featureNames	logFC	AveExpr	t	P.Value	adj.P.Val	B	ENTREZID	SYMBOL	GENENAME	ENSEMBL
A_23_P360213	2.846	13.91	62.4	6.33E-12	2.75E-07	15.11	NA	NA	NA	NA
A_24_P913056	1.882	11.38	51.66	2.80E-11	4.05E-07	14.72	5339	PLEC	plectin	ENSG00000178209
A_24_P89457	1.578	8.428	42.11	1.40E-10	1.22E-06	14.16	1026	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21 Cip1)	ENSG00000124762
A_23_P66774	1.242	9.884	37.06	3.83E-10	2.37E-06	13.73	124975	GGT6	gamma-glutamyltransferase 6	ENSG00000167741
A_24_P402261	1.528	6.955	34	7.53E-10	2.97E-06	13.4	440836	ODF3B	outer dense fiber of sperm tails 3B	ENSG00000177989
A_24_P181731	1.279	8.919	31.89	1.25E-09	3.65E-06	13.13	8425	LTBP4	latent transforming growth factor beta binding protein 4	ENSG00000090006
A_23_P132932	1.298	7.919	31.81	1.27E-09	3.65E-06	13.12	1609	DGKQ	diacylglycerol kinase theta 110kDa	ENSG00000145214
A_23_P256603	2.585	9.822	31.58	1.35E-09	3.65E-06	13.09	4301	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog Drosophila); translocated to 4	ENSG00000130396
A_24_P155058	1.685	7.75	30.78	1.65E-09	3.97E-06	12.98	3551	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells kinase beta	ENSG00000104365
A_23_P254888	1.204	10.76	29.84	2.09E-09	4.46E-06	12.84	7791	ZYX	zyxin	ENSG00000159840
A_24_P37665	1.249	9.541	29.73	2.16E-09	4.46E-06	12.82	10861	SLC26A1	solute carrier family 26 (sulfate transporter) member 1	ENSG00000145217
A_24_P350124	1.861	9.379	29.26	2.45E-09	4.82E-06	12.75	57674	RNF213	ring finger protein 213	ENSG00000173821 ENSG00000180843
A_23_P26468	1.298	8.838	28.34	3.14E-09	5.48E-06	12.59	9028	RHBDL1	rhomboid veinlet-like 1 (Drosophila)	ENSG00000103269
A_23_P107735	1.246	8.351	28.32	3.16E-09	5.48E-06	12.59	973	CD79A	CD79a molecule immunoglobulin-associated alpha	ENSG00000105369
A_23_P56150	1.086	9.017	27.84	3.61E-09	6.01E-06	12.51	84839	RAX2	retina and anterior neural fold homeobox 2	ENSG00000173976
A_23_P49443	1.148	8.329	27.62	3.84E-09	6.01E-06	12.47	115	ADCY9	adenylate cyclase 9	ENSG00000162104
A_24_P281497	1.527	8.86	27.1	4.46E-09	6.04E-06	12.38	116983	ACAP3	ArfGAP with coiled-coil ankyrin repeat and PH domains 3	ENSG00000131584
A_32_P173298	1.169	9.915	26.56	5.22E-09	6.37E-06	12.27	23450	SF3B3	splicing factor 3b subunit 3 130kDa	ENSG00000189091
A_23_P56673	0.9955	7.405	26.51	5.29E-09	6.37E-06	12.26	83444	INO80B	INO80 complex subunit B	ENSG00000115274
A_23_P30972	1.401	9.13	26.25	5.72E-09	6.70E-06	12.21	10973	ASCC3	activating signal cointegrator 1 complex subunit 3	ENSG00000112249
A_24_P237231	0.8976	9.881	25.81	6.53E-09	7.26E-06	12.13	150094	SIK1	salt-inducible kinase 1	ENSG00000142178
A_24_P117866	0.8837	9.857	25.47	7.24E-09	7.65E-06	12.06	118	ADD1	adducin 1 (alpha)	ENSG00000087274
A_32_P217471	0.8735	7.911	25.01	8.34E-09	8.15E-06	11.96	4430	MYO1B	myosin IB	ENSG00000128641
A_24_P247408	1.583	7.637	24.71	9.19E-09	8.15E-06	11.89	399851	LOC399851	hypothetical gene supported by AY129010	NA
A_24_P290856	1.235	7.612	24.71	9.18E-09	8.15E-06	11.9	5802	PTPRS	protein tyrosine phosphatase receptor type S	ENSG00000105426
A_23_P13711	1.352	7.962	24.7	9.21E-09	8.15E-06	11.89	8085	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	ENSG00000167548
A_23_P215642	1.151	8.568	24.19	1.09E-08	8.88E-06	11.78	64759	TNS3	tensin 3	ENSG00000136205
A_24_P915734	1.112	7.288	23.78	1.24E-08	9.79E-06	11.69	100289490	LOC100289490	hypothetical protein LOC100289490	NA
A_24_P117902	1.26	10.11	22.95	1.63E-08	1.12E-05	11.49	114884	OSBPL10	oxysterol binding protein-like 10	ENSG00000144645

A_32_P161292	1.751	7.534	22.86	1.69E-08	1.12E-05	11.46	91351	DDX60L	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60-like	ENSG00000181381
A_23_P135310	0.9246	6.958	22.35	2.01E-08	1.25E-05	11.34	6812	STXBP1	syntaxin binding protein 1	ENSG00000136854
A_23_P118086	0.93	9.124	22.22	2.10E-08	1.27E-05	11.3	124044	SPATA2L	spermatogenesis associated 2-like	ENSG00000158792
A_23_P142671	1.448	11.08	22.2	2.11E-08	1.27E-05	11.3	130557	ZNF513	zinc finger protein 513	ENSG00000163795
A_24_P209389	1.845	8.194	22.18	2.13E-08	1.27E-05	11.29	51085	MLXIPL	MLX interacting protein-like	ENSG00000009950
A_23_P204079	1.31	8.487	21.92	2.33E-08	1.33E-05	11.22	8620	NPFF	neuropeptide FF-amide peptide precursor	ENSG00000139574
A_24_P109524	0.9707	8.005	21.75	2.48E-08	1.35E-05	11.18	54434	SSH1	slingshot homolog 1 (Drosophila)	ENSG00000084112
A_24_P895892	1.508	8.004	21.57	2.65E-08	1.40E-05	11.13	23102	TBC1D2B	TBC1 domain family member 2B	ENSG00000167202
A_23_P218302	1.267	8.351	21.5	2.71E-08	1.42E-05	11.11	84656	GLYR1	glyoxylate reductase 1 homolog (Arabidopsis)	ENSG00000140632
A_24_P301954	0.8043	6.599	20.73	3.61E-08	1.72E-05	10.89	114130	MGC16384	hypothetical LOC114130	NA
A_32_P141374	1.466	10.21	20.66	3.70E-08	1.73E-05	10.87	352954	GATS	GATS stromal antigen 3 opposite strand	ENSG00000160844
A_24_P392723	1.207	6.947	20.65	3.71E-08	1.73E-05	10.87	114819	CROCCL2	ciliary rootlet coiled-coil rootletin-like 2	NA
A_23_P206466	0.8801	8.979	20.54	3.87E-08	1.78E-05	10.84	57524	CASKIN1	CASK interacting protein 1	ENSG00000167971
A_24_P124097	0.7078	10.64	20.49	3.95E-08	1.78E-05	10.82	64855	FAM129B	family with sequence similarity 129 member B	ENSG00000136830
A_24_P914155	1.203	7.382	20.49	3.94E-08	1.78E-05	10.82	159195	USP54	ubiquitin specific peptidase 54	ENSG00000166348
A_23_P157943	1.312	7.768	20.44	4.02E-08	1.78E-05	10.81	11253	MAN1B1	mannosidase alpha class 1B member 1	ENSG00000177239
A_24_P478495	1.025	8.754	20.37	4.13E-08	1.80E-05	10.79	728229	TMEM191B	transmembrane protein 191B	NA
A_23_P55926	0.7774	10.45	20.24	4.34E-08	1.81E-05	10.75	7376	NR1H2	nuclear receptor subfamily 1 group H member 2	ENSG00000131408
A_23_P66017	1.201	7.645	19.79	5.18E-08	1.97E-05	10.61	112476	PRRT2	proline-rich transmembrane protein 2	ENSG00000167371
A_32_P146815	0.8286	7.805	19.5	5.79E-08	2.06E-05	10.52	4257	MGST1	microsomal glutathione S-transferase 1	ENSG00000008394
A_24_P41170	0.9863	5.953	19.16	6.64E-08	2.15E-05	10.41	54477	PLEKHA5	pleckstrin homology domain containing family A member 5	ENSG00000052126
A_23_P63219	0.9093	8.79	18.92	7.32E-08	2.25E-05	10.33	23126	POGZ	pogo transposable element with ZNF domain	ENSG00000143442
A_23_P368740	1.048	7.241	18.78	7.74E-08	2.25E-05	10.28	83933	HDAC10	histone deacetylase 10	ENSG00000100429
A_24_P130865	0.9055	6.816	18.66	8.15E-08	2.32E-05	10.24	23133	PHF8	PHD finger protein 8	ENSG00000172943
A_23_P256663	1.177	9.098	18.65	8.17E-08	2.32E-05	10.24	8484	GALR3	galanin receptor 3	ENSG00000128310
A_24_P326635	0.9927	9.505	18.55	8.54E-08	2.35E-05	10.2	156	ADRBK1	adrenergic beta receptor kinase 1	ENSG00000173020
A_32_P37592	2.374	9.635	18.55	8.54E-08	2.35E-05	10.2	677769	SCARNA17	small Cajal body-specific RNA 17	NA
A_24_P170801	0.9868	6.584	18.5	8.69E-08	2.35E-05	10.19	727957	HEATR7A	HEAT repeat containing 7A	ENSG00000179832
A_24_P25668	1.248	6.606	18.49	8.73E-08	2.35E-05	10.18	1815	DRD4	dopamine receptor D4	ENSG00000069696
A_23_P77807	1.466	8.856	18.38	9.15E-08	2.39E-05	10.14	10743	RAI1	retinoic acid induced 1	ENSG00000108557
A_23_P255011	0.9194	10.72	18.33	9.34E-08	2.42E-05	10.13	56886	UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	ENSG00000136731
A_23_P397371	1.373	11.01	18.21	9.83E-08	2.44E-05	10.08	27434	POLM	polymerase (DNA directed) mu	ENSG00000122678
A_24_P58331	1.217	10.01	18.01	1.07E-07	2.54E-05	10.01	79877	DCAKD	dephospho-CoA kinase domain containing	ENSG00000172992
A_24_P44891	0.9473	9.725	17.94	1.11E-07	2.61E-05	9.986	30000	TNPO2	transportin 2	ENSG00000105576
A_24_P68050	1.313	6.823	17.85	1.15E-07	2.66E-05	9.954	83985	SPNS1	spinster homolog 1 (Drosophila)	ENSG00000169682

A_23_P304530	0.7879	8.176	17.83	1.16E-07	2.68E-05	9.946	254910	LCE5A	late cornified envelope 5A	ENSG00000186207
A_24_P81789	1.61	10.31	17.76	1.20E-07	2.73E-05	9.92	54509	RHOF	ras homolog gene family member F (in filopodia)	ENSG00000139725
A_23_P130731	0.689	9.242	17.71	1.22E-07	2.76E-05	9.904	79735	TBC1D17	TBC1 domain family member 17	ENSG00000104946
A_32_P222450	0.9984	8.614	17.65	1.25E-07	2.81E-05	9.88	25907	TMEM158	transmembrane protein 158	NA
A_23_P208779	0.7148	10.2	17.6	1.28E-07	2.82E-05	9.863	54869	EPS8L1	EPS8-like 1	ENSG00000131037
A_23_P331028	1.748	13.73	17.59	1.29E-07	2.82E-05	9.859	23389	MED13L	mediator complex subunit 13-like	ENSG00000123066
A_23_P38190	1.294	8.385	17.36	1.42E-07	3.07E-05	9.773	94103	ORMDL3	ORM1-like 3 (S. cerevisiae)	ENSG00000172057
A_24_P416059	1.233	10.29	17.33	1.44E-07	3.07E-05	9.76	4123	MAN2C1	mannosidase alpha class 2C member 1	ENSG00000140400
A_24_P285158	0.8546	8.81	17.27	1.48E-07	3.10E-05	9.739	127943	FCRLB	Fc receptor-like B	ENSG00000162746
A_23_P142013	1.212	7.464	17.22	1.52E-07	3.13E-05	9.719	56949	XAB2	XPA binding protein 2	ENSG00000076924
A_24_P330030	0.7844	7.003	17.2	1.53E-07	3.15E-05	9.71	220064	ORAOV1	oral cancer overexpressed 1	ENSG00000149716
A_24_P161463	0.6808	11.65	17.01	1.67E-07	3.28E-05	9.635	441951	C20orf199	chromosome 20 open reading frame 199	NA
A_23_P26426	0.9494	10.58	17	1.67E-07	3.28E-05	9.635	27132	CPNE7	copine VII	ENSG00000178773
A_23_P150919	0.6118	8.952	16.94	1.72E-07	3.36E-05	9.61	84876	ORAI1	ORAI calcium release-activated calcium modulator 1	ENSG00000182500
A_24_P10674	1.11	10.46	16.64	1.98E-07	3.63E-05	9.489	115703	ARHGAP33	Rho GTPase activating protein 33	ENSG00000004777
A_24_P24263	0.9439	6.696	16.63	1.98E-07	3.63E-05	9.487	10611	PDLIM5	PDZ and LIM domain 5	ENSG00000163110
A_23_P23227	0.5915	8.617	16.62	2.00E-07	3.64E-05	9.481	5586	PKN2	protein kinase N2	ENSG00000065243
A_23_P103084	1.482	8.131	16.49	2.12E-07	3.75E-05	9.43	10043	TOM1	target of myb1 (chicken)	ENSG00000100284
A_23_P416191	0.6782	6.674	16.46	2.15E-07	3.75E-05	9.418	259290	TAS2R31	taste receptor type 2 member 31	NA
A_24_P914495	0.7774	9.579	16.46	2.15E-07	3.75E-05	9.418	2011	MARK2	MAP/microtubule affinity-regulating kinase 2	ENSG00000072518
A_23_P130619	1.304	8.47	16.42	2.18E-07	3.79E-05	9.403	6813	STXBP2	syntaxin binding protein 2	ENSG00000076944
A_23_P47086	0.9778	7.067	16.37	2.24E-07	3.86E-05	9.379	57830	KRTAP5-8	keratin associated protein 5-8	ENSG00000204572 ENSG00000241233
A_24_P272160	1.141	7.98	16.27	2.35E-07	3.99E-05	9.338	23218	NBEAL2	neurobeachin-like 2	ENSG00000160796
A_32_P390781	1.49	7.771	16.11	2.54E-07	4.24E-05	9.271	57455	REXO1	REX1 RNA exonuclease 1 homolog (S. cerevisiae)	ENSG00000079313
A_23_P130761	1.031	7.705	16.07	2.59E-07	4.26E-05	9.254	1628	DBP	D site of albumin promoter (albumin D-box) binding protein	ENSG00000105516
A_23_P384056	0.7579	9.864	16.05	2.61E-07	4.26E-05	9.248	64770	CCDC14	coiled-coil domain containing 14	ENSG00000175455
A_32_P14669	0.9213	8.039	15.92	2.78E-07	4.51E-05	9.191	7617	ZNF66	zinc finger protein 66	NA
A_23_P405282	0.8287	8.178	15.89	2.82E-07	4.54E-05	9.178	284365	MGC45922	hypothetical LOC284365	NA
A_24_P938293	0.7322	10.64	15.88	2.83E-07	4.54E-05	9.175	3280	HES1	hairy and enhancer of split 1 (Drosophila)	ENSG00000114315
A_32_P98298	1.133	7.438	15.82	2.92E-07	4.61E-05	9.148	1850	DUSP8	dual specificity phosphatase 8	ENSG00000184545
A_32_P148726	1.311	8.007	15.81	2.92E-07	4.61E-05	9.147	389741	MGC21881	hypothetical locus MGC21881	NA
A_23_P48455	0.8693	7.475	15.77	2.99E-07	4.64E-05	9.126	81693	AMN	amnionless homolog (mouse)	ENSG00000166126
A_23_P131115	0.9626	8.221	15.76	3.00E-07	4.64E-05	9.121	4782	NFIC	nuclear factor I/C (CCAAT-binding transcription factor)	ENSG00000141905
A_24_P410516	1.375	9.287	15.74	3.03E-07	4.65E-05	9.113	440295	GOLGA6L9	golgin A6 family-like 9	ENSG00000196648 ENSG00000197978

A_24_P800604	1.391	10.5	15.71	3.07E-07	4.67E-05	9.101	286077	FAM83H	family with sequence similarity 83 member H	ENSG00000180921
A_23_P105307	0.5418	8.676	15.65	3.16E-07	4.71E-05	9.077	1606	DGKA	diacylglycerol kinase alpha 80kDa	ENSG00000065357
A_24_P230156	0.7384	7.904	15.6	3.24E-07	4.82E-05	9.053	8629	JRK	jerky homolog (mouse)	ENSG00000234616
A_23_P56304	0.6131	7.778	15.5	3.41E-07	4.98E-05	9.008	80264	ZNF430	zinc finger protein 430	ENSG00000118620
A_24_P649582	0.9726	8.803	15.5	3.41E-07	4.98E-05	9.009	253039	LOC253039	hypothetical LOC253039	NA
A_23_P37569	0.6674	7.481	15.42	3.55E-07	5.07E-05	8.972	4122	MAN2A2	mannosidase alpha class 2A member 2	ENSG00000196547
A_23_P36364	0.6785	8.172	15.39	3.60E-07	5.09E-05	8.959	7070	THY1	Thy-1 cell surface antigen	ENSG00000154096
A_32_P20288	1.026	8.732	15.32	3.73E-07	5.15E-05	8.928	64839	FBXL17	F-box and leucine-rich repeat protein 17	ENSG00000145743
A_32_P163368	0.6159	5.943	15.17	4.02E-07	5.39E-05	8.861	8993	PGLYRP1	peptidoglycan recognition protein 1	ENSG00000008438
A_23_P371794	1.121	8.565	15.13	4.11E-07	5.43E-05	8.841	784	CACNB3	calcium channel voltage-dependent beta 3 subunit	ENSG00000167535
A_24_P162172	1.516	8.706	15.1	4.15E-07	5.46E-05	8.831	80208	SPG11	spastic paraplegia 11 (autosomal recessive)	ENSG00000104133
A_24_P222043	1.447	11.13	15.03	4.31E-07	5.53E-05	8.796	3159	HMGA1	high mobility group AT-hook 1	ENSG00000137309
A_24_P273063	1.161	8.413	15.03	4.31E-07	5.53E-05	8.797	79870	BAALC	brain and acute leukemia cytoplasmic	ENSG00000164929
A_24_P51360	0.7495	9.724	15.03	4.32E-07	5.53E-05	8.795	51520	LARS	leucyl-tRNA synthetase	ENSG00000133706
A_32_P157192	0.8492	5.933	14.93	4.54E-07	5.67E-05	8.751	22826	DNAJC8	DnaJ (Hsp40) homolog subfamily C member 8	ENSG00000126698
A_24_P665504	0.7669	7.609	14.91	4.60E-07	5.73E-05	8.739	100132062	LOC100132062	hypothetical LOC100132062	ENSG00000238035
A_23_P90189	0.9521	10.91	14.86	4.71E-07	5.83E-05	8.717	27113	BBC3	BCL2 binding component 3	ENSG00000105327
A_23_P204828	1.326	8.672	14.79	4.89E-07	5.94E-05	8.682	7181	NR2C1	nuclear receptor subfamily 2 group C member 1	ENSG00000120798
A_23_P118113	1.952	8.194	14.75	4.99E-07	5.98E-05	8.664	6650	SOLH	small optic lobes homolog (Drosophila)	ENSG00000103326
A_23_P115118	0.6958	11.16	14.74	5.00E-07	5.98E-05	8.663	656	BMP8B	bone morphogenetic protein 8b	ENSG00000116985
A_24_P42436	0.8095	7.531	14.6	5.38E-07	6.26E-05	8.595	9743	ARHGAP32	Rho GTPase activating protein 32	ENSG00000134909
A_23_P329271	0.6451	10.36	14.56	5.51E-07	6.31E-05	8.573	4157	MC1R	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	ENSG00000198211
A_23_P55911	0.8424	7.341	14.52	5.61E-07	6.36E-05	8.558	126070	ZNF440	zinc finger protein 440	ENSG00000171295
A_23_P349310	0.6486	7.906	14.47	5.78E-07	6.41E-05	8.53	27327	TNRC6A	trinucleotide repeat containing 6A	ENSG00000090905
A_32_P867789	1.199	7.742	14.47	5.77E-07	6.41E-05	8.532	57642	COL20A1	collagen type XX alpha 1	ENSG00000101203
A_23_P116587	0.9692	6.204	14.46	5.81E-07	6.41E-05	8.525	4975	OMP	olfactory marker protein	NA
A_24_P73817	0.6618	6.425	14.42	5.92E-07	6.49E-05	8.507	339105	POL3S	polyserase 3	ENSG00000151006
A_24_P238649	0.9374	6.751	14.36	6.12E-07	6.60E-05	8.477	388677	NOTCH2NL	Notch homolog 2 (Drosophila) N-terminal like	ENSG00000213240
A_23_P323154	0.7668	7.617	14.31	6.29E-07	6.74E-05	8.453	84662	GLIS2	GLIS family zinc finger 2	ENSG00000126603
A_23_P202156	1.218	11.02	14.29	6.34E-07	6.74E-05	8.444	4791	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	ENSG00000077150
A_24_P142495	1.197	9.352	14.25	6.47E-07	6.76E-05	8.426	81850	KRTAP1-3	keratin associated protein 1-3	ENSG00000221880
A_23_P396135	1.14	8.236	14.22	6.58E-07	6.82E-05	8.41	1482	NKX2-5	NK2 transcription factor related locus 5 (Drosophila)	ENSG00000183072
A_24_P350744	1.199	8.352	14.21	6.61E-07	6.82E-05	8.406	22889	KIAA0907	KIAA0907	ENSG00000132680

