

Table S7 Model estimates for probe sets with time effect q-value <0.05 and expression level decreased from baseline.

Probe Set ID	Gene Symbol	Gene Name	Time Effect 3 mg/kg	Time Effect 10 mg/kg	Dose Effect Pre-Tx	Dose Effect Post-Tx	Interaction Effect	Time Effect <i>P</i> -value	Dose Effect <i>P</i> -value	Interaction <i>P</i> -value	Time Effect q-value	Dose Effect q-value	Interaction q-value
205338_s_at	DCT ^M	tyrosinase-related protein-2	-1.572	-0.365	-0.878	0.328	1.207	0.002	0.148	0.052	0.044	0.461	0.796
206696_at	GPR143	G protein-coupled receptor 143	-1.372	-0.267	-1.055	0.051	1.105	0.002	0.076	0.044	0.046	0.454	0.796
220245_at	SLC45A2 ^M	solute carrier family 45, member 2	-1.176	-0.393	-0.056	0.726	0.783	0.002	0.245	0.101	0.045	0.496	0.796
219464_at	CA14	carbonic anhydrase XIV	-1.144	-0.004	-1.000	0.14	1.14	0.002	0.043	0.012	0.046	0.453	0.796
219107_at	BCAN	brevican	-1.009	-0.132	-0.853	0.024	0.877	0.001	0.033	0.022	0.039	0.453	0.796
214475_x_at	CAPN3	calpain 3, (p94)	-0.995	-0.476	-0.705	-0.187	0.519	<.001	0.31	0.159	0.028	0.513	0.796
221644_s_at	SLC45A2	solute carrier family 45, member 2	-0.988	-0.237	-0.070	0.681	0.751	0.001	0.102	0.043	0.035	0.458	0.796
220425_x_at	ROPN1B	roporin, rhophilin associated protein 1B	-0.976	-0.460	-0.222	0.294	0.516	<.001	0.363	0.136	0.025	0.527	0.796
211890_x_at	CAPN3	calpain 3, (p94)	-0.926	-0.389	-0.669	-0.132	0.537	<.001	0.236	0.116	0.029	0.492	0.796
204187_at	GMPR	guanosine monophosphate reductase	-0.902	-0.159	-0.483	0.26	0.743	<.001	0.023	0.02	0.029	0.453	0.796
210944_s_at	CAPN3	calpain 3, (p94)	-0.827	-0.338	-0.627	-0.138	0.489	0.001	0.274	0.122	0.034	0.504	0.796
91920_at	BCAN	brevican	-0.807	-0.262	-0.574	-0.029	0.545	<.001	0.057	0.048	0.025	0.453	0.796
210963_s_at	GYG2	glycogenin 2	-0.793	-0.040	-0.591	0.163	0.754	<.001	0.003	0.003	0.025	0.453	0.796
210964_s_at	GYG2	glycogenin 2	-0.783	-0.099	-0.598	0.087	0.685	0.001	0.013	0.015	0.032	0.453	0.796
205376_at	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	-0.732	-0.099	-0.549	0.085	0.633	0.001	0.023	0.024	0.04	0.453	0.796
212445_s_at	NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like	-0.671	-0.279	-0.550	-0.158	0.393	<.001	0.137	0.111	0.028	0.46	0.796
209681_at	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	-0.601	-0.252	-0.191	0.159	0.349	0.002	0.293	0.169	0.048	0.508	0.796
212807_s_at	SORT1	sortilin 1	-0.600	-0.379	-0.178	0.043	0.221	0.001	0.32	0.375	0.034	0.516	0.809
222258_s_at	SH3BP4	SH3-domain binding protein 4	-0.596	-0.373	-0.056	0.168	0.223	0.001	0.56	0.386	0.039	0.582	0.81
218402_s_at	HPS4	Hermansky-Pudlak syndrome 4	-0.551	-0.137	-0.399	0.014	0.414	0.001	0.064	0.054	0.04	0.453	0.796
203702_s_at	TTLL4	tubulin tyrosine ligase-like family, member 4	-0.550	-0.083	-0.360	0.107	0.467	0.002	0.071	0.029	0.044	0.454	0.796
222116_s_at	TBC1D16	TBC1 domain family, member 16	-0.536	-0.303	-0.277	-0.044	0.233	0.001	0.322	0.297	0.038	0.516	0.797
