

Symbol	Title	Averages						P-Values		
		0 mg		5 mg		20 mg		Two-way ANOVA		
		WT	TG	WT	TG	WT	TG	WT vs TG	Drug	Interxn
<b>Increased in Transgenic (571)</b>										
Aass	aminoadipate-semialdehyde synthase	-0.37	-0.15	-0.12	0.622	-0.65	0.697	0.00167	0.213337	0.154576
Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	-0.27	0.253	-0.38	-0.1	-0.29	0.836	0.011312	0.242142	0.349122
Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), mem	-0.21	0.179	-0.18	0.096	-0.64	0.795	0.005547	0.915543	0.107444
Abhd4	abhydrolase domain containing 4	-0.07	0.241	-0.48	0.662	-0.45	0.129	0.008427	0.64772	0.384045
Abi1	abl-interactor 1	-0.3	0.829	-0.24	0.189	-0.58	0.221	0.001895	0.31928	0.504527
Abi2	abl-interactor 2	-0.22	0.609	-0.04	0.402	-0.69	0.03	0.008966	0.149621	0.805943
Acadm	acyl-Coenzyme A dehydrogenase, medium chain	-0.18	0.635	-0.05	0.262	-0.7	0.118	0.011042	0.206213	0.63446
Acads	acyl-Coenzyme A dehydrogenase, short chain	-0.01	0.53	-0.64	0.45	-0.51	0.235	0.001853	0.348373	0.650995
Acbd5	acyl-Coenzyme A binding domain containing 5	-0.16	0.91	-0.03	0.027	-0.79	0.148	0.005097	0.064154	0.170032
Accs	1-aminocyclopropane-1-carboxylate synthase homolog	-0.41	0.227	-0.67	0.76	-0.08	0.238	0.001509	0.833387	0.153362
Acer3	alkaline ceramidase 3	-0.32	0.764	-0.28	0.172	-0.56	0.33	0.001549	0.493887	0.550081
Aco1	aconitase 1	-0.07	0.536	-0.08	0.124	-0.72	0.272	0.019439	0.340244	0.446978
Adam17	a disintegrin and metallopeptidase domain 17	-0.08	0.421	-0.29	0.689	-0.78	0.087	0.00176	0.114821	0.688113
Adamts18	a disintegrin-like and metallopeptidase (reprolysin type	-0.44	0.106	-0.49	0.594	-0.04	0.319	0.010196	0.583036	0.470837
Adk	adenosine kinase	-0.13	0.811	-0.45	0.522	-0.69	0.033	0.000374	0.069532	0.894293
AF251705	cDNA sequence AF251705	-0.78	0.669	-0.33	0.328	-0.21	0.471	0.000186	0.795369	0.287966
AF529169	cDNA sequence AF529169	-0.31	0.078	-0.43	0.428	-0.44	0.711	0.001723	0.699153	0.433986
Aif1	allograft inflammatory factor 1	-0.65	1.004	-0.61	0.78	-0.55	0.194	4.81E-08	0.323408	0.1704
Ak2	adenylate kinase 2	-0.51	0.076	-0.06	0.617	-0.38	0.316	0.011025	0.260981	0.983706
Aldh1l2	aldehyde dehydrogenase 1 family, member L2	-0.38	1.283	-0.22	0.139	-0.23	-0.43	0.008324	0.020038	0.003627
Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	-0.52	0.373	-0.29	0.4	-0.22	0.349	0.005873	0.881705	0.867784
Alg6	asparagine-linked glycosylation 6 homolog (yeast, alph	-0.41	0.413	-0.16	0.42	-0.5	0.317	0.004469	0.774562	0.908249
Alox5ap	arachidonate 5-lipoxygenase activating protein	-0.01	0.613	-0.64	0.644	-0.28	-0.27	0.00993	0.149636	0.102864
Amz1	archaelysin family metallopeptidase 1	-0.26	0.051	-0.26	1.014	-0.38	-0.13	0.013072	0.085599	0.150027
Angpt1	angiopoietin 1	-0.39	0.598	-0.24	0.48	-0.63	0.284	0.000598	0.531269	0.899668
Ankrd10	ankyrin repeat domain 10	-0.12	0.922	-0.36	0.239	-0.5	-0.07	0.005814	0.068281	0.561907
Anxa2	annexin A2	-0.12	-0.32	-0.19	0.568	-0.62	0.665	0.012566	0.373505	0.044415
Anxa3	annexin A3	-0.61	1.122	-0.74	0.581	-0.76	0.583	3.87E-11	0.20768	0.570939
Anxa4	annexin A4	0.269	0.565	-0.5	0.233	-0.73	0.198	0.008585	0.055422	0.546405
Anxa5	annexin A5	-0.19	0.561	-0.43	0.537	-0.5	0.103	0.002535	0.441503	0.82711

Ap4m1	adaptor-related protein complex AP-4, mu 1	-0.19	0.649	-0.36	0.339	-0.62	0.267	0.001601	0.40064	0.94664
Apaf1	apoptotic peptidase activating factor 1	-0.19	0.952	-0.5	0.3	-0.58	0.133	0.000354	0.089852	0.728154
Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange f	-0.25	0.741	0.065	0.371	-0.86	0.028	0.00316	0.041471	0.447215
Arhgap25	Rho GTPase activating protein 25	-0.39	0.59	-0.29	0.444	-0.68	0.419	0.000221	0.685009	0.819853
Arhgap5	Rho GTPase activating protein 5	0.008	0.916	-0.31	0.078	-0.64	0.041	0.007947	0.031552	0.675732
Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	-0.29	0.258	-0.26	0.47	-0.57	0.445	0.00319	0.854886	0.739694
Arid4b	AT rich interactive domain 4B (RBP1-like)	-0.25	0.854	-0.21	0.028	-0.71	0.392	0.001085	0.230167	0.231506
Arl8b	ADP-ribosylation factor-like 8B	-0.08	0.787	-0.35	0.127	-0.52	0.129	0.009188	0.159501	0.807122
Arpc1b	actin related protein 2/3 complex, subunit 1B	-0.83	0.48	-0.46	0.676	-0.26	0.523	9.99E-06	0.458616	0.613866
Arsk	arylsulfatase K	-0.46	0.972	-0.14	0.253	-0.27	-0.21	0.011191	0.244708	0.056826
Asb6	ankyrin repeat and SOCS box-containing 6	-0.46	0.59	-0.51	0.502	-0.2	0.183	0.001455	0.961107	0.46481
Aspg	asparaginase homolog (S. cerevisiae)	-0.62	1.052	-0.44	0.446	-0.86	0.584	6.17E-09	0.328376	0.243577
Asph	aspartate-beta-hydroxylase	-0.24	0.936	-0.48	0.009	-0.35	0.237	0.002884	0.134789	0.456802
Atg10	autophagy-related 10 (yeast)	-0.36	0.193	-0.21	0.415	-0.59	0.609	0.00195	0.829707	0.498848
Atp4a	ATPase, H+/K+ exchanging, gastric, alpha polypeptide	-0.22	0.35	-0.61	0.803	-0.26	-0.01	0.003094	0.704305	0.131542
Atp6v0d2	ATPase, H+ transporting, lysosomal V0 subunit D2	-0.06	0.541	-0.45	0.11	-0.44	0.359	0.011977	0.399339	0.913184
Atpbd3	ATP binding domain 3	-0.45	0.189	-0.28	0.61	-0.25	0.24	0.0098	0.632085	0.802968
AU020206	expressed sequence AU020206	-0.86	0.966	-0.75	0.976	-0.68	0.542	2.95E-14	0.622031	0.247798
Axl	AXL receptor tyrosine kinase	-0.4	0.473	-0.62	0.519	-0.54	0.661	1.59E-05	0.913532	0.821706
B2m	beta-2 microglobulin	-0.54	1.008	-0.6	0.788	-0.82	0.311	2.75E-09	0.108029	0.664128
B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltran	-0.46	0.269	-0.46	0.412	-0.19	0.496	0.003338	0.707097	0.951389
Bag2	BCL2-associated athanogene 2	-0.67	0.456	0.019	0.634	-0.54	0.209	0.000894	0.187298	0.661126
Bag3	BCL2-associated athanogene 3	0.136	0.591	-0.69	-0.04	-0.37	0.419	0.011773	0.058644	0.850503
BC002059	cDNA sequence BC002059	-0.39	0.731	-0.31	0.333	-0.22	-0.03	0.011395	0.623805	0.321263
BC016495	cDNA sequence BC016495	-0.23	0.651	-0.26	0.334	-0.42	0.017	0.013965	0.40659	0.770561
BC028528	cDNA sequence BC028528	-0.63	0.438	-0.11	0.114	-0.35	0.651	0.002516	0.708235	0.291298
BC052040	cDNA sequence BC052040	-0.74	0.633	0.283	0.199	-0.5	0.26	0.005545	0.419775	0.049271
Bcas2	breast carcinoma amplified sequence 2	-0.08	0.892	-0.39	0.112	-0.56	0.128	0.004093	0.080841	0.725634
Bcl2a1a	B-cell leukemia/lymphoma 2 related protein A1a	-0.86	0.933	-0.69	0.67	-0.66	0.787	2.12E-12	0.941147	0.55068
Blnk	B-cell linker	-0.5	1.046	-0.67	0.458	-0.48	0.303	1.46E-06	0.271512	0.346061
Brd4	bromodomain containing 4	-0.78	-0.03	-0.37	0.818	-0.16	0.592	0.000205	0.036945	0.656878
Btg1	B-cell translocation gene 1, anti-proliferative	-0.16	0.92	-0.33	-0.11	-0.66	0.438	0.001181	0.090246	0.22447
C1qa	complement component 1, q subcomponent, alpha po	-0.8	1.183	-0.7	0.589	-0.71	0.644	5.36E-13	0.39868	0.172469
C1qb	complement component 1, q subcomponent, beta poly	-0.73	1.228	-0.64	0.747	-0.76	0.356	4.11E-12	0.097212	0.124443

C1qc	complement component 1, q subcomponent, C chain	-0.93	0.977	-0.76	0.847	-0.6	0.657	4.87E-14	0.995766	0.25767
C3ar1	complement component 3a receptor 1	-0.93	0.755	-0.76	0.745	-0.51	0.875	1.68E-12	0.411516	0.770822
C5ar1	complement component 5a receptor 1	-0.09	-0.18	-0.45	0.452	-0.53	0.788	0.004313	0.661415	0.053107
C78859	expressed sequence C78859	-0.34	1.152	-0.26	0.259	-0.72	0.056	9.68E-05	0.029292	0.183693
C85492	expressed sequence C85492	-0.49	0.369	0.006	0.243	-0.45	0.401	0.012827	0.820242	0.519953
Capg	capping protein (actin filament), gelsolin-like	-0.51	0.957	-0.56	0.54	-0.65	0.373	6.02E-07	0.374618	0.661865
Casp8	caspase 8	-0.3	0.454	-0.52	0.704	-0.46	0.2	0.000524	0.702071	0.582841
Ccdc59	coiled-coil domain containing 59	-0.34	0.434	-0.51	0.102	-0.45	0.837	0.000374	0.378399	0.480553
Ccl3	chemokine (C-C motif) ligand 3	-0.87	1.18	-0.76	0.653	-0.69	0.693	6.66E-15	0.51304	0.137896
Ccl6	chemokine (C-C motif) ligand 6	-0.85	1.335	-0.73	0.709	-0.84	0.595	0	0.073717	0.036579
Ccl9	chemokine (C-C motif) ligand 9	-0.11	0.93	-0.51	0.437	-0.56	-0.09	0.000867	0.042299	0.560592
Ccnk	cyclin K	-0.47	0.436	-0.38	0.599	-0.29	0.198	0.002113	0.863012	0.680447
Ccr5	chemokine (C-C motif) receptor 5	-0.21	0.635	-0.37	0.542	-0.41	-0.11	0.007307	0.278313	0.547719
Cd14	CD14 antigen	-0.62	1.133	-0.84	0.592	-0.88	0.793	6.44E-15	0.104419	0.675741
Cd151	CD151 antigen	-0.26	0.342	-0.12	0.426	-0.69	0.368	0.004244	0.579586	0.653412
Cd163	CD163 antigen	-0.1	0.352	-0.27	0.157	-0.64	0.558	0.006879	0.801056	0.358668
Cd180	CD180 antigen	-0.6	0.415	-0.53	0.335	-0.31	0.795	6.01E-05	0.389312	0.911719
Cd200	CD200 antigen	-0.35	0.3	-0.2	0.38	-0.5	0.441	0.005363	0.909843	0.82452
Cd200r2	CD200 receptor 2	-0.12	0.568	-0.61	0.743	-0.51	4E-04	0.000596	0.239696	0.30345
Cd274	CD274 antigen	-0.36	0.356	-0.29	0.689	-0.37	0.044	0.006408	0.489178	0.653674
Cd300lf	CD300 antigen like family member F	-0.19	0.143	-0.46	0.737	-0.35	0.15	0.008581	0.72906	0.325323
Cd302	CD302 antigen	-0.41	0.305	-0.07	0.179	-0.54	0.613	0.005916	0.926442	0.327311
Cd33	CD33 antigen	-0.76	0.858	-0.46	0.157	-0.33	0.692	6.27E-06	0.462528	0.172914
Cd44	CD44 antigen	-0.2	0.763	-0.22	0.447	-0.58	-0.12	0.006005	0.097569	0.691831
Cd48	CD48 antigen	-0.58	0.766	-0.79	0.894	-0.86	0.707	2.4E-12	0.711361	0.713504
Cd53	CD53 antigen	-0.92	1.041	-0.76	0.644	-0.56	0.754	2.37E-13	0.711033	0.219384
Cd68	CD68 antigen	-0.81	1.27	-0.84	0.726	-0.7	0.569	5.55E-16	0.169138	0.076517
Cd83	CD83 antigen	-0.27	0.603	-0.22	-0.02	-0.48	0.467	0.009437	0.636353	0.412297
Cd84	CD84 antigen	-0.66	1.075	-0.66	0.653	-0.74	0.508	1.89E-10	0.356413	0.496344
Cd86	CD86 antigen	-0.46	1.073	-0.43	0.62	-0.92	0.263	4.86E-08	0.035747	0.585849
Cd9	CD9 antigen	-0.76	0.774	-0.38	0.898	-0.77	0.398	6.58E-09	0.181094	0.726933
Cdc6	cell division cycle 6 homolog ( <i>S. cerevisiae</i> )	-0.71	0.347	0.185	0.623	-0.54	0.203	0.002502	0.076886	0.565156
Cdc7	cell division cycle 7 ( <i>S. cerevisiae</i> )	-0.2	0.839	-0.35	-0.19	-0.43	0.437	0.006045	0.14268	0.296461
Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	-0.44	0.376	-0.51	0.525	-0.24	0.375	0.0014	0.948059	0.783145

Chpt1	choline phosphotransferase 1	-0.03	0.877	-0.17	0.045	-0.65	0.015	0.017568	0.04741	0.510126
Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase	-0.69	0.096	-0.14	0.231	-0.08	0.656	0.013148	0.155671	0.75113
Clec1a	C-type lectin domain family 1, member a	-0.64	0.37	-0.33	0.731	-0.4	0.368	0.000161	0.489427	0.861852
Clec5a	C-type lectin domain family 5, member a	-0.7	0.758	-0.37	0.229	-0.33	0.551	8.32E-05	0.812337	0.307833
Clec7a	C-type lectin domain family 7, member a	-0.8	1.381	-0.79	0.708	-0.83	0.554	0	0.024385	0.029864
Clic1	chloride intracellular channel 1	-0.59	0.534	-0.19	0.677	-0.62	0.305	9.28E-05	0.353383	0.888569
Cmklr1	chemokine-like receptor 1	-0.37	0.764	-0.23	-0.09	-0.51	0.545	0.001945	0.481331	0.180576
Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	-0.35	0.504	-0.77	0.702	-0.43	0.437	1.53E-05	0.919828	0.442869
Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	-0.34	0.917	-0.33	0.19	-0.59	0.29	0.000373	0.274136	0.444001
Cmtm7	CKLF-like MARVEL transmembrane domain containing 7	-0.48	0.691	-0.14	0.417	-0.21	-0.16	0.019624	0.508255	0.196511
Cnot4	CCR4-NOT transcription complex, subunit 4	-0.05	0.576	-0.28	0.452	-0.55	-0.09	0.018194	0.158075	0.910864
Cntn6	contactin 6	-0.58	0.178	0.002	0.373	-0.29	0.393	0.019976	0.452143	0.80339
Col11a1	collagen, type XI, alpha 1	-0.11	0.386	-0.08	0.083	-0.94	0.716	0.001556	0.680765	0.028883
Commd6	COMM domain containing 6	-0.01	0.204	-0.08	0.435	-0.91	0.384	0.006963	0.286055	0.173361
Commd8	COMM domain containing 8	-0.09	0.559	-0.34	-0.13	-0.49	0.557	0.013061	0.299646	0.396643
Creg1	cellular repressor of E1A-stimulated genes 1	-0.69	-0.13	-0.06	0.711	-0.21	0.432	0.008033	0.044189	0.935507
Crip1	cysteine-rich protein 1 (intestinal)	-0.51	0.364	-0.28	0.38	-0.33	0.461	0.002827	0.886613	0.943437
Csf1	colony stimulating factor 1 (macrophage)	-0.05	0.875	-0.35	-0.09	-0.56	0.268	0.007564	0.070911	0.48354
Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity	-0.34	0.353	-0.95	0.417	0.088	0.5	0.000794	0.152535	0.233801
Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (alpha)	-0.71	0.495	-0.41	0.759	-0.17	0.153	0.00029	0.599451	0.227228
Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (alpha)	-0.66	0.428	-0.56	0.519	-0.06	0.447	0.000374	0.542576	0.511903
Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta	-0.47	0.695	-1.06	0.363	-0.31	0.902	2.51E-08	0.027035	0.849963
Ctsa	cathepsin A	-0.65	0.135	-0.22	0.721	-0.39	0.482	0.000535	0.215664	0.963998
Ctsb	cathepsin B	-0.67	-0	-0.38	0.532	-0.15	0.735	0.000928	0.092539	0.894886
Ctsc	cathepsin C	-0.51	0.637	-0.03	0.51	-0.85	0.366	7.43E-05	0.225404	0.41377
Ctsd	cathepsin D	-0.9	1.182	-0.6	0.726	-0.77	0.575	2.75E-14	0.439262	0.086819
Ctsl	cathepsin L	-0.7	0.387	-0.37	0.916	-0.52	0.391	5.95E-06	0.244781	0.784883
Ctsz	cathepsin Z	-0.63	0.799	-0.22	0.765	-0.62	0.057	1.69E-05	0.118286	0.38164
Cttnbp2nl	CTTNBP2 N-terminal like	-0.43	0.908	-0.4	0.564	-0.45	-0.06	0.000267	0.205564	0.251063
Cx3cr1	chemokine (C-X3-C) receptor 1	-0.41	0.704	-0.36	0.004	-0.31	0.486	0.002983	0.50837	0.461017
Cxadr	coxsackie virus and adenovirus receptor	-0.26	0.28	-0.18	0.88	-0.87	0.208	0.000235	0.057765	0.551239
Cyba	cytochrome b-245, alpha polypeptide	-0.68	0.648	-0.67	0.684	-0.54	0.69	3.64E-08	0.92891	0.964615
Cybb	cytochrome b-245, beta polypeptide	-0.73	0.36	-0.41	0.37	-0.15	0.665	0.000353	0.304689	0.837754
Cyld	cyldromatosis (turban tumor syndrome)	-0.21	0.62	-0.28	0.305	-0.62	0.265	0.002942	0.449032	0.872759

Cyp2c54	cytochrome P450, family 2, subfamily c, polypeptide 54	-0.25	0.98	-0.23	0.048	-0.38	-0.05	0.014732	0.132808	0.20736
Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	-0.08	0.117	-0.55	0.117	-0.66	1.075	0.000266	0.305704	0.019927
Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	-0.19	0.613	-0.69	0.241	-0.23	0.334	0.002834	0.347838	0.829437
D14Ertd66	DNA segment, Chr 14, ERATO Doi 668, expressed	-0.26	0.361	-0.69	0.873	-0.7	0.478	3.14E-06	0.716188	0.2086
D17H6S56	DNA segment, Chr 17, human D6S56E 5	-0.71	0.523	-0.85	0.554	0.159	0.445	4.19E-05	0.19502	0.089114
Daam2	dishevelled associated activator of morphogenesis 2	0.287	0.491	-0.34	0.003	-0.96	0.534	0.004719	0.068685	0.050779
Dap	death-associated protein	-0.74	-0.06	-0.07	0.586	-0.21	0.567	0.004425	0.057234	0.975086
Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	-0.43	-0.02	-0.39	0.109	-0.11	0.884	0.011171	0.092529	0.574469
Dcun1d1	DCN1, defective in cullin neddylation 1, domain containing	0.004	0.807	-0.06	0.043	-0.86	0.147	0.00959	0.039415	0.27617
Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-0.14	0.775	-0.31	0.174	-0.56	0.158	0.005657	0.207724	0.775484
Def8	differentially expressed in FDCP 8	-0.33	0.723	-0.16	0.201	-0.38	0.044	0.018497	0.501067	0.463783
Dhrs3	dehydrogenase/reductase (SDR family) member 3	-0.4	0.526	-0.27	0.733	-0.53	0.03	0.001008	0.251129	0.72546
Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-0.03	0.735	-0.22	0.055	-0.62	0.16	0.017382	0.148806	0.645031
Dock2	dedicator of cyto-kinesis 2	-0.44	0.904	-0.59	0.705	-0.79	0.339	1.03E-07	0.191543	0.903481
Dpy19l3	dpy-19-like 3 (C. elegans)	0.214	0.275	-0.33	0.709	-0.76	-0.1	0.017397	0.043372	0.251637
Dpy19l4	dpy-19-like 4 (C. elegans)	-0.41	0.755	-0.3	0.52	-0.61	0.157	0.000266	0.339819	0.748597
Dsn1	DSN1, MIND kinetochore complex component, homolog	0.051	0.391	-0.4	-0.03	-0.69	0.718	0.004651	0.332818	0.123116
Dtx4	deltex 4 homolog (Drosophila)	-0.15	0.722	-0.91	0.16	-0.09	0.354	0.00127	0.060914	0.537849
Duox1	dual oxidase 1	-0.11	0.49	-0.43	0.407	-0.42	0.125	0.011319	0.551138	0.882511
Eef1d	eukaryotic translation elongation factor 1 delta (guanine)	-0.04	0.669	-0.28	0.052	-0.64	0.317	0.008913	0.228538	0.584212
EG232599	predicted gene, EG232599	-0.7	0.127	0.108	0.286	-0.36	0.616	0.008882	0.224077	0.370153
EG574403	predicted gene, EG574403	-0.34	0.65	-0.25	0.01	-0.52	0.553	0.002311	0.653028	0.33129
EG634650	predicted gene, EG634650	-0.29	0.28	-0.4	0.739	-0.4	0.135	0.00346	0.596926	0.538707
EG665937	predicted gene, EG665937	-0.18	0.64	-0.63	0.449	-0.83	0.635	3.48E-06	0.380435	0.477191
Ehbp111	EH domain binding protein 1-like 1	-0.3	0.569	-0.06	0.296	-0.88	0.462	0.000587	0.410626	0.241742
Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	-0.47	0.138	0.169	0.695	-0.68	0.207	0.006895	0.051644	0.818488
Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural	-0.11	0.497	-0.56	0.422	-0.26	0.077	0.013276	0.59142	0.572784
Elk3	ELK3, member of ETS oncogene family	-0.15	0.733	-0.31	0.16	-0.67	0.326	0.002041	0.260234	0.649328
Emr1	EGF-like module containing, mucin-like, hormone receptor	-0.51	0.323	-0.15	0.658	-0.44	0.203	0.002963	0.380663	0.943755
ENSMUSG	predicted gene, ENSMUSG00000073738	-0.53	0.222	-0.11	0.584	-0.24	0.148	0.018592	0.42965	0.817877
Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	-0.25	0.388	-0.56	0.014	-0.15	0.629	0.009477	0.237329	0.942485
Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	-0.59	0.098	-0.33	0.188	-0.06	0.76	0.007659	0.129512	0.88537
Etohd2	ethanol decreased 2	-0.33	0.637	-0.45	0.475	-0.76	0.52	2.12E-05	0.611622	0.777382
Exdl1	exonuclease 3'-5' domain-like 1	-0.26	0.297	-0.27	0.433	-0.55	0.408	0.004436	0.881809	0.804268

Eya4	eyes absent 4 homolog (Drosophila)	-0.37	0.732	-0.43	0.278	-0.48	0.371	0.000533	0.623831	0.795597
F3	coagulation factor III	-0.32	0.619	-0.39	0.15	-0.38	0.417	0.003398	0.683229	0.794785
Fam114a1	family with sequence similarity 114, member A1	-0.45	0.47	0.222	0.452	-0.75	0.146	0.006332	0.103389	0.418913
Fam116a	family with sequence similarity 116, member A	-0.21	0.818	-0.17	0.151	-0.73	0.243	0.002052	0.177889	0.414462
Fam164c	family with sequence similarity 164, member C	-0.26	0.289	-0.06	0.439	-0.84	0.486	0.001681	0.463211	0.295025
Fam176a	family with sequence similarity 176, member A	-0.24	0.663	-0.58	-0.06	-0.34	0.654	0.001299	0.144587	0.680956
Fam70a	family with sequence similarity 70, member A	-0.31	0.816	0.091	0.201	-0.84	0.154	0.002484	0.097335	0.166163
Fam83d	family with sequence similarity 83, member D	-0.21	0.542	-0.1	0.035	-0.79	0.599	0.002445	0.654841	0.10947
Fbxl5	F-box and leucine-rich repeat protein 5	-0.28	0.896	-0.14	-0.05	-0.45	0.147	0.013719	0.254116	0.20606
Fbxo8	F-box protein 8	-0.16	0.689	-0.14	0.267	-0.9	0.335	0.000808	0.168108	0.363389
Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide	-0.82	1.197	-0.59	0.782	-0.75	0.378	1.82E-12	0.163923	0.087649
Fcgr1	Fc receptor, IgG, high affinity I	-0.72	0.782	-0.59	0.508	-0.13	0.307	3.34E-05	0.895076	0.156002
Fcgr2b	Fc receptor, IgG, low affinity IIb	-0.65	1.302	-0.81	0.618	-0.55	0.291	8.38E-11	0.070653	0.040953
Fcgr3	Fc receptor, IgG, low affinity III	-0.7	1.326	-0.74	0.512	-0.55	0.355	1.62E-10	0.089447	0.039302
Fcrls	Fc receptor-like S, scavenger receptor	-0.8	1.197	-0.59	0.555	-0.64	0.481	1.37E-10	0.428896	0.083771
Ffar2	free fatty acid receptor 2	-0.34	0.565	-0.42	0.027	-0.1	0.366	0.019505	0.492665	0.703522
Fli1	Friend leukemia integration 1	-0.65	0.025	-0.29	0.741	-0.09	0.341	0.004412	0.160884	0.59007
Fmn1	formin 1	-0.42	0.793	-0.19	0.305	-0.45	0.078	0.00356	0.448034	0.409879
Fnip2	folliculin interacting protein 2	-0.52	0.562	-0.41	0.692	-0.15	-0.06	0.002557	0.708172	0.151056
Frmd4a	FERM domain containing 4A	-0.4	0.992	-0.09	0.145	-0.37	-0.13	0.011886	0.186581	0.084513
Frs2	fibroblast growth factor receptor substrate 2	-0.31	0.242	-0.48	0.436	-0.2	0.367	0.009604	0.917185	0.803768
Ftsjd1	FtsJ methyltransferase domain containing 1	-0.17	0.661	-0.31	0.38	-0.43	-0.04	0.013042	0.300161	0.767091
Fuca2	fucosidase, alpha-L- 2, plasma	-0.06	0.176	-0.25	0.593	-0.72	0.282	0.006583	0.418931	0.41502
Fxyd4	FXDY domain-containing ion transport regulator 4	-0.36	0.322	-0.49	0.521	-0.1	0.181	0.011266	0.981625	0.498743
G3bp1	Ras-GTPase-activating protein SH3-domain binding p	-0.34	0.468	-0.79	0.184	0.087	0.472	0.004133	0.145285	0.591728
Gabre	gamma-aminobutyric acid (GABA-A) receptor, subunit	-0.18	0.011	-0.39	0.175	-0.36	0.761	0.014723	0.526643	0.317729
Gal	galanin	-0.57	0.862	-0.39	0.248	-0.36	0.356	0.000208	0.746428	0.313833
Gal3st4	galactose-3-O-sulfotransferase 4	-0.12	0.68	-0.25	0.344	-0.57	-0.01	0.011302	0.177489	0.914795
Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	-0.14	0.453	-0.53	0.572	-0.28	-0.01	0.01063	0.618516	0.395635
Galnt12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	-0.42	0.155	-0.7	0.34	0.259	0.419	0.019323	0.171509	0.347004
Galr1	galanin receptor 1	-0.21	0.377	-0.38	0.343	-0.36	0.287	0.013441	0.920206	0.978292
Gcc1	golgi coiled coil 1	0.103	0.077	-0.21	0.43	-0.85	0.443	0.011537	0.506184	0.095584
Gen1	Gen homolog 1, endonuclease (Drosophila)	-0.06	0.582	-0.09	0.406	-0.86	0.09	0.005376	0.070324	0.735702
Gfap	glial fibrillary acidic protein	-0.63	1.301	-0.52	0.398	-0.78	0.426	1.02E-09	0.063026	0.079318

Ggta1	glycoprotein galactosyltransferase alpha 1, 3	-0.73	0.607	-0.76	1.044	-0.7	0.673	5.49E-12	0.607659	0.464078
Glipr1	GLI pathogenesis-related 1 (glioma)	-0.41	0.685	-0.63	0.512	-0.46	0.406	3.76E-05	0.758027	0.872553
Gbra2	glycine receptor, alpha 2 subunit	-0.56	0.076	0.075	0.274	-0.47	0.67	0.009252	0.338214	0.296929
Glt8d1	glycosyltransferase 8 domain containing 1	0.192	0.604	-0.3	0.28	-0.84	0.1	0.009839	0.040951	0.664006
Gm1604A	gene model 1604A, (NCBI)	-0.46	0.279	-0.04	0.651	-0.55	0.198	0.00437	0.23611	0.994194
Gmfg	glia maturation factor, gamma	-0.16	0.443	-0.16	0.663	-0.65	-0.08	0.008768	0.095419	0.901426
Gngt2	guanine nucleotide binding protein (G protein), gamma	-0.43	0.771	-0.33	0.267	-0.4	0.25	0.001384	0.676893	0.539154
Gp49a	glycoprotein 49 A	-0.7	0.977	-0.92	0.906	-0.84	0.742	1.11E-16	0.513983	0.780031
Gpr65	G-protein coupled receptor 65	-0.22	0.423	-0.68	0.186	-0.42	0.775	0.000308	0.289087	0.629419
Gpr84	G protein-coupled receptor 84	-0.27	0.509	-0.57	0.84	-0.97	0.528	1.59E-07	0.279654	0.297189
Gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)	-0.43	0.345	-0.48	0.457	-0.42	0.605	0.00035	0.885326	0.915559
Grik2	glutamate receptor, ionotropic, kainate 2 (beta 2)	-0.01	0.86	-0.37	-0.12	-0.58	0.312	0.0072	0.055949	0.466138
Grin2d	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	-0.37	0.387	-0.53	0.278	-0.17	0.475	0.004677	0.659957	0.963843
Grn	granulin	-0.54	1.264	-0.39	0.455	-0.77	0.158	1.63E-07	0.029148	0.099012
Gsn	gelsolin	-0.56	0.101	-0.11	0.828	-0.44	0.249	0.00229	0.117198	0.873383
Gtf2a2	general transcription factor II A, 2	-0.3	-0.2	-0.26	0.475	-0.41	0.709	0.009781	0.344479	0.240641
Gusb	glucuronidase, beta	-0.58	1.164	-0.45	0.189	-0.82	0.668	1.1E-08	0.159053	0.054739
H2afy2	H2A histone family, member Y2	-0.31	0.316	-0.24	0.155	-0.41	0.552	0.011443	0.93001	0.663764
H2-D1	histocompatibility 2, D region locus 1	-0.82	0.021	-0.47	0.926	-0.15	0.576	2.63E-05	0.032326	0.395044
H2-L	histocompatibility 2, D region	-0.8	0.491	-0.49	0.583	-0.16	0.498	4.42E-05	0.507917	0.520121
H2-Ob	histocompatibility 2, O region beta locus	-0.2	0.901	-0.76	0.46	-0.29	-0	0.000395	0.13629	0.203747
H60c	histocompatibility 60c	-0.34	0.85	-0.37	0.163	-0.34	0.144	0.004191	0.396057	0.428103
Hap1	huntingtin-associated protein 1	-0.42	0.232	-0.22	0.21	-0.26	0.531	0.01686	0.757488	0.841521
Havcr2	hepatitis A virus cellular receptor 2	-0.65	0.882	-0.36	0.558	-0.62	0.347	2.46E-06	0.56862	0.447205
Hcrt	hypocretin	-0.43	0.851	-0.18	0.235	-0.26	-0.08	0.013496	0.450557	0.169984
Hells	helicase, lymphoid specific	0.052	0.471	-0.47	0.385	-0.63	0.234	0.00537	0.306496	0.700702
Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl term	-0.16	0.509	-0.39	-0.17	-0.35	0.627	0.014819	0.260085	0.459245
Herc5	hect domain and RLD 5	-0.45	0.587	-0.25	0.715	-0.72	0.216	8.02E-05	0.218976	0.984049
Hexa	hexosaminidase A	-0.29	0.962	-0.38	0.36	-0.55	0.026	0.00056	0.121507	0.466408
Hexb	hexosaminidase B	-0.78	1.243	-0.65	0.742	-0.66	0.31	1.05E-11	0.158011	0.046577
Hgf	hepatocyte growth factor	-0.71	0.52	-0.05	0.167	-0.12	0.317	0.014259	0.803762	0.228056
Hhex	hematopoietically expressed homeobox	-0.46	0.572	-0.21	0.201	-0.67	0.672	0.000202	0.969876	0.261395
Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	-0.41	0.504	-0.3	0.638	-0.55	0.214	0.000606	0.508775	0.951963
Hsp25-ps1	heat shock protein 25, pseudogene 1	-0.04	0.778	-0.55	0.145	-0.43	0.176	0.00553	0.126064	0.940586