A_24_P918157	0.7936	6.492	14.17	6.78E-07	6.90E-05	8.383	9139	CBFA2T2	core-binding factor runt domain alpha subunit 2; translocated to 2	ENSG00000078699
A_24_P373976	1.474	9.074	14.14	6.88E-07	6.92E-05	8.37	6385	SDC4	syndecan 4	ENSG00000124145
A_24_P932451	0.7944	6.609	14.11	6.98E-07	6.97E-05	8.356	29994	BAZ2B	bromodomain adjacent to zinc finger domain 2B	ENSG00000123636
A_24_P213884	1.265	8.683	14.02	7.33E-07	7.12E-05	8.31	7148	TNXB	tenascin XB	ENSG00000168477 ENSG00000229353 ENSG00000233323
A_24_P238543	1.062	7.787	14.02	7.33E-07	7.12E-05	8.31	5255	PHKA1	phosphorylase kinase alpha 1 (muscle)	ENSG00000067177
A_23_P84670	0.8323	7.706	14	7.43E-07	7.16E-05	8.298	2902	GRIN1	glutamate receptor ionotropic N-methyl D-aspartate 1	ENSG00000176884
A_23_P34018	0.5482	12.89	13.99	7.47E-07	7.17E-05	8.293	6170	RPL39	ribosomal protein L39	ENSG00000198918
A_24_P316102	1.295	8.826	13.95	7.63E-07	7.24E-05	8.274	8028	MLLT10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog Drosophila); translocated to 10	ENSG00000078403
A_24_P37887	1.46	10.87	13.95	7.62E-07	7.24E-05	8.274	285601	GPR150	G protein-coupled receptor 150	ENSG00000178015
A_23_P409723	0.7565	6.563	13.92	7.73E-07	7.29E-05	8.261	254896	MGC31957	hypothetical protein MGC31957	NA
A_23_P368187	1.221	9.106	13.89	7.89E-07	7.39E-05	8.242	4665	NAB2	NGFI-A binding protein 2 (EGR1 binding protein 2)	ENSG00000166886
A_23_P72840	0.6353	6.883	13.88	7.92E-07	7.39E-05	8.239	54344	DPM3	dolichyl-phosphate mannosyltransferase polypeptide 3	ENSG00000179085
A_24_P337867	0.5687	7.683	13.87	7.97E-07	7.42E-05	8.232	80228	ORAI2	ORAI calcium release-activated calcium modulator 2	ENSG00000160991
A_24_P926770	0.9559	7.466	13.86	8.03E-07	7.42E-05	8.226	26020	LRP10	low density lipoprotein receptor-related protein 10	ENSG00000197324
A_23_P395365	0.5063	6.534	13.85	8.04E-07	7.42E-05	8.225	954	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2	ENSG00000054179
A_23_P3900	0.9053	7.144	13.83	8.12E-07	7.42E-05	8.215	23558	WBP2	WW domain binding protein 2	ENSG00000132471
A_24_P126873	0.7635	7.676	13.83	8.13E-07	7.42E-05	8.214	6830	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	ENSG00000109111
A_24_P355609	1.071	8.353	13.83	8.16E-07	7.42E-05	8.211	116535	MRGPRF	MAS-related GPR member F	ENSG00000172935
A_24_P775659	0.5164	6.92	13.83	8.14E-07	7.42E-05	8.213	23217	ZFR2	zinc finger RNA binding protein 2	ENSG00000105278
A_32_P38467	0.5143	11.55	13.81	8.25E-07	7.45E-05	8.2	100093630	SNHG8	small nucleolar RNA host gene 8 (non-protein coding)	NA
A_24_P729905	1.213	9.372	13.7	8.74E-07	7.74E-05	8.147	653268	AGAP7	ArfGAP with GTPase domain ankyrin repeat and PH domain 7	ENSG00000204169
A_32_P66091	0.6782	6.049	13.68	8.84E-07	7.79E-05	8.136	8844	KSR1	kinase suppressor of ras 1	ENSG00000141068
A_24_P340853	0.748	6.75	13.67	8.91E-07	7.83E-05	8.128	84875	PARP10	poly (ADP-ribose) polymerase family member 10	ENSG00000178685
A_24_P8318	0.6823	7.902	13.65	8.98E-07	7.87E-05	8.122	27125	AFF4	AF4/FMR2 family member 4	ENSG00000072364
A_32_P98227	1.064	7.382	13.65	9.01E-07	7.88E-05	8.118	11155	LDB3	LIM domain binding 3	ENSG00000122367
A_23_P401524	0.7734	9.28	13.64	9.07E-07	7.91E-05	8.112	1339	COX6A2	cytochrome c oxidase subunit VIa polypeptide 2	ENSG00000156885
A_23_P114707	1.159	8.002	13.63	9.10E-07	7.92E-05	8.109	9563	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	ENSG00000049239
A_23_P251216	0.9729	6.294	13.59	9.30E-07	8.06E-05	8.089	55187	VPS13D	vacuolar protein sorting 13 homolog D (S. cerevisiae)	ENSG00000048707

A_23_P550	0.5646	8.311	13.59	9.28E-07	8.06E-05	8.09	405	ARNT	aryl hydrocarbon receptor nuclear translocator	ENSG00000143437
A_32_P86150	0.8743	8.248	13.57	9.42E-07	8.14E-05	8.077	440387	CTRB2	chymotrypsinogen B2	ENSG00000168928
A_24_P291016	0.7005	8.072	13.5	9.81E-07	8.36E-05	8.039	25	ABL1	c-abl oncogene 1 receptor tyrosine kinase	ENSG00000097007
A_23_P6561	0.9068	8.125	13.46	1.00E-06	8.48E-05	8.018	55096	FLJ10213	hypothetical protein FLJ10213	NA
A_24_P555791	0.6566	6.844	13.46	1.00E-06	8.48E-05	8.018	8924	HERC2	hect domain and RLD 2	ENSG00000128731
A_24_P930276	0.6755	7.222	13.46	1.00E-06	8.48E-05	8.018	4779	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	ENSG00000082641
A_23_P209408	0.6452	7.848	13.44	1.01E-06	8.52E-05	8.011	843	CASP10	caspase 10 apoptosis-related cysteine peptidase	ENSG00000003400
A_24_P139229	1.543	8.315	13.43	1.02E-06	8.54E-05	8.004	23275	POFUT2	protein O-fucosyltransferase 2	ENSG00000186866
A_24_P358244	1.14	9.913	13.4	1.04E-06	8.66E-05	7.985	22879	MON1B	MON1 homolog B (yeast)	ENSG00000103111
A_24_P331711	0.5323	6.814	13.38	1.05E-06	8.68E-05	7.977	284486	THEM5	thioesterase superfamily member 5	ENSG00000196407
A_24_P58283	1.036	8.705	13.37	1.05E-06	8.68E-05	7.972	6670	SP3	Sp3 transcription factor	ENSG00000172845
A_32_P93328	1.058	8.064	13.37	1.05E-06	8.68E-05	7.974	100134713	LOC100134713	hypothetical protein LOC100134713	NA
A_23_P9926	1.088	9.018	13.36	1.06E-06	8.68E-05	7.967	83882	TSPAN10	tetraspanin 10	ENSG00000182612
A_32_P180741	0.6903	6.464	13.36	1.06E-06	8.68E-05	7.967	10188	TNK2	tyrosine kinase non-receptor 2	ENSG00000061938
A_23_P138000	0.8307	7.165	13.34	1.07E-06	8.72E-05	7.957	10500	SEMA6C	sema domain transmembrane domain (TM) and cytoplasmic domain (semaphorin) 6C	ENSG00000143434
A_23_P8797	1.219	8.448	13.32	1.09E-06	8.81E-05	7.943	5383	PMS2L5	postmeiotic segregation increased 2-like 5	ENSG00000123965
A_24_P40061	0.8674	7.702	13.28	1.11E-06	8.87E-05	7.925	114823	LENG8	leukocyte receptor cluster (LRC) member 8	ENSG00000167615
A_23_P68868	0.8149	8.477	13.25	1.13E-06	8.98E-05	7.908	55000	TUG1	taurine upregulated 1 (non-protein coding)	NA
A_23_P11936	0.8808	7.15	13.21	1.15E-06	9.10E-05	7.885	91544	UBXN11	UBX domain protein 11	ENSG00000158062
A_23_P9688	0.7516	8.77	13.21	1.15E-06	9.10E-05	7.887	1783	DYNC1LI2	dynein cytoplasmic 1 light intermediate chain 2	ENSG00000135720
A_24_P366735	1.091	7.152	13.2	1.16E-06	9.11E-05	7.882	57492	ARID1B	AT rich interactive domain 1B (SWI1-like)	ENSG00000049618
A_24_P415618	1.149	8.912	13.18	1.17E-06	9.18E-05	7.871	22877	MLXIP	MLX interacting protein	ENSG00000175727
A_23_P29985	0.7995	7.55	13.17	1.18E-06	9.18E-05	7.864	152992	C4orf23	chromosome 4 open reading frame 23	ENSG00000155275
A_23_P207596	0.5722	8.967	13.16	1.19E-06	9.20E-05	7.858	4763	NF1	neurofibromin 1	ENSG00000196712
A_32_P184518	0.4428	12.46	13.16	1.19E-06	9.20E-05	7.856	6144	RPL21	ribosomal protein L21	ENSG00000122026
A_23_P258381	0.9406	8.243	13.15	1.19E-06	9.22E-05	7.853	92369	SPSB4	splA/ryanodine receptor domain and SOCS box containing 4	ENSG00000175093
A_24_P333901	0.6285	8.149	13.12	1.21E-06	9.32E-05	7.838	23334	KIAA0467	KIAA0467	ENSG00000198198
A_23_P150664	1.289	10.63	13.11	1.22E-06	9.38E-05	7.83	387733	IFITM5	interferon induced transmembrane protein 5	ENSG00000206013
A_24_P222454	0.7893	6.257	12.99	1.31E-06	9.79E-05	7.767	51535	PPHLN1	periphilin 1	ENSG00000134283
A_24_P399871	0.6262	10.7	12.99	1.31E-06	9.79E-05	7.763	8911	CACNA1I	calcium channel voltage-dependent T type alpha 1I subunit	ENSG00000100346
A_32_P120638	0.6659	7.203	12.99	1.31E-06	9.79E-05	7.764	92105	INTS4	integrator complex subunit 4	ENSG00000149262
A_24_P102726	0.7208	8.504	12.97	1.33E-06	9.85E-05	7.752	5498	PPOX	protoporphyrinogen oxidase	ENSG00000143224
A_23_P106258	0.4757	6.58	12.92	1.37E-06	0.0001003	7.725	283600	C14orf68	chromosome 14 open reading frame 68	ENSG00000140107

A_23_P107775	0.5092	6.247	12.91	1.37E-06	0.0001006	7.721	147744	TMEM190	transmembrane protein 190	ENSG00000160472
A_23_P342688	0.7353	6.434	12.9	1.38E-06	0.0001009	7.714	84960	KIAA1984	KIAA1984	ENSG00000213213
A_23_P136413	1.336	8.731	12.89	1.39E-06	0.0001011	7.708	4326	MMP17	matrix metallopeptidase 17 (membrane-inserted)	ENSG00000198598
A_23_P417282	0.5974	8.084	12.83	1.44E-06	0.0001034	7.677	3480	IGF1R	insulin-like growth factor 1 receptor	ENSG00000140443
A_23_P168419	1.092	8.092	12.82	1.45E-06	0.0001041	7.668	58508	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	ENSG00000055609
A_24_P9346	0.861	6.744	12.74	1.52E-06	0.0001081	7.624	8831	SYNGAP1	synaptic Ras GTPase activating protein 1 homolog (rat)	ENSG00000197283 ENSG00000227460
A_24_P404593	0.9859	7.665	12.73	1.53E-06	0.0001087	7.617	51816	CECR1	cat eye syndrome chromosome region candidate 1	ENSG00000093072
A_32_P319880	0.7636	7.161	12.7	1.56E-06	0.0001096	7.601	57654	KIAA1530	KIAA1530	ENSG00000163945
A_23_P85853	0.7222	9.206	12.69	1.57E-06	0.0001098	7.595	79639	TMEM53	transmembrane protein 53	ENSG00000126106
A_24_P147910	0.7232	12.14	12.67	1.58E-06	0.0001103	7.584	10801	9-Sep	septin 9	ENSG00000184640
A_24_P163574	1.019	6.997	12.65	1.60E-06	0.0001107	7.574	64599	GIGYF1	GRB10 interacting GYF protein 1	ENSG00000146830
A_23_P402751	1.988	13.8	12.63	1.62E-06	0.0001115	7.564	7088	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog Drosophila)	ENSG00000196781
A_32_P110751	0.8634	9.795	12.61	1.64E-06	0.0001128	7.549	1974	EIF4A2	eukaryotic translation initiation factor 4A2	ENSG00000156976
A_24_P143758	0.7005	8.17	12.58	1.67E-06	0.0001137	7.535	100190939	LOC100190939	hypothetical LOC100190939	NA
A_32_P129621	0.6782	9.386	12.57	1.68E-06	0.0001146	7.527	6868	ADAM17	ADAM metallopeptidase domain 17	ENSG00000151694
A_23_P167093	1.046	8.853	12.52	1.73E-06	0.0001167	7.498	3425	IDUA	iduronidase alpha-L-	ENSG00000127415
A_24_P662086	0.5599	7.014	12.47	1.78E-06	0.0001186	7.471	100128961	GAPDHL7	glyceraldehyde-3-phosphate dehydrogenase-like 7 pseudogene	NA
A_24_P212129	0.5748	8.481	12.45	1.80E-06	0.0001198	7.46	7581	ZNF33A	zinc finger protein 33A	ENSG00000189180
A_24_P12651	0.9911	7.825	12.37	1.90E-06	0.0001236	7.411	23087	TRIM35	tripartite motif-containing 35	ENSG00000104228
A_23_P99891	0.5889	8.673	12.34	1.94E-06	0.0001252	7.391	59274	MESDC1	mesoderm development candidate 1	ENSG00000140406
A_24_P932760	1.022	7.184	12.33	1.95E-06	0.0001258	7.386	3831	KLC1	kinesin light chain 1	ENSG00000126214
A_23_P209316	0.5261	7.765	12.32	1.96E-06	0.0001261	7.38	905	CCNT2	cyclin T2	ENSG00000082258
A_24_P305345	0.5761	6.123	12.32	1.96E-06	0.0001261	7.379	30835	CD209	CD209 molecule	ENSG00000090659
A_23_P16476	0.948	7.349	12.29	2.00E-06	0.0001266	7.362	83855	KLF16	Kruppel-like factor 16	ENSG00000129911
A_24_P280390	0.9822	7.393	12.29	2.00E-06	0.0001266	7.361	200312	RNF215	ring finger protein 215	ENSG00000099999
A_24_P106502	1.845	7.987	12.28	2.01E-06	0.0001266	7.355	29964	PRICKLE4	prickle homolog 4 (Drosophila)	ENSG00000124593
A_24_P293089	0.9348	10.24	12.28	2.01E-06	0.0001266	7.358	163033	ZNF579	zinc finger protein 579	ENSG00000218891
A_24_P313576	0.4476	6.833	12.26	2.02E-06	0.0001271	7.349	6844	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	ENSG00000220205
A_24_P921584	1.045	9.457	12.24	2.05E-06	0.0001284	7.335	226	ALDOA	aldolase A fructose-bisphosphate	ENSG00000149925
A_23_P116435	0.5837	7.312	12.21	2.09E-06	0.0001297	7.319	51214	IGF2AS	insulin-like growth factor 2 antisense	ENSG00000099869
A_23_P90339	0.6712	9.51	12.21	2.10E-06	0.0001297	7.316	8175	SF3A2	splicing factor 3a subunit 2 66kDa	ENSG00000104897
A_32_P360193	1.457	7.821	12.21	2.10E-06	0.0001297	7.315	144132	DNHD1	dynein heavy chain domain 1	ENSG00000179532
A_23_P101480	0.6254	7.097	12.18	2.13E-06	0.000131	7.298	22983	MAST1	microtubule associated serine/threonine kinase 1	ENSG00000105613
A_23_P91802	0.7408	10.77	12.16	2.16E-06	0.0001312	7.286	1890	TYMP	thymidine phosphorylase	ENSG00000025708