212632_at	STX7	syntaxin 7	-0.521	-0.317	-0.280	-0.076	0.204	0.001	0.144	0.343	0.034	0.46	0.8
208029_s_at	LAPTM4B	lysosomal protein	-0.519	-0.423	-0.264	-0.169	0.095	0.001	0.076	0.7	0.041	0.454	0.862

		transmembrane 4 beta											
209108_at	TSPAN6	tetraspanin 6	-0.514	-0.588	0.296	0.222	-0.074	0.001	0.815	0.781	0.033	0.645	0.869
220272_at	BNC2	basonuclin 2	-0.513	-0.234	-0.474	-0.195	0.28	<.001	0.048	0.141	0.028	0.453	0.796
205677_s_at	DLEU1	deleted in lymphocytic leukemia 1 (non-protein coding)	-0.505	-0.232	-0.043	0.23	0.273	0.001	0.368	0.178	0.038	0.529	0.797
216048_s_at	RHOBTB3	Rho-related BTB domain containing 3	-0.499	-0.461	-0.178	-0.139	0.039	0.001	0.358	0.87	0.035	0.526	0.883
202975_s_at	RHOBTB3	Rho-related BTB domain containing 3	-0.499	-0.508	-0.153	-0.162	-0.009	<.001	0.475	0.969	0.028	0.557	0.892
209238_at	STX3	syntaxin 3	-0.498	-0.355	-0.316	-0.174	0.143	0.001	0.367	0.521	0.038	0.529	0.835
201535_at	UBL3	ubiquitin-like 3	-0.494	-0.270	-0.195	0.029	0.224	0.002	0.285	0.296	0.045	0.507	0.797
202976_s_at	RHOBTB3	Rho-related BTB domain containing 3	-0.487	-0.398	-0.047	0.042	0.089	<.001	0.548	0.657	0.026	0.579	0.857
202946_s_at	BTBD3	BTB (POZ) domain containing 3	-0.484	-0.230	-0.344	-0.091	0.254	0.002	0.082	0.227	0.05	0.454	0.797
204040_at	RNF144A	ring finger protein 144A	-0.475	-0.244	-0.211	0.019	0.231	<.001	0.178	0.205	0.029	0.472	0.797
219641_at	DET1	de-etiolated homolog 1	-0.473	-0.280	-0.322	-0.129	0.193	0.001	0.116	0.338	0.039	0.458	0.798
211844_s_at	NRP2	neuropilin 2	-0.469	-0.223	-0.215	0.031	0.246	0.001	0.206	0.198	0.039	0.482	0.797
204527_at	MYO5A	myosin VA (heavy chain 12, myoxin)	-0.463	-0.489	0.004	-0.022	-0.026	0.002	0.67	0.919	0.047	0.609	0.888
203612_at	BYSL	bystin-like	-0.457	-0.134	-0.435	-0.112	0.323	0.002	0.019	0.074	0.042	0.453	0.796
212290_at	SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-0.448	-0.126	-0.149	0.173	0.322	<.001	0.157	0.043	0.028	0.464	0.796
205673_s_at	ASB9	ankyrin repeat and SOCS box-containing 9	-0.441	-0.013	-0.453	-0.025	0.428	<.001	0.004	0.004	0.026	0.453	0.796
216059_at	PAX3	paired box 3	-0.437	-0.137	-0.343	-0.042	0.301	0.002	0.056	0.088	0.045	0.453	0.796
219051_x_at	METRNL	meteorin, glial cell differentiation regulator	-0.436	-0.083	-0.472	-0.118	0.353	<.001	0.015	0.023	0.03	0.453	0.796
209109_s_at	TSPAN6	tetraspanin 6	-0.433	-0.409	0.238	0.262	0.024	<.001	0.725	0.903	0.028	0.621	0.887
204107_at	NFYA	nuclear transcription factor Y, alpha	-0.423	-0.031	-0.400	-0.009	0.392	<.001	0.001	0.005	0.025	0.453	0.796
202873_at	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	-0.421	-0.247	-0.137	0.038	0.175	0.002	0.503	0.343	0.044	0.565	0.8
204109_s_at	NFYA	nuclear transcription factor Y, alpha	-0.417	-0.072	-0.433	-0.088	0.345	0.002	0.004	0.034	0.044	0.453	0.796
204992_s_at	PFN2	profilin 2	-0.407	-0.547	-0.240	-0.380	-0.139	0.001	0.199	0.546	0.032	0.48	0.839