Hspa4l	heat shock protein 4 like	-0.09	0.63	-0.09	0.366	-0.85	0.113	0.004329	0.082827	0.695997
Hspb6	heat shock protein, alpha-crystallin-related, B6	-0.42	0.021	-0.05	0.847	-0.43	0.081	0.014202	0.085941	0.714561
Htr4	5 hydroxytryptamine (serotonin) receptor 4	-0.4	1.027	-0.25	0.405	-0.55	-0.1	0.000552	0.079322	0.198264
Iah1	isoamyl acetate-hydrolyzing esterase 1 homolog (S. ce	-0.15	0.789	-0.39	0.019	-0.59	0.421	0.001754	0.196422	0.538571
Ica1l	islet cell autoantigen 1-like	-0.12	0.644	-0.35	-0.08	-0.4	0.386	0.018731	0.308599	0.631624
Icam1	intercellular adhesion molecule 1	-0.35	-0.06	-0.33	0.443	-0.48	0.821	0.001574	0.417683	0.225089
Ifi27	interferon, alpha-inducible protein 27	-0.42	0.232	-0.45	0.881	-0.99	0.812	2.57E-08	0.329888	0.058689
Ifi30	interferon gamma inducible protein 30	-0.14	0.624	-0.42	0.27	-0.76	0.506	0.000293	0.380496	0.549839
Ifi35	interferon-induced protein 35	-0.5	0.402	-0.03	0.572	-0.34	-0.01	0.017884	0.331424	0.646764
Ifit3	interferon-induced protein with tetratricopeptide repeat	-0.42	0.199	-0.16	0.596	-0.52	0.356	0.00376	0.488586	0.913466
Ifitm3	interferon induced transmembrane protein 3	-0.47	-0.2	-0.27	0.813	-0.13	0.29	0.018313	0.123732	0.351093
Ifnar2	interferon (alpha and beta) receptor 2	0.479	0.225	-0.51	0.02	-0.93	0.692	0.006281	0.077994	0.004565
Igbb1	immunoglobulin (CD79A) binding protein 1	-0.85	0.534	-0.28	0.371	0.294	0.07	0.013733	0.503305	0.027492
Igf1	insulin-like growth factor 1	-0.33	1.175	-0.77	0.393	-0.67	0.353	9.17E-08	0.023906	0.606467
Igf2r	insulin-like growth factor 2 receptor	-0.66	0.484	-0.08	0.534	-0.19	0.022	0.010143	0.499316	0.309971
Igsf5	immunoglobulin superfamily, member 5	-0.41	0.186	-0.4	0.637	-0.46	0.501	0.00071	0.736594	0.726457
Ihh	Indian hedgehog	-0.39	0.71	-0.25	0.431	-0.28	-0.11	0.010991	0.472527	0.311352
Il13ra1	interleukin 13 receptor, alpha 1	-0.74	0.03	0.022	0.332	-0.3	0.724	0.004899	0.103716	0.471116
Il2rg	interleukin 2 receptor, gamma chain	-0.58	0.486	-0.34	0.249	-0.02	0.302	0.011378	0.778631	0.471167
Il6ra	interleukin 6 receptor, alpha	-0.23	0.145	-0.57	-0.1	-0.17	0.97	0.006878	0.046022	0.36307
Ino80d	INO80 complex subunit D	0.059	0.535	-0.61	0.486	-0.6	0.182	0.001822	0.215985	0.573445
Inpp5d	inositol polyphosphate-5-phosphatase D	-0.65	0.869	-0.67	0.734	-0.44	0.312	2.38E-07	0.790734	0.275409
Irak4	interleukin-1 receptor-associated kinase 4	-0.13	0.316	-0.63	0.034	-0.27	0.725	0.005682	0.194803	0.653451
Irf5	interferon regulatory factor 5	-0.19	0.854	-0.87	0.769	-0.7	0.24	1.95E-07	0.077258	0.317727
Irf9	interferon regulatory factor 9	-0.42	0.476	-0.35	0.793	-0.43	0.019	0.000988	0.350734	0.483798
Itch	itchy, E3 ubiquitin protein ligase	-0.21	0.761	-0.05	0.471	-0.6	-0.28	0.015135	0.033684	0.532781
Itgam	integrin alpha M	-0.35	0.869	-0.47	0.479	-0.43	0.024	0.000471	0.279513	0.410089
Itgax	integrin alpha X	-0.68	1.4	-0.54	0.558	-0.61	0.087	2.23E-09	0.024624	0.008848
Itgb2	integrin beta 2	-0.78	1.136	-0.71	0.767	-0.82	0.606	1.62E-14	0.32223	0.378861
Itpril2	inositol 1,4,5-triphosphate receptor interacting protein-	-0.28	0.462	-0.36	0.645	-0.47	0.068	0.003144	0.471486	0.741675
Jakmip3	janus kinase and microtubule interacting protein 3	-0.81	0.45	-0.21	0.491	0.138	0.063	0.011926	0.499932	0.085729
Jmjd6	jumonji domain containing 6	-0.02	0.56	-0.28	-0	-0.82	0.624	0.00189	0.305089	0.122476
Kcnj3	potassium inwardly-rectifying channel, subfamily J, me	-0.36	0.367	-0.22	0.546	-0.36	0.095	0.013213	0.633911	0.86101
Kcnk6	potassium inwardly-rectifying channel, subfamily K, me	-0.84	0.406	-0.39	0.476	-0.23	0.708	3.04E-05	0.259861	0.766302



Kctd12	potassium channel tetramerisation domain containing	-0.05	0.869	-0.34	0.02	-0.61	0.202	0.00552	0.075874	0.603557
Kif3b	kinesin family member 3B	-0.87	0.322	-0.43	0.403	-0.17	0.853	2.43E-05	0.080762	0.801124
Klhl20	kelch-like 20 (Drosophila)	0.039	0.579	-0.25	0.545	-0.72	-0.14	0.011109	0.038596	0.896013
Klhl6	kelch-like 6 (Drosophila)	-0.41	0.934	-0.56	0.557	-0.77	0.381	4.76E-07	0.212126	0.900359
Krt32	keratin 32	0.01	0.639	-0.23	0.411	-0.67	-0.1	0.015616	0.064223	0.991359
Lair1	leukocyte-associated Ig-like receptor 1	-0.19	0.882	-0.79	0.67	-0.97	0.504	3.53E-09	0.047284	0.630847
Laptm5	lysosomal-associated protein transmembrane 5	-0.69	1.309	-0.64	0.651	-0.8	0.374	2.59E-12	0.041496	0.100815
Larp7	La ribonucleoprotein domain family, member 7	-0.44	0.077	0.157	0.384	-0.69	0.567	0.007743	0.29395	0.206315
Lass6	LAG1 homolog, ceramide synthase 6	0.07	0.666	-0.45	0.24	-0.53	0.066	0.014015	0.123129	0.982609
Lca5	Leber congenital amaurosis 5 (human)	-0.14	0.634	-0.32	0.034	-0.46	0.337	0.013017	0.416177	0.721312
Lcorl	ligand dependent nuclear receptor corepressor-like	-0.01	0.773	-0.11	-0.05	-0.8	0.268	0.010322	0.084401	0.221677
Lcp1	lymphocyte cytosolic protein 1	-0.6	1.233	-0.53	0.508	-0.56	0.141	2.06E-07	0.106663	0.069878
Lcp2	lymphocyte cytosolic protein 2	-0.04	0.984	-0.57	0.372	-0.39	-0.26	0.003916	0.021345	0.230745
Ldlrad3	low density lipoprotein receptor class A domain contain	-0.4	0.655	-0.3	0.163	-0.6	0.59	0.000345	0.788664	0.411916
Ldoc1	leucine zipper, down-regulated in cancer 1	-0.46	0.698	-0.52	0.199	0.133	0.064	0.017722	0.58392	0.130433
Leprot	leptin receptor overlapping transcript	-0.06	0.909	-0.21	0.15	-0.75	0.063	0.003814	0.035297	0.552188
Lgals3	lectin, galactose binding, soluble 3	-0.71	0.016	-0.19	0.762	-0.57	0.769	2.25E-05	0.057399	0.51155
Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	-0.72	0.419	-0.23	0.927	-0.66	0.389	2.62E-06	0.104314	0.975743
Lgals9	lectin, galactose binding, soluble 9	-0.5	0.24	-0.84	0.658	-0.02	0.541	0.000128	0.310897	0.213559
Lgi4	leucine-rich repeat LGI family, member 4	-0.47	0.491	-0.22	0.511	-0.4	0.188	0.003237	0.712811	0.827656
Lhx9	LIM homeobox protein 9	0.026	0.915	-0.39	-0.28	-0.55	0.362	0.009286	0.022369	0.293532
Limk2	LIM motif-containing protein kinase 2	-0.32	0.072	-0.31	0.44	-0.3	0.453	0.016231	0.773147	0.798777
Lmf1	lipase maturation factor 1	-0.54	0.361	0.002	0.686	-0.35	-0.08	0.015269	0.161877	0.569814
Lnx2	ligand of numb-protein X 2	-0.63	0.31	-0.23	0.426	-0.1	0.31	0.010124	0.612564	0.685532
Lonp2	lon peptidase 2, peroxisomal	0.217	0.601	-0.14	0.107	-0.95	0.207	0.014966	0.033572	0.250365
Lpcat2	lysophosphatidylcholine acyltransferase 2	-0.42	0.198	0.042	0.622	-0.62	0.24	0.006998	0.181801	0.882359
Lpl	lipoprotein lipase	-0.83	0.434	-0.6	0.6	-0.4	0.913	6.96E-08	0.195173	0.971663
Lpxn	leupaxin	-0.6	0.399	-0.65	0.386	-0.15	0.712	0.000101	0.267935	0.946217
Lrmp	lymphoid-restricted membrane protein	-0.31	0.503	-0.37	0.389	-0.29	0.153	0.010667	0.867425	0.80967
Lrrc33	leucine rich repeat containing 33	-0.86	0.639	-0.59	0.403	-0.12	0.676	4.61E-06	0.252983	0.391772
Lrrc8a	leucine rich repeat containing 8A	-0.63	-0.02	-0.28	0.414	-0.1	0.662	0.006719	0.129909	0.969127
Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	-0.16	0.735	-0.19	0.493	-0.53	-0.25	0.013256	0.063303	0.578009
Lsp1	lymphocyte specific 1	-0.47	0.598	-0.48	0.154	0.025	0.277	0.011612	0.577217	0.412715
Lypd1	Ly6/Plaur domain containing 1	0.057	0.588	-0.71	0.558	-0.64	0.199	0.000371	0.148635	0.434348

Lyz1	lysozyme 1	-0.57	1.348	-0.57	0.264	-0.73	0.452	3.11E-09	0.030891	0.060816
Lyz2	lysozyme 2	-0.75	1.265	-0.79	0.662	-0.79	0.608	2.55E-15	0.114817	0.176629
Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family	-0.86	0.449	-0.77	0.759	0.311	0.243	5.33E-05	0.179386	0.005976
Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	0.082	0.563	-0.4	0.316	-0.62	0.105	0.012505	0.165379	0.901979
Mamdc2	MAM domain containing 2	-0.41	0.933	0.071	0.294	-0.52	-0.23	0.011623	0.065842	0.102472
Mapk1ip1	mitogen-activated protein kinase 1 interacting protein 1	-0.17	0.843	-0.22	0.054	-0.68	0.267	0.003142	0.165019	0.384138
Matn2	matrilin 2	-0.16	0.871	-0.26	0.077	-0.61	0.188	0.004181	0.137989	0.49484
Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	-0.03	0.775	-0.33	0.011	-0.68	0.333	0.00422	0.118015	0.51392
Med13	mediator complex subunit 13	-0.03	0.813	-0.2	0.061	-0.69	0.126	0.011166	0.076879	0.550899
Med19	mediator of RNA polymerase II transcription, subunit 19	-0.26	1.048	-0.14	-0.03	-0.45	-0.03	0.012955	0.088206	0.112087
Mettl11a	Methyltransferase like 11A (Mettl11a), mRNA	-0.24	0.713	-0.39	-0.01	-0.29	0.3	0.013705	0.369335	0.642812
Mettl6	methyltransferase like 6	-0.09	0.705	-0.74	0.243	-0.04	0.004	0.016081	0.184168	0.266144
Mfsd9	major facilitator superfamily domain containing 9	-0.42	0.733	-0.38	0.576	-0.76	0.364	1.24E-05	0.387372	0.926254
Minpp1	multiple inositol polyphosphate histidine phosphatase 1	-0.1	0.734	-0.19	0.122	-0.68	0.199	0.007984	0.180963	0.586468
Mlc1	megalencephalic leukoencephalopathy with subcortical maldevelopment 1	-0.16	0.386	-0.03	0.453	-0.73	0.142	0.013263	0.224458	0.797179
Mlh3	mutL homolog 3 (E coli)	-0.22	0.825	-0.45	0.478	-0.51	-0.02	0.001035	0.16444	0.602651
Mlph	melanophilin	-0.26	0.615	-0.35	0.235	-0.32	0.176	0.012323	0.661611	0.819366
Mlxipl	MLX interacting protein-like	-0.45	0.752	-0.44	0.537	-0.7	0.419	8.58E-06	0.564566	0.914248
Mobk12a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	-0.75	0.107	-0.31	0.501	0.052	0.477	0.005758	0.136816	0.731905
Morc3	microorchidia 3	-0.33	0.694	-0.1	0.258	-0.66	0.234	0.002992	0.392365	0.503822
Mpeg1	macrophage expressed gene 1	-1.04	1.015	-0.79	0.802	-0.5	0.721	1.78E-15	0.763413	0.075936
Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	-0.12	0.68	-0.63	0.475	-0.28	-0.04	0.004777	0.297788	0.344427
Mrpl32	mitochondrial ribosomal protein L32	-0.34	0.44	-0.27	0.097	-0.48	0.635	0.003311	0.850347	0.459981
Mrpl36	mitochondrial ribosomal protein L36	-0.41	0.661	-0.46	0.355	-0.35	0.306	0.001003	0.813175	0.788303
Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6c	-0.14	0.693	-0.51	0.309	-0.49	0.227	0.002006	0.32352	0.977138
Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6d	-0.1	0.755	-0.52	-0.07	-0.52	0.536	0.001652	0.113538	0.576556
Msn	moesin	-0.27	0.99	-0.59	0.642	-0.66	0.008	9.79E-06	0.041221	0.454774
Mt2	metallothionein 2	-0.79	0.072	-0.2	0.321	0.047	0.631	0.008818	0.067755	0.830138
Mtcp1	mature T-cell proliferation 1	-0.02	0.41	-0.18	0.356	-0.72	0.208	0.013829	0.312829	0.694126
Mttp	microsomal triglyceride transfer protein	-0.28	0.17	-0.3	0.047	-0.34	0.743	0.015381	0.537569	0.428647
Myc	myelocytomatosis oncogene	-0.22	-0.05	-0.63	0.596	-0.49	0.809	0.000235	0.571097	0.087192
Myo1e	myosin IE	-0.36	0.59	-0.4	0.568	-0.28	-0.02	0.004662	0.630388	0.411044
Myt1	myelin transcription factor 1	-0.54	-0.02	-0.19	0.955	-0.46	0.311	0.000909	0.065693	0.538247
Naalad2	N-acetylated alpha-linked acidic dipeptidase 2	-0.2	0.878	-0.53	0.263	-0.51	0.207	0.000597	0.169001	0.802487

Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease III)	-0.66	0.363	-0.19	0.74	-0.62	0.467	3.85E-05	0.264178	0.958522
Naip2	NLR family, apoptosis inhibitory protein 2	-0.45	0.787	-0.29	0.477	-0.63	0.223	0.000147	0.386534	0.68458
Naip5	NLR family, apoptosis inhibitory protein 5	-0.62	0.816	-0.47	0.279	-0.39	0.538	2.58E-05	0.746834	0.446135
Ncf1	neutrophil cytosolic factor 1	-0.75	-0	-0.3	0.775	-0.28	0.638	0.000156	0.058643	0.839542
Ncf2	neutrophil cytosolic factor 2	-0.65	1.064	-0.5	0.748	-0.91	0.425	9.6E-11	0.103564	0.531548
Nckap1l	NCK associated protein 1 like	-0.4	1.185	-0.44	0.352	-0.6	0.059	2.03E-05	0.048243	0.175701
Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcine	-0.39	0.79	0.015	-0.08	-0.5	0.281	0.013563	0.562434	0.104374
Nfe2l2	nuclear factor, erythroid derived 2, like 2	-0.18	0.563	-0.03	0.271	-0.66	0.116	0.018207	0.271222	0.684132
Nmnat3	nicotinamide nucleotide adenylyltransferase 3	-0.08	0.412	-0.36	0.341	-0.45	0.194	0.019369	0.645803	0.942855
Nol3	nucleolar protein 3 (apoptosis repressor with CARD do	-0.08	0.286	-0.78	0.134	-0.44	0.924	0.000264	0.113839	0.203219
Nov	nephroblastoma overexpressed gene	-0.17	0.714	-0.56	0.179	-0.32	0.244	0.004604	0.304659	0.864242
Npc2	Niemann Pick type C2	-0.5	0.229	-0.09	0.882	-0.59	0.145	0.001006	0.071981	0.894575
Npl	N-acetylneuraminate pyruvate lyase	-0.29	0.463	-0.31	0.149	-0.37	0.426	0.011079	0.863499	0.83862
Npy2r	neuropeptide Y receptor Y2	0.109	0.696	-0.52	0.039	-0.55	0.285	0.009012	0.078942	0.879084
Nsun7	NOL1/NOP2/Sun domain family, member 7	-0.1	0.218	-0.43	0.57	-0.62	0.397	0.002305	0.788661	0.41271
Nt5e	5' nucleotidase, ecto	-0.3	0.137	-0.61	0.418	-0.1	0.498	0.007724	0.551832	0.61027
Nubpl	nucleotide binding protein-like	-0.22	0.466	0.105	0.485	-0.89	0.124	0.005268	0.06327	0.559103
Nup133	nucleoporin 133	-0.5	0.195	-0.41	0.841	-0.24	0.184	0.001715	0.439508	0.365258
Oasl2	2'-5' oligoadenylate synthetase-like 2	-0.37	0.131	-0.43	1.014	-0.43	0.142	0.000612	0.229455	0.19023
Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (L	-0.08	0.827	-0.61	0.109	-0.17	0.011	0.017679	0.111592	0.460472
Ormd2	ORM1-like 2 (S. cerevisiae)	0.139	0.594	-0.07	0.246	-0.92	0.053	0.019019	0.028761	0.508473
Osbpl11	oxysterol binding protein-like 11	-0.24	0.599	-0.52	0.448	-0.29	0.086	0.004865	0.629725	0.585189
Osmr	oncostatin M receptor	-0.54	1.055	-0.68	0.619	-0.79	0.495	9.53E-10	0.199983	0.75808
OTTMUSG	predicted gene, OTTMUSG00000003311	-0.05	0.861	-0.5	0.412	-0.81	0.178	0.000121	0.038373	0.986989
Oxct1	3-oxoacid CoA transferase 1	0.111	0.808	-0.42	0.276	-0.68	-0.03	0.005961	0.024228	0.995882
P2ry13	purinergic receptor P2Y, G-protein coupled 13	-0.53	1.026	-0.45	0.394	-0.09	-0.2	0.001537	0.370338	0.016414
P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	-0.42	0.988	-0.96	0.415	-0.11	0.229	9.68E-06	0.112136	0.075776
Parp3	poly (ADP-ribose) polymerase family, member 3	-0.51	0.284	0.037	0.574	-0.65	0.343	0.002187	0.234456	0.739421
Pat1	protein associated with topoisomerase II homolog 1 (y	-0.03	0.477	-0.4	0.125	-0.45	0.342	0.019186	0.480956	0.87714
Pcdhb7	protocadherin beta 7	-0.54	0.222	0.09	0.45	-0.5	0.356	0.010193	0.335036	0.685256
Pcdhb9	protocadherin beta 9	-0.32	1.049	-0.36	0.262	-0.66	0.155	0.000134	0.085959	0.383578
Pcmt2	protein-L-isoaspartate (D-aspartate) O-methyltransfera	0.089	0.751	-0.15	0.144	-0.8	0.032	0.0168	0.031437	0.654107
Pde3b	phosphodiesterase 3B, cGMP-inhibited	-0.52	1.011	-0.29	0.417	-0.51	0.042	0.000144	0.227343	0.176674
Pdhx	pyruvate dehydrogenase complex, component X	-0.44	0.159	-0.17	0.365	-0.42	0.57	0.006164	0.6916	0.717772

Pdia5	protein disulfide isomerase associated 5	-0.59	0.739	-0.27	0.199	-0.06	0.124	0.009262	0.93354	0.151558
Pea15a	phosphoprotein enriched in astrocytes 15A	-0.46	0.542	-1.01	0.662	-0.34	0.705	1.18E-07	0.362984	0.329953
Pgap1	post-GPI attachment to proteins 1	-0.28	0.512	-0.21	0.368	-0.49	0.176	0.009566	0.637427	0.942742
Phb	prohibitin	-0.06	0.78	-0.55	0.429	-0.9	0.384	1.86E-05	0.074534	0.705972
Phxr4	per-hexamer repeat gene 4	-0.12	0.29	-0.61	0.478	-0.29	0.289	0.007781	0.88481	0.52152
Pign	phosphatidylinositol glycan anchor biosynthesis, class	0.185	0.476	-0.46	0.359	-0.72	0.191	0.007564	0.138568	0.53491
Pik3cg	phosphoinositide-3-kinase, catalytic, gamma polypepti	-0.47	0.959	-0.46	0.258	-0.52	0.378	3.85E-05	0.397426	0.413204
Pitrm1	pitrilysin metallepetidase 1	-0.24	0.852	-0.33	0.239	-0.76	0.341	0.000217	0.190138	0.564438
Pkd2	polycystic kidney disease 2	-0.31	0.652	-0.23	-0.05	-0.54	0.581	0.00286	0.573109	0.244579
Pkib	protein kinase inhibitor beta, cAMP dependent, testis s	-0.27	1.052	-0.59	0.037	-0.28	0.181	0.001081	0.066358	0.286534
Plat	plasminogen activator, tissue	0.157	0.614	-0.49	-0.03	-0.55	0.35	0.017174	0.090834	0.692611
Plaur	plasminogen activator, urokinase receptor	-0.22	0.876	-0.34	0.297	-0.74	0.241	0.000265	0.135026	0.700556
Plice1	phospholipase C, epsilon 1	-0.44	0.775	-0.39	0.441	-0.76	0.499	7.06E-06	0.54787	0.689036
Plcg2	phospholipase C, gamma 2	-0.07	0.834	-0.48	0.42	-0.71	0.104	0.000407	0.062386	0.982502
Pld4	phospholipase D family, member 4	-0.36	0.242	-0.25	0.405	-0.56	0.582	0.00188	0.898132	0.609813
Plek	pleckstrin	-0.8	1.126	-0.62	0.805	-0.79	0.476	5.72E-13	0.252284	0.238213
Plekhf1	pleckstrin homology domain containing, family F (with	-0.36	0.485	-0.54	0.044	4E-04	0.458	0.014732	0.294736	0.810539
Pmp22	peripheral myelin protein 22	-0.4	0.856	-0.59	0.584	-0.67	0.349	2.2E-06	0.346419	0.904056
Pnpla7	patatin-like phospholipase domain containing 7	-0.3	0.428	-0.55	0.388	-0.28	0.387	0.002725	0.865006	0.894487
Pon3	paraoxonase 3	-0.32	0.228	-0.16	0.637	-0.63	0.296	0.003144	0.384343	0.817344
Pp11r	placental protein 11 related	-0.62	0.963	-0.3	0.182	-0.54	0.471	2.61E-05	0.653667	0.138826
Ppfia2	protein tyrosine phosphatase, receptor type, f polypept	-0.09	0.595	-0.37	0.197	-0.47	0.202	0.01416	0.396178	0.977029
Prdx1	peroxiredoxin 1	-0.03	0.694	-0.25	0.35	-0.76	0.077	0.004101	0.082246	0.924915
Prdx6	peroxiredoxin 6	0.262	0.467	-0.61	0.475	-0.6	0.024	0.010545	0.088689	0.334959
Prnp	prion protein	-0.81	0.36	-0.61	0.683	-0.43	0.915	4.67E-08	0.16734	0.935226
Prokr2	prokineticin receptor 2	-0.39	0.568	0.099	0.333	-0.57	0.055	0.018228	0.278075	0.501866
Pros1	protein S (alpha)	-0.39	0.949	-0.38	0.671	-0.51	-0.21	0.00019	0.055788	0.156129
Psen1	presenilin 1	-0.62	0.541	-0.6	0.411	-0.36	0.744	8.97E-06	0.538503	0.966352
Psmb8	proteasome (prosome, macropain) subunit, beta type 8	-0.79	0.412	-0.52	0.623	-0.22	0.618	1.36E-05	0.365774	0.777918
Psmb9	proteasome (prosome, macropain) subunit, beta type 9	-0.65	0.344	-0.65	0.491	0.231	0.333	0.002584	0.28187	0.161144
Psmd10	proteasome (prosome, macropain) 26S subunit, non-A	-0.35	0.727	-0.02	0.272	-0.62	0.089	0.006716	0.267694	0.428791
Psmd6	proteasome (prosome, macropain) 26S subunit, non-A	-0.04	0.616	-0.12	0.128	-0.76	0.25	0.011757	0.205195	0.452026
Psme2	proteasome (prosome, macropain) 28 subunit, beta	-0.35	-0.06	-0.01	0.45	-0.6	0.607	0.01015	0.372336	0.271703
Psrc1	proline/serine-rich coiled-coil 1	-0.33	0.509	-0.83	0.218	0.01	0.498	0.001636	0.153645	0.631022

Ptpn6	protein tyrosine phosphatase, non-receptor type 6	-0.59	0.845	-0.26	-0.03	-0.33	0.502	0.000856	0.59487	0.120088
Ptrf	polymerase I and transcript release factor	-0.35	0.358	-0.27	0.577	-0.28	0.039	0.016467	0.681794	0.675354
Pttg1ip	pituitary tumor-transforming 1 interacting protein	8E-04	0.647	-0	0.224	-0.95	0.151	0.007382	0.044814	0.327787
Pus7l	pseudouridylylase synthase 7 homolog ( <i>S. cerevisiae</i> )-lik	-0.22	-0.1	-0.56	0.37	-0.13	0.662	0.015435	0.322775	0.365874
Pycard	PYD and CARD domain containing	-0.57	1.017	-0.54	0.498	-0.4	0.159	1.09E-05	0.428942	0.167831
Pygb	brain glycogen phosphorylase	-0.15	0.8	-0.46	0.077	-0.38	0.21	0.006741	0.199214	0.766433
Qars	glutaminyl-tRNA synthetase	-0.09	0.658	-0.28	0.026	-0.52	0.287	0.016064	0.320395	0.67746
Qser1	glutamine and serine rich 1	-0.22	0.765	-0.15	0.249	-0.51	-0.04	0.015891	0.207224	0.574926
Rab24	RAB24, member RAS oncogene family	-0.6	0.094	-0.2	0.513	-0.15	0.408	0.011227	0.332096	0.960616
Rab32	RAB32, member RAS oncogene family	-0.47	0.766	-0.15	0.389	-0.33	-0.08	0.008098	0.423234	0.250596
Rab39	RAB39, member RAS oncogene family	0.07	0.717	-0.18	-0.01	-0.75	0.221	0.017583	0.081369	0.409754
Rab3b	RAB3B, member RAS oncogene family	-0.27	0.725	-0.29	0.054	-0.33	0.213	0.01555	0.493341	0.558718
Rab71l	RAB7, member RAS oncogene family-like 1	-0.21	0.199	-0.33	0.671	-0.41	0.126	0.012107	0.598787	0.600269
Rassf4	Ras association (RalGDS/AF-6) domain family membe	-0.33	0.152	-0.74	0.461	0.14	0.357	0.012928	0.383991	0.250112
Rbl1	retinoblastoma-like 1 (p107)	-0.24	0.524	0.012	0.189	-0.79	0.387	0.005225	0.458706	0.248475
Rbm18	RNA binding motif protein 18	-0.3	1.075	-0.16	0.191	-0.58	-0.09	0.002431	0.046909	0.162078
Rbm41	RNA binding motif protein 41	0.144	0.211	-0.32	0.518	-0.72	0.166	0.019434	0.285045	0.325624
Rcn1	reticulocalbin 1	-0.58	0.874	-0.41	0.406	-0.1	-0.05	0.001879	0.735382	0.060673
Rcor1	REST corepressor 1	-0.09	0.864	-0.18	0.054	-0.62	0.069	0.013	0.085405	0.483315
Rdbp	RD RNA-binding protein	-0.58	0.232	-0.48	0.343	0.13	0.433	0.011694	0.297892	0.621789
Rftn2	raftlin family member 2	0.334	0.248	-0.76	0.551	-0.59	0.213	0.005532	0.211153	0.056317
Rgs1	regulator of G-protein signaling 1	-0.18	0.854	-0.36	0.414	-0.62	-0.01	0.001263	0.089398	0.765916
Rgs10	regulator of G-protein signalling 10	-0.4	0.492	-0.03	0.324	-0.62	0.328	0.004387	0.617121	0.558545
Rgs19	regulator of G-protein signaling 19	-0.14	0.794	-0.13	0.146	-0.63	0.05	0.013283	0.129228	0.553443
Rhbdd1	rhomboid domain containing 1	-0.48	0.288	-0.22	0.247	-0.25	0.491	0.011868	0.779957	0.861032
Rims1	regulating synaptic membrane exocytosis 1	-0.33	0.486	-0.17	0.689	-0.45	-0.14	0.009359	0.177469	0.5907
Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase	0.122	0.298	-0.56	0.623	-0.47	0.008	0.015733	0.341334	0.239634
Rnase4	ribonuclease, RNase A family 4	-0.45	1.055	-0.89	0.747	-0.89	0.575	8.81E-13	0.061476	0.913054
Rnasen	ribonuclease III, nuclear	-0.12	0.779	-0.18	0.356	-0.7	-0.04	0.005465	0.062735	0.823787
Rnf12	ring finger protein 12	-0.05	0.796	-0.23	0.377	-0.62	-0.19	0.012283	0.036557	0.776678
Rnf135	ring finger protein 135	-0.22	-0.1	-0.66	1.148	-0.29	0.136	0.00087	0.304805	0.006432
Rnf144a	ring finger protein 144A	-0.32	0.828	-0.57	0.163	-0.19	0.21	0.002665	0.314702	0.452812
Rnh1	ribonuclease/angiogenin inhibitor 1	-0.57	-0.11	-0.31	0.659	-0.4	0.765	0.000427	0.114034	0.447386
Robo1	roundabout homolog 1 ( <i>Drosophila</i> )	0.175	0.787	-0.49	0.16	-0.59	0.025	0.011814	0.026276	0.997027