A_24_P48983	0.9297	7.952	12.15	2.17E-06	0.0001314	7.281	90060	CCDC120	coiled-coil domain containing 120	ENSG00000147144
A_32_P83997	0.5591	11.31	12.15	2.17E-06	0.0001314	7.28	10313	RTN3	reticulon 3	ENSG00000133318
A_23_P167401	0.6775	7.638	12.14	2.18E-06	0.0001314	7.276	56125	PCDHB11	protocadherin beta 11	ENSG00000197479
A_24_P718503	0.5983	8.076	12.14	2.18E-06	0.0001314	7.277	100130152	LOC100130152	hypothetical protein LOC100130152	NA
A_24_P450194	0.5489	6.055	12.13	2.21E-06	0.0001321	7.267	400960	LOC400960	hypothetical gene supported by BC040598	NA
A_23_P97892	0.7491	7.817	12.12	2.22E-06	0.0001326	7.261	8861	LDB1	LIM domain binding 1	ENSG00000198728
A_23_P40896	0.592	7.223	12.09	2.26E-06	0.0001339	7.241	55186	SLC25A36	solute carrier family 25 member 36	ENSG00000114120
A_24_P264790	2.058	9.898	12.08	2.28E-06	0.0001342	7.236	4054	LTBP3	latent transforming growth factor beta binding protein 3	ENSG00000168056
A_32_P97798	0.5831	6.395	12.07	2.28E-06	0.0001344	7.233	10628	TXNIP	thioredoxin interacting protein	ENSG00000117289
A_24_P278602	0.9016	7.032	12.04	2.33E-06	0.0001363	7.214	10068	IL18BP	interleukin 18 binding protein	ENSG00000137496
A_23_P258570	0.4385	8.907	12.03	2.34E-06	0.0001365	7.211	5716	PSMD10	proteasome (prosome macropain) 26S subunit non-ATPase 10	ENSG00000101843
A_23_P208900	0.541	6.9	12.02	2.36E-06	0.0001369	7.202	10501	SEMA6B	sema domain transmembrane domain (TM) and cytoplasmic domain (semaphorin) 6B	ENSG00000167680
A_32_P143336	0.7056	9.185	12	2.39E-06	0.0001375	7.189	92249	LOC92249	hypothetical LOC92249	NA
A_24_P187197	0.9936	7.177	11.96	2.44E-06	0.0001397	7.168	440300	LOC440300	chondroitin sulfate proteoglycan 4 pseudogene	NA
A_32_P145764	0.8359	8.393	11.94	2.47E-06	0.000141	7.155	730495	LOC730495	hypothetical protein LOC730495	NA
A_23_P39336	1.061	8.689	11.93	2.50E-06	0.000142	7.144	23770	FKBP8	FK506 binding protein 8 38kDa	ENSG00000105701
A_23_P253389	0.8795	11.78	11.92	2.51E-06	0.000142	7.142	6522	SLC4A2	solute carrier family 4 anion exchanger member 2 (erythrocyte membrane protein band 3-like 1)	ENSG00000164889
A_23_P320290	0.6709	7.263	11.92	2.50E-06	0.000142	7.143	152485	ZNF827	zinc finger protein 827	ENSG00000151612
A_24_P353709	0.6512	9.073	11.92	2.51E-06	0.0001421	7.139	8704	B4GALT2	UDP-Gal:betaGlcNAc beta 1 4-galactosyltransferase polypeptide 2	ENSG00000117411
A_32_P930375	0.8235	5.733	11.88	2.58E-06	0.000145	7.116	619343	C8orf68	chromosome 8 open reading frame 68	NA
A_23_P105562	0.5069	6.333	11.86	2.60E-06	0.0001455	7.105	7450	VWF	von Willebrand factor	ENSG00000110799
A_23_P344515	1.322	8.883	11.86	2.61E-06	0.0001455	7.105	750	C16orf3	chromosome 16 open reading frame 3	ENSG00000221819
A_23_P18993	0.5197	6.349	11.83	2.65E-06	0.0001472	7.087	166968	MIER3	mesoderm induction early response 1 family member 3	ENSG00000155545
A_23_P97195	0.4503	8.295	11.83	2.65E-06	0.0001472	7.088	56181	FAM54B	family with sequence similarity 54 member B	ENSG00000117640
A_23_P71867	0.4593	7.444	11.81	2.69E-06	0.0001481	7.074	3590	IL11RA	interleukin 11 receptor alpha	ENSG00000137070
A_23_P120513	0.8683	7.71	11.79	2.73E-06	0.0001495	7.06	128653	C20orf141	chromosome 20 open reading frame 141	ENSG00000198326 ENSG00000241690
A_24_P108401	0.6472	9.317	11.75	2.80E-06	0.0001518	7.036	354	KLK3	kallikrein-related peptidase 3	ENSG00000142515
A_23_P339191	0.5636	9.136	11.73	2.83E-06	0.0001528	7.024	867	CBL	Cas-Br-M (murine) ecotropic retroviral transforming sequence	ENSG00000110395
A_24_P241862	1.25	9.255	11.73	2.83E-06	0.0001528	7.023	8498	RANBP3	RAN binding protein 3	ENSG00000031823
A_23_P500824	0.8798	7.86	11.71	2.86E-06	0.0001536	7.013	6853	SYN1	synapsin I	ENSG00000008056
A_32_P159445	1.112	9.298	11.71	2.87E-06	0.0001536	7.011	23096	IQSEC2	IQ motif and Sec7 domain 2	ENSG00000124313
A_24_P922808	0.6526	7.101	11.7	2.89E-06	0.0001542	7.002	51029	PPPDE1	PPPDE peptidase domain containing 1	ENSG00000121644

A_23_P142173	0.6401	6.571	11.69	2.90E-06	0.0001546	6.999	9704	DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	ENSG00000134815
A_23_P33573	0.5082	6.887	11.68	2.93E-06	0.0001554	6.991	3850	KRT3	keratin 3	ENSG00000186442
A_23_P142421	1.018	9.489	11.66	2.97E-06	0.0001567	6.977	9757	MLL4	myeloid/lymphoid or mixed-lineage leukemia 4	ENSG00000105663
A_32_P14187	1.217	7.43	11.66	2.97E-06	0.0001567	6.977	7020	TFAP2A	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	ENSG00000137203
A_23_P88710	0.4864	10.13	11.65	2.98E-06	0.0001568	6.973	25963	TMEM87A	transmembrane protein 87A	ENSG00000103978
A_24_P315535	0.8317	8.687	11.65	2.98E-06	0.0001567	6.975	200734	SPRED2	sprouty-related EVH1 domain containing 2	ENSG00000198369
A_24_P384397	0.8101	8.882	11.65	2.98E-06	0.0001567	6.975	125950	RAVER1	ribonucleoprotein PTB-binding 1	ENSG00000161847
A_23_P97652	0.9513	7.996	11.64	3.00E-06	0.0001576	6.966	387509	GPR153	G protein-coupled receptor 153	ENSG00000158292
A_23_P164042	0.6334	6.632	11.61	3.06E-06	0.0001591	6.949	2081	ERN1	endoplasmic reticulum to nucleus signaling 1	ENSG00000178607
A_23_P129629	0.7149	7.184	11.6	3.08E-06	0.0001593	6.943	4504	MT3	metallothionein 3	ENSG00000087250
A_23_P329727	2.244	9.265	11.6	3.07E-06	0.0001593	6.945	23162	MAPK8IP3	mitogen-activated protein kinase 8 interacting protein 3	ENSG00000138834
A_23_P34554	0.9933	8.384	11.6	3.09E-06	0.0001596	6.939	777	CACNA1E	calcium channel voltage-dependent R type alpha 1E subunit	ENSG00000198216
A_23_P87432	1.327	7.937	11.6	3.07E-06	0.0001593	6.945	114822	RHPN1	rhophilin Rho GTPase binding protein 1	ENSG00000158106
A_23_P355471	0.961	7.373	11.59	3.10E-06	0.0001598	6.937	6915	TBXA2R	thromboxane A2 receptor	ENSG00000006638
A_24_P352200	0.6489	6.736	11.59	3.10E-06	0.0001599	6.935	79591	C10orf76	chromosome 10 open reading frame 76	ENSG00000120029
A_24_P258235	0.6417	5.982	11.54	3.20E-06	0.0001639	6.903	26338	OR5L2	olfactory receptor family 5 subfamily L member 2	ENSG00000205030
A_23_P16189	0.5161	5.956	11.53	3.23E-06	0.0001642	6.896	5582	PRKCG	protein kinase C gamma	ENSG00000126583
A_23_P21570	1.215	9.7	11.51	3.26E-06	0.0001649	6.886	64067	NPAS3	neuronal PAS domain protein 3	ENSG00000151322
A_32_P951	0.8391	7.784	11.51	3.26E-06	0.0001649	6.886	280664	WFDC10B	WAP four-disulfide core domain 10B	ENSG00000182931
A_32_P41461	1.127	7.987	11.49	3.31E-06	0.0001664	6.872	10163	WASF2	WAS protein family member 2	ENSG00000158195
A_23_P137157	0.7532	6.518	11.48	3.33E-06	0.0001669	6.864	5973	RENBP	renin binding protein	ENSG00000102032
A_24_P392486	0.6476	11.85	11.48	3.32E-06	0.0001667	6.868	339344	MYPOP	Myb-related transcription factor partner of profilin	ENSG00000176182
A_23_P201940	0.6496	6.24	11.45	3.39E-06	0.000169	6.848	25802	LMOD1	leiomodin 1 (smooth muscle)	ENSG00000163431
A_23_P66948	0.4331	7.788	11.44	3.41E-06	0.0001692	6.842	64762	FAM59A	family with sequence similarity 59 member A	ENSG00000141441
A_24_P16856	0.8241	6.671	11.39	3.53E-06	0.0001727	6.808	8227	SFRS17A	splicing factor arginine/serine-rich 17A	ENSG00000197976
A_32_P139738	1.034	7.721	11.39	3.53E-06	0.0001728	6.807	440362	HERC2P4	hect domain and RLD 2 pseudogene 4	NA
A_23_P167537	0.7161	7.701	11.33	3.68E-06	0.0001782	6.767	10814	CPLX2	complexin 2	ENSG00000145920
A_23_P69206	0.4004	6.435	11.32	3.70E-06	0.0001787	6.761	6533	SLC6A6	solute carrier family 6 (neurotransmitter transporter taurine) member 6	ENSG00000131389
A_24_P375728	1.005	7.711	11.32	3.71E-06	0.0001787	6.76	92154	MTSS1L	metastasis suppressor 1-like	ENSG00000132613
A_23_P317796	1.081	8.528	11.27	3.81E-06	0.0001826	6.733	346606	MOGAT3	monoacylglycerol O-acyltransferase 3	ENSG00000106384
A_23_P80473	0.6971	8.222	11.17	4.09E-06	0.0001904	6.663	166012	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13	ENSG00000180767
A_24_P235098	0.8435	9.396	11.16	4.11E-06	0.0001908	6.658	94234	FOXQ1	forkhead box Q1	ENSG00000164379
A_23_P107394	0.9714	10.15	11.14	4.17E-06	0.0001917	6.645	84667	HES7	hairy and enhancer of split 7 (Drosophila)	ENSG00000179111

A_24_P143599	0.6626	7.262	11.14	4.16E-06	0.0001917	6.647	23250	ATP11A	ATPase class VI type 11A	ENSG00000068650
A_23_P113682	0.8143	7.651	11.1	4.28E-06	0.0001944	6.618	142680	SLC34A3	solute carrier family 34 (sodium phosphate) member 3	ENSG00000198569
A_32_P143980	1.006	8.423	11.1	4.29E-06	0.0001946	6.616	3106	HLA-B	major histocompatibility complex class I B	ENSG00000234745
A_32_P200165	0.7393	6.245	11.1	4.29E-06	0.0001946	6.615	1994	ELAVL1	ELAV (embryonic lethal abnormal vision Drosophila)-like 1 (Hu antigen R)	ENSG00000066044
A_23_P213216	1.497	10.28	11.09	4.33E-06	0.0001953	6.608	7469	WHSC2	Wolf-Hirschhorn syndrome candidate 2	ENSG00000185049
A_23_P102622	0.6708	7.048	11.08	4.33E-06	0.0001953	6.607	8785	MATN4	matrilin 4	ENSG00000124159
A_23_P26294	0.8204	12.64	11.08	4.33E-06	0.0001954	6.606	25823	TPSG1	tryptase gamma 1	ENSG00000116176
A_24_P269101	0.6215	6.95	11.06	4.40E-06	0.0001967	6.592	4762	NEUROG1	neurogenin 1	ENSG00000181965
A_23_P109122	1.131	8.183	11.05	4.44E-06	0.0001979	6.582	57593	EBF4	early B-cell factor 4	ENSG00000088881
A_23_P25790	0.5582	10.81	11.04	4.47E-06	0.0001986	6.576	64403	CDH24	cadherin 24 type 2	ENSG00000139880
A_23_P253405	0.6267	9.088	11.01	4.54E-06	0.0002005	6.561	1317	SLC31A1	solute carrier family 31 (copper transporters) member 1	ENSG00000136868
A_23_P217068	0.4381	15.07	11	4.59E-06	0.0002017	6.549	6136	RPL12	ribosomal protein L12	ENSG00000197958
A_23_P35148	0.6442	7.842	10.99	4.61E-06	0.000202	6.546	6884	TAF13	TAF13 RNA polymerase II TATA box binding protein (TBP)-associated factor 18kDa	ENSG00000197780
A_23_P122815	0.4614	11.21	10.98	4.65E-06	0.000203	6.537	813	CALU	calumenin	ENSG00000128595
A_24_P287780	0.6391	7.353	10.97	4.69E-06	0.0002041	6.528	5119	CHMP1A	chromatin modifying protein 1A	ENSG00000131165
A_23_P254970	0.7476	6.728	10.96	4.72E-06	0.0002046	6.522	55599	RNPC3	RNA-binding region (RNP1 RRM) containing 3	ENSG00000185946
A_23_P119395	0.8955	7.928	10.95	4.74E-06	0.0002049	6.518	2696	GIPR	gastric inhibitory polypeptide receptor	ENSG00000010310
A_23_P153549	1.14	8.72	10.91	4.88E-06	0.0002087	6.489	2906	GRIN2D	glutamate receptor ionotropic N-methyl D-aspartate 2D	ENSG00000105464
A_32_P216841	0.7921	7.149	10.9	4.90E-06	0.0002093	6.484	132671	SPATA18	spermatogenesis associated 18 homolog (rat)	ENSG00000163071
A_23_P11309	1.586	8.55	10.88	4.97E-06	0.0002119	6.47	55558	PLXNA3	plexin A3	ENSG00000130827
A_24_P848662	0.6888	7.871	10.87	5.01E-06	0.0002132	6.462	100131582	LOC100131582	hypothetical protein LOC100131582	NA
A_23_P428738	0.9673	8.125	10.85	5.06E-06	0.0002139	6.453	283	ANG	angiogenin ribonuclease RNase A family 5	ENSG00000214274
A_23_P434289	1.374	7.807	10.85	5.09E-06	0.0002142	6.448	118442	GPR62	G protein-coupled receptor 62	ENSG00000180929
A_24_P203315	0.6657	5.993	10.85	5.08E-06	0.0002142	6.449	254263	CNIH2	cornichon homolog 2 (Drosophila)	ENSG00000174871
A_24_P315066	1.139	8.308	10.84	5.10E-06	0.0002145	6.445	83637	ZMIZ2	zinc finger MIZ-type containing 2	ENSG00000122515
A_23_P165186	0.637	8.307	10.82	5.17E-06	0.0002161	6.431	55957	LIN37	lin-37 homolog (C. elegans)	ENSG00000188223
A_24_P24244	1.01	8.705	10.82	5.20E-06	0.0002169	6.426	1822	ATN1	atrophin 1	ENSG00000111676
A_32_P735636	0.5896	6.666	10.81	5.20E-06	0.000217	6.425	55739	CARKD	carbohydrate kinase domain containing	ENSG00000213995
A_24_P935804	0.5056	5.965	10.8	5.26E-06	0.000219	6.414	285331	CCDC66	coiled-coil domain containing 66	ENSG00000180376
A_24_P372833	0.6385	6.13	10.79	5.29E-06	0.0002193	6.409	9651	PLCH2	phospholipase C eta 2	ENSG00000149527
A_32_P74615	0.876	7.18	10.79	5.29E-06	0.0002193	6.409	389058	SP5	Sp5 transcription factor	ENSG00000204335
A_23_P306148	0.9194	10.69	10.69	5.67E-06	0.0002293	6.34	5371	PML	promyelocytic leukemia	ENSG00000140464
A_23_P98402	0.3802	10.02	10.67	5.76E-06	0.0002309	6.324	51092	SIDT2	SID1 transmembrane family member 2	ENSG00000149577
A_24_P349676	1.046	7.988	10.67	5.75E-06	0.0002309	6.325	55663	ZNF446	zinc finger protein 446	ENSG00000083838

A_24_P586390	0.8012	8.712	10.67	5.74E-06	0.0002306	6.328	441124	LOC441124	hypothetical gene supported by AK093729; BX647918	NA
A_24_P286527	1.055	8.844	10.66	5.80E-06	0.0002317	6.317	64792	RABL5	RAB member RAS oncogene family-like 5	ENSG00000128581
A_24_P311771	0.8407	8.167	10.66	5.78E-06	0.0002311	6.321	51663	ZFR	zinc finger RNA binding protein	ENSG00000056097
A_32_P834166	0.5628	6.457	10.65	5.81E-06	0.0002318	6.316	100128843	LOC100128843	similar to DNA polymerase epsilon catalytic subunit protein	ENSG00000233881
A_24_P386334	1.652	9.87	10.64	5.87E-06	0.000233	6.306	56904	SH3GLB2	SH3-domain GRB2-like endophilin B2	ENSG00000148341
A_32_P26092	0.453	6.02	10.64	5.86E-06	0.0002328	6.308	7293	TNFRSF4	tumor necrosis factor receptor superfamily member 4	ENSG00000186827
A_23_P153351	0.4368	11.87	10.62	5.95E-06	0.0002354	6.291	645	BLVRB	biliverdin reductase B (flavin reductase (NADPH))	ENSG00000090013
A_24_P918387	0.808	6.483	10.62	5.94E-06	0.0002352	6.293	5426	POLE	polymerase (DNA directed) epsilon	ENSG00000177084
A_24_P922909	0.9973	7.839	10.62	5.94E-06	0.0002351	6.294	4297	MLL	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog Drosophila)	ENSG00000118058
A_23_P34888	1.09	7.318	10.61	6.00E-06	0.0002362	6.283	27159	CHIA	chitinase acidic	ENSG00000134216
A_24_P328446	1.764	7.617	10.61	6.00E-06	0.0002362	6.284	3196	TLX2	T-cell leukemia homeobox 2	ENSG00000115297
A_23_P218434	0.971	9.05	10.6	6.03E-06	0.0002365	6.279	7769	ZNF226	zinc finger protein 226	ENSG00000167380
A_24_P311856	0.6041	6.317	10.6	6.03E-06	0.0002365	6.278	1297	COL9A1	collagen type IX alpha 1	ENSG00000112280
A_23_P74668	1.035	8.027	10.58	6.11E-06	0.0002383	6.265	93190	C1orf158	chromosome 1 open reading frame 158	ENSG00000157330
A_23_P329016	1.064	10.03	10.57	6.18E-06	0.0002403	6.254	92715	WDR85	WD repeat domain 85	ENSG00000148399
A_24_P324577	1.15	7.714	10.57	6.15E-06	0.0002396	6.258	57612	KIAA1466	KIAA1466 gene	NA
A_23_P111797	0.5024	8.282	10.56	6.22E-06	0.000241	6.247	84214	DKFZp434F142	hypothetical DKFZp434F142	NA
A_23_P369983	0.667	8.918	10.56	6.20E-06	0.0002405	6.251	147965	FAM98C	family with sequence similarity 98 member C	ENSG00000130244
A_32_P175349	0.7227	7.31	10.55	6.27E-06	0.0002415	6.24	100128942	LOC100128942	hypothetical protein LOC100128942	ENSG00000204277
A_24_P202978	0.6106	8.915	10.54	6.28E-06	0.0002417	6.237	8897	MTMR3	myotubularin related protein 3	ENSG00000100330
A_24_P929754	0.8131	8.631	10.54	6.30E-06	0.0002417	6.235	2872	MKNK2	MAP kinase interacting serine/threonine kinase 2	ENSG00000099875
A_23_P320095	0.8303	7.745	10.5	6.48E-06	0.0002472	6.207	27254	CSDC2	cold shock domain containing C2 RNA binding	ENSG00000172346
A_24_P416595	0.9935	7.686	10.5	6.49E-06	0.0002474	6.205	284346	ZNF575	zinc finger protein 575	ENSG00000176472
A_23_P142037	0.9805	6.726	10.48	6.58E-06	0.0002493	6.192	5989	RFX1	regulatory factor X 1 (influences HLA class II expression)	ENSG00000132005
A_24_P229350	0.4655	7.206	10.48	6.58E-06	0.0002493	6.191	91010	FMNL3	formin-like 3	ENSG00000161791
A_24_P285378	1.314	8.401	10.48	6.55E-06	0.0002489	6.197	56063	C1orf91	chromosome 1 open reading frame 91	ENSG00000160055
A_24_P400528	2.114	7.661	10.48	6.58E-06	0.0002493	6.191	84629	TNRC18	trinucleotide repeat containing 18	ENSG00000182095
A_24_P206121	1.314	9.1	10.47	6.60E-06	0.0002494	6.189	3779	KCNMB1	potassium large conductance calcium-activated channel subfamily M beta member 1	ENSG00000145936
A_23_P34877	0.4504	7.943	10.46	6.66E-06	0.0002506	6.179	64783	RBM15	RNA binding motif protein 15	ENSG00000162775
A_23_P91278	0.5779	6.922	10.46	6.68E-06	0.0002507	6.177	4773	NFATC2	nuclear factor of activated T-cells cytoplasmic calcineurin-dependent 2	ENSG00000101096
A_23_P125772	0.5758	6.871	10.41	6.93E-06	0.0002579	6.14	26576	SRPK3	SFRS protein kinase 3	ENSG00000184343

