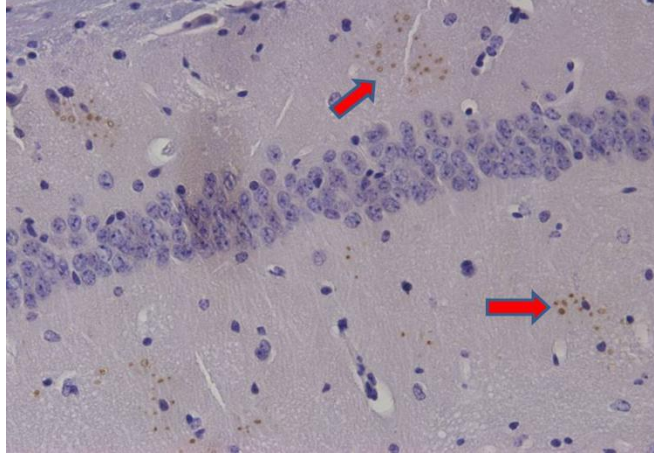


Transcriptional signaling pathways inversely regulated in Alzheimer's disease and glioblastoma multiform

Timothy Liu, Ding Ren, Xiaoping Zhu, Zheng Yin, Guangxu Jin, Zhen Zhao, Daniel Robinson, Xuping Li, Kelvin Wong, Kemi Cui, Hong Zhao, Stephen TC Wong

A



Supp Fig 1. A β plaque formation in AD mouse model

Stains indicate A β plaques that have formed in the brains of 12-month old APPswe transgenic mice

Transcriptional signaling pathways inversely regulated in Alzheimer's disease and glioblastoma multiforme

Timothy Liu, Ding Ren, Xiaoping Zhu, Zheng Yin, Guangxu Jin, Zhen Zhao, Daniel Robinson, Xuping Li, Kelvin Wong, Kemi Cui, Hong Zhao, Stephen TC

Supplementary Table 1. Differentially expressed genes enriched in GBM- and AD+ group