202609_at	EPS8	epidermal growth factor receptor pathway substrate 8	-0.405	-0.348	0.035	0.092	0.057	<.001	0.864	0.732	0.025	0.657	0.866
215415_s_at	LYST ¹	lysosomal trafficking regulator	-0.395	-0.272	-0.223	-0.101	0.123	<.001	0.104	0.445	0.029	0.458	0.825
203545_at	ALG8	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog	-0.390	-0.141	0.01	0.259	0.249	0.002	0.268	0.125	0.048	0.503	0.796

206748_s_at	SPAG9	sperm associated antigen 9	-0.388	-0.150	-0.372	-0.133	0.238	0.002	0.069	0.131	0.044	0.454	0.796
201485_s_at	RCN2	reticulocalbin 2, EF-hand calcium binding domain	-0.381	-0.270	-0.180	-0.069	0.111	<.001	0.373	0.464	0.027	0.53	0.828
212503_s_at	DIP2C	DIP2 disco-interacting protein 2 homolog C	-0.380	-0.350	0.079	0.109	0.029	0.002	0.841	0.883	0.05	0.65	0.885
205880_at	PRKD1	protein kinase D1	-0.380	-0.364	-0.110	-0.095	0.016	0.002	0.218	0.937	0.049	0.487	0.89
219372_at	IFT81	intraflagellar transport 81 homolog	-0.379	-0.217	-0.087	0.076	0.162	0.001	0.615	0.313	0.039	0.595	0.797
212676_at	NF1	neurofibromin 1	-0.374	-0.047	-0.268	0.059	0.326	<.001	0.016	0.012	0.028	0.453	0.796
207515_s_at	POLR1C	polymerase (RNA) I polypeptide C	-0.374	-0.192	-0.280	-0.098	0.182	0.001	0.105	0.211	0.032	0.458	0.797
221759_at	G6PC3	glucose 6 phosphatase, catalytic, 3	-0.373	-0.210	-0.268	-0.105	0.163	<.001	0.087	0.234	0.025	0.454	0.797
213133_s_at	GCSH	similar to Glycine cleavage system H protein	-0.369	-0.225	0.094	0.238	0.144	0.002	0.496	0.374	0.043	0.564	0.809
212797_at	SORT1	sortilin 1	-0.368	-0.030	-0.108	0.231	0.338	0.001	0.012	0.01	0.032	0.453	0.796
209537_at	EXTL2	exostoses (multiple)-like 2	-0.365	-0.339	-0.063	-0.038	0.026	<.001	0.495	0.869	0.025	0.563	0.883
218464_s_at	C17orf63	chromosome 17 open reading frame 63	-0.363	-0.158	-0.251	-0.046	0.205	<.001	0.031	0.108	0.025	0.453	0.796
212996_s_at	URB1	URB1 ribosome biogenesis 1 homolog	-0.357	-0.077	-0.491	-0.211	0.28	0.001	0.008	0.03	0.032	0.453	0.796
213391_at	DPY19L4	dpy-19-like 4	-0.356	-0.335	-0.123	-0.101	0.021	<.001	0.361	0.874	0.025	0.527	0.884
218595_s_at	HEATR1	HEAT repeat containing 1	-0.356	-0.075	-0.278	0.003	0.281	0.002	0.054	0.046	0.045	0.453	0.796
208677_s_at	BSG	basigin (Ok blood group)	-0.352	-0.232	-0.344	-0.225	0.119	0.002	0.164	0.454	0.045	0.468	0.826
210415_s_at	ODF2	outer dense fiber of sperm tails 2	-0.350	-0.100	-0.393	-0.143	0.251	<.001	0.001	0.045	0.029	0.453	0.796
203631_s_at	GPRC5B	G protein-coupled receptor, family C, group 5, member B	-0.349	-0.164	-0.189	-0.005	0.185	<.001	0.207	0.15	0.028	0.483	0.796
201733_at	CLCN3	chloride channel 3	-0.345	-0.257	-0.136	-0.048	0.088	0.002	0.185	0.583	0.044	0.473	0.845
203188_at	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	-0.332	-0.244	-0.059	0.029	0.089	0.002	0.735	0.575	0.048	0.625	0.842
219376_at	ZNF322B	zinc finger protein 322B	-0.329	-0.208	-0.124	-0.003	0.121	<.001	0.178	0.315	0.025	0.472	0.797
200662_s_at	TOMM20	similar to translocase of outer mitochondrial membrane 20 homolog;	-0.328	-0.237	-0.178	-0.087	0.091	<.001	0.345	0.497	0.028	0.523	0.833
