4.709	7.989	8.841	0.8
28902	216207_x	IGKV1D-13	Hs.390427	2	2p12	7.052	7.783	12.056	0.8
79670	220933_s	ZCCHC6	Hs.136398	9	9q21	6.411	7.015	7.504	0.8
894	200953_s	CCND2	Hs.376071	12	12p13	6.032	6.591	8.467	0.8
1520	202901_x	CTSS	Hs.181301	1	1q21	4.964	8.167	8.522	0.82
3059	202957_at	HCLS1	Hs.14601	3	3q13	5.87	8.608	9.197	0.81
7305	204122_at	TYROBP	Hs.515369	19	19q13.1	6.731	9.395	10.195	0.81
11010	204221_x	GLIPR1	Hs.205558						
			Hs.591034	12	12q21.2	4.511	5.368	6.318	0.81
5790	204960_at	PTPRCAP	Hs.155975	11	11q13.3	5.979	6.378	7.547	0.8
25816	208296_x	TNFAIP8	Hs.271955	5	5q23.1	6.419	7.957	8.362	0.81
3122	208894_at	HLA-DRA	Hs.520048	6	6p21.3	10.277	12.307	12.397	0.82
6955	210972_x	TRA@	Hs.74647	14	14q11.2	5.638	7.751	9.252	0.81
27292	213598_at	DIMT1L	Hs.533222	5	5q11-q14	5.704	6.355	6.758	0.81
199	215051_x	AIF1	Hs.76364	6	6p21.3	7.631	9.972	9.996	0.82
6955	216191_s	TRA@	Hs.74647	14	14q11.2	4.052	4.193	4.899	0.8
3128	217362_x	HLA-DRB6	Hs.534322	6	6p21.3	7.025	8.156	8.639	0.81
51284	220146_at	TLR7	Hs.443036 X		Xp22.3	4.075	4.873	6.3	0.8
2263	203638_s	FGFR2	Hs.533683	10	10q26	8.658	8.215	6.851	-0.79
11163	206302_s	NUDT4	Hs.591008	12	12q21	8.261	7.382	6.39	-0.79
1431	208660_at	CS	Hs.430606						
			Hs.633044	12	12q13.2-q1	9.261	8.926	8.657	-0.79

23710	208869_s	GABARAPI	Hs.524250	12	12p13.2	8.735	8.004	7.172	-0.79
5733	210834_s	PTGER3	Hs.445000	1	1p31.2	4.607	4.185	4.081	-0.81
1329	213735_s	COX5B	Hs.1342	2	2cen-q13	10.722	10.547	9.852	-0.8
3929	214461_at	LBP	Hs.154078	20	20q11.23-q	7.619	6.534	4.444	-0.81
	217249_x	NA	NA	NA	NA	9.315	9.075	8.778	-0.79
28958	218026_at	CCDC56	Hs.16059	17	17q21	10.601	10.227	9.235	-0.8
10768	200850_s	AHCYL1	Hs.485365						
			Hs.592725	1	1p13.2	10.883	10.546	9.723	-0.8
1337	200925_at	COX6A1	Hs.497118	12	12q24.2	11.665	11.47	10.806	-0.8
10105	201489_at	PPIF	Hs.381072	10	10q22-q23	7.943	7.472	7.281	-0.8
4717	203478_at	NDUFC1	Hs.84549	4	4q28.2-q31	10.348	10.078	9.523	-0.8
7369	206716_at	UMOD	Hs.164470	16	16p12.3	12.918	10.363	8.806	-0.8
5523	209633_at	PPP2R3A	Hs.518155	3	3q22.1	9.936	9.13	8.114	-0.79
363	216219_at	AQP6	Hs.54505	12	12q13	7.225	6.606	6.324	-0.79
10659	202156_s	CUGBP2	Hs.309288	10	10p13	4.878	5.502	6.214	0.8
7456	202663_at	WASPIP	Hs.591641	2	2q31.1	4.785	5.177	6.167	0.8
1436	203104_at	CSF1R	Hs.483829	5	5q33-q35	6.201	8.575	8.862	0.81
2215	204007_at	FCGR3B	Hs.372679	1	1q23	5.633	8.107	8.772	0.82
2313	204236_at	FLI1	Hs.504281	11	11q24.1-q2	5.005	5.942	7.241	0.79
5698	204279_at	PSMB9	Hs.132682	6	6p21.3	6.621	9.436	9.569	0.82
10563	205242_at	CXCL13	Hs.100431	4	4q21	3.896	5.251	8.362	0.8
3603	209827_s	IL16	Hs.459095	15	15q26.3	5.705	6.101	7.519	0.8
652128	211637_x	LOC652128	Hs.643624	14	NA	5.003	6.021	9.706	0.8
2760	212737_at	GM2A	Hs.483873	5	5q31.3-q33	6.562	7.925	8.459	0.81
55016	219574_at	1-Mar	Hs.591701						
			Hs.608487	4	4q32.3	4.303	7.006	7.292	0.81
10170	219799_s	DHRS9	Hs.179608	2	2q31.1	4.752	5.569	5.983	0.81
397	201288_at	ARHGDI3	Hs.504877	12	12p12.3	8.592	9.989	10.859	0.8
3965	203236_s	LGALS9	Hs.81337	17	17q11.1	6.354	7.611	7.718	0.81
597	205681_at	BCL2A1	Hs.227817	15	15q24.3	4.111	6.443	7.209	0.81
5966	206036_s	REL	Hs.631886	2	2p13-p12	4.581	5.325	5.899	0.8
7852	209201_x	CXCR4	Hs.421986	2	2q21	5.442	6.196	9.379	0.8
942	210895_s	CD86	Hs.171182	3	3q21	4.449	7.709	7.892	0.81
3122	210982_s	HLA-DRA	Hs.520048	6	6p21.3	9.911	12.069	12.258	0.81
2533	211795_s	FYB	Hs.370503	5	5p13.1	4.912	7.485	7.332	0.82
3113	211990_at	HLA-DPA1	Hs.347270	6	6p21.3	9.995	12.082	12.448	0.81
	217235_x	NA	NA	NA	NA	6.432	6.585	10.952	0.8
58533	217789_at	SNX6	Hs.583855	14	14q13.2	7.111	7.814	8.385	0.8
116496	217966_s	C1orf24	Hs.518662	1	1q25	4.68	4.943	5.665	0.79
1462	221731_x	CSPG2	Hs.443681	5	5q14.3	5.877	8.68	9.806	0.8
6793	40420_at	STK10	Hs.519756	5	5q35.1	5.52	5.909	6.588	0.8
10131	201391_at	TRAP1	Hs.30345	16	16p13.3	8.196	7.924	7.551	-0.8
6390	202675_at	SDHB	Hs.465924	1	1p36.1-p35	9.104	8.67	7.934	-0.8

7164	203786_s	TPD52L1	Hs.591347		6 6q22-q23	9.179	8.524	7.95	-0.79
6997	206286_s	TDGF1	Hs.385870		3 3p21.31	7.856	6.413	5.853	-0.78
873	209213_at	CBR1	Hs.88778		21 21q22.13	8.392	8.165	7.352	-0.8
5805	209694_at	PTS	Hs.503860		11 11q22.3-q2	8.971	8.282	7.818	-0.8
23077	201959_s	MYCBP2	Hs.591221		13 13q22	7.465	7.729	8.583	0.79
6503	203761_at	SLA	Hs.75367		8 8q22.3-qter 8q24	6.272	7.593	8.524	0.8
1462	204620_s	CSPG2	Hs.443681		5 5q14.3	5.996	8.56	9.663	0.79
10154	206471_s	PLXNC1	Hs.584845		12 12q23.3	3.911	4.229	4.47	0.8
9859	207719_x	CEP170	Hs.533635						
	212829_at	NA	NA	NA	1 1q44	6.459	7.169	7.974	0.8
					NA	7.439	7.719	8.366	0.79
200316	214995_s	APOBEC3F	Hs.441124		22 22q13.1	4.585	5.952	6.023	0.82
652745	216401_x	LOC65274	NA	Un	NA	6.472	6.811	11.598	0.8
55577	218231_at	NAGK	Hs.7036		2 2p13.3	7.68	8.707	9.039	0.81
51816	219505_at	CECR1	Hs.170310		22 22q11.2	6.441	8.735	9.131	0.81
4166	221059_s	CHST6	Hs.487510		16 16q22	7.253	8.03	8.679	0.78
3094	200093_s	HINT1	Hs.483305		5 5q31.2	10.988	10.613	10.342	-0.79
1351	201119_s	COX8A	Hs.433901		11 11q12-q13	10.806	10.392	9.888	-0.79
1350	201134_x	COX7C	Hs.430075		5 5q14	12.283	11.907	11.538	-0.79
481	201243_s	ATP1B1	Hs.291196		1 1q24	10.922	10.282	9.901	-0.8
7965	202138_x	JTV1	Hs.301613						
			Hs.520205		7 7p22	8.989	8.448	8.283	-0.81
4694	202298_at	NDUFA1	Hs.534168	X	Xq24	10.742	10.353	10.283	-0.8
10939	202486_at	AFG3L2	Hs.528996		18 18p11	7.23	6.949	6.345	-0.8
4745	206089_at	NELL1	Hs.502145		11 11p15.2-p1	6.008	5.256	5.13	-0.8
1410	209283_at	CRYAB	Hs.408767		11 11q22.3-q2	12.006	11.416	9.325	-0.79
29088	218027_at	MRPL15	Hs.18349		8 8q11.2-q13	9.121	8.865	8.272	-0.78
1520	202902_s	CTSS	Hs.181301		1 1q21	6	10.31	10.325	0.81
2350	204829_s	FOLR2	Hs.433159		11 11q13.3-q1	6.232	8.006	8.083	0.8
10385	205298_s	BTN2A2	Hs.373938		6 6p22.1	5.985	6.701	6.903	0.8
27074	205569_at	LAMP3	Hs.518448		3 3q26.3-q27	3.996	4.626	5.437	0.79
942	205685_at	CD86	Hs.171182		3 3q21	4.878	5.628	6.081	0.8
11119	207485_x	BTN3A1	Hs.191510		6 6p22.1	5.703	6.642	6.726	0.81
1231	207794_at	CCR2	Hs.395						
			Hs.511794		3 3p21.31	4.182	4.283	5.115	0.79
953	209473_at	ENTPD1	Hs.576612		10 10q24	6.231	6.655	7.718	0.79
6404	209879_at	SELPLG	Hs.591014		12 12q24	5.301	6.064	7.055	0.8
	211645_x	NA	NA	NA	NA	5.722	6.476	11.698	0.79
926	215332_s	CD8B	Hs.405667						
			Hs.610012		2 2p12	3.91	3.983	4.427	0.79
960	217523_at	CD44	Hs.502328		11 11p13	4.239	4.554	6.021	0.79
51703	218322_s	ACSL5	Hs.11638		10 10q25.1-q2	5.732	6.14	6.968	0.78

51278	218611_at	IER5	Hs.15725	1	1q25.3	5.348	6.234	7.409	0.78
79866	219544_at	C13orf34	Hs.643464	13	13q22.1	4.561	4.88	5.287	0.81
81606	221011_s	LBH	Hs.567598	2	2p23.1	6.286	6.972	7.554	0.78
25900	36030_at	HOM-TES-	Hs.15243	12	12p13.3	5.705	6.134	6.631	0.79
7965	209971_x	JTV1	Hs.301613						
			Hs.520205	7	7p22	8.629	8.145	7.962	-0.8
4697	217773_s	NDUFA4	Hs.50098	7	7p21.3	11.451	10.959	10.462	-0.79
79711	218305_at	IPO4	Hs.411865	14	14q12	7.03	6.721	6.459	-0.78
684	201641_at	BST2	Hs.118110	19	19p13.2	6.369	7.977	8.501	0.79
10123	202208_s	ARL4C	Hs.111554	2	2q37.1	6.285	6.546	7.747	0.79
8905	203299_s	AP1S2	Hs.121592 X		Xp22.2	5.5	5.795	6.131	0.79
8905	203300_x	AP1S2	Hs.121592 X		Xp22.2	5.549	7.28	7.632	0.81
1231	206978_at	CCR2	Hs.395						
			Hs.511794	3	3p21.31	4.175	4.389	6.897	0.79
3824	207796_x	KLRD1	Hs.562457	12	12p13	4.179	4.306	4.626	0.79
9750	209829_at	C6orf32	Hs.559459	6	6p22.3-p21	4.336	4.734	5.536	0.79
3502	211430_s	IGHG3	Hs.510635	14	14q32.33	8.234	10.344	13.461	0.79
1193	213415_at	CLIC2	Hs.632837 X		Xq28	5.148	6.752	7.082	0.8
80833	221087_s	APOL3	Hs.474737	22	22q13.1	6.393	7.692	7.802	0.8
4072	201839_s	TACSTD1	Hs.542050	2	2p21	10.455	10.038	9.208	-0.78
539	216954_x	ATP5O	Hs.409140	21	21q22.1-q22.2				
					21q22.11	7.538	7.249	6.994	-0.78
5250	200030_s	SLC25A3	Hs.290404	12	12q23	11.318	11	10.691	-0.79
5816	205336_at	PVALB	Hs.295449	22	22q12-q13.1				
					22q13.1	7.279	6.206	4.883	-0.78
23516	212110_at	SLC39A14	Hs.491232	8	8p21.3	9.156	8.308	7.269	-0.77
5777	206687_s	PTPN6	Hs.63489	12	12p13	6.568	7.14	7.646	0.79
10863	208268_at	ADAM28	Hs.174030	8	8p21.2	4.041	4.17	4.773	0.79
4673	208754_s	NAP1L1	Hs.524599						
			Hs.643135	12	12q21.2	7.767	8.015	8.535	0.78
6362	209924_at	CCL18	Hs.143961	17	17q11.2	4.992	6.23	6.878	0.81
4068	210116_at	SH2D1A	Hs.349094 X		Xq25-q26	4.007	4.358	5.724	0.78
25816	210260_s	TNFAIP8	Hs.271955	5	5q23.1	6.869	8.506	8.978	0.8
5724	211661_x	PTAFR	Hs.433540	1	1p35-p34.3	5.485	6.222	6.818	0.8
651629	215176_x	LOC651629	NA Un		NA	6.88	8.206	13.053	0.79
3493	216557_x	IGHA1	Hs.510635	14	14q32.33	5.732	6.056	10.323	0.79
3108	217478_s	HLA-DMA	Hs.351279	6	6p21.3	7.707	9.746	10.141	0.8
	43511_s_a	NA	NA NA		NA	5.731	6.159	6.614	0.79
27089	201568_at	UQCQRQ	Hs.146602	5	5q31.1	10.901	10.355	9.986	-0.79
80347	201913_s	COASY	Hs.296422	17	17q12-q21	8.448	8.103	7.571	-0.78
1595	202314_at	CYP51A1	Hs.417077	7	7q21.2-q21	8.044	7.198	6.731	-0.78
4728	203190_at	NDUFS8	Hs.90443	11	11q13	8.83	8.271	7.758	-0.78
3775	204679_at	KCNK1	Hs.208544	1	1q42-q43	7.539	7.024	6.503	-0.78

8613	212230_at	PPAP2B	Hs.405156						
			Hs.638793	1	1pter-p22.1	9.438	8.578	8.234	-0.8
25994	217845_x	HIGD1A	Hs.7917	3	3p22.1	10.952	10.592	10.207	-0.78
2633	202270_at	GBP1	Hs.62661	1	1p22.2	7.078	9.988	9.999	0.81
836	202763_at	CASP3	Hs.141125	4	4q34	5.424	6.414	6.761	0.8
8869	203217_s	ST3GAL5	Hs.415117	2	2p11.2	5.802	6.353	6.828	0.78
9839	203603_s	ZFHX1B	Hs.34871	2	2q22	5.345	6.453	7.366	0.78
5999	204337_at	RGS4	Hs.386726	1	1q23.3	4.614	5.848	5.969	0.8
	204552_at	NA	NA	NA	NA	4.48	4.723	5.55	0.79
3717	205842_s	JAK2	Hs.591081	9	9p24	5.307	6.351	6.614	0.79
4208	209200_at	MEF2C	Hs.444409	5	5q14	6.079	6.254	7.623	0.79
3458	210354_at	IFNG	Hs.856	12	12q14	4.107	5.311	4.935	0.81
	211908_x	NA	NA	NA	NA	5.418	5.541	8.479	0.79
10117	212592_at	ENAM	Hs.381568	4	4q13.3	6.475	7.165	11.16	0.79
167227	212919_at	DCP2	Hs.443875	5	5q22.2	7.396	8.089	8.327	0.78
9910	213982_s	RABGAP1L	Hs.585378						
			Hs.591475						
			Hs.615081	1	1q24	5.299	5.571	6.811	0.78
7940	215633_x	LST1	Hs.436066	6	6p21.3	6.353	7.411	8.015	0.8
51296	219593_at	SLC15A3	Hs.237856	11	11q12.2	5.546	6.615	6.959	0.8
10989	200955_at	IMMT	Hs.148559	2	2p11.2				
						9.039	8.464	8.194	-0.79
5092	203557_s	PCBD1	Hs.3192	10	10q22	8.872	8.273	7.583	-0.79
10787	207738_s	NCKAP1	Hs.516633	2	2q32	9.052	8.707	8.369	-0.79
80273	212432_at	GRPEL1	Hs.443723	4	4p16	8.395	7.97	7.401	-0.78
1737	213149_at	DLAT	Hs.335551	11	11q23.1	7.848	7.244	6.423	-0.77
25994	221896_s	HIGD1A	Hs.7917	3	3p22.1	10.572	10.08	9.581	-0.77
5538	200975_at	PPT1	Hs.3873	1	1p32	9.681	10.175	10.345	0.78
2589	201722_s	GALNT1	Hs.514806	18	18q12.1	6.909	7.644	8.111	0.79
5900	209050_s	RALGDS	Hs.106185	9	9q34.3	6.087	6.843	7.247	0.78
90634	213375_s	CG018	Hs.161220	13	13q12-q13	6.514	7.489	7.945	0.78
	217157_x	NA	NA	NA	NA	6.298	6.61	10.625	0.79
339562	217480_x	LOC33956	Hs.449972	2	2p11.1	6.427	6.924	10.997	0.79
51177	218223_s	PLEKHO1	Hs.438824	1	1q21.2	5.541	6.784	7.52	0.79
79037	219812_at	MGC2463	Hs.521075	7	7q22.1	4.977	5.056	6.008	0.79
6362	32128_at	CCL18	Hs.143961	17	17q11.2	3.873	4.806	5.478	0.8
4700	202000_at	NDUFA6	Hs.274416	22	22q13.2-q1	7.955	7.572	6.793	-0.78
11030	209487_at	RBPMS	Hs.334587	8	8p12-p11	8.979	8.573	7.606	-0.77
573	211475_s	BAG1	Hs.377484	9	9p12	8.12	7.521	7.052	-0.78
51142	217720_at	CHCHD2	Hs.389996						
			Hs.547257	7	7p11.2	10.827	10.5	10.444	-0.79
54458	217794_at	PRR13	Hs.426359						
			Hs.631599	12	12q12	9.912	9.863	9.145	-0.79