Robo2	roundabout homolog 2 (Drosophila)	-0.33	0.55	-0.39	0.522	-0.33	0.061	0.005034	0.698816	0.628818
RP23-12I2	serine-arginine repressor protein	-0.17	0.795	-0.3	0.112	-0.65	0.308	0.002096	0.221093	0.55928
Rpl21	ribosomal protein L21	-0.48	0.414	-0.44	0.643	-0.72	0.673	4.45E-06	0.852066	0.653269
Runx1	runt related transcription factor 1	-0.34	1.229	-0.41	-0.14	-0.21	0.018	0.003881	0.034333	0.030225
Ryr3	ryanodine receptor 3	0.085	0.389	-0.52	0.351	-0.52	0.247	0.012125	0.421293	0.6166
Sall1	sal-like 1 (Drosophila)	-0.22	0.702	-0.12	0.317	-0.67	0.088	0.00557	0.199187	0.715346
Samsn1	SAM domain, SH3 domain and nuclear localization sig	-0.61	0.952	-0.55	0.941	-0.78	0.196	2.51E-09	0.065991	0.390057
Sash3	SAM and SH3 domain containing 3	-0.17	0.711	-0.71	0.368	-0.36	0.253	0.000685	0.301382	0.728338
Sat1	spermidine/spermine N1-acetyl transferase 1	-0.42	0.697	-0.37	0.445	-0.79	0.553	8.87E-06	0.637165	0.6233
Scamp2	secretory carrier membrane protein 2	-0.95	0.653	-0.32	0.923	-0.26	0.108	3.95E-06	0.176814	0.052878
Scd3	stearoyl-coenzyme A desaturase 3	-0.07	0.554	-0.39	0.143	-0.55	0.373	0.007469	0.431344	0.801754
Scel	sciellin	0.275	0.5	-0.31	-0.21	-0.89	0.655	0.008924	0.061349	0.022077
Scfd1	Sec1 family domain containing 1	-0.63	0.362	-0.03	0.378	-0.39	0.403	0.004578	0.598437	0.621941
Scn9a	sodium channel, voltage-gated, type IX, alpha	-0.38	0.308	-0.22	-0.22	-0.32	0.897	0.0105	0.229581	0.127836
Scp2	sterol carrier protein 2, liver	0.022	0.622	-0.28	-0.03	-0.63	0.358	0.016738	0.213419	0.475727
Scpep1	serine carboxypeptidase 1	-0.21	0.801	-0.29	0.29	-0.68	0.193	0.001103	0.186927	0.758125
Scrg1	scrapie responsive gene 1	-0.24	0.607	-0.51	0.027	-0.25	0.452	0.007094	0.341082	0.877052
Scrib	scribbled homolog (Drosophila)	-0.42	0.419	-0.26	0.33	-0.4	0.413	0.004175	0.991687	0.901989
Sema3d	sema domain, immunoglobulin domain (Ig), short basi	-0.34	0.913	-0.39	0.515	-0.65	0.081	8.73E-05	0.129054	0.63328
Sema4a	sema domain, immunoglobulin domain (Ig), transmem	0.029	0.829	-0.06	0.026	-0.87	0.126	0.010374	0.027206	0.26009
Serinc3	serine incorporator 3	-0.19	0.556	-0.34	0.314	-0.6	0.34	0.002465	0.585673	0.890873
Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, memb	0.006	0.549	-0.12	0.41	-0.76	-0.03	0.017075	0.069458	0.929473
Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, memb	-0.32	0.661	-0.23	-0.12	-0.58	0.683	0.00166	0.491241	0.124975
Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	-0.4	0.935	-0.55	0.479	-0.76	0.43	8.05E-07	0.244098	0.845904
Sgk1	serum/glucocorticoid regulated kinase 1	-0.58	0.251	-0.41	0.031	0.068	0.722	0.010873	0.09536	0.806366
Sgpp1	sphingosine-1-phosphate phosphatase 1	-0.18	0.941	-0.23	0.304	-0.7	-0.03	0.001798	0.040923	0.569695
Siglec5	sialic acid binding Ig-like lectin 5	-0.58	1.125	-0.56	0.24	-0.44	0.383	3.26E-06	0.249429	0.152547
Siglech	sialic acid binding Ig-like lectin H	-0.66	1.169	-0.6	0.392	-0.36	0.249	9.93E-07	0.317613	0.057392
Siva1	SIVA1, apoptosis-inducing factor	-0.22	0.62	-0.56	0.133	-0.11	0.214	0.017563	0.404657	0.695278
Sla	src-like adaptor	-0.26	0.832	-0.57	0.551	-0.39	-0.05	0.000602	0.220285	0.305214
Slc11a1	solute carrier family 11 (proton-coupled divalent metal	-0.81	1.052	-0.75	0.696	-0.66	0.657	1.22E-12	0.752458	0.381434
Slc22a4	solute carrier family 22 (organic cation transporter), me	-0.54	-0.15	-0.16	0.351	-0.29	0.825	0.006913	0.108574	0.4343
Slc25a45	solute carrier family 25, member 45	-0.3	0.44	-0.26	0.337	-0.54	0.4	0.0035	0.890076	0.852564
Slc35c2	solute carrier family 35, member C2	-0.55	-0.19	-0.48	0.439	0.054	0.77	0.00666	0.03153	0.626502

Slc37a2	solute carrier family 37 (glycerol-3-phosphate transporter)	-0.33	0.431	-0.04	0.604	-0.69	0.105	0.00379	0.16181	0.965667
Slc39a11	solute carrier family 39 (metal ion transporter), member 11	-0.61	0.717	-0.64	0.609	-0.42	0.482	1.98E-06	0.964491	0.689873
Slc44a2	solute carrier family 44, member 2	-0.26	0.16	-0.16	0.756	-0.45	0.002	0.019784	0.228514	0.6622
Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	-0.31	-0.25	-0.69	0.824	-0.08	0.52	0.002699	0.2018	0.041082
Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9	-0.52	0.472	-0.39	0.566	-0.39	0.361	0.000431	0.912535	0.908892
Slco2b1	solute carrier organic anion transporter family, member 2B1	-0.75	0.912	-0.93	0.641	-0.2	0.498	7.28E-09	0.432521	0.086026
Smc4	structural maintenance of chromosomes 4	-0.45	0.897	-0.33	0.47	-0.07	-0.38	0.012069	0.295137	0.018049
Smek2	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	-0.15	0.794	-0.38	-0.12	-0.37	0.31	0.01469	0.170424	0.521107
Snrnp35	small nuclear ribonucleoprotein 35 (U11/U12)	-0.47	0.741	-0.33	0.402	-0.44	0.229	0.000595	0.713684	0.601083
Snx12	sorting nexin 12	-0.1	0.539	-0.32	0.128	-0.48	0.295	0.017751	0.509016	0.874445
Snx2	sorting nexin 2	0.062	0.624	-0.32	0.083	-0.63	0.232	0.017836	0.169165	0.749876
Sorbs1	sorbin and SH3 domain containing 1	-0.47	-0.01	-0.7	0.439	0.034	0.755	0.001639	0.068758	0.489489
Sos2	Son of sevenless homolog 2 (Drosophila)	-0.12	0.844	-0.13	0.156	-0.71	0.052	0.007567	0.075737	0.499749
Sparc	secreted acidic cysteine rich glycoprotein	-0.52	0.126	-0.45	0.5	-0.29	0.705	0.000595	0.381792	0.812757
Spata6	spermatogenesis associated 6	-0.51	-0.08	-0.29	0.33	-0.11	0.693	0.016148	0.159535	0.828791
Spats1	spermatogenesis associated, serine-rich 1	-0.22	0.099	-0.15	0.505	-0.52	0.326	0.019576	0.635259	0.695638
Spib	Spi-B transcription factor (Spi-1/PU.1 related)	-0.08	0.182	-0.94	0.087	0.098	0.678	0.010925	0.023808	0.417401
Spopl	speckle-type POZ protein-like	-0.07	0.967	-0.19	0.013	-0.7	0.089	0.005918	0.034486	0.337886
Spp1	secreted phosphoprotein 1	-0.32	0.643	-0.53	0.209	-0.39	0.486	0.000774	0.549848	0.92833
Srgn	serglycin	-0.47	0.159	-0.45	0.499	-0.33	0.659	0.00074	0.550024	0.800526
St18	suppression of tumorigenicity 18	-0.02	0.253	-0.51	0.212	-0.47	0.571	0.008231	0.660341	0.447267
Stard9	START domain containing 9	-0.47	0.499	-0.32	0.478	-0.33	0.232	0.002824	0.91669	0.793312
Stat1	signal transducer and activator of transcription 1	-0.1	0.355	-0.73	0.908	-0.57	0.189	8.43E-05	0.454375	0.092445
Stat3	signal transducer and activator of transcription 3	-0.33	0.668	-0.63	0.067	-0.09	0.421	0.003776	0.230032	0.708102
Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	-0.52	0.721	-0.1	0.452	-0.52	0.089	0.001537	0.374075	0.430659
Stra13	stimulated by retinoic acid 13	-0.32	0.4	-0.54	0.439	-0.13	0.217	0.009111	0.942435	0.588883
Strap	serine/threonine kinase receptor associated protein	-0.1	0.827	-0.22	0.009	-0.67	0.243	0.006191	0.127138	0.407309
Stx2	syntaxin 2	-0.34	0.54	-0.57	0.351	-0.03	0.134	0.011481	0.771684	0.388969
Stxbp3a	syntaxin binding protein 3A	-0.33	0.671	-0.09	0.309	-0.56	0.096	0.007874	0.36916	0.613419
Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	-0.35	0.562	-0.39	0.47	-0.32	0.119	0.004493	0.782693	0.70221
Surf4	surfeit gene 4	0.04	0.715	-0.35	0.22	-0.68	0.124	0.006903	0.090776	0.929641
Syk	spleen tyrosine kinase	-0.02	0.524	-0.73	-0.09	-0.34	0.701	0.00279	0.051495	0.65876
Syngr1	synaptogyrin 1	-0.31	0.922	-0.61	0.069	-0.48	0.531	7.33E-05	0.126375	0.604778
Syngr2	synaptogyrin 2	-0.44	0.681	-0.27	0.705	-0.77	0.207	2.92E-05	0.17071	0.95066

Syt3	synaptotagmin III	-0.17	0.397	-0.36	0.251	-0.54	0.48	0.004796	0.838807	0.712164
Tacr3	tachykinin receptor 3	0.088	0.428	-0.13	0.542	-0.97	0.082	0.004892	0.031192	0.467375
Taf12	TAF12 RNA polymerase II, TATA box binding protein (	0.096	0.543	-0.52	0.216	-0.47	0.186	0.01703	0.219436	0.885701
Tapbp	TAP binding protein	-0.42	0.092	-0.3	0.355	-0.22	0.542	0.013882	0.581947	0.917111
Tbp	TATA box binding protein	-0.32	0.719	-0.08	0.308	-0.52	-0	0.011342	0.277518	0.526306
Tbxas1	thromboxane A synthase 1, platelet	-0.6	0.94	-0.58	0.856	-0.54	0.073	2.77E-07	0.21039	0.133826
Tchp	trichoplein, keratin filament binding	-0.57	0.999	-0.26	0.221	-0.25	0.022	0.001712	0.506143	0.062253
Tcirg1	T-cell, immune regulator 1, ATPase, H+ transporting, I	-0.4	1.001	-0.57	0.648	-0.69	0.163	9.58E-07	0.100696	0.556977
Tec	cytoplasmic tyrosine kinase, Dscr28C related (Drosoph	-0.56	0.336	-0.37	0.307	-0	0.373	0.012721	0.608215	0.697534
Tgfb1	transforming growth factor, beta 1	-0.56	0.76	-0.56	0.161	-0.37	0.701	2.4E-05	0.37664	0.546313
Tgfr2	transforming growth factor, beta receptor II	-0.58	0.842	-0.59	0.764	-0.6	0.303	2.7E-07	0.505546	0.547277
Tgoln1	trans-golgi network protein	0.137	0.69	-0.36	0.259	-0.64	-0.03	0.018427	0.050012	0.992487
Thbs4	thrombospondin 4	-0.48	0.058	-0.66	0.487	0.011	0.648	0.001844	0.157435	0.53172
Tjap1	tight junction associated protein 1	0.063	0.256	-0.5	0.281	-0.5	0.416	0.01523	0.662224	0.464878
Tlr13	toll-like receptor 13	-0.58	1.259	-0.49	0.37	-0.72	0.342	3.92E-08	0.080663	0.107954
Tlr2	toll-like receptor 2	-0.66	0.83	-0.4	0.658	-0.64	0.356	9.54E-07	0.538595	0.59265
Tmem106a	transmembrane protein 106A	-0.31	0.307	-0.47	0.096	-0.12	0.551	0.018363	0.435132	0.98539
Tmem119	transmembrane protein 119	-0.31	0.599	-0.24	0.514	-0.54	0.073	0.003062	0.364614	0.882086
Tmem123	transmembrane protein 123	-0.18	0.396	-0.11	0.435	-0.6	0.115	0.018787	0.369141	0.956564
Tmem159	transmembrane protein 159	-0.34	0.067	-0.56	0.278	-0.1	0.7	0.007496	0.255156	0.724462
Tmem176a	transmembrane protein 176A	-0.14	0.705	-0.08	0.091	-0.8	0.308	0.004854	0.212068	0.268982
Tmem176b	transmembrane protein 176B	-0.24	0.52	-0.24	0.49	-0.86	0.398	0.000261	0.350733	0.590817
Tmem206	transmembrane protein 206	-0.15	0.596	-0.22	0.749	-0.56	-0.35	0.009175	0.027021	0.407045
Tmem77	transmembrane protein 77	-0.5	0.369	-0.14	0.603	-0.29	0.051	0.011438	0.467301	0.66686
Tmlhe	trimethyllysine hydroxylase, epsilon	-0.25	0.906	-0.03	0.111	-0.6	-0.02	0.012763	0.106392	0.240965
Tnfaip6	tumor necrosis factor alpha induced protein 6	-0.12	0.218	-0.24	0.379	-0.61	0.403	0.011785	0.826362	0.54536
Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2	-0.09	0.707	-0.51	0.619	-0.68	0.029	0.000393	0.088627	0.734997
Trem2	triggering receptor expressed on myeloid cells 2	-0.8	1.315	-0.81	0.596	-0.63	0.55	3.52E-14	0.133937	0.042452
Trim30	tripartite motif-containing 30	-0.77	0.385	-0.6	0.665	-0.07	0.501	4.46E-05	0.329913	0.400468
Trim34	tripartite motif-containing 34	-0.51	0.167	-0.2	1.031	-0.47	0.054	0.000839	0.054065	0.420933
Uap1l1	UDP-N-acetylglucosamine pyrophosphorylase 1-like 1	-0.7	0.506	-0.08	0.546	-0.34	0.19	0.001863	0.469439	0.466461
Ube2w	ubiquitin-conjugating enzyme E2W (putative)	-0.25	0.671	0.204	0.263	-0.77	-0.02	0.019774	0.063466	0.308422
Ubfd1	ubiquitin family domain containing 1	0.202	0.594	-0.05	-0.14	-1.06	0.496	0.008593	0.047887	0.013291
Uevld	UEV and lactate/malate dehydrogenase domains	-0.31	0.704	-0.85	-0.04	0.317	0.273	0.01497	0.026174	0.161635



Ugdh	UDP-glucose dehydrogenase	-0.38	0.559	-0.26	0.451	-0.52	0.237	0.001967	0.670493	0.924336
Unc93b1	unc-93 homolog B1 (C. elegans)	-0.26	0.714	-0.36	0.312	-0.66	0.356	0.000454	0.425241	0.808776
Upp2	uridine phosphorylase 2	0.032	0.284	-0.38	0.11	-0.78	0.752	0.002302	0.603451	0.072025
Vav1	vav 1 oncogene	-0.61	0.202	-0.31	0.608	-0.02	0.204	0.011382	0.465888	0.478736
Vbp1	von Hippel-Lindau binding protein 1	-0.04	0.598	-0.02	0.104	-0.87	0.296	0.010169	0.173418	0.22822
Vim	vimentin	-0.4	0.86	-0.37	0.405	-0.94	0.569	6.62E-07	0.281043	0.351181
Vnn1	vanin 1	-0.11	0.113	-0.48	0.34	-0.38	0.541	0.011687	0.886882	0.481202
Vps54	vacuolar protein sorting 54 (yeast)	0.117	0.494	-0.17	0.222	-0.98	0.357	0.004295	0.10988	0.171013
Vwa5a	von Willebrand factor A domain containing 5A	-0.51	0.948	-0.27	0.665	-0.86	0.173	1.2E-06	0.053534	0.554115
Was	Wiskott-Aldrich syndrome homolog (human)	-0.41	0.893	-0.56	0.263	-0.09	0.031	0.002801	0.394148	0.13558
Wasf2	WAS protein family, member 2	-0.55	0.403	-0.47	1.087	-0.53	0.148	7.97E-06	0.150014	0.239043
Wdr26	WD repeat domain 26	-0.43	1.178	-0.24	0.124	-0.43	-0.04	0.001112	0.088661	0.047027
Wdr33	WD repeat domain 33	-0.04	0.544	-0.11	0.211	-0.75	0.204	0.015528	0.228619	0.576718
Wdr51b	WD repeat domain 51B	-0.6	0.381	0.033	-0.13	-0.32	0.729	0.012799	0.5382	0.081833
Wsb1	WD repeat and SOCS box-containing 1	-0.23	0.711	0.032	0.13	-0.73	0.18	0.01015	0.21927	0.286889
X99384	cDNA sequence X99384	-0.41	-0.05	-0.19	0.425	-0.34	0.598	0.013518	0.41973	0.634988
Ybx1	Y box protein 1	-0.2	0.297	-0.54	0.557	-0.35	0.287	0.004075	0.964358	0.592359
Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-0.14	0.51	-0.16	0.39	-0.78	0.246	0.003547	0.267759	0.696303
Zbtb8b	zinc finger and BTB domain containing 8b	-0.26	0.632	-0.43	0.06	-0.27	0.35	0.010565	0.477548	0.804107
Zcchc10	zinc finger, CCHC domain containing 10	0.105	0.399	-0.42	0.155	-0.63	0.417	0.013133	0.377244	0.466108
Zcchc4	zinc finger, CCHC domain containing 4	-0.12	0.719	-0.05	0.091	-0.7	0.14	0.017227	0.165317	0.418407
Zfp109	zinc finger protein 109	-0.14	0.463	-0.36	0.191	-0.42	0.314	0.017404	0.693006	0.95587
Zfp182	zinc finger protein 182	0.055	0.76	-0.63	0.05	-0.27	0.112	0.019899	0.067797	0.83892
Zfp189	zinc finger protein 189	-0.23	0.509	-0.52	0.219	-0.26	0.357	0.007422	0.637761	0.97382
Zfp191	zinc finger protein 191	-0.07	0.265	-0.16	0.473	-0.82	0.354	0.004734	0.375718	0.365623
Zfp36	zinc finger protein 36	-0.32	0.607	-0.54	0.433	-0.43	0.351	0.000459	0.759878	0.946024
Zfp429	zinc finger protein 429	-0.14	0.605	-0.4	0.216	-0.56	0.353	0.003307	0.459305	0.881832
Zfp592	zinc finger protein 592	-0.26	0.129	-0.29	0.668	-0.67	0.46	0.001104	0.554733	0.423491
Zfp62	zinc finger protein 62	-0.12	0.755	-0.24	0.095	-0.57	0.163	0.011657	0.21177	0.653829
Zkscan6	zinc finger with KRAB and SCAN domains 6	-0.25	0.775	-0.14	0.46	-0.55	-0.19	0.008123	0.082416	0.535035
Zscan10	zinc finger and SCAN domain containing 10	-0.53	0.067	-0.16	0.707	-0.47	0.454	0.00155	0.237414	0.83448
<b>Decreased in Transgenic (364)</b>										
39878	membrane-associated ring finger (C3HC4) 6	-0.04	-0.75	0.583	-0.22	0.522	-0.16	0.003651	0.08837	0.979288
40063	septin 7	-0.01	-0.93	0.461	-0.16	0.748	-0.19	0.000679	0.022909	0.821249

Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	0.04	-0.64	0.071	-0.47	0.933	-0	0.003403	0.020102	0.788038
Acta1	actin, alpha 1, skeletal muscle	0.275	-0.59	0.135	-0.39	0.581	-0.1	0.007615	0.356877	0.860712
Actg1	actin, gamma, cytoplasmic 1	-0.05	-0.82	0.393	-0.17	0.561	0.015	0.012882	0.048546	0.916859
Aebp2	AE binding protein 2	-0.04	-0.6	0.371	-0.19	0.597	-0.2	0.013329	0.210413	0.908077
Ahcy	S-adenosylhomocysteine hydrolase	-0.5	-0.18	0.842	-0.67	0.59	-0.05	0.008785	0.083976	0.006575
Ahcy1	S-adenosylhomocysteine hydrolase-like 1	0.647	-0.92	0.062	-0.29	0.673	-0.33	5.91E-05	0.466306	0.094594
Ak5	adenylate kinase 5	0.033	-0.6	0.077	-0.28	0.913	-0.2	0.004779	0.088672	0.428982
Akap11	A kinase (PRKA) anchor protein 11	-0.08	-0.66	0.053	-0.11	0.893	-0.15	0.016487	0.049401	0.338886
Ankrd50	ankyrin repeat domain 50	0.475	-0.04	0.306	-0.27	0.308	-0.83	0.003251	0.276582	0.516149
Ano4	anoctamin 4	0.596	-0.21	0.268	-0.37	0.23	-0.59	0.003233	0.459299	0.945612
Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	0.252	-0.72	0.084	-0.14	0.533	-0.1	0.017586	0.34072	0.479085
Aplp1	amyloid beta (A4) precursor-like protein 1	0.065	-0.87	0.287	-0.24	0.813	-0.15	0.001048	0.043123	0.69253
Apoa1bp	apolipoprotein A-I binding protein	0.156	-0.76	0.335	-0.33	0.386	0.117	0.016417	0.200567	0.568701
Arl5b	ADP-ribosylation factor-like 5B	0.665	-0.01	0.326	-0.33	0.027	-0.74	0.005006	0.075235	0.980221
Armcx5	armadillo repeat containing, X-linked 5	-0.02	-0.86	0.626	0.034	0.232	-0.09	0.019534	0.038606	0.694257
Arpc3	actin related protein 2/3 complex, subunit 3	0.066	-0.85	0.334	0.114	0.537	-0.29	0.009164	0.093071	0.446087
Arpp21	cyclic AMP-regulated phosphoprotein, 21	0.952	-0.83	0.738	-0.59	0.709	-1.16	1.11E-16	0.143819	0.234839
Asphd1	aspartate beta-hydroxylase domain containing 1	0.035	-0.51	0.134	-0.05	0.706	-0.37	0.019185	0.398628	0.347337
Atg3	autophagy-related 3 (yeast)	0.44	-0.5	0.371	-0.36	0.193	-0.24	0.007385	0.993264	0.714685
Atl2	atlastin GTPase 2	0.153	-0.15	0.447	0.223	0.313	-1.01	0.011141	0.068677	0.114069
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.228	-0.98	0.201	0.082	0.815	-0.46	0.000284	0.085989	0.068582
Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	0.161	-0.7	-0	0.254	0.747	-0.55	0.009793	0.316658	0.028188
Atp5b	ATP synthase, H+ transporting mitochondrial F1 comp	-0.17	-0.66	0.463	-0.31	0.738	-0.1	0.00482	0.0445	0.819935
Atp5d	ATP synthase, H+ transporting, mitochondrial F1 comp	0.316	-0.77	0.41	-0.35	0.41	-0.12	0.001917	0.448408	0.647457
Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 comp	0.407	-1.02	0.488	0.015	0.17	-0.2	0.002164	0.160799	0.137466
Atp5g3	ATP synthase, H+ transporting, mitochondrial F0 comp	-0.09	-0.79	0.301	-0.28	0.809	-0.03	0.004229	0.021636	0.90497
Atp5h	ATP synthase, H+ transporting, mitochondrial F0 comp	0.198	-1.15	0.462	-0.04	0.462	-0.07	0.00105	0.026036	0.240986
Atp5j	ATP synthase, H+ transporting, mitochondrial F0 comp	0.232	-0.92	0.503	-0.18	0.571	-0.32	0.000257	0.149596	0.711072
Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 co	0.195	-0.73	0.293	-0.12	0.494	-0.23	0.007949	0.362638	0.698189
Atp5l	ATP synthase, H+ transporting, mitochondrial F0 comp	0.222	-0.87	0.254	-0.21	0.523	-0.03	0.005589	0.163386	0.523319
Atp5o	ATP synthase, H+ transporting, mitochondrial F1 comp	0.238	-0.9	0.355	0.011	0.434	-0.25	0.004238	0.186395	0.407341
Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein	0.032	-0.73	0.771	-0.15	0.387	-0.38	0.001042	0.084261	0.951768
Atp6v0d1	ATPase, H+ transporting, lysosomal V0 subunit D1	0.302	-0.7	0.077	-0.16	0.721	-0.34	0.002455	0.423834	0.301132
Atp6v1g1	ATPase, H+ transporting, lysosomal V1 subunit G1	-0.14	-0.68	0.57	0.126	0.488	-0.41	0.012152	0.042356	0.722753

Atp6v1g2	ATPase, H <sup>+</sup> transporting, lysosomal V1 subunit G2	0.124	-0.93	0.12	-0.01	0.68	-0.08	0.00869	0.059362	0.276895
Atpaf1	ATP synthase mitochondrial F1 complex assembly fac	0.14	-0.65	0.222	-0.12	0.569	-0.24	0.012476	0.372034	0.692333
AU023762	expressed sequence AU023762	0.509	-0.59	0.355	-0.19	0.164	-0.35	0.005366	0.840816	0.566442
B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransfer	0.766	-0.92	0.205	-0.3	0.723	-0.64	4.11E-07	0.890885	0.059564
Basp1	brain abundant, membrane attached signal protein 1	-0.07	-0.72	0.378	-0.17	0.624	-0.11	0.011063	0.08502	0.952183
Bat2l	HLA-B associated transcript 2-like	0.151	-0.55	-0.02	0.266	0.732	-0.65	0.015394	0.52716	0.021227
BC024659	cDNA sequence BC024659	0.267	-0.49	0.029	-0.22	0.605	-0.26	0.01595	0.582504	0.573207
BC033915	cDNA sequence BC033915	0.217	-0.87	0.196	-0.33	0.593	0.086	0.004817	0.08456	0.546766
BC042720	cDNA sequence BC042720	0.187	-0.27	-0.01	-0.3	0.858	-0.51	0.00529	0.524153	0.157204
Bcr	breakpoint cluster region	0.555	0.045	0.119	-0.56	0.218	-0.42	0.017326	0.209522	0.957546
Brd2	bromodomain containing 2	-0.01	-0.64	0.229	-0.47	0.929	-0.1	0.00137	0.033789	0.76098
Brdt	bromodomain, testis-specific	0.358	-0.72	0.25	0.132	0.36	-0.49	0.007481	0.454273	0.256525
Bsdc1	BSD domain containing 1	0.054	-0.7	0.509	-0.5	0.773	-0.21	0.000215	0.111087	0.885961
Btbd6	BTB (POZ) domain containing 6	0.006	-0.2	0.322	-0.57	0.705	-0.28	0.006384	0.469752	0.370016
Camk2a	calcium/calmodulin-dependent protein kinase II alpha	-0.05	-0.79	0.172	0.099	0.718	-0.22	0.01938	0.064488	0.317188
Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	0.31	-0.47	0.166	-0.41	0.655	-0.34	0.002476	0.609674	0.783498
Car2	carbonic anhydrase 2	0.584	-0.44	0.52	-0.31	0.348	-0.8	5.39E-05	0.437178	0.849296
Cck	cholecystokinin	0.535	-0.24	-0.16	-0.48	0.747	-0.47	0.001866	0.186233	0.306038
Ccl27a	chemokine (C-C motif) ligand 27A	0.309	-0.53	0.398	-0.47	0.8	-0.59	3.18E-05	0.72864	0.547622
Cct7	chaperonin containing Tcp1, subunit 7 (eta)	0.006	-0.66	0.596	-0.06	0.466	-0.42	0.003818	0.140975	0.908674
Cdc34	cell division cycle 34 homolog (S. cerevisiae)	0.312	-0.2	0.341	-0.63	0.258	-0.13	0.01663	0.749302	0.612819
Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	0.613	-0.65	0.474	-0.05	-0.24	-0.27	0.015502	0.293119	0.121094
Cdh22	cadherin 22	-0.18	-0.39	0.534	-0.49	0.549	-0.04	0.017134	0.205436	0.404383
Cfl2	cofilin 2, muscle	0.08	-0.57	0.531	-0.31	0.721	-0.51	0.000284	0.371429	0.592632
Chchd10	coiled-coil-helix-coiled-coil-helix domain containing 10	0.27	-0.63	0.79	-0.22	0.249	-0.54	0.000311	0.204482	0.929531
Chgb	chromogranin B	0.088	-0.69	0.088	-0.18	0.816	-0.2	0.006316	0.128702	0.435263
Chmp4b	chromatin modifying protein 4B	0.066	-0.79	0.433	-0.15	0.371	-0.01	0.01762	0.147643	0.737649
Cit	citron	0.14	-0.63	0.352	-0.25	0.722	-0.41	0.000994	0.376546	0.657716
Ckb	creatine kinase, brain	-0.01	-0.81	0.311	-0.35	0.841	-0.06	0.001385	0.024374	0.916185
Clk2	CDC-like kinase 2	0.182	-0.65	0.257	0.057	0.498	-0.43	0.011235	0.43095	0.43641
Clta	clathrin, light polypeptide (Lca)	0.166	-0.51	0.409	-0.47	0.344	-0.01	0.01475	0.553657	0.697756
Cmpk1	cytidine monophosphate (UMP-CMP) kinase 1	0.019	-0.74	0.659	0.224	0.211	-0.45	0.012986	0.026242	0.853142
Cnbp	cellular nucleic acid binding protein	-0.01	-0.59	0.098	-0.23	0.832	-0.16	0.012035	0.11125	0.537446
Cnp	2',3'-cyclic nucleotide 3' phosphodiesterase	0.023	-0.93	0.471	-0.19	0.713	-0.18	0.000662	0.032129	0.864498

Coq7	demethyl-Q 7	0.169	-0.26	0.516	-0.11	0.389	-0.74	0.004237	0.447516	0.491899
Cox4i1	cytochrome c oxidase subunit IV isoform 1	0.004	-0.82	0.225	-0.18	0.658	0.032	0.013865	0.048333	0.784811
Cox5a	cytochrome c oxidase, subunit Va	0.161	-0.88	0.746	-0.52	0.824	-0.44	4.76E-07	0.07379	0.876503
Cox5b	cytochrome c oxidase, subunit Vb	0.004	-0.78	0.245	-0.25	0.854	-0.15	0.002114	0.045494	0.673874
Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	0.096	-0.48	0.185	-0.3	0.645	-0.2	0.014266	0.39796	0.826405
Cox6c	cytochrome c oxidase, subunit VIc	0.109	-0.74	0.215	-0.19	0.747	-0.23	0.003309	0.16133	0.604261
Cox7a2	cytochrome c oxidase, subunit VIIa 2	0.225	-0.81	0.335	-0.05	0.457	-0.26	0.00538	0.293022	0.568082
Cplx1	complexin 1	0.184	-0.47	-0.09	-0.49	0.824	-0.02	0.011468	0.057968	0.75543
Cplx2	complexin 2	0.006	-0.54	0.219	-0.3	0.699	-0.14	0.01359	0.20174	0.847788
Crhbp	corticotropin releasing hormone binding protein	0.511	-0.75	0.808	-0.4	0.545	-0.84	4.37E-08	0.288561	0.932742
Csnk1e	casein kinase 1, epsilon	0.202	-0.54	0.099	-0.43	0.777	-0.18	0.003438	0.206212	0.771341
Csnk2b	casein kinase 2, beta polypeptide	0.075	-0.83	0.108	-0.29	0.654	0.194	0.018246	0.028978	0.643143
Ctbp1	C-terminal binding protein 1	0.117	-0.77	0.152	-0.31	0.676	0.045	0.008996	0.074089	0.770688
Ctnnd2	catenin (cadherin associated protein), delta 2	0.634	-0.36	0.232	-0.2	0.158	-0.57	0.005309	0.51813	0.650365
Cuta	cutA divalent cation tolerance homolog (E. coli)	0.332	-0.41	0.47	-0.24	0.086	-0.31	0.019073	0.765251	0.826574
Cxxc5	CXXC finger 5	0.194	-0.47	-0.1	-0.41	1.033	-0.31	0.001542	0.078574	0.186408
Cyc1	cytochrome c-1	0.277	-0.67	0.497	-0.37	0.218	-0.04	0.007158	0.584246	0.467185
Cyfp2	cytoplasmic FMR1 interacting protein 2	0.4	-0.44	-0.03	-0.6	0.878	-0.29	0.000502	0.107812	0.57311
D11Bwg05	DNA segment, Chr 11, Brigham & Women's Genetics	0.302	-0.3	-0.18	-0.57	0.748	-0.05	0.017334	0.060118	0.791311
Ddn	dendrin	0.101	-0.61	0.126	-0.62	0.872	0.058	0.00203	0.020461	0.983761
Ddx1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	0.002	-0.48	0.467	-0.24	0.725	-0.53	0.001284	0.400259	0.406619
Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	0.514	0.109	0.128	-0.67	0.44	-0.56	0.003358	0.141708	0.590474
Dennd5a	DENN/MADD domain containing 5A	0.572	-0.63	0.434	-0.36	0.67	-0.8	1.81E-06	0.930257	0.448411
Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	0.257	-0.51	0.505	-0.11	0.386	-0.61	0.002053	0.47341	0.812414
Dkk3	dickkopf homolog 3 (Xenopus laevis)	0.218	0.092	0.07	-0.27	0.611	-0.73	0.017127	0.659496	0.106361
Dnalc4	dynein, axonemal, light chain 4	0.177	-0.57	-0.19	-0.39	0.88	0.02	0.014294	0.028419	0.493677
Dstn	destrin	0.266	-0.6	0.615	-0.53	0.131	0.038	0.005673	0.664041	0.198292
Dusp14	dual specificity phosphatase 14	0.159	-0.55	0.311	-0.08	0.525	-0.43	0.00813	0.574652	0.654895
Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase)	0.243	-0.72	0.23	-0.52	0.873	-0.21	0.000163	0.103669	0.835482
Dvl1	dishevelled, dsh homolog 1 (Drosophila)	0.273	-0.71	0.184	0.025	0.408	-0.28	0.018693	0.524318	0.405327
Dynll1	dynein light chain LC8-type 1	0.43	-0.54	0.141	-0.47	0.547	-0.2	0.002508	0.522945	0.831278
Eef1a2	eukaryotic translation elongation factor 1 alpha 2	0.082	-0.79	-0.03	-0.23	0.785	0.092	0.017535	0.027163	0.503121
Eef2	eukaryotic translation elongation factor 2	0.088	-0.72	0.228	-0.22	0.694	-0.15	0.005929	0.154317	0.762413
Efhd2	EF hand domain containing 2	0.268	-0.11	0.515	-0.37	0.208	-0.55	0.009531	0.647201	0.694746