218561_s_at	LYRM4	LYR motif containing 4	-0.325	-0.323	-0.206	-0.204	0.001	0.001	0.084	0.994	0.032	0.454	0.893
213854_at	SYNGR1	synaptogyrin 1	-0.324	-0.214	0.079	0.189	0.11	<.001	0.664	0.357	0.025	0.607	0.803

206414_s_at	DDEF2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	-0.323	-0.373	-0.077	-0.127	-0.051	0.001	0.342	0.772	0.037	0.522	0.869
218187_s_at	C8orf33	chromosome 8 open reading frame 33	-0.314	-0.206	-0.267	-0.159	0.108	0.002	0.177	0.456	0.048	0.472	0.827
203867_s_at	NLE1	notchless homolog 1	-0.313	-0.135	-0.248	-0.071	0.178	0.001	0.054	0.142	0.034	0.453	0.796
205135_s_at	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	-0.305	-0.175	-0.163	-0.033	0.13	<.001	0.12	0.252	0.026	0.458	0.797
221532_s_at	WDR61	WD repeat domain 61	-0.305	-0.220	-0.144	-0.058	0.086	0.002	0.118	0.544	0.044	0.458	0.839
212294_at	GNG12	guanine nucleotide binding protein (G protein), gamma 12	-0.302	-0.245	-0.219	-0.163	0.057	0.001	0.389	0.685	0.038	0.535	0.859
211159_s_at	PPP2R5D	protein phosphatase 2, regulatory subunit B', delta isoform	-0.302	-0.051	-0.186	0.064	0.251	0.002	0.024	0.037	0.046	0.453	0.796
212539_at	CHD1L	chromodomain helicase DNA binding protein 1-like	-0.301	-0.232	-0.153	-0.085	0.068	0.001	0.646	0.617	0.038	0.601	0.85
205097_at	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	-0.301	-0.512	0.087	-0.123	-0.210	<.001	0.498	0.287	0.029	0.564	0.797
219880_at	---		-0.297	-0.441	-0.007	-0.151	-0.145	<.001	0.686	0.365	0.025	0.612	0.805
213823_at	HOXA11	homeobox A11	-0.296	-0.028	-0.226	0.042	0.268	0.001	0.04	0.019	0.041	0.453	0.796
200973_s_at	TSPAN3	tetraspanin 3	-0.296	-0.347	0.018	-0.034	-0.051	<.001	0.889	0.718	0.025	0.661	0.865
221586_s_at	E2F5 ^c	E2F transcription factor 5, p130-binding	-0.293	-0.001	-0.322	-0.030	0.292	0.002	0.062	0.013	0.048	0.453	0.796
201674_s_at	AKAP1	A kinase (PRKA) anchor protein 1	-0.290	-0.228	0.017	0.08	0.063	0.002	0.855	0.655	0.046	0.655	0.856
221235_s_at	LOC644617	hypothetical LOC644617	-0.290	-0.298	-0.227	-0.235	-0.008	0.002	0.094	0.96	0.044	0.454	0.892
222013_x_at	FAM86B1	family with sequence similarity 86, member B1	-0.283	-0.191	-0.178	-0.087	0.091	0.001	0.247	0.438	0.033	0.496	0.824
204063_s_at	ULK2	unc-51-like kinase 2	-0.283	-0.078	-0.092	0.113	0.205	0.002	0.067	0.072	0.046	0.453	0.796
202749_at	WRB	tryptophan rich basic protein	-0.283	-0.148	-0.083	0.052	0.135	0.001	0.181	0.224	0.033	0.472	0.797
215720_s_at	NFYA	nuclear transcription factor Y, alpha	-0.280	-0.049	-0.275	-0.043	0.232	<.001	0.003	0.014	0.025	0.453	0.796
216986_s_at	IRF4 ^l	interferon regulatory factor 4	-0.279	-0.120	-0.133	0.026	0.159	0.002	0.323	0.18	0.049	0.516	0.797
204184_s_at	ADRBK2	adrenergic, beta, receptor kinase 2	-0.275	-0.123	-0.127	0.025	0.152	0.001	0.318	0.17	0.038	0.515	0.796
217935_s_at	UQCC	ubiquinol-cytochrome c reductase complex chaperone	-0.275	-0.127	-0.323	-0.175	0.148	0.001	0.087	0.18	0.038	0.454	0.797