64960	221437_s	MRPS15	Hs.352839		1	1p35-p34.1	7.764	7.337	7.078	-0.79
7805	201721_s	LAPTM5	Hs.371021		1	1p34	7.754	10.635	11.281	0.8
4673	204528_s	NAP1L1	Hs.524599							
			Hs.643135		12	12q21.2	7.937	8.261	8.819	0.77
1439	205159_at	CSF2RB	Hs.592192		22	22q13.1	4.391	7.019	8.224	0.78
26191	208010_s	PTPN22	Hs.535276		1	1p13.3-p13	3.707	3.947	4.185	0.79
9473	210785_s	C1orf38	Hs.10649		1	1p35.3	4.868	6.561	7.247	0.8
651961	211643_x	NA	NA	NA		NA	5.886	6.171	11.152	0.79
1540	213295_at	CYLD	Hs.578973		16	16q12.1	6.08	6.312	7.119	0.78
923	213958_at	CD6	Hs.502710		11	11q13	6.264	6.353	6.966	0.77
1540	221905_at	CYLD	Hs.578973		16	16q12.1	4.662	4.995	5.682	0.78
2115	221911_at	ETV1	Hs.22634		7	7p21.3	4.17	4.435	5.563	0.77
316	205082_s	AOX1	Hs.406238		2	2q33	8.51	7.066	5.748	-0.78
509	208870_x	ATP5C1	Hs.271135		10	10p15.1	11.799	11.41	10.86	-0.78
29078	219006_at	C6orf66	Hs.591333		6	6q16.1	8.543	7.852	7.476	-0.78
3133	200904_at	HLA-E	Hs.118354		6	6p21.3	9.118	10.374	10.568	0.79
10659	202158_s	CUGBP2	Hs.309288		10	10p13	4.458	4.828	5.89	0.78
5567	202742_s	PRKACB	Hs.487325		1	1p36.1	6.141	6.909	7.206	0.78
1230	205098_at	CCR1	Hs.301921		3	3p21	5.588	8.271	8.148	0.79
10561	214059_at	IFI44	Hs.82316		1	1p31.1	4.221	4.322	4.546	0.76
3493	216510_x	IGHA1	Hs.510635		14	14q32.33	4.427	4.638	9.998	0.78
920	203547_at	CD4	Hs.631659		12	12pter-p12	6.326	7.129	7.818	0.77
9232	203554_x	PTTG1	Hs.350966		5	5q35.1	5.776	7.648	7.093	0.8
940	206545_at	CD28	Hs.591629		2	2q33	3.849	3.916	4.268	0.78
149628	208965_s	PYHIN1	Hs.380250		1	1q23.1	5.673	7.272	7.953	0.79
23240	209760_at	KIAA0922	Hs.205572		4	4q31.3	5.05	5.311	5.713	0.78
7940	210629_x	LST1	Hs.436066		6	6p21.3	6.188	7.343	7.841	0.78
647478	211644_x	NA	NA	NA		NA	5.907	6.601	12.166	0.78
	211650_x	NA	NA	NA		NA	5.411	5.56	8.821	0.78
3507	216491_x	IGHM	Hs.510635		14	14q32.33	5.153	5.883	10.115	0.78
51075	201175_at	TXNDC14	Hs.166011		11	11cen-q22.1	9.353	8.9	8.719	-0.78
9521	204905_s	EEF1E1	Hs.631818		6	6p24.3-p25	8.602	7.852	7.511	-0.77
6539	206058_at	SLC6A12	Hs.437174		12	12p13	7.377	6.922	5.346	-0.77
6609	209420_s	SMPD1	Hs.498173		11	11p15.4-p1	7.914	7.674	6.363	-0.77
26284	212087_s	ERAL1	Hs.3426		17	17q11.2	6.472	6.084	5.887	-0.78
135138	214204_at	PACRG	Hs.25791		6	6q26	4.916	4.651	4.375	-0.78
3081	214307_at	HGD	Hs.368254							
			Hs.616526		3	3q21-q23	8.181	7.196	5.153	-0.79
51144	217869_at	HSD17B12	Hs.132513		11	11p11.2	9.794	9.29	8.923	-0.78
4718	218101_s	NDUFC2	Hs.407860		11	11q14.1	10.066	9.662	9.378	-0.78
103910	221474_at	MRLC2	Hs.464472		18	18p11.31	11.563	11.229	11.105	-0.77
23284	209867_s	LPHN3	Hs.28391							
			Hs.411097		4	4q13.1	4.735	4.347	4.303	-0.78

51109	217776_at	RDH11	Hs.226007	14	14q24.1	10.543	10.019	9.151	-0.77
83658	217918_at	DYNLRB1	Hs.531876	20	20q11.21	9.971	9.447	9.295	-0.77
10982	202501_at	MAPRE2	Hs.532824	18	18q12.1	6.939	7.451	7.722	0.79
7318	203281_s	UBE1L	Hs.16695	3	3p21	6.312	6.734	7.293	0.77
10403	204162_at	KNTC2	Hs.414407	18	18p11.32	4.159	5.172	4.891	0.8
355	204780_s	FAS	Hs.244139	10	10q24.1	6.929	7.826	8.216	0.77
313	205639_at	AOAH	Hs.488007	7	7p14-p12	5.466	5.895	6.881	0.78
952	205692_s	CD38	Hs.479214	4	4p15	4.821	6.455	7.12	0.79
3500	211633_x	IGHG1	Hs.510635	14	14q32.33	4.925	5.013	9.313	0.78
28461	211635_x	IGHV1-69	Hs.634941	14	14q32.32-q	5.175	5.241	9.474	0.78
	216576_x	NA	NA	NA	NA	5.184	5.811	10.86	0.78
64231	219666_at	MS4A6A	Hs.523702	11	11q12.1	6.531	9.571	9.168	0.8
2101	1487_at	ESRRA	Hs.110849	11	11q13	7.347	7.132	6.41	-0.76
6392	202026_at	SDHD	Hs.356270	11	11q23	10.772	10.427	9.671	-0.77
2263	208228_s	FGFR2	Hs.533683	10	10q26	7.718	7.418	5.892	-0.77
5747	208820_at	PTK2	Hs.395482	8	8q24-qter	8.469	8.244	7.776	-0.76
25828	209077_at	TXN2	Hs.211929	22	22q13.1	7.927	7.489	7.377	-0.78
7434	211598_x	VIPR2	Hs.490817	7	7q36.3	7.005	6.851	6.729	-0.76
3910	202202_s	LAMA4	Hs.213861	6	6q21	4.973	5.533	6.728	0.77
1936	203113_s	EEF1D	Hs.333388	8	8q24.3	9.531	9.733	10.387	0.77
5142	203708_at	PDE4B	Hs.198072	1	1p31	5.473	6.348	7.95	0.77
3385	204949_at	ICAM3	Hs.75516	19	19p13.3-p1	5.883	6.174	7.747	0.77
54900	207734_at	LAX1	Hs.272794	1	1q32.1	4.401	4.552	5.607	0.78
3479	209541_at	IGF1	Hs.160562	12	12q22-q23	4.735	5.698	6.63	0.76
28461	211634_x	IGHV1-69	Hs.634941	14	14q32.32-q	5.09	5.278	10.085	0.78
3119	211654_x	HLA-DQB1	Hs.409934						
			Hs.534322	6	6p21.3	7.01	9.939	10.026	0.78
	212386_at	NA	NA	NA	NA	6.674	6.995	8.867	0.78
23347	212569_at	SMCHD1	Hs.8118	18	18p11.32	6.233	6.632	7.432	0.78
27250	212594_at	PDCD4	Hs.232543	10	10q24	5.72	5.838	6.433	0.77
27334	214615_at	P2RY10	Hs.296433 X		Xq21.1	3.784	3.819	4.336	0.78
10161	218589_at	P2RY5	Hs.123464	13	13q14	7.639	8.108	8.744	0.76
4722	201740_at	NDUFS3	Hs.502528	11	11p11.11	8.981	8.65	8.337	-0.77
687	203543_s	KLF9	Hs.150557						
			Hs.602267	9	9q13	7.724	5.992	5.799	-0.78
3094	207721_x	HINT1	Hs.483305	5	5q31.2	11.193	10.96	10.588	-0.77
5523	209632_at	PPP2R3A	Hs.518155	3	3q22.1	7.871	7.672	6.743	-0.77
55847	218597_s	ZCD1	Hs.370102	10	10q21.1	9.094	7.933	6.917	-0.77
2001	220625_s	ELF5	Hs.11713	11	11p13-p12	5.617	4.575	4.409	-0.78
2110	33494_at	ETFDH	Hs.155729	4	4q32-q35	6.733	6.09	5.441	-0.77
10409	202391_at	BASP1	Hs.201641	5	5p15.1-p14	7.179	7.716	9.347	0.77
1130	203518_at	LYST	Hs.532411	1	1q42.1-q42	5.026	5.294	6.714	0.77
4283	203915_at	CXCL9	Hs.77367	4	4q21	4.972	11.34	10.666	0.81

1675	205382_s	CFD	Hs.155597	19	19p13.3	5.879	7.184	8.127	0.76
23643	206584_at	LY96	Hs.69328	8	8q21.11	6.098	9.126	9.673	0.79
3822	206785_s	KLRC2	Hs.591157	12	12p13	4.043	4.691	5.528	0.77
10943	207551_s	MSL3L1	Hs.307924 X		Xp22.3	6.655	6.773	7.665	0.77
9473	207571_x	C1orf38	Hs.10649	1	1p35.3	4.861	6.207	6.875	0.78
4048	208771_s	LTA4H	Hs.524648	12	12q22	8.822	9.101	9.429	0.76
	212387_at	NA	NA		NA	6.106	6.469	7.866	0.77
28517	215524_x	TRDV2	Hs.74647	14	14q11	3.89	4.095	4.312	0.76
971	215925_s	CD72	Hs.116481	9	9p13.3	4.51	6.118	6.109	0.79
2908	216321_s	NR3C1	Hs.122926	5	5q31.3	7.851	8.29	8.648	0.77
712	218232_at	C1QA	Hs.632379	1	1p36.12	6.795	11.129	10.665	0.8
51303	219117_s	FKBP11	Hs.119177	12	12q13.12	7.296	7.748	9.516	0.78
64092	220330_s	SAMSN1	Hs.473341						
			Hs.570423	21	21q11	5.053	8.272	8.941	0.79
55423	220485_s	SIRPG	Hs.590883	20	20p13	5.028	5.137	5.774	0.78
55707	220731_s	NECAP2	Hs.437385	1	1p36.13	6.71	7.439	7.809	0.78
7462	221581_s	LAT2	Hs.520943	7	7q11.23	5.153	5.605	6.881	0.78
28299	221671_x	IGKV1-5	Hs.449621	2	2p12	10.048	10.941	13.481	0.78
10768	200848_at	AHCYL1	Hs.485365						
			Hs.592725	1	1p13.2	9.044	8.696	7.584	-0.77
4259	201403_s	MGST3	Hs.191734	1	1q23	11.216	11.051	10.352	-0.77
573	202387_at	BAG1	Hs.377484	9	9p12	7.532	7.106	6.857	-0.76
23530	202783_at	NNT	Hs.482043	5	5p13.1-5ce	8.606	8.387	7.399	-0.76
4485	205614_x	MST1	Hs.349110						
			Hs.512587	3	3p21	8.265	7.886	7.247	-0.76
509	205711_x	ATP5C1	Hs.271135	10	10p15.1	11.521	11.171	10.514	-0.77
1288	213992_at	COL4A6	Hs.145586 X		Xq22	5.03	4.519	4.047	-0.76
79789	221042_s	CLMN	Hs.301478	14	14q32.13	6.501	6.071	5.419	-0.76
7805	201720_s	LAPTM5	Hs.371021	1	1p34	6.556	9.923	9.836	0.79
4318	203936_s	MMP9	Hs.297413	20	20q11.2-q1	5.233	5.416	6.938	0.76
240	204446_s	ALOX5	Hs.89499	10	10q11.2	5.245	7.484	8.807	0.78
3669	204698_at	ISG20	Hs.459265	15	15q26	5.422	6.692	7.311	0.76
5778	204852_s	PTPN7	Hs.402773	1	1q32.1	4.86	5.334	5.872	0.76
1475	204971_at	CSTA	Hs.518198	3	3q21	4.672	6.927	8.029	0.78
958	205153_s	CD40	Hs.472860	20	20q12-q13.	5.38	6.145	6.449	0.77
10866	206082_at	HCP5	Hs.549053	6	6p21.3	5.867	7.527	7.35	0.8
931	210356_x	MS4A1	Hs.438040	11	11q12	4.247	4.381	5.777	0.77
9859	212746_s	CEP170	Hs.533635						
			Hs.644237	1	1q44	5.571	6.466	6.688	0.77
28299	214836_x	IGKV1-5	Hs.449621	2	2p12	7.738	8.565	11.437	0.78
391427	217378_x	LOC39142	NA	2	2q14.1	6.489	6.986	11.751	0.78
1112	218031_s	CHES1	Hs.434286						
			Hs.621371	14	14q31.3	5.451	6.379	6.884	0.77

2217	218831_s	FCGRT	Hs.111903	19	19q13.3	7.675	8.382	8.485	0.77
3514	221651_x	IGKC	Hs.449621	2	2p12	10.034	10.989	13.515	0.78
3689	202803_s	ITGB2	Hs.375957	21	21q22.3	5.421	8.351	8.652	0.78
4938	202869_at	OAS1	Hs.524760	12	12q24.1	6.246	8.063	7.541	0.78
9603	204702_s	NFE2L3	Hs.404741	7	7p15-p14	4.11	4.976	5.422	0.78
7351	208998_at	UCP2	Hs.80658	11	11q13	6.838	8.742	8.947	0.78
3535	209138_x	IGL@	Hs.449585	22	22q11.1-q1	9.208	9.969	13.655	0.77
6373	210163_at	CXCL11	Hs.632592	4	4q21.2	3.734	7.914	8.312	0.79
958	215346_at	CD40	Hs.472860	20	20q12-q13.	6.098	6.667	6.987	0.77
4063	215967_s	LY9	Hs.403857	1	1q21.3-q22	5.024	5.139	6.049	0.77
10578	37145_at	GNLY	Hs.105806	2	2p12-q11	4.353	4.375	5.952	0.78
80183	44790_s_a	C13orf18	Hs.98117	13	13q14.12	4.111	4.408	5.69	0.76
1340	201441_at	COX6B1	Hs.431668	19	19q13.1	10.515	10.139	9.803	-0.76
5909	203911_at	RAP1GAP	Hs.148178	1	1p36.1-p35	8.647	8.105	6.622	-0.77
9071	205328_at	CLDN10	Hs.157002						
			Hs.534377						
			Hs.597167	13	13q31-q34	10.23	9.444	8.693	-0.77
2813	208473_s	GP2	Hs.53985	16	16p12	5.916	5.183	5.12	-0.77
5265	211429_s	SERPINA1	Hs.525557	14	14q32.1	12.402	11.073	10.303	-0.78
10102	212656_at	TSFM	Hs.632704	12	12q13-q14	7.834	7.281	6.756	-0.78
56922	218440_at	MCCC1	Hs.47649	3	3q27	8.366	7.888	6.96	-0.76
4154	201153_s	MBNL1	Hs.478000						
			Hs.558914	3	3q25	8.582	8.69	9.424	0.77
7128	202644_s	TNFAIP3	Hs.591338	6	6q23	6.442	7.442	8.207	0.77
27250	202731_at	PDCD4	Hs.232543	10	10q24	4.962	6.192	6.341	0.78
10320	205039_s	ZNFN1A1	Hs.435949	7	7p13-p11.1	6.348	6.908	7.08	0.76
4125	209166_s	MAN2B1	Hs.334626						
			Hs.356769	19	19cen-q13.	6.357	6.861	7.407	0.76
57157	209780_at	PHTF2	Hs.203965	7	7q11.23-q2	6.486	7.117	7.696	0.76
2313	210786_s	FLI1	Hs.504281	11	11q24.1-q2	4.483	5.093	5.545	0.78
356	210865_at	FASLG	Hs.2007	1	1q23	4.239	4.407	4.631	0.75
28831	211798_x	IGLJ3	Hs.449585	22	22q11.1-q1	5.582	5.93	10.481	0.77
115207	212192_at	KCTD12	Hs.109438	13	13q22.3	9.667	10.105	10.486	0.75
23048	212288_at	FNBP1	Hs.189409	9	9q34	6.874	7.698	8.118	0.76
23213	212344_at	SULF1	Hs.409602	8	8q13.2-q13	6.087	6.303	7.244	0.77
	214777_at	NA	NA		NA	5.882	6.029	11.899	0.77
3492	214916_x	IGH@	Hs.510635	14	14q32.33	5.393	5.393	9.379	0.77
3495	214973_x	IGHD	Hs.510635	14	14q32.33	5.621	5.82	10.059	0.77
10308	219540_at	ZNF267	Hs.460645	16	16p11.2	5.95	7.173	7.459	0.76
79772	220122_at	MCTP1	Hs.591248	5	5q15	4.269	5.69	6.103	0.76
7388	202233_s	UQCRH	Hs.481571	1	1p33	10.892	10.739	10.433	-0.76
4712	203613_s	NDUFB6	Hs.493668	9	9p21.1	9.817	9.332	8.952	-0.76
3084	206343_s	NRG1	Hs.453951	8	8p21-p12	5.539	4.753	4.325	-0.75

760	209301_at	CA2	Hs.155097		8 8q22	9.923	9.427	8.025	-0.77
8738	209833_at	CRADD	Hs.38533						
			Hs.591016		12 12q21.33-q	7.337	6.962	6.625	-0.76
1672	210397_at	DEFB1	Hs.32949		8 8p23.2-p23	11.873	11.358	9.967	-0.76
4485	216320_x	MST1	Hs.349110						
			Hs.512587		3 3p21	8.322	7.847	6.979	-0.75
55366	218326_s	LGR4	Hs.502176		11 11p14-p13	9.295	8.924	8.011	-0.75
51016	219203_at	C14orf122	Hs.271614		14 14q11.2	6.685	6.428	6.175	-0.75
7849	121_at	PAX8	Hs.469728		2 2q12-q14	9.69	9.56	8.57	-0.76
11171	200870_at	STRAP	Hs.504895		12 12p12.3	9.587	9.212	8.99	-0.76
23365	201334_s	ARHGEF12	Hs.24598		11 11q23.3	10.256	9.899	9.413	-0.75
1528	207843_x	CYB5A	Hs.465413		18 18q23	11.009	10.621	9.212	-0.76
4191	209036_s	MDH2	Hs.520967		7 7p12.3-q11	9.553	9.205	8.678	-0.76
6048	209111_at	RNF5	Hs.512071						
			Hs.534342		6 6p21.3	9.11	8.936	8.016	-0.77
83451	221927_s	ABHD11	Hs.520943		7 7q11.23	7.376	6.989	6.623	-0.76
9857	204373_s	CEP350	Hs.413045		1 1p36.13-q4	6.249	7.239	7.486	0.76
9252	204633_s	RPS6KA5	Hs.510225		14 14q31-q32.	4.743	5.106	5.809	0.76
2219	205237_at	FCN1	Hs.440898		9 9q34	4.428	4.851	7.083	0.75
4938	205552_s	OAS1	Hs.524760		12 12q24.1	5.563	7.349	6.913	0.79
10538	205965_at	BATF	Hs.509964		14 14q24.3	5.785	5.952	6.539	0.76
953	207691_x	ENTPD1	Hs.576612		10 10q24	4.594	5.592	6.372	0.77
3055	208018_s	HCK	Hs.126521		20 20q11-q12	5.357	6.553	7.463	0.77
861	209360_s	RUNX1	Hs.149261						
			Hs.612648		21 21q22.3	5.806	6.283	7.529	0.75
23347	212579_at	SMCHD1	Hs.8118		18 18p11.32	5.99	6.657	7.595	0.75
23526	212873_at	HMHA1	Hs.465521		19 19p13.3	5.738	6.209	6.924	0.76
3514	214669_x	IGKC	Hs.449621		2 2p12	8.264	9.202	12.193	0.77
91353	215946_x	CTA-246H3	Hs.567636		22 22q11.23	6.637	6.998	10.183	0.77
	217227_x	NA	NA	NA	NA	6.257	6.572	10.365	0.77
64108	219684_at	RTP4	Hs.43388		3 3q27.3	5.409	6.655	6.696	0.79
7099	221060_s	TLR4	Hs.174312		9 9q32-q33	4.872	5.84	6.391	0.77
958	35150_at	CD40	Hs.472860		20 20q12-q13.	6.933	7.515	7.839	0.78
79602	201346_at	ADIPOR2	Hs.371642		12 12p13.31	8.124	7.71	7.574	-0.76
4817	202891_at	NIT1	Hs.146406		1 1q21-q22	8.311	8.15	7.545	-0.77
2271	203033_x	FH	Hs.498239		1 1q42.1	8.542	8.036	7.624	-0.76
3336	205133_s	HSPE1	Hs.1197		2 2q33.1	9.583	8.954	8.494	-0.76
5563	207709_at	PRKAA2	Hs.591439		1 1p31	4.863	4.571	4.319	-0.76
7153	201292_at	TOP2A	Hs.156346		17 17q21-q22	4.145	6.095	4.929	0.79
4689	205147_x	NCF4	Hs.474781		22 22q13.1	4.736	5.588	6.169	0.77
11184	206296_x	MAP4K1	Hs.95424		19 19q13.1-q1	5.123	5.15	5.849	0.76
10109	208679_s	ARPC2	Hs.529303		2 2q36.1	10.414	11.107	11.283	0.78
27350	209584_x	APOBEC3C	Hs.441124		22 22q13.1-q1	5.367	6.241	6.379	0.77