EG433923	predicted gene, EG433923	-0.03	-0.88	0.617	-0.01	0.468	-0.25	0.003345	0.030702	0.929717
EG627798	predicted gene, EG627798	-0.1	-0.84	0.314	-0.02	0.642	-0.07	0.016759	0.031486	0.748885
EG667723	predicted gene, EG667723	0.118	-0.57	0.726	-0.22	0.273	-0.39	0.002656	0.27368	0.872909
Ei24	etoposide induced 2.4 mRNA	0.023	-0.55	0.698	-0.29	0.526	-0.47	0.000748	0.276976	0.707172
Eif1	eukaryotic translation initiation factor 1	0.036	-0.94	0.426	-0.04	0.487	-0.07	0.007779	0.046324	0.657265
Eif3d	eukaryotic translation initiation factor 3, subunit D	-0.17	-0.57	0.399	-0.18	0.669	-0.19	0.015578	0.113691	0.754375
Eif3i	eukaryotic translation initiation factor 3, subunit I	0.065	-0.81	0.31	-0.09	0.7	-0.27	0.002962	0.110789	0.584502
Eif4h	eukaryotic translation initiation factor 4H	0.088	-0.77	0.202	-0	0.647	-0.25	0.01003	0.167441	0.435817
Eif5a	eukaryotic translation initiation factor 5A	0.049	-0.74	0.486	-0.38	0.513	-0.01	0.004216	0.132026	0.831568
Elof1	elongation factor 1 homolog (ELF1, <i>S. cerevisiae</i> )	0.558	-0.58	0.184	-0.18	0.186	-0.29	0.011474	0.984346	0.405372
ENSMUSG	predicted gene, ENSMUSG00000043801	0.035	-0.93	0.427	-0.11	0.596	-0.12	0.003067	0.04454	0.767644
ENSMUSG	predicted gene, ENSMUSG00000045799	0.209	-0.73	0.195	-0.37	0.449	0.156	0.019025	0.174281	0.56926
ENSMUSG	predicted gene, ENSMUSG00000066693	0.035	-0.8	0.506	-0.19	0.364	0.001	0.013129	0.114058	0.72347
ENSMUSG	predicted gene, ENSMUSG00000068529	0.162	-0.91	0.397	-0.43	0.601	0.069	0.001078	0.056193	0.648971
ENSMUSG	predicted gene, ENSMUSG00000075401	0.005	-0.53	0.356	-0.2	0.678	-0.36	0.005626	0.338618	0.64793
Ets2	E26 avian leukemia oncogene 2, 3' domain	0.292	-0.26	-0.12	-0.33	0.782	-0.42	0.009804	0.407001	0.249408
Faf1	Fas-associated factor 1	-0.07	-0.58	0.436	-0.53	0.919	-0.23	0.000341	0.064676	0.510856
Fam100b	family with sequence similarity 100, member B	0.258	-0.62	0.187	-0.26	0.469	-0.13	0.01434	0.524986	0.77777
Fam108a	family with sequence similarity 108, member A	0.163	-0.6	0.038	-0.52	1.056	-0.22	0.000344	0.032096	0.418062
Fam115a	family with sequence similarity 115, member A	0.56	-0.12	0.216	-1	0.419	-0.14	0.000805	0.071714	0.470089
Fam152a	family with sequence similarity 152, member A	0.724	0.076	0.343	-0.79	-0.11	-0.3	0.007171	0.055916	0.272466
Fam81a	family with sequence similarity 81, member A	0.242	-0.57	0.713	-0.47	0.583	-0.58	2.17E-05	0.58054	0.761291
Fez1	fasciculation and elongation protein zeta 1 (zygin I)	0.051	-0.93	0.112	0.077	0.895	-0.3	0.002068	0.030034	0.096526
Fgfr2	fibroblast growth factor receptor 2	0.403	-0.45	0.73	0.044	-0.06	-0.75	0.002471	0.028253	0.947844
Foxj3	forkhead box J3	-0.07	-0.49	0.182	-0.24	0.803	-0.23	0.013841	0.175444	0.515758
Frmd6	FERM domain containing 6	0.377	-0.75	0.045	-0.3	0.507	0.003	0.010001	0.292799	0.397407
Frmpd1	FERM and PDZ domain containing 1	0.155	-1.05	0.609	0.138	0.151	-0.13	0.007689	0.022206	0.245205
Fst	follicle-stimulating hormone receptor	0.989	-0.24	0.39	-0.6	-0.26	-0.4	0.000835	0.039409	0.124434
Fut9	fucosyltransferase 9	0.489	0.115	0.488	-0.69	-0.03	-0.41	0.010581	0.192425	0.306051
Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit 1	0.141	-0.64	0.805	-0.57	0.685	-0.51	4.2E-06	0.318783	0.524971
Gcc2	GRIP and coiled-coil domain containing 2	0.384	-0.15	0.525	-0.12	0.125	-0.82	0.005116	0.142377	0.765245
Gdap1	ganglioside-induced differentiation-associated-protein 1	0.425	0.167	0.3	-0.82	0.271	-0.37	0.00734	0.172893	0.348166
Gdf10	growth differentiation factor 10	0.385	-0.78	0.041	0.064	0.443	-0.27	0.015366	0.593262	0.149693
Ghitm	growth hormone inducible transmembrane protein	0.149	-0.69	0.422	0.105	0.29	-0.36	0.019447	0.224442	0.689479

Git1	G protein-coupled receptor kinase-interactor 1	0.176	-0.5	0.191	-0.29	0.646	-0.3	0.007122	0.537981	0.746742
Gls2	glutaminase 2 (liver, mitochondrial)	0.468	-0.81	0.368	-0.31	0.543	-0.38	0.000129	0.64368	0.57507
Gna11	guanine nucleotide binding protein, alpha 11	0.105	-0.91	0.31	-0.25	0.707	-0.07	0.001626	0.050172	0.736584
Gnb5	guanine nucleotide binding protein (G protein), beta 5	0.146	-0.97	0.351	0.068	0.463	-0.17	0.006724	0.074289	0.367228
Gng3	guanine nucleotide binding protein (G protein), gamma	0.1	-0.85	0.198	-0.01	0.574	-0.11	0.015642	0.115734	0.464902
Got1	glutamate oxaloacetate transaminase 1, soluble	0.317	-0.78	0.156	-0.14	0.389	-0.05	0.017849	0.423466	0.385213
Gp1bb	glycoprotein Ib, beta polypeptide	0.161	-0.79	0.042	0.019	0.694	-0.23	0.012372	0.189462	0.220357
Gpm6b	glycoprotein m6b	0.132	-0.82	0.266	0.068	0.633	-0.37	0.004121	0.161667	0.3145
Gpr25	G protein-coupled receptor 25	-0.15	-0.43	0.042	-0.23	0.976	-0.24	0.017125	0.081003	0.19162
Gpr37	G protein-coupled receptor 37	0.223	-0.87	0.437	-0.3	0.434	-0.03	0.002488	0.192156	0.573073
Gps1	G protein pathway suppressor 1	0.196	-0.58	0.502	-0.06	0.181	-0.31	0.018952	0.399213	0.89123
Gpt	glutamic pyruvic transaminase, soluble	-0.01	-0.3	0.499	-0.08	0.638	-0.77	0.002385	0.432408	0.149178
Grm2	glutamate receptor, metabotropic 2	0.345	-0.19	0.036	-0.5	0.793	-0.54	0.001419	0.414857	0.292617
Grm3	glutamate receptor, metabotropic 3	0.441	-0.52	0.536	-0.69	0.469	-0.33	7.51E-05	0.869636	0.75551
Grpel1	GrpE-like 1, mitochondrial	0.151	-0.63	0.635	-0.38	0.308	-0.17	0.003224	0.426849	0.67005
Gstm5	glutathione S-transferase, mu 5	0.284	-1.08	0.283	-0.28	0.494	0.166	0.001991	0.044291	0.169268
Gtpbp5	GTP binding protein 5	0.359	-0.43	0.227	-0.47	0.432	-0.2	0.006938	0.740155	0.966042
Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+	0.49	0.169	0.341	-0.65	0.08	-0.47	0.014681	0.162822	0.533652
Higd1b	HIG1 domain family, member 1B	0.048	-0.41	0.147	-0.45	0.785	-0.16	0.008744	0.193944	0.706331
Higd2a	HIG1 domain family, member 2A	0.19	-0.89	0.187	-0.18	0.538	0.051	0.0105	0.104408	0.441604
Hipk2	homeodomain interacting protein kinase 2	0.992	-0.35	0.024	-0.43	-0.11	-0.26	0.007875	0.123732	0.110251
Hopx	HOP homeobox	0.715	-0.03	0.108	-0.19	0.081	-0.76	0.012048	0.076918	0.626987
Hpca	hippocalcin	0.555	-0.52	0.058	-0.76	0.337	0.225	0.006775	0.102024	0.238919
Hs2st1	heparan sulfate 2-O-sulfotransferase 1	-0.15	-0.46	0.543	0.261	0.617	-0.84	0.004234	0.040472	0.066486
Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	0.154	-0.64	0.418	-0.31	0.385	-0.09	0.010551	0.412652	0.855568
Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A mem	0.126	-0.91	0.596	-0.24	0.502	-0.19	0.000644	0.089672	0.834911
Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	0.151	-0.6	0.395	-0.38	0.397	-0.04	0.011987	0.422444	0.829313
Ids	iduronate 2-sulfatase	0.208	-0.67	0.308	-0.4	0.477	-0.01	0.007371	0.311905	0.810988
Ier2	immediate early response 2	0.163	-0.31	0.448	-0.25	0.485	-0.59	0.00387	0.827173	0.603551
Invs	inversin	0.176	-0.19	0.102	-0.69	0.777	-0.22	0.004513	0.163019	0.560495
Iqsec1	IQ motif and Sec7 domain 1	0.082	-0.63	0.344	-0.68	0.476	0.341	0.011488	0.050344	0.310712
Iqsec3	IQ motif and Sec7 domain 3	0.3	-0.64	0.125	-0.08	0.71	-0.51	0.001813	0.642546	0.216049
Irgq	immunity-related GTPase family, Q	0.591	-0.2	0.098	-0.13	0.243	-0.68	0.011323	0.40007	0.473314
Itm2a	integral membrane protein 2A	0.347	-0.49	0.607	-0.11	0.043	-0.48	0.007079	0.298688	0.87589

Itpr1	inositol 1,4,5-triphosphate receptor 1	0.641	-0.23	0.163	-0.31	0.415	-0.77	0.000788	0.400969	0.472718
Jtb	jumping translocation breakpoint	0.417	-0.46	0.429	-0.26	0.204	-0.41	0.005183	0.826822	0.905749
Kcnmb4	potassium large conductance calcium-activated chann	0.202	-0.73	-0.19	-0.22	0.87	-0.02	0.011629	0.036996	0.226226
Kcnq5	potassium voltage-gated channel, subfamily Q, memb	0.497	-0.19	0.424	-0.75	0.033	-0.08	0.009476	0.567268	0.215459
Kif5a	kinesin family member 5A	0.28	-1	0.551	0.01	0.448	-0.42	0.000264	0.082304	0.427871
Klc1	kinesin light chain 1	-0.02	-0.76	0.272	-0.18	0.925	-0.32	0.00094	0.055413	0.373921
Klhdc3	kelch domain containing 3	0.163	-0.52	0.353	-0.54	0.71	-0.24	0.000949	0.339595	0.894496
Lancl2	LanC (bacterial lantibiotic synthetase component C)-lik	-0.08	-0.73	0.278	-0.03	0.813	-0.32	0.004886	0.06924	0.373126
Ldha	lactate dehydrogenase A	0.369	-0.76	0.329	-0.18	0.513	-0.38	0.000909	0.58021	0.569519
Ldhb	lactate dehydrogenase B	0.1	-1.01	0.449	0.121	0.453	-0.23	0.004235	0.03523	0.409222
Lgr4	leucine-rich repeat-containing G protein-coupled recep	0.748	-0.31	0.265	-0.39	-0.04	-0.38	0.007312	0.352451	0.48433
Lingo1	leucine rich repeat and Ig domain containing 1	-0.14	-0.55	0.536	-0.01	0.556	-0.44	0.010135	0.128225	0.600243
Lmbrd1	LMBR1 domain containing 1	-0.24	-0.48	0.095	0.147	0.98	-0.53	0.018263	0.101912	0.018883
Lphn1	latrophilin 1	0.081	-0.76	0.258	0.141	0.67	-0.48	0.004947	0.16117	0.204475
Lrpap1	low density lipoprotein receptor-related protein associa	-0.11	-0.5	0.195	-0.25	0.874	-0.25	0.009268	0.124107	0.393679
Lrrc14	leucine rich repeat containing 14	-0.17	-0.45	0.53	-0.11	0.564	-0.39	0.014559	0.201351	0.541945
Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	0.139	-0.83	0.147	0.011	0.569	-0.13	0.017819	0.161303	0.378641
Mast2	microtubule associated serine/threonine kinase 2	0.336	-0.62	0.198	-0.03	0.49	-0.48	0.005543	0.753269	0.381494
Mdh1	malate dehydrogenase 1, NAD (soluble)	0.029	-0.97	0.455	-0.11	0.694	-0.2	0.000817	0.026185	0.722347
Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	0.115	-0.75	0.45	-0.29	0.356	0.037	0.012297	0.217073	0.642079
Mllt6	myeloid/lymphoid or mixed-lineage leukemia (trithorax	-0.05	-0.82	0.157	0.091	0.82	-0.28	0.008791	0.044362	0.201783
Mrpl22	mitochondrial ribosomal protein L22	0.234	-0.57	0.337	-0.34	0.554	-0.3	0.002697	0.624347	0.955192
Mrps30	mitochondrial ribosomal protein S30	0.095	-0.06	0.146	-0.74	0.701	-0.15	0.012092	0.167697	0.395538
Mtap1s	microtubule-associated protein 1S	0.172	-0.37	0.293	-0.63	0.617	-0.13	0.003904	0.341722	0.8193
Mtap2	microtubule-associated protein 2	0.825	-0.24	0.132	-0.49	0.18	-0.52	0.001493	0.188442	0.719559
Myl4	myosin, light polypeptide 4	-0.04	-0.69	0.317	-0.19	0.936	-0.39	0.000721	0.0785	0.309516
Myrip	myosin VIIA and Rab interacting protein	0.151	-0.42	0.214	-0.2	0.835	-0.63	0.001064	0.719133	0.157581
Myt1l	myelin transcription factor 1-like	-0.11	-0.58	0.861	-0.2	0.581	-0.6	0.000177	0.057977	0.399776
Nap1l1	nucleosome assembly protein 1-like 1	-0.05	-0.5	0.545	-0.11	0.414	-0.34	0.016399	0.270086	0.883098
Nap1l2	nucleosome assembly protein 1-like 2	-0.09	-0.8	0.501	-0.18	0.558	-0.06	0.007895	0.046084	0.989534
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcompl	0.316	-0.57	0.269	-0.29	0.315	-0.12	0.01648	0.773347	0.760009
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcompl	0.271	-0.95	0.381	-0.37	0.67	-0.12	0.000186	0.100809	0.649653
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomple	0.325	-0.8	0.482	-0.04	0.05	-0.13	0.017147	0.328491	0.295974
Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomple	0.214	-0.85	0.269	-0.19	0.523	-0.07	0.005463	0.190168	0.568545

Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomple	0.226	-0.61	0.119	-0.38	0.688	-0.12	0.005106	0.237742	0.828603
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomple	0.296	-0.75	0.508	-0.38	0.331	-0.11	0.001954	0.467774	0.57425
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomple	0.324	-0.83	0.121	-0.4	0.951	-0.28	6.22E-05	0.084252	0.36624
Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex un	0.125	-0.5	0.266	-0.34	0.805	-0.41	0.001236	0.42447	0.503201
Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	0.454	-0.6	0.168	-0.4	0.5	-0.23	0.002376	0.668189	0.720603
Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	0.13	-0.72	0.329	-0.59	0.526	0.244	0.006014	0.061976	0.493723
Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	0.03	-0.76	0.401	-0.29	0.781	-0.25	0.00081	0.093526	0.834681
Nelf	nasal embryonic LHRH factor	0.394	-0.33	-0.22	-0.43	0.69	-0.18	0.017853	0.16519	0.516688
Ngef	neuronal guanine nucleotide exchange factor	-0.1	-0.64	0.341	-0.19	0.678	-0.14	0.013477	0.1028	0.860177
Nkiras1	NFKB inhibitor interacting Ras-like protein 1	0.63	-0.45	0.026	-0.05	0.31	-0.58	0.007516	0.751617	0.21507
Npas4	neuronal PAS domain protein 4	0.311	-0.67	0.494	0.023	0.21	-0.46	0.005659	0.29094	0.693763
Npy	neuropeptide Y	0.288	-0.86	0.377	-0.06	0.731	-0.59	7.32E-05	0.239943	0.245405
Nr1d2	nuclear receptor subfamily 1, group D, member 2	-0	-0	0.363	-0.74	0.538	-0.16	0.01865	0.458709	0.189558
Nr3c2	nuclear receptor subfamily 3, group C, member 2	0.157	-0.76	0.436	-0.01	0.319	-0.24	0.013178	0.239404	0.726116
Nrn1	neuritin 1	0.265	-0.66	0.147	-0.28	0.759	-0.32	0.00135	0.352129	0.518144
Nsf	N-ethylmaleimide sensitive fusion protein	-0.01	-0.72	0.172	-0.17	0.753	-0.1	0.01221	0.075964	0.684714
Nt5c3l	5'-nucleotidase, cytosolic III-like	0.105	-0.57	0.749	-0.42	0.379	-0.31	0.000856	0.392078	0.633859
Ogn	osteoglycin	0.649	-0.6	0.373	-0.06	-0.13	-0.35	0.012097	0.411401	0.200463
Olfm1	olfactomedin 1	0.133	-0.53	0.008	-0.4	0.774	-0.05	0.012814	0.110582	0.784511
Omg	oligodendrocyte myelin glycoprotein	0.199	-0.41	0.391	-0.16	0.419	-0.49	0.008013	0.767898	0.824031
OTTMUSG	predicted gene, OTTMUSG00000014243	0.548	-0.63	-0.33	-0.34	0.704	-0.07	0.007672	0.085707	0.130088
OTTMUSG	predicted gene, OTTMUSG00000014892	-0.04	-0.52	0.283	-0.45	0.678	-0	0.013225	0.122229	0.906349
Pabpc1	poly A binding protein, cytoplasmic 1	-0.06	-0.6	0.504	-0.39	0.651	-0.16	0.003088	0.15231	0.823443
Pam	peptidylglycine alpha-amidating monooxygenase	0.018	-0.53	0.573	-0.6	0.419	0.058	0.006287	0.262313	0.372321
Pank4	pantothenate kinase 4	0.541	-0.26	-0.04	-0.15	0.381	-0.56	0.01674	0.681194	0.363009
Pard6a	par-6 (partitioning defective 6,) homolog alpha (C. eleg	-0.32	-0.38	0.342	-0.23	0.975	-0.39	0.006082	0.081854	0.079476
Pcbp4	poly(rC) binding protein 4	-0.02	-0.53	0.081	-0.48	0.861	0.038	0.010831	0.032219	0.855986
Pctk2	PCTAIRE-motif protein kinase 2	-0	-0.41	0.52	-0.48	0.653	-0.32	0.001808	0.453155	0.529487
Pdha1	pyruvate dehydrogenase E1 alpha 1	-0.08	-0.56	0.457	-0.08	0.634	-0.42	0.0067	0.201078	0.578003
Pebp1	phosphatidylethanolamine binding protein 1	0.151	-0.87	0.107	-0.2	0.573	0.142	0.019093	0.062665	0.444583
Pef1	penta-EF hand domain containing 1	0.158	-0.5	0.109	-0.21	0.633	-0.26	0.016677	0.500936	0.650756
Pfn2	profilin 2	0.11	-0.94	0.343	-0.31	0.632	0.058	0.002149	0.03686	0.673508
Pftk1	PFTAIRE protein kinase 1	0.217	-0.47	0.094	-0.34	0.708	-0.28	0.006364	0.440748	0.664482
Pgk1	phosphoglycerate kinase 1	0.128	-0.66	0.321	-0.21	0.577	-0.23	0.005864	0.328632	0.876276



Pla2g7	phospholipase A2, group VII (platelet-activating factor	0.782	-0.55	0.363	-0.06	-0.3	-0.37	0.013679	0.185206	0.094483
Pldn	pallidin	0.151	-1.07	0.661	-0.05	0.239	-0.06	0.002338	0.027132	0.275794
Plekhb1	pleckstrin homology domain containing, family B (evec	0.144	-0.9	0.09	-0.08	0.643	-0.01	0.013295	0.073334	0.344401
Plekhb2	pleckstrin homology domain containing, family B (evec	0.215	-0.66	0.481	0.061	0.22	-0.4	0.013022	0.253106	0.755774
Plekhg1	pleckstrin homology domain containing, family G (with	0.283	-0.6	0.421	-0.33	0.716	-0.58	0.000101	0.689249	0.599367
Plp1	proteolipid protein (myelin) 1	0.121	-0.6	0.334	-0.18	0.562	-0.31	0.00666	0.426967	0.8399
Polb	polymerase (DNA directed), beta	0.5	-0.23	0.342	-0.17	0.074	-0.59	0.014278	0.387111	0.938309
Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	0.177	-0.46	0.179	0.028	0.588	-0.58	0.011336	0.726041	0.25538
Pou4f1	POU domain, class 4, transcription factor 1	0.764	-0.07	0.443	-0.65	-0.14	-0.43	0.002609	0.08289	0.371307
Ppib	peptidylprolyl isomerase B	0.12	-0.69	0.203	-0.39	0.677	-0.01	0.006284	0.115207	0.93648
Ppme1	protein phosphatase methylesterase 1	0.265	-0.52	0.308	-0.57	0.554	-0.12	0.002466	0.413988	0.944306
Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	0.155	-1.01	0.231	-0.13	0.578	0.057	0.005877	0.042682	0.355503
Ppp1r16b	protein phosphatase 1, regulatory (inhibitor) subunit 16	0.316	-0.22	-0.01	-0.76	0.626	-0	0.011552	0.068766	0.9403
Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0.069	-0.57	0.387	-0.78	0.614	0.221	0.002699	0.04148	0.390008
Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit,	0.198	-0.78	0.38	-0.18	0.461	-0.17	0.004722	0.291351	0.76311
Prdx5	peroxiredoxin 5	0.218	-0.84	0.394	-0.26	0.556	-0.17	0.001316	0.218853	0.775231
Prickle1	prickle like 1 (Drosophila)	0.442	-0.21	0.016	-0.15	0.62	-0.79	0.00312	0.753564	0.110885
Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	0.299	-0.79	0.199	-0.3	0.587	-0.11	0.002824	0.267675	0.600057
Prkcb	protein kinase C, beta	0.719	-0.25	0.171	-0.57	0.106	-0.27	0.006202	0.332231	0.609999
Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolo	0.155	-0.79	0.574	-0.1	0.318	-0.25	0.004215	0.180458	0.806353
Prss12	protease, serine, 12 neurotrypsin (motopsin)	-0.05	-0.62	0.46	-0.2	0.771	-0.42	0.001311	0.154379	0.51529
Pthlh	parathyroid hormone-like peptide	0.127	-0.33	0.789	-0.49	0.188	-0.32	0.003181	0.661322	0.311712
Pttg1	pituitary tumor-transforming gene 1	0.086	-0.81	0.261	-0.2	0.722	-0.15	0.003116	0.093123	0.708027
Pvalb	parvalbumin	0.482	-0.53	0.269	-0.47	0.797	-0.64	1.48E-05	0.806822	0.445075
Rab2a	RAB2A, member RAS oncogene family	-0.06	-0.88	0.417	-0.17	0.549	0.062	0.011242	0.030098	0.846924
Rab6	RAB6, member RAS oncogene family	0.185	-0.57	0.258	-0.58	0.443	0.187	0.015801	0.181379	0.585058
Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	0.641	-0.14	0.335	-0.49	0.153	-0.58	0.002178	0.287439	0.988176
Rasal2	RAS protein activator like 2	0.186	-0.79	0.469	-0.59	0.551	0.078	0.000749	0.105829	0.544628
Reep1	receptor accessory protein 1	-0.11	-0.51	0.677	-0.02	0.494	-0.57	0.003927	0.102859	0.534555
Rgs4	regulator of G-protein signaling 4	0.277	-0.71	0.556	0.029	0.534	-0.78	0.000112	0.157369	0.365146
Rgs7bp	regulator of G-protein signalling 7 binding protein	0.551	0.129	0.192	-0.46	0.295	-0.75	0.004862	0.127902	0.567288
Rhebl1	Ras homolog enriched in brain like 1	0.281	-0.66	0.543	-0.05	0.081	-0.28	0.013914	0.326673	0.633935
Rnf11	ring finger protein 11	0.102	-0.45	0.271	-0.45	0.758	-0.29	0.002455	0.355947	0.703375
Rnf26	ring finger protein 26	0.322	-1.16	0.106	-0.12	0.671	0.031	0.00104	0.026746	0.078453

Rtn3	reticulon 3	0.145	-0.88	0.371	-0.06	0.493	-0.17	0.005262	0.134284	0.6074
Rtn4	reticulon 4	0.038	-0.78	0.36	-0.16	0.864	-0.4	0.000407	0.087651	0.429373
Rundc3b	RUN domain containing 3B	-0.07	-0.54	0.777	-0.14	0.216	-0.3	0.013063	0.124699	0.720057
Rusc1	RUN and SH3 domain containing 1	0.216	-0.89	0.297	-0.07	0.579	-0.24	0.002383	0.177429	0.453862
Sag	retinal S-antigen	0.127	-0.99	0.296	0.142	0.593	-0.28	0.003659	0.052661	0.229744
Satb2	special AT-rich sequence binding protein 2	0.361	-0.11	0.08	-0.08	0.467	-0.77	0.015055	0.659049	0.196985
Scg2	secretogranin II	0.321	-0.83	0.843	-0.47	0.09	-0.07	0.000349	0.295012	0.095243
Scg3	secretogranin III	0.101	-0.64	0.483	-0.26	0.356	-0.11	0.012003	0.353705	0.870449
Scn1b	sodium channel, voltage-gated, type I, beta	0.456	-0.65	-0.33	0.032	0.822	-0.44	0.005542	0.429975	0.010042
Sdf4	stromal cell derived factor 4	-0.02	-0.81	0.223	-0.15	0.676	0.002	0.01538	0.045815	0.770039
Sdhb	succinate dehydrogenase complex, subunit B, iron sulf	0.171	-0.97	0.371	-0.2	0.56	-0.05	0.001937	0.073543	0.550725
Sepw1	selenoprotein W, muscle 1	0.229	-0.57	-0.08	-0.31	0.747	-0.09	0.014078	0.153051	0.536558
Sgjp1	SH3-domain GRB2-like (endophilin) interacting protein	-0	-0.54	0.534	-0.1	0.642	-0.58	0.001432	0.248486	0.454649
Skp1a	S-phase kinase-associated protein 1A	-0.03	-0.53	0.446	-0.33	0.526	-0.13	0.012979	0.281308	0.902291
Slc23a2	solute carrier family 23 (nucleobase transporters), mem	0.301	-0.66	0.417	0.285	0.349	-0.79	0.00243	0.093306	0.182566
Slc25a26	solute carrier family 25 (mitochondrial carrier, phosph	0.103	-0.62	0.178	-0.35	0.795	-0.18	0.003405	0.155809	0.754291
Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine	-0.06	-0.84	0.387	-0.08	0.73	-0.21	0.003319	0.037549	0.7075
Slc30a4	solute carrier family 30 (zinc transporter), member 4	0.367	-0.37	0.624	-0.36	0.231	-0.56	0.001056	0.610862	0.909395
Slc48a1	solute carrier family 48 (heme transporter), member 1	0.373	-0.77	0.265	-0.02	0.492	-0.45	0.001782	0.538633	0.318747
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	0.05	-0.65	0.331	0.106	0.521	-0.43	0.014567	0.228299	0.481619
Snap25	synaptosomal-associated protein 25	0.125	-0.86	0.319	-0.25	0.649	-0.08	0.002393	0.088681	0.767288
Snrnp27	small nuclear ribonucleoprotein 27 (U4/U6.U5)	0.321	-0.39	0.018	-0.29	0.564	-0.3	0.016517	0.682919	0.653838
Snx3	sorting nexin 3	0.378	-0.73	0.032	-0.33	0.533	0.007	0.009012	0.258774	0.42814
Snx33	sorting nexin 33	0.389	-0.14	0.202	-0.09	0.364	-0.78	0.010593	0.512447	0.351283
Sorl1	sortilin-related receptor, LDLR class A repeats-contain	0.113	-0.42	0.421	-0.41	0.681	-0.43	0.001187	0.64072	0.624327
Sox18	SRY-box containing gene 18	0.294	-0.56	0.044	-0.07	0.554	-0.34	0.016247	0.742011	0.366911
Sparcl1	SPARC-like 1	0.322	-0.79	0.31	-0.44	0.629	-0.15	0.000491	0.261995	0.784579
Spna2	spectrin alpha 2	0.157	-0.83	0.328	-0.09	0.638	-0.31	0.001943	0.179831	0.560118
Srfbp1	serum response factor binding protein 1	0.091	-0.06	0.683	-0.74	0.196	-0.18	0.010017	0.989692	0.087794
Srr	serine racemase	0.031	-0.79	0.322	-0.25	0.682	-0.08	0.00444	0.078384	0.906931
Sst	somatostatin	0.283	-0.96	0.555	-0.45	1.046	-0.59	1.23E-08	0.059783	0.410841
Stmn3	stathmin-like 3	0.389	-0.8	0.391	-0.44	0.465	-0.13	0.000593	0.443212	0.590055
Stmn4	stathmin-like 4	0.394	-0.79	0.277	-0.35	0.764	-0.41	5.8E-05	0.405552	0.525104
Stt3b	STT3, subunit of the oligosaccharyltransferase comple	0.746	-0.11	0.312	-0.75	0.119	-0.4	0.00105	0.141379	0.645858

Stx6	syntaxin 6	0.192	-0.69	0.236	-0.6	1.21	-0.43	1.08E-06	0.025502	0.201972
Suds3	suppressor of defective silencing 3 homolog (S. cerevi	0.141	-0.41	0.412	-0.63	0.662	-0.23	0.001101	0.413941	0.70141
Syn2	synapsin II	0.298	-0.21	-0.03	-0.78	0.632	0.041	0.013358	0.050885	0.915714
Syngr3	synaptogyrin 3	0.063	-0.17	0.147	-0.54	0.867	-0.39	0.003833	0.323091	0.229836
Syt1	synaptotagmin I	0.005	-0.77	0.25	-0.12	0.714	-0.15	0.007688	0.083662	0.673037
Tacc2	transforming, acidic coiled-coil containing protein 2	0.009	-0.55	0.218	-0	0.712	-0.44	0.011305	0.331208	0.298607
Tbcb	tubulin folding cofactor B	0.242	-0.66	0.402	-0.36	0.262	0.019	0.014602	0.522796	0.536865
Tbx18	T-box18	0.699	-0.43	0.038	-0.04	0.101	-0.47	0.019584	0.574971	0.232196
Tet1	tet oncogene 1	0.407	0.077	0.281	-0.69	0.207	-0.32	0.018155	0.340376	0.569115
Them2	thioesterase superfamily member 2	0.204	-0.63	0.259	-0.38	0.581	-0.12	0.005008	0.345114	0.948763
Timm10	translocase of inner mitochondrial membrane 10 homod	0.307	-0.9	0.177	-0.28	0.592	-0.01	0.00252	0.142901	0.409086
Tmem125	transmembrane protein 125	-0.11	-0.78	0.496	-0.31	0.482	0.148	0.01613	0.039427	0.719199
Tmem151a	transmembrane protein 151A	0.229	-0.54	-0.01	-0.25	0.676	-0.17	0.015949	0.334083	0.558239
Tmem178	transmembrane protein 178	0.295	0.103	0.057	-0.35	0.634	-0.76	0.007962	0.479975	0.104426
Tmem214	transmembrane protein 214	0.508	-0.1	0.495	-0.79	-0.11	-0.06	0.014337	0.449233	0.085334
Tmem30a	transmembrane protein 30A	-0.06	-0.7	0.532	-0.34	0.508	4E-04	0.00748	0.096128	0.824661
Tmem59l	transmembrane protein 59-like	0.322	-0.88	0.151	-0.56	0.894	-0.05	7.17E-05	0.022742	0.666797
Tmsb4x	thymosin, beta 4, X chromosome	-0.14	-0.81	0.346	-0.19	0.707	0.014	0.010784	0.020477	0.95821
Tnc	tenascin C	0.292	-0.2	0.391	-0.26	0.267	-0.55	0.013103	0.761155	0.86995
Tpm1	tropomyosin 1, alpha	0.011	-0.84	0.466	-0.21	0.553	-0.06	0.00447	0.067431	0.919354
Trak2	trafficking protein, kinesin binding 2	0.702	-0.37	0.457	-0.28	0.288	-0.9	4.06E-05	0.187866	0.692437
Trim44	tripartite motif-containing 44	-0.14	-0.72	0.161	-0.16	0.862	-0.06	0.014045	0.022679	0.598689
Trim7	tripartite motif-containing 7	-0.11	-0.48	0.395	-0.26	0.817	-0.39	0.00303	0.206764	0.358212
Tro	trophinin	0.147	-0.38	0.545	-0.27	0.345	-0.44	0.006564	0.701394	0.872867
Trp63	transformation related protein 63	0.131	-0.87	0.151	-0.18	0.774	-0.1	0.002974	0.060642	0.478059
Tspan7	tetraspanin 7	0.094	-0.89	0.285	-0.4	0.837	-0.03	0.000539	0.022303	0.870356
Ttc9b	tetratricopeptide repeat domain 9B	0.018	-0.51	0.193	-0.26	0.732	-0.23	0.011945	0.266473	0.668989
Ttl5	tubulin tyrosine ligase-like family, member 5	0.357	-0.27	0.337	-0.45	0.212	-0.24	0.017573	0.951641	0.869325
Tuba1b	tubulin, alpha 1B	-0.05	-0.64	0.417	-0.22	0.526	-0.09	0.016323	0.163125	0.997667
Tuba4a	tubulin, alpha 4A	0.005	-0.73	0.471	-0.15	0.479	-0.15	0.009833	0.146161	0.979306
Tubb3	tubulin, beta 3	0.209	-0.75	0.602	-0.39	0.353	-0.12	0.001466	0.329771	0.617255
Tubb5	tubulin, beta 5	-0.01	-0.72	0.412	-0.17	0.706	-0.29	0.002447	0.118067	0.777787
Tulp4	tubby like protein 4	0.425	-0.28	0.412	-0.18	0.054	-0.5	0.018078	0.492446	0.970822
Txndc13	thioredoxin domain containing 13	-0.16	-0.52	0.826	-0.47	0.446	-0.15	0.002329	0.144149	0.250828