A_24_P16036	0.3525	9.032	10.4	6.96E-06	0.0002583	6.136	391356	C2orf79	chromosome 2 open reading frame 79	ENSG00000184924
A_24_P933688	2.11	7.18	10.39	7.00E-06	0.000259	6.13	89797	NAV2	neuron navigator 2	ENSG00000166833
A_32_P206839	0.5839	8.158	10.39	7.02E-06	0.0002597	6.126	100288911	LOC100288911	hypothetical protein LOC100288911	NA
A_23_P120435	1.189	9.558	10.37	7.12E-06	0.0002611	6.112	140686	WFDC3	WAP four-disulfide core domain 3	ENSG00000124116
A_23_P257407	0.5847	11.51	10.37	7.11E-06	0.0002608	6.114	27158	NDOR1	NADPH dependent diflavin oxidoreductase 1	ENSG00000188566
A_23_P94133	0.7802	7.915	10.36	7.15E-06	0.0002614	6.108	10940	POP1	processing of precursor 1 ribonuclease P/MRP subunit (S. cerevisiae)	ENSG00000104356
A_24_P923765	1.047	9.794	10.36	7.14E-06	0.0002611	6.11	399664	MEX3D	mex-3 homolog D (C. elegans)	ENSG00000181588
A_23_P131139	0.364	6.569	10.35	7.23E-06	0.0002633	6.097	116093	DIRC1	disrupted in renal carcinoma 1	ENSG00000174325
A_32_P157228	0.4169	7.774	10.35	7.20E-06	0.0002627	6.101	25909	AHCTF1	AT hook containing transcription factor 1	ENSG00000153207
A_24_P202329	0.7515	6.652	10.34	7.28E-06	0.0002644	6.091	146880	LOC146880	hypothetical LOC146880	NA
A_32_P168670	0.8286	6.342	10.34	7.26E-06	0.0002641	6.093	55016	1-Mar	membrane-associated ring finger (C3HC4) 1	ENSG00000145416
A_23_P15101	0.5781	8.543	10.31	7.41E-06	0.0002675	6.073	79838	TMC5	transmembrane channel-like 5	ENSG00000103534
A_23_P53724	0.8895	7.048	10.31	7.40E-06	0.0002675	6.074	9746	CLSTN3	calsyntenin 3	ENSG00000139182
A_24_P295999	0.5127	8.543	10.26	7.66E-06	0.0002725	6.039	920	CD4	CD4 molecule	ENSG00000010610
A_23_P353704	0.9581	9.121	10.24	7.81E-06	0.0002758	6.02	56261	GPCPD1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	ENSG00000125772
A_24_P315500	1.06	8.144	10.24	7.78E-06	0.0002754	6.024	100130557	LOC100130557	hypothetical LOC100130557	NA
A_24_P368943	0.678	7.775	10.24	7.78E-06	0.0002754	6.024	2128	EVX1	even-skipped homeobox 1	ENSG00000106038
A_24_P382579	0.4908	6.735	10.24	7.78E-06	0.0002754	6.024	5020	OXT	oxytocin prepropeptide	ENSG00000101405
A_23_P303891	0.7267	8.407	10.23	7.88E-06	0.0002774	6.011	353133	LCE1C	late cornified envelope 1C	ENSG00000197084
A_24_P85365	1.02	7.06	10.19	8.10E-06	0.0002832	5.984	8509	NDST2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	ENSG00000166507
A_23_P34402	0.6922	9.763	10.18	8.15E-06	0.0002845	5.977	23385	NCSTN	nicastrin	ENSG00000162736
A_24_P161036	0.4063	10.02	10.18	8.15E-06	0.0002845	5.977	641371	ACOT1	acyl-CoA thioesterase 1	ENSG00000184227
A_24_P112803	0.9979	7.931	10.17	8.19E-06	0.0002846	5.972	6656	SOX1	SRY (sex determining region Y)-box 1	ENSG00000182968
A_24_P213503	0.6637	7.778	10.17	8.18E-06	0.0002846	5.974	5791	PTPRE	protein tyrosine phosphatase receptor type E	ENSG00000132334
A_32_P64038	0.7442	10.55	10.17	8.19E-06	0.0002846	5.972	400590	LOC400590	hypothetical LOC400590	NA
A_23_P422071	0.4766	9.279	10.15	8.30E-06	0.0002877	5.959	8705	B3GALT4	UDP-Gal:betaGlcNAc beta 1 3-galactosyltransferase polypeptide 4	ENSG00000206285 ENSG00000226936 ENSG00000235155 ENSG00000235863 ENSG00000236802
A_24_P221385	0.8467	8.937	10.12	8.51E-06	0.000293	5.934	84288	EFCAB2	EF-hand calcium binding domain 2	ENSG00000203666
A_23_P318486	0.9234	8.239	10.07	8.80E-06	0.0003001	5.9	219293	ATAD3C	ATPase family AAA domain containing 3C	ENSG00000215915
A_24_P933180	0.6113	7.117	10.07	8.86E-06	0.0003015	5.894	2677	GGCX	gamma-glutamyl carboxylase	ENSG00000115486
A_23_P210379	0.5364	12.22	10.06	8.89E-06	0.0003018	5.89	55738	ARFGAP1	ADP-ribosylation factor GTPase activating protein 1	ENSG00000101199
A_24_P218056	1.002	7.701	10.05	8.94E-06	0.0003032	5.884	23386	NUDCD3	NudC domain containing 3	ENSG00000015676

A_23_P303390	0.3282	6.263	10.04	9.03E-06	0.0003054	5.874	4613	MYCN	v-myc myelocytomatosis viral related oncogene neuroblastoma derived (avian)	ENSG00000134323
A_24_P256243	1.006	7.44	10.03	9.10E-06	0.0003073	5.867	6757	SSX2	synovial sarcoma X breakpoint 2	ENSG00000157950 ENSG00000187754 ENSG00000241476
A_23_P41634	0.7279	8.381	10.02	9.18E-06	0.0003087	5.858	57763	ANKRA2	ankyrin repeat family A (RFXANK-like) 2	ENSG00000164331
A_23_P259580	1.547	9.475	10.01	9.23E-06	0.0003096	5.852	6892	TAPBP	TAP binding protein (tapasin)	ENSG00000206208 ENSG00000231925
A_23_P432545	0.7041	7.83	10.01	9.23E-06	0.0003096	5.852	283229	EFCAB4A	EF-hand calcium binding domain 4A	ENSG00000177685
A_23_P76529	0.8136	7.934	10	9.28E-06	0.0003102	5.847	3695	ITGB7	integrin beta 7	ENSG00000139626
A_24_P348989	0.7364	6.411	10	9.29E-06	0.0003102	5.846	11024	LILRA1	leukocyte immunoglobulin-like receptor subfamily A (with TM domain) member 1	ENSG00000104974
A_23_P373031	1.138	7.902	9.981	9.42E-06	0.0003128	5.831	775	CACNA1C	calcium channel voltage-dependent L type alpha 1C subunit	ENSG00000151067
A_24_P367812	0.4446	6.959	9.977	9.46E-06	0.0003132	5.828	650392	LOC650392	hypothetical protein LOC650392	NA
A_23_P85441	0.4606	7.191	9.967	9.52E-06	0.0003145	5.821	57549	IGSF9	immunoglobulin superfamily member 9	ENSG00000085552
A_23_P71778	1.482	9.03	9.963	9.56E-06	0.0003154	5.818	389812	LCN15	lipocalin 15	ENSG00000177984
A_24_P319635	0.7845	9.864	9.954	9.62E-06	0.0003167	5.811	4170	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	ENSG00000143384
A_32_P311737	1.136	7.799	9.953	9.62E-06	0.0003167	5.811	26030	PLEKHG3	pleckstrin homology domain containing family G (with RhoGef domain) member 3	ENSG00000126822
A_32_P194032	1.067	9.121	9.946	9.67E-06	0.0003178	5.805	91694	LONRF1	LON peptidase N-terminal domain and ring finger 1	ENSG00000154359
A_23_P19036	0.6731	10.07	9.945	9.68E-06	0.0003178	5.804	10318	TNIP1	TNFAIP3 interacting protein 1	ENSG00000145901
A_23_P431734	1.11	7.415	9.942	9.70E-06	0.0003178	5.802	51312	SLC25A37	solute carrier family 25 member 37	ENSG00000147454
A_24_P612446	-0.7424	6.069	-9.941	9.71E-06	0.0003179	5.801	221477	C6orf89	chromosome 6 open reading frame 89	ENSG00000198663
A_23_P165548	-1.058	7.521	-9.943	9.69E-06	0.0003178	5.803	64342	HS1BP3	HCLS1 binding protein 3	ENSG00000118960
A_23_P428373	-0.9436	6.024	-9.949	9.65E-06	0.0003174	5.807	254958	REXO1L1	REX1 RNA exonuclease 1 homolog (S. cerevisiae)-like 1	ENSG00000205176
A_23_P256021	-0.8486	12.45	-9.953	9.62E-06	0.0003167	5.81	81887	LAS1L	LAS1-like (S. cerevisiae)	ENSG00000001497
A_24_P277576	-0.3803	5.773	-9.968	9.51E-06	0.0003145	5.822	9319	TRIP13	thyroid hormone receptor interactor 13	ENSG00000071539
A_23_P365149	-1.066	8.861	-9.976	9.46E-06	0.0003132	5.828	10295	BCKDK	branched chain ketoacid dehydrogenase kinase	ENSG00000103507
A_23_P128396	-0.5978	8.121	-9.98	9.43E-06	0.0003128	5.83	80196	RNF34	ring finger protein 34	ENSG00000170633
A_23_P86037	-0.4948	5.743	-9.983	9.41E-06	0.0003128	5.832	55585	UBE2Q1	ubiquitin-conjugating enzyme E2Q family member 1	ENSG00000160714
A_23_P212844	-1.056	10.08	-9.984	9.41E-06	0.0003128	5.833	10460	TACC3	transforming acidic coiled-coil containing protein 3	ENSG00000013810
A_32_P72447	-0.9156	12.33	-9.994	9.34E-06	0.0003111	5.841	27338	UBE2S	ubiquitin-conjugating enzyme E2S	ENSG00000108106
A_23_P68452	-1.044	8.483	-9.999	9.30E-06	0.0003105	5.844	51006	SLC35C2	solute carrier family 35 member C2	ENSG00000080189
A_23_P15937	-0.4279	8.064	-10	9.27E-06	0.0003102	5.848	4087	SMAD2	SMAD family member 2	ENSG00000175387
A_24_P377269	-0.4445	13.23	-10.01	9.24E-06	0.0003096	5.852	3308	HSPA4	heat shock 70kDa protein 4	ENSG00000170606
A_23_P28279	-0.836	9.324	-10.02	9.17E-06	0.0003086	5.859	10120	ACTR1B	ARP1 actin-related protein 1 homolog B centractin beta (yeast)	ENSG00000115073

A_23_P41872	-0.9454	9.091	-10.02	9.16E-06	0.0003083	5.86	11285	B4GALT7	xylosylprotein beta 1 4-galactosyltransferase polypeptide 7 (galactosyltransferase I)	ENSG00000027847
A_23_P86421	-0.7419	8.107	-10.02	9.19E-06	0.0003088	5.857	8031	NCOA4	nuclear receptor coactivator 4	ENSG00000138293
A_24_P106297	-0.7465	7.644	-10.02	9.15E-06	0.0003082	5.862	23600	AMACR	alpha-methylacyl-CoA racemase	ENSG00000082196 ENSG00000242110
A_23_P58482	-0.6837	10.21	-10.05	8.95E-06	0.0003032	5.884	4245	MGAT1	mannosyl (alpha-1 3-)-glycoprotein beta-1 2-N-acetylglucosaminyltransferase	ENSG00000131446
A_24_P79955	-0.6559	7.723	-10.05	8.96E-06	0.0003032	5.882	9939	RBM8A	RNA binding motif protein 8A	ENSG00000131795
A_23_P27493	-0.6259	9.207	-10.06	8.87E-06	0.0003015	5.893	56342	PPAN	peter pan homolog (Drosophila)	ENSG00000130810
A_24_P916251	-0.3429	6.404	-10.06	8.88E-06	0.0003015	5.892	6158	RPL28	ribosomal protein L28	ENSG00000108107
A_23_P360983	-0.3864	7.934	-10.07	8.83E-06	0.0003007	5.897	91942	NDUFAF2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex assembly factor 2	ENSG00000164182
A_23_P120947	-1.029	12.05	-10.08	8.75E-06	0.0002988	5.906	2547	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6	ENSG00000196419
A_23_P142322	-1.116	10.38	-10.08	8.76E-06	0.000299	5.905	1153	CIRBP	cold inducible RNA binding protein	ENSG00000099622
A_24_P192197	-1.099	8.936	-10.08	8.73E-06	0.0002987	5.908	56897	WRNIP1	Werner helicase interacting protein 1	ENSG00000124535
A_23_P29855	-0.3701	9.63	-10.09	8.68E-06	0.0002973	5.914	8615	USO1	USO1 homolog vesicle docking protein (yeast)	ENSG00000138768
A_24_P140391	-0.9803	8.197	-10.09	8.72E-06	0.0002984	5.91	84992	PIGY	phosphatidylinositol glycan anchor biosynthesis class Y	ENSG00000145337
A_23_P23966	-0.5611	8.035	-10.11	8.55E-06	0.000294	5.929	118738	ZNF488	zinc finger protein 488	ENSG00000165388
A_23_P28980	-0.6278	8.314	-10.11	8.57E-06	0.0002942	5.927	128869	PIGU	phosphatidylinositol glycan anchor biosynthesis class U	ENSG00000101464
A_23_P120915	-0.904	7.746	-10.12	8.50E-06	0.000293	5.935	129138	ANKRD54	ankyrin repeat domain 54	ENSG00000100124
A_24_P320526	-0.6496	7.849	-10.13	8.45E-06	0.0002915	5.941	64771	C6orf106	chromosome 6 open reading frame 106	ENSG00000196821
A_23_P136916	-0.702	10.73	-10.17	8.21E-06	0.0002849	5.97	64743	WDR13	WD repeat domain 13	ENSG00000101940
A_23_P3514	-0.6533	9.351	-10.17	8.20E-06	0.0002846	5.972	29105	C16orf80	chromosome 16 open reading frame 80	ENSG00000070761
A_23_P109928	-0.5422	10.47	-10.18	8.16E-06	0.0002846	5.976	9861	PSMD6	proteasome (prosome macropain) 26S subunit non-ATPase 6	ENSG00000163636
A_23_P160598	-0.4569	10.08	-10.18	8.13E-06	0.0002842	5.98	114034	TOE1	target of EGR1 member 1 (nuclear)	ENSG00000132773
A_24_P225448	-0.9844	6.945	-10.2	8.01E-06	0.000281	5.994	1465	CSRP1	cysteine and glycine-rich protein 1	ENSG00000159176
A_24_P396375	-1.801	8.243	-10.21	7.97E-06	0.0002795	6	1889	ECE1	endothelin converting enzyme 1	ENSG00000117298
A_23_P214658	-0.4895	6.625	-10.22	7.93E-06	0.0002786	6.004	5089	PBX2	pre-B-cell leukemia homeobox 2	ENSG00000204304 ENSG00000206315 ENSG00000224952 ENSG00000225987 ENSG00000232005 ENSG00000236353 ENSG00000237344
A_23_P150365	-0.3258	12.11	-10.23	7.87E-06	0.0002772	6.013	25996	REXO2	REX2 RNA exonuclease 2 homolog (S. cerevisiae)	ENSG00000076043
A_23_P208516	-0.448	11.83	-10.24	7.82E-06	0.0002761	6.019	79143	MBOAT7	membrane bound O-acyltransferase domain containing 7	ENSG00000125505
A_23_P370989	-0.44	6	-10.24	7.80E-06	0.0002758	6.021	4173	MCM4	minichromosome maintenance complex component 4	ENSG00000104738

A_23_P166910	-0.4679	8.196	-10.26	7.69E-06	0.0002729	6.036	23317	DNAJC13	DnaJ (Hsp40) homolog subfamily C member 13	ENSG00000138246
A_32_P28365	-0.8796	6.174	-10.26	7.68E-06	0.0002728	6.037	4678	NASP	nuclear autoantigenic sperm protein (histone-binding)	ENSG00000132780
A_24_P122050	-0.8387	8.421	-10.27	7.65E-06	0.0002724	6.041	9491	PSMF1	proteasome (prosome macropain) inhibitor subunit 1 (PI31)	ENSG00000125818
A_24_P393844	-0.7031	9.229	-10.27	7.63E-06	0.0002724	6.043	1802	DPH2	DPH2 homolog (S. cerevisiae)	ENSG00000132768
A_24_P849801	-1.01	9.045	-10.27	7.65E-06	0.0002724	6.041	6146	RPL22	ribosomal protein L22	ENSG00000116251
A_23_P212706	-0.5532	8.678	-10.29	7.52E-06	0.0002692	6.058	64422	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	ENSG00000144848
A_23_P252913	-0.4309	6.565	-10.29	7.52E-06	0.0002692	6.058	55212	BBS7	Bardet-Biedl syndrome 7	ENSG00000138686
A_24_P11965	-1.272	12.01	-10.29	7.52E-06	0.0002692	6.058	93621	MRFAP1	Mof4 family associated protein 1	ENSG00000179010
A_23_P432506	-0.3573	5.609	-10.3	7.48E-06	0.0002687	6.064	253868	C20orf200	chromosome 20 open reading frame 200	ENSG00000174403
A_24_P740705	-0.4779	11.83	-10.3	7.45E-06	0.000268	6.067	91582	RPS19BP1	ribosomal protein S19 binding protein 1	ENSG00000187051
A_23_P105519	-0.6332	6.31	-10.31	7.42E-06	0.0002678	6.071	51729	WBP11	WW domain binding protein 11	ENSG00000084463
A_23_P146187	-0.617	6.456	-10.31	7.44E-06	0.0002678	6.069	23212	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	ENSG00000179041
A_23_P209477	-1.487	8.975	-10.31	7.44E-06	0.0002678	6.069	5496	PPM1G	protein phosphatase 1G (formerly 2C) magnesium-dependent gamma isoform	ENSG00000115241
A_23_P154025	-0.6599	11.16	-10.32	7.37E-06	0.0002669	6.078	6741	SSB	Sjogren syndrome antigen B (autoantigen La)	ENSG00000138385
A_23_P89509	-0.6062	10.37	-10.33	7.31E-06	0.0002653	6.086	10615	SPAG5	sperm associated antigen 5	ENSG00000076382
A_23_P349817	-0.5143	7.261	-10.36	7.13E-06	0.0002611	6.111	2963	GTF2F2	general transcription factor IIF polypeptide 2 30kDa	ENSG00000188342
A_32_P22257	-0.8798	11.6	-10.36	7.17E-06	0.0002619	6.105	3150	HMGN1	high-mobility group nucleosome binding domain 1	ENSG00000205581
A_23_P141636	-0.6723	11.69	-10.37	7.10E-06	0.0002608	6.116	9775	EIF4A3	eukaryotic translation initiation factor 4A3	ENSG00000141543
A_23_P14193	-0.6183	7.27	-10.37	7.13E-06	0.0002611	6.112	5983	RFC3	replication factor C (activator 1) 3 38kDa	ENSG00000133119
A_23_P207014	-0.4662	9.275	-10.38	7.07E-06	0.0002599	6.12	5889	RAD51C	RAD51 homolog C (S. cerevisiae)	ENSG00000108384
A_23_P9677	-0.6626	6.597	-10.38	7.05E-06	0.0002599	6.122	54910	SEMA4C	sema domain immunoglobulin domain (Ig) transmembrane domain (TM) and short cytoplasmic domain (semaphorin) 4C	ENSG00000168758
A_32_P201496	-1.213	7.644	-10.38	7.04E-06	0.0002598	6.123	171568	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	ENSG00000100413
A_23_P258093	-0.4304	10.97	-10.4	6.98E-06	0.0002586	6.133	10554	AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase alpha)	ENSG00000204310 ENSG00000206324 ENSG00000226467 ENSG00000227642 ENSG00000228892 ENSG00000235758 ENSG00000236873
A_23_P373645	-0.5477	8.482	-10.4	6.96E-06	0.0002583	6.135	10431	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	ENSG00000138297 ENSG00000204152
A_23_P149664	-0.427	9.302	-10.41	6.88E-06	0.000257	6.146	653659	TMEM183B	transmembrane protein 183B	ENSG00000163444
A_23_P160631	-0.6372	13.27	-10.41	6.89E-06	0.0002571	6.145	7203	CCT3	chaperonin containing TCP1 subunit 3 (gamma)	ENSG00000163468
A_24_P4661	-1.258	9.958	-10.41	6.91E-06	0.0002573	6.143	9538	EI24	etoposide induced 2.4 mRNA	ENSG00000149547