1462	211571_s	CSPG2	Hs.443681	5	5q14.3	5.268	7.358	8.366	0.77
3105	213932_x	HLA-A	Hs.181244	6	6p21.3	11.512	12.62	12.203	0.8
1521	214450_at	CTSW	Hs.416848	11	11q13.1	5.155	5.393	6.04	0.75
3107	216526_x	HLA-C	Hs.77961						
			Hs.449621						
			Hs.591791	6	6p21.3	10.731	11.862	11.561	0.8
11009	221601_s	IL24	Hs.58831						
			Hs.642714	1	1q32	4.546	4.635	6.105	0.77
391	203175_at	RHOG	Hs.501728	11	11p15.5-p1	7.27	7.811	8.164	0.74
3662	204562_at	IRF4	Hs.401013	6	6p25-p23	5.505	5.552	6.607	0.76
6348	205114_s	CCL3	Hs.514107	17	17q11-q21	5.071	7	8.067	0.77
6932	205255_x	TCF7	Hs.573153	5	5q31.1	6.526	6.84	7.171	0.75
608	206641_at	TNFRSF17	Hs.2556	16	16p13.1	3.852	3.866	7.877	0.77
3119	209823_x	HLA-DQB1	Hs.409934						
			Hs.534322	6	6p21.3	6.083	9.44	9.176	0.79
3516	211974_x	RBPSUH	Hs.479396	4	4p15.2	8.442	9.09	9.238	0.76
28831	214677_x	IGLJ3	Hs.449585	22	22q11.1-q1	9.3	9.981	13.59	0.77
3535	215379_x	IGL@	Hs.449585	22	22q11.1-q1	7.748	8.168	11.649	0.77
4940	218400_at	OAS3	Hs.528634	12	12q24.2	5.301	6.3	6.28	0.76
9685	201769_at	CLINT1	Hs.132853	5	5q23.1-q33	9.445	9.211	8.791	-0.75
8859	204090_at	STK19	Hs.534847	6	6p21.3	7.829	7.327	7.104	-0.75
2021	204824_at	ENDOG	Hs.591905	9	9q34.1	6.427	6.253	5.468	-0.76
549	205052_at	AUH	Hs.175905	9	9q22.31	9.652	9.018	7.882	-0.76
5733	208169_s	PTGER3	Hs.445000	1	1p31.2	5.333	5.043	4.684	-0.76
5037	210825_s	PEBP1	Hs.433863	12	12q24.23	11.047	10.114	9.873	-0.77
57017	212228_s	COQ9	Hs.513632	16	16q13	9.251	9.087	7.928	-0.77
9728	212450_at	KIAA0256	Hs.9997	15	15q21.1	8.513	8.286	7.951	-0.75
1528	217021_at	CYB5A	Hs.465413	18	18q23	5.155	4.998	4.849	-0.77
23788	217772_s	MTCH2	Hs.269944	11	11p11.2	9.263	9.052	8.466	-0.76
51015	218170_at	ISOC1	Hs.483296	5	5q22.1-q33	8.561	7.896	7.56	-0.75
80775	218897_at	MGC10993	Hs.439991	2	2q14.2	5.821	5.277	4.762	-0.76
4154	201151_s	MBNL1	Hs.478000						
			Hs.558914	3	3q25	6.233	7.207	7.828	0.76
9263	202693_s	STK17A	Hs.268887	7	7p12-p14	6.421	7.037	8.101	0.75
5567	202741_at	PRKACB	Hs.487325	1	1p36.1	8.61	8.979	9.507	0.76
6793	203047_at	STK10	Hs.519756	5	5q35.1	5.47	5.903	6.463	0.75
2215	204006_s	FCGR3B	Hs.372679	1	1q23	4.827	8.727	8.865	0.78
2207	204232_at	FCER1G	Hs.433300	1	1q23	7.036	10.261	10.252	0.78
1462	204619_s	CSPG2	Hs.443681	5	5q14.3	4.99	6.242	7.801	0.75
10125	205590_at	RASGRP1	Hs.591127	15	15q15	6.514	6.684	7.44	0.75
3575	205798_at	IL7R	Hs.591742	5	5p13	4.902	5.226	7.192	0.74
3431	208012_x	SP110	Hs.145150	2	2q37.1	6.384	7.258	7.771	0.76
3431	209762_x	SP110	Hs.145150	2	2q37.1	5.987	6.826	7.586	0.75

7096	210176_at	TLR1	Hs.575090						
			Hs.621817	4	4p14	4.697	6.38	6.744	0.76
23180	212646_at	RAFTLIN	Hs.98910	3	3p24.3	6.187	6.782	7.761	0.75
5965	212917_x	RECQL	Hs.235069	12	12p12	6.415	7.241	7.543	0.76
5142	215671_at	PDE4B	Hs.198072	1	1p31	3.683	3.765	4.047	0.75
3493	217360_x	IGHA1	Hs.510635	14	14q32.33	4.732	4.822	7.67	0.76
10320	220704_at	ZNFN1A1	Hs.435949	7	7p13-p11.1	3.927	3.974	4.699	0.76
1852	205777_at	DUSP9	Hs.144879 X		Xq28	7.766	6.871	6.092	-0.75
735	206727_at	C9	Hs.481980	5	5p14-p12	4.839	3.835	3.735	-0.74
2180	207275_s	ACSL1	Hs.406678	4	4q34-q35	10.038	9.77	8.203	-0.76
2104	207981_s	ESRRG	Hs.444225	1	1q41	8.656	8.15	6.282	-0.76
213	211298_s	ALB	Hs.418167	4	4q11-q13	9.542	4.019	4.016	-0.78
26519	218408_at	TIMM10	Hs.235750	11	11q12.1-q1	7.612	7.497	6.982	-0.75
10352	218766_s	WARS2	Hs.523506	1	1p13.3-p13	5.688	5.566	5.058	-0.75
79837	218942_at	PIP5K2C	Hs.144502	12	12q13.3	7.778	7.545	7.049	-0.74
79568	219176_at	FLJ22555	Hs.154494	2	2q33.1	8.306	7.881	7.232	-0.75
7001	39729_at	PRDX2	Hs.631612	19	19p13.2	10.383	10.059	9.002	-0.75
9246	201649_at	UBE2L6	Hs.425777	11	11q12	7.643	9.334	9.134	0.78
1389	201988_s	CREBL2	Hs.591156	12	12p13	7.437	7.856	8.208	0.74
8439	203269_at	NSMAF	Hs.372000	8	8q12-q13	6.822	7.086	7.671	0.75
81553	208092_s	FAM49A	Hs.467769	2	2p24.3	4.683	5.284	5.851	0.75
26156	212018_s	RSL1D1	Hs.592044	16	16p13.13	7.647	8.081	8.215	0.75
4687	214084_x	NCF1	Hs.520943	7	7q11.23	4.645	5.032	5.561	0.75
51192	219161_s	CKLF	Hs.15159	16	16q21	7.1	7.699	8.53	0.75
3032	201007_at	HADHB	Hs.534639	2	2p23	10.635	10.152	9.833	-0.76
5236	201968_s	PGM1	Hs.1869	1	1p31	8.776	8.437	7.661	-0.75
3929	211652_s	LBP	Hs.154078	20	20q11.23-q	6.864	6.509	5.313	-0.76
2271	214170_x	FH	Hs.498239	1	1q42.1	9.351	8.676	8.117	-0.75
51081	217932_at	MRPS7	Hs.71787	17	17q25	7.693	7.548	7.008	-0.75
60488	217942_at	MRPS35	Hs.311072	12	12p11	8.428	7.995	7.365	-0.76
53343	218375_at	NUDT9	Hs.149500	4	4q22.1	7.768	7.344	6.961	-0.74
27247	218946_at	HIRIP5	Hs.430439	2	2p15-p13	8.15	7.654	7.34	-0.74
5152	205593_s	PDE9A	Hs.473927	21	21q22.3	6.537	5.716	5.63	-0.75
539	200818_at	ATP5O	Hs.409140	21	21q22.1-q22.2				
					21q22.11	11.236	10.785	10.5	-0.75
10935	201619_at	PRDX3	Hs.523302	10	10q25-q26	10.692	10.531	9.89	-0.75
36	205355_at	ACADSB	Hs.81934	10	10q26.13	7.428	6.387	5.514	-0.76
38	205412_at	ACAT1	Hs.232375	11	11q22.3-q2	11.109	10.564	8.945	-0.75
1466	207030_s	CSRP2	Hs.530904	12	12q21.1	9.374	8.754	7.508	-0.75
1528	209366_x	CYB5A	Hs.465413	18	18q23	11.28	10.81	9.461	-0.75
1632	209759_s	DCI	Hs.403436	16	16p13.3	8.165	7.081	6.728	-0.75
729	210168_at	C6	Hs.481992	5	5p13	6.988	5.094	5.046	-0.76
11223	213380_x	MSTP9	Hs.349110						

			Hs.475654		1 1p36.13	7.912	7.414	6.674	-0.74
1491	217127_at	CTH	Hs.19904		1 1p31.1	7.023	5.866	4.71	-0.75
26999	220999_s	CYFIP2	Hs.519702		5 5q33.3	8.511	8.009	7.076	-0.74
4242	204153_s	MFNG	Hs.517603		22 22q12	5.405	5.469	6.461	0.75
10964	204439_at	IFI44L	Hs.389724		1 1p31.1	4.932	8.337	7.819	0.79
100	204639_at	ADA	Hs.255479		20 20q12-q13.	5.053	5.877	6.218	0.77
1230	205099_s	CCR1	Hs.301921		3 3p21	4.692	7.18	6.105	0.78
7185	205599_at	TRAF1	Hs.531251		9 9q33-q34	5.193	5.301	5.818	0.75
4063	210370_s	LY9	Hs.403857		1 1q21.3-q22	4.2	4.278	4.7	0.74
6373	211122_s	CXCL11	Hs.632592		4 4q21.2	3.821	9.344	7.992	0.79
23347	212577_at	SMCHD1	Hs.8118		18 18p11.32	5.546	6.21	6.641	0.76
116496	217967_s	C1orf24	Hs.518662		1 1q25	5.549	6.095	7.608	0.74
55080	218746_at	TAPBPL	Hs.504597		12 12p13.31	6.465	6.926	7.436	0.73
55601	218986_s	FLJ20035	Hs.591710		4 4q32.3	6.497	7.633	7.847	0.75
3778	221584_s	KCNMA1	Hs.144795		10 10q22.3	5.314	6.43	6.642	0.75
3659	202531_at	IRF1	Hs.436061		5 5q31.1	5.809	8.051	7.936	0.77
4067	202626_s	LYN	Hs.491767						
			Hs.614775		8 8q13	5.603	8.055	7.698	0.77
7128	202643_s	TNFAIP3	Hs.591338		6 6q23	4.981	6.436	6.964	0.77
976	202910_s	CD97	Hs.466039		19 19p13	5.378	6.219	6.933	0.75
	202970_at	NA	NA	NA	NA	5.88	6.065	6.151	0.74
6304	203408_s	SATB1	Hs.517717		3 3p23	6.613	6.686	7.422	0.75
355	204781_s	FAS	Hs.244139		10 10q24.1	5.878	6.701	7.281	0.74
3684	205786_s	ITGAM	Hs.172631		16 16p11.2	5.437	7.246	7.256	0.77
945	206120_at	CD33	Hs.83731		19 19q13.3	5.534	6.466	6.576	0.76
6509	212811_x	SLC1A4	Hs.323878		2 2p15-p13	5.808	5.846	6.359	0.75
7852	217028_at	CXCR4	Hs.421986		2 2q21	5.881	6.433	9.704	0.75
8635	217983_s	RNASET2	Hs.529989		6 6q27	7.852	10.063	10.434	0.77
8635	217984_at	RNASET2	Hs.529989		6 6q27	7.897	9.931	10.061	0.77
54855	220306_at	FAM46C	Hs.356216		1 1p12	4.734	4.848	5.976	0.76
6647	200642_at	SOD1	Hs.443914		21 21q22.1				
					21q22.11	11.682	11.246	10.898	-0.75
389840	200979_at	MAP3K15	Hs.471144 X		Xp22.12	7.766	7.137	6.548	-0.73
3426	203854_at	CFI	Hs.312485		4 4q25	10.479	10.078	9.18	-0.74
5774	203997_at	PTPN3	Hs.436429		9 9q31	7.659	7.537	6.842	-0.75
27069	209249_s	GHITM	Hs.352656		10 10q23.1	10.67	10.448	9.946	-0.75
509	213366_x	ATP5C1	Hs.271135		10 10p15.1	11.575	11.23	10.614	-0.75
27013	200070_at	C2orf24	Hs.4973		2 2q35	8.517	8.139	7.741	-0.74
351	200602_at	APP	Hs.642685		21 21q21.2				
					21q21.3	10.177	9.996	9.576	-0.75
1347	201597_at	COX7A2	Hs.70312		6 6q12	11.349	10.858	10.648	-0.76
1345	201754_at	COX6C	Hs.351875		8 8q22-q23	11.276	10.674	10.551	-0.75
5265	202833_s	SERPINA1	Hs.525557		14 14q32.1	12.394	10.815	10.044	-0.75

6337	203453_at	SCNN1A	Hs.591047	12	12p13	10.097	9.692	8.578	-0.74
2039	204505_s	EPB49	Hs.106124	8	8p21.1	7.214	6.911	6.705	-0.73
27069	209248_at	GHITM	Hs.352656	10	10q23.1	10.433	9.914	9.49	-0.75
1646	209699_x	AKR1C2	Hs.460260						
			Hs.567256	10	10p15-p14	9.324	8.724	6.909	-0.74
1327	213758_at	COX4I1	Hs.433419	16	16q22-qter	5.602	4.953	5.04	-0.77
8802	217874_at	SUCLG1	Hs.270428	2	2p11.2	11.243	10.848	9.374	-0.75
5950	219140_s	RBP4	Hs.50223	10	10q23-q24	9.46	6.839	6.1	-0.76
3988	201847_at	LIPA	Hs.127445	10	10q23.2-q2	9.23	10.831	10.774	0.78
10769	201939_at	PLK2	Hs.398157						
			Hs.642858	5	5q12.1-q13	4.865	5.817	6.108	0.75
23064	201964_at	SETX	Hs.460317	9	9q34.13	6.445	6.859	7.212	0.74
6503	203760_s	SLA	Hs.75367	8	8q22.3-qter				
					8q24	5.586	6.61	6.843	0.76
4690	204725_s	NCK1	Hs.477693	3	3q21	6.216	6.706	7.263	0.75
3431	209761_s	SP110	Hs.145150	2	2q37.1	6.131	7.128	7.724	0.76
51752	209788_s	ARTS-1	Hs.436186	5	5q15	6.493	7.609	8.152	0.74
11314	209933_s	CD300A	Hs.9688	17	17q25.1	5.451	6.617	7.246	0.75
9103	211395_x	FCGR2C	Hs.352642	1	1q23.3	5.7	7.302	7.721	0.75
	211639_x	NA	NA	NA	NA	5.104	5.545	9.096	0.76
10561	214453_s	IFI44	Hs.82316	1	1p31.1	5.855	7.279	7.323	0.77
11031	217762_s	RAB31	Hs.99528	18	18p11.3	6.868	8.327	8.865	0.75
51571	217916_s	FAM49B	Hs.126941	8	8q24.21	7.528	8.39	8.645	0.76
51303	219118_at	FKBP11	Hs.119177	12	12q13.12	5.933	6.188	7.901	0.76
27128	219183_s	PSCD4	Hs.170944	22	22q12.3-q1	5.834	6.678	7.203	0.75
64167	219759_at	LRAP	Hs.591249	5	5q15	4.242	7.518	6.895	0.76
10906	35254_at	TRAFD1	Hs.5148	12	12q	6.251	6.635	6.684	0.76
11329	202951_at	STK38	Hs.409578	6	6p21	7.5	7.844	8.07	0.73
7188	204352_at	TRAF5	Hs.523930	1	1q32	5.406	5.708	6.786	0.74
10537	205890_s	UBD	Hs.44532	6	6p21.3	7.027	10.223	9.538	0.77
10261	206420_at	IGSF6	Hs.530902	16	16p12-p13	4.22	6.782	6.296	0.77
5026	210448_s	P2RX5	Hs.408615	17	17p13.3	4.894	4.973	5.571	0.75
3903	210644_s	LAIR1	Hs.572535	19	19q13.4	5.304	7.735	7.711	0.76
4162	211042_x	MCAM	Hs.599039	11	11q23.3	5.294	5.723	5.956	0.73
4068	211210_x	SH2D1A	Hs.349094 X		Xq25-q26	5.262	5.527	6.002	0.73
149013	214722_at	KIAA1245	Hs.515947						
			Hs.534675	1	1q21.2	7.711	8.169	8.838	0.74
55233	214812_s	MOBK1B	Hs.196437	2	2p13.1	8.748	9.235	9.299	0.74
3535	215121_x	IGL@	Hs.449585	22	22q11.1-q1	9.302	9.847	13.306	0.76
28823	217179_x	IGLV1-44	Hs.449601	22	22q11.2	5.914	6.151	10.794	0.76
51311	220832_at	TLR8	Hs.272410 X		Xp22	4.234	5.565	5.251	0.76
3945	201030_x	LDHB	Hs.446149	12	12p12.2-p1	12.591	12.282	11.445	-0.74
25874	202427_s	BRP44	Hs.517768	1	1q24	9.842	9.596	8.437	-0.74

51020	203259_s	HDDC2	Hs.32826	6	6q13-q24.3	9.194	8.385	8.205	-0.76
2813	206681_x	GP2	Hs.53985	16	16p12	6.262	5.809	5.713	-0.75
10229	209745_at	COQ7	Hs.157113	16	16p13.11-p	5.81	5.666	5.45	-0.73
10434	212449_s	LYPLA1	Hs.435850	8	8q11.23	10.004	9.731	9.426	-0.73
10102	214331_at	TSFM	Hs.632704	12	12q13-q14	5.549	4.887	4.817	-0.75
55540	219255_x	IL17RB	Hs.558512	3	3p21.1	10.301	10.02	7.009	-0.74
81892	221434_s	C14orf156	Hs.445498	14	14q24.3	9.08	8.581	8.444	-0.74
4881	32625_at	NPR1	Hs.490330	1	1q21-q22	7.135	6.858	6.535	-0.74
360	39248_at	AQP3	Hs.234642	9	9p13	10.072	9.7	8.084	-0.75
409	203388_at	ARRB2	Hs.435811	17	17p13	5.488	6.346	6.556	0.74
580	205345_at	BARD1	Hs.591642	2	2q34-q35	5.215	6.012	6.377	0.75
1178	206207_at	CLC	Hs.889	19	19q13.1	4.254	4.57	6.431	0.72
829	208374_s	CAPZA1	Hs.514934	1	1p13.2	9.265	9.807	10.018	0.75
3507	209374_s	IGHM	Hs.510635	14	14q32.33	6.749	6.868	11.098	0.75
972	209619_at	CD74	Hs.591258	5	5q32	11.174	12.675	12.697	0.77
81553	209683_at	FAM49A	Hs.467769	2	2p24.3	4.036	4.403	5.759	0.74
3105	215313_x	HLA-A	Hs.181244	6	6p21.3	11.237	12.557	12.253	0.78
3105	217436_x	HLA-A	Hs.181244	6	6p21.3	8.4	10.111	9.71	0.79
50807	221039_s	DDEF1	Hs.106015	8	8q24.1-q24	4.888	5.656	5.813	0.75
3134	221875_x	HLA-F	Hs.519972	6	6p21.3	9.08	11.003	10.777	0.79
1327	200086_s	COX4I1	Hs.433419	16	16q22-qter	11.343	10.825	10.811	-0.75
9553	203781_at	MRPL33	Hs.515879	2	2p21	10.228	9.553	9.545	-0.76
384	203946_s	ARG2	Hs.632330	14	14q24.1-q2	9.278	8.601	5.415	-0.73
1645	204151_x	AKR1C1	Hs.460260						
			Hs.567256	10	10p15-p14	10.013	9.447	7.795	-0.73
617	207618_s	BCS1L	Hs.471401	2	2q33	6.802	6.481	6.268	-0.74
4695	209224_s	NDUFA2	Hs.534333	5	5q31	9.818	9.731	9.309	-0.74
6309	211423_s	SC5DL	Hs.287749	11	11q23.3	8.968	8.209	7.748	-0.74
6038	213397_x	RNASE4	Hs.283749	14	14q11.1	9.133	7.904	7.451	-0.74
498	213738_s	ATP5A1	Hs.298280	18	18q12-q21	11.934	11.612	11.015	-0.74
375057	213925_at	C1orf95	Hs.116827						
			Hs.592751	1	1q42.12	5.695	5.217	5.165	-0.75
1528	215726_s	CYB5A	Hs.465413	18	18q23	11.083	10.447	9.155	-0.75
79135	221620_s	FAM121B	Hs.495851 X		Xp22.11	8.298	7.594	6.739	-0.75
51011	222056_s	FAHD2A	Hs.546387	2	2p24.3-p11	7.378	6.908	6.436	-0.74
8859	36019_at	STK19	Hs.534847	6	6p21.3	7.463	6.945	6.794	-0.73
1606	203385_at	DGKA	Hs.524488	12	12q13.3	5.861	5.864	6.75	0.75
7941	206214_at	PLA2G7	Hs.584823	6	6p21.2-p12	4.205	4.808	5.955	0.74
2589	201723_s	GALNT1	Hs.514806	18	18q12.1	6.221	7.736	7.541	0.78
4599	202086_at	MX1	Hs.517307	21	21q22.3	7.157	8.338	8.54	0.75
6925	203753_at	TCF4	Hs.569908	18	18q21.1	7.062	7.124	8.667	0.75
3134	204806_x	HLA-F	Hs.519972	6	6p21.3	8.777	10.726	10.399	0.78
54941	207735_at	RNF125	Hs.272800						