Ubac1	ubiquitin associated domain containing 1	0.442	-0.29	0.32	-0.22	0.2	-0.53	0.010908	0.69172	0.936631
Ube2k	ubiquitin-conjugating enzyme E2K (UBC1 homolog, ye	-0.05	-0.74	0.484	-0.09	0.43	-0.11	0.018621	0.1053	0.967504
Ubl5	ubiquitin-like 5	-0.05	-0.48	0.484	-0.24	0.479	-0.23	0.016998	0.356318	0.857548
Ubn1	ubiquitin 1	0.269	-0.16	0.338	-0.67	0.305	-0.13	0.016745	0.667563	0.558298
Ubqln1	ubiquilin 1	0.458	-0.38	0.446	-0.27	0.354	-0.69	0.000682	0.647245	0.847121
Ubxn6	UBX domain protein 6	0.178	-0.69	0.193	-0.12	0.721	-0.37	0.002845	0.344592	0.404591
Ufc1	ubiquitin-fold modifier conjugating enzyme 1	0.11	-0.9	0.209	0.032	0.581	-0.13	0.011699	0.09178	0.371271
Ufsp2	UFM1-specific peptidase 2	0.123	-0.81	0.524	-0.11	0.281	-0.09	0.011017	0.165383	0.649282
Uqcrfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur p	0.114	-1.05	0.479	-0.04	0.562	-0.18	0.000953	0.030007	0.520663
Usp22	ubiquitin specific peptidase 22	0.025	-0.89	0.179	-0.08	0.69	-0.01	0.011751	0.036298	0.523168
Vdac1	voltage-dependent anion channel 1	0.178	-0.9	0.193	-0.3	0.796	-0.07	0.000953	0.047399	0.58887
Vdac2	voltage-dependent anion channel 2	0.05	-0.86	0.474	-0.29	0.724	-0.18	0.000486	0.055438	0.957862
Vgf	VGF nerve growth factor inducible	0.455	-0.65	0.803	-0.63	0.235	-0.32	2.71E-05	0.792094	0.275577
Vps29	vacuolar protein sorting 29 (S. pombe)	0.059	-0.83	0.617	-0.1	0.266	-0.1	0.009339	0.095023	0.673849
Vsn1	visinin-like 1	0.084	-0.97	0.428	-0.14	0.756	-0.27	0.000307	0.036615	0.621216
Wbp5	WW domain binding protein 5	0.249	-0.62	0.953	-0.28	-0.05	-0.35	0.001156	0.111982	0.268126
Wnt7b	wingless-related MMTV integration site 7B	0.359	-0.55	-0.22	-0.39	0.71	0.006	0.017447	0.083099	0.44312
Wwp2	WW domain containing E3 ubiquitin protein ligase 2	0.383	-0.68	-0.04	-0.09	0.656	-0.33	0.005697	0.552993	0.1755
Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	-0.02	-0.56	0.383	-0.38	0.591	-0.07	0.010827	0.207075	0.938551
Zcrb1	zinc finger CCHC-type and RNA binding motif 1	0.16	-0.45	0.742	-0.13	0.52	-0.9	6.58E-05	0.145836	0.325586
Zdhhc17	zinc finger, DHHC domain containing 17	0.302	-0.49	0.312	0.104	0.445	-0.75	0.003719	0.429911	0.254118
Zfp704	zinc finger protein 704	0.354	-0.16	0.159	-0	0.406	-0.81	0.013515	0.545973	0.217263
<b>Linear Increase (234)</b>										
39879	membrane-associated ring finger (C3HC4) 7	-0.55	-0.61	-0.04	0.238	0.647	0.301	0.852685	0.002809	0.575686
Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	-1.1	-1.11	-0.11	0.222	0.908	1.186	0.104851	0	0.461109
Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	-0.75	-0.32	-0.37	0.496	0.372	0.605	0.031821	0.002827	0.529049
Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	-0.92	-1.24	0.218	0.19	1.016	0.705	0.166972	1.65E-13	0.690363
Abhd12	abhydrolase domain containing 12	-0.58	-0.32	-0.08	-0.14	0.446	0.69	0.548766	0.004213	0.830454
Acaca	acetyl-Coenzyme A carboxylase alpha	-0.75	-0.12	-0.32	0.217	1.011	0.017	0.809088	0.004632	0.007194
Acer2	alkaline ceramidase 2	-0.48	-0.61	-0.75	0.367	0.875	0.587	0.268862	1.94E-05	0.014244
Acs1	acyl-CoA synthetase long-chain family member 1	-0.73	-1.26	0.262	0.185	0.992	0.49	0.043067	4.35E-10	0.51384
Acs13	acyl-CoA synthetase long-chain family member 3	-0.66	-0.49	-0.35	0.245	0.365	0.904	0.058463	0.000248	0.711895
Actr2	ARP2 actin-related protein 2 homolog (yeast)	-0.28	-0.78	0.217	-0.16	0.563	0.393	0.156634	0.004986	0.855294
Actr3	ARP3 actin-related protein 3 homolog (yeast)	-0.36	-0.46	0.4	-0.51	0.688	0.239	0.046565	0.015255	0.385612

Agt	angiotensinogen (serpin peptidase inhibitor, clade A, n	-0.63	-0.8	-0.12	0.099	0.653	0.78	0.796085	9.61E-06	0.742679
Als2	Amyotrophic lateral sclerosis 2 (juvenile) homolog (hur	-0.47	-0.54	-0.04	0.011	0.759	0.274	0.491538	0.004636	0.641737
Ankrd37	ankyrin repeat domain 37	-0.45	-0.69	0.06	0.008	0.531	0.512	0.669246	0.002323	0.922358
Ano8	anoctamin 8	-0.53	-0.28	-0.15	-0.07	0.797	0.267	0.781185	0.008554	0.396527
Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family,	-0.46	-0.76	-0.39	0.405	0.706	0.471	0.697856	0.000315	0.092193
Anubl1	AN1, ubiquitin-like, homolog (Xenopus laevis)	-0.57	-0.37	-0.04	0.105	0.419	0.466	0.607548	0.016334	0.96935
Apoc1	apolipoprotein C-I	-1.1	-0.97	0.021	0.072	0.999	0.992	0.693718	5.44E-15	0.929519
Apod	apolipoprotein D	-1	-1.12	-0.09	0.202	0.913	1.088	0.405452	6.66E-16	0.476744
Apoe	apolipoprotein E	-0.79	-0.92	-0.01	0.158	0.83	0.726	0.924952	7.53E-08	0.795898
Arf5	ADP-ribosylation factor 5	0.13	-1.03	-0.11	0.011	0.727	0.151	0.024607	0.01139	0.090488
Arrdc4	arrestin domain containing 4	-0.69	-0.6	0.113	0.079	0.848	0.262	0.443696	0.000332	0.445158
Atxn10	ataxin 10	-0.03	-0.78	0.242	-0.48	0.555	0.418	0.028598	0.011454	0.499718
B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransfer	-0.28	-0.68	-0.15	0.152	0.172	0.742	0.525591	0.0106	0.250553
B4galnt4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-0.42	-0.77	0.143	0.118	0.745	0.155	0.183971	0.002303	0.62546
Bag5	BCL2-associated athanogene 5	-0.48	-0.5	0.166	0.073	0.706	0.033	0.296016	0.018637	0.493663
BC024814	cDNA sequence BC024814	-0.7	-0.3	0.012	0.218	0.579	0.24	0.716272	0.011546	0.447283
BC057552	cDNA sequence BC057552	-0.43	-0.54	-0.23	-0	0.535	0.654	0.742601	0.00212	0.840608
Bcas3	breast carcinoma amplified sequence 3	-0.32	-0.66	-0.25	0.06	0.56	0.565	0.969657	0.003164	0.553354
Braf	Braf transforming gene	-0.38	-0.63	-0.24	0.364	0.333	0.53	0.459014	0.009976	0.363913
Brd8	bromodomain containing 8	-0.54	-0.46	0.092	-0.02	0.493	0.447	0.915217	0.008831	0.948951
Bre	brain and reproductive organ-expressed protein	-0.1	-0.89	0.199	-0.15	0.103	0.757	0.497728	0.009414	0.046049
Btf3l4	basic transcription factor 3-like 4	-0.5	-0.56	-0.11	0.158	0.603	0.403	0.993882	0.004473	0.719076
C1qbp	complement component 1, q subcomponent binding p	-0.39	-0.55	0.238	-0.19	0.852	0.021	0.052464	0.012291	0.526673
Ccdc136	coiled-coil domain containing 136	-0.27	-0.74	-0.04	0.254	0.436	0.313	0.685962	0.016638	0.463806
Ccdc21	coiled-coil domain containing 21	-0.57	-0.62	0.179	0.03	0.515	0.468	0.738085	0.00194	0.980004
Cd47	CD47 antigen (Rh-related antigen, integrin-associated	-0.35	-0.89	0.085	0.18	0.518	0.397	0.431151	0.001782	0.545171
Cenpp	centromere protein P	-0.62	-0.26	0.059	-0.35	0.666	0.533	0.805234	0.00246	0.414821
Cfl1	cofilin 1, non-muscle	-0.07	-0.97	0.147	-0.24	0.644	0.397	0.033018	0.002685	0.492464
Cirbp	cold inducible RNA binding protein	-0.61	-0.66	0.106	0.157	0.424	0.577	0.833164	0.000954	0.93903
Col4a3bp	collagen, type IV, alpha 3 (Goodpasture antigen) bindi	-0.73	-0.87	0.028	0.395	0.531	0.634	0.613005	8.59E-06	0.63731
Col9a1	collagen, type IX, alpha 1	-0.68	-0.99	0.307	0.019	0.396	0.924	0.914551	7.89E-07	0.176049
Coq3	coenzyme Q3 homolog, methyltransferase (yeast)	-0.62	-0.5	0.163	0.128	0.414	0.431	0.89247	0.005566	0.967321
Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	-0.69	-0.31	-0.07	-0.15	0.957	0.314	0.619788	0.000615	0.197649
Crebzf	CREB/ATF bZIP transcription factor	-0.31	-0.52	-0.2	0.061	0.63	0.313	0.721572	0.018878	0.607766

Crkrs	CDC2-related kinase, arginine/serine-rich	-0.44	-0.65	0.499	-0.31	0.362	0.521	0.236479	0.00464	0.252388
Crybb1	crystallin, beta B1	-0.51	-0.66	-0.52	0.106	0.675	0.883	0.294945	1.04E-05	0.346676
Cxcl12	chemokine (C-X-C motif) ligand 12	-0.19	-1.09	-0.08	0.012	0.731	0.523	0.130023	0.000108	0.179927
Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide	-0.75	-0.27	-0.55	0.263	0.982	0.377	0.284869	0.000119	0.024342
Cyp4f15	cytochrome P450, family 4, subfamily f, polypeptide 15	-0.66	-0.44	0.16	-0.27	0.277	0.949	0.505005	0.000517	0.148586
Dbndd2	dysbindin (dystrobrevin binding protein 1) domain cont	-0.8	-0.4	-0.32	0.349	0.581	0.622	0.10727	0.000318	0.526081
Dbp	D site albumin promoter binding protein	-0.43	-0.63	0.243	-0.14	0.5	0.437	0.380832	0.00609	0.864359
Dcxr	dicarbonyl L-xylulose reductase	-0.63	-0.26	-0.38	0.252	0.218	0.837	0.025791	0.005057	0.876948
Ddc	dopa decarboxylase	-0.34	-0.76	-0.31	0.188	0.115	1.069	0.124493	0.000444	0.043745
Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	-0.37	-0.58	0.188	-0.09	0.143	0.689	0.931331	0.016844	0.326686
Dgat2	diacylglycerol O-acyltransferase 2	-0.51	-0.53	-0.12	-0.08	0.947	0.304	0.371987	0.000689	0.419777
Dgcr14	DiGeorge syndrome critical region gene 14	-0.31	-0.72	0.223	-0.01	0.774	5E-04	0.055402	0.010689	0.643796
Dhdds	dehydrodolichyl diphosphate synthase	-0.36	-0.57	-0.16	-0.01	0.645	0.431	0.710394	0.005669	0.780144
Dido1	death inducer-obliterator 1	-0.6	-0.37	-0.28	0.349	0.479	0.443	0.264066	0.009435	0.537063
Diras2	DIRAS family, GTP-binding RAS-like 2	-0.51	-0.48	-0.08	0.202	0.339	0.525	0.507843	0.013193	0.917861
Dnaic1	dynein, axonemal, intermediate chain 1	-0.44	-0.45	-0.53	0.499	0.251	0.671	0.045987	0.01063	0.198275
Dnajc16	DnaJ (Hsp40) homolog, subfamily C, member 16	-0.21	-0.82	0.131	-0.13	0.715	0.254	0.068893	0.005307	0.839252
Dnajc30	DnaJ (Hsp40) homolog, subfamily C, member 30	-0.28	-0.61	0.008	-0.12	0.873	0.101	0.091584	0.009913	0.545619
Eef2k	eukaryotic elongation factor-2 kinase	-0.27	-0.58	-0.18	-0.09	0.893	0.201	0.217219	0.005282	0.412697
Eftud1	elongation factor Tu GTP binding domain containing 1	-0.54	-0.34	-0.15	0.047	0.696	0.319	0.975179	0.009528	0.544321
EG629732	predicted gene, EG629732	-0.22	-0.7	-0.24	0.274	0.628	0.216	0.611018	0.017437	0.187347
Eid1	EP300 interacting inhibitor of differentiation 1	-0.12	-0.74	0.031	-0.14	0.659	0.248	0.106553	0.018191	0.758369
Eif2b3	eukaryotic translation initiation factor 2B, subunit 3	-0.38	-0.46	0.044	-0.16	0.904	0.037	0.11904	0.014787	0.363873
Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, struc	-0.37	-0.74	0.37	-0.16	0.652	0.209	0.066631	0.004988	0.964125
Eif4b	eukaryotic translation initiation factor 4B	-0.51	-0.72	-0.32	0.286	0.709	0.53	0.756624	0.000231	0.26328
Eif5	eukaryotic translation initiation factor 5	-0.31	-0.98	0.138	0.169	0.772	0.15	0.073086	0.000722	0.385918
Eml2	echinoderm microtubule associated protein like 2	-0.43	-0.65	0.056	0.031	0.598	0.367	0.521198	0.005062	0.928737
Eng	endoglin	-0.14	-0.66	-0.25	0.03	0.378	0.596	0.973877	0.015624	0.337241
ENSMUSG	predicted gene, ENSMUSG00000058905	0.007	-0.89	0.078	-0.13	0.636	0.209	0.039345	0.019241	0.496305
Ewsr1	Ewing sarcoma breakpoint region 1	-0.31	-0.66	0.069	-0.1	0.783	0.184	0.129028	0.007738	0.768107
Fads2	fatty acid desaturase 2	-1.04	-0.8	-0.03	0.278	0.768	0.852	0.262406	1.92E-09	0.879034
Fam120b	family with sequence similarity 120, member B	-0.36	-0.45	-0.01	-0.16	0.341	0.636	0.935185	0.016809	0.736187
Foxp4	forkhead box P4	-0.46	-0.88	0.094	0.053	0.668	0.481	0.347657	0.000223	0.789278
Fxyd6	FXYD domain-containing ion transport regulator 6	-0.31	-0.78	-0.21	0.337	0.543	0.376	0.895552	0.004562	0.214626

Fzd2	frizzled homolog 2 (Drosophila)	-0.38	-0.57	-0.21	0.037	0.863	0.239	0.434909	0.00362	0.335329
Gaa	glucosidase, alpha, acid	-0.31	-0.68	-0.08	0.172	0.106	0.748	0.475574	0.011856	0.242668
Gas8	growth arrest specific 8	-0.65	-0.15	-0.58	0.418	0.673	0.34	0.100073	0.008174	0.070011
Ggt1	gamma-glutamyltransferase 1	-0.89	-0.74	-0.03	0.089	0.378	1.202	0.062247	4.54E-08	0.242806
Gle1	GLE1 RNA export mediator (yeast)	-0.3	-0.53	-0.12	-0.14	0.731	0.334	0.390469	0.008381	0.819121
Gltscr2	glioma tumor suppressor candidate region gene 2	-0.21	-0.79	-0.22	-0.09	0.914	0.338	0.145054	0.000677	0.358062
Gm1821	gene model 1821, (NCBI)	-0.23	-0.8	0.303	-0.15	0.688	0.126	0.033116	0.009921	0.97451
Gm967	gene model 967, (NCBI)	-0.74	-0.6	-0.07	0.312	0.387	0.729	0.209663	0.000204	0.897088
Gnb4	guanine nucleotide binding protein (G protein), beta 4	-0.28	-0.67	0.042	0.045	0.222	0.607	0.999022	0.018014	0.451074
Gne	glucosamine	-0.51	-0.65	-0.13	0.133	0.686	0.454	0.875127	0.001002	0.665643
Got2	glutamate oxaloacetate transaminase 2, mitochondrial	-0.26	-0.85	0.018	-0.13	0.714	0.451	0.160546	0.000971	0.726938
Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	-0.76	-0.37	-0.13	0.37	0.46	0.466	0.214496	0.003006	0.674849
Gpc5	glypican 5	-0.13	-0.82	-0.05	-0.03	0.424	0.53	0.444844	0.009781	0.35564
Gpi1	glucose phosphate isomerase 1	0.059	-0.88	-0.14	-0.04	0.596	0.31	0.12629	0.018141	0.224295
Gpr146	G protein-coupled receptor 146	-0.28	-0.77	-0.2	0.272	0.427	0.504	0.929373	0.006144	0.275297
Grhr	glyoxylate reductase/hydroxypyruvate reductase	-0.52	-0.29	-0.24	0.067	0.255	0.742	0.169095	0.013909	0.909475
Grwd1	glutamate-rich WD repeat containing 1	-0.29	-0.66	0.412	-0.39	0.623	0.258	0.037832	0.011791	0.701041
Gsk3b	glycogen synthase kinase 3 beta	-0.21	-0.62	0.029	-0.28	0.409	0.631	0.496869	0.009633	0.529207
Gtrgeo22	gene trap ROSA b-geo 22	-0.61	-0.61	-0.13	0.279	0.613	0.466	0.710913	0.000823	0.606441
H1f0	H1 histone family, member 0	-0.36	-0.73	0.178	-0.01	0.56	0.329	0.285484	0.006073	0.949568
Hdgfrp3	hepatoma-derived growth factor, related protein 3	-0.45	-0.46	0.053	-0.04	0.6	0.293	0.590036	0.017771	0.88115
Hint1	histidine triad nucleotide binding protein 1	0.077	-1.07	-0.03	0.117	0.267	0.525	0.299665	0.011742	0.03267
Hyi	hydroxypyruvate isomerase homolog (E. coli)	-0.52	-0.6	0.17	-0.06	0.555	0.439	0.561714	0.003287	0.96856
Ier3	immediate early response 3	-0.35	-0.44	-0.09	-0.16	0.51	0.522	0.841247	0.012986	0.984514
Ifi47	interferon gamma inducible protein 47	-0.12	-0.77	-0.35	0.152	0.64	0.385	0.587725	0.007009	0.150781
Igfbp4	insulin-like growth factor binding protein 4	-0.25	-0.6	-0.36	0.07	1.202	-0.1	0.069828	0.002125	0.009044
Iitfg1	integrin alpha FG-GAP repeat containing 1	-0.37	-0.65	0.038	0.207	0.589	0.159	0.476244	0.015461	0.596179
Iitih3	inter-alpha trypsin inhibitor, heavy chain 3	-0.66	-0.52	0.212	-0.07	0.111	0.934	0.319017	0.000967	0.151691
Iitm2b	integral membrane protein 2B	-0.16	-0.92	0.04	-0.04	0.781	0.229	0.053255	0.002615	0.48889
Jag2	jagged 2	-0.39	-0.51	0.149	-0.19	0.732	0.204	0.186679	0.013122	0.790248
Kcna5	potassium voltage-gated channel, shaker-related subfa	-0.57	-0.48	0.279	-0.07	0.117	0.739	0.619726	0.007336	0.263641
Kcnp4	Kv channel interacting protein 4	-0.51	-0.42	-0.13	-0.07	0.786	0.352	0.701044	0.003565	0.609775
Kpna3	karyopherin (importin) alpha 3	-0.63	-0.24	-0.33	0.246	0.643	0.35	0.361387	0.010255	0.31133
Larp6	La ribonucleoprotein domain family, member 6	-0.13	-0.73	-0.2	0.073	0.619	0.306	0.381658	0.016201	0.340127

Lgi3	leucine-rich repeat LGI family, member 3	-0.44	-0.66	-0.37	0.101	0.888	0.454	0.79437	0.000211	0.243466
Lmna	lamin A	-0.65	-0.61	0.181	0.128	0.792	0.168	0.366212	0.000888	0.457454
Lpcat3	lysophosphatidylcholine acyltransferase 3	-1.02	-1.17	0.209	0.238	0.763	0.972	0.849884	4.06E-14	0.629833
Lrrtm4	leucine rich repeat transmembrane neuronal 4	-0.52	-0.3	-0.29	0.2	0.625	0.313	0.584877	0.018644	0.402753
Ly6a	lymphocyte antigen 6 complex, locus A	-0.56	-0.66	-0.26	0.097	0.711	0.665	0.747625	9.41E-05	0.666486
Lyrn4	LYR motif containing 4	0.096	-0.86	0.078	-0.31	0.165	0.732	0.282442	0.019532	0.037587
Mal	myelin and lymphocyte protein, T-cell differentiation pr	-0.54	-0.91	-0.19	0.263	0.663	0.677	0.87344	1.53E-05	0.317422
Map2k5	mitogen-activated protein kinase kinase 5	-0.66	-0.23	-0.12	-0.04	0.525	0.577	0.443534	0.005317	0.780974
Mare	alpha globin regulatory element containing gene	-0.48	-0.74	0.072	0.133	0.559	0.435	0.658325	0.001497	0.862981
Mast1	microtubule associated serine/threonine kinase 1	-0.39	-0.55	0.153	-0.26	0.787	0.245	0.12738	0.006021	0.812104
Mbp	myelin basic protein	-0.11	-0.81	0.06	-0.13	0.742	0.18	0.049149	0.011045	0.667518
Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial	-0.2	-0.87	-0.31	-0.07	0.868	0.515	0.24629	0.000127	0.24865
Meg3	maternally expressed 3	-0.32	-1.08	0.136	0.088	0.826	0.274	0.046446	0.000104	0.412906
Mepce	methylphosphate capping enzyme	-0.59	-0.29	-0.17	0.139	0.877	0.064	0.786781	0.011776	0.096086
Mfsd2	major facilitator superfamily domain containing 2	-1.02	-0.72	0.03	-0.05	0.819	0.978	0.486687	7.03E-10	0.684959
Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-lik	-1.04	-1.25	0.21	0.095	1.192	0.767	0.050244	0	0.585657
Mobb	myelin-associated oligodendrocytic basic protein	-0.27	-0.59	-0.24	-0.05	0.513	0.599	0.953568	0.005531	0.660339
Mrps26	mitochondrial ribosomal protein S26	-0.39	-0.57	0.106	-0.06	0.942	-0.05	0.065076	0.009292	0.273538
Myip	myosin regulatory light chain interacting protein	-0.66	-0.35	-0.26	0.342	0.694	0.265	0.50226	0.005649	0.199513
Naaa	N-acylethanolamine acid amidase	-0.47	-0.59	0.009	0.184	0.323	0.526	0.727347	0.009414	0.843647
Ncl	nucleolin	-0.33	-0.68	0.13	0.103	0.392	0.355	0.582945	0.017267	0.835155
Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosami	-0.25	-0.57	-0.38	0.196	0.62	0.348	0.97693	0.015017	0.253526
Nsg2	neuron specific gene family member 2	-0.39	-0.79	0.019	0.22	0.834	0.074	0.177476	0.002022	0.246555
Ntan1	N-terminal Asn amidase	-0.33	-0.63	0.315	-0.28	0.486	0.4	0.18829	0.01329	0.698544
Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	-0.42	-0.54	-0.26	0.399	0.241	0.571	0.237984	0.016238	0.434208
Oaz2	ornithine decarboxylase antizyme 2	0.058	-0.81	-0.08	-0.2	0.632	0.317	0.079562	0.017348	0.425032
OTTMUSG	predicted gene, OTTMUSG00000016246	-0.23	-0.81	0.276	-0.09	0.717	0.081	0.032511	0.009392	0.887612
OTTMUSG	predicted gene, OTTMUSG00000025463	-0.2	-0.56	0.033	-0.3	0.66	0.333	0.174722	0.01616	0.998628
Ovgp1	oviductal glycoprotein 1	-0.82	-0.22	0.209	-0.15	0.477	0.559	0.640694	0.003144	0.259368
Pabpn1	poly(A) binding protein, nuclear 1	-0.51	-0.63	0.375	-0.24	0.477	0.519	0.338808	0.002278	0.50004
Pacsin1	protein kinase C and casein kinase substrate in neuro	-0.3	-0.72	-0.09	0.045	0.813	0.206	0.213064	0.004229	0.42608
Pcm1	pericentriolar material 1	-0.3	-0.67	0.036	-0.09	0.552	0.436	0.411199	0.007997	0.893014
Pde1b	phosphodiesterase 1B, Ca2+-calmodulin dependent	-0.5	-0.69	-0.17	0.222	0.657	0.465	0.993366	0.00083	0.512932
Pex6	peroxisomal biogenesis factor 6	-0.31	-0.66	0.161	-0.17	0.482	0.466	0.35225	0.009624	0.827089



Pfkm	phosphofructokinase, muscle	-0.15	-0.82	-0.02	0.159	0.78	-0.02	0.077605	0.017012	0.205037
Phb2	prohibitin 2	-0.3	-0.5	0.387	-0.53	0.751	0.168	0.020797	0.016565	0.468898
Phlda3	pleckstrin homology-like domain, family A, member 3	-0.46	-0.44	-0	-0.02	0.365	0.562	0.792403	0.015857	0.933039
Pkm2	pyruvate kinase, muscle	0.062	-0.86	-0.05	-0.14	0.789	0.115	0.02139	0.016889	0.345894
Plcb4	phospholipase C, beta 4	-0.36	-0.81	-0.07	-0.12	0.312	0.995	0.78581	0.000166	0.123373
Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	-0.5	-0.53	-0.24	-0.1	0.579	0.797	0.635622	0.000274	0.903369
Prkce	protein kinase C, epsilon	-0.14	-0.79	0.01	-0.16	0.715	0.296	0.091645	0.006889	0.712092
Prom1	prominin 1	-0.89	-0.75	0.044	-0.09	0.846	0.846	0.995225	3.43E-08	0.850054
Prpf40b	PRP40 pre-mRNA processing factor 40 homolog B (ye	-0.56	-0.69	-0.32	0.355	0.502	0.705	0.273309	0.000228	0.354535
Psap	prosaposin	-0.24	-0.79	-0.13	0.318	0.522	0.265	0.62225	0.011995	0.237198
Ptpre	protein tyrosine phosphatase, receptor type, E	-0.25	-0.67	-0.04	-0.1	0.885	0.131	0.093375	0.006587	0.498682
Rab4a	RAB4A, member RAS oncogene family	-0.6	-0.37	-0.08	-0.03	0.411	0.695	0.443184	0.003693	0.910186
Rabl3	RAB, member of RAS oncogene family-like 3	-0.34	-0.71	0.246	-0.33	0.725	0.359	0.070634	0.002389	0.920586
Rac1	RAS-related C3 botulinum substrate 1	-0.26	-0.82	0.063	0.164	0.626	0.165	0.211713	0.008903	0.491061
Ramp2	receptor (calcitonin) activity modifying protein 2	-0.33	-0.56	-0.46	0.346	0.218	0.771	0.117671	0.007598	0.186048
Rap2b	RAP2B, member of RAS oncogene family	-0.75	-0.29	-0.25	0.383	0.369	0.59	0.066821	0.004303	0.771972
Rapgef1	Rap guanine nucleotide exchange factor (GEF)-like 1	-0.64	-0.34	-0.17	0.013	0.812	0.363	0.962952	0.001863	0.387846
Rarres2	retinoic acid receptor responder (tazarotene induced) 2	-0.46	-0.51	0.004	0.14	0.039	0.788	0.256803	0.013594	0.383363
Rasgef1a	RasGEF domain family, member 1A	-0.47	-0.65	0.041	0.029	0.939	0.089	0.144038	0.00188	0.306019
Rbm3	RNA binding motif protein 3	-0.71	-0.81	0.16	0.096	0.617	0.639	0.827995	1.69E-05	0.972297
Rcbtb1	regulator of chromosome condensation (RCC1) and B	-0.15	-0.77	0.112	-0.07	0.857	-0.04	0.021307	0.015877	0.467961
Reck	reversion-inducing-cysteine-rich protein with kazal mot	-0.71	-0.59	-0.02	0.316	0.537	0.466	0.591382	0.000674	0.782035
Reep5	receptor accessory protein 5	-0.32	-0.69	-0.01	0.114	0.702	0.174	0.30111	0.009912	0.524585
Rgma	RGM domain family, member A	-0.28	-0.55	-0.27	0.132	0.385	0.554	0.683238	0.019309	0.537197
Rhob	ras homolog gene family, member B	-0.23	-0.61	0.013	-0.19	0.569	0.41	0.320772	0.014375	0.923207
Rltpr	RGD motif, leucine rich repeats, tropomodulin domain	-0.26	-0.53	-0.19	-0.01	0.704	0.256	0.484599	0.019007	0.561787
Rnf167	ring finger protein 167	-0.13	-0.82	-0.02	-0.05	0.595	0.351	0.194717	0.009948	0.528977
Rpl13a	ribosomal protein L13a	-0.14	-0.91	0.041	-0.01	0.615	0.329	0.128249	0.005276	0.457713
Rpl18	ribosomal protein L18	-0.27	-0.69	0.035	0.041	0.634	0.202	0.25948	0.017195	0.713718
Rpl19	ribosomal protein L19	-0.12	-0.93	0.244	-0.02	0.472	0.269	0.086763	0.012099	0.540011
Rpl4	ribosomal protein L4	-0.2	-0.83	0.298	-0.05	0.669	0.054	0.030648	0.012994	0.866692
Rpl7	ribosomal protein L7	-0.54	-0.66	0.033	0.231	0.512	0.41	0.973389	0.002435	0.832898
Rps15	ribosomal protein S15	-0.28	-0.78	0.311	-0.14	0.699	0.15	0.040962	0.006739	0.986789
Rps25	ribosomal protein S25	-0.16	-0.88	0.182	-0.03	0.504	0.312	0.133425	0.010344	0.614478