A_23_P115861	-0.4592	6.021	-10.42	6.87E-06	0.0002568	6.148	220992	ZNF485	zinc finger protein 485	ENSG00000198298
A_23_P145408	-0.5471	9.491	-10.42	6.87E-06	0.0002568	6.148	2519	FUCA2	fucosidase alpha-L- 2 plasma	ENSG00000001036
A_23_P255569	-0.9233	9.879	-10.45	6.73E-06	0.0002523	6.169	64118	DUS1L	dihydrouridine synthase 1-like (S. cerevisiae)	ENSG00000169718
A_23_P122375	-0.6866	6.57	-10.46	6.68E-06	0.0002507	6.177	60685	ZFAND3	zinc finger AN1-type domain 3	ENSG00000156639
A_23_P140088	-0.3787	6.084	-10.46	6.65E-06	0.0002503	6.182	79621	RNASEH2B	ribonuclease H2 subunit B	ENSG00000136104
A_32_P230547	-0.6449	7.31	-10.47	6.61E-06	0.0002494	6.187	85440	DOCK7	dedicator of cytokinesis 7	ENSG00000116641
A_32_P89073	-0.7489	7.592	-10.47	6.60E-06	0.0002494	6.188	90378	SAMD1	sterile alpha motif domain containing 1	NA
A_23_P123866	-0.5208	7.262	-10.48	6.59E-06	0.0002493	6.191	51271	UBAP1	ubiquitin associated protein 1	ENSG00000165006
A_23_P52082	-0.6441	6.411	-10.48	6.58E-06	0.0002493	6.192	25896	INTS7	integrator complex subunit 7	ENSG00000143493
A_23_P104065	-0.9675	7.759	-10.49	6.51E-06	0.0002478	6.203	23463	ICMT	isoprenylcysteine carboxyl methyltransferase	ENSG00000116237
A_24_P190424	-1.688	8.172	-10.49	6.54E-06	0.0002487	6.198	4218	RAB8A	RAB8A member RAS oncogene family	ENSG00000167461
A_24_P269398	-0.6362	7.341	-10.52	6.40E-06	0.0002445	6.22	835	CASP2	caspase 2 apoptosis-related cysteine peptidase	ENSG00000106144
A_23_P24960	-1.04	8.234	-10.53	6.35E-06	0.0002432	6.228	79731	NARS2	asparaginyl-tRNA synthetase 2 mitochondrial (putative)	ENSG00000137513
A_23_P36408	-0.5366	6.963	-10.53	6.35E-06	0.0002432	6.227	65082	VPS33A	vacuolar protein sorting 33 homolog A (S. cerevisiae)	ENSG00000139719
A_24_P266035	-0.5953	8.051	-10.53	6.34E-06	0.0002432	6.228	27292	DIMT1L	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	ENSG00000086189
A_23_P108641	-0.5139	8.138	-10.54	6.29E-06	0.0002417	6.236	84908	FAM136A	family with sequence similarity 136 member A	ENSG00000035141
A_23_P119464	-0.8013	6.883	-10.55	6.24E-06	0.0002414	6.244	85415	RHPN2	rhophilin Rho GTPase binding protein 2	ENSG00000131941
A_23_P120982	-0.4158	5.569	-10.55	6.27E-06	0.0002415	6.24	10343	PKDREJ	polycystic kidney disease (polycystin) and REJ homolog (sperm receptor for egg jelly homolog sea urchin)	ENSG00000130943
A_23_P256223	-0.508	7.049	-10.55	6.25E-06	0.0002414	6.242	7411	VBP1	von Hippel-Lindau binding protein 1	ENSG00000155959
A_23_P340728	-1.148	7.075	-10.55	6.26E-06	0.0002414	6.242	5663	PSEN1	presenilin 1	ENSG00000080815
A_23_P42368	-0.6472	7.429	-10.55	6.27E-06	0.0002415	6.239	51534	VTA1	Vps20-associated 1 homolog (S. cerevisiae)	ENSG00000009844
A_23_P50020	-0.512	6.59	-10.57	6.15E-06	0.0002396	6.259	9382	COG1	component of oligomeric golgi complex 1	ENSG00000166685
A_24_P328819	-0.5956	7.255	-10.58	6.11E-06	0.0002383	6.266	60684	C4orf41	chromosome 4 open reading frame 41	ENSG00000168538
A_23_P35609	-0.8438	8.046	-10.59	6.09E-06	0.0002383	6.269	7390	UROS	uroporphyrinogen III synthase	ENSG00000188690
A_23_P392383	-0.6527	7.146	-10.59	6.10E-06	0.0002383	6.267	23367	LARP1	La ribonucleoprotein domain family member 1	ENSG00000155506
A_23_P88848	-0.8859	7.716	-10.59	6.06E-06	0.0002375	6.273	54920	DUS2L	dihydrouridine synthase 2-like SMM1 homolog (S. cerevisiae)	ENSG00000167264
A_23_P208523	-0.7048	6.739	-10.61	5.98E-06	0.0002361	6.287	79165	LENG1	leukocyte receptor cluster (LRC) member 1	ENSG00000105617
A_23_P257945	-0.4035	9.48	-10.61	6.01E-06	0.0002362	6.283	3052	HCCS	holocytochrome c synthase (cytochrome c heme-lyase)	ENSG00000004961
A_23_P345887	-0.5741	6.347	-10.61	5.98E-06	0.0002361	6.287	2673	GFPT1	glutamine-fructose-6-phosphate transaminase 1	ENSG00000198380
A_23_P47955	-0.4601	6.614	-10.61	5.99E-06	0.0002362	6.285	4940	OAS3	2'-5'-oligoadenylate synthetase 3 100kDa	ENSG00000111331
A_23_P2935	-0.5778	6.16	-10.63	5.90E-06	0.0002337	6.301	283635	FAM177A1	family with sequence similarity 177 member A1	ENSG00000151327

A_23_P164035	-1.362	7.817	-10.65	5.83E-06	0.0002323	6.312	5705	PSMC5	proteasome (prosome macropain) 26S subunit ATPase 5	ENSG00000087191
A_23_P167789	-0.4487	6.413	-10.65	5.82E-06	0.000232	6.314	51307	FAM53C	family with sequence similarity 53 member C	ENSG00000120709
A_23_P157861	-1.524	7.358	-10.66	5.77E-06	0.0002311	6.322	57109	REXO4	REX4 RNA exonuclease 4 homolog (S. cerevisiae)	ENSG00000148300
A_23_P154522	-0.4595	7.36	-10.68	5.70E-06	0.0002296	6.334	57504	MTA3	metastasis associated 1 family member 3	ENSG00000057935
A_23_P501745	-1.211	7.433	-10.68	5.69E-06	0.0002294	6.336	5192	PEX10	peroxisomal biogenesis factor 10	ENSG00000157911
A_23_P78372	-0.5452	6.627	-10.68	5.71E-06	0.0002297	6.333	9984	THOC1	THO complex 1	ENSG00000079134
A_23_P145388	-0.6	13.37	-10.7	5.61E-06	0.0002277	6.35	23787	MTCH1	mitochondrial carrier homolog 1 (C. elegans)	ENSG00000137409
A_23_P39116	-0.7993	11.72	-10.7	5.63E-06	0.0002281	6.348	3978	LIG1	ligase I DNA ATP-dependent	ENSG00000105486
A_23_P8139	-0.6907	6.858	-10.7	5.64E-06	0.0002282	6.346	7629	ZNF76	zinc finger protein 76 (expressed in testis)	ENSG00000065029
A_23_P40354	-0.435	8.817	-10.73	5.51E-06	0.0002249	6.368	22919	MAPRE1	microtubule-associated protein RP/EB family member 1	ENSG00000101367
A_23_P41327	-0.9193	7.405	-10.73	5.52E-06	0.0002249	6.366	55646	LYAR	Ly1 antibody reactive homolog (mouse)	ENSG00000145220
A_23_P120237	-0.363	11.35	-10.75	5.43E-06	0.0002222	6.382	56910	STARD7	StAR-related lipid transfer (START) domain containing 7	ENSG00000084090
A_23_P94795	-0.8553	9.516	-10.75	5.43E-06	0.0002221	6.383	7004	TEAD4	TEA domain family member 4	ENSG00000197905
A_23_P106439	-0.5477	7.851	-10.76	5.39E-06	0.0002217	6.39	91433	RCCD1	RCC1 domain containing 1	ENSG00000166965
A_23_P26799	-0.395	8.069	-10.76	5.38E-06	0.0002216	6.391	9526	MPDU1	mannose-P-dolichol utilization defect 1	ENSG00000129255
A_24_P308628	-0.6437	7.251	-10.76	5.41E-06	0.0002221	6.387	51409	HEMK1	HemK methyltransferase family member 1	ENSG00000114735
A_23_P46928	-0.4787	14.2	-10.77	5.37E-06	0.0002214	6.393	5214	PFKP	phosphofructokinase platelet	ENSG00000067057
A_24_P146603	-0.5685	10.4	-10.78	5.33E-06	0.00022	6.402	9188	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	ENSG00000165732
A_23_P15705	-0.7241	12.92	-10.79	5.31E-06	0.0002193	6.406	5694	PSMB6	proteasome (prosome macropain) subunit beta type 6	ENSG00000142507
A_32_P51084	-0.3927	10.54	-10.8	5.27E-06	0.000219	6.413	23165	NUP205	nucleoporin 205kDa	ENSG00000155561
A_23_P161446	-0.6031	7.293	-10.81	5.22E-06	0.0002173	6.423	2665	GDI2	GDP dissociation inhibitor 2	ENSG00000057608
A_23_P80342	-0.6313	8.275	-10.83	5.13E-06	0.0002149	6.44	10454	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	ENSG00000100324
A_24_P132813	-0.5524	5.79	-10.83	5.15E-06	0.0002155	6.436	93377	OPALIN	oligodendrocytic myelin paranodal and inner loop protein	ENSG00000197430
A_23_P158627	-0.3937	9.853	-10.84	5.12E-06	0.0002149	6.441	79050	NOC4L	nucleolar complex associated 4 homolog (S. cerevisiae)	ENSG00000184967
A_23_P168629	-0.7363	9.747	-10.84	5.11E-06	0.0002148	6.443	55131	RBM28	RNA binding motif protein 28	ENSG00000106344
A_23_P132948	-0.3752	6.894	-10.85	5.06E-06	0.0002139	6.453	1998	ELF2	E74-like factor 2 (ets domain transcription factor)	ENSG00000109381
A_23_P158662	-0.9618	10.08	-10.85	5.06E-06	0.0002139	6.453	2873	GPS1	G protein pathway suppressor 1	ENSG00000169727
A_24_P73158	-1.818	10.3	-10.85	5.07E-06	0.000214	6.451	2237	FEN1	flap structure-specific endonuclease 1	ENSG00000168496
A_24_P118844	-0.5275	5.938	-10.88	4.96E-06	0.0002115	6.473	23331	TTC28	tetratricopeptide repeat domain 28	ENSG00000100154
A_23_P72961	-1.504	9.094	-10.91	4.86E-06	0.0002084	6.492	5631	PRPS1	phosphoribosyl pyrophosphate synthetase 1	ENSG00000147224
A_23_P28420	-0.8574	10.87	-10.94	4.77E-06	0.0002054	6.512	29789	OLA1	Obg-like ATPase 1	ENSG00000138430
A_23_P57268	-0.5825	6.526	-10.94	4.77E-06	0.0002054	6.512	1525	CXADR	coxsackie virus and adenovirus receptor	ENSG00000154639

A_24_P148836	-0.4027	5.943	-10.94	4.79E-06	0.000206	6.508	200942	KLHDC8B	kelch domain containing 8B	ENSG00000185909
A_32_P154091	-0.3899	7.721	-10.94	4.76E-06	0.0002054	6.513	389641	LOC389641	hypothetical gene supported by AK124295	NA
A_24_P13572	-0.7167	6.602	-10.95	4.75E-06	0.0002053	6.515	1743	DLST	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	ENSG00000119689
A_23_P154330	-0.5122	8.111	-10.96	4.70E-06	0.0002041	6.526	10190	TXNDC9	thioredoxin domain containing 9	ENSG00000115514
A_23_P43820	-0.4615	6.22	-10.96	4.70E-06	0.0002041	6.526	84879	MFSD2A	major facilitator superfamily domain containing 2A	ENSG00000168389
A_24_P407717	-0.8881	8.783	-10.96	4.72E-06	0.0002047	6.521	2885	GRB2	growth factor receptor-bound protein 2	ENSG00000177885
A_23_P40072	-0.5718	6.484	-10.97	4.69E-06	0.0002041	6.529	4528	MTIF2	mitochondrial translational initiation factor 2	ENSG00000085760
A_23_P68889	-0.6558	11.57	-10.97	4.67E-06	0.000204	6.531	51493	C22orf28	chromosome 22 open reading frame 28	ENSG00000100220
A_24_P321626	-0.9756	7.48	-10.97	4.68E-06	0.0002041	6.53	55703	POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	ENSG00000013503
A_23_P29885	-0.4896	12.14	-10.99	4.62E-06	0.0002024	6.543	10296	MAEA	macrophage erythroblast attacher	ENSG00000090316
A_24_P108351	-0.4738	7.103	-10.99	4.60E-06	0.0002019	6.547	11100	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	ENSG00000105323
A_23_P310317	-0.4883	12.41	-11	4.59E-06	0.0002017	6.55	6949	TCOF1	Treacher Collins-Franceschetti syndrome 1	ENSG00000070814
A_23_P97157	-0.49	8.606	-11	4.58E-06	0.0002017	6.551	55705	IPO9	importin 9	ENSG00000198700
A_23_P24987	-0.3485	6.15	-11.01	4.55E-06	0.0002008	6.558	6302	TSPAN31	tetraspanin 31	ENSG00000135452
A_24_P66270	-0.976	8.003	-11.01	4.54E-06	0.0002005	6.56	653639	LYPLA2P1	lysophospholipase II pseudogene 1	NA
A_23_P149975	-0.6024	10.83	-11.05	4.44E-06	0.0001979	6.583	83641	FAM107B	family with sequence similarity 107 member B	ENSG00000065809
A_23_P154539	-0.8727	12.77	-11.06	4.39E-06	0.0001967	6.593	24148	PRPF6	PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)	ENSG00000101161
A_23_P56933	-0.8869	10.35	-11.07	4.38E-06	0.0001965	6.596	57142	RTN4	reticulon 4	ENSG00000115310
A_23_P67648	-0.8447	12.09	-11.07	4.37E-06	0.0001965	6.597	826	CAPNS1	calpain small subunit 1	ENSG00000126247
A_24_P139742	-0.4804	6.25	-11.07	4.38E-06	0.0001966	6.595	64802	NMNAT1	nicotinamide nucleotide adenylyltransferase 1	ENSG00000173614
A_24_P171345	-0.5668	7.801	-11.07	4.37E-06	0.0001965	6.598	9698	PUM1	pumilio homolog 1 (Drosophila)	ENSG00000134644
A_24_P276490	-1.1	6.99	-11.08	4.35E-06	0.0001961	6.601	11313	LYPLA2	lysophospholipase II	ENSG00000011009
A_23_P41246	-0.6063	10.04	-11.11	4.26E-06	0.0001939	6.622	10227	MFSD10	major facilitator superfamily domain containing 10	ENSG00000109736
A_23_P96087	-0.9979	9.679	-11.11	4.25E-06	0.0001935	6.625	8971	H1FX	H1 histone family member X	ENSG00000184897
A_24_P335358	-1.435	10.2	-11.11	4.25E-06	0.0001935	6.626	80324	PUS1	pseudouridylate synthase 1	ENSG00000177192
A_23_P140511	-0.4653	9.209	-11.12	4.24E-06	0.0001932	6.629	10845	CLPX	ClpX caseinolytic peptidase X homolog (E. coli)	ENSG00000166855
A_23_P16673	-0.5003	9.538	-11.12	4.21E-06	0.0001926	6.634	1265	CNN2	calponin 2	ENSG00000064666
A_23_P63681	-0.505	8.194	-11.12	4.23E-06	0.0001931	6.63	3416	IDE	insulin-degrading enzyme	ENSG00000119912
A_23_P30024	-0.6952	9.045	-11.13	4.20E-06	0.0001925	6.637	4790	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	ENSG00000109320
A_32_P88415	-0.8888	6.192	-11.13	4.19E-06	0.0001925	6.638	91977	MYOZ3	myozenin 3	ENSG00000164591
A_23_P202374	-0.4771	9.084	-11.14	4.16E-06	0.0001917	6.645	1355	COX15	COX15 homolog cytochrome c oxidase assembly protein (yeast)	ENSG00000014919

A_23_P49033	-0.7945	8.793	-11.15	4.15E-06	0.0001917	6.648	6642	SNX1	sorting nexin 1	ENSG00000028528
A_24_P254177	-0.4537	7.283	-11.15	4.14E-06	0.0001913	6.652	79086	C19orf42	chromosome 19 open reading frame 42	ENSG00000214046
A_23_P329152	-0.3879	10.66	-11.16	4.10E-06	0.0001907	6.66	3609	ILF3	interleukin enhancer binding factor 3 90kDa	ENSG00000129351
A_23_P51754	-1.067	8.21	-11.18	4.07E-06	0.0001903	6.668	5906	RAP1A	RAP1A member of RAS oncogene family	ENSG00000116473
A_23_P13502	-0.3772	12.63	-11.19	4.03E-06	0.000189	6.678	51287	CHCHD8	coiled-coil-helix-coiled-coil-helix domain containing 8	ENSG00000181924
A_23_P54147	-0.6413	7.234	-11.19	4.04E-06	0.0001894	6.676	51199	NIN	ninein (GSK3B interacting protein)	ENSG00000100503
A_32_P57810	-0.5024	5.984	-11.2	4.00E-06	0.0001884	6.685	114804	RNF157	ring finger protein 157	ENSG00000141576
A_23_P152651	-0.5465	9.191	-11.21	3.99E-06	0.0001881	6.688	11325	DDX42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	ENSG00000198231
A_23_P152218	-0.9057	8.183	-11.22	3.96E-06	0.000187	6.696	1874	E2F4	E2F transcription factor 4 p107/p130-binding	ENSG00000205250
A_24_P257971	-1.104	7.419	-11.22	3.96E-06	0.000187	6.694	10999	SLC27A4	solute carrier family 27 (fatty acid transporter) member 4	ENSG00000167114
A_23_P436476	-0.7642	8.205	-11.25	3.88E-06	0.0001842	6.716	23029	RBM34	RNA binding motif protein 34	ENSG00000188739
A_23_P97573	-0.5674	6.632	-11.25	3.87E-06	0.0001842	6.717	9129	PRPF3	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	ENSG00000117360
A_24_P828949	-0.4644	6.516	-11.25	3.88E-06	0.0001842	6.715	55110	MAGOHB	mago-nashi homolog B (Drosophila)	ENSG00000111196
A_23_P106463	-0.7564	8.961	-11.27	3.83E-06	0.0001829	6.728	4947	OAZ2	ornithine decarboxylase antizyme 2	ENSG00000180304
A_23_P154507	-0.5169	10.1	-11.27	3.83E-06	0.0001829	6.729	9270	ITGB1BP1	integrin beta 1 binding protein 1	ENSG00000119185
A_24_P277615	-1.105	7.551	-11.27	3.82E-06	0.0001829	6.731	81786	TRIM7	tripartite motif-containing 7	ENSG00000146054
A_23_P161231	-1.119	7.011	-11.28	3.80E-06	0.0001821	6.737	81855	SFXN3	sideroflexin 3	ENSG00000107819
A_24_P347198	-0.6254	8.825	-11.28	3.80E-06	0.0001821	6.737	8562	DENR	density-regulated protein	ENSG00000139726
A_23_P129486	-0.5454	10.68	-11.29	3.76E-06	0.000181	6.745	51734	SEPX1	selenoprotein X 1	ENSG00000198736
A_23_P77321	-0.4613	6.59	-11.33	3.69E-06	0.0001782	6.766	23168	RTF1	Rtf1 Paf1/RNA polymerase II complex component homolog (S. cerevisiae)	ENSG00000137815
A_24_P131173	-0.7541	6.485	-11.35	3.62E-06	0.000176	6.783	79762	C1orf115	chromosome 1 open reading frame 115	ENSG00000162817
A_23_P70748	-0.6452	9.196	-11.4	3.50E-06	0.0001716	6.817	85021	REPS1	RALBP1 associated Eps domain containing 1	ENSG00000135597
A_23_P100486	-0.4393	11.65	-11.41	3.49E-06	0.0001716	6.818	79001	VKORC1	vitamin K epoxide reductase complex subunit 1	ENSG00000167397
A_23_P120002	-0.6097	6.661	-11.42	3.46E-06	0.0001703	6.828	3431	SP110	SP110 nuclear body protein	ENSG00000135899
A_23_P137731	-0.7279	7.53	-11.43	3.45E-06	0.0001698	6.832	79577	CDC73	cell division cycle 73 Paf1/RNA polymerase II complex component homolog (S. cerevisiae)	ENSG00000134371
A_23_P57588	-1.188	7.422	-11.43	3.43E-06	0.0001696	6.837	51512	GTSE1	G-2 and S-phase expressed 1	ENSG00000075218
A_24_P327815	-1.332	10.05	-11.44	3.41E-06	0.0001693	6.841	10963	STIP1	stress-induced-phosphoprotein 1	ENSG00000168439
A_23_P108574	-0.4716	6.715	-11.45	3.40E-06	0.000169	6.846	23683	PRKD3	protein kinase D3	ENSG00000115825
A_23_P256855	-0.7436	7.775	-11.45	3.40E-06	0.000169	6.844	57510	XPO5	exportin 5	ENSG00000124571
A_23_P258621	-0.4969	8.015	-11.45	3.40E-06	0.000169	6.845	8634	RTCD1	RNA terminal phosphate cyclase domain 1	ENSG00000137996
A_23_P16615	-0.7504	10.72	-11.47	3.35E-06	0.0001671	6.861	4670	HNRNPM	heterogeneous nuclear ribonucleoprotein M	ENSG00000099783
A_23_P151634	-1.388	8.121	-11.48	3.34E-06	0.000167	6.863	11198	SUPT16H	suppressor of Ty 16 homolog (S. cerevisiae)	ENSG00000092201