218307_at	RSAD1	radical S-adenosyl methionine domain	-0.274	-0.218	-0.056	<.001	0.056	0.001	0.795	0.649	0.035	0.64	0.853

		containing 1											
221229_s_at	FLJ20628	tRNA methyltransferase 61 homolog B	-0.272	-0.263	-0.124	-0.114	0.009	0.001	0.294	0.945	0.034	0.509	0.892
203284_s_at	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	-0.271	-0.463	0.209	0.017	-0.192	<.001	0.747	0.268	0.027	0.628	0.797
204944_at	PTPRG ^C	protein tyrosine phosphatase, receptor type, G	-0.269	-0.465	-0.089	-0.285	-0.196	0.001	0.333	0.293	0.034	0.519	0.797
213304_at	KIAA0423	family with sequence similarity 179, member B	-0.268	-0.176	-0.078	0.014	0.092	<.001	0.343	0.379	0.028	0.522	0.81
208837_at	TMED3	transmembrane emp24 protein transport domain containing 3	-0.262	-0.416	-0.169	-0.323	-0.154	0.001	0.427	0.376	0.035	0.544	0.809
202019_s_at	LANCL1	LanC lantibiotic synthetase component C-like 1	-0.256	-0.407	-0.032	-0.184	-0.151	0.002	0.074	0.399	0.044	0.454	0.812
208796_s_at	CCNG1	cyclin G1	-0.254	-0.322	-0.013	-0.082	-0.068	0.001	0.393	0.641	0.038	0.537	0.853
200659_s_at	PHB ^C	prohibitin	-0.250	-0.188	-0.147	-0.085	0.062	0.001	0.338	0.567	0.034	0.521	0.841
209777_s_at	SLC19A1	solute carrier family 19 (folate transporter), member 1	-0.250	-0.038	-0.142	0.07	0.213	0.002	0.122	0.033	0.047	0.458	0.796
218709_s_at	IFT52	intraflagellar transport 52 homolog	-0.249	-0.302	-0.142	-0.195	-0.053	0.001	0.21	0.705	0.038	0.483	0.863
211763_s_at	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	-0.249	-0.285	0.047	0.011	-0.036	<.001	0.559	0.775	0.028	0.582	0.869
212745_s_at	BBS4	Bardet-Biedl syndrome 4	-0.245	-0.211	-0.185	-0.151	0.033	0.002	0.096	0.785	0.046	0.455	0.87
213675_at	---		-0.241	-0.405	0.08	-0.084	-0.164	<.001	0.723	0.264	0.025	0.621	0.797
203526_s_at	APC ^{I,C}	adenomatous polyposis coli	-0.233	-0.185	0.009	0.057	0.048	0.002	0.499	0.665	0.044	0.564	0.857
200972_at	TSPAN3	tetraspanin 3	-0.233	-0.241	0.058	0.05	-0.008	0.001	0.948	0.95	0.039	0.675	0.892
215931_s_at	ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2	-0.230	-0.197	-0.026	0.007	0.033	0.002	0.967	0.776	0.049	0.679	0.869
204065_at	CHST10	carbohydrate sulfotransferase 10	-0.229	-0.134	-0.080	0.014	0.094	0.002	0.675	0.36	0.049	0.61	0.803
213508_at	C14orf147	chromosome 14 open reading frame 147	-0.227	-0.550	0.121	-0.202	-0.323	0.002	0.313	0.147	0.045	0.514	0.796
208822_s_at	DAP3	death associated protein 3	-0.227	-0.084	-0.093	0.051	0.143	0.002	0.291	0.131	0.048	0.508	0.796
201380_at	CRTAP	cartilage associated protein	-0.219	-0.400	-0.125	-0.306	-0.181	0.001	0.146	0.269	0.038	0.46	0.797
221488_s_at	CUTA	cutA divalent cation tolerance homolog	-0.219	-0.219	0.017	0.016	<.001	<.001	0.933	0.996	0.029	0.671	0.894
216305_s_at	C2orf3	chromosome 2 open reading frame 3	-0.218	-0.200	-0.189	-0.171	0.018	0.001	0.172	0.862	0.032	0.471	0.882

200929_at	TMED10	transmembrane emp24-like trafficking protein 10	-0.218	-0.217	-0.049	-0.047	0.002	0.001	0.995	0.988	0.038	0.685	0.892