Rps3	ribosomal protein S3	-0.28	-0.65	0.333	-0.27	0.738	0.093	0.028999	0.016105	0.882918
Rrp1	ribosomal RNA processing 1 homolog ( <i>S. cerevisiae</i> )	-0.23	-0.92	-0.14	0.337	0.546	0.337	0.550015	0.003385	0.136035
Rrp15	ribosomal RNA processing 15 homolog ( <i>S. cerevisiae</i> )	-0.51	-0.57	-0.14	0.031	0.674	0.518	0.952995	0.001155	0.842395
Rsad2	radical S-adenosyl methionine domain containing 2	-0.66	-0.49	-0.18	0.347	0.37	0.638	0.178605	0.001824	0.811367
Sbsn	suprabasin	-0.42	-0.85	-0.22	0.311	0.954	0.189	0.320963	0.000205	0.052604
Scd1	stearoyl-Coenzyme A desaturase 1	-1.21	-1.2	0.18	0.329	0.896	1.014	0.415023	0	0.864773
Scd2	stearoyl-Coenzyme A desaturase 2	-1.07	-1.27	0.172	0.421	0.918	0.812	0.901383	1.11E-16	0.372868
Scg5	secretogranin V	-0.11	-0.83	0.006	-0.1	0.661	0.307	0.110662	0.008407	0.586954
Sec14l1	SEC14-like 1 ( <i>S. cerevisiae</i> )	-0.07	-0.79	-0.25	-0.05	1.006	0.089	0.04127	0.003031	0.114611
Sergef	secretion regulating guanine nucleotide exchange factor	-0.17	-0.95	-0.07	0.027	0.511	0.582	0.394219	0.001417	0.231862
Sf3b3	Splicing factor 3b, subunit 3, mRNA (cDNA clone IMAC)	-0.33	-0.73	0.154	0.089	0.533	0.248	0.315014	0.010854	0.853135
Sf4	splicing factor 4	-0.57	-0.86	0.168	0.172	0.676	0.382	0.397527	0.000146	0.828391
Sfrs5	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	-0.26	-0.82	0.165	0.081	0.538	0.244	0.207164	0.009028	0.730634
Sh3glb2	SH3-domain GRB2-like endophilin B2	-0.15	-0.68	-0.24	-0.01	0.98	0.053	0.087476	0.006475	0.13154
Slc25a28	solute carrier family 25, member 28	-0.66	-0.57	-0.01	0.133	0.712	0.395	0.905369	0.000754	0.684772
Slc26a8	solute carrier family 26, member 8	-0.56	-0.48	-0.2	0.252	0.566	0.432	0.591198	0.004649	0.610052
Slc30a1	solute carrier family 30 (zinc transporter), member 1	-0.15	-1.02	0.101	0.041	0.769	0.163	0.031165	0.002025	0.353639
Slit3	slit homolog 3 ( <i>Drosophila</i> )	-0.62	-0.34	-0.06	0.148	0.574	0.325	0.747248	0.01253	0.639244
Smarb1	SWI/SNF related, matrix associated, actin dependent	-0.18	-0.72	0.18	-0.26	0.61	0.306	0.086455	0.014844	0.924587
Smn1	survival motor neuron 1	-0.41	-0.58	0.006	0.063	0.407	0.503	0.987763	0.010928	0.89817
Snhg10	small nucleolar RNA host gene (non-protein coding) 10	-0.52	-0.75	0.069	0.25	0.3	0.631	0.698931	0.001161	0.60205
Sox10	SRY-box containing gene 10	-0.51	-0.55	-0.44	0.511	0.62	0.371	0.347306	0.00283	0.088631
Sox17	SRY-box containing gene 17	-0.65	-0.61	-0.06	0.218	0.533	0.57	0.622092	0.00058	0.889841
Spata7	spermatogenesis associated 7	-0.58	-0.45	-0.09	0.285	0.705	0.151	0.944449	0.00834	0.275487
Sreb1	sterol regulatory element binding transcription factor 1	-1.16	-1.26	0.282	0.193	1.006	0.931	0.422335	0	0.994842
Sri	sorcin	-0.32	-0.7	-0.11	0.163	0.461	0.477	0.902103	0.00744	0.553024
Supt5h	suppressor of Ty 5 homolog ( <i>S. cerevisiae</i> )	-0.21	-0.8	0.15	-0	0.607	0.191	0.120797	0.014081	0.766337
Sys1	SYS1 Golgi-localized integral membrane protein homolog	-0.7	-0.32	-0.09	0.044	1.092	0.004	0.397744	0.001468	0.022333
Taf9	TAF9 RNA polymerase II, TATA box binding protein (T	-0.28	-0.74	0.348	-0.11	0.61	0.129	0.059591	0.014077	0.999327
Tcta	T-cell leukemia translocation altered gene	-0.54	-0.58	-0.32	0.331	0.311	0.795	0.121701	0.001122	0.451301
Tctex1d2	Tctex1 domain containing 2	-0.42	-0.81	-0.1	0.333	0.414	0.543	0.801285	0.001525	0.366623
Tdo2	tryptophan 2,3-dioxygenase	-0.26	-0.71	0.152	-0.31	0.803	0.284	0.049567	0.003168	0.991226
Tenc1	tensin like C1 domain-containing phosphatase	-0.39	-0.51	-0.17	0.088	0.555	0.411	0.999861	0.013304	0.757329
Tgm2	transglutaminase 2, C polypeptide	-0.66	-0.66	-0.39	0.18	0.708	0.822	0.290124	6.04E-06	0.521178

Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	-0.33	-0.45	0.075	-0.27	0.606	0.355	0.348579	0.019998	0.933531
Tlcd1	TLC domain containing 1	-0.3	-0.59	0.227	-0.25	0.45	0.435	0.302728	0.019087	0.750423
Tmem39a	transmembrane protein 39a	-0.15	-0.66	-0.49	0.248	0.394	0.608	0.536814	0.010602	0.114486
Tmem66	transmembrane protein 66	-0.43	-0.88	0.154	0.157	0.753	0.206	0.157088	0.000604	0.587186
Tprgl	transformation related protein 63 regulated like	-0.36	-0.75	0.266	-0.19	0.363	0.635	0.431699	0.002857	0.398555
Trim28	tripartite motif-containing 28	-0.43	-0.49	0.11	-0.23	0.616	0.418	0.416969	0.007758	0.897409
Trim35	tripartite motif-containing 35	-0.26	-1.06	-0.24	-0	0.93	0.549	0.139292	6.66E-06	0.1399
Trmt6	tRNA methyltransferase 6 homolog (S. cerevisiae)	-0.63	-0.52	-0.17	0.467	0.616	0.244	0.601186	0.003406	0.228352
Txnl4a	thioredoxin-like 4A	-0.73	-0.4	0.119	0.166	0.478	0.399	0.686829	0.004348	0.784152
Vps37b	vacuolar protein sorting 37B (yeast)	-0.72	-0.34	-0.2	0.176	0.714	0.4	0.537373	0.001888	0.39239
Vtn	vitronectin	0.126	-0.95	-0.21	-0.09	0.857	0.163	0.020306	0.005575	0.100817
Wdr42a	WD repeat domain 42A	-0.34	-0.51	0.094	-0.2	0.346	0.583	0.76763	0.019471	0.667769
Xpo6	exportin 6	-0.49	-0.28	-0.45	0.272	0.529	0.443	0.254217	0.016917	0.398289
Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	-0.07	-0.75	-0.04	-0.23	0.485	0.533	0.269406	0.010747	0.464283
Zdhhc8	zinc finger, DHHC domain containing 8	-0.29	-0.63	0.034	-0.18	0.934	0.094	0.055615	0.005774	0.525658
Zfp687	zinc finger protein 687	-0.56	-0.26	-0.13	-0.03	0.714	0.292	0.975979	0.013352	0.471971
Zkscan16	Zinc finger with KRAB and SCAN domains 16 (Zkscan16)	-0.55	-0.58	-0.06	0.19	0.697	0.3	0.802735	0.002613	0.550172
Znf512b	zinc finger protein 512B	-0.33	-0.5	-0.25	0.072	0.798	0.202	0.550982	0.011655	0.312924
Zyx	zyxin	-0.33	-0.63	-0.08	-0.02	0.85	0.183	0.215934	0.005257	0.468174
<b>Linear Decrease (173)</b>										
Acbd3	acyl-Coenzyme A binding domain containing 3	0.105	0.761	0.076	0.111	-0.6	-0.39	0.222515	0.01119	0.569465
Acn9	ACN9 homolog (S. cerevisiae)	0.528	0.572	-0.09	-0.13	-0.56	-0.32	0.749044	0.006142	0.891732
Adam1a	a disintegrin and metallopeptidase domain 1a	0.824	0.215	-0.05	-0.19	-0.01	-0.85	0.026672	0.005269	0.472916
Akap13	A kinase (PRKA) anchor protein 13	0.638	0.331	0.01	-0.19	-0.58	-0.24	0.814011	0.015923	0.525625
Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	0.979	0.436	0.076	-0.31	-0.55	-0.68	0.110287	3.1E-05	0.730546
Alg8	asparagine-linked glycosylation 8 homolog (yeast, alpha)	0.313	0.625	-0.17	0.095	-0.53	-0.3	0.283301	0.019733	0.991662
Amacr	alpha-methylacyl-CoA racemase	0.186	0.559	0.643	-0.41	-0.77	-0.17	0.906003	0.014089	0.011162
Amot	angiominin	0.348	0.745	0.34	-0.48	-0.26	-0.65	0.250453	0.003733	0.107107
Ampd3	adenosine monophosphate deaminase 3	0.081	0.967	-0.02	-0.13	-0.68	-0.13	0.067892	0.008225	0.224079
Apc	adenomatosis polyposis coli	0.383	1.086	-0.14	-0.05	-0.68	-0.53	0.156472	3.36E-05	0.465473
Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain	0.453	0.471	-0.11	-0.01	0.111	-0.91	0.210216	0.016802	0.111049
Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	0.401	0.693	-0	-0.2	-0.51	-0.35	0.729259	0.006631	0.703264
Armet	arginine-rich, mutated in early stage tumors	0.73	0.43	0.023	-0.1	-0.69	-0.42	0.828971	0.001082	0.604478
Aspn	asporin	0.237	0.716	0.431	-0.1	-0.9	-0.34	0.467478	0.000847	0.1105

Avl9	AVL9 homolog ( <i>S. cerevisiae</i> )	0.216	0.708	0.085	-0.09	-0.09	-0.78	0.608448	0.015163	0.147403
Baz1b	bromodomain adjacent to zinc finger domain, 1B	0.501	0.371	-0.03	0.224	-0.42	-0.65	0.884555	0.007125	0.690503
Bbs7	Bardet-Biedl syndrome 7 (human)	0.569	0.392	0.078	-0.28	-0.92	0.143	0.45793	0.01289	0.033965
BC018507	cDNA sequence BC018507	-0	0.927	-0.17	0.357	-0.61	-0.4	0.020648	0.005227	0.46308
Bdh1	3-hydroxybutyrate dehydrogenase, type 1	0.056	0.946	-0.15	0.161	-0.41	-0.52	0.134984	0.007169	0.236504
Btbd7	BTB (POZ) domain containing 7	0.235	0.706	-0.22	0.231	-0.79	-0.12	0.031256	0.010601	0.913771
Bxdc2	brix domain containing 2	0.458	0.763	0.152	-0.21	-0.63	-0.5	0.918356	0.00064	0.491499
C78339	expressed sequence C78339	0.237	0.681	0.101	-0.07	-0.54	-0.37	0.554773	0.015823	0.600505
Caprin1	cell cycle associated protein 1	0.367	0.448	0.418	-0.18	-0.48	-0.57	0.420111	0.009347	0.504093
Cav1	caveolin 1, caveolae protein	0.598	0.543	-0.13	0.093	-0.52	-0.59	0.896322	0.001443	0.848185
Ccdc127	coiled-coil domain containing 127	0.65	0.565	-0.44	0.153	-0.87	-0.07	0.059559	0.00099	0.2565
Ccnb2	cyclin B2	0.345	0.831	-0.35	0.113	-0.48	-0.41	0.161931	0.002903	0.7283
Ccp1	cell cycle progression 1	0.452	0.584	0.066	-0.12	-0.84	-0.13	0.36886	0.004994	0.313033
Cdk5rap1	CDK5 regulatory subunit associated protein 1	0.579	0.415	-0.3	0.103	-0.66	-0.15	0.310477	0.012892	0.484516
Cep170	centrosomal protein 170	0.431	0.536	-0.25	0.131	-0.34	-0.49	0.653513	0.016548	0.682835
Chordc1	cysteine and histidine-rich domain (CHORD)-containing	0.734	0.586	-0.01	-0.28	-0.57	-0.48	0.647276	0.000428	0.813278
Col20a1	collagen, type XX, alpha 1	0.255	0.624	-0.27	0.346	-0.34	-0.58	0.319359	0.015217	0.341542
Creb3l2	cAMP responsive element binding protein 3-like 2	0.218	0.675	-0.35	0.466	-0.5	-0.46	0.070713	0.010059	0.426522
Cryab	crystallin, alpha B	0.859	0.287	-0.1	-0.1	-0.4	-0.6	0.270779	0.001857	0.609602
Cyp51	cytochrome P450, family 51	0.474	1.056	-0.01	0.148	-1.09	-0.53	0.033971	1.69E-07	0.616554
Dhcr7	7-dehydrocholesterol reductase	0.494	0.448	-0.02	0.014	-0.88	-0.07	0.27569	0.009155	0.279944
Dio2	deiodinase, iodothyronine, type II	0.816	0.464	0.008	-0.25	-0.46	-0.61	0.274651	0.000477	0.939351
Dleu2	deleted in lymphocytic leukemia, 2	0.311	0.643	0.247	0.047	-0.55	-0.66	0.981289	0.001694	0.624972
Dmp1	dentin matrix protein 1	0.595	0.948	-0.22	-0.03	-0.81	-0.45	0.168398	1.04E-05	0.927611
Dpy19l1	dpy-19-like 1 ( <i>C. elegans</i> )	0.389	0.4	0.036	0.123	0.05	-1	0.188903	0.015018	0.103653
Dr1	down-regulator of transcription 1	0.208	0.864	0.063	-0.32	-0.8	0.048	0.11789	0.007373	0.07901
Ece2	endothelin converting enzyme 2	0.412	0.652	-0.12	-0.01	-0.63	-0.28	0.341267	0.006769	0.928699
Edem3	ER degradation enhancer, mannosidase alpha-like 3	0.29	0.705	-0	0.063	-0.79	-0.23	0.154833	0.005272	0.690818
Egfl6	EGF-like-domain, multiple 6	0.799	0.716	-0.19	-0.02	-0.48	-0.84	0.667899	8.76E-06	0.611011
Ell2	elongation factor RNA polymerase II 2	0.041	0.864	0.176	-0.17	-0.7	-0.13	0.148464	0.017546	0.121734
Epha5	Eph receptor A5	0.516	0.47	-0.25	0.264	-0.78	-0.22	0.156308	0.005304	0.515612
Epha6	Eph receptor A6	0.482	0.957	-0.37	0.079	-0.69	-0.41	0.076562	8.27E-05	0.931525
Ets1	E26 avian leukemia oncogene 1, 5' domain	0.363	0.549	-0.11	0.172	-0.42	-0.53	0.627189	0.013156	0.796943
Exoc3	exocyst complex component 3	0.511	0.392	0.18	0.139	-0.62	-0.61	0.834925	0.001905	0.976087

F13a1	coagulation factor XIII, A1 subunit	0.44	0.536	0.232	-0.03	-0.59	-0.58	0.827168	0.002375	0.819446
Fam13c	family with sequence similarity 13, member C	0.073	0.867	-0.12	0.189	-0.61	-0.31	0.057129	0.01011	0.635241
Fbxo18	F-box protein 18	0.36	0.575	0.388	-0.57	-0.15	-0.59	0.10667	0.019947	0.145306
Fbxw8	F-box and WD-40 domain protein 8	0.402	0.536	0.027	0.055	-0.55	-0.45	0.722376	0.008871	0.984182
Fcho2	FCH domain only 2	0.165	0.808	-0.15	-0.01	-0.64	-0.11	0.077894	0.018979	0.686356
Fosl2	fos-like antigen 2	0.48	0.353	0.157	0.059	-0.41	-0.65	0.533152	0.009249	0.971253
Fut11	fucosyltransferase 11	0.507	0.257	0.208	0.003	-0.54	-0.46	0.626632	0.017365	0.834265
Gigyf2	GRB10 interacting GYF protein 2	0.114	0.891	0.186	0.184	-0.74	-0.56	0.172278	0.000436	0.3542
Gja1	gap junction protein, alpha 1	0.435	0.737	-0.25	0.021	-0.42	-0.49	0.482448	0.003159	0.793312
Gm879	gene model 879, (NCBI)	0.358	0.667	-0.22	0.05	-0.78	-0.04	0.074921	0.010032	0.686634
Gmps	guanine monphosphate synthetase	0.151	1.133	-0.3	0.005	-0.62	-0.27	0.020397	0.000821	0.400392
Golga7	golgi autoantigen, golgin subfamily a, 7	0.781	0.24	-0.07	-0.09	-0.54	-0.37	0.592997	0.007249	0.470431
Hectd2	HECT domain containing 2	0.139	0.89	0.285	-0.33	-0.69	-0.23	0.400441	0.005659	0.052489
Hhip	Hedgehog-interacting protein	0.889	0.371	-0.18	-0.16	-0.37	-0.6	0.29878	0.000785	0.646127
Hiat1	hippocampus abundant gene transcript 1	0.254	0.743	0.1	-0.08	-0.79	-0.18	0.207223	0.006249	0.358085
Hist1h2ab	histone cluster 1, H2ab	0.612	0.49	0.142	-0.39	-0.52	-0.35	0.506233	0.005191	0.502052
Hist1h2bb	histone cluster 1, H2bb	0.492	0.471	0.156	-0.02	-0.79	-0.31	0.703413	0.00383	0.517887
Hist1h3b	histone cluster 1, H3b	0.578	0.498	-0.13	-0.11	-0.48	-0.37	0.943844	0.00804	0.953547
Hist2h3c2	histone cluster 2, H3c2	0.569	0.542	-0.05	0.402	-1.01	-0.45	0.14054	4.68E-05	0.514139
Hnrmpm	heterogeneous nuclear ribonucleoprotein M	0.426	0.606	-0.09	-0.1	-0.51	-0.31	0.624635	0.012145	0.930739
Hspa5	heat shock protein 5	0.559	0.486	-0.06	0.124	-0.72	-0.4	0.54757	0.002325	0.790618
Hsph1	heat shock 105kDa/110kDa protein 1	0.399	0.545	-0.05	0.109	-0.67	-0.31	0.367833	0.009219	0.923581
Idi1	isopentenyl-diphosphate delta isomerase	0.695	0.863	0.055	0.161	-0.91	-0.85	0.576655	3.53E-08	0.974396
Igj	immunoglobulin joining chain	0.299	0.493	-0.15	0.351	-0.73	-0.25	0.11602	0.015355	0.850972
Ing1	inhibitor of growth family, member 1	0.353	0.768	0.336	-0.48	-0.39	-0.54	0.43453	0.002919	0.109815
Ints8	integrator complex subunit 8	0.408	0.818	-0.22	0.049	-0.42	-0.59	0.481277	0.001212	0.585176
Iws1	IWS1 homolog (S. cerevisiae)	0.695	0.104	-0.46	0.596	-0.43	-0.57	0.645443	0.008718	0.015368
Jhdm1d	jumonji C domain-containing histone demethylase 1 homolog	0.434	0.963	-0.24	0.054	-0.85	-0.31	0.044752	8.32E-05	0.880515
Kbtbd2	kelch repeat and BTB (POZ) domain containing 2	0.21	0.736	0.284	0.023	-0.45	-0.75	0.958228	0.001639	0.281643
Kctd21	potassium channel tetramerisation domain containing 21	0.489	0.76	0.181	-0.07	-0.87	-0.46	0.533118	0.000101	0.460543
Klk6	kallikrein related-peptidase 6	-0.08	1.062	-0.13	0.062	-0.3	-0.49	0.111758	0.012832	0.068511
Lap3	leucine aminopeptidase 3	0.623	0.596	-0.11	0.325	-0.68	-0.75	0.608714	4.69E-05	0.594248
Lgr6	leucine-rich repeat-containing G protein-coupled receptor 6	0.596	0.424	-0.14	-0.04	-0.79	-0.08	0.384463	0.008666	0.321421
Lhfp12	lipoma HMGIC fusion partner-like 2	0.275	0.734	-0.52	0.281	-0.37	-0.36	0.085972	0.014608	0.422756

Lin7c	lin-7 homolog C ( <i>C. elegans</i> )	0.239	0.606	0.169	-0.1	-0.84	-0.03	0.21623	0.019971	0.196568
Lix1	limb expression 1 homolog (chicken)	0.544	0.44	-0.19	0.045	-0.42	-0.42	0.851989	0.01453	0.848127
Megf10	multiple EGF-like-domains 10	0.649	0.482	0.068	-0.01	-0.72	-0.49	0.982963	0.00075	0.770192
Mkks	McKusick-Kaufman syndrome protein	0.67	0.892	-0.13	-0.21	-0.66	-0.54	0.691956	1.47E-05	0.840869
Mlec	malectin	0.481	0.389	-0.14	0.195	-0.2	-0.73	0.696218	0.015453	0.359516
Mmd2	monocyte to macrophage differentiation-associated 2	0.21	0.689	0.236	-0.21	-0.58	-0.29	0.665856	0.018418	0.272965
Mmgt1	membrane magnesium transporter 1	0.91	0.436	0.137	-0.26	-0.65	-0.62	0.211182	5.43E-05	0.606599
Mpdz	multiple PDZ domain protein	0.412	0.517	-0.28	0.301	-0.54	-0.4	0.262701	0.011695	0.679725
Mrp63	mitochondrial ribosomal protein 63	0.325	0.853	-0.08	0.107	-0.6	-0.55	0.27794	0.000783	0.69908
Mrpl35	mitochondrial ribosomal protein L35	0.655	0.242	0.124	-0.05	-0.43	-0.58	0.316612	0.00926	0.891447
Mtap	methylthioadenosine phosphorylase	0.372	0.578	-0.17	0.361	-0.89	-0.22	0.050304	0.002667	0.710749
Nasp	nuclear autoantigenic sperm protein (histone-binding)	0.53	0.349	-0.15	0.338	-0.51	-0.58	0.741292	0.005898	0.49605
Nipa1	non imprinted in Prader-Willi/Angelman syndrome 1 homolog	0.711	0.652	-0.22	-0.06	-0.66	-0.43	0.627026	0.000239	0.8644
Nop16	NOP16 nucleolar protein homolog (yeast)	0.326	0.796	-0.17	-0.09	-0.51	-0.3	0.303835	0.006433	0.803974
Nudt5	nudix (nucleoside diphosphate linked moiety X)-type m	0.572	0.7	0.112	-0.05	-0.7	-0.62	0.959429	0.000118	0.857085
Obfc2a	oligonucleotide/oligosaccharide-binding fold containing	0.224	0.65	0.126	0.021	-0.55	-0.43	0.555405	0.012791	0.682722
OTTMUSG	predicted gene, OTTMUSG00000003825	0.233	0.824	-0.25	0.018	-0.53	-0.24	0.122176	0.011077	0.836208
Palld	palladin, cytoskeletal associated protein	0.599	0.541	-0.37	0.106	-0.36	-0.52	0.710258	0.003908	0.517951
Pank1	pantothenate kinase 1	0.83	0.103	-0.08	-0.05	-0.34	-0.54	0.223142	0.01332	0.426394
Paqr4	progesterone and adipoQ receptor family member IV	0.671	0.256	-0.03	0.128	-0.3	-0.77	0.320797	0.005293	0.502085
Paqr6	progesterone and adipoQ receptor family member VI	0.882	0.263	-0.27	0.163	-0.55	-0.54	0.801787	0.000962	0.179289
Pbk	PDZ binding kinase	0.552	0.428	0.068	-0.24	-0.58	-0.25	0.892736	0.015021	0.564364
Pdia6	protein disulfide isomerase associated 6	0.853	0.227	-0.09	-0.08	-0.47	-0.5	0.371417	0.003402	0.476774
Phf14	PHD finger protein 14	0.192	0.641	0.125	0.043	-0.93	-0.03	0.083953	0.012499	0.25634
Plcl1	phospholipase C-like 1	0.471	0.57	0.096	-0.25	-0.22	-0.66	0.350223	0.008338	0.631141
Pnpla8	patatin-like phospholipase domain containing 8	0.334	0.662	-0.2	0.24	-0.57	-0.44	0.228303	0.005875	0.868682
Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma	1.093	0.191	0.032	-0.4	-0.41	-0.6	0.024497	0.000249	0.405787
Ptgs2	prostaglandin-endoperoxide synthase 2	0.336	0.608	0.156	-0.14	-0.64	-0.29	0.659557	0.011684	0.506409
Rbm12b	RNA binding motif protein 12B	0.288	0.738	-0.23	0.119	-0.77	-0.1	0.046163	0.008271	0.861776
Rbm28	RNA binding motif protein 28	0.473	0.635	-0.04	0.22	-0.58	-0.69	0.658357	0.000517	0.799786
Rbm4	RNA binding motif protein 4	0.319	0.528	0.224	-0.13	-0.51	-0.42	0.943715	0.019822	0.633266
Rcan1	regulator of calcineurin 1	0.405	0.506	-0	0.008	-0.39	-0.52	0.97762	0.017225	0.928493
Rmnd1	required for meiotic nuclear division 1 homolog ( <i>S. cerevisiae</i> )	0.815	0.315	-0.44	0.463	-0.55	-0.65	0.650531	0.00035	0.034116
Rnf128	ring finger protein 128	0.173	0.716	0.265	-0.23	-0.65	-0.22	0.514441	0.01812	0.170494

Rngtt	RNA guanylyltransferase and 5'-phosphatase	0.528	0.477	0.362	-0.46	-0.56	-0.36	0.354065	0.007223	0.200359
Rpe	ribulose-5-phosphate-3-epimerase	0.294	0.826	-0.08	0.06	-0.6	-0.44	0.252844	0.002275	0.753241
Rpusd2	RNA pseudouridylyl synthase domain containing 2	0.343	0.494	0.416	-0.14	-1.13	0.027	0.273582	0.002908	0.0116
Rsf1	remodeling and spacing factor 1	0.643	0.572	-0.08	-0.24	-0.57	-0.34	0.988519	0.002101	0.78135
S100b	S100 protein, beta polypeptide, neural	0.569	1.158	-0.21	0.036	-0.92	-0.57	0.049774	6.83E-08	0.762546
Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like	0.459	0.961	0.157	-0.27	-0.81	-0.45	0.508782	3.42E-05	0.187827
Sbk1	SH3-binding kinase 1	0.862	0.503	0.028	-0.19	-0.47	-0.77	0.193074	6.96E-05	0.967961
Sbno1	sno, strawberry notch homolog 1 (Drosophila)	0.28	0.851	-0.2	0.128	-0.77	-0.24	0.049141	0.002087	0.900942
Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase)	0.639	0.587	0.095	-0.04	-0.61	-0.68	0.714437	0.000213	0.988947
Sdf2l1	stromal cell-derived factor 2-like 1	0.7	0.465	-0.33	0.031	-0.55	-0.34	0.635039	0.002987	0.574054
Serbp1	Serpine1 mRNA binding protein 1	0.488	0.566	0.164	-0.39	-0.68	-0.15	0.933248	0.008048	0.193231
Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1	0.687	0.375	0.069	-0.04	-0.53	-0.59	0.510541	0.00199	0.898935
Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding)	0.48	0.576	-0.04	-0.17	-0.58	-0.25	0.69469	0.009598	0.753286
Shank2	SH3/ankyrin domain gene 2 (Shank2), transcript variant 1	0.682	0.665	0.03	-0.37	-0.59	-0.42	0.713768	0.000377	0.59462
Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	0.535	0.368	0.121	-0.17	-0.65	-0.22	0.967454	0.019074	0.45083
Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	0.458	0.435	0.01	0.062	-0.33	-0.64	0.706513	0.01316	0.820729
Slc45a4	solute carrier family 45, member 4	0.271	0.768	-0.19	0.159	-0.65	-0.3	0.105129	0.005669	0.958944
Slc5a3	solute carrier family 5 (inositol transporters), member 3	0.399	0.67	0.098	0.033	-0.91	-0.26	0.228981	0.001109	0.466046
Smchd1	SMC hinge domain containing 1	0.349	0.792	0.316	-0.33	-0.66	-0.42	0.966343	0.00125	0.137516
Snappc3	small nuclear RNA activating complex, polypeptide 3	0.374	0.624	0.107	-0.13	-0.63	-0.31	0.651893	0.008365	0.599825
Snrnp48	small nuclear ribonucleoprotein 48 (U11/U12)	0.229	0.763	0.085	0.23	-0.94	-0.31	0.063811	0.000687	0.662907
Sod2	superoxide dismutase 2, mitochondrial	0.434	0.502	0.158	0.17	-0.8	-0.46	0.558206	0.001269	0.834475
Solh	small optic lobes homolog (Drosophila)	0.725	0.475	-0.03	-0.08	-0.51	-0.61	0.57537	0.000843	0.936801
Sox2	SRY-box containing gene 2	0.469	0.288	0.339	-0.09	-0.68	-0.34	0.711962	0.013781	0.436418
Sphk2	sphingosine kinase 2	0.311	0.819	0.026	-0.28	-0.68	-0.15	0.314263	0.004986	0.273807
Spink10	serine peptidase inhibitor, Kazal type 10	0.385	0.727	-0.09	-0.1	-0.72	-0.16	0.223478	0.004907	0.634101
Stk4	serine/threonine kinase 4	0.219	0.76	0.066	-0.08	-0.32	-0.59	0.859085	0.010555	0.357786
Syvn1	synovial apoptosis inhibitor 1, synoviolin	0.281	0.693	0.036	0.187	-0.72	-0.43	0.241187	0.002355	0.906118
Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)	0.377	0.885	-0.02	-0.11	-0.98	-0.09	0.056166	0.000368	0.204148
Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)	0.363	0.719	0.346	-0.12	-0.77	-0.5	0.815834	0.000481	0.28193
Tcfap2d	transcription factor AP-2, delta	0.329	0.588	0.301	-0.06	-0.71	-0.41	0.79104	0.003739	0.456761
Tcfcp2	transcription factor CP2	0.272	0.602	0.194	-0.04	-0.44	-0.55	0.98597	0.01183	0.62263
Them4	thioesterase superfamily member 4	0.515	0.793	0.124	-0.42	-0.67	-0.32	0.896006	0.000546	0.223302
Tjp1	tight junction protein 1	0.397	0.425	-0.02	0.202	-0.45	-0.55	0.848764	0.014185	0.867927

Tmem100	transmembrane protein 100	0.588	0.661	0.044	-0.15	-0.84	-0.3	0.536801	0.000429	0.421144
Tnrc6a	trinucleotide repeat containing 6a	0.405	0.442	-0.29	0.331	-0.76	-0.13	0.082076	0.019317	0.522481
Tprkb	Tp53rk binding protein	0.593	0.443	-0.02	0.045	-0.94	-0.13	0.307456	0.00235	0.222479
Tra2a	transformer 2 alpha homolog (Drosophila)	0.282	0.761	-0.29	0.036	-0.58	-0.16	0.102127	0.012791	0.966954
Tsga10	testis specific 10	0.457	0.619	0.047	-0.11	-0.72	-0.27	0.532625	0.003969	0.585371
Tspan12	tetraspanin 12	0.282	0.879	-0.02	0.004	-0.78	-0.31	0.126456	0.001153	0.581129
Ttl12	tubulin tyrosine ligase-like family, member 12	0.244	0.744	0.054	-0.24	-0.11	-0.64	0.666108	0.017191	0.208829
Uba5	ubiquitin-like modifier activating enzyme 5	0.396	0.402	0.588	-0.51	-0.68	-0.19	0.398512	0.019436	0.024502
Ubl4	ubiquitin-like 4	0.244	0.843	-0.02	-0.17	-0.69	-0.14	0.173224	0.00646	0.366024
Urb2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	0.144	0.807	-0.36	0.479	-0.22	-0.78	0.180549	0.004126	0.032766
Usp31	ubiquitin specific peptidase 31	0.403	0.656	-0.04	-0.07	-0.36	-0.57	0.982053	0.006701	0.743492
Vill	villin-like	0.236	0.751	-0.33	0.117	-0.22	-0.51	0.367425	0.019614	0.348955
Vps13a	vacuolar protein sorting 13A (yeast)	0.304	0.908	-0.28	0.234	-0.43	-0.67	0.210646	0.000629	0.270047
Vti1a	vesicle transport through interaction with t-SNAREs ho	0.446	0.378	0.34	-0.24	-0.97	0.038	0.603338	0.012487	0.024199
Xbp1	X-box binding protein 1	0.653	0.414	0.287	-0.29	-0.65	-0.43	0.39448	0.002109	0.391358
Ythdf3	YTH domain family 3	0.128	0.801	0.107	-0.08	-0.8	-0.09	0.102103	0.012103	0.234237
Zbtb41	zinc finger and BTB domain containing 41 homolog	0.386	0.537	0.105	-0.12	-0.14	-0.75	0.358517	0.015249	0.461435
Zc3h15	zinc finger CCCH-type containing 15	0.454	0.674	0.161	-0.26	-0.87	-0.13	0.449719	0.001982	0.136451
Zdhhc5	zinc finger, DHHC domain containing 5	0.313	0.696	-0.3	0.182	-0.63	-0.23	0.090199	0.010535	0.985445
Zfp367	zinc finger protein 367	0.494	0.535	-0.07	-0.01	-0.37	-0.57	0.893075	0.007503	0.895136
Zfp826	zinc finger protein 826	0.379	0.778	-0.28	0.297	-0.8	-0.34	0.042066	0.000742	0.950403
Zmym1	zinc finger, MYM domain containing 1	0.469	0.633	0.01	-0.2	-0.46	-0.43	0.978781	0.005762	0.820808
Zxdc	ZXD family zinc finger C	-0.16	0.999	0.076	0.081	-0.6	-0.28	0.041617	0.016597	0.128491
<b>5&amp;20 + (127)</b>										
Abhd14b	abhydrolase domain containing 14b	-0.51	-0.73	0.248	0.449	0.209	0.313	0.907452	0.002864	0.761208
Acat1	acetyl-Coenzyme A acetyltransferase 1	-0.66	-0.63	0.372	0.05	0.639	0.229	0.327873	0.001072	0.716071
Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde re	-0.57	-0.99	0.575	0.187	0.698	0.061	0.031102	2.94E-05	0.875769
Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	-0.86	-0.44	0.01	0.405	0.374	0.548	0.158631	0.000656	0.892243
Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	-0.54	-0.54	0.397	0.138	0.479	0.064	0.360599	0.01224	0.794797
Amdhd2	amidohydrolase domain containing 2	-0.37	-0.67	0.376	0.516	0.276	-0.16	0.430685	0.008148	0.613354
Apbb2	amyloid beta (A4) precursor protein-binding, family B, t	-0.65	-0.5	0.422	0.036	0.676	0.03	0.217693	0.00455	0.395647
Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4	-0.36	-0.8	0.424	0.083	0.357	0.25	0.232129	0.006678	0.852239
Atp11b	ATPase, class VI, type 11B	-0.44	-0.99	-0.08	0.554	0.454	0.455	0.894604	0.000165	0.108879
B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltr	-0.58	-0.59	-0.14	0.499	0.215	0.594	0.163438	0.003256	0.539198