A_23_P123256	-0.9934	7.251	-11.49	3.31E-06	0.0001664	6.872	11333	PDAP1	PDGFA associated protein 1	ENSG00000106244
A_23_P150092	-0.7876	10.75	-11.49	3.31E-06	0.0001665	6.87	22929	SEPHS1	selenophosphate synthetase 1	ENSG00000086475
A_23_P200439	-0.5484	6.409	-11.5	3.29E-06	0.0001658	6.878	103	ADAR	adenosine deaminase RNA-specific	ENSG00000160710
A_23_P2143	-0.5782	10.35	-11.51	3.26E-06	0.0001649	6.885	9789	SPCS2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	ENSG00000118363
A_23_P33482	-0.5741	6.471	-11.52	3.25E-06	0.0001649	6.889	7405	UVRAG	UV radiation resistance associated gene	ENSG00000198382
A_23_P97265	-0.7614	10.19	-11.53	3.22E-06	0.0001642	6.897	54865	GPATCH4	G patch domain containing 4	ENSG00000160818
A_32_P103060	-0.5535	6.869	-11.56	3.17E-06	0.0001624	6.914	7555	CNBP	CCHC-type zinc finger nucleic acid binding protein	ENSG00000169714
A_23_P159227	-1.323	9.117	-11.57	3.14E-06	0.0001612	6.922	8751	ADAM15	ADAM metallopeptidase domain 15	ENSG00000143537
A_23_P68610	-1.322	11.06	-11.58	3.12E-06	0.0001605	6.928	22974	TPX2	TPX2 microtubule-associated homolog (Xenopus laevis)	ENSG00000088325
A_23_P12816	-0.9665	7.609	-11.59	3.11E-06	0.00016	6.933	3070	HELLS	helicase lymphoid-specific	ENSG00000119969
A_23_P141917	-0.7135	7.446	-11.6	3.07E-06	0.0001593	6.945	7297	TYK2	tyrosine kinase 2	ENSG00000105397
A_23_P100779	-0.6235	7.139	-11.61	3.05E-06	0.000159	6.951	7343	UBTF	upstream binding transcription factor RNA polymerase I	ENSG00000108312
A_24_P941845	-0.6673	6.139	-11.63	3.02E-06	0.0001577	6.962	29925	GMPPB	GDP-mannose pyrophosphorylase B	ENSG00000173540
A_23_P119254	-0.7213	9.331	-11.64	3.01E-06	0.0001576	6.964	55723	ASF1B	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	ENSG00000105011
A_32_P218332	-0.5312	9.37	-11.65	2.99E-06	0.000157	6.971	197322	ACSF3	acyl-CoA synthetase family member 3	ENSG00000176715
A_23_P15511	-1.279	12.28	-11.68	2.93E-06	0.0001554	6.99	1655	DDX5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	ENSG00000108654
A_23_P416686	-0.3961	6.674	-11.7	2.89E-06	0.0001542	7.003	56834	GPR137	G protein-coupled receptor 137	ENSG00000173264
A_23_P63751	-0.4782	10.91	-11.7	2.88E-06	0.000154	7.007	10935	PRDX3	peroxiredoxin 3	ENSG00000165672
A_24_P338636	-0.6252	8.136	-11.7	2.89E-06	0.0001542	7.004	11171	STRAP	serine/threonine kinase receptor associated protein	ENSG00000023734
A_24_P204697	-0.6109	6.321	-11.71	2.87E-06	0.0001536	7.012	29774	POM121L9P	POM121 membrane glycoprotein-like 9 (rat) pseudogene	NA
A_23_P153783	-0.4854	7.254	-11.74	2.82E-06	0.0001525	7.027	7392	USF2	upstream transcription factor 2 c-fos interacting	ENSG00000105698
A_23_P32320	-0.5713	8.074	-11.74	2.81E-06	0.0001525	7.03	79058	ASPSCR1	alveolar soft part sarcoma chromosome region candidate 1	ENSG00000169696
A_23_P92824	-0.6375	6.495	-11.74	2.82E-06	0.0001525	7.028	83734	ATG10	ATG10 autophagy related 10 homolog (S. cerevisiae)	ENSG00000152348
A_24_P942002	-0.6506	6.671	-11.77	2.76E-06	0.0001505	7.049	23527	ACAP2	ArfGAP with coiled-coil ankyrin repeat and PH domains 2	ENSG00000114331
A_23_P213000	-1.187	10.2	-11.78	2.74E-06	0.0001496	7.057	9948	WDR1	WD repeat domain 1	ENSG00000071127
A_23_P28057	-1.202	12.77	-11.78	2.74E-06	0.0001496	7.056	7064	THOP1	thimet oligopeptidase 1	ENSG00000172009
A_23_P501134	-0.6456	7.032	-11.79	2.72E-06	0.0001493	7.063	3980	LIG3	ligase III DNA ATP-dependent	ENSG00000005156
A_24_P11307	-1.245	9.211	-11.81	2.69E-06	0.0001481	7.074	10768	AHCYL1	adenosylhomocysteinase-like 1	ENSG00000168710
A_32_P98683	-0.4441	9.902	-11.81	2.70E-06	0.0001483	7.071	4302	MLLT6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog Drosophila); translocated to 6	ENSG00000108292
A_23_P122624	-0.8389	7.905	-11.82	2.68E-06	0.0001479	7.079	84946	LTV1	LTV1 homolog (S. cerevisiae)	ENSG00000135521
A_24_P39508	-0.6656	6.964	-11.86	2.60E-06	0.0001455	7.107	123920	CMTM3	CKLF-like MARVEL transmembrane domain containing 3	ENSG00000140931

A_32_P199301	-0.8958	7.957	-11.87	2.58E-06	0.0001452	7.113	7027	TFDP1	transcription factor Dp-1	ENSG00000198176
A_23_P102988	-1.033	6.546	-11.9	2.54E-06	0.0001433	7.129	10587	TXNRD2	thioredoxin reductase 2	ENSG00000184470
A_24_P89701	-0.4402	11.76	-11.91	2.52E-06	0.0001424	7.136	3614	IMPDH1	IMP (inosine monophosphate) dehydrogenase 1	ENSG00000106348
A_23_P66487	-1.249	8.292	-11.99	2.41E-06	0.0001383	7.181	6603	SMARCD2	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily d member 2	ENSG00000108604
A_24_P76740	-0.5697	7.792	-12	2.38E-06	0.0001374	7.192	200014	CC2D1B	coiled-coil and C2 domain containing 1B	ENSG00000154222
A_23_P102351	-1.394	7.177	-12.01	2.37E-06	0.0001372	7.198	9486	CHST10	carbohydrate sulfotransferase 10	ENSG00000115526
A_32_P332	-1.132	6.517	-12.01	2.37E-06	0.0001372	7.197	151325	MYADML	myeloid-associated differentiation marker-like	NA
A_23_P42684	-0.5463	6.058	-12.03	2.34E-06	0.0001365	7.207	55025	FLJ20712	hypothetical FLJ20712	NA
A_24_P121271	-0.3995	9.071	-12.04	2.33E-06	0.0001363	7.215	11052	CPSF6	cleavage and polyadenylation specific factor 6 68kDa	ENSG00000111605
A_23_P143089	-0.678	7.857	-12.06	2.30E-06	0.0001351	7.226	4358	MPV17	MpV17 mitochondrial inner membrane protein	ENSG00000115204
A_23_P257863	-0.598	12.31	-12.08	2.26E-06	0.0001339	7.241	22948	CCT5	chaperonin containing TCP1 subunit 5 (epsilon)	ENSG00000150753
A_23_P434421	-0.9521	8.304	-12.1	2.25E-06	0.0001334	7.248	219771	CCNY	cyclin Y	ENSG00000108100
A_23_P9591	-1.161	12.58	-12.1	2.25E-06	0.0001334	7.248	10960	LMAN2	lectin mannose-binding 2	ENSG00000169223
A_23_P120839	-0.5611	8.492	-12.11	2.22E-06	0.0001326	7.259	24144	TFIP11	tuftelin interacting protein 11	ENSG00000100109
A_23_P7083	-0.6217	6.967	-12.13	2.20E-06	0.000132	7.269	92070	C4orf42	chromosome 4 open reading frame 42	ENSG00000196810
A_23_P138461	-0.9641	7.11	-12.14	2.19E-06	0.0001317	7.272	56652	C10orf2	chromosome 10 open reading frame 2	ENSG00000107815
A_23_P53015	-0.9194	7.639	-12.15	2.18E-06	0.0001314	7.278	64852	TUT1	terminal uridylyl transferase 1 U6 snRNA-specific	ENSG00000149016
A_23_P364890	-1.186	7.899	-12.17	2.14E-06	0.000131	7.294	9810	RNF40	ring finger protein 40	ENSG00000103549
A_23_P140725	-0.4372	7.143	-12.19	2.12E-06	0.0001306	7.306	9742	IFT140	intraflagellar transport 140 homolog (Chlamydomonas)	ENSG00000187535
A_23_P363954	-0.8861	5.978	-12.19	2.12E-06	0.0001306	7.305	7069	THRSP	thyroid hormone responsive (SPOT14 homolog rat)	ENSG00000151365
A_24_P242820	-0.4959	8.078	-12.19	2.13E-06	0.0001308	7.302	7247	TSN	translin	ENSG00000211460
A_23_P257057	-0.6705	8.841	-12.2	2.11E-06	0.0001303	7.309	51337	C8orf55	chromosome 8 open reading frame 55	ENSG00000130193
A_23_P162807	-0.6014	8.855	-12.21	2.10E-06	0.0001297	7.315	10240	MRPS31	mitochondrial ribosomal protein S31	ENSG00000102738
A_24_P343255	-0.6288	7.018	-12.21	2.10E-06	0.0001297	7.316	116138	KLHDC3	kelch domain containing 3	ENSG00000124702
A_23_P107661	-1.258	10.12	-12.24	2.06E-06	0.0001284	7.333	5518	PPP2R1A	protein phosphatase 2 (formerly 2A) regulatory subunit A alpha isoform	ENSG00000105568
A_23_P117778	-0.8116	7.975	-12.27	2.02E-06	0.0001271	7.349	84993	UBL7	ubiquitin-like 7 (bone marrow stromal cell-derived)	ENSG00000138629
A_23_P116679	-0.7616	9.056	-12.28	2.01E-06	0.0001266	7.358	5036	PA2G4	proliferation-associated 2G4 38kDa	ENSG00000170515
A_23_P214603	-0.569	10.41	-12.28	2.01E-06	0.0001266	7.356	10211	FLOT1	flotillin 1	ENSG00000137312 ENSG00000206379 ENSG00000206480 ENSG00000230143 ENSG00000232280
A_23_P13425	-0.5176	10.94	-12.29	2.00E-06	0.0001266	7.361	975	CD81	CD81 molecule	ENSG00000110651
A_23_P425516	-0.5177	6.373	-12.29	1.99E-06	0.0001266	7.364	26262	TSPAN17	tetraspanin 17	ENSG00000048140

A_23_P91293	-0.6529	7.72	-12.31	1.97E-06	0.0001261	7.376	9217	VAPB	VAMP (vesicle-associated membrane protein)-associated protein B and C	ENSG00000124164
A_24_P413437	-0.9954	11.48	-12.31	1.97E-06	0.0001261	7.376	4841	NONO	non-POU domain containing octamer-binding	ENSG00000147140
A_32_P139079	-0.974	12.52	-12.31	1.97E-06	0.0001263	7.373	26135	SERBP1	SERPINE1 mRNA binding protein 1	ENSG00000142864
A_23_P67971	-0.6559	8.306	-12.37	1.89E-06	0.0001236	7.413	130589	GALM	galactose mutarotase (aldose 1-epimerase)	ENSG00000143891
A_23_P77833	-0.6331	6.958	-12.38	1.89E-06	0.0001236	7.416	9489	PGS1	phosphatidylglycerophosphate synthase 1	ENSG00000087157
A_24_P99639	-0.4611	6.036	-12.38	1.89E-06	0.0001236	7.418	284086	NEK8	NIMA (never in mitosis gene a)- related kinase 8	ENSG00000160602
A_24_P38944	-0.9449	8.764	-12.4	1.86E-06	0.0001229	7.431	79080	CCDC86	coiled-coil domain containing 86	ENSG00000110104
A_24_P303974	-0.7187	8.686	-12.44	1.82E-06	0.0001203	7.453	8872	CDC123	cell division cycle 123 homolog (S. cerevisiae)	ENSG00000151465
A_23_P99260	-0.7327	12.58	-12.45	1.81E-06	0.0001202	7.455	10988	METAP2	methionyl aminopeptidase 2	ENSG00000111142
A_24_P818005	-0.5645	8.256	-12.48	1.78E-06	0.0001183	7.475	79089	TMUB2	transmembrane and ubiquitin-like domain containing 2	ENSG00000168591
A_23_P3450	-0.5263	6.674	-12.5	1.75E-06	0.000117	7.487	27229	TUBGCP4	tubulin gamma complex associated protein 4	ENSG00000137822
A_32_P162338	-0.7105	11.24	-12.5	1.75E-06	0.000117	7.487	7170	TPM3	tropomyosin 3	ENSG00000143549
A_23_P88249	-0.8778	7.921	-12.51	1.75E-06	0.000117	7.491	55147	RBM23	RNA binding motif protein 23	ENSG00000100461
A_32_P22622	-0.555	7.043	-12.52	1.74E-06	0.0001167	7.497	8602	NOP14	NOP14 nucleolar protein homolog (yeast)	ENSG00000087269
A_32_P213389	-0.8819	6.704	-12.53	1.72E-06	0.000116	7.506	7259	TSPYL1	TSPY-like 1	ENSG00000189241
A_23_P16139	-0.7388	7.747	-12.54	1.72E-06	0.0001159	7.508	10523	CHERP	calcium homeostasis endoplasmic reticulum protein	ENSG00000085872
A_23_P108604	-0.8368	10.41	-12.56	1.69E-06	0.0001147	7.524	9448	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	ENSG00000071054
A_24_P39454	-1.414	6.993	-12.58	1.67E-06	0.0001137	7.535	54617	INO80	INO80 homolog (S. cerevisiae)	ENSG00000128908
A_23_P68087	-0.4835	10.29	-12.59	1.66E-06	0.0001137	7.538	471	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	ENSG00000138363
A_23_P132248	-0.5313	7.592	-12.63	1.62E-06	0.0001115	7.564	55954	ZMAT5	zinc finger matrin type 5	ENSG00000100319
A_23_P7361	-0.7997	8.177	-12.63	1.62E-06	0.0001115	7.562	79071	ELOVL6	ELOVL family member 6 elongation of long chain fatty acids (FEN1/Elo2 SUR4/Elo3-like yeast)	ENSG00000170522
A_23_P56213	-1.148	7.203	-12.65	1.60E-06	0.0001107	7.575	57655	GRAMD1A	GRAM domain containing 1A	ENSG00000089351
A_24_P294719	-0.4709	6.131	-12.65	1.61E-06	0.0001109	7.572	23197	FAF2	Fas associated factor family member 2	ENSG00000113194
A_23_P1199	-0.4713	11.25	-12.67	1.58E-06	0.0001103	7.586	11164	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	ENSG00000165609
A_32_P113436	-0.6948	6.121	-12.69	1.57E-06	0.0001098	7.595	144983	HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1-like 2	ENSG00000139675 ENSG00000242466
A_24_P276703	-0.6917	9.633	-12.71	1.55E-06	0.0001091	7.609	23435	TARDBP	TAR DNA binding protein	ENSG00000120948
A_24_P29401	-0.5201	6.15	-12.75	1.51E-06	0.0001077	7.629	5295	PIK3R1	phosphoinositide-3-kinase regulatory subunit 1 (alpha)	ENSG00000145675
A_24_P332971	-0.5775	8.927	-12.77	1.50E-06	0.0001067	7.64	285855	RPL7L1	ribosomal protein L7-like 1	ENSG00000146223
A_24_P338145	-0.4513	9.848	-12.83	1.44E-06	0.0001034	7.677	30968	STOML2	stomatin (EPB72)-like 2	ENSG00000165283
A_23_P1280	-0.5656	8.137	-12.86	1.42E-06	0.0001023	7.69	51008	ASCC1	activating signal cointegrator 1 complex subunit 1	ENSG00000138303

A_23_P138693	-0.7069	7.597	-12.87	1.41E-06	0.0001019	7.697	9397	NMT2	N-myristoyltransferase 2	ENSG00000152465
A_24_P3973	-1.183	7.421	-12.87	1.40E-06	0.0001018	7.7	3181	HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1	ENSG00000122566
A_23_P101655	-0.6323	10.36	-12.9	1.38E-06	0.0001008	7.717	81	ACTN4	actinin alpha 4	ENSG00000130402
A_23_P118690	-0.589	8.182	-12.9	1.39E-06	0.0001009	7.712	7756	ZNF207	zinc finger protein 207	ENSG00000010244
A_23_P207766	-0.4682	9.445	-12.95	1.34E-06	9.89E-05	7.741	396	ARHGDIA	Rho GDP dissociation inhibitor (GDI) alpha	ENSG00000141522
A_23_P201086	-1.544	7.417	-12.96	1.34E-06	9.85E-05	7.748	375	ARF1	ADP-ribosylation factor 1	ENSG00000143761
A_23_P2077	-1.299	6.24	-12.96	1.33E-06	9.85E-05	7.749	256144	OR4C3	olfactory receptor family 4 subfamily C member 3	ENSG00000176547
A_23_P49082	-0.7345	10.39	-12.96	1.34E-06	9.85E-05	7.748	10101	NUBP2	nucleotide binding protein 2 (MinD homolog E. coli)	ENSG00000095906
A_23_P10870	-0.512	8.1	-12.98	1.32E-06	9.81E-05	7.758	22845	DOLK	dolichol kinase	ENSG00000175283
A_24_P313756	-0.7156	10.91	-12.99	1.31E-06	9.79E-05	7.763	84617	TUBB6	tubulin beta 6	ENSG00000176014
A_23_P210886	-0.8085	8.225	-13.03	1.28E-06	9.64E-05	7.786	598	BCL2L1	BCL2-like 1	ENSG00000171552
A_23_P19061	-0.5348	6.452	-13.05	1.27E-06	9.54E-05	7.799	92181	UBTD2	ubiquitin domain containing 2	ENSG00000168246
A_24_P269006	-0.5836	7.149	-13.05	1.27E-06	9.54E-05	7.799	501	ALDH7A1	aldehyde dehydrogenase 7 family member A1	ENSG00000164904
A_32_P38145	-0.975	8.771	-13.05	1.27E-06	9.56E-05	7.795	11252	PACSIN2	protein kinase C and casein kinase substrate in neurons 2	ENSG00000100266
A_23_P202696	-0.5462	6.622	-13.06	1.26E-06	9.53E-05	7.805	55709	KBTBD4	kelch repeat and BTB (POZ) domain containing 4	ENSG00000123444
A_23_P124927	-0.4985	8.64	-13.07	1.25E-06	9.53E-05	7.807	10636	RGS14	regulator of G-protein signaling 14	ENSG00000169220
A_24_P237766	-0.5663	6.798	-13.08	1.24E-06	9.47E-05	7.816	6397	SEC14L1	SEC14-like 1 (S. cerevisiae)	ENSG00000129657
A_23_P23575	-0.8649	11.15	-13.1	1.23E-06	9.41E-05	7.823	27173	SLC39A1	solute carrier family 39 (zinc transporter) member 1	ENSG00000143570
A_23_P66872	-0.5762	9.743	-13.1	1.23E-06	9.41E-05	7.825	50628	GEMIN4	gem (nuclear organelle) associated protein 4	ENSG00000179409
A_23_P60537	-0.6245	8.207	-13.14	1.20E-06	9.26E-05	7.847	9128	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	ENSG00000136875
A_23_P20683	-0.5323	9.427	-13.18	1.18E-06	9.18E-05	7.867	9933	KIAA0020	KIAA0020	ENSG00000080608
A_23_P64650	-0.5455	11.03	-13.18	1.18E-06	9.18E-05	7.867	10102	TSFM	Ts translation elongation factor mitochondrial	ENSG00000123297
A_24_P942945	-0.5439	6.363	-13.18	1.18E-06	9.18E-05	7.867	57211	GPR126	G protein-coupled receptor 126	ENSG00000112414
A_24_P297078	-0.5051	7.052	-13.2	1.16E-06	9.11E-05	7.881	57136	C20orf3	chromosome 20 open reading frame 3	ENSG00000101474
A_24_P64329	-1.234	8.864	-13.22	1.14E-06	9.07E-05	7.893	282974	STK32C	serine/threonine kinase 32C	ENSG00000165752
A_24_P258051	-0.7133	7.449	-13.23	1.14E-06	9.06E-05	7.898	84930	MASTL	microtubule associated serine/threonine kinase-like	ENSG00000120539
A_23_P143190	-1.278	10.5	-13.28	1.11E-06	8.87E-05	7.922	4605	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	ENSG00000101057
A_23_P353056	-0.4393	9.825	-13.3	1.10E-06	8.82E-05	7.932	9854	C2CD2L	C2CD2-like	ENSG00000172375
A_23_P414269	-1.224	7.613	-13.3	1.10E-06	8.82E-05	7.934	90121	TSR2	TSR2 20S rRNA accumulation homolog (S. cerevisiae)	ENSG00000158526
A_24_P163477	-0.5945	7.27	-13.3	1.09E-06	8.82E-05	7.936	55278	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	ENSG00000130348
A_24_P233960	-0.7302	9.227	-13.31	1.09E-06	8.82E-05	7.938	81609	SNX27	sorting nexin family member 27	ENSG00000143376