203068	212320_at	TUBB	Hs.638727 Hs.533059 Hs.636480	18 18q12.1	4.351	4.581	5.074	0.74
55013	218802_at	CCDC109E	Hs.234149	6 6p21.33	9.291	9.867	10.317	0.74
29108	221666_s	PYCARD	Hs.499094	4 4q25	5.577	7.528	7.683	0.76
7454	38964_r_at	WAS	Hs.2157 X	16 16p12-p11. Xp11.4-p11	5.707	7.179	7.539	0.75
11034	201022_s	DSTN	Hs.304192 Hs.635105	20 20p12.1	11.569	11.217	10.99	-0.73
3396	204868_at	ICT1	Hs.407955	17 17q25.1	7.395	6.898	6.629	-0.74
5715	207805_s	PSMD9	Hs.131151	12 12q24.31-q	8.125	7.943	7.436	-0.73
4724	209303_at	NDUFS4	Hs.528222	5 5q11.1	9.197	8.699	8.403	-0.74
7849	209552_at	PAX8	Hs.469728	2 2q12-q14	8.959	8.546	7.521	-0.73
1466	211126_s	CSRP2	Hs.530904	12 12q21.1	8.678	8.145	6.872	-0.73
634	211889_x	CEACAM1	Hs.512682	19 19q13.2	6.234	5.938	5.741	-0.73
80273	212434_at	GRPEL1	Hs.443723	4 4p16	7.704	7.331	6.876	-0.73
56245	220543_at	C21orf62	Hs.517235	21 21q22.1	5.429	5.15	4.732	-0.72
27141	221188_s	CIDEB	Hs.130685 Hs.642693 Hs.642695	14 14q12	8.843	8.176	7.433	-0.73
139322	222269_at	FAM121A	Hs.512181 X	Xq21.1	5.162	4.898	4.763	-0.73
10904	201032_at	BLCAP	Hs.472651	20 20q11.2-q1	8.286	8.153	7.888	-0.72
4714	201227_s	NDUFB8	Hs.523215	10 10q23.2-q2	10.607	10.224	9.864	-0.75
1717	201790_s	DHCR7	Hs.503134	11 11q13.2-q1	5.986	5.733	5.267	-0.72
4709	203371_s	NDUFB3	Hs.109760	2 2q31.3	9.705	9.445	9.011	-0.73
2230	203647_s	FDX1	Hs.744	11 11q22	8.891	8.462	8.103	-0.74
435	204608_at	ASL	Hs.632015	7 7cen-q11.2	8.194	7.704	6.584	-0.74
211	205633_s	ALAS1	Hs.476308	3 3p21.1	8.008	7.866	6.968	-0.74
33	206068_s	ACADL	Hs.471277	2 2q34-q35	7.097	6.505	4.957	-0.73
29956	222212_s	LASS2	Hs.643565	1 1q21.2	9.702	9.653	8.587	-0.74
376267	59697_at	RAB15	Hs.512492	14 14q23.3	6.465	6.219	5.917	-0.73
8664	200005_at	EIF3S7	Hs.55682	22 22q13.1	8.858	9.18	9.586	0.73
2200	202766_s	FBN1	Hs.591133	15 15q21.1	6.254	7.903	8.097	0.75
6314	204516_at	ATXN7	Hs.476595	3 3p21.1-p12	6.716	7.677	7.82	0.73
4689	207677_s	NCF4	Hs.474781	22 22q13.1	4.645	5.315	5.976	0.74
5175	208981_at	PECAM1	Hs.514412	17 17q23	8.156	8.297	9.713	0.74
3043	209116_x	HBB	Hs.523443	11 11p15.5	5.787	12.45	11.755	0.76
3106	209140_x	HLA-B	Hs.77961	6 6p21.3	11.179	12.843	12.589	0.78
4068	211211_x	SH2D1A	Hs.349094 X	Xq25-q26	4.489	4.539	5.103	0.74
56833	219386_s	SLAMF8	Hs.438683	1 1q23.2	4.841	6.754	8.076	0.76
51063	57715_at	FAM26B	Hs.241545	10 10pter-q26.	5.91	6.082	6.687	0.72
740	201717_at	MRPL49	Hs.75859	11 11q13	9.05	8.682	8.364	-0.73
2110	205530_at	ETFDH	Hs.155729	4 4q32-q35	6.558	5.81	4.984	-0.74
48	207071_s	ACO1	Hs.642741	9 9p22-q32				

				9p22-p13	9.087	8.453	7.253	-0.74
10632	208745_at	ATP5L	Hs.486360	11 11q23.3	9.608	9.054	8.594	-0.73
10656	209781_s	KHDRBS3	Hs.444558	8 8q24.2	6.593	6.088	5.693	-0.73
3420	210418_s	IDH3B	Hs.436405	20 20p13	8.312	7.945	7.704	-0.75
1350	213846_at	COX7C	Hs.430075	5 5q14	9.272	8.635	8.435	-0.74
1645	216594_x	AKR1C1	Hs.460260					
			Hs.567256	10 10p15-p14	9.164	8.725	7.034	-0.73
54927	217972_at	CHCHD3	Hs.444467	7 7q32.3-q33	8.004	7.651	7.249	-0.72
353189	222071_s	SLCO4C1	Hs.127648	5 5q21.2	9.241	8.671	6.453	-0.73
4082	201670_s	MARCKS	Hs.519909	6 6q22.2	5.69	7.955	8.224	0.76
2589	201724_s	GALNT1	Hs.514806	18 18q12.1	6.605	7.732	7.797	0.75
6890	202307_s	TAP1	Hs.352018	6 6p21.3	6.468	8.647	8.208	0.76
4261	205101_at	CIITA	Hs.126714	16 16p13	5.014	5.185	5.61	0.72
3717	205841_at	JAK2	Hs.591081	9 9p24	4.28	4.841	4.92	0.75
9834	206478_at	KIAA0125	Hs.632338					
			Hs.640199	14 14q32.33	4.314	4.327	5.797	0.74
11262	207777_s	SP140	Hs.632549	2 2q37.1	4.322	4.478	5.725	0.73
3106	211911_x	HLA-B	Hs.77961	6 6p21.3	10.272	12.469	12.072	0.78
857	212097_at	CAV1	Hs.74034	7 7q31.1	7.093	9.082	9.199	0.74
493	212135_s	ATP2B4	Hs.343522	1 1q32.1	7.111	7.403	7.738	0.73
8473	212307_s	OGT	Hs.405410 X	Xq13	5.334	6.498	6.743	0.74
91316	213502_x	LOC91316	Hs.148656	22 22q11.23	8.25	8.423	11.609	0.75
27071	219290_x	DAPP1	Hs.436271	4 4q25-q27	5.231	5.502	5.931	0.73
64127	220066_at	CARD15	Hs.592072	16 16q21	4.065	4.142	4.662	0.74
29992	222218_s	PILRA	Hs.444407	7 7q22.1	5.085	6.257	6.569	0.74
23307	31826_at	KIAA0674	Hs.522351	9 9q32	7.22	7.694	7.724	0.75
3669	33304_at	ISG20	Hs.459265	15 15q26	5.662	6.658	7.272	0.74
5341	203470_s	PLEK	Hs.468840	2 2p14	6.191	8	7.811	0.76
154	206170_at	ADRB2	Hs.591251	5 5q31-q32	4.46	4.612	5.496	0.73
838	207500_at	CASP5	Hs.213327	11 11q22.2-q2	4.86	5.119	5.201	0.73
284119	208789_at	PTRF	Hs.437191	17 17q21.31	6.922	7.58	7.995	0.72
3071	209734_at	NCKAP1L	Hs.182014	12 12q13.1	5.825	7.599	7.697	0.75
3135	210514_x	HLA-G	Hs.181244					
			Hs.512152	6 6p21.3	8.36	9.894	9.636	0.78
	211641_x	NA	NA NA	NA	6.048	6.117	9.047	0.75
3043	211696_x	HBB	Hs.523443	11 11p15.5	5.848	12.516	11.816	0.76
23231	212311_at	KIAA0746	Hs.479384	4 4p15.2	6.633	6.904	8.224	0.74
3107	214459_x	HLA-C	Hs.77961					
			Hs.449621					
			Hs.591791	6 6p21.3	10.937	12.349	12.075	0.78
	216412_x	NA	NA NA	NA	6.09	6.163	9.025	0.75
3535	216846_at	IGL@	Hs.449585	22 22q11.1-q1	5.42	5.433	6.607	0.74
474344	219777_at	GIMAP6	Hs.438823	7 NA	6.755	7.046	8.447	0.73

4698	201304_at	NDUFA5	Hs.643550	7	7q32	10.004	9.616	9.061	-0.73
51678	205429_s	MPP6	Hs.533355	7	7p15	4.77	4.63	4.27	-0.72
7306	205694_at	TYRP1	Hs.270279	9	9p23	6.983	6.197	4.307	-0.73
1622	209389_x	DBI	Hs.78888	2	2q12-q21	9.998	9.969	9.084	-0.73
5283	209625_at	PIGH	Hs.553497	14	14q11-q24	7.248	6.418	6.182	-0.74
1737	212568_s	DLAT	Hs.335551	11	11q23.1	8.09	7.667	6.579	-0.71
51647	218074_at	FAM96B	Hs.9825	16	16q22.1-q2	9.439	9.124	8.822	-0.72
27329	219803_at	ANGPTL3	Hs.209153	1	1p31.1-p22	7.933	6.381	4.616	-0.74
50617	220197_at	ATP6V0A4	Hs.98967	7	7q33-q34	7.673	7.595	5.466	-0.74
1809	201431_s	DPYSL3	Hs.519659	5	5q32	5.448	5.51	6.592	0.72
1535	203028_s	CYBA	Hs.513803	16	16q24	8.496	9.987	9.883	0.75
1536	203922_s	CYBB	Hs.292356 X		Xp21.1	5.26	7.744	7.716	0.76
9844	204513_s	ELMO1	Hs.304578	7	7p14.2	4.771	5.073	5.79	0.73
3671	207191_s	ISLR	Hs.513022	15	15q23-q24	5.082	5.418	6.097	0.71
1438	211287_x	CSF2RA	Hs.520937 X						
			Y		Xp22.32 an	4.652	4.937	5.176	0.73
3135	211529_x	HLA-G	Hs.181244						
			Hs.512152	6	6p21.3	9.521	11.214	10.915	0.78
	214768_x	NA	NA NA		NA	5.511	5.649	10.887	0.74
2760	35820_at	GM2A	Hs.483873	5	5q31.3-q33	6.332	7.151	7.642	0.74
1717	201791_s	DHCR7	Hs.503134	11	11q13.2-q1	6.081	5.747	5.727	-0.73
4728	203189_s	NDUFS8	Hs.90443	11	11q13	7.263	6.756	6.292	-0.72
8835	203373_at	SOCS2	Hs.485572	12	12q	8.058	6.43	6.85	-0.74
10063	203880_at	COX17	Hs.534383	3	3q13.33	8.806	7.997	8.045	-0.75
4285	204305_at	MIPEP	Hs.507498	13	13q12	7.4	7.08	6.125	-0.73
6299	206893_at	SALL1	Hs.135787	16	16q12.1	7.226	6.562	5.062	-0.72
57019	208968_s	CIAPIN1	Hs.4900	16	16q13-q21	8.269	8.007	7.674	-0.72
6307	209146_at	SC4MOL	Hs.105269						
			Hs.593050	4	4q32-q34	9.222	8.279	7.703	-0.71
7164	210372_s	TPD52L1	Hs.591347	6	6q22-q23	6.819	6.496	5.882	-0.72
515	211755_s	ATP5F1	Hs.514870	1	1p13.2	11.527	11.265	10.723	-0.73
5438	212955_s	POLR2I	Hs.47062	19	19q12	8.237	7.738	7.501	-0.74
51109	217775_s	RDH11	Hs.226007	14	14q24.1	8.209	7.706	7.133	-0.72
26073	217806_s	POLDIP2	Hs.241543	17	17q11.2	8.059	7.855	7.103	-0.73
4708	218201_at	NDUFB2	Hs.324250	7	7q34	9.418	8.969	8.659	-0.73
9577	57540_at	BRE	Hs.11916						
			Hs.258314	2	2p23.2	8.059	7.341	6.737	-0.74
10051	201664_at	SMC4	Hs.58992	3	3q26.1	6.117	7.315	7.225	0.75
6035	201785_at	RNASE1	Hs.78224	14	14q11.2	9.353	10.161	10.836	0.72
8445	202971_s	DYRK2	Hs.173135	12	12q15	4.489	5.312	5.337	0.75
3759	206765_at	KCNJ2	Hs.1547	17	17q23.1-q2	4.554	5.625	5.874	0.73
2206	207496_at	MS4A2	Hs.386748	11	11q13	3.842	3.837	4.626	0.74
2833	207681_at	CXCR3	Hs.198252 X		Xq13	4.708	4.868	5.255	0.71

355	215719_x	FAS	Hs.244139	10	10q24.1	5.477	6.85	7.005	0.73
26586	218252_at	CKAP2	Hs.444028						
			Hs.449585						
			Hs.521482	13	13q14	5.075	6.221	6.118	0.74
9935	218559_s	MAFB	Hs.642679	20	20q11.2-q1	7.094	9.213	9.604	0.74
5007	201800_s	OSBP	Hs.502688	11	11q12-q13	8.179	8.047	7.527	-0.72
5494	203966_s	PPM1A	Hs.592298	14	14q23.1	8.618	8.325	7.808	-0.72
6788	204068_at	STK3	Hs.492333	8	8q22.2	7.973	7.414	6.838	-0.72
23600	209424_s	AMACR	Hs.508343	5	5p13.2-q11	8.805	8.372	6.634	-0.72
5213	210976_s	PFKM	Hs.75160	12	12q13.3	8.371	8.173	7.17	-0.72
1646	211653_x	AKR1C2	Hs.460260						
			Hs.567256	10	10p15-p14	9.356	8.918	6.818	-0.72
5037	211941_s	PEBP1	Hs.433863	12	12q24.23	10.638	9.967	9.519	-0.74
63968	213447_at	PWCR1	Hs.555970	15	15q11.2	8.126	7.722	7.473	-0.72
55788	218191_s	LMBRD1	Hs.271643	6	6q13	10.297	10.031	9.645	-0.73
4708	218200_s	NDUFB2	Hs.324250	7	7q34	10.727	10.18	9.889	-0.73
26873	222025_s	OPLAH	Hs.305882	8	8q24.3	5.431	4.889	4.571	-0.72
64919	219528_s	BCL11B	Hs.510396	14	14q32.2	4.176	4.196	5.007	0.74
7318	1294_at	UBE1L	Hs.16695	3	3p21	6.437	6.836	7.096	0.72
6124	201154_x	RPL4	Hs.186350						
			Hs.591306	15	15q22	11.582	11.622	12.036	0.72
10019	203320_at	SH2B3	Hs.506784	12	12q24	6.161	6.899	7.478	0.71
2530	203988_s	FUT8	Hs.118722	14	14q24.3	5.711	6.206	6.542	0.73
4687	204961_s	NCF1	Hs.520943	7	7q11.23	4.576	5.095	5.553	0.72
4673	208752_x	NAP1L1	Hs.524599						
			Hs.643135	12	12q21.2	9.146	9.497	9.926	0.72
3107	208812_x	HLA-C	Hs.77961						
			Hs.449621						
			Hs.591791	6	6p21.3	11.215	12.501	12.288	0.77
3493	211868_x	IGHA1	Hs.510635	14	14q32.33	6.004	6.115	10.224	0.74
472	212672_at	ATM	Hs.435561	11	11q22-q23	6.865	6.968	7.724	0.72
116984	213618_at	CENTD1	Hs.479451	4	4p14	5.283	5.766	6.511	0.72
	217258_x	NA	NA	NA	NA	5.666	5.788	10.005	0.74
55711	220615_s	MLSTD1	Hs.298851	12	12p11.22	4.842	5.293	5.541	0.72
4706	202077_at	NDUFAB1	Hs.189716	16	16p12.1	10.554	9.744	9.686	-0.74
2263	203639_s	FGFR2	Hs.533683	10	10q26	6.755	6.714	5.411	-0.76
5188	204300_at	PET112L	Hs.119316	4	4q27-q28	6.607	6.455	6.037	-0.73
9131	205512_s	PDCD8	Hs.424932 X		Xq25-q26	8.868	8.57	6.716	-0.72
3827	206054_at	KNG1	Hs.77741	3	3q27	11.052	8.721	7.508	-0.72
2888	206204_at	GRB14	Hs.411881	2	2q22-q24	7.65	7.17	6.518	-0.73
1014	206517_at	CDH16	Hs.513660	16	16q22.1	9.917	9.937	7.916	-0.73
9173	207526_s	IL1RL1	Hs.66	2	2q12	7.01	4.919	5.259	-0.75
39	209608_s	ACAT2	Hs.571037	6	6q25.3-q26	7.48	6.851	6.571	-0.71