BC004004	cDNA sequence BC004004	-0.58	-0.84	0.302	0.113	0.979	-0	0.032382	9.32E-05	0.272186
Bcat1	branched chain aminotransferase 1, cytosolic	-0.19	-0.83	-0.14	0.54	0.384	0.175	0.823495	0.019068	0.08506
Bsg	basigin	0.002	-1.06	0.176	0.134	0.201	0.445	0.232258	0.012023	0.07108
Casc4	cancer susceptibility candidate 4	-0.5	-0.51	0.203	0.07	0.32	0.418	0.948998	0.017379	0.9315
Cbr1	carbonyl reductase 1	-0.51	-0.61	-0.17	0.558	0.469	0.257	0.558342	0.006202	0.22822
Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	-0.7	-0.5	-0.09	0.444	0.681	0.195	0.715703	0.0018	0.199743
Cog2	component of oligomeric golgi complex 2	-0.48	-0.83	0.439	0.365	-0.11	0.582	0.693727	0.000944	0.174302
Copb2	coatamer protein complex, subunit beta 2 (beta prime)	-0.19	-0.89	0.259	0.314	0.457	-0.01	0.131741	0.011837	0.433368
Crip2	cysteine rich protein 2	-0.24	-0.85	0.274	0.209	0.376	0.168	0.23619	0.013179	0.644187
Csde1	cold shock domain containing E1, RNA binding	-0.54	-0.5	0.479	0.465	0.058	0.043	0.986013	0.007005	0.994348
Cul2	cullin 2	-0.42	-0.66	0.363	0.432	0.176	0.089	0.736093	0.009365	0.883084
Dbi	diazepam binding inhibitor	-0.66	-0.97	0.36	0.534	-0.16	0.86	0.160339	4.31E-06	0.034839
Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-0.27	-1.07	0.49	0.252	0.446	0.071	0.045775	0.000775	0.586369
Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-li	-0.45	-0.78	0.584	0.121	0.471	0.022	0.086552	0.002575	0.96957
Denr	density-regulated protein	-0.56	-0.53	0.493	-0.16	0.553	0.207	0.190357	0.007217	0.509899
Dis3	DIS3 mitotic control homolog (S. cerevisiae)	-0.31	-0.77	0.132	0.202	0.156	0.547	0.997215	0.011049	0.364896
Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	-0.52	-0.59	0.187	0.305	0.529	0.082	0.585925	0.009275	0.637086
Edn1	endothelin 1	-0.61	-0.52	0.145	0.471	0.116	0.402	0.341775	0.007704	0.916345
EG665989	predicted gene, EG665989	-0.6	-0.67	0.147	0.254	0.416	0.453	0.915405	0.001436	0.956562
Eif1a	eukaryotic translation initiation factor 1A	-0.69	-0.28	0.576	0.361	0.037	0.029	0.802549	0.010112	0.574542
Elovl5	ELOVL family member 5, elongation of long chain fatty	-0.98	-1.07	0.349	0.279	0.837	0.575	0.431585	2.39E-10	0.890916
Emcn	endomucin	-0.4	-0.69	0.123	0.286	0.315	0.334	0.879698	0.012361	0.74339
Eno3	enolase 3, beta muscle	-0.74	-0.69	0.256	0.55	0.541	0.088	0.878163	0.00022	0.400532
Eps15l1	epidermal growth factor receptor pathway substrate 15	-0.49	-0.6	0.466	0.043	0.123	0.444	0.774558	0.011483	0.469253
Esam	endothelial cell-specific adhesion molecule	-0.15	-0.95	0.193	0.291	0.499	0.037	0.111142	0.010506	0.308633
Exosc1	exosome component 1	-0.46	-0.64	0.309	0.133	0.583	0.054	0.231391	0.009977	0.800397
Fads1	fatty acid desaturase 1	-0.54	-0.9	0.291	0.313	0.402	0.4	0.631036	0.000281	0.759471
Fasn	fatty acid synthase	-1.02	-1.2	0.408	0.19	0.92	0.688	0.181231	9.27E-14	0.989121
Fbxo3	F-box protein 3	-0.49	-0.63	0.69	0.005	0.061	0.347	0.462645	0.006971	0.265728
Fbxo7	F-box protein 7	-0.87	-0.37	0.161	0.256	0.565	0.312	0.626479	0.001265	0.426461
Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegan	-0.59	-0.48	0.01	0.369	0.27	0.427	0.397938	0.011744	0.91111
Gstm1	glutathione S-transferase, mu 1	-0.43	-0.74	-0.03	0.359	0.333	0.476	0.757453	0.004171	0.506112
Gstt3	glutathione S-transferase, theta 3	-0.61	-0.41	0.241	0.421	-0.09	0.458	0.215599	0.016906	0.793948
Gtl3	gene trap locus 3	-0.52	-0.5	0.522	0.171	0.021	0.305	0.949591	0.017424	0.579957

Gucy1b3	guanylate cyclase 1, soluble, beta 3	-0.2	-0.96	0.291	0.034	0.536	0.225	0.071002	0.004682	0.651788
Hadh	hydroxyacyl-Coenzyme A dehydrogenase	-0.27	-0.86	0.014	0.696	0.204	0.161	0.938497	0.006065	0.103914
Haghl	hydroxyacylglutathione hydrolase-like	-0.22	-0.91	0.181	0.201	0.555	0.121	0.134899	0.007638	0.485733
Hes6	hairy and enhancer of split 6 (Drosophila)	-0.43	-0.6	0.172	0.553	-0.09	0.381	0.353562	0.014126	0.526046
Hirip3	HIRA interacting protein 3	-0.67	-0.34	0.372	0.421	0.112	0.137	0.58315	0.013859	0.849628
Hnrmpd	heterogeneous nuclear ribonucleoprotein D	-0.36	-0.79	0.301	0.121	0.211	0.48	0.644942	0.006369	0.501449
Hnrpd1	heterogeneous nuclear ribonucleoprotein D-like	-0.44	-0.76	0.387	0.443	0.245	0.091	0.570482	0.003394	0.819862
Hook2	hook homolog 2 (Drosophila)	-0.39	-0.73	-0.16	0.708	0.348	0.181	0.615832	0.007556	0.09225
Htra2	HtrA serine peptidase 2	-0.84	-0.43	0.208	0.362	0.486	0.259	0.63211	0.001301	0.540737
Ilvbl	ilvB (bacterial acetolactate synthase)-like	-0.5	-0.96	0.442	0.307	0.308	0.352	0.426649	0.000242	0.661175
Inmt	indolethylamine N-methyltransferase	-0.73	-0.35	0.217	0.289	0.184	0.429	0.342788	0.010165	0.871441
Inpp5e	inositol polyphosphate-5-phosphatase E	-0.52	-0.48	-0	0.293	0.255	0.459	0.479373	0.019078	0.908025
Itfg3	integrin alpha FG-GAP repeat containing 3	-0.3	-0.73	-0.02	0.373	0.58	0.045	0.440537	0.017908	0.250145
Itih5	inter-alpha (globulin) inhibitor H5	-0.36	-0.76	-0.03	0.349	0.101	0.653	0.464189	0.006678	0.242148
Ivd	isovaleryl coenzyme A dehydrogenase	-0.21	-0.83	0.254	0.041	0.187	0.497	0.487494	0.015458	0.315302
Krt12	keratin 12	-0.38	-0.72	0.257	0.16	0.542	0.108	0.241287	0.010285	0.846643
Lactb2	lactamase, beta 2	-0.73	-0.39	0.238	0.524	-0.14	0.538	0.073029	0.004691	0.761046
Lect1	leukocyte cell derived chemotaxin 1	-0.28	-0.78	0.346	0.288	-0.23	0.611	0.689008	0.011447	0.076277
Lgals7	lectin, galactose binding, soluble 7	-0.77	-0.53	0.132	0.266	0.616	0.311	0.931067	0.000757	0.609498
Lmo4	LIM domain only 4	-0.27	-0.9	1E-04	0.584	0.645	-0.13	0.240748	0.004024	0.03817
Man2b2	mannosidase 2, alpha B2	-0.74	-0.35	0.059	0.379	0.086	0.606	0.093836	0.00748	0.942055
Matn4	matrilin 4	-0.41	-0.93	0.414	0.525	6E-04	0.347	0.923619	0.000561	0.294259
Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	-0.39	-0.64	0.319	0.357	-0.11	0.426	0.667052	0.017617	0.433041
Mfsd4	major facilitator superfamily domain containing 4	-0.5	-0.68	0.449	-0.12	0.839	-0	0.025557	0.002178	0.495586
Mllt10	myeloid/lymphoid or mixed-lineage leukemia (trithorax	-0.65	-0.42	0.545	0.207	0.406	-0.06	0.432338	0.008855	0.462772
Msh3	MutS homolog 3 (E. coli) (Msh3), mRNA	-0.39	-0.85	0.219	0.45	0.282	0.239	0.713915	0.00316	0.508998
Mtch2	mitochondrial carrier homolog 2 (C. elegans)	-0.29	-0.86	0.374	0.046	0.51	0.164	0.092589	0.006346	0.903351
Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	-0.16	-0.85	0.708	0.184	0.25	-0.2	0.02412	0.007463	0.913238
Nol5a	nucleolar protein 5A	-0.66	-0.65	0.51	0.228	0.025	0.544	0.729842	0.00105	0.375329
Ntf3	neurotrophin 3	-0.41	-0.75	-0.08	0.448	0.181	0.568	0.430344	0.00487	0.296974
Nudt14	nudix (nucleoside diphosphate linked moiety X)-type n	-0.34	-0.8	0.145	0.445	-0.24	0.742	0.246087	0.005017	0.048776
Nudt6	nudix (nucleoside diphosphate linked moiety X)-type n	-0.66	-0.18	0.009	0.861	-0.16	0.176	0.02308	0.018862	0.662903
Osgepl1	O-sialoglycoprotein endopeptidase-like 1	-0.36	-0.82	0.387	0.036	0.469	0.247	0.159163	0.004502	0.921675
P4hb	prolyl 4-hydroxylase, beta polypeptide	-0.43	-0.65	0.263	0.284	0.127	0.384	0.936649	0.013825	0.740869

Pard6g	par-6 partitioning defective 6 homolog gamma (C. eleg)	-0.56	-0.52	0.66	0.021	0.041	0.361	0.709594	0.009616	0.259157
Pcbp2	poly(rC) binding protein 2	-0.4	-0.76	-0.03	0.493	0.342	0.322	0.839739	0.005788	0.335082
Pcyox1	prenylcysteine oxidase 1	-0.41	-0.81	-0.25	0.831	0.614	-0.01	0.933475	0.00142	0.005222
Pdlim4	PDZ and LIM domain 4	-0.85	-0.52	0.051	0.57	0.221	0.553	0.089941	0.00039	0.927511
Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomera	-0.41	-0.66	0.012	0.384	0.037	0.609	0.350216	0.012094	0.360752
Podxl	podocalyxin-like	-0.4	-0.85	0.218	0.226	0.777	-0.02	0.081314	0.001835	0.37148
Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	-0.43	-0.63	0.164	0.26	0.434	0.182	0.635983	0.015528	0.829497
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPa	-0.36	-0.83	0.566	0.117	0.18	0.286	0.267479	0.004227	0.547381
Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	-0.44	-0.64	0.283	0.009	0.44	0.333	0.439684	0.009561	0.963289
Qpctl	glutaminy-peptide cyclotransferase-like	-0.72	-0.29	0.494	-0.14	0.307	0.392	0.873549	0.013895	0.195489
Rab33a	RAB33A, member of RAS oncogene family	-0.58	-0.49	0.266	0.129	0.528	0.156	0.578352	0.011783	0.744488
Rad51ap1	RAD51 associated protein 1	-0.23	-0.84	0.228	0.068	0.13	0.588	0.67092	0.010754	0.208268
Rbbp4	retinoblastoma binding protein 4	-0.57	-0.47	0.067	0.306	0.248	0.428	0.484954	0.015643	0.976602
Rel1	RELT-like 1	-0.61	-0.48	0.14	0.328	0.752	-0.11	0.447609	0.007396	0.138135
Rpl41	ribosomal protein L41	-0.16	-0.91	0.072	0.561	0.387	-0.02	0.359598	0.011233	0.104241
Rsad1	radical S-adenosyl methionine domain containing 1	-0.49	-0.66	0.238	0.096	0.626	0.175	0.302082	0.004899	0.845802
Sar1a	SAR1 gene homolog A (S. cerevisiae)	-0.32	-0.95	0.281	0.498	0.659	-0.23	0.061103	0.001044	0.124971
Scrn1	secernin 1	-0.36	-0.7	0.7	0.09	0.465	-0.22	0.025349	0.007262	0.822756
Scube2	signal peptide, CUB domain, EGF-like 2	-0.5	-0.54	0.443	-0.08	0.49	0.182	0.248633	0.014426	0.720804
Sephs1	selenophosphate synthetase 1	-0.39	-0.67	0.247	0.241	0.432	0.116	0.428286	0.015718	0.859501
Sephs2	selenophosphate synthetase 2	-0.32	-0.77	0.341	5E-04	0.351	0.351	0.283759	0.01069	0.732708
Sirt5	sirtuin 5 (silent mating type information regulation 2 ho	-0	-1.03	0.107	0.293	0.477	0.055	0.083021	0.016924	0.125085
Slc6a6	solute carrier family 6 (neurotransmitter transporter, ta	-0.47	-0.94	0.165	0.212	0.837	0.149	0.104157	0.000167	0.394208
Slco1a4	solute carrier organic anion transporter family, membe	-0.37	-0.81	0.349	0.377	0.547	-0.14	0.13	0.003928	0.467577
Son	Son DNA binding protein	-0.5	-0.73	0.208	0.395	0.459	0.147	0.627513	0.003115	0.666863
Sstr2	somatostatin receptor 2	-0.34	-0.73	0.038	0.315	0.643	0.036	0.325363	0.011269	0.30847
Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog	-0.38	-0.96	0.094	0.272	0.513	0.403	0.476045	0.000645	0.42452
Stard10	START domain containing 10	-0.22	-0.85	0.202	0.153	0.59	0.061	0.102525	0.01234	0.582508
Syt12	synaptotagmin-like 2	-0.26	-1.13	0.219	0.219	0.746	0.117	0.028562	0.000265	0.263183
Tada2l	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	-0.53	-1.06	0.082	0.613	0.689	0.155	0.40872	1.66E-05	0.073088
Tfdp1	transcription factor Dp 1	-0.4	-0.65	0.495	0.234	0.267	0.028	0.323861	0.013742	0.999233
Tgds	TDP-glucose 4,6-dehydratase	-0.61	-0.43	0.368	0.521	0.288	-0.12	0.930371	0.007747	0.545312
Tipin	timeless interacting protein	-0.51	-0.71	0.325	0.139	0.496	0.24	0.374678	0.003211	0.992711
Tjp2	tight junction protein 2	-0.26	-0.85	0.259	0.203	0.274	0.317	0.42125	0.010766	0.537801

Tm9sf3	transmembrane 9 superfamily member 3	-0.16	-0.89	0.32	0.456	0.168	0.027	0.320847	0.011816	0.342661
Tmem86a	transmembrane protein 86A	-0.38	-0.65	0.096	0.189	0.384	0.333	0.768203	0.017089	0.844236
Trim3	tripartite motif-containing 3	-0.4	-0.82	-0.03	0.528	0.466	0.204	0.862139	0.003257	0.212096
Trnau1ap	tRNA selenocysteine 1 associated protein 1	-0.75	-0.56	0.265	0.249	0.64	0.173	0.684364	0.000913	0.502555
Ttrap	Traf and Tnf receptor associated protein	-0.43	-0.6	0.68	0.22	0.196	-0.08	0.223536	0.008091	0.883545
Ttyh2	tweety homolog 2 (Drosophila)	-0.25	-0.85	0.046	0.291	0.445	0.254	0.457947	0.010098	0.373951
Usp2	ubiquitin specific peptidase 2	-0.37	-0.85	0.43	0.17	0.351	0.22	0.233827	0.003768	0.835342
Vps11	vacuolar protein sorting 11 (yeast)	-0.53	-0.79	0.16	0.217	0.522	0.4	0.651374	0.000797	0.861596
Xab2	XPA binding protein 2	-0.21	-0.88	0.408	0.469	0.292	-0.14	0.155312	0.005296	0.45305
Xpa	xeroderma pigmentosum, complementation group A	-0.41	-0.62	0.062	0.325	0.264	0.361	0.844584	0.018746	0.734579
Zbtb22	zinc finger and BTB domain containing 22	-0.6	-0.74	0.499	0.041	0.404	0.374	0.377052	0.000879	0.744305
Zc3h14	zinc finger CCCH type containing 14	-0.7	-0.67	0.454	-0.07	0.682	0.3	0.210037	0.000276	0.592679
Zdhhc4	zinc finger, DHHC domain containing 4	-0.54	-0.67	0.064	0.282	0.534	0.315	0.860618	0.002793	0.740207
Zfp821	zinc finger protein 821	-0.37	-0.61	-0.1	0.416	0.824	-0.18	0.313541	0.017497	0.038527
Zfp90	zinc finger protein 90	-0.38	-0.86	0.08	0.571	0.612	-0.06	0.342518	0.001913	0.098859
<b>5&amp;20 - (131)</b>										
Ak3l1	adenylate kinase 3-like 1	0.342	0.709	-0.43	0.131	-0.49	-0.23	0.11387	0.012546	0.875314
Appl1	adaptor protein, phosphotyrosine interaction, PH domain containing 1	0.515	0.851	-0.21	-0.32	-0.42	-0.38	0.705641	0.000678	0.736753
Asrgl1	asparaginase like 1	0.906	0.528	-0.33	-0.07	-0.59	-0.48	0.999719	8.75E-05	0.475904
Atg12	autophagy-related 12 (yeast)	0.431	0.814	-0.37	-0.17	-0.48	-0.18	0.231157	0.002767	0.950593
Atl3	atlastin GTPase 3	0.465	0.616	-0.3	-0.55	-0.1	-0.11	0.883275	0.007626	0.804339
Bbs1	Bardet-Biedl syndrome 1 (human)	0.72	0.328	0.008	-0.55	-0.17	-0.37	0.119055	0.012352	0.83533
Bbx	bobby sox homolog (Drosophila)	0.519	0.695	-0.13	-0.56	-0.37	-0.13	0.986047	0.003368	0.465433
BC026590	cDNA sequence BC026590	0.387	0.644	-0.14	-0.2	-0.26	-0.4	0.945238	0.018581	0.789913
BC049349	cDNA sequence BC049349	0.027	1.033	0.074	-0.62	-0.61	0.192	0.10784	0.00893	0.006255
Bicd2	bicaudal D homolog 2 (Drosophila)	0.414	0.639	-0.52	-0.25	0.129	-0.39	0.983564	0.010854	0.337795
Camkk2	calcium/calmodulin-dependent protein kinase kinase 2	0.098	0.965	-0.61	-0.36	-0.09	0.087	0.073508	0.003942	0.433865
Camsap1	calmodulin regulated spectrin-associated protein 1	0.552	0.464	-0.52	-0.13	-0.53	0.155	0.184731	0.015755	0.430405
Ccar1	cell division cycle and apoptosis regulator 1	0.765	0.418	0.268	-0.72	-0.5	-0.27	0.115067	0.001925	0.100761
Ccdc93	coiled-coil domain containing 93	0.785	0.231	-0.07	-0.4	-0.39	-0.22	0.335324	0.015256	0.464206
Clint1	clathrin interactor 1	0.266	1.006	-0.22	-0.25	-0.27	-0.46	0.455782	0.0019	0.242445
Cnr1	cannabinoid receptor 1 (brain)	0.368	0.734	-0.38	-0.05	-0.55	-0.07	0.113918	0.009795	0.966267
Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	0.55	0.496	-0.24	-0.15	0.201	-0.86	0.15359	0.009873	0.106873
Creb1	cAMP responsive element binding protein 1	0.467	0.585	0.303	-0.62	-0.17	-0.56	0.098354	0.009159	0.210346

Cycs	cytochrome c, somatic	0.409	0.598	0.303	-0.57	-0.68	-0.05	0.938076	0.01225	0.035457
Cyhr1	cysteine and histidine rich 1	0.57	0.683	-0.41	-0.2	-0.38	-0.24	0.52752	0.002525	0.986194
D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	0.357	0.7	-0.29	-0.04	-0.58	-0.11	0.15949	0.013271	0.938365
Der1	Der1-like domain family, member 1	0.276	0.869	-0.27	-0.16	-0.48	-0.17	0.170561	0.007156	0.722512
Dhcr24	24-dehydrocholesterol reductase	0.318	1.248	-0.54	-0.04	-0.22	-0.67	0.130579	1.86E-05	0.029647
Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	0.402	0.698	-0.16	-0.38	-0.54	0.002	0.404941	0.010481	0.434104
Dtna	dystrobrevin alpha	0.4	0.715	-0.21	-0.28	-0.62	0.018	0.236567	0.008642	0.495814
Dusp16	dual specificity phosphatase 16	0.674	0.307	-0.52	-0.35	-0.02	-0.14	0.670443	0.012408	0.675787
EG240055	predicted gene, EG240055	0.605	0.519	-0.53	-0.02	-0.13	-0.46	0.905499	0.007359	0.362677
Eif4ebp2	eukaryotic translation initiation factor 4E binding protein	0.408	0.749	-0.3	-0.54	-0.45	0.177	0.311582	0.003581	0.324303
Epb4.1l2	erythrocyte protein band 4.1-like 2	0.051	1.086	-0.33	0.014	-0.14	-0.58	0.182346	0.004975	0.043401
Ephx2	epoxide hydrolase 2, cytoplasmic	0.577	0.644	-0.48	0.13	-0.55	-0.32	0.20713	0.001931	0.632815
Exog	endo/exonuclease (5'-3'), endonuclease G-like	0.619	0.248	-1.01	0.27	-0.34	0.171	0.042996	0.019036	0.01712
Fam126b	family with sequence similarity 126, member B	0.5	0.536	0.092	-0.51	-0.48	-0.14	0.757342	0.015512	0.286049
Fam173b	family with sequence similarity 173, member B	0.504	0.661	-0.75	-0.15	0.067	-0.32	0.608735	0.002738	0.247085
Fam62b	family with sequence similarity 62, member B	0.711	0.409	-0.29	-0.3	-0.33	-0.23	0.773714	0.007866	0.787458
Fbxl7	F-box and leucine-rich repeat protein 7	-0.11	1.183	-0.35	-0.17	-0.26	-0.17	0.029537	0.01125	0.072088
Fgfr3	fibroblast growth factor receptor 3	0.426	0.634	-0.34	-0.25	-0.17	-0.28	0.803533	0.016246	0.879791
Fusip1	FUS interacting protein (serine-arginine rich) 1	0.29	0.885	-0.27	-0.06	-0.76	-0.03	0.032726	0.003279	0.647131
Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit	0.418	0.692	-0.16	-0.13	-0.55	-0.24	0.400147	0.007451	0.885787
Gamt	guanidinoacetate methyltransferase	0.508	0.61	-0.2	-0.32	-0.77	0.191	0.188666	0.006277	0.148903
Gem	GTP binding protein (gene overexpressed in skeletal m	0.05	1.003	-0.14	-0.45	-0.46	0.099	0.09696	0.013112	0.091963
Gldc	glycine decarboxylase	0.732	0.775	0.063	-0.52	-0.55	-0.49	0.476069	4.35E-05	0.399661
Gbbp1l1	GC-rich promoter binding protein 1-like 1	0.425	0.912	-0.47	-0.03	-0.45	-0.34	0.141129	0.000827	0.780733
Gpt2	glutamic pyruvate transaminase (alanine aminotransfe	0.295	0.82	-0.36	-0.17	-0.59	0.06	0.065009	0.008747	0.730949
Grin2c	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	0.11	0.926	-0.65	-0.18	-0.04	-0.08	0.091518	0.008975	0.343324
H3f3b	H3 histone, family 3B	0.267	0.97	-0.11	-0.44	-0.32	-0.31	0.597159	0.002962	0.20475
Hdac4	histone deacetylase 4	0.168	0.898	-0.51	-0.09	0.097	-0.49	0.428972	0.012051	0.073722
Helz	helicase with zinc finger domain	0.574	0.488	0.127	-0.59	-0.51	-0.1	0.586445	0.011064	0.173576
Hip1	huntingtin interacting protein 1	0.642	0.384	-0.46	-0.02	-0.39	-0.18	0.595963	0.016913	0.502026
Hist3h2a	histone cluster 3, H2a	0.549	0.98	-0.44	-0.37	-0.43	-0.25	0.321566	8.37E-05	0.80282
Hmmr	hyaluronan mediated motility receptor (RHAMM)	0.463	0.578	-0.41	-0.27	0.035	-0.38	0.824245	0.015415	0.594587
Hspa1b	heat shock protein 1B	0.338	0.748	-0.45	-0.17	-0.51	0.086	0.081606	0.010899	0.8692
Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	0.31	0.811	-0.31	-0.09	-0.42	-0.25	0.229171	0.008914	0.842469

Itsn1	intersectin 1 (SH3 domain protein 1A)	0.266	0.708	-0.82	0.186	0.035	-0.33	0.133705	0.019351	0.068944
Kalrn	kalirin, RhoGEF kinase	0.964	0.086	-0.18	-0.49	-0.17	-0.3	0.070332	0.007944	0.401084
Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	0.321	0.749	-0.21	-0.12	-0.73	0.037	0.081611	0.010377	0.521132
Kcnj16	potassium inwardly-rectifying channel, subfamily J, me	0.456	0.891	-0.36	-0.41	-0.06	-0.47	0.981052	0.000798	0.345629
Kctd6	potassium channel tetramerisation domain containing	0.492	0.569	-0.14	-0.4	-0.41	-0.1	0.870973	0.015029	0.65208
Kif1b	kinesin family member 1B	0.871	0.076	-0.54	-0.31	0.063	-0.23	0.231392	0.011866	0.228478
Larp4	La ribonucleoprotein domain family, member 4	0.34	0.708	-0.21	-0.12	-0.61	-0.07	0.180575	0.014123	0.747394
Lman2l	lectin, mannose-binding 2-like	0.782	0.604	-0.45	-0.01	-0.68	-0.26	0.315338	0.00024	0.452237
Lonrf3	LON peptidase N-terminal domain and ring finger 3	0.308	0.78	-0.24	-0.39	0.018	-0.42	0.874833	0.011535	0.308546
Lrp4	low density lipoprotein receptor-related protein 4	0.906	0.202	-0.13	-0.38	-0.57	-0.09	0.508286	0.005085	0.12405
Man1a2	mannosidase, alpha, class 1A, member 2	0.194	1.007	-0.39	-0.05	-0.55	-0.13	0.030378	0.003471	0.682393
Mbn1	muscleblind-like 1 (Drosophila)	0.299	0.808	-0.12	-0.52	-0.28	-0.14	0.744664	0.00995	0.318744
Mdga2	MAM domain containing glycosylphosphatidylinositol a	0.335	0.797	-0.08	-0.25	-0.55	-0.2	0.383674	0.006672	0.535228
Med20	mediator complex subunit 20	0.528	0.587	-0.21	-0.51	-0.25	-0.14	0.869904	0.008217	0.768517
Msc	musculin	0.795	0.334	-0.07	-0.52	-0.14	-0.44	0.096719	0.005563	0.952391
Myo6	myosin VI	0.429	0.679	-0.25	-0.06	-0.18	-0.59	0.956209	0.007709	0.48327
N4bp1	NEDD4 binding protein 1	0.604	0.518	-0.38	-0.53	-0.13	-0.1	0.778191	0.004654	0.957075
Nat14	N-acetyltransferase 14	0.779	0.33	-0.17	-0.3	-0.27	-0.4	0.337638	0.007298	0.826101
Ncapg2	non-SMC condensin II complex, subunit G2	0.328	0.806	0.038	-0.45	-0.65	-0.02	0.385801	0.00607	0.121279
Ncoa5	nuclear receptor coactivator 5	0.2	0.989	-0.57	-0.12	-0.21	-0.2	0.085574	0.004048	0.409393
Ncoa7	nuclear receptor coactivator 7	0.53	0.809	-0.2	-0.51	-0.31	-0.28	0.99346	0.000966	0.599671
Nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)	0.429	0.713	-0.4	-0.28	-0.3	-0.14	0.444416	0.007456	0.961273
Nipbl	Nipped-B homolog (Drosophila)	0.351	0.679	-0.23	-0.52	-0.32	0.079	0.546702	0.014064	0.465563
Nkd2	naked cuticle 2 homolog (Drosophila)	0.219	0.902	-0.49	-0.22	-0.44	0.1	0.041715	0.006884	0.77798
Nomo1	nodal modulator 1	0.167	0.926	-0.48	0.157	-0.36	-0.34	0.053453	0.008559	0.406735
Nras	neuroblastoma ras oncogene	0.318	0.819	-0.2	-0.2	-0.5	-0.19	0.281133	0.007415	0.698542
Nupl1	nucleoporin like 1	0.248	0.801	-0.16	-0.39	-0.57	0.137	0.160796	0.014878	0.246447
Nxph2	neurexophilin 2	0.346	1.045	-0.28	-0.27	-0.02	-0.75	0.971551	0.000326	0.041316
Oscar	osteoclast associated receptor	0.593	0.555	-0.73	-0.11	-0.21	-0.09	0.329108	0.003848	0.503264
Paqr8	progesterin and adipoQ receptor family member VIII	0.723	0.729	-0.51	-0.07	-0.5	-0.37	0.408584	0.000166	0.730949
Parg	poly (ADP-ribose) glycohydrolase	0.171	0.87	-0.54	0.113	-0.42	-0.13	0.028136	0.015857	0.746983
Pcdh20	protocadherin 20	0.415	0.65	0.048	-0.36	-0.35	-0.38	0.783429	0.012098	0.564777
Phip	pleckstrin homology domain interacting protein	0.371	0.792	-0.09	-0.66	-0.54	0.171	0.430132	0.003588	0.071541
Phkg1	phosphorylase kinase gamma 1	0.381	0.689	-0.39	-0.2	-0.27	-0.18	0.433597	0.014984	0.938873