A_24_P254285	-0.6487	7.61	-13.31	1.09E-06	8.81E-05	7.942	92667	C20orf72	chromosome 20 open reading frame 72	ENSG00000125871
A_23_P15466	-0.8415	8.406	-13.33	1.08E-06	8.75E-05	7.952	6341	SCO1	SCO cytochrome oxidase deficient homolog 1 (yeast)	ENSG00000133028
A_23_P77430	-0.4375	11.43	-13.34	1.07E-06	8.72E-05	7.957	54496	PRMT7	protein arginine methyltransferase 7	ENSG00000132600
A_23_P103837	-0.6182	8.681	-13.35	1.07E-06	8.72E-05	7.961	9898	UBAP2L	ubiquitin associated protein 2-like	ENSG00000143569
A_24_P225961	-1.188	7.352	-13.37	1.05E-06	8.68E-05	7.974	1605	DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	ENSG00000173402
A_23_P332340	-0.5844	5.861	-13.38	1.05E-06	8.68E-05	7.976	283385	MORN3	MORN repeat containing 3	ENSG00000139714
A_24_P382637	-0.6853	7.13	-13.39	1.04E-06	8.68E-05	7.98	26164	GTPBP5	GTP binding protein 5 (putative)	ENSG00000101181
A_23_P39656	-0.4994	7.837	-13.41	1.03E-06	8.63E-05	7.992	64320	RNF25	ring finger protein 25	ENSG00000163481
A_24_P157388	-0.9427	6.578	-13.43	1.02E-06	8.54E-05	8.004	55573	CDV3	CDV3 homolog (mouse)	ENSG00000091527
A_23_P118038	-0.8572	10.35	-13.5	9.79E-07	8.36E-05	8.04	10204	NUTF2	nuclear transport factor 2	ENSG00000102898
A_23_P9416	-0.4877	10.47	-13.52	9.66E-07	8.28E-05	8.053	48	ACO1	aconitase 1 soluble	ENSG00000122729
A_23_P102517	-0.7206	7.493	-13.54	9.59E-07	8.24E-05	8.06	5147	PDE6D	phosphodiesterase 6D cGMP-specific rod delta	ENSG00000156973
A_23_P133227	-0.4858	9.532	-13.55	9.50E-07	8.18E-05	8.069	3035	HARS	histidyl-tRNA synthetase	ENSG00000170445
A_23_P17307	-0.7401	11.99	-13.56	9.45E-07	8.15E-05	8.073	55257	C20orf20	chromosome 20 open reading frame 20	ENSG00000101189
A_23_P25141	-0.5599	7.407	-13.59	9.33E-07	8.08E-05	8.086	55832	CAND1	cullin-associated and neddylation-dissociated 1	ENSG00000111530
A_23_P135364	-0.923	8.509	-13.69	8.80E-07	7.77E-05	8.14	1841	DTYMK	deoxythymidylate kinase (thymidylate kinase)	ENSG00000168393
A_23_P251927	-1.272	8.282	-13.72	8.66E-07	7.70E-05	8.155	54927	CHCHD3	coiled-coil-helix-coiled-coil-helix domain containing 3	ENSG00000106554
A_32_P165112	-0.5754	7.978	-13.76	8.47E-07	7.55E-05	8.176	116143	WDR92	WD repeat domain 92	ENSG00000221823 ENSG00000243667
A_23_P126057	-0.4327	10.56	-13.77	8.40E-07	7.50E-05	8.183	6342	SCP2	sterol carrier protein 2	ENSG00000116171
A_23_P14083	-0.6569	9.909	-13.79	8.33E-07	7.47E-05	8.191	347902	AMIGO2	adhesion molecule with Ig-like domain 2	ENSG00000139211
A_23_P82068	-1.029	11.35	-13.8	8.26E-07	7.45E-05	8.199	51406	NOL7	nucleolar protein 7 27kDa	ENSG00000225921
A_23_P59836	-0.6369	6.536	-13.82	8.20E-07	7.44E-05	8.206	55798	METTL2B	methyltransferase like 2B	ENSG00000165055
A_23_P422193	-0.9924	7.495	-13.84	8.12E-07	7.42E-05	8.216	6839	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	ENSG00000101945
A_23_P92132	-0.7561	10.11	-13.84	8.09E-07	7.42E-05	8.218	7866	IFRD2	interferon-related developmental regulator 2	ENSG00000214706
A_23_P83453	-1.119	8.583	-13.85	8.06E-07	7.42E-05	8.222	6599	SMARCC1	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily c member 1	ENSG00000173473
A_23_P23221	-1.017	10.22	-13.88	7.92E-07	7.39E-05	8.238	1647	GADD45A	growth arrest and DNA-damage-inducible alpha	ENSG00000116717
A_23_P30377	-0.5806	8.042	-13.94	7.68E-07	7.27E-05	8.267	9879	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	ENSG00000145833
A_23_P160283	-0.5666	7.15	-13.97	7.56E-07	7.20E-05	8.282	27252	KLHL20	kelch-like 20 (Drosophila)	ENSG00000076321
A_23_P165355	-0.7797	8.027	-13.99	7.46E-07	7.17E-05	8.294	10056	FARSB	phenylalanyl-tRNA synthetase beta subunit	ENSG00000116120
A_23_P54834	-0.6541	8.91	-14.01	7.40E-07	7.15E-05	8.302	51388	NIP7	nuclear import 7 homolog (S. cerevisiae)	ENSG00000132603
A_23_P136805	-0.8327	7.817	-14.04	7.25E-07	7.06E-05	8.321	9824	ARHGAP11A	Rho GTPase activating protein 11A	ENSG00000198826

A_23_P97906	-0.6855	8.375	-14.05	7.21E-07	7.05E-05	8.326	22978	NT5C2	5'-nucleotidase cytosolic II	ENSG00000076685
A_24_P100517	-0.9002	8.689	-14.06	7.16E-07	7.05E-05	8.332	89958	C9orf140	chromosome 9 open reading frame 140	ENSG00000186193
A_32_P135902	-0.6686	6.696	-14.06	7.20E-07	7.05E-05	8.327	1973	EIF4A1	eukaryotic translation initiation factor 4A1	ENSG00000161960
A_23_P203344	-0.6246	8.397	-14.09	7.08E-07	7.00E-05	8.343	80829	ZFP91	zinc finger protein 91 homolog (mouse)	ENSG00000186660
A_24_P232252	-0.57	5.923	-14.09	7.08E-07	7.00E-05	8.342	6505	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter system Xag) member 1	ENSG00000106688
A_32_P132796	-0.8174	7.776	-14.1	7.01E-07	6.97E-05	8.351	9577	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	ENSG00000158019
A_32_P63182	-0.658	8.402	-14.1	7.03E-07	6.97E-05	8.35	2923	PDIA3	protein disulfide isomerase family A member 3	ENSG00000167004
A_24_P144504	-0.8063	6.948	-14.12	6.95E-07	6.97E-05	8.359	79184	BRCC3	BRCA1/BRCA2-containing complex subunit 3	ENSG00000185515
A_23_P402610	-1.015	6.695	-14.15	6.83E-07	6.91E-05	8.375	5198	PFAS	phosphoribosylformylglycinamidine synthase	ENSG00000178921
A_24_P205364	-1.26	7.448	-14.15	6.86E-07	6.92E-05	8.372	6470	SHMT1	serine hydroxymethyltransferase 1 (soluble)	ENSG00000176974
A_23_P103588	-0.6427	5.804	-14.16	6.79E-07	6.90E-05	8.381	3158	HMGCS2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)	ENSG00000134240
A_23_P29555	-0.6119	11.09	-14.17	6.77E-07	6.90E-05	8.384	6396	SEC13	SEC13 homolog (S. cerevisiae)	ENSG00000157020
A_23_P39024	-0.5836	8.287	-14.18	6.72E-07	6.89E-05	8.391	84292	WDR83	WD repeat domain 83	ENSG00000123154
A_23_P165280	-1.11	10.79	-14.21	6.64E-07	6.82E-05	8.402	5434	POLR2E	polymerase (RNA) II (DNA directed) polypeptide E 25kDa	ENSG00000099817
A_23_P46118	-0.6675	7.132	-14.21	6.62E-07	6.82E-05	8.405	1122	CHML	choroideremia-like (Rab escort protein 2)	ENSG00000203668
A_23_P374351	-1.054	7	-14.24	6.51E-07	6.76E-05	8.42	222658	KCTD20	potassium channel tetramerisation domain containing 20	ENSG00000112078
A_23_P7101	-0.947	10.81	-14.24	6.51E-07	6.76E-05	8.42	7884	SLBP	stem-loop binding protein	ENSG00000163950
A_32_P199736	-0.8069	6.322	-14.24	6.52E-07	6.76E-05	8.419	11261	CHP	calcium binding protein P22	ENSG00000187446
A_23_P38497	-0.9325	9.042	-14.26	6.45E-07	6.76E-05	8.429	8402	SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier) member 11	ENSG00000108528
A_23_P144622	-1.636	8.246	-14.27	6.42E-07	6.75E-05	8.432	10007	GNPDA1	glucosamine-6-phosphate deaminase 1	ENSG00000113552
A_24_P389517	-0.7648	10.35	-14.27	6.40E-07	6.75E-05	8.436	3190	HNRNPK	heterogeneous nuclear ribonucleoprotein K	ENSG00000165119
A_24_P237265	-0.6851	7.344	-14.28	6.39E-07	6.75E-05	8.438	5594	MAPK1	mitogen-activated protein kinase 1	ENSG00000100030
A_24_P280029	-1.248	8.025	-14.29	6.35E-07	6.74E-05	8.443	57026	PDXP	pyridoxal (pyridoxine vitamin B6) phosphatase	ENSG00000100092 ENSG00000241360
A_23_P165937	-0.6825	6.714	-14.3	6.30E-07	6.74E-05	8.45	79980	DSN1	DSN1 MIND kinetochore complex component homolog (S. cerevisiae)	ENSG00000149636
A_23_P75978	-0.4895	9.537	-14.34	6.18E-07	6.65E-05	8.468	81570	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	ENSG00000162129
A_23_P502609	-0.6488	9.354	-14.36	6.12E-07	6.60E-05	8.477	9091	PIGQ	phosphatidylinositol glycan anchor biosynthesis class Q	ENSG00000007541
A_23_P216355	-0.9722	8.773	-14.38	6.04E-07	6.56E-05	8.49	4796	NFKBIL2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	ENSG00000160949
A_23_P16573	-1.264	7.933	-14.41	5.96E-07	6.50E-05	8.501	54555	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	ENSG00000105671
A_23_P215265	-0.4834	7.79	-14.43	5.90E-07	6.48E-05	8.51	2768	GNA12	guanine nucleotide binding protein (G protein) alpha 12	ENSG00000146535

A_23_P135769	-0.8788	14.04	-14.46	5.80E-07	6.41E-05	8.526	60	ACTB	actin beta	ENSG00000075624
A_24_P378368	-0.9839	6.392	-14.47	5.75E-07	6.41E-05	8.534	8720	MBTPS1	membrane-bound transcription factor peptidase site 1	ENSG00000140943
A_23_P213344	-0.854	8.295	-14.48	5.74E-07	6.41E-05	8.537	1729	DIAPH1	diaphanous homolog 1 (Drosophila)	ENSG00000131504
A_24_P26897	-0.4986	6.087	-14.48	5.74E-07	6.41E-05	8.537	3632	INPP5A	inositol polyphosphate-5-phosphatase 40kDa	ENSG00000068383
A_24_P53519	-0.7618	8.558	-14.48	5.74E-07	6.41E-05	8.535	10036	CHAF1A	chromatin assembly factor 1 subunit A (p150)	ENSG00000167670
A_23_P135499	-0.5329	6.436	-14.51	5.64E-07	6.37E-05	8.552	25932	CLIC4	chloride intracellular channel 4	ENSG00000169504
A_23_P91657	-1.03	8.258	-14.52	5.61E-07	6.36E-05	8.556	2130	EWSR1	Ewing sarcoma breakpoint region 1	ENSG00000182944
A_23_P98898	-0.8096	6.582	-14.54	5.55E-07	6.32E-05	8.567	1017	CDK2	cyclin-dependent kinase 2	ENSG00000123374
A_23_P208446	-0.7159	9.983	-14.55	5.53E-07	6.31E-05	8.571	6294	SAFB	scaffold attachment factor B	ENSG00000160633
A_23_P370434	-0.6315	12.09	-14.58	5.45E-07	6.26E-05	8.583	708	C1QBP	complement component 1 q subcomponent binding protein	ENSG00000108561
A_23_P208416	-0.8834	6.793	-14.59	5.43E-07	6.26E-05	8.588	79939	SLC35E1	solute carrier family 35 member E1	ENSG00000127526
A_23_P47735	-0.6383	6.519	-14.62	5.33E-07	6.21E-05	8.604	84957	RELT	RELT tumor necrosis factor receptor	ENSG00000054967
A_23_P55064	-0.8987	7.628	-14.62	5.32E-07	6.21E-05	8.605	55135	WRAP53	WD repeat containing antisense to TP53	ENSG00000141499
A_23_P165891	-0.6634	7.497	-14.64	5.26E-07	6.17E-05	8.615	9014	TAF1B	TATA box binding protein (TBP)-associated factor RNA polymerase I B 63kDa	ENSG00000115750
A_24_P305597	-0.8297	11.51	-14.67	5.20E-07	6.12E-05	8.627	11047	ADRM1	adhesion regulating molecule 1	ENSG00000130706
A_23_P166122	-0.7341	7.34	-14.68	5.17E-07	6.11E-05	8.631	10621	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F 39 kDa	ENSG00000132664
A_23_P345707	-0.4661	6.474	-14.7	5.12E-07	6.07E-05	8.641	90381	C15orf42	chromosome 15 open reading frame 42	ENSG00000140534
A_24_P63608	-0.4969	11.34	-14.7	5.11E-07	6.07E-05	8.642	55651	NHP2	NHP2 ribonucleoprotein homolog (yeast)	ENSG00000145912
A_32_P88479	-0.4463	11.39	-14.7	5.12E-07	6.07E-05	8.64	23313	C22orf9	chromosome 22 open reading frame 9	ENSG00000100364
A_23_P70045	-0.7036	12.07	-14.74	5.00E-07	5.98E-05	8.662	9555	H2AFY	H2A histone family member Y	ENSG00000113648
A_23_P154070	-0.4592	12.8	-14.77	4.92E-07	5.94E-05	8.677	7277	TUBA4A	tubulin alpha 4a	ENSG00000127824
A_23_P32722	-0.5555	6.478	-14.77	4.92E-07	5.94E-05	8.677	79797	ZNF408	zinc finger protein 408	ENSG00000175213
A_23_P152995	-0.4879	5.793	-14.79	4.88E-07	5.94E-05	8.685	6532	SLC6A4	solute carrier family 6 (neurotransmitter transporter serotonin) member 4	ENSG00000108576
A_23_P58353	-0.9111	12.47	-14.81	4.83E-07	5.91E-05	8.694	3184	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1 37kDa)	ENSG00000138668
A_23_P64010	-0.6441	10.19	-14.85	4.74E-07	5.83E-05	8.711	23788	MTCH2	mitochondrial carrier homolog 2 (C. elegans)	ENSG00000109919
A_23_P102743	-0.6808	6.775	-14.93	4.53E-07	5.67E-05	8.752	51605	TRMT6	tRNA methyltransferase 6 homolog (S. cerevisiae)	ENSG00000089195
A_23_P18465	-0.6901	7.925	-14.97	4.44E-07	5.61E-05	8.77	5981	RFC1	replication factor C (activator 1) 1 145kDa	ENSG00000035928

A_32_P78528	-1.235	12.9	-14.99	4.41E-07	5.59E-05	8.777	203068	TUBB	tubulin beta	ENSG00000183311 ENSG00000196230 ENSG00000224156 ENSG00000227739 ENSG00000229684 ENSG00000232421 ENSG00000232575 ENSG00000235067
A_23_P476	-0.8259	7.552	-15.03	4.31E-07	5.53E-05	8.798	9019	MPZL1	myelin protein zero-like 1	ENSG00000197965
A_23_P354170	-1.242	7.45	-15.04	4.28E-07	5.53E-05	8.803	54965	PIGX	phosphatidylinositol glycan anchor biosynthesis class X	ENSG00000163964
A_23_P423480	-0.7155	8.676	-15.05	4.28E-07	5.53E-05	8.804	219743	TYSND1	trypsin domain containing 1	ENSG00000156521
A_32_P174790	-0.6382	6.962	-15.08	4.20E-07	5.47E-05	8.82	439990	LOC439990	hypothetical gene supported by BC009626; BC048265	NA
A_23_P106708	-0.6992	17.31	-15.09	4.19E-07	5.47E-05	8.823	6187	RPS2	ribosomal protein S2	ENSG00000140988
A_24_P296424	-0.5649	7.256	-15.1	4.17E-07	5.46E-05	8.828	1201	CLN3	ceroid-lipofuscinosis neuronal 3	ENSG00000188603
A_32_P10003	-0.6286	6.653	-15.14	4.07E-07	5.42E-05	8.849	113457	TUBA3D	tubulin alpha 3d	ENSG00000075886 ENSG00000198033
A_23_P98431	-0.6741	13.28	-15.2	3.96E-07	5.33E-05	8.875	3145	HMBS	hydroxymethylbilane synthase	ENSG00000149397
A_23_P166193	-0.554	7.726	-15.21	3.95E-07	5.33E-05	8.877	55741	EDEM2	ER degradation enhancer mannosidase alpha-like 2	ENSG00000088298
A_23_P95470	-0.6587	9.873	-15.21	3.94E-07	5.33E-05	8.877	977	CD151	CD151 molecule (Raph blood group)	ENSG00000177697
A_23_P5586	-0.5881	9.522	-15.24	3.87E-07	5.29E-05	8.894	10199	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	ENSG00000124383
A_23_P131771	-0.9058	6.343	-15.32	3.72E-07	5.15E-05	8.929	7165	TPD52L2	tumor protein D52-like 2	ENSG00000101150
A_32_P18824	-0.5428	10.22	-15.36	3.65E-07	5.10E-05	8.948	29117	BRD7	bromodomain containing 7	ENSG00000166164
A_32_P8666	-0.8228	8.998	-15.41	3.56E-07	5.07E-05	8.969	644063	LOC644063	similar to heterogeneous nuclear ribonucleoprotein K	NA
A_23_P153583	-1.397	7.88	-15.42	3.54E-07	5.06E-05	8.976	5536	PPP5C	protein phosphatase 5 catalytic subunit	ENSG00000011485
A_23_P79942	-0.713	9.004	-15.43	3.52E-07	5.06E-05	8.979	80025	PANK2	pantothenate kinase 2	ENSG00000125779
A_23_P126186	-0.8025	9.257	-15.44	3.51E-07	5.06E-05	8.983	8560	DEGS1	degenerative spermatocyte homolog 1 lipid desaturase (Drosophila)	ENSG00000143753
A_24_P130962	-1.408	8.685	-15.47	3.45E-07	5.01E-05	8.997	64222	TOR3A	torsin family 3 member A	ENSG00000186283
A_24_P313744	-0.5232	10.21	-15.54	3.34E-07	4.93E-05	9.027	9097	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	ENSG00000101557
A_23_P8380	-0.5655	8.233	-15.67	3.13E-07	4.70E-05	9.085	78996	C7orf49	chromosome 7 open reading frame 49	ENSG00000122783
A_23_P105392	-0.8402	12.79	-15.69	3.11E-07	4.69E-05	9.092	10576	CCT2	chaperonin containing TCP1 subunit 2 (beta)	ENSG00000166226
A_23_P130194	-0.5349	13.11	-15.69	3.11E-07	4.69E-05	9.091	5831	PYCR1	pyrroline-5-carboxylate reductase 1	ENSG00000183010
A_23_P49646	-1.004	8.35	-15.75	3.01E-07	4.64E-05	9.121	5636	PRPSAP2	phosphoribosyl pyrophosphate synthetase-associated protein 2	ENSG00000141127
A_32_P88626	-0.8521	7.417	-15.86	2.86E-07	4.56E-05	9.165	65979	PHACTR4	phosphatase and actin regulator 4	ENSG00000204138
A_23_P55998	-0.9411	9.905	-15.88	2.82E-07	4.54E-05	9.176	6510	SLC1A5	solute carrier family 1 (neutral amino acid transporter) member 5	ENSG00000105281
A_23_P21436	-1.021	8.933	-16.07	2.59E-07	4.26E-05	9.254	26147	PHF19	PHD finger protein 19	ENSG00000119403
A_24_P636318	-0.8716	6.928	-16.24	2.38E-07	4.02E-05	9.325	130074	FAM168B	family with sequence similarity 168 member B	ENSG00000152102