3418	210046_s	IDH2	Hs.513141	15	15q26.1	9.173	9.264	8.05	-0.74
57237	213839_at	KIAA0500	Hs.593760	14	14q32.2	7.692	7.308	6.604	-0.71
55163	218511_s	PNPO	Hs.631742	17	17q21.32	7.94	7.513	6.66	-0.73
10097	200728_at	ACTR2	Hs.393201	2	2p14	9.207	10.041	10.42	0.72
25832	201103_x	NBPF14	Hs.467587						
			Hs.515947						
			Hs.534675						
			Hs.607640	1	1q12-1q21.	9.267	9.362	9.96	0.72
2533	205285_s	FYB	Hs.370503	5	5p13.1	5.089	5.989	6.291	0.74
10578	205495_s	GNLY	Hs.105806	2	2p12-q11	4.339	4.388	6.032	0.72
6850	207540_s	SYK	Hs.371720	9	9q22	5.382	5.969	6.519	0.73
3135	211528_x	HLA-G	Hs.181244						
			Hs.512152	6	6p21.3	10.013	11.662	11.276	0.77
3040	211745_x	HBA2	Hs.449630	16	16p13.3	5.556	11.655	11.048	0.76
23213	212354_at	SULF1	Hs.409602	8	8q13.2-q13	6.152	6.609	7.91	0.72
6125	213689_x	RPL5	Hs.180946						
			Hs.532359	1	1p22.1	6.318	6.657	7.365	0.71
3535	215214_at	IGL@	Hs.449585	22	22q11.1-q1	5.474	5.592	9.716	0.74
	217281_x	NA	NA		NA	5.645	5.871	10.156	0.74
64581	221698_s	CLEC7A	Hs.143929	12	12p13.2	5.357	7.076	7.77	0.74
292	200657_at	SLC25A5	Hs.632282 X		Xq24-q26	11.18	10.746	10.144	-0.72
1152	200884_at	CKB	Hs.173724	14	14q32	7.992	8.522	6.786	-0.73
3775	204678_s	KCNK1	Hs.208544	1	1q42-q43	6.019	5.47	5.311	-0.71
3201	206289_at	HOXA4	Hs.595822	7	7p15-p14	6.239	5.812	5.805	-0.73
486	207434_s	FXVD2	Hs.413137	11	11q23	10.786	10.66	9.338	-0.72
10476	210149_s	ATP5H	Hs.514465	17	17q25	11.545	11.342	10.885	-0.72
57460	212686_at	PPM1H	Hs.435479	12	12q14.1-q1	6.626	6.277	5.704	-0.71
51186	217975_at	WBP5	Hs.533287 X		Xq22.1-q22	9.919	9.735	9.331	-0.71
3773	219564_at	KCNJ16	Hs.463985	17	17q23.1-q2	11.4	11.257	10.386	-0.72
767	220234_at	CA8	Hs.491813	8	8q11-q12	5.242	5.003	4.773	-0.71
4329	221589_s	ALDH6A1	Hs.293970	14	14q24.3	10.436	9.651	7.061	-0.73
1666	202447_at	DECR1	Hs.492212	8	8q21.3	9.883	9.643	8.865	-0.73
379	203586_s	ARL4D	Hs.183153						
			Hs.633470	17	17q12-q21	7.101	6.872	6.222	-0.71
7280	204141_at	TUBB2A	Hs.300701	6	6p25	9.4	8.871	7.552	-0.71
64849	205244_s	SLC13A3	Hs.250281	20	20q12-q13.	9.706	8.484	6.285	-0.72
5037	205353_s	PEBP1	Hs.433863	12	12q24.23	10.938	9.962	9.427	-0.73
2352	206371_at	FOLR3	Hs.352	11	11q13	5.737	5.265	5.009	-0.72
3760	207142_at	KCNJ3	Hs.591606	2	2q24.1	4.3	4.271	3.886	-0.73
23710	208868_s	GABARAPI	Hs.524250	12	12p13.2	8.402	7.584	7.026	-0.71
1738	209095_at	DLD	Hs.131711	7	7q31-q32	10.115	9.873	8.916	-0.73
3420	210014_x	IDH3B	Hs.436405	20	20p13	8.248	7.836	7.585	-0.73
9455	217080_s	HOMER2	Hs.578443	15	15q24.3	5.124	4.975	4.906	-0.71

3827	217512_at	KNG1	Hs.77741	3	3q27	7.97	6.499	5.489	-0.71
4338	218212_s	MOCS2	Hs.163645	5	5q11	8.194	7.851	7.217	-0.72
25979	220690_s	DHRS7B	Hs.386989	17	17p12	7.424	7.254	6.701	-0.71
51204	221069_s	CCDC44	Hs.174134	17	17q23.3	7.265	6.931	6.199	-0.71
79971	221958_s	GPR177	Hs.22137	1	1p31.3	8.381	7.938	7.24	-0.71
4074	200901_s	M6PR	Hs.134084	12	12p13	8.09	8.509	8.687	0.73
1445	202329_at	CSK	Hs.77793	15	15q23-q25	6.405	6.771	7.482	0.71
6223	202649_x	RPS19	Hs.438429	19	19q13.2	11.029	11.433	11.884	0.71
27250	202730_s	PDCD4	Hs.232543	10	10q24	6.473	6.653	7.034	0.72
9695	203279_at	EDEM1	Hs.224616	3	3p26.2	6.572	6.677	7.277	0.71
2146	203358_s	EZH2	Hs.444082	7	7q35-q36	4.13	4.699	4.886	0.72
5366	204285_s	PMAIP1	Hs.96	18	18q21.32	4.163	4.725	5.402	0.73
3627	204533_at	CXCL10	Hs.632586	4	4q21	5.802	11.268	9.442	0.77
10109	207988_s	ARPC2	Hs.529303	2	2q36.1	8.9	9.393	9.656	0.73
79168	208594_x	LILRA6	Hs.241797	19	19q13.4	5.108	5.389	5.664	0.71
3039	211699_x	HBA1	Hs.449630	16	16p13.3	5.579	11.246	10.526	0.76
3107	211799_x	HLA-C	Hs.77961						
			Hs.449621						
			Hs.591791	6	6p21.3	9.066	11.154	10.758	0.77
79158	212959_s	GNPTAB	Hs.46850	12	12q23.2	6.86	7.902	8.231	0.71
5771	213136_at	PTPN2	Hs.123352	18	18p11.3-p1	7.737	7.93	8.743	0.72
6223	213414_s	RPS19	Hs.438429	19	19q13.2	11.487	11.951	12.27	0.71
3039	214414_x	HBA1	Hs.449630	16	16p13.3	5.593	12.311	11.828	0.76
3039	217414_x	HBA1	Hs.449630	16	16p13.3	5.757	11.615	11.014	0.75
7704	205883_at	ZBTB16	Hs.591945	11	11q23.1	6.709	5.31	5.288	-0.73
10437	201422_at	IFI30	Hs.14623	19	19p13.1	8.84	10.361	10.628	0.74
1604	201926_s	CD55	Hs.527653	1	1q32	6.469	7.068	7.882	0.7
2633	202269_x	GBP1	Hs.62661	1	1p22.2	6.524	10.275	9.163	0.77
4247	203102_s	MGAT2	Hs.93338	14	14q21	7.384	7.885	8.319	0.71
1606	211272_s	DGKA	Hs.524488	12	12q13.3	4.176	4.216	4.859	0.72
6670	213168_at	SP3	Hs.531587	2	2q31	8.137	8.5	8.931	0.71
4811	202007_at	NID1	Hs.356624	1	1q43	7.86	7.585	6.987	-0.73
1622	202428_x	DBI	Hs.78888	2	2q12-q21	11.414	11.339	10.468	-0.72
10671	203261_at	DCTN6	Hs.158427	8	8p12-p11	9.018	8.672	8.487	-0.71
5639	205617_at	PRRG2	Hs.35101	19	19q13.33	5.402	5.226	4.93	-0.71
8547	205866_at	FCN3	Hs.333383	1	1p36.11	7.339	5.448	5.547	-0.74
22837	211032_at	COBLL1	Hs.470457	2	2q24.3	4.153	3.927	3.932	-0.73
79589	219263_at	RNF128	Hs.496542 X		Xq22.3	8.69	8.121	6.389	-0.71
65987	219545_at	KCTD14	Hs.17296	11	11q14.1	6.441	6.067	5.554	-0.69
23677	222258_s	SH3BP4	Hs.516777	2	2q37.1-q37	8.661	8.016	7.696	-0.72
7289	221964_at	TULP3	Hs.198853	12	12p13.3	6.473	6.204	6.004	-0.71
1512	202295_s	CTSH	Hs.148641	15	15q24-q25	11.331	10.747	10.319	-0.71
2877	202831_at	GPX2	Hs.2704	14	14q24.1	7.14	6.815	5.957	-0.71

9650	203207_s	MTFR1	Hs.444831	8	8q13.1	7.234	6.625	5.641	-0.71
4616	209304_x	GADD45B	Hs.110571	19	19p13.3	8.824	7.506	7.673	-0.76
23600	209426_s	AMACR	Hs.508343	5	5p13.2-q11	8.832	8.64	6.425	-0.71
6470	209980_s	SHMT1	Hs.513987						
			Hs.636044						
			Hs.642675	17	17p11.2	8.526	8.345	6.244	-0.72
8416	211712_s	ANXA9	Hs.591483	1	1q21	6.678	6.016	5.346	-0.72
2813	214324_at	GP2	Hs.53985	16	16p12	5.256	4.621	4.605	-0.73
4705	217860_at	NDUFA10	Hs.277677	2	2q37.3	9.113	8.724	8.553	-0.72
79799	219948_x	UGT2A3	Hs.122583	4	4q13.2	9.252	8.268	5.516	-0.71
6557	220281_at	SLC12A1	Hs.123116	15	15q15-q21.	11.412	9.864	8.386	-0.71
64922	220376_at	LRRC19	Hs.128071	9	9p21.2	8.443	7.939	5.275	-0.72
26355	220942_x	C3orf28	Hs.584881	3	3q21.1	10.537	10.588	9.737	-0.73
140545	220991_s	RNF32	Hs.490715	7	7q36	3.675	3.604	3.559	-0.71
7431	201426_s	VIM	Hs.533317						
			Hs.633873	10	10p13	10.51	12.044	11.913	0.75
54739	206133_at	BIRC4BP	Hs.441975	17	17p13.2	5.575	6.643	6.387	0.74
7409	206219_s	VAV1	Hs.116237	19	19p13.2	5.123	5.788	6.381	0.71
7903	206925_at	ST8SIA4	Hs.308628	5	5q21	3.959	4.46	4.853	0.73
5175	208983_s	PECAM1	Hs.514412	17	17q23	6.497	7.379	8.967	0.73
4192	209035_at	MDK	Hs.82045	11	11p11.2	5.623	6.432	6.296	0.73
6509	209610_s	SLC1A4	Hs.323878	2	2p15-p13	4.738	4.877	5.525	0.71
3135	211530_x	HLA-G	Hs.181244						
			Hs.512152	6	6p21.3	8.026	9.148	8.978	0.76
28831	211881_x	IGLJ3	Hs.449585	22	22q11.1-q1	5.311	5.214	9.25	0.73
3493	216542_x	IGHA1	Hs.510635	14	14q32.33	6.106	6.225	9.54	0.72
3537	216560_x	IGLC1	NA	22	22q11.2	5.541	5.332	10.532	0.73
3500	217022_s	IGHG1	Hs.510635	14	14q32.33	7.783	7.216	12.2	0.73
3500	217236_x	IGHG1	Hs.510635	14	14q32.33	4.417	4.624	5.773	0.71
11031	217764_s	RAB31	Hs.99528	18	18p11.3	7.653	8.57	9.099	0.72
51393	219282_s	TRPV2	Hs.279746	17	17p11.2	6.129	6.256	6.882	0.71
55803	219358_s	CENTA2	Hs.514063	17	17q11.2	5.929	7.009	7.011	0.74
51338	219607_s	MS4A4A	Hs.325960	11	11q12	6.613	10.02	9.49	0.75
259266	219918_s	ASPM	Hs.121028	1	1q31	3.743	5.731	4.417	0.75
3956	201105_at	LGALS1	Hs.445351	22	22q13.1	9.27	10.618	10.79	0.73
7127	202510_s	TNFAIP2	Hs.525607	14	14q32	6.177	7.104	7.577	0.71
713	202953_at	C1QB	Hs.8986	1	1p36.12	6.731	10.604	10.488	0.74
1643	203409_at	DDB2	Hs.643521	11	11p12-p11	5.175	5.683	5.988	0.71
953	209474_s	ENTPD1	Hs.576612	10	10q24	4.449	5.382	6.316	0.74
7100	210166_at	TLR5	Hs.135853	1	1q41-q42	5.486	5.644	6.353	0.72
1838	215565_at	DTNB	Hs.307720	2	2p24	4.202	4.141	5.863	0.73
100	216705_s	ADA	Hs.255479	20	20q12-q13.	4.62	4.797	4.962	0.71
23166	38487_at	STAB1	Hs.301989	3	3p21.1	6.502	7.509	8.058	0.71

9420	207386_at	CYP7B1	Hs.491869	8	8q21.3	4.444	4.239	4.132	-0.71
4616	207574_s	GADD45B	Hs.110571	19	19p13.3	9.174	7.417	7.645	-0.75
11030	209488_s	RBPMS	Hs.334587	8	8p12-p11	9.004	8.989	7.797	-0.72
10560	209681_at	SLC19A2	Hs.30246	1	1q23.3	7.002	6.418	5.309	-0.69
1622	211070_x	DBI	Hs.78888	2	2q12-q21	11.369	11.288	10.418	-0.72
6505	213664_at	SLC1A1	Hs.444915	9	9p24	9.607	9.024	7.121	-0.71
23368	216347_s	PPP1R13B	Hs.436113	14	14q32.33	6.738	6.328	6.122	-0.7
5564	201834_at	PRKAB1	Hs.6061	12	12q24.1	7.774	7.608	7.131	-0.69
267	202204_s	AMFR	Hs.295137	16	16q21	7.584	6.761	6.598	-0.7
4711	203621_at	NDUFB5	Hs.518424	3	3q26.33	10.325	10.027	9.607	-0.71
10247	203790_s	HRSP12	Hs.18426	8	8q22	10.301	9.393	7.238	-0.72
5437	209302_at	POLR2H	Hs.432574	3	3q28	7.955	7.777	7.5	-0.71
599	209311_at	BCL2L2	Hs.410026	14	14q11.2-q1	7.774	7.33	6.974	-0.7
27077	210534_s	EPPB9	Hs.462445	17	17p11.2	6.277	6.088	5.774	-0.71
622	211715_s	BDH1	Hs.274539	3	3q29	6.508	6.365	5.376	-0.72
374655	213657_s	ZNF710	Hs.459311	15	15q26.1	7.213	7.071	5.634	-0.71
2017	214073_at	CTTN	Hs.632133	11	11q13	5.799	5.182	4.788	-0.7
79611	219616_at	FLJ21963	Hs.259559	12	12q21.31	6.185	5.979	5.162	-0.71
63933	220094_s	C6orf79	Hs.214043	6	6p24.3-p23	7.821	7.466	6.563	-0.72
10636	38290_at	RGS14	Hs.9347	5	5q35.3	6.26	6.02	5.812	-0.7
103	201786_s	ADAR	Hs.12341	1	1q21.1-q21	9.04	9.287	9.536	0.71
4175	201930_at	MCM6	Hs.444118	2	2q21	7.034	8.076	8.139	0.73
1278	202403_s	COL1A2	Hs.489142	7	7q22.1	8.747	10.352	10.134	0.73
4067	202625_at	LYN	Hs.491767						
			Hs.614775	8	8q13	5.932	7.502	7.952	0.72
6502	203625_x	SKP2	Hs.23348	5	5p13	5.136	5.907	5.985	0.71
1112	205022_s	CHES1	Hs.434286						
			Hs.621371	14	14q31.3	6.072	6.221	7.032	0.7
1009	207172_s	CDH11	Hs.116471	16	16q22.1	5.523	5.796	6.633	0.7
926	207979_s	CD8B	Hs.405667						
			Hs.610012	2	2p12	4.926	5.281	5.883	0.7
2268	208438_s	FGR	Hs.1422	1	1p36.2-p36	5.121	5.504	6.254	0.7
3106	208729_x	HLA-B	Hs.77961	6	6p21.3	10.124	12.465	11.916	0.76
330	210538_s	BIRC3	Hs.127799	11	11q22	6.528	7.422	8.349	0.71
	213891_s	NA	NA	NA	NA	6.637	6.69	8.485	0.72
51465	217826_s	UBE2J1	Hs.163776	6	6q15	7.184	7.532	8.44	0.71
79686	219563_at	C14orf139	Hs.41502	14	14q32.13	5.194	5.42	6.681	0.71
79895	220416_at	ATP8B4	Hs.511311	15	15q21.2	4.118	4.735	4.989	0.71
80215	220918_at	C21orf96	Hs.149261	21	21q22.12	5.469	5.429	6.307	0.73
4082	201669_s	MARCKS	Hs.519909	6	6q22.2	8.208	9.706	10.246	0.71
865	202370_s	CBFB	Hs.460988	16	16q22.1	6.974	7.547	8.093	0.71
1880	205419_at	EBI2	Hs.784	13	13q32.3	4.302	4.155	6.855	0.73
1359	205624_at	CPA3	Hs.646	3	3q21-q25	5.112	4.837	9.982	0.73

3588	209575_at	IL10RB	Hs.512211	21	21q22.1-q22.2				
					21q22.11	6.575	7.626	7.757	0.72
5272	209723_at	SERPINB9	Hs.104879	6	6p25	5.17	6.284	7.117	0.71
23213	212353_at	SULF1	Hs.409602	8	8q13.2-q13	5.635	6.313	7.966	0.7
23313	212421_at	C22orf9	Hs.592207	22	22q13.31	4.956	5.253	5.591	0.7
3535	216853_x	IGL@	Hs.449585	22	22q11.1-q1	5.5	5.503	9.43	0.73
3043	217232_x	HBB	Hs.523443	11	11p15.5	6.424	12.111	11.582	0.73
51466	217838_s	EVL	Hs.125867	14	14q32.2	6.027	6.144	7.434	0.72
55656	218905_at	INTS8	Hs.521693						
			Hs.567387	8	8q22.1	7.062	7.546	7.904	0.7
1540	39582_at	CYLD	Hs.578973	16	16q12.1	5.639	5.764	6.469	0.7
5372	203467_at	PMM1	Hs.75835	22	22q13.2	7.189	6.897	6.229	-0.7
6835	205224_at	SURF2	Hs.159448	9	9q34.2	6.259	5.424	5.675	-0.74
2911	207299_s	GRM1	Hs.32945	6	6q24	4.202	4.027	3.976	-0.72
4704	208969_at	NDUFA9	Hs.75227	12	12p13.3	9.572	9.367	8.922	-0.7
3758	210402_at	KCNJ1	Hs.527830	11	11q24	10.458	10.245	8.304	-0.69
26027	214763_at	ACOT11	Hs.234786	1	1p32.3	6.282	6.147	5.267	-0.71
79696	220107_s	C14orf140	Hs.48642	14	14q24.3	5.561	5.157	4.884	-0.73
2475	202288_at	FRAP1	Hs.338207	1	1p36.2	5.663	5.48	5.407	-0.7
4701	202785_at	NDUFA7	Hs.333427	19	19p13.2	8.236	8	7.713	-0.71
2230	203646_at	FDX1	Hs.744	11	11q22	7.875	7.422	7.116	-0.71
4129	204041_at	MAOB	Hs.46732 X		Xp11.23	9.042	8.462	7.772	-0.71
2690	205498_at	GHR	Hs.125180	5	5p13-p12	7.556	6.168	5.233	-0.71
9139	207625_s	CBFA2T2	Hs.153934	20	20q11	6.406	6.206	5.984	-0.7
7905	208873_s	REEP5	Hs.429608	5	5q22-q23	10.31	10.011	9.606	-0.7
64963	211595_s	MRPS11	Hs.111286	15	15q25	7.667	7.453	7.251	-0.7
79154	218756_s	MGC4172	Hs.462859	17	17q12	5.525	5.148	4.593	-0.71
54869	221655_x	EPS8L1	Hs.438862	19	19q13.42	6.346	5.991	5.976	-0.71
3157	221750_at	HMGCS1	Hs.397729	5	5p14-p13	7.114	6.596	6.432	-0.71
10051	201663_s	SMC4	Hs.58992	3	3q26.1	5.287	6.705	6.391	0.73
2149	203989_x	F2R	Hs.482562	5	5q13	5.965	7.718	7.118	0.73
5999	204338_s	RGS4	Hs.386726	1	1q23.3	4.238	4.492	4.605	0.71
8638	205660_at	OASL	Hs.118633	12	12q24.2	5.14	5.553	5.756	0.7
5583	206099_at	PRKCH	Hs.333907	14	14q22-q23	4.666	4.802	5.327	0.7
719	209906_at	C3AR1	Hs.591148	12	12p13.31	7.081	8.389	9.142	0.72
2191	209955_s	FAP	Hs.516493	2	2q23	4.409	4.533	5.841	0.71
9103	210992_x	FCGR2C	Hs.352642	1	1q23.3	5.802	7.223	7.51	0.72
28461	211640_x	IGHV1-69	Hs.634941	14	14q32.32-q	5.057	4.977	8.409	0.73
3500	211649_x	IGHG1	Hs.510635	14	14q32.33	5.586	5.536	8.269	0.73
3133	217456_x	HLA-E	Hs.118354	6	6p21.3	8.778	10.282	9.989	0.76
29969	217599_s	MDFIC	Hs.427236	7	7q31.1-q31	3.991	4.123	4.383	0.71
23129	38671_at	PLXND1	Hs.301685	3	3q21.3	6.436	6.907	7.263	0.71
7284	201113_at	TUFM	Hs.12084	16	16p11.2	9.378	8.938	8.574	-0.7