220768_s_at	CSNK1G3	casein kinase 1, gamma 3	-0.215	-0.307	0.035	-0.058	-0.092	0.001	0.634	0.481	0.035	0.599	0.831
205231_s_at	EPM2A	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)	-0.210	-0.131	-0.165	-0.085	0.08	0.002	0.193	0.395	0.045	0.477	0.811
206961_s_at	MED20	mediator complex subunit 20	-0.206	-0.076	-0.030	0.101	0.131	<.001	0.162	0.078	0.028	0.466	0.796
208716_s_at	TMCO1	transmembrane and coiled-coil domains 1	-0.205	-0.114	0.054	0.145	0.091	0.002	0.428	0.309	0.046	0.544	0.797
202300_at	HBXIP	hepatitis B virus x interacting protein	-0.204	-0.133	-0.009	0.062	0.071	0.001	0.549	0.42	0.038	0.58	0.82
205217_at	TIMM8A	translocase of inner mitochondrial membrane 8 homolog A	-0.204	-0.048	-0.095	0.061	0.156	0.002	0.108	0.056	0.045	0.458	0.796
212122_at	RHOQ, RHOQP2	ras homolog gene family, member Q	-0.201	-0.233	0.113	0.081	-0.032	0.002	0.886	0.783	0.047	0.66	0.869
218437_s_at	LZTFL1	leucine zipper transcription factor-like 1	-0.199	-0.305	-0.083	-0.188	-0.105	<.001	0.6	0.377	0.028	0.592	0.809
201059_at	CTTN ^C	cortactin	-0.195	-0.189	-0.073	-0.067	0.006	0.001	0.253	0.953	0.039	0.498	0.892
203733_at	DEXI	dexamethasone-induced transcript	-0.194	-0.316	0.049	-0.073	-0.122	0.002	0.763	0.392	0.049	0.632	0.81
214052_x_at	BAT2D1	proline-rich coiled-coil 2C	-0.192	-0.064	-0.121	0.007	0.128	<.001	0.147	0.065	0.029	0.46	0.796
202033_s_at	RB1CC1	RB1-inducible coiled-coil 1	-0.192	-0.288	-0.119	-0.215	-0.096	0.002	0.322	0.455	0.043	0.516	0.827
211976_at	RPL35P2, RPL35P1, rpl35	ribosomal protein L35; ribosomal protein L35 pseudogene 1; ribosomal protein L35 pseudogene 2	-0.191	-0.289	-0.146	-0.245	-0.098	0.001	0.211	0.441	0.041	0.484	0.824
214877_at	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	-0.187	-0.161	-0.199	-0.173	0.025	<.001	0.362	0.747	0.025	0.527	0.867
211094_s_at	NF1	nuclear transcription factor Y, alpha	-0.181	-0.140	-0.061	-0.020	0.041	0.002	0.32	0.636	0.046	0.516	0.853
212987_at	FBXO9	F-box protein 9	-0.176	-0.246	-0.028	-0.097	-0.070	0.002	0.433	0.54	0.046	0.546	0.838
202371_at	TCEAL4	transcription elongation factor A (SII)-like 4	-0.176	-0.313	0.251	0.114	-0.137	<.001	0.488	0.246	0.028	0.561	0.797
208251_at	KCNC4	potassium voltage-gated channel, Shaw-related subfamily, member 4	-0.169	-0.040	-0.126	0.003	0.129	0.002	0.157	0.06	0.049	0.464	0.796
202034_x_at	RB1CC1	RB1-inducible coiled-coil 1	-0.167	-0.306	-0.045	-0.184	-0.139	<.001	0.252	0.236	0.03	0.498	0.797

204823_at	NAV3	neuron navigator 3; similar to neuron navigator 3	-0.165	-0.537	0.67	0.298	-0.372	0.001	0.018	0.071	0.039	0.453	0.796
214462_at	SOCS6	suppressor of cytokine signaling 6	-0.161	-0.150	-0.040	-0.029	0.011	0.001	0.151	0.881	0.034	0.462	0.885
210974_s_at	AP3D1 ¹	adaptor-related protein complex 3, delta 1 subunit	-0.159	-0.123	-0.081	-0.046	0.035	0.002	0.348	0.64	0.045	0.524	0.853