A_23_P3424	-0.7556	9.836	-16.28	2.34E-07	3.99E-05	9.342	54913	RPP25	ribonuclease P/MRP 25kDa subunit	ENSG00000178718
A_23_P86917	-0.6098	11.49	-16.31	2.30E-07	3.95E-05	9.356	8772	FADD	Fas (TNFRSF6)-associated via death domain	ENSG00000168040
A_23_P83736	-0.7256	8.859	-16.39	2.22E-07	3.83E-05	9.39	3622	ING2	inhibitor of growth family member 2	ENSG00000168556
A_23_P52978	-1.051	7.736	-16.44	2.17E-07	3.77E-05	9.41	27339	PRPF19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	ENSG00000110107
A_23_P137715	-0.615	7.556	-16.46	2.14E-07	3.75E-05	9.419	57645	POGK	pogo transposable element with KRAB domain	ENSG00000143157
A_23_P25336	-0.9474	6.923	-16.47	2.14E-07	3.75E-05	9.422	51228	GLTP	glycolipid transfer protein	ENSG00000139433
A_23_P131723	-0.8421	11.89	-16.49	2.11E-07	3.75E-05	9.431	10971	YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta polypeptide	ENSG00000134308
A_23_P46627	-0.6124	9.929	-16.6	2.01E-07	3.65E-05	9.476	51094	ADIPOR1	adiponectin receptor 1	ENSG00000159346
A_23_P71014	-0.922	10.64	-16.67	1.95E-07	3.60E-05	9.501	114049	WBSCR22	Williams Beuren syndrome chromosome region 22	ENSG00000071462
A_23_P17575	-1.001	13.68	-16.7	1.92E-07	3.55E-05	9.516	191	AHCY	adenosylhomocysteinase	ENSG00000101444
A_24_P80204	-0.6939	12.84	-16.71	1.91E-07	3.55E-05	9.519	7851	MALL	mal T-cell differentiation protein-like	ENSG00000144063
A_23_P36129	-0.7628	8.665	-16.74	1.88E-07	3.52E-05	9.532	26007	DAK	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	ENSG00000149476
A_23_P216402	-0.7756	7.672	-16.78	1.85E-07	3.47E-05	9.548	83549	UCK1	uridine-cytidine kinase 1	ENSG00000130717
A_32_P512061	-0.6972	6.787	-16.8	1.84E-07	3.46E-05	9.554	2630	GBAP1	glucosidase beta acid pseudogene 1	NA
A_23_P12849	-0.6806	8.337	-16.83	1.80E-07	3.43E-05	9.568	84893	FBXO18	F-box protein helicase 18	ENSG00000134452
A_23_P65741	-0.5753	8.699	-16.83	1.81E-07	3.43E-05	9.566	115752	DIS3L	DIS3 mitotic control homolog (S. cerevisiae)-like	ENSG00000166938
A_23_P431776	-0.771	7.337	-16.85	1.79E-07	3.42E-05	9.575	2118	ETV4	ets variant 4	ENSG00000175832
A_23_P17773	-1.648	7.071	-16.89	1.76E-07	3.38E-05	9.588	83606	C22orf13	chromosome 22 open reading frame 13	ENSG00000138867
A_23_P130648	-0.7603	8.862	-16.91	1.75E-07	3.38E-05	9.596	10755	GIPC1	GIPC PDZ domain containing family member 1	ENSG00000123159
A_24_P791515	-0.5389	6.28	-16.92	1.74E-07	3.38E-05	9.602	10492	SYNCRIP	synaptotagmin binding cytoplasmic RNA interacting protein	ENSG00000135316
A_23_P1145	-0.9057	7.861	-17.01	1.67E-07	3.28E-05	9.638	55149	MTPAP	mitochondrial poly(A) polymerase	ENSG00000107951
A_24_P405313	-1.084	6.815	-17.05	1.63E-07	3.27E-05	9.654	8604	SLC25A12	solute carrier family 25 (mitochondrial carrier Aralar) member 12	ENSG00000115840
A_23_P138507	-0.6146	7.799	-17.06	1.63E-07	3.27E-05	9.657	983	CDK1	cyclin-dependent kinase 1	ENSG00000170312
A_24_P353619	-0.9833	6.223	-17.1	1.60E-07	3.25E-05	9.671	249	ALPL	alkaline phosphatase liver/bone/kidney	ENSG00000162551
A_23_P2601	-0.5845	13.76	-17.12	1.59E-07	3.25E-05	9.679	7184	HSP90B1	heat shock protein 90kDa beta (Grp94) member 1	ENSG00000166598
A_23_P134477	-1.009	10.92	-17.24	1.50E-07	3.12E-05	9.727	84310	C7orf50	chromosome 7 open reading frame 50	ENSG00000146540
A_23_P167263	-0.7177	7.564	-17.29	1.47E-07	3.09E-05	9.745	79960	PHF17	PHD finger protein 17	ENSG00000077684
A_23_P113441	-0.8938	6.345	-17.32	1.45E-07	3.07E-05	9.756	55164	SHQ1	SHQ1 homolog (S. cerevisiae)	ENSG00000144736
A_23_P171054	-0.7949	6.229	-17.33	1.45E-07	3.07E-05	9.759	2002	ELK1	ELK1 member of ETS oncogene family	ENSG00000126767
A_23_P75453	-0.9216	8.704	-17.5	1.34E-07	2.90E-05	9.825	4221	MEN1	multiple endocrine neoplasia I	ENSG00000133895
A_23_P416242	-0.9537	6.652	-17.54	1.31E-07	2.86E-05	9.841	115992	RNF166	ring finger protein 166	ENSG00000158717
A_32_P194264	-0.8042	7.359	-17.59	1.28E-07	2.82E-05	9.86	494143	CHAC2	ChaC cation transport regulator homolog 2 (E. coli)	ENSG00000143942

A_24_P397107	-0.7729	7.861	-17.67	1.24E-07	2.79E-05	9.889	993	CDC25A	cell division cycle 25 homolog A (S. pombe)	ENSG00000164045
A_24_P314571	-0.7046	8.471	-17.71	1.22E-07	2.76E-05	9.903	147841	SPC24	SPC24 NDC80 kinetochore complex component homolog (S. cerevisiae)	ENSG00000161888
A_32_P197511	-0.5722	8.905	-17.86	1.14E-07	2.66E-05	9.959	114984	FLYWCH2	FLYWCH family member 2	ENSG00000162076
A_23_P71146	-1.094	9.282	-17.87	1.14E-07	2.66E-05	9.96	5425	POLD2	polymerase (DNA directed) delta 2 regulatory subunit 50kDa	ENSG00000106628
A_23_P106575	-0.673	10.16	-18.02	1.07E-07	2.54E-05	10.02	2806	GOT2	glutamic-oxaloacetic transaminase 2 mitochondrial (aspartate aminotransferase 2)	ENSG00000125166
A_23_P424513	-0.7607	8.048	-18.03	1.07E-07	2.54E-05	10.02	10048	RANBP9	RAN binding protein 9	ENSG00000010017
A_24_P108779	-0.7702	6.784	-18.08	1.04E-07	2.52E-05	10.04	79734	KCTD17	potassium channel tetramerisation domain containing 17	ENSG00000100379
A_23_P252052	-0.5774	6.986	-18.13	1.02E-07	2.48E-05	10.06	11259	FILIP1L	filamin A interacting protein 1-like	ENSG00000168386
A_23_P121405	-0.7575	8.51	-18.16	1.00E-07	2.47E-05	10.07	29890	RBM15B	RNA binding motif protein 15B	ENSG00000179837
A_23_P125408	-1.091	8.538	-18.16	1.01E-07	2.47E-05	10.06	83475	DOHH	deoxyhypusine hydroxylase/monooxygenase	ENSG00000129932
A_23_P52219	-0.7393	7.75	-18.21	9.85E-08	2.44E-05	10.08	10613	ERLIN1	ER lipid raft associated 1	ENSG00000107566
A_24_P283928	-0.686	7.234	-18.21	9.84E-08	2.44E-05	10.08	79035	OBFC2B	oligonucleotide/oligosaccharide-binding fold containing 2B	ENSG00000139579
A_23_P77776	-0.5696	11.49	-18.26	9.62E-08	2.43E-05	10.1	6427	SFRS2	splicing factor arginine/serine-rich 2	ENSG00000161547
A_23_P148372	-0.7703	9.884	-18.4	9.07E-08	2.39E-05	10.15	1478	CSTF2	cleavage stimulation factor 3' pre-RNA subunit 2 64kDa	ENSG00000101811
A_23_P46964	-0.838	7.875	-18.48	8.77E-08	2.35E-05	10.18	55662	HIF1AN	hypoxia inducible factor 1 alpha subunit inhibitor	ENSG00000166135
A_23_P64954	-0.7914	7.937	-18.58	8.41E-08	2.35E-05	10.21	8078	USP5	ubiquitin specific peptidase 5 (isopeptidase T)	ENSG00000111667
A_23_P117797	-0.9377	8.429	-18.79	7.71E-08	2.25E-05	10.29	54982	CLN6	ceroid-lipofuscinosis neuronal 6 late infantile variant	ENSG00000128973
A_23_P126457	-0.727	7.967	-18.82	7.62E-08	2.25E-05	10.29	81875	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	ENSG00000143319
A_23_P164000	-1.273	9.676	-18.82	7.64E-08	2.25E-05	10.29	26168	SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	ENSG00000161956
A_32_P150130	-0.9575	6.627	-18.89	7.40E-08	2.25E-05	10.32	59339	PLEKHA2	pleckstrin homology domain containing family A (phosphoinositide binding specific) member 2	ENSG00000169499
A_24_P93887	-0.71	8.078	-18.9	7.38E-08	2.25E-05	10.32	55588	MED29	mediator complex subunit 29	ENSG00000063322
A_23_P141738	-0.7183	8.144	-18.94	7.27E-08	2.25E-05	10.33	6760	SS18	synovial sarcoma translocation chromosome 18	ENSG00000141380
A_23_P103070	-0.7371	9.142	-19.08	6.86E-08	2.19E-05	10.38	7533	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta polypeptide	ENSG00000128245
A_24_P141629	-0.6967	7.515	-19.09	6.82E-08	2.19E-05	10.38	63901	FAM111A	family with sequence similarity 111 member A	ENSG00000166801
A_23_P44617	-0.7157	8.237	-19.16	6.63E-08	2.15E-05	10.41	22820	COPG	coatomer protein complex subunit gamma	ENSG00000181789
A_24_P48139	-0.7366	7.064	-19.27	6.36E-08	2.12E-05	10.44	23536	ADAT1	adenosine deaminase tRNA-specific 1	ENSG00000065457
A_23_P310590	-0.6246	6.654	-19.32	6.22E-08	2.09E-05	10.46	220323	OAF	OAF homolog (Drosophila)	ENSG00000184232
A_24_P236251	-1.079	6.193	-19.33	6.20E-08	2.09E-05	10.46	8788	DLK1	delta-like 1 homolog (Drosophila)	ENSG00000185559
A_23_P17430	-1.157	6.755	-19.44	5.94E-08	2.06E-05	10.5	55544	RBM38	RNA binding motif protein 38	ENSG00000132819

A_32_P12610	-0.7468	8.359	-19.47	5.86E-08	2.06E-05	10.51	1876	E2F6	E2F transcription factor 6	ENSG00000169016
A_23_P100196	-0.9002	9.098	-19.55	5.68E-08	2.04E-05	10.53	9100	USP10	ubiquitin specific peptidase 10	ENSG00000103194
A_24_P124973	-0.6956	6.236	-19.65	5.46E-08	1.98E-05	10.57	56160	NDNL2	necdin-like 2	ENSG00000185115
A_23_P42065	-1.253	8.074	-19.66	5.43E-08	1.98E-05	10.57	27242	TNFRSF21	tumor necrosis factor receptor superfamily member 21	ENSG00000146072
A_24_P278367	-0.8186	9.659	-19.7	5.36E-08	1.98E-05	10.58	10121	ACTR1A	ARP1 actin-related protein 1 homolog A centractin alpha (yeast)	ENSG00000138107
A_32_P159347	-0.8827	11.11	-19.77	5.22E-08	1.97E-05	10.6	220988	HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	ENSG00000170144
A_23_P23303	-0.9883	8.707	-19.95	4.86E-08	1.89E-05	10.66	9156	EXO1	exonuclease 1	ENSG00000174371
A_23_P81463	-0.7776	7.525	-20.02	4.72E-08	1.86E-05	10.68	54505	DHX29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	ENSG00000067248
A_24_P394246	-1.014	7.911	-20.25	4.32E-08	1.81E-05	10.75	51246	SHISA5	shisa homolog 5 (Xenopus laevis)	ENSG00000164054
A_24_P276864	-1.478	8.76	-20.32	4.21E-08	1.81E-05	10.77	55627	SMPD4	sphingomyelin phosphodiesterase 4 neutral membrane (neutral sphingomyelinase-3)	ENSG00000136699
A_23_P346405	-0.7317	6.48	-20.35	4.16E-08	1.80E-05	10.78	90550	CCDC109A	coiled-coil domain containing 109A	ENSG00000156026
A_23_P501770	-0.8546	6.78	-20.43	4.03E-08	1.78E-05	10.81	84126	ATRIP	ATR interacting protein	ENSG00000164053
A_23_P102965	-0.7788	7.731	-20.9	3.38E-08	1.65E-05	10.94	23786	BCL2L13	BCL2-like 13 (apoptosis facilitator)	ENSG00000099968
A_23_P163481	-0.8182	9.162	-20.9	3.38E-08	1.65E-05	10.94	701	BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	ENSG00000156970
A_23_P374782	-0.7696	9.061	-20.98	3.28E-08	1.64E-05	10.96	30011	SH3KBP1	SH3-domain kinase binding protein 1	ENSG00000147010
A_23_P58588	-0.9054	6.209	-21.08	3.17E-08	1.60E-05	10.99	6586	SLIT3	slit homolog 3 (Drosophila)	ENSG00000184347
A_23_P56630	-1.033	7.18	-21.32	2.89E-08	1.48E-05	11.06	6772	STAT1	signal transducer and activator of transcription 1 91kDa	ENSG00000115415
A_23_P52986	-1.007	7.189	-21.65	2.57E-08	1.38E-05	11.15	220001	VWCE	von Willebrand factor C and EGF domains	ENSG00000167992
A_24_P142269	-0.8898	7.033	-21.74	2.49E-08	1.35E-05	11.18	8479	HIRIP3	HIRA interacting protein 3	ENSG00000149929
A_24_P126060	-0.8017	9.8	-21.84	2.41E-08	1.34E-05	11.2	1654	DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 X-linked	ENSG00000215301
A_23_P63067	-0.6811	13.34	-22.01	2.26E-08	1.33E-05	11.25	7818	DAP3	death associated protein 3	ENSG00000132676
A_23_P79161	-0.759	12.57	-22.33	2.02E-08	1.25E-05	11.33	27166	PRELID1	PRELI domain containing 1	ENSG00000169230
A_23_P110606	-0.7809	6.662	-22.78	1.73E-08	1.14E-05	11.45	9794	MAML1	mastermind-like 1 (Drosophila)	ENSG00000161021
A_23_P19257	-0.8829	10.97	-22.9	1.66E-08	1.12E-05	11.48	347734	SLC35B2	solute carrier family 35 member B2	ENSG00000157593
A_24_P101391	-1.517	11.79	-22.96	1.63E-08	1.12E-05	11.49	4904	YBX1	Y box binding protein 1	ENSG00000065978
A_23_P49521	-0.8956	7.459	-23.4	1.40E-08	1.03E-05	11.6	6426	SFRS1	splicing factor arginine/serine-rich 1	ENSG00000136450
A_24_P96234	-1.05	8.546	-23.51	1.35E-08	1.03E-05	11.62	81890	QTRT1	queuine tRNA-ribosyltransferase 1	ENSG00000213339
A_23_P138105	-1.535	6.797	-23.72	1.26E-08	9.79E-06	11.67	54797	MED18	mediator complex subunit 18	ENSG00000130772
A_24_P252020	-0.9346	7.147	-23.77	1.24E-08	9.79E-06	11.68	90933	TRIM41	tripartite motif-containing 41	ENSG00000146063
A_24_P546375	-1.004	6.655	-24.25	1.06E-08	8.86E-06	11.79	342096	GOLGA6A	golgin A6 family member A	ENSG00000159289
A_23_P93823	-1.182	7.54	-24.29	1.05E-08	8.86E-06	11.8	5982	RFC2	replication factor C (activator 1) 2 40kDa	ENSG00000049541
A_23_P337201	-0.8178	9.718	-24.55	9.64E-09	8.36E-06	11.86	6731	SRP72	signal recognition particle 72kDa	ENSG00000174780
A_24_P128205	-0.8466	8.615	-24.73	9.12E-09	8.15E-06	11.9	5707	PSMD1	proteasome (prosome macropain) 26S subunit non-ATPase 1	ENSG00000173692

A_23_P161552	-1.218	7.977	-25.71	6.74E-09	7.31E-06	12.1	84364	ARFGAP2	ADP-ribosylation factor GTPase activating protein 2	ENSG00000149182
A_23_P13338	-0.9022	7.246	-25.88	6.39E-09	7.26E-06	12.14	80789	INTS5	integrator complex subunit 5	ENSG00000185085
A_24_P36847	-1.192	10.21	-26.69	5.02E-09	6.37E-06	12.3	1660	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	ENSG00000135829
A_23_P153050	-0.97	7.654	-26.75	4.93E-09	6.37E-06	12.31	54890	ALKBH5	alkB alkylation repair homolog 5 (E. coli)	ENSG00000091542
A_23_P202143	-1.12	7.846	-27.19	4.34E-09	6.04E-06	12.39	9221	NOLC1	nucleolar and coiled-body phosphoprotein 1	ENSG00000166197
A_23_P217411	-1.026	9.519	-27.59	3.88E-09	6.01E-06	12.46	8243	SMC1A	structural maintenance of chromosomes 1A	ENSG00000072501
A_24_P408083	-0.9529	9.124	-29.78	2.13E-09	4.46E-06	12.83	1786	DNMT1	DNA (cytosine-5-)-methyltransferase 1	ENSG00000130816
A_23_P136787	-2.113	7.639	-31.15	1.50E-09	3.82E-06	13.03	84296	GINS4	GINS complex subunit 4 (Sld5 homolog)	ENSG00000147536
A_23_P162866	-1.167	13.22	-32.97	9.60E-10	3.47E-06	13.27	3320	HSP90AA1	heat shock protein 90kDa alpha (cytosolic) class A member 1	ENSG00000080824
A_24_P287075	-1.29	7.956	-34.13	7.32E-10	2.97E-06	13.41	5871	MAP4K2	mitogen-activated protein kinase kinase kinase kinase 2	ENSG00000168067