4650	217297_s	MYO9B	Hs.123198	19	19p13.1	5.013	5.351	5.467	0.7
56833	219385_at	SLAMF8	Hs.438683	1	1q23.2	5.476	6.475	6.803	0.71
6389	201093_x	SDHA	Hs.440475	5	5p15	9.294	9.177	8.638	-0.7
1429	202950_at	CRYZ	Hs.83114	1	1p31-p22	10.829	10.454	9.419	-0.7
3698	204987_at	ITIH2	Hs.75285	10	10p15	5.15	4.98	4.824	-0.71
6342	211733_x	SCP2	Hs.476365						
			Hs.632399	1	1p32	10.579	10.364	9.94	-0.69
3081	214308_s	HGD	Hs.368254						
			Hs.616526	3	3q21-q23	8.314	8.216	5.849	-0.7
23286	216074_x	WWC1	Hs.484047	5	5q35.1	6.429	6.364	5.505	-0.7
55151	218772_x	TMEM38B	Hs.411925	9	9q31.2	7.157	6.97	5.896	-0.69
26063	219664_s	DECR2	Hs.9235	16	16p13.3	8.081	7.485	7.108	-0.7
9673	32091_at	KIAA0446	Hs.532375	1	1q22	7.975	7.243	6.718	-0.7
10099	200972_at	TSPAN3	Hs.5062	15	15q24.3	10.14	10.006	9.467	-0.69
2017	201059_at	CTTN	Hs.632133	11	11q13	8.61	8.267	7.842	-0.69
3420	201509_at	IDH3B	Hs.436405	20	20p13	7.619	7.174	7.057	-0.72
84747	202365_at	MGC5139	Hs.127610	12	12q24.31	8.368	8.155	7.886	-0.68
4594	202960_s	MUT	Hs.485527	6	6p21	9.149	8.664	7.501	-0.7
5264	203335_at	PHYH	Hs.498732	10	10pter-p11.	10.168	9.43	8.057	-0.71
3708	203710_at	ITPR1	Hs.567295	3	3p26-p25	7.724	7.351	7.012	-0.69
3081	205221_at	HGD	Hs.368254						
			Hs.616526	3	3q21-q23	8.743	8.573	5.912	-0.7
1491	206085_s	CTH	Hs.19904	1	1p31.1	4.972	4.678	4.146	-0.69
5162	208911_s	PDHB	Hs.161357	3	3p21.1-p14	8.218	8.09	7.484	-0.7
57142	211509_s	RTN4	Hs.429581	2	2p16.3	11.229	11.253	10.802	-0.71
3306	211538_s	HSPA2	Hs.432648	14	14q24.1	8.708	7.257	7.039	-0.69
57509	212096_s	MTUS1	Hs.7946	8	8p22	8.252	7.785	7.404	-0.68
23014	212231_at	FBXO21	Hs.159699	12	12q24.22	7.874	7.697	7.046	-0.7
55353	214039_s	LAPTM4B	Hs.492314	8	8q22.1	11.237	10.774	10.321	-0.69
55748	217752_s	CNDP2	Hs.149185	18	18q22.3	10.796	10.804	9.82	-0.71
55365	218345_at	HCA112	Hs.438823	7	7q36.1	10.97	10.797	9.735	-0.68
5827	219076_s	PXMP2	Hs.430299	12	12q24.33	8.091	7.435	6.204	-0.7
79632	220150_s	C6orf60	Hs.443789	6	6q22.31	5.658	5.367	4.988	-0.68
8507	201341_at	ENC1	Hs.104925	5	5q12-q13.3	6.383	6.918	7.525	0.68
3039	204018_x	HBA1	Hs.449630	16	16p13.3	5.929	11.491	10.74	0.73
4277	206247_at	MICB	Hs.211580	6	6p21.3	4.45	5.122	5.794	0.7
3431	208392_x	SP110	Hs.145150	2	2q37.1	5.569	5.895	6.295	0.68
3479	209540_at	IGF1	Hs.160562	12	12q22-q23	4.504	4.774	5.56	0.69
8542	209546_s	APOL1	Hs.114309	22	22q13.1	6.871	8.271	7.951	0.73
2130	211825_s	EWSR1	Hs.374477	22	22q12.2	4.672	5.153	5.647	0.69
23102	212796_s	TBC1D2B	Hs.567426	15	15q24.3-q2	6.56	7.179	7.593	0.7
4082	213002_at	MARCKS	Hs.519909	6	6q22.2	4.846	5.438	5.837	0.7
10396	213106_at	ATP8A1	Hs.435052	4	4p14-p12	5.22	5.34	6.611	0.69

6955	213830_at	TRA@	Hs.74647	14	14q11.2	4.682	4.763	5.115	0.69
9555	214500_at	H2AFY	Hs.420272						
			Hs.599225	5	5q31.3-q32	5.063	5.903	6.296	0.7
55167	218733_at	MSL2L1	Hs.18631	3	3q22.2	5.745	5.966	6.448	0.69
5660	200866_s	PSAP	Hs.523004	10	10q21-q22	9.195	10.235	10.003	0.71
6142	200869_at	RPL18A	Hs.337766	19	19p13	10.503	11.059	11.49	0.69
7175	201731_s	TPR	Hs.279640	1	1q25	8.046	8.431	8.513	0.69
6241	201890_at	RRM2	Hs.226390	2	2p25-p24	4.119	6.934	5.74	0.73
9792	202656_s	SERTAD2	Hs.591569	2	2p14	6.697	7.725	7.597	0.71
6310	203232_s	ATXN1	Hs.434961	6	6p23	7.016	7.371	7.746	0.69
6504	206181_at	SLAMF1	Hs.523660	1	1q22-q23	4.294	4.326	5.15	0.7
304	208816_x	ANXA2P2	Hs.534301	9	9p13	8.457	8.999	9.255	0.71
10092	211963_s	ARPC5	Hs.518609	1	1q25.3	9.422	10.176	10.411	0.71
6432	213649_at	SFRS7	Hs.309090	2	2p22.1	6.696	6.899	7.809	0.68
91543	213797_at	RSAD2	Hs.17518	2	2p25.2	4.704	5.885	5.807	0.73
23048	213940_s	FNBP1	Hs.189409	9	9q34	6.615	7.07	7.256	0.7
51696	218603_at	HECA	Hs.197644	6	6q23-q24	7.283	7.37	8.585	0.7
81567	221253_s	TXNDC5	Hs.150837	6	6p24.3	9.922	10.011	11.312	0.71
223	201612_at	ALDH9A1	Hs.2533	1	1q23.1	10.154	9.883	9.469	-0.7
3321	202421_at	IGSF3	Hs.171057	1	1p13	8.191	8.024	6.839	-0.69
10040	204485_s	TOM1L1	Hs.153504	17	17q23.2	8.479	7.902	6.799	-0.69
9971	206340_at	NR1H4	Hs.282735	12	12q23.1	8.457	8.084	6.371	-0.69
28513	206898_at	CDH19	Hs.42771	18	18q22-q23	4.004	3.766	3.763	-0.71
81689	209274_s	HBLD2	Hs.449291	9	9q21.33	9.13	8.638	8.105	-0.69
11212	209384_at	PROSC	Hs.304792						
			Hs.608177	8	8p11.2	9.103	8.794	8.536	-0.69
10579	211382_s	TACC2	Hs.501252						
			Hs.643068	10	10q26	6.023	5.575	5.052	-0.69
9673	212683_at	KIAA0446	Hs.532375	1	1q22	7.419	6.743	6.394	-0.71
50486	213524_s	G0S2	Hs.432132	1	1q32.2-q41	8.239	7.735	7.433	-0.69
10053	218261_at	AP1M2	Hs.18894	19	19p13.2	7.62	7.22	6.226	-0.7
79717	218341_at	PPCS	Hs.473495	1	1p34.2	8.359	7.918	7.684	-0.68
51099	218739_at	ABHD5	Hs.19385	3	3p21	6.458	6.375	5.684	-0.69
55129	218910_at	TMEM16K	Hs.17949	3	3p22.1-p21	7.358	7.151	6.707	-0.69
10857	201121_s	PGRMC1	Hs.90061		Xq22-q24	10.646	10.302	9.625	-0.71
523	201972_at	ATP6V1A	Hs.477155	3	3q13.2-q13	10.489	10.401	9.79	-0.7
51706	202263_at	CYB5R1	Hs.334832	1	1p36.13-q4	8.247	8.162	7.57	-0.7
6988	203054_s	TCTA	Hs.517962	3	3p21	8.086	7.862	7.322	-0.7
10651	203517_at	MTX2	Hs.470728	2	2q31.1	8.065	7.411	7.035	-0.68
6038	205158_at	RNASE4	Hs.283749	14	14q11.1	7.971	7.297	6.416	-0.69
486	205674_x	FXD2	Hs.413137	11	11q23	11.837	11.817	10.56	-0.7
6915	207554_x	TBXA2R	Hs.442530	19	19p13.3	5.245	5.051	5.008	-0.69
8801	214835_s	SUCLG2	Hs.186512	3	3p14.1	9.163	8.714	7.948	-0.69

29796	218190_s	UCRC	Hs.284292	22	22cen-q12.	11.082	10.942	10.407	-0.69
10158	219630_at	PDZK1IP1	Hs.431099	1	1p33	11.49	11.354	10.109	-0.69
1797	38157_at	DOM3Z	Hs.153299	6	6p21.3	6.633	6.433	6.291	-0.68
8761	201064_s	PABPC4	Hs.169900	1	1p32-p36	7.115	7.81	8.196	0.7
25832	201104_x	NBPF14	Hs.467587						
			Hs.515947						
			Hs.534675						
			Hs.607640	1	1q12-1q21.	8.491	8.885	9.065	0.69
25939	204502_at	SAMHD1	Hs.580681	20	20pter-q12	5.477	7.47	7.501	0.73
8843	205220_at	GPR109B	Hs.458425	12	12q24.31	4.044	4.141	4.628	0.69
7351	208997_s	UCP2	Hs.80658	11	11q13	6.605	8.352	8.187	0.71
4615	209124_at	MYD88	Hs.82116	3	3p22	8.335	8.725	9.247	0.68
9181	209435_s	ARHGEF2	Hs.568509	1	1q21-q22	7.077	7.307	7.787	0.69
25900	209721_s	HOM-TES-	Hs.15243	12	12p13.3	6.248	6.444	6.831	0.68
961	211075_s	CD47	Hs.446414	3	3q13.1-q13	7.734	8.883	9.041	0.7
3119	212999_x	HLA-DQB1	Hs.409934						
			Hs.534322	6	6p21.3	5.354	8.204	8.472	0.68
3310	213418_at	HSPA6	Hs.352642	1	1q23	5.097	6.135	7.213	0.7
3384	213620_s	ICAM2	Hs.431460	17	17q23-q25	7.226	7.41	8.838	0.7
93349	214791_at	LOC93349	Hs.369056	2	2q37.1	4.945	6.131	6.23	0.71
150759	221973_at	LOC150759	Hs.503463	2	2q11.2	4.938	5.255	5.971	0.69
1278	202404_s	COL1A2	Hs.489142	7	7q22.1	6.439	9.095	8.324	0.71
9768	202503_s	KIAA0101	Hs.81892	15	15q22.31	4.84	7.878	6.693	0.71
7456	202665_s	WASPIP	Hs.591641	2	2q31.1	5.593	6.259	6.462	0.68
558	202686_s	AXL	Hs.590970	19	19q13.1	5.747	7.06	7.121	0.71
5366	204286_s	PMAIP1	Hs.96	18	18q21.32	3.851	4.242	5.103	0.69
7130	206026_s	TNFAIP6	Hs.437322	2	2q23.3	3.864	4.205	4.536	0.69
3159	206074_s	HMGA1	Hs.518805						
			Hs.640435	6	6p21	5.774	6.453	7.51	0.69
9735	206316_s	KNTC1	Hs.300559	12	12q24.31	4.477	4.843	5.034	0.7
2533	211794_at	FYB	Hs.370503	5	5p13.1	5.554	6.239	6.307	0.7
94431	216908_x	LOC94431	Hs.632170	16	16p12.1	5.537	6.045	6.308	0.69
11031	217763_s	RAB31	Hs.99528	18	18p11.3	6.274	8.431	8.258	0.73
29028	218782_s	ATAD2	Hs.370834	8	8q24.13	3.899	4.928	4.203	0.73
9380	201347_x	GRHPR	Hs.155742	9	9q12	9.198	8.556	7.938	-0.69
10160	201910_at	FARP1	Hs.403917	13	13q32.2	8.735	8.56	7.912	-0.69
6720	202308_at	SREBF1	Hs.592123	17	17p11.2	5.685	5.64	5.349	-0.69
6902	203667_at	TBCA	Hs.291212	5	5q14.1	10.561	10.204	9.894	-0.68
6450	204979_s	SH3BGR	Hs.473847	21	21q22.3	6.075	5.638	5.427	-0.71
7037	208691_at	TFRC	Hs.529618	3	3q29	9.343	7.733	7.621	-0.69
5340	209978_s	PLG	Hs.143436	6	6q26	8.96	7.308	5.562	-0.69
9540	210609_s	TP53I3	Hs.50649	2	2p23.3	7.23	6.946	6.475	-0.67
1495	210844_x	CTNNA1	Hs.534797	5	5q31	9.949	9.89	9.409	-0.68

8801	212459_x	SUCLG2	Hs.186512	3	3p14.1	9.646	9.319	8.32	-0.68
4499	212859_x	MT1M	Hs.643532	16	16q13	11.448	11.003	10.512	-0.69
374655	213658_at	ZNF710	Hs.459311	15	15q26.1	6.253	6.079	4.82	-0.7
5446	213695_at	PON3	Hs.440967	7	7q21.3	5.577	4.95	4.817	-0.69
708	214214_s	C1QBP	Hs.555866	17	17p13.3	8.588	8.505	7.99	-0.68
8801	215772_x	SUCLG2	Hs.186512	3	3p14.1	9.678	9.408	8.522	-0.68
55739	217940_s	FLJ10769	Hs.408324	13	13q34	7.797	7.552	7.246	-0.69
56898	218285_s	BDH2	Hs.124696	4	4q24	10.869	10.225	9.357	-0.69
56652	218590_at	PEO1	Hs.22678	10	10q23.3-24	5.281	4.978	5.016	-0.73
80150	218857_s	ASRGL1	Hs.535326	11	11q12.3	9.018	8.572	7.319	-0.69
	221275_s	NA	NA	NA	NA	4.414	4.296	4.17	-0.68
55650	51146_at	PIGV	Hs.259605	1	1p36.11	6.068	5.53	5.5	-0.7
10053	65517_at	AP1M2	Hs.18894	19	19p13.2	7.23	6.841	5.987	-0.69
1327	202698_x	COX4I1	Hs.433419	16	16q22-qter	11.621	11.406	11.177	-0.69
2181	201662_s	ACSL3	Hs.471461	2	2q34-q35	7.757	7.48	7.204	-0.68
1942	202023_at	EFNA1	Hs.516664	1	1q21-q22	8.629	8.049	7.246	-0.68
9650	203208_s	MTFR1	Hs.444831	8	8q13.1	8.687	7.899	7.05	-0.68
4646	203216_s	MYO6	Hs.149387	6	6q13	9.022	8.688	7.841	-0.68
8835	203372_s	SOCS2	Hs.485572	12	12q	5.329	4.741	4.698	-0.68
8100	204703_at	IFT88	Hs.187376	13	13q12.1	7.661	7.52	7.144	-0.68
2638	204965_at	GC	Hs.418497	4	4q12-q13	7.686	3.805	3.865	-0.7
11145	209581_at	HRASLS3	Hs.502775	11	11q12.3-q1	8.791	8.706	7.973	-0.69
51406	213838_at	NOL7	Hs.643500	6	6p23	7.409	7	6.616	-0.69
9380	216308_x	GRHPR	Hs.155742	9	9q12	9.131	8.518	8.055	-0.69
55214	218717_s	LEPREL1	Hs.374191	3	3q28	8.53	8.972	7.677	-0.72
32	221928_at	ACACB	Hs.234898	12	12q24.11	6.566	6.071	5.866	-0.68
374655	37590_g_a	ZNF710	Hs.459311	15	15q26.1	6.301	6.258	5.158	-0.7
23077	201960_s	MYCBP2	Hs.591221	13	13q22	7.441	7.563	8.431	0.7
1536	203923_s	CYBB	Hs.292356 X		Xp21.1	4.742	8.626	8.572	0.72
6916	208130_s	TBXAS1	Hs.520757	7	7q34-q35	5.021	5.967	6.366	0.7
1027	209112_at	CDKN1B	Hs.238990	12	12p13.1-p1	8.676	8.921	9.521	0.68
3459	211676_s	IFNGR1	Hs.520414	6	6q23-q24	7.294	8.276	8.826	0.7
23253	212286_at	ANKRD12	Hs.464585	18	18p11.22	5.83	6.89	7.07	0.7
3117	213831_at	HLA-DQA1	Hs.387679	6	6p21.3	5.548	10.17	10.259	0.68
54918	217947_at	CMTM6	Hs.380627						
			Hs.440494	3	3p22.3	9.606	10.258	10.316	0.71
144195	202497_x	SLC2A14	Hs.419240	12	12p13.31	5.867	6.658	7.04	0.69
4190	200978_at	MDH1	Hs.526521	2	2p13.3	11.243	10.9	9.976	-0.69
2109	202942_at	ETFB	Hs.74047	19	19q13.3	8.571	8.117	7.456	-0.69
6492	206876_at	SIM1	Hs.520293	6	6q16.3-q21	7.416	6.908	6.452	-0.67
25814	208833_s	ATXN10	Hs.475125	22	22q13.31	9.628	9.312	9.222	-0.67
8824	209667_at	CES2	Hs.282975	16	16q22.1	9.948	9.068	7.618	-0.69
11046	213083_at	SLC35D2	Hs.494556						

			Hs.593332	9	9q22.32	7.947	7.849	6.945	-0.68
90627	213103_at	STARD13	Hs.507704	13	13q12-q13	6.075	5.806	5.819	-0.7
161291	213285_at	TMEM30B	Hs.146180	14	14q23.1	7.547	6.918	6.457	-0.67
52	215227_x	ACP1	Hs.558296	2	2p25	8.332	8.114	7.741	-0.68
9445	217731_s	ITM2B	Hs.446450	13	13q14.3	11.896	11.581	11.262	-0.68
79886	219276_x	C9orf82	Hs.178357	9	9p21.2	8.45	7.979	7.305	-0.66
80004	219395_at	RBM35B	Hs.436585						
			Hs.592053	16	16q22.1	6.83	6.381	5.828	-0.66
255812	222021_x	SDHAL1	Hs.566872						
			Hs.586058	3	3q29	9.526	9.298	8.759	-0.68
10097	200729_s	ACTR2	Hs.393201	2	2p14	8.618	9.578	9.778	0.69
5108	202174_s	PCM1	Hs.491148	8	8p22-p21.3	7.931	8.383	8.424	0.69
3796	203086_at	KIF2	Hs.558351	5	5q12-q13	4.837	5.055	5.248	0.68
10859	207104_x	LILRB1	Hs.67846	19	19q13.4	5.824	6.246	7.361	0.68
5696	209040_s	PSMB8	Hs.180062	6	6p21.3	7.059	9.031	8.701	0.72
6241	209773_s	RRM2	Hs.226390	2	2p25-p24	4.728	8.088	6.008	0.71
26278	213262_at	SACS	Hs.159492	13	13q12	4.681	4.953	5.771	0.67
3535	216430_x	IGL@	Hs.449585	22	22q11.1-q1	5.377	5.384	7.444	0.71
51465	217825_s	UBE2J1	Hs.163776	6	6q15	6.657	6.578	7.933	0.7
11177	217985_s	BAZ1A	Hs.509140	14	14q12-q13	5.468	6.175	6.592	0.69
9448	218181_s	MAP4K4	Hs.431550	2	2q11.2-q12	5.215	5.432	6.208	0.68
64761	218543_s	PARP12	Hs.12646	7	7q34	5.617	6.543	6.769	0.69
6614	219519_s	SIGLEC1	Hs.31869	20	20p13	5.348	6.926	6.784	0.71
4729	202941_at	NDUFV2	Hs.464572	18	18p11.31-p	9.544	9.496	9.007	-0.68
22977	206469_x	AKR7A3	Hs.6980	1	1p35.1-p36	8.521	7.594	6.839	-0.69
501	208951_at	ALDH7A1	Hs.483239	5	5q31	8.099	7.749	6.963	-0.7
204	208967_s	AK2	Hs.470907	1	1p34	9.305	9.412	8.537	-0.7
5104	209443_at	SERPINA5	Hs.510334	14	14q32.1	9.185	8.122	6.954	-0.68
51399	217958_at	TRAPPC4	Hs.524078	11	11q23.3	8.967	8.345	8.137	-0.68
27018	217963_s	NGFRAP1	Hs.448588 X		Xq22.2	10.817	10.567	9.965	-0.69
65985	218434_s	AACS	Hs.169054	12	12q24.31	6.869	6.557	6.14	-0.68
10166	218653_at	SLC25A15	Hs.631772	13	13q14	6.574	6.125	5.776	-0.66
54996	219527_at	MOSC2	Hs.369042	1	1q41	6.904	6.601	5.569	-0.7
6451	201312_s	SH3BGRL	Hs.108029 X		Xq13.3	10.045	10.236	10.404	0.68
302	201590_x	ANXA2	Hs.511605	15	15q21-q22	11.033	11.731	11.917	0.7
23166	204150_at	STAB1	Hs.301989	3	3p21.1	6.377	7.328	7.755	0.69
1009	207173_x	CDH11	Hs.116471	16	16q22.1	6.209	6.808	8.161	0.68
3958	208949_s	LGALS3	Hs.531081	14	14q21-q22	10.08	10.514	10.812	0.67
3486	212143_s	IGFBP3	Hs.450230	7	7p13-p12	7.135	9.158	8.785	0.69
3507	215949_x	IGHM	Hs.510635	14	14q32.33	6.614	6.571	8.897	0.69
2896	216041_x	GRN	Hs.514220	17	17q21.32	8.552	9.532	9.59	0.68
3500	217260_x	IGHG1	Hs.510635	14	14q32.33	4.701	4.664	4.98	0.69
80351	218228_s	TNKS2	Hs.329327	10	10q23.3	6.62	7.257	7.534	0.69