GBM	p-value (GBM)	AD	p-value (AD)	[AD]-[GBM]	Gene Symbol	Description
-19.0053	0	2.90436	8.00E-14	21.90966	CXCR4	chemokine (C-X-C motif) receptor 4
-17.0223	0	1.59531	4.19E-11	18.61761	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
-15.7619	3.80E-15	1.55059	6.89E-09	17.31249	NES	nestin
-14.5191	1.89E-25	2.33212	4.72E-15	16.85122	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
-13.2316	5.97E-22	1.84979	5.63E-19	15.08139	C21orf62	chromosome 21 open reading frame 62
-7.41736	1.21E-24	1.5886	6.41E-11	9.00596	TCF7L1	transcription factor 7-like 1 (T-cell specific, HMG-box)
-6.76226	2.69E-14	1.90321	8.41E-07	8.66547	SPP1	secreted phosphoprotein 1
-5.86117	1.95E-10	1.75826	2.76E-14	7.61943	ANGPT2	angiopoietin 2
-5.6675	6.41E-08	1.88748	4.39E-12	7.55498	AEBP1	AE binding protein 1
-5.64867	3.35E-42	1.84838	6.30E-19	7.49705	PTBP1	polypyrimidine tract binding protein 1
-5.81855	7.90E-34	1.51352	6.06E-09	7.33207	DENND2A	DENN/MADD domain containing 2A
-5.43669	3.19E-12	1.69113	2.33E-09	7.12782	GBP2	guanylate binding protein 2, interferon-inducible
-5.41383	1.23E-41	1.56233	7.91E-09	6.97616	EFNA1	ephrin-A1
-4.62267	1.04E-27	2.09584	1.18E-20	6.71851	DDR1	discoidin domain receptor tyrosine kinase 1
-4.64805	4.61E-19	2.01807	8.07E-16	6.66612	CALD1	caldesmon 1
-4.99189	2.24E-22	1.57084	1.94E-10	6.56273	DTYMK	deoxythymidylate kinase (thymidylate kinase)
-4.74692	5.60E-18	1.8122	3.14E-11	6.55912	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A
-3.88905	4.31E-08	2.47215	1.94E-11	6.3612	ZBTB20	zinc finger and BTB domain containing 20
-4.68899	4.16E-26	1.56706	2.45E-10	6.25605	SYK	spleen tyrosine kinase
-4.14684	1.20E-25	1.96033	1.39E-13	6.10717	VEZF1	vascular endothelial zinc finger 1
-4.48733	1.05E-19	1.5205	4.97E-11	6.00783	BAZ1A	bromodomain adjacent to zinc finger domain, 1A
-4.38735	6.87E-26	1.42505	7.89E-07	5.8124	HEATR2	HEAT repeat containing 2
-3.88255	3.47E-14	1.85299	4.38E-19	5.73554	TIMELESS	<i>timeless</i> homolog (Drosophila)
-3.18841	3.78E-13	2.53509	2.66E-15	5.7235	ERBB2IP	erbB2 interacting protein
-3.52176	3.22E-11	2.07833	1.51E-12	5.60009	LAMB2	laminin, beta 2 (laminin S)
-3.06204	4.58E-07	2.50823	1.10E-14	5.57027	MSX1	msh homeobox 1
-2.99046	4.22E-23	2.45698	2.59E-19	5.44744	TNPO1	transportin 1
-3.94351	6.80E-27	1.4899	2.34E-08	5.43341	NECAP2	NECAP endocytosis associated 2
-3.16239	4.86E-15	2.26682	2.37E-16	5.42921	SERPINB6	serpin peptidase inhibitor, clade B (ovalbumin), member 6
-3.64234	2.29E-16	1.76981	2.43E-07	5.41215	LAMP2	lysosomal-associated membrane protein 2
-3.60566	1.42E-10	1.65278	8.57E-10	5.25844	SMAD1	SMAD family member 1
-3.07934	6.32E-18	2.17592	1.75E-12	5.25526	BGN	biglycan
-3.17502	1.16E-12	2.02173	1.47E-13	5.19675	CEBPD	CCAAT/enhancer binding protein (C/EBP), delta
-3.71517	3.92E-15	1.40543	4.82E-08	5.1206	CHD1	chromodomain helicase DNA binding protein 1
-3.21798	3.83E-22	1.89548	3.45E-11	5.11346	PKN2	protein kinase N2
-3.59339	5.85E-25	1.50148	1.21E-08	5.09487	G3BP1	GTPase activating protein (SH3 domain) binding protein 1
-2.51583	4.31E-09	2.35692	2.13E-21	4.87275	C6orf145	PX domain containing 1 (Previous name: chromosome 6 open reading frame 145)
-1.98044	1.25E-07	2.87561	2.00E-18	4.85605	GOLIM4	golgi integral membrane protein 4
-2.64538	8.00E-10	2.19857	1.22E-13	4.84395	HLA-E	major histocompatibility complex, class I, E
-3.11744	1.29E-15	1.60757	2.57E-10	4.72501	SDCCAG3	serologically defined colon cancer antigen 3
-2.88873	1.06E-12	1.72948	4.82E-15	4.61821	STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)
-2.15023	1.42E-08	2.40808	2.71E-25	4.55831	FAM63A	family with sequence similarity 63, member A
-3.01971	1.10E-21	1.48649	2.84E-08	4.5062	SLC39A1	solute carrier family 39 (zinc transporter), member 1
-2.76503	5.73E-14	1.67962	6.04E-15	4.44465	ELF1	E74-like factor 1 (ets domain transcription factor)