Ptar1	protein prenyltransferase alpha subunit repeat containi	0.315	0.805	-0.13	-0.28	-0.19	-0.48	0.939884	0.00892	0.391247
Qk	quaking	0.419	0.822	-0.35	-0.17	-0.53	-0.15	0.188362	0.002759	0.919037
Rab22a	RAB22A, member RAS oncogene family	0.435	0.618	-0.5	-0.27	-0	-0.27	0.849343	0.012202	0.663819
Rab2b	RAB2B, member RAS oncogene family	0.424	0.884	-0.43	-0.07	-0.59	-0.18	0.087739	0.001128	0.983893
Rab8b	RAB8B, member RAS oncogene family	0.711	0.561	-0.1	-0.27	-0.47	-0.45	0.679597	0.001184	0.940809
Rabep1	rabaptin, RAB GTPase binding effector protein 1	0.226	0.927	-0.07	-0.23	-0.77	-0.01	0.069918	0.003765	0.205244
Rabgap1l	RAB GTPase activating protein 1-like	0.193	0.865	-0.05	-0.63	-0.62	0.316	0.144777	0.008142	0.021821
Rgs5	regulator of G-protein signaling 5	0.816	0.642	0.009	-0.48	-0.53	-0.48	0.369463	9.03E-05	0.615764
Rlbp1	retinaldehyde binding protein 1	0.836	0.568	-0.23	-0.2	-0.76	-0.24	0.685768	0.00016	0.369809
Rnf32	ring finger protein 32	0.454	0.771	-0.26	-0.16	-0.36	-0.42	0.620956	0.003055	0.818419
Rorb	RAR-related orphan receptor beta	0.637	0.45	-0.05	-0.52	-0.49	-0.05	0.763019	0.009605	0.299172
Scin	scinderin	0.441	0.806	-0.23	-0.4	-0.52	-0.06	0.360478	0.002566	0.52269
Scn8a	sodium channel, voltage-gated, type VIII, alpha	0.201	0.846	-0.4	-0.42	0.086	-0.25	0.698004	0.010118	0.252771
Sertad3	SERTA domain containing 3	0.612	0.356	-0.48	-0.26	0.118	-0.38	0.472895	0.019891	0.485555
Sipa1l3	signal-induced proliferation-associated 1 like 3	0.389	0.756	-0.31	-0.38	-0.26	-0.16	0.590112	0.007168	0.768532
Slc15a4	solute carrier family 15, member 4	0.395	0.773	-0.65	0.07	-0.29	-0.26	0.12433	0.005043	0.494466
Slc25a18	solute carrier family 25 (mitochondrial carrier), membe	0.844	0.107	0.186	-0.54	-0.22	-0.45	0.020266	0.017035	0.617699
Slc4a4	solute carrier family 4 (anion exchanger), member 4	0.575	0.522	-0.31	-0.63	0.101	-0.26	0.313014	0.004279	0.850188
Snx1	sorting nexin 1	0.469	0.499	-0.21	-0.05	-0.94	0.238	0.056136	0.01495	0.0999
Snx16	sorting nexin 16	0.593	0.637	-0.31	-0.1	-0.77	-0.05	0.169365	0.001849	0.478546
Spred1	sprouty protein with EVH-1 domain 1, related sequenc	0.557	0.689	-0.17	-0.5	-0.49	-0.07	0.757967	0.002381	0.429793
Spry3	sprouty homolog 3 (Drosophila)	0.298	1.011	-0.14	-0.42	-0.3	-0.39	0.626882	0.001321	0.19703
Synj1	synaptojanin 1	0.4	0.536	-0.42	-0.43	-0.12	0.046	0.706172	0.019375	0.953288
Synj2bp	synaptojanin 2 binding protein	0.392	0.701	-0.54	0.05	-0.32	-0.26	0.198669	0.010953	0.678961
Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	0.111	0.897	0.089	-0.82	-0.39	0.189	0.516822	0.010395	0.007578
Tmem33	transmembrane protein 33	0.269	1.006	-0.1	-0.22	-0.83	-0.05	0.044105	0.000825	0.200224
Tmem50b	transmembrane protein 50B	0.978	0.019	-0.21	-0.41	0.02	-0.5	0.020284	0.011095	0.415095
Tpmt	thiopurine methyltransferase	0.765	0.652	-0.29	-0.14	-0.65	-0.35	0.627219	0.000178	0.759977
Trio	triple functional domain (PTPRF interacting)	0.418	0.685	-0.06	-0.37	-0.45	-0.19	0.779611	0.010264	0.546055
Trpc5	transient receptor potential cation channel, subfamily C	0.559	0.406	-0.05	-0.72	-0.1	-0.11	0.25788	0.018126	0.514697
Trps1	trichorhinophalangeal syndrome I (human)	0.224	0.864	-0.1	-0.29	-0.44	-0.2	0.347629	0.011774	0.39275
Ttbk2	tau tubulin kinase 2	0.37	0.646	-0.31	-0.01	-0.24	-0.42	0.598745	0.019848	0.673555
Ttc14	tetratricopeptide repeat domain 14	0.531	0.597	-0.27	-0.13	-0.76	0.042	0.163781	0.005645	0.385593
Uba6	ubiquitin-like modifier activating enzyme 6	0.595	0.757	0.224	-0.63	-0.46	-0.46	0.31031	0.00033	0.151307

Ubxn7	UBX domain protein 7	0.334	0.67	-0.1	-0.17	-0.05	-0.65	0.651715	0.017995	0.305763
Upf2	UPF2 regulator of nonsense transcripts homolog (yeas	0.44	0.694	-0.41	-0.11	-0.55	-0.04	0.148772	0.007437	0.895823
Usp45	ubiquitin specific petidase 45	0.593	0.89	-0.23	-0.21	-0.68	-0.34	0.338489	8.91E-05	0.830501
Wdr59	WD repeat domain 59	0.576	0.552	-0.13	-0.49	-0.11	-0.41	0.351426	0.007728	0.834841
Wnt2	wingless-related MMTV integration site 2	0.58	1.006	-0.35	-0.43	-0.39	-0.38	0.588619	3.72E-05	0.62203
Zbtb7a	zinc finger and BTB domain containing 7a	0.423	0.859	-0.52	-0.27	-0.16	-0.28	0.429028	0.001624	0.633794
Zfp180	zinc finger protein 180	0.128	0.877	-0.09	-0.15	-0.79	0.109	0.029223	0.014702	0.214266
Zfp236	zinc finger protein 236	0.295	0.902	-0.27	-0.02	-0.53	-0.31	0.137623	0.002983	0.766347
Zfp318	zinc finger protein 318	0.504	0.767	-0.63	-0.39	-0.33	0.11	0.185117	0.000752	0.926196
Zfp451	zinc finger protein 451	0.492	0.579	-0.19	-0.47	-0.32	-0.09	0.951547	0.012895	0.696394
Zfp652	zinc finger protein 652	0.479	0.642	-0.68	0.104	-0.37	-0.16	0.112842	0.007213	0.512331
<b>20 + (97)</b>										
Adarb1	adenosine deaminase, RNA-specific, B1	-0.35	-0.13	-0.43	-0.17	0.464	0.643	0.375443	0.010229	0.990596
Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	-0.28	-0.31	-0.49	-0.02	0.232	0.872	0.140519	0.007974	0.499956
Aip	aryl-hydrocarbon receptor-interacting protein	0.161	-0.39	-0.39	-0.52	0.841	0.235	0.077801	0.004499	0.669428
Ap1gbp1	AP1 gamma subunit binding protein 1	-0.55	0.102	0.204	-0.71	0.712	0.308	0.341325	0.014629	0.026215
Arl4d	ADP-ribosylation factor-like 4D	-0.49	0.057	-0.49	-0.09	0.23	0.849	0.033216	0.010516	0.928245
Arpc1a	actin related protein 2/3 complex, subunit 1A	-0.04	-0.75	-0.07	-0.31	0.638	0.463	0.128998	0.005678	0.62323
Atp13a2	ATPase type 13A2	-0.04	-0.33	-0.7	-0.33	0.328	1.039	0.246446	0.000169	0.187683
Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-0.07	-0.49	-0.22	-0.27	0.535	0.485	0.492125	0.018546	0.785887
AV039307	expressed sequence AV039307	-0.5	0.118	-0.51	-0.14	1.078	0.007	0.894459	0.006217	0.007718
Bcas1	breast carcinoma amplified sequence 1	-0.08	-0.07	-0.42	-0.54	0.209	0.899	0.421135	0.003311	0.336985
Bend5	BEN domain containing 5	-0.47	-0.28	-0.22	-0.13	0.992	0.122	0.411443	0.0057	0.140238
Btg3	B-cell translocation gene 3	-0.06	-0.23	-0.51	-0.33	0.691	0.415	0.71059	0.006198	0.738104
C1qI2	complement component 1, q subcomponent-like 2	-0.16	0.033	-0.57	-0.25	0.684	0.281	0.879818	0.01683	0.448356
Camk2g	calcium/calmodulin-dependent protein kinase II gamm	-0.44	-0.35	-0.38	0.023	1.281	-0.13	0.157816	0.001544	0.002557
Capn5	calpain 5	-0.28	-0.47	-0.48	0.194	0.713	0.307	0.917875	0.01198	0.168732
Casq2	calsequestrin 2	-0.35	-0.12	-0.28	-0.28	0.991	0.069	0.335196	0.01143	0.124869
Ccdc86	coiled-coil domain containing 86	-0.27	-0.25	-0.28	-0.27	0.393	0.671	0.684923	0.014905	0.883085
Ccnj1	cyclin J-like	-0.54	-0.22	-0.15	-0.2	0.901	0.241	0.589514	0.004989	0.248736
Clip4	CAP-GLY domain containing linker protein family, mer	-0.27	-0.07	-0.33	-0.35	0.782	0.249	0.634971	0.016021	0.467387
Crtc1	CREB regulated transcription coactivator 1	0.097	-0.16	-0.95	0.007	0.603	0.373	0.510669	0.006495	0.065256
Cygb	cytoglobin	-0.42	0.118	-0.56	-0.4	0.596	0.711	0.251037	0.000706	0.719343
D18Ert65	DNA segment, Chr 18, ERATO Doi 653, expressed	-0.05	-0.59	-0.25	-0.23	0.5	0.565	0.551343	0.011502	0.547734



Dab1	disabled homolog 1 (Drosophila)	-0.28	-0.23	-0.16	-0.47	0.486	0.664	0.919064	0.006609	0.701225
Deaf1	deformed epidermal autoregulatory factor 1 (Drosophila)	-0.31	-0.31	-0.33	-0.16	0.505	0.604	0.715409	0.009915	0.960672
Dgcr6	DiGeorge syndrome critical region gene 6	-0.51	-0.34	-0.17	-0.44	0.8	0.673	0.751114	0.000146	0.717181
Dgkh	diacylglycerol kinase, eta	-0.13	-0.6	-0.06	-0.55	0.985	0.312	0.020012	0.000698	0.923824
Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30 (Dhx30),	-0.36	0.004	-0.11	-0.53	0.388	0.645	0.788917	0.016828	0.380367
Dnm1	dynamamin 1	-0.1	-0.41	-0.21	-0.49	0.932	0.252	0.078537	0.003142	0.747494
Dpysl4	dihydropyrimidinase-like 4	-0.39	-0.31	0.186	-0.51	0.969	0.068	0.034898	0.009118	0.202719
Ensa	endosulfine alpha	-0.11	-0.45	-0.08	-0.5	0.796	0.311	0.088259	0.007531	0.971998
Faah	fatty acid amide hydrolase	-0.2	-0.4	-0.56	-0	0.585	0.559	0.645902	0.005962	0.417409
Fbxo2	F-box protein 2	0.097	-0.44	-0.67	-0.14	0.923	0.177	0.28297	0.004073	0.063397
Fbxw2	F-box and WD-40 domain protein 2	-0.41	-0.45	-0.47	0.09	0.7	0.538	0.623664	0.001677	0.419902
Fgf14	fibroblast growth factor 14	-0.14	-0.38	-0.58	0.009	0.493	0.576	0.55213	0.011605	0.388947
Ikzf2	IKAROS family zinc finger 2	-0.41	-0.09	-0.29	-0.24	0.2	0.867	0.161066	0.01286	0.583045
Itpka	inositol 1,4,5-trisphosphate 3-kinase A	-0.12	-0.55	-0.2	-0.17	0.799	0.19	0.177409	0.018691	0.546665
Kcnq2	potassium voltage-gated channel, subfamily Q, memb	0.244	-0.44	-0.39	-0.58	0.624	0.467	0.155063	0.003344	0.603138
Kif13a	kinesin family member 13A	-0.08	-0.27	-0.29	-0.51	0.792	0.345	0.239623	0.004894	0.896157
Klf13	Kruppel-like factor 13	-0.38	-0.51	0.026	-0.42	0.881	0.391	0.136489	0.001022	0.787747
Krt73	keratin 73	-0.15	-0.13	-0.47	-0.33	0.818	0.268	0.594767	0.007535	0.470492
Loh12cr1	loss of heterozygosity, 12, chromosomal region 1 hom	-0.03	-0.43	-0.49	-0.39	1.004	0.296	0.150388	0.000615	0.355095
Lrtm2	leucine-rich repeats and transmembrane domains 2	-0.24	-0.44	-0.39	0.02	0.618	0.401	0.991064	0.017039	0.509583
MacroD1	MACRO domain containing 1	-0.28	-0.47	-0.05	-0.28	0.292	0.763	0.941097	0.011017	0.43411
Mdga1	MAM domain containing glycosylphosphatidylinositol a	-0.1	-0.76	-0.04	-0.3	0.632	0.502	0.148198	0.003738	0.64099
Msto1	misato homolog 1 (Drosophila)	-0.45	-0.22	-0.18	-0.13	0.142	0.863	0.177956	0.017639	0.512476
Ncaph2	non-SMC condensin II complex, subunit H2	-0.23	-0.47	-0.37	-0.17	0.256	0.951	0.35452	0.002656	0.279508
Ncrna0008	non-protein coding RNA 86	-0.46	0.227	-0.52	-0.17	0.599	0.392	0.257551	0.019744	0.326374
Nfkbia	nuclear factor of kappa light polypeptide gene enhance	-0.61	-0.05	-0.45	0.132	0.232	0.801	0.020053	0.01295	0.998921
Nkain4	Na+/K+ transporting ATPase interacting 4	-0.18	-0.51	-0.08	-0.37	0.919	0.192	0.065747	0.006184	0.711383
Nr2c1	nuclear receptor subfamily 2, group C, member 1	-0.24	-0.17	-0.17	-0.43	0.28	0.741	0.719822	0.019025	0.498223
Numbl	numb-like	-0.01	-0.62	-0.27	-0.2	0.622	0.402	0.30694	0.015273	0.528479
Pcdhga1	protocadherin gamma subfamily A, 1	0.003	-0.45	-0.4	-0.26	0.912	0.155	0.141099	0.00885	0.306467
Pde10a	phosphodiesterase 10A	0.111	-0.47	0.169	-0.81	0.24	0.704	0.124441	0.01807	0.041871
Phyhip	phytanoyl-CoA hydroxylase interacting protein	-0.26	-0.47	-0.37	-0.11	0.59	0.602	0.941257	0.003822	0.733455
Pik3ip1	phosphoinositide-3-kinase interacting protein 1	-0.32	-0.49	-0.34	0.02	0.551	0.56	0.796264	0.006476	0.664324
Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12	0.083	-0.51	-0.45	-0.33	0.481	0.668	0.699984	0.004117	0.343525

Ppp5c	protein phosphatase 5, catalytic subunit	-0.1	-0.65	0.101	-0.43	0.705	0.315	0.046515	0.011287	0.955256
Prrt3	proline-rich transmembrane protein 3	-0.19	-0.58	-0.03	-0.28	0.893	0.148	0.059718	0.0091	0.691361
Ptk2b	PTK2 protein tyrosine kinase 2 beta	-0.04	-0.69	-0.26	-0.15	0.508	0.568	0.516916	0.008467	0.359758
Rab40b	Rab40b, member RAS oncogene family	-0.03	-0.3	-0.41	-0.38	0.873	0.222	0.229471	0.006493	0.511302
Rbm12	RNA binding motif protein 12	-0.44	-0.26	-0.06	-0.22	0.819	0.191	0.41319	0.016562	0.408446
Rbm39	RNA binding motif protein 39	-0.37	-0.48	0.017	-0.34	0.506	0.654	0.660743	0.00392	0.697332
Rexo1	REX1, RNA exonuclease 1 homolog ( <i>S. cerevisiae</i> )	0.13	-0.71	-0.26	-0.47	0.449	0.775	0.30321	0.001528	0.129199
Rgs9	regulator of G-protein signaling 9	-0.4	-0.31	-0.28	-0.03	0.62	0.405	0.867741	0.016933	0.742028
Rhou	ras homolog gene family, member U	-0.55	-0.07	-0.39	-0.28	0.404	0.927	0.114042	0.000836	0.726872
Rnf170	ring finger protein 170	-0.66	0.256	0.125	-0.63	0.926	0.074	0.307384	0.01347	0.002942
Rundc3a	RUN domain containing 3A	0.047	-0.94	-0.27	-0.26	0.878	0.441	0.038367	0.000298	0.194125
Sbf1	SET binding factor 1	-0.01	-0.48	-0.29	-0.33	0.83	0.231	0.131862	0.010663	0.61578
Sf1	splicing factor 1	0.07	-0.64	-0.52	0.046	0.202	0.771	0.55525	0.017759	0.050401
Sf3b2	splicing factor 3b, subunit 2	-0.07	-0.84	-0.12	-0.27	0.762	0.463	0.086407	0.001196	0.52706
Sfrs14	splicing factor, arginine/serine-rich 14	-0.05	-0.13	-0.61	-0.26	0.735	0.304	0.841064	0.008489	0.424432
Slc2a4	solute carrier family 2 (facilitated glucose transporter),	-0.74	-0.56	-0.39	-0.25	0.982	0.97	0.587375	6.12E-09	0.908008
Slc35e1	solute carrier family 35, member E1	0.173	-0.41	-0.61	-0.17	0.389	0.562	0.96235	0.018196	0.22021
Slc4a3	solute carrier family 4 (anion exchanger), member 3	-0.33	-0.42	-0.09	-0.21	0.476	0.568	0.874023	0.013516	0.931763
Snd1	staphylococcal nuclease and tudor domain containing	-0.31	-0.41	-0.2	-0.19	0.542	0.56	0.914623	0.009195	0.976269
Sort1	sortilin 1	-0.05	-0.14	-0.41	-0.46	0.395	0.659	0.865065	0.00831	0.815307
Spsb1	splA/ryanodine receptor domain and SOCS box containi	-0.73	-0	-0.48	0.163	0.54	0.578	0.051261	0.005623	0.432819
St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,	-0.07	-0.63	-0.44	-0.04	0.718	0.409	0.508622	0.005388	0.251083
St6galnac6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,	-0.07	-0.39	-0.35	-0.42	1.016	0.172	0.084314	0.002466	0.390088
Stk35	serine/threonine kinase 35	-0.04	-0.19	-0.51	-0.41	0.198	0.933	0.341686	0.003057	0.299066
Stxbp6	syntaxin binding protein 6 (amisyn)	-0.65	0.077	-0.48	-0.06	0.737	0.452	0.221493	0.003872	0.202166
Swap70	SWA-70 protein	-0.28	-0.39	-0.05	-0.29	0.757	0.253	0.258821	0.017808	0.799875
Sycp3	synaptonemal complex protein 3	-0.45	0.058	-0.25	-0.37	0.098	0.968	0.08292	0.010299	0.229675
Tap2	transporter 2, ATP-binding cassette, sub-family B (MD	-0.32	-0.45	-0.64	0.268	0.524	0.608	0.228647	0.004196	0.169387
Tarbp2	TAR (HIV) RNA binding protein 2	-0.34	-0.09	-0.42	-0.49	1.018	0.356	0.486554	0.000315	0.258263
Tha1	threonine aldolase 1	-0.06	-0.13	-0.49	-0.31	0.458	0.52	0.80942	0.018154	0.92137
Tlk2	tousled-like kinase 2 ( <i>Arabidopsis</i> )	-0.09	-0.27	-0.66	0.003	0.739	0.252	0.990599	0.018238	0.147201
Txnip	thioredoxin interacting protein	-0.17	-0.52	-0.62	-0.1	0.377	0.99	0.256616	0.000334	0.170842
Unk	unkempt homolog ( <i>Drosophila</i> )	-0.24	-0.6	-0.29	-0.1	0.747	0.449	0.521703	0.0027	0.601805
Usp52	ubiquitin specific peptidase 52	-0.06	-0.35	-0.17	-0.49	0.845	0.191	0.089456	0.012944	0.794438

Wbp2	WW domain binding protein 2	-0.16	-0.52	-0.38	5E-04	0.503	0.51	0.973265	0.017415	0.483685
Wdr32	WD repeat domain 32	-0.13	-0.13	-0.41	-0.35	0.595	0.421	0.88108	0.01588	0.922238
Wdr73	WD repeat domain 73	-0.03	-0.62	-0.27	-0.13	1.083	-0.09	0.021333	0.010855	0.076012
Wdr91	WD repeat domain 91	-0.34	-0.52	-0.48	0.142	0.654	0.524	0.671086	0.00278	0.310229
Xdh	xanthine dehydrogenase	-0.76	0.049	-0.36	-0.09	0.634	0.61	0.135513	0.002007	0.338511
Zfp580	zinc finger protein 580	0.038	-0.68	-0.25	-0.3	0.671	0.451	0.173604	0.005807	0.507421
Zmiz2	zinc finger, MIZ-type containing 2	-0.29	-0.37	-0.19	-0.32	0.942	0.223	0.204364	0.004442	0.478836
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Abcf3	ATP-binding cassette, sub-family F (GCN20), member	0.142	0.446	0.299	0.185	-0.9	-0.14	0.193362	0.012866	0.338516
Adcyap1	adenylate cyclase activating polypeptide 1	0.403	0.124	0.355	0.147	-0.52	-0.54	0.504853	0.016637	0.903744
Azi2	5-azacytidine induced gene 2	0.686	0.099	0.232	0.204	-0.64	-0.64	0.382789	0.001488	0.524581
C1galt1c1	C1GALT1-specific chaperone 1	0.125	0.508	0.334	0.256	-0.79	-0.4	0.344814	0.003842	0.66653
Cbx5	chromobox homolog 5 (Drosophila HP1a)	0.342	0.369	0.306	0.095	-0.45	-0.66	0.601062	0.008613	0.904954
Ccdc25	coiled-coil domain containing 25	0.042	0.707	0.131	0.191	-0.43	-0.58	0.440837	0.014164	0.376759
Cetn2	centrin 2	0.21	0.382	0.526	0.086	-1.06	-0.13	0.348026	0.002574	0.062489
Copz2	coatamer protein complex, subunit zeta 2	0.056	0.306	0.213	0.557	-0.7	-0.4	0.225747	0.006906	0.987409
Cpsf2	cleavage and polyadenylation specific factor 2	0.199	0.101	0.734	-0.05	-0.51	-0.48	0.244524	0.019056	0.348877
Cxcl2	chemokine (C-X-C motif) ligand 2	0.004	0.159	0.017	0.95	-0.59	-0.52	0.102465	0.002293	0.254784
Dcun1d2	DCN1, defective in cullin neddylation 1, domain contain	-0.16	0.801	0.047	0.379	-0.6	-0.37	0.039692	0.016265	0.409053
Ddr2	discoidin domain receptor family, member 2	0.171	0.023	0.389	0.485	-0.99	-0.09	0.237707	0.004738	0.176349
Derl2	Der1-like domain family, member 2	0.092	0.681	-0.08	0.388	-0.71	-0.32	0.050791	0.010296	0.945442
Dpp7	dipeptidylpeptidase 7	0.106	0.376	0.028	0.555	-0.82	-0.22	0.059099	0.013347	0.841925
Ebf1	early B-cell factor 1	0.031	0.031	0.411	0.566	-0.55	-0.49	0.764897	0.005975	0.966853
Ednrb	endothelin receptor type B	0.606	0.011	0.632	0.059	-0.61	-0.76	0.059006	0.000479	0.659865
Fermt2	fermitin family homolog 2 (Drosophila)	0.565	0.273	0.249	0.113	-0.34	-0.89	0.175413	0.00199	0.77464
Fkbp14	FK506 binding protein 14	0.453	0.245	0.141	0.31	-0.97	-0.2	0.308837	0.004024	0.246018
Gnpda2	glucosamine-6-phosphate deaminase 2	0.211	0.3	0.412	0.128	-0.73	-0.31	0.761296	0.016216	0.512087
Gpr177	G protein-coupled receptor 177	0.315	0.074	0.752	0.042	-0.71	-0.5	0.295043	0.002419	0.291073
Heatr5a	HEAT repeat containing 5A	-0.05	0.669	0.246	0.248	-0.82	-0.22	0.070045	0.01087	0.427299
Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	0.436	0.315	0.134	0.272	-1.11	-0.06	0.128857	0.002722	0.102386
Hist1h3a	histone cluster 1, H3a	0.516	0.221	0.022	0.36	-0.67	-0.48	0.756991	0.00576	0.544191
Hmgn1	high mobility group nucleosomal binding domain 1	0.177	-0.01	0.595	0.215	-0.91	-0.09	0.730336	0.011634	0.098638
Igdcc4	immunoglobulin superfamily, DCC subclass, member	0.301	0.689	0.169	0.329	-0.6	-0.85	0.657782	0.000115	0.519347
Igh-6	immunoglobulin heavy chain 6 (heavy chain of IgM)	0.232	0.087	0.205	0.589	-0.71	-0.42	0.466553	0.00587	0.637933



Acp1	acid phosphatase 1, soluble	-0.68	-0.15	0.254	0.76	-0.28	0.152	0.045838	0.009874	0.987352
Angptl1	angiopoietin-like 1	0.326	-0.39	0.941	0.202	-0.59	-0.56	0.037887	0.000529	0.290102
Bdh2	3-hydroxybutyrate dehydrogenase, type 2	-0.36	-0.27	0.461	0.606	-0.71	0.272	0.093257	0.009447	0.241018
Bzw1	basic leucine zipper and W2 domains 1	-0.23	-0.53	0.809	0.185	0.001	-0.26	0.112114	0.014918	0.804069
Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	-0.4	-0.43	0.481	0.488	-0.28	0.136	0.60275	0.016525	0.715401
Cpsf3	cleavage and polyadenylation specificity factor 3	-0.49	-0.43	0.464	0.54	-0.21	0.127	0.534568	0.009351	0.87454
Ctps2	cytidine 5'-triphosphate synthase 2	-0.91	0.008	0.546	0.626	-0.16	-0.02	0.106423	0.002047	0.26242
Cyb5b	cytochrome b5 type B	0.061	-0.21	-0.2	1.143	-0.64	-0.18	0.026476	0.008317	0.018325
Donson	downstream neighbor of SON	-0.4	-0.11	0.456	0.6	0.077	-0.6	0.73735	0.014088	0.224515
Dppa5a	developmental pluripotency associated 5A	-0.14	-0.02	0.34	0.609	-0.75	-0.03	0.133	0.019117	0.588738
Dtymk	deoxythymidylate kinase	-0.37	-0.5	0.697	0.293	0.166	-0.31	0.17707	0.011512	0.833068
Efhc1	EF-hand domain (C-terminal) containing 1	-0.33	-0.55	0.417	0.567	-0.18	0.053	0.828874	0.012481	0.733485
Eif4a1	eukaryotic translation initiation factor 4A1	-0.42	-0.42	0.485	0.457	-0.08	-0.02	0.954139	0.019575	0.989013
Etf1	eukaryotic translation termination factor 1	-0.22	-0.66	0.316	0.655	0.203	-0.35	0.377682	0.011496	0.274483
Etfdh	electron transferring flavoprotein, dehydrogenase	-0.12	-0.3	0.708	0.336	-0.24	-0.4	0.335128	0.014974	0.932304
Fbxl12	F-box and leucine-rich repeat protein 12	-0.58	-0.47	0.716	0.517	-0.33	0.163	0.568963	0.00081	0.489539
Kdr	kinase insert domain protein receptor	0.109	-0.46	0.419	0.762	-0.42	-0.46	0.704757	0.002315	0.293871
Lrch1	leucine-rich repeats and calponin homology (CH) dom	-0.18	-0.5	0.219	0.797	-0.59	0.222	0.137857	0.012114	0.133959
Lrch4	leucine-rich repeats and calponin homology (CH) dom	-0.41	-0.04	0.218	0.822	-0.59	0.036	0.031072	0.014256	0.889652
Nbn	nibrin	-0.3	-0.45	0.47	0.732	0.01	-0.48	0.611575	0.003061	0.446456
Pofut2	protein O-fucosyltransferase 2	-0.15	-0.59	0.328	0.758	-0.08	-0.31	0.743175	0.007882	0.319205
Ranbp2	RAN binding protein 2	-0.33	0.25	0.35	0.61	-0.43	-0.39	0.234401	0.016933	0.673245
Rbbp6	retinoblastoma binding protein 6	-0.63	-0.13	0.669	0.331	0.172	-0.36	0.607735	0.014614	0.190536
Slbp	stem-loop binding protein	-0.2	0.207	0.954	0.042	-0.4	-0.57	0.336162	0.005043	0.07941
Slc22a5	solute carrier family 22 (organic cation transporter), me	-0.46	-0.21	0.72	0.7	-0.32	-0.4	0.840318	0.000351	0.831663
Slc26a2	solute carrier family 26 (sulfate transporter), member 2	-0.4	0.132	0.547	0.573	-0.32	-0.48	0.586706	0.006326	0.489474
Slc7a9	solute carrier family 7 (cationic amino acid transporter,	-0.4	-0.1	0.384	0.935	-0.53	-0.26	0.111463	0.000844	0.866036
Slco4c1	solute carrier organic anion transporter family, membe	-0.33	-0.13	0.602	0.423	-0.59	0.039	0.380245	0.018443	0.409191
Smcr7	Smith-Magenis syndrome chromosome region, candid	-0.28	-0.59	0.51	0.679	0.006	-0.36	0.495634	0.002677	0.617611
Snx9	sorting nexin 9	-0.35	-0.28	0.621	0.445	-0.47	0.043	0.590404	0.012792	0.514768
Syap1	synapse associated protein 1	-0.43	-0.23	0.64	0.389	-0.39	0.036	0.626323	0.016931	0.532972
Sypl	synaptophysin-like protein	-0.07	-0.7	0.42	0.577	-0.29	1E-04	0.808285	0.013998	0.265673
Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding prot	-0.02	-0.06	0.543	0.487	-0.51	-0.45	0.964117	0.006815	0.977831
Tctn3	tectonic family member 3	-0.04	-0.05	0.134	0.87	-0.23	-0.69	0.709654	0.00718	0.127509

Tgfbra1	transforming growth factor, beta receptor associated p	-0.62	-0.05	0.432	0.713	0.308	-0.72	0.801294	0.003599	0.012648
Tmem41b	transmembrane protein 41B	-0.55	-0.08	0.469	0.641	-0.14	-0.29	0.499177	0.009646	0.588798
Tsfn	Ts translation elongation factor, mitochondrial	-0.43	-0.43	0.697	0.301	0.021	-0.16	0.44008	0.012143	0.808879
Txndc1	thioredoxin domain containing 1	-0.43	0.032	0.57	0.501	-0.67	0.043	0.131263	0.011255	0.408599
Ube3a	ubiquitin protein ligase E3A	-0.29	-0.44	0.629	0.417	-0.22	-0.12	0.734322	0.013718	0.860257
Vldlr	very low density lipoprotein receptor	-0.3	-0.17	0.608	0.46	-0.38	-0.2	0.829238	0.014586	0.846219
Wdr16	WD repeat domain 16	0.108	-0.54	0.462	0.538	-0.15	-0.48	0.222844	0.017278	0.486444
Wdr19	WD repeat domain 19	-0.02	-0.09	0.334	0.62	-0.38	-0.46	0.857935	0.017091	0.791832
Xpo7	exportin 7	-0.36	-0.4	0.426	0.616	-0.45	0.168	0.301603	0.011315	0.53298
Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	0.03	-0.56	0.423	0.744	-0.2	-0.5	0.427868	0.003659	0.288835
Zbtb46	zinc finger and BTB domain containing 46	-0.65	0.304	0.386	0.654	-0.36	-0.24	0.065126	0.01471	0.321056
<b>5 - (26)</b>										
Add2	adducin 2 (beta)	0.367	0.555	-0.63	-0.35	-0.16	0.225	0.254872	0.010608	0.949189
Akap2	A kinase (PRKA) anchor protein 2	0.364	0.07	0.038	-1.11	0.079	0.53	0.155036	0.007072	0.022532
Arid5b	AT rich interactive domain 5B (MRF1-like)	-0.09	0.362	-0.98	0.016	0.33	0.409	0.035919	0.014272	0.290777
Bbs12	Bardet-Biedl syndrome 12 (human)	0.266	0.387	-0.69	-0.31	-0.18	0.539	0.098132	0.017315	0.606557
Brf1	BRF1 homolog, subunit of RNA polymerase III transcri	0.015	0.277	-0.59	-0.43	0.328	0.419	0.49692	0.015772	0.961056
Camk2b	calcium/calmodulin-dependent protein kinase II, beta	0.456	-0.3	-0.7	-0.32	0.297	0.499	0.800392	0.010895	0.124877
Cbx7	chromobox homolog 7	0.058	-0.02	-0.22	-0.8	0.163	0.815	0.99289	0.004512	0.11202
Chd7	chromodomain helicase DNA binding protein 7	0.395	0.042	-0.18	-0.85	0.416	0.144	0.080956	0.016699	0.776029
Csmd1	CUB and Sushi multiple domains 1	0.425	0.238	-0.38	-0.63	0.003	0.332	0.88928	0.019006	0.585623
Diap2	diaphanous homolog 2 (Drosophila)	-0.03	0.51	-0.4	-0.7	0.444	0.231	0.969988	0.00755	0.30582
Dopey2	dopey family member 2	-0.04	0.415	-0.16	-0.86	0.402	0.29	0.62388	0.012661	0.161728
Fbf1	Fas (TNFRSF6) binding factor 1	-0.08	0.091	-0.63	-0.43	0.19	0.874	0.140321	0.002443	0.614874
Glpr11l	GLI pathogenesis-related 1 like 1	0.306	0.19	-0.2	-0.92	0.476	0.136	0.106381	0.007014	0.58121
Il34	interleukin 34	0.508	0.22	-0.71	-0.29	0.037	0.212	0.679951	0.017313	0.497346
Kcns1	K+ voltage-gated channel, subfamily S, 1	0.077	0.116	-0.28	-0.87	0.766	0.196	0.115075	0.002038	0.461113
Klhl11	kelch-like 11 (Drosophila)	0.334	0.513	-0.54	-0.42	0.017	0.112	0.598517	0.017244	0.990397
Lime1	Lck interacting transmembrane adaptor 1	0.597	0.096	-0.32	-0.68	-0.16	0.421	0.699313	0.016254	0.151882
Mfhas1	malignant fibrous histiocytoma amplified sequence 1	0.383	0.478	-0.22	-0.72	0.156	-0.07	0.405445	0.016352	0.626966
Mrps27	mitochondrial ribosomal protein S27	0.368	0.443	-0.64	-0.4	0.312	-0.07	0.932019	0.010226	0.569551
Mterfd1	MTERF domain containing 1	0.508	-0.08	-0.65	-0.44	0.211	0.396	0.791891	0.01089	0.326691
Ptges2	prostaglandin E synthase 2	0.281	0.272	-0.4	-0.85	0.359	0.334	0.502785	0.002301	0.696754
Sec22c	SEC22 vesicle trafficking protein homolog C (S. cerevi	0.48	0.53	-0.22	-0.94	0.08	0.082	0.346457	0.001562	0.330622





