65244	218324_s	SPATS2	Hs.146679	12	12q13.12	4.749	5.129	5.36	0.68
11221	221563_at	DUSP10	Hs.497822	1	1q41	4.806	5.256	5.75	0.69
3028	202282_at	HADH2	Hs.171280 X		Xp11.2	9.192	8.985	8.566	-0.69
6697	203458_at	SPR	Hs.301540	2	2p14-p12	7.292	7.078	6.642	-0.67
2639	203500_at	GCDH	Hs.532699	19	19p13.2	6.92	6.38	6.277	-0.7
11163	206303_s	NUDT4	Hs.591008	12	12q21	6.77	6.433	5.752	-0.68
23479	209075_s	NIFUN	Hs.350702						
			Hs.615131	12	12q24.1	11.62	10.93	10.923	-0.69
8644	209160_at	AKR1C3	Hs.78183	10	10p15-p14	10.718	9.838	7.671	-0.68
5340	209977_at	PLG	Hs.143436	6	6q26	8.521	7.111	5.507	-0.68
7416	212038_s	VDAC1	Hs.519320	5	5q31	9.8	9.656	9.298	-0.67
51071	218102_at	DERA	Hs.39429	12	12p12.3	8.947	8.519	7.899	-0.69
27129	218934_s	HSPB7	Hs.502612	1	1p36.23-p3	5.737	5.459	5.24	-0.67
64080	219222_at	RBKS	Hs.11916	2	2p23.3	7.702	7.102	6.678	-0.69
51287	220647_s	CHCHD8	Hs.475387	11	11q13.4	8.253	8.002	7.664	-0.69
32	49452_at	ACACB	Hs.234898	12	12q24.11	6.847	5.757	5.548	-0.67
6772	200887_s	STAT1	Hs.470943	2	2q32.2	9.526	11.488	11.059	0.72
6117	201529_s	RPA1	Hs.461925	17	17p13.3	5.455	6.105	6.272	0.68
6515	202499_s	SLC2A3	Hs.419240	12	12p13.3	4.734	6.078	6.531	0.69
9873	203620_s	FCHSD2	Hs.577053	11	11q13.4	5.916	6.675	7.206	0.68
8875	205922_at	VNN2	Hs.293130	6	6q23-q24	4.833	6.019	5.856	0.72
388344	212191_x	LOC38834	Hs.448879	17	17p11.2	11.329	11.57	11.763	0.67
6137	212734_x	RPL13	Hs.410817	16	16q24.3				
					17p11.2	12.064	12.263	12.401	0.67
302	213503_x	ANXA2	Hs.511605	15	15q21-q22	10.713	11.454	11.734	0.7
57730	214723_x	KIAA1641	Hs.532921						
			Hs.541894						
			Hs.632866	2	2q11.2	3.931	4.748	4.668	0.71
3120	215536_at	HLA-DQB2	Hs.554753	6	6p21	5.627	5.724	6.157	0.67
567	216231_s	B2M	Hs.534255	15	15q21-q22.	12.477	13.025	12.884	0.71
28461	216541_x	IGHV1-69	Hs.634941	14	14q32.32-q	4.89	4.749	7.734	0.71
27258	202209_at	LSM3	Hs.111632	3	3p25.1	9.651	9.421	8.953	-0.67
23530	202784_s	NNT	Hs.482043	5	5p13.1-5ce	7.492	7.357	6.344	-0.69
3920	203042_at	LAMP2	Hs.496684 X		Xq24	9.657	9.304	8.347	-0.67
9743	203431_s	RICS	Hs.440379	11	11q24-q25	5.062	4.614	4.387	-0.68
6484	203759_at	ST3GAL4	Hs.591947	11	11q23-q24	5.855	5.505	5.422	-0.68
9920	204301_at	KBTBD11	Hs.5333	8	8p23.3	7.016	7.184	5.655	-0.69
5334	205934_at	PLCL1	Hs.153322	2	2q33	7.052	6.106	4.863	-0.67
1187	207047_s	CLCNKA	Hs.591533	1	1p36	8.217	7.93	5.671	-0.68
563	209309_at	AZGP1	Hs.546239	7	7q22.1	9.478	7.817	5.408	-0.69
10265	210239_at	IRX5	Hs.435730	16	16q11.2-q1	4.922	4.634	4.421	-0.66
6819	211470_s	SULT1C1	Hs.436123	2	2q11.1-q11	9.417	9.053	6.633	-0.68
4499	216336_x	MT1M	Hs.643532	16	16q13	10.215	10.042	9.561	-0.67

563	217014_s	AZGP1	Hs.546239	7	7q22.1	7.679	6.54	5.687	-0.68
54502	218035_s	FLJ20273	Hs.518727	4	4p13-p12	10.365	10.255	9.126	-0.67
26589	219244_s	MRPL46	Hs.534261	15	15q24-q25	7.523	7.215	6.804	-0.68
3133	200905_x	HLA-E	Hs.118354	6	6p21.3	9.711	11.429	11.117	0.74
6748	201004_at	SSR4	Hs.409223 X		Xq28	9.927	9.867	11.215	0.71
79888	201818_at	AYTL2	Hs.368853	5	5p15.33	6.117	7.122	7.088	0.7
5552	201858_s	PRG1	Hs.1908	10	10q22.1	9.015	10.658	10.763	0.71
22823	203345_s	MTF2	Hs.591449	1	1p22.1	6.669	7.506	7.422	0.68
4085	203362_s	MAD2L1	Hs.591697	4	4q27	4.136	5.847	5.039	0.7
4016	203570_at	LOXL1	Hs.65436	15	15q24-q25				
					15q22	5.642	6.437	6.793	0.67
5965	205091_x	RECQL	Hs.235069	12	12p12	5.926	6.769	6.971	0.67
3904	207509_s	LAIR2	Hs.43803	19	19q13.4	4.984	5.296	5.527	0.68
3039	209458_x	HBA1	Hs.449630	16	16p13.3	5.791	11.529	10.86	0.71
51465	217823_s	UBE2J1	Hs.163776	6	6q15	7.169	7.238	8.62	0.69
79180	217992_s	EFHD2	Hs.465374	1	1p36.21	5.395	6.106	6.329	0.69
57730	220940_at	KIAA1641	Hs.532921						
			Hs.541894						
			Hs.632866	2	2q11.2	4.867	5.487	5.542	0.69
79365	221530_s	BHLHB3	Hs.177841	12	12p11.23-p	5.556	6.234	7.579	0.67
10120	202135_s	ACTR1B	Hs.98791	2	2q11.1-q11	7.285	7.165	6.919	-0.67
4594	202959_at	MUT	Hs.485527	6	6p21	7.189	6.817	5.858	-0.67
6183	204331_s	MRPS12	Hs.411125	19	19q13.1-q1	7.57	7.324	6.943	-0.67
33	206069_s	ACADL	Hs.471277	2	2q34-q35	6.401	5.485	4.582	-0.68
4723	208714_at	NDUFV1	Hs.7744	11	11q13	9.23	9.218	8.511	-0.68
5435	209511_at	POLR2F	Hs.436578	22	22q13.1	7.517	7.091	7.16	-0.7
84263	209513_s	HSDL2	Hs.59486	9	9q32	8.292	7.86	6.905	-0.69
2653	213133_s	GCSH	Hs.546256						
			Hs.575922	16	16q23.2	8.72	8.006	7.4	-0.69
22977	216381_x	AKR7A3	Hs.6980	1	1p35.1-p36	8.415	7.38	6.599	-0.68
29911	218780_at	HOOK2	Hs.30792	19	19p13.13	6.366	6.428	5.814	-0.68
54995	219133_at	OXSM	Hs.55781	3	3p24.2	7.606	7.391	6.71	-0.68
7145	221246_x	TNS1	Hs.471381	2	2q35-q36	7.442	7.162	6.869	-0.68
2037	201719_s	EPB41L2	Hs.486470	6	6q23	6.687	7.211	7.434	0.68
3459	202727_s	IFNGR1	Hs.520414	6	6q23-q24	9.061	9.396	9.962	0.67
3660	203275_at	IRF2	Hs.374097	4	4q34.1-q35	4.96	6.34	6.433	0.68
7133	203508_at	TNFRSF1E	Hs.256278	1	1p36.3-p36	5.91	6.455	7.301	0.67
9111	203964_at	NMI	Hs.54483	2	2p24.3-q21	7.666	8.753	8.744	0.69
80301	204436_at	PLEKHQ1	Hs.458575	15	15q22.1	5.826	6.367	6.793	0.68
8543	209205_s	LMO4	Hs.436792	1	1p22.3	6.087	6.452	7.027	0.67
490	209281_s	ATP2B1	Hs.506276	12	12q21.3	5.688	6.241	6.484	0.68
8728	209765_at	ADAM19	Hs.483944	5	5q32-q33	5.508	5.544	5.949	0.68
85236	209806_at	HIST1H2BI	Hs.437275	6	6p21.33	7.226	8.367	8.441	0.69

3486	210095_s	IGFBP3	Hs.450230	7	7p13-p12	8.753	10.409	10.358	0.68
8832	211192_s	CD84	Hs.398093	1	1q24	4.305	5.155	5.065	0.7
240	214366_s	ALOX5	Hs.89499	10	10q11.2	4.313	4.657	5.344	0.68
10112	218755_at	KIF20A	Hs.73625	5	5q31	4.11	4.972	4.582	0.71
5583	218764_at	PRKCH	Hs.333907	14	14q22-q23	6.61	6.51	7.653	0.69
51291	218913_s	GMIP	Hs.49427	19	19p12-p11	5.238	5.526	5.941	0.67
5791	221840_at	PTPRE	Hs.127022	10	10q26	5.6	6.286	7.453	0.67
6925	222146_s	TCF4	Hs.569908	18	18q21.1	6.689	6.544	8.466	0.7
5019	202780_at	OXCT1	Hs.278277	5	5p13.1	8.102	7.254	7.013	-0.67
10912	204121_at	GADD45G	Hs.9701	9	9q22.1-q22	5.402	4.997	5	-0.68
10636	204280_at	RGS14	Hs.9347	5	5q35.3	6.171	5.997	5.537	-0.67
56288	210094_s	PARD3	Hs.131489	10	10p11.22-p	7.058	7.108	6.54	-0.68
7113	211689_s	TMPRSS2	Hs.439309	21	21q22.3	5.577	5.686	4.478	-0.69
987	212692_s	LRBA	Hs.480938	4	4q31.3	8.024	7.774	7.484	-0.66
5096	212694_s	PCCB	Hs.63788	3	3q21-q22	8.293	7.69	6.63	-0.69
513	213041_s	ATP5D	Hs.418668	19	19p13.3	8.281	7.704	7.323	-0.67
229	214424_s	ALDOB	Hs.530274	9	9q21.3-q22	5.027	4.557	4.464	-0.69
4494	217165_x	MT1F	Hs.513626	16	16q13	10.411	10.252	9.104	-0.67
28973	217408_at	MRPS18B	Hs.118354	6	6p21.3	8.94	8.372	8.418	-0.67
79616	219227_at	CCNJL	Hs.14070	5	5q33.3	4.55	4.114	4.311	-0.7
8450	202214_s	CUL4B	Hs.102914 X		Xq23	7.642	7.961	8.082	0.66
2200	202765_s	FBN1	Hs.591133	15	15q21.1	5.242	6.291	6.159	0.7
6275	203186_s	S100A4	Hs.557609	1	1q21	8.218	9.238	10.031	0.67
3384	204683_at	ICAM2	Hs.431460	17	17q23-q25	6.332	6.552	7.664	0.67
6188	208692_at	RPS3	Hs.546286	11	11q13.3-q1	10.654	10.928	11.228	0.67
11167	208782_at	FSTL1	Hs.591316	3	3q13.33	8.972	9.898	9.893	0.69
302	210427_x	ANXA2	Hs.511605	15	15q21-q22	10.946	11.686	11.871	0.69
5912	213923_at	RAP2B	Hs.98643	3	3q25.2	6.821	8.632	8.508	0.7
1281	215076_s	COL3A1	Hs.443625	2	2q31	9.173	12.021	10.539	0.72
50615	219971_at	IL21R	Hs.210546	16	16p11	3.877	3.963	4.216	0.66
25865	38269_at	PRKD2	Hs.466987	19	19q13.3	6.169	6.532	6.973	0.66
6614	44673_at	SIGLEC1	Hs.31869	20	20p13	5.477	6.362	6.323	0.68
3419	202070_s	IDH3A	Hs.591110	15	15q25.1-q2	7.364	7.116	6.67	-0.66
2947	202554_s	GSTM3	Hs.2006	1	1p13.3	10.051	9.527	8.242	-0.65
7525	202933_s	YES1	Hs.194148	18	18p11.31-p	8.411	8.119	7.333	-0.66
10965	202982_s	ACOT2	Hs.446685	14	14q24.3	7.917	7.301	6.358	-0.67
3029	205012_s	HAGH	Hs.157394						
			Hs.513265	16	16p13.3	8.265	7.582	7.005	-0.69
744	205413_at	MPPED2	Hs.289795	11	11p13	5.49	5	4.054	-0.67
2168	205892_s	FABP1	Hs.380135	2	2p11	10.271	8.76	5.073	-0.67
6119	209507_at	RPA3	Hs.487540	7	7p22	9.099	8.628	8.284	-0.67
23216	212350_at	TBC1D1	Hs.176503	4	4p14	8.42	8.428	7.871	-0.68
4616	213560_at	GADD45B	Hs.110571	19	19p13.3	6.188	5.814	5.867	-0.7

2998	214621_at	GYS2	Hs.82614	12	12p12.2	3.746	3.651	3.603	-0.68
1370	216223_at	CPN2	Hs.528368	3	3q29	5.435	4.396	4.243	-0.7
57820	217988_at	CCNB1IP1	Hs.107003	14	14q11.2	8.718	7.964	7.732	-0.67
23554	219274_at	TSPAN12	Hs.16529	7	7q31.31	9.692	9.092	8.082	-0.67
79746	219298_at	ECHDC3	Hs.22242	10	10p14	8.556	8.475	6.637	-0.68
894	200951_s	CCND2	Hs.376071	12	12p13	4.672	4.662	5.285	0.68
2202	201842_s	EFEMP1	Hs.76224	2	2p16	9.19	10.186	10.103	0.68
9697	202369_s	TRAM2	Hs.520182	6	6p21.1-p12	6.41	7.312	7.385	0.69
7040	203085_s	TGFB1	Hs.155218	19	19q13.2				
					19q13.1	5.373	6.987	6.899	0.68
4033	204674_at	LRMP	Hs.124922	12	12p12.1	6.91	7.309	7.984	0.66
3087	204689_at	HHEX	Hs.118651	10	10q23.33	4.86	5.074	5.526	0.68
5450	205267_at	POU2AF1	Hs.128180	11	11q23.1	4.364	4.233	7.951	0.7
5368	205901_at	PNOC	Hs.88218	8	8p21	4.424	4.465	5.762	0.68
10462	206682_at	CLEC10A	Hs.54403	17	17p13.1	5.274	5.094	7.129	0.69
0	212546_s	NA	NA	NA	NA	6.384	6.96	7.155	0.68
5965	212918_at	RECQL	Hs.235069	12	12p12	6.664	7.501	7.942	0.66
675	214727_at	BRCA2	Hs.34012	13	13q12.3	3.619	3.842	3.706	0.69
9705	206135_at	ST18	Hs.147170	8	8q11.23	3.89	3.703	3.718	-0.69
10920	214260_at	COPS8	Hs.531713	2	2q37.3	4.379	4.292	4.207	-0.66
5721	201762_s	PSME2	Hs.434081						
			Hs.512410	14	14q11.2	9.612	10.735	10.364	0.7
9734	205659_at	HDAC9	Hs.196054	7	7p21.1	5.254	5.17	5.989	0.69
10863	208269_s	ADAM28	Hs.174030	8	8p21.2	5.494	5.746	6.062	0.64
2534	210105_s	FYN	Hs.390567	6	6q21	7.713	8.057	8.588	0.68
6124	211710_x	RPL4	Hs.186350						
			Hs.591306	15	15q22	11.845	11.886	12.233	0.67
352961	214186_s	3.8-1	Hs.132807	6	6p21.3	6.399	6.475	6.716	0.66
3514	217145_at	IGKC	Hs.449621	2	2p12	3.959	3.83	5.754	0.7
51313	219872_at	C4orf18	Hs.567498	4	4q32.1	4.243	4.457	5.004	0.68
6500	200718_s	SKP1A	Hs.171626	5	5q31	11.49	11.41	11.117	-0.66
11034	201021_s	DSTN	Hs.304192						
			Hs.635105	20	20p12.1	11.002	10.862	10.559	-0.66
2631	201816_s	GBAS	Hs.591069	7	7p12	9.21	9.075	8.506	-0.65
7172	203672_x	TPMT	Hs.444319	6	6p22.3	7.193	6.842	6.196	-0.67
5191	205420_at	PEX7	Hs.280932	6	6q21-q22.2	5.71	5.009	4.798	-0.66
462	210049_at	SERPINC1	Hs.75599	1	1q23-q25.1	4.575	4.184	4.074	-0.68
4580	210386_s	MTX1	Hs.490874	1	1q21	7.817	7.439	7.311	-0.68
221154	212410_at	EFHA1	Hs.412103	13	13q12.11	9.822	9.454	8.855	-0.67
57142	214629_x	RTN4	Hs.429581	2	2p16.3	11.121	11.028	10.638	-0.67
	217625_x	NA	NA	NA	NA	5.674	5.321	5.118	-0.66
54948	217980_s	MRPL16	Hs.530734	11	NA	8.497	7.98	7.701	-0.66
79818	219741_x	ZNF552	Hs.560727	19	19q13.43	5.723	5.182	4.977	-0.66