218203_at	ALG5	asparagine-linked glycosylation 5, dolichyl-phosphate beta- glucosyltransferase homolog	-0.158	-0.209	0.219	0.168	-0.051	0.001	0.272	0.593	0.039	0.504	0.846
203866_at	NLE1	notchless homolog 1	-0.158	-0.063	-0.100	-0.004	0.095	0.002	0.251	0.146	0.046	0.497	0.796
212229_s_at	FBXO21	F-box protein 21	-0.155	-0.307	-0.069	-0.220	-0.151	0.001	0.181	0.219	0.038	0.472	0.797
204498_s_at	ADCY9	adenylate cyclase 9	-0.154	-0.067	-0.061	0.027	0.087	0.002	0.153	0.178	0.046	0.463	0.797
212505_s_at	KIAA0892	MAU2 chromatid cohesion factor homolog	-0.150	-0.102	-0.153	-0.105	0.048	0.002	0.107	0.484	0.045	0.458	0.831
202440_s_at	ST5 ^C	suppression of tumorigenicity 5	-0.147	-0.354	-0.040	-0.248	-0.207	0.001	0.022	0.134	0.038	0.453	0.796
200719_at	SKP1	S-phase kinase- associated protein 1	-0.139	-0.380	-0.001	-0.242	-0.241	0.001	0.087	0.102	0.039	0.454	0.796
212169_at	FKBP9	FK506 binding protein 9, 63 kDa	-0.138	-0.439	-0.204	-0.505	-0.301	0.002	0.063	0.081	0.044	0.453	0.796
221279_at	GDAP1	ganglioside-induced differentiation- associated protein 1	-0.127	-0.191	0.024	-0.040	-0.064	<.001	0.565	0.349	0.025	0.584	0.801
200983_x_at	CD59	CD59 molecule, complement regulatory protein	-0.111	-0.293	0.168	-0.014	-0.183	0.001	0.437	0.114	0.041	0.546	0.796
200984_s_at	CD59	CD59 molecule, complement regulatory protein	-0.090	-0.378	0.219	-0.069	-0.288	0.002	0.253	0.048	0.044	0.498	0.796
202853_s_at	RYK	RYK receptor-like tyrosine kinase	-0.090	-0.224	0.046	-0.088	-0.134	0.002	0.478	0.143	0.046	0.558	0.796
210844_x_at	CTNNA1	catenin (cadherin- associated protein), alpha 1, 102kDa	-0.085	-0.211	-0.027	-0.154	-0.127	0.001	0.064	0.111	0.034	0.453	0.796
208407_s_at	CTNND1	catenin (cadherin- associated protein), delta 1	-0.082	-0.423	0.164	-0.177	-0.341	0.002	0.223	0.04	0.048	0.487	0.796
219078_at	GPATCH2	G patch domain containing 2	-0.081	-0.325	0.025	-0.219	-0.244	<.001	0.116	0.032	0.03	0.458	0.796
203141_s_at	AP3B1 ¹	adaptor-related protein complex 3, beta 1 subunit	-0.069	-0.215	0.058	-0.088	-0.146	<.001	0.318	0.049	0.028	0.515	0.796
200811_at	CIRBP	cold inducible RNA	-0.068	-0.423	0.035	-0.320	-0.355	<.001	0.023	0.01	0.025	0.453	0.796

		binding protein											
200711_s_at	SKP1	S-phase kinase-associated protein 1	−0.063	−0.233	0.058	−0.112	−0.170	0.001	0.061	0.042	0.034	0.453	0.796
200985_s_at	CD59 ^I	CD59 molecule, complement regulatory protein	−0.062	−0.381	0.215	−0.105	−0.320	<.001	0.066	0.008	0.025	0.453	0.796
213040_s_at	NPTXR	neuronal pentraxin receptor	−0.020	−0.322	0.175	−0.127	−0.302	<.001	0.017	0.006	0.029	0.453	0.796
212417_at	SCAMP1	secretory carrier membrane protein 1	−0.015	−0.368	0.169	−0.184	−0.354	<.001	0.055	0.005	0.028	0.453	0.796
208733_at	RAB2A	RAB2A, member RAS oncogene family	−0.013	−0.180	0.201	0.034	−0.167	0.002	0.019	0.018	0.05	0.453	0.796
200810_s_at	CIRBP	cold inducible RNA binding protein	−0.008	−0.376	0.031	−0.337	−0.368	<.001	0.006	0.003	0.025	0.453	0.796

I = immune related; C = cancer related; M = melanoma related