51084	220753_s	CRYL1	Hs.370703	13	13q12.11	9.604	8.867	7.625	-0.67
376267	221810_at	RAB15	Hs.512492	14	14q23.3	6.031	5.847	5.511	-0.66
32	43427_at	ACACB	Hs.234898	12	12q24.11	6.689	5.722	5.65	-0.66
356	211333_s	FASLG	Hs.2007	1	1q23	4.023	4.206	4.316	0.66
5830	203244_at	PEX5	Hs.567327	12	12p13.3	7.218	7.122	6.476	-0.66
22928	200961_at	SEPHS2	Hs.118725	16	16p11.2	9.867	9.762	8.475	-0.67
10449	202003_s	ACAA2	Hs.200136	18	18q21.1	10.553	10.312	9.009	-0.67
3419	202069_s	IDH3A	Hs.591110	15	15q25.1-q2	7.639	7.283	6.792	-0.65
9663	202460_s	LPIN2	Hs.132342	18	18p11.31	8.014	7.524	7.435	-0.65
10497	202893_at	UNC13B	Hs.493791	9	9p12-p11	7.677	7.249	6.832	-0.67
4023	203549_s	LPL	Hs.180878	8	8p22	6.772	5.474	5.493	-0.67
4598	204056_s	MVK	Hs.130607	12	12q24	6.641	6.422	6.205	-0.64
8800	205160_at	PEX11A	Hs.31034	15	15q26.1	6.389	6.087	5.682	-0.66
6819	205342_s	SULT1C1	Hs.436123	2	2q11.1-q11	9.073	8.911	6.705	-0.67
3292	205829_at	HSD17B1	Hs.50727	17	17q11-q21	4.183	4.114	3.916	-0.67
521	207335_x	ATP5I	Hs.85539	4	4p16.3	9.691	8.781	8.746	-0.68
64087	209623_at	MCCC2	Hs.167531	5	5q12-q13	8.91	8.336	7.44	-0.67
27335	212716_s	EIF3S12	Hs.314359	19	19q13.2	10.708	9.896	10.163	-0.69
23051	217367_s	ZHX3	Hs.380133	20	20q12	6.13	5.712	5.244	-0.65
6134	200725_x	RPL10	Hs.534404 X		Xq28	11.72	11.829	12.079	0.66
7533	201020_at	YWHAH	Hs.226755	22	22q12.3	6.808	7.527	7.801	0.67
2771	201040_at	GNAI2	Hs.77269	3	3p21	6.595	7.126	7.604	0.66
2162	203305_at	F13A1	Hs.335513	6	6p25.3-p24	8.428	10.435	9.964	0.67
3604	207536_s	TNFRSF9	Hs.193418	1	1p36	4.571	5.104	5.283	0.66
25865	209282_at	PRKD2	Hs.466987	19	19q13.3	5.44	5.537	5.779	0.66
4247	211061_s	MGAT2	Hs.93338	14	14q21	6.781	7.237	7.536	0.66
55573	212010_s	CDV3	Hs.642726	3	3q22.1	9.669	9.936	10.258	0.67
	212382_at	NA	NA NA		NA	4.98	4.98	5.916	0.67
9645	212472_at	MICAL2	Hs.501928	11	11p15.3	5.253	5.693	5.878	0.67
10781	214686_at	ZNF266	Hs.465838	19	19p13.2	6.527	6.697	7.27	0.65
	214949_at	NA	NA NA		NA	5.82	6.148	6.329	0.66
3538	216365_x	IGLC2	NA	22	22q11.2	5.664	5.465	8.266	0.7
5996	216834_at	RGS1	Hs.75256	1	1q31	5.853	6.593	9.117	0.68
10695	217931_at	TNRC5	Hs.414099	6	6pter-p12.1	6.866	7.032	7.55	0.65
83440	220980_s	ADPGK	Hs.513013	15	15q24.1	7.463	7.785	8.172	0.66
158747	221895_at	MOSPD2	Hs.190043 X		Xp22.2	6.417	6.994	7.006	0.68
5900	209051_s	RALGDS	Hs.106185	9	9q34.3	5.569	5.832	6.156	0.65
2896	200678_x	GRN	Hs.514220	17	17q21.32	8.652	9.473	9.621	0.66
7097	204924_at	TLR2	Hs.519033	4	4q32	6.346	7.585	8.019	0.69
1396	205081_at	CRIP1	Hs.70327	14	14q32.33	6.557	6.746	7.839	0.65
27240	205484_at	SIT1	Hs.88012	9	9p13-p12	5.152	5.351	6.172	0.66
7177	205683_x	TPSAB1	Hs.405479	16	16p13.3	5.124	4.837	8.87	0.69
54504	208146_s	CPVL	Hs.233389						

			Hs.449281							
			Hs.449585							
			Hs.539824	7	7p15-p14	8.335	8.594	9.253	0.66	
23208	209198_s	SYT11	Hs.32984	1	1q21.2	4.305	4.52	4.679	0.67	
11214	209534_x	AKAP13	Hs.459211	15	15q24-q25	6.368	6.676	7.191	0.65	
472	210858_x	ATM	Hs.435561	11	11q22-q23	6.692	8.339	8.221	0.67	
23231	212314_at	KIAA0746	Hs.479384	4	4p15.2	8.188	7.899	9.295	0.68	
23307	212663_at	KIAA0674	Hs.522351	9	9q32	7.694	8.102	8.085	0.67	
54491	219694_at	FAM105A	Hs.591751	5	5p15.2	5.226	5.615	5.985	0.66	
11009	221602_s	IL24	Hs.58831							
			Hs.642714	1	1q32	5.544	5.623	6.535	0.67	
5142	222326_at	PDE4B	Hs.198072	1	1p31	3.867	4.14	4.304	0.66	
23552	205271_s	CCRK	Hs.522274	9	9q22.1	6	5.662	5.681	-0.69	
27109	206993_at	ATP5S	Hs.438489	14	14q22.1	5.021	4.723	4.495	-0.65	
23277	212456_at	KIAA0664	Hs.22616	17	17p13.3	8.338	7.983	7.601	-0.65	
23189	213005_s	ANKRD15	Hs.306764	9	9p24.3	8.411	8.227	7.195	-0.66	
51181	217973_at	DCXR	Hs.9857	17	17q25.3	9.277	8.186	7.553	-0.67	
55111	218290_at	PLEKHJ1	Hs.501353	19	19p13.3	7.068	6.941	6.624	-0.66	
29093	218339_at	MRPL22	Hs.483924	5	5q33.1-q33	8.018	7.81	7.271	-0.65	
114884	219073_s	OSBPL10	Hs.150122	3	3p22.3	8.206	8.017	7.022	-0.65	
64577	220148_at	ALDH8A1	Hs.486520	6	6q23.2	10.089	9.349	6.387	-0.67	
401428	222290_at	OR2A20P	Hs.591830	7	7q35	4.738	4.641	4.34	-0.65	
	222354_at	NA	NA	NA	NA	5.412	4.965	4.963	-0.71	
25820	201880_at	ARIH1	Hs.268787	15	15q24	6.888	7.145	7.434	0.66	
10217	201904_s	CTDSPL	Hs.475963	3	3p21.3	7.609	7.35	6.763	-0.65	
587	203576_at	BCAT2	Hs.512670	19	19q13	7.719	7.544	6.847	-0.65	
866	206325_at	SERPINA6	Hs.532635	14	14q32.1	6.641	5.94	5.203	-0.67	
10211	208749_x	FLOT1	Hs.179986	6	6p21.3	9.112	8.92	8.646	-0.67	
521	209492_x	ATP5I	Hs.85539	4	4p16.3	10.849	10.153	10.04	-0.66	
23769	210414_at	FLRT1	Hs.584876	11	11q12-q13	4.722	4.652	4.446	-0.65	
2263	211401_s	FGFR2	Hs.533683	10	10q26	5.427	5.442	4.675	-0.7	
645745	211456_x	LOC645745	Hs.632513	1	1q43	11.516	11.367	10.629	-0.65	
55970	212294_at	GNG12	Hs.431101	1	1p31.3	9.298	9.182	8.778	-0.65	
11046	213082_s	SLC35D2	Hs.494556							
			Hs.593332	9	9q22.32	6.709	6.553	6.214	-0.65	
23016	213648_at	EXOSC7	Hs.115792	3	3p21.31	6.229	6.063	5.83	-0.66	
10682	213787_s	EBP	Hs.632801	X	Xp11.23-p1	7.488	7.113	6.6	-0.66	
	213929_at	NA	NA	NA	NA	5.766	5.313	4.715	-0.65	
646278	217520_x	LOC646278	Hs.597835	15	15q13.1	4.788	4.537	4.42	-0.65	
79639	219462_at	TMEM53	Hs.22157	1	1p34.1	6.195	6.086	5.664	-0.65	
81689	221425_s	HBLD2	Hs.449291	9	9q21.33	7.171	7.212	6.571	-0.67	
51606	221504_s	ATP6V1H	Hs.491737	8	8p22-q22.3	8.357	8.358	7.398	-0.68	
9501	221614_s	RPH3AL	Hs.461807	17	17p13.3	6.332	5.931	5.791	-0.66	

3692	221953_s	ITGB4BP	Hs.632277	20	20q12	7.047	6.66	6.296	-0.68
55101	45828_at	FLJ10241	Hs.351099	19	19q13.2	8.329	8.198	7.557	-0.66
10541	201305_x	ANP32B	Hs.494604	9	9q22.32	8.32	8.692	8.963	0.66
8087	201637_s	FXR1	Hs.478407	3	3q28	8.088	8.504	8.677	0.66
1277	202310_s	COL1A1	Hs.172928	17	17q21.33	6.081	8.897	7.827	0.67
5699	202659_at	PSMB10	Hs.9661	16	16q22.1	6.905	8.163	8.14	0.68
11040	204269_at	PIM2	Hs.496096 X		Xp11.23	5.99	5.825	7.127	0.69
8405	204640_s	SPOP	Hs.463382	17	17q21.33	6.979	7.263	7.471	0.65
6003	210258_at	RGS13	Hs.497220	1	1q31.2	3.638	3.607	4.23	0.69
23304	212756_s	UBR2	Hs.529925	6	6p21.1	6.53	6.912	7.169	0.66
6355	214038_at	CCL8	Hs.271387	17	17q11.2	5.073	9.087	8.962	0.68
6203	217747_s	RPS9	Hs.467284						
			Hs.546288	19	19q13.4	10.621	10.85	11.296	0.65
79709	218473_s	GLT25D1	Hs.418795	19	19p13.11	6.204	6.651	6.89	0.66
55100	219193_at	WDR70	Hs.213690	5	5p13.2	6.06	6.604	6.628	0.67
3735	200079_s	KARS	Hs.3100	16	16q23-q24	9.09	9.509	9.744	0.66
7453	200629_at	WARS	Hs.497599	14	14q32.31	8.209	10.255	9.815	0.67
3437	204747_at	IFIT3	Hs.47338	10	10q24	6.828	8.648	7.599	0.69
9744	205213_at	CENTB1	Hs.337242	17	17p13.1	5.288	5.115	6.288	0.68
5294	206370_at	PIK3CG	Hs.32942	7	7q22.3	3.84	3.829	4.199	0.66
647460	216517_at	NA	NA NA		NA	4.369	4.428	6.118	0.67
64780	218376_s	MICAL1	Hs.33476	6	6q21	5.793	5.949	6.476	0.67
	49111_at	NA	NA NA		NA	5.774	5.895	6.175	0.65
89853	52975_at	FAM125B	Hs.162659	9	9q33.3	5.687	5.841	5.939	0.64
9588	200845_s	PRDX6	Hs.573688	1	1q25.1	10.047	9.782	9.568	-0.64
6856	201260_s	SYPL1	Hs.80919	7	7q22.2	8.865	8.574	8.321	-0.65
6382	201286_at	SDC1	Hs.224607	2	2p24.1	8.637	7.893	7.305	-0.64
8165	201675_at	AKAP1	Hs.463506	17	17q21-q23	8.074	7.823	7.186	-0.65
64849	205243_at	SLC13A3	Hs.250281	20	20q12-q13.	10.026	8.731	6.43	-0.67
3977	205876_at	LIFR	Hs.133421	5	5p13-p12	4.807	4.572	4.37	-0.66
11170	207547_s	FAM107A	Hs.506357	3	3p21.1	6.551	6.39	5.831	-0.64
799	207886_s	CALCR	Hs.489127	7	7q21.3	4.377	4.263	4.172	-0.65
5151	212521_s	PDE8A	Hs.9333	15	15q25.3	7.557	7.414	6.833	-0.66
390940	213556_at	LOC390940	Hs.22049	19	19q13.31	5.515	5.382	5.135	-0.64
4499	217546_at	MT1M	Hs.643532	16	16q13	6.976	5.568	5.273	-0.65
56647	218264_at	BCCIP	Hs.370292	10	10q26.1	6.509	5.817	5.692	-0.66
54148	218558_s	MRPL39	Hs.420696	21	21q21.3	8.258	7.893	7.457	-0.65
51074	218698_at	APIP	Hs.447794	11	11p13	7.66	7.389	7.092	-0.66
10319	219407_s	LAMC3	Hs.201805	9	9q31-q34	5.679	5.25	5.263	-0.67
4285	36830_at	MIPEP	Hs.507498	13	13q12	6.549	6.165	5.14	-0.66
55036	220592_at	CCDC40	Hs.202542	17	17q25.3	4.418	4.363	4.286	-0.67
2171	202345_s	FABP5	Hs.408061	8	8q21.13	5.619	7.073	7.934	0.66
22823	203346_s	MTF2	Hs.591449	1	1p22.1	5.494	6.639	6.364	0.68

5090	204082_at	PBX3	Hs.428027	9	9q33-q34	6.066	6.52	6.66	0.66
3665	208436_s	IRF7	Hs.166120	11	11p15.5	6.084	6.193	7.003	0.66
8826	210840_s	IQGAP1	Hs.430551	15	15q26.1	7.367	8.56	8.709	0.66
23253	212289_at	ANKRD12	Hs.464585	18	18p11.22	6.194	6.612	6.819	0.65
4174	216237_s	MCM5	Hs.517582	22	22q13.1	5.024	5.843	5.815	0.68
55114	218076_s	ARHGAP17	Hs.373793	16	16p12.1	6.949	7.234	7.587	0.65
55704	221078_s	KIAA1212	Hs.292925	2	2p16.1	4.615	5.127	5.345	0.67
51237	221286_s	PACAP	Hs.409563	5	5q23-5q31	5.934	5.4	8.308	0.69
167153	222282_at	PAPD4	Hs.418198	5	5q14.1	5.557	6.358	6.788	0.65
4677	200027_at	NARS	Hs.465224	18	18q21.2-q2	11.011	10.665	10.303	-0.65
1185	203950_s	CLCN6	Hs.193043	1	1p36	5.566	5.439	5.309	-0.65
10966	204547_at	RAB40B	Hs.484068	17	17q25.3	7.36	6.878	5.989	-0.65
11062	205762_s	DUS4L	Hs.97627	7	7q22-q31	4.253	4.118	3.993	-0.65
1184	206704_at	CLCN5	Hs.49114 X		Xp11.23-p1	6.331	6.319	4.9	-0.67
51382	208898_at	ATP6V1D	Hs.272630	14	14q23-q24.	9.731	9.39	8.991	-0.65
7381	209065_at	UQCRB	Hs.131255	8	8q22	8.241	7.684	6.712	-0.65
80303	209343_at	EFHD1	Hs.516769						
			Hs.642960	2	2q37.1	9.713	9.078	8.017	-0.66
10211	210142_x	FLOT1	Hs.179986	6	6p21.3	9.224	8.969	8.707	-0.65
9577	211566_x	BRE	Hs.11916						
			Hs.258314	2	2p23.2	7.759	7.589	7.401	-0.65
23065	212395_s	KIAA0090	Hs.439200	1	1p36.13	5.586	5.598	5.117	-0.66
84193	212465_at	SETD3	Hs.510407	14	14q32.2	8.964	8.432	8.288	-0.67
23286	213085_s	WWC1	Hs.484047	5	5q35.1	8.045	7.867	7.151	-0.64
23366	213424_at	KIAA0895	Hs.6224	7	7p14.2	5.566	4.898	4.224	-0.65
6752	214597_at	SSTR2	Hs.514451	17	17q24	4.785	4.184	4.244	-0.68
57001	218981_at	ACN9	Hs.592269	7	7q21.3	7.152	6.46	5.703	-0.66
55112	219251_s	WDR60	Hs.389945	7	7q36.3	6.559	6.214	5.892	-0.64
55277	219718_at	FLJ10986	Hs.444301	1	1p32.1	6.844	6.466	6.2	-0.67
54943	220372_at	C21orf55	Hs.458308	21	21q22.11	4.556	4.46	4.262	-0.66
11160	221542_s	SPFH2	Hs.125849	8	8p11.2	6.28	6.223	5.643	-0.65
5527	201877_s	PPP2R5C	Hs.368264	14	14q32	7.524	7.709	8.194	0.65
3429	202411_at	IFI27	Hs.532634	14	14q32	7.56	8.884	8.952	0.66
9702	203492_x	CEP57	Hs.101014	11	11q21	5.747	6.431	6.133	0.68
571	204194_at	BACH1	Hs.154276	21	21q22.11	6.551	7.554	7.904	0.66
10735	209023_s	STAG2	Hs.496710						
			Hs.624663 X		Xq25	6.424	7.306	7.535	0.66
6929	210776_x	TCF3	Hs.371282	19	19p13.3	6.427	6.504	7.035	0.66
23225	212316_at	NUP210	Hs.475525	3	3p25.1	5.158	5.32	5.684	0.65
23312	212820_at	DMXL2	Hs.511386	15	15q21.2	6.772	7.572	8.033	0.65
26112	212886_at	CCDC69	Hs.132994	5	5q33.1	5.577	5.478	6.366	0.68
3087	215933_s	HHEX	Hs.118651	10	10q23.33	4.289	4.683	5.452	0.65
4815	219594_at	NINJ2	Hs.504422	12	12p13	4.776	4.976	5.219	0.66

56938	220658_s	ARNTL2	Hs.434269	12	12p12.2-p1	4.129	4.322	4.758	0.66
203197	221865_at	C9orf91	Hs.522357	9	9q32	4.508	4.646	4.869	0.64
2235	203116_s	FECH	Hs.465221	18	18q21.3	7.396	6.994	6.637	-0.65
10165	203775_at	SLC25A13	Hs.489190	7	7q21.3	7.229	6.601	5.91	-0.66
5345	205075_at	SERPINF2	Hs.159509	17	17p13	7.577	6.501	6.332	-0.65
6443	205120_s	SGCB	Hs.438953	4	4q12	8.067	7.924	7.146	-0.65
9185	205645_at	REPS2	Hs.186810 X		Xp22.2	6.165	5.388	5.332	-0.66
1188	205985_x	CLCNKB	Hs.352243	1	1p36	7.87	7.824	6.056	-0.66
288	206385_s	ANK3	Hs.499725	10	10q21	9.763	9.665	7.438	-0.65
10693	206587_at	CCT6B	Hs.73072	17	17q12	4.883	4.727	4.591	-0.65
10246	207097_s	SLC17A2	Hs.591802	6	6p21.3	4.346	4.199	4.133	-0.65
5861	208724_s	RAB1A	Hs.310645	2	2p14	11.164	11.036	10.718	-0.65
7381	209066_x	UQCRB	Hs.131255	8	8q22	11.288	10.919	10.658	-0.64
10478	211754_s	SLC25A17	Hs.474938	22	22q13.2	6.974	6.619	6.458	-0.66
6526	212944_at	SLC5A3	Hs.302742	21	21q22.12	9.263	8.494	8.227	-0.63
4862	213462_at	NPAS2	Hs.156832						
			Hs.638925	2	2q11.2	6.82	6.331	5.999	-0.65
23786	217955_at	BCL2L13	Hs.631672	22	22q11	7.612	7.629	6.817	-0.66
28998	218049_s	MRPL13	Hs.333823	8	8q22.1-q22	8.533	8.434	7.707	-0.65
4696	218563_at	NDUFA3	Hs.198269	19	19q13.42	9.859	9.583	9.32	-0.66
10451	218807_at	VAV3	Hs.267659	1	1p13.3	9.384	8.894	8.239	-0.65
55351	219686_at	STK32B	Hs.133062	4	4p16.2-p16	6.482	6.285	5.734	-0.65
55727	220297_at	BTBD7	Hs.525549	14	14q32.12-q	5.165	4.947	4.736	-0.64
934	266_s_at	CD24	Hs.375108	6	6q21	11.166	11.017	10.437	-0.66
662	37226_at	BNIP1	Hs.145726	5	5q33-q34	5.21	5.155	5.068	-0.65
9741	200673_at	LAPTM4A	Hs.467807	2	2p24.1	11.373	11.277	10.958	-0.65