-2.31955	4.37E-10	2.01794	9.27E-13	4.33749	VGLL4	vestigial like 4 (Drosophila)
-2.27348	2.19E-08	1.95519	3.35E-23	4.22867	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
-1.93025	8.83E-07	2.29448	6.11E-10	4.22473	NIPBL	Nipped-B homolog (Drosophila)
-2.55914	1.69E-14	1.64399	1.77E-12	4.20313	CTDSP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1
-2.42312	4.42E-30	1.72389	7.18E-15	4.14701	RBM38	RNA binding motif protein 38
-2.29197	2.19E-10	1.81327	1.45E-16	4.10524	RAF1	v-raf-1 murine leukemia viral oncogene homolog 1
-2.69259	3.30E-13	1.40503	2.20E-06	4.09762	ABHD4	abhydrolase domain containing 4
-2.43697	1.75E-21	1.62345	6.86E-12	4.06042	TGIF2	TGFB-induced factor homeobox 2
-2.41145	2.10E-06	1.64861	1.20E-08	4.06006	KLF6	Kruppel-like factor 6
-2.19036	3.96E-14	1.77242	1.31E-10	3.96278	TROVE2	TROVE domain family, member 2
-2.26591	2.16E-13	1.68546	1.07E-13	3.95137	C1orf144	SUZ RNA binding domain containing 1 (Previous name: chromosome 1 open reading frame 144)
-2.51365	1.40E-19	1.42601	7.51E-07	3.93966	MYO1F	myosin IF
-2.31378	3.95E-19	1.50931	7.73E-09	3.82309	DDAH2	dimethylarginine dimethylaminohydrolase 2
-2.27207	5.50E-12	1.51163	3.22E-08	3.7837	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)
-1.96875	1.70E-09	1.73408	3.46E-15	3.70283	LSM14A	<i>LSM14A</i> , SCD6 homolog A (<i>S. cerevisiae</i>)
-1.76377	1.24E-06	1.93745	4.49E-22	3.70122	TCF3	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)
-2.00923	3.14E-18	1.57677	1.34E-10	3.586	CDK2AP1	cyclin-dependent kinase 2 associated protein 1
-1.8925	6.83E-15	1.60154	3.27E-13	3.49404	EEF1D	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
-1.77413	5.60E-18	1.66466	4.43E-13	3.43879	C7orf26	chromosome 7 open reading frame 26
-1.72232	1.82E-13	1.67786	1.80E-13	3.40018	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
-1.82373	2.27E-08	1.53305	1.92E-09	3.35678	INPPL1	inositol polyphosphate phosphatase-like 1
-1.89756	1.11E-07	1.3988	3.00E-06	3.29636	FTSJ3	FtsJ homolog 3 (<i>E. coli</i>)
-1.73929	1.62E-06	1.55294	1.44E-12	3.29223	DOCK6	dedicator of cytokinesis 6
-1.69777	6.01E-06	1.50283	1.12E-08	3.2006	MAML1	mastermind-like 1 (Drosophila)
-1.51592	3.03E-07	1.43796	4.01E-07	2.95388	NUP214	nucleoporin 214kDa

Transcriptional signaling pathways inversely regulated in Alzheimer's disease and glioblastoma multiform

Timothy Liu, Ding Ren, Xiaoping Zhu, Zheng Yin, Guangxu Jin, Zhen Zhao, Daniel Robinson, Xuping Li, Kelvin Wong, Kemi

supplementary Table 2. Differentially expressed genes enriched in GBM+ and AD- group

GBM	p-value (GBM)	AD	p-value (AD)	[GBM] - [AD]	Gene Symbol	Description
69.8354	9.36E-24	-5.03278	1.47E-12	74.86818	VSNL1	visinin-like 1
66.1181	5.38E-38	-2.22593	1.99E-12	68.34403	SLC17A7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7
50.0319	2.53E-21	-2.92639	7.63E-09	52.95829	SYT1	synaptotagmin I
48.0145	2.70E-24	-2.59281	4.94E-09	50.60731	SNAP91	synaptosomal-associated protein, 91kDa homolog (mouse)
41.9258	0	-2.02067	4.06E-13	43.94647	CACNG3	calcium channel, voltage-dependent, gamma subunit 3
33.9691	8.53E-18	-5.50808	4.89E-18	39.47718	SNAP25	synaptosomal-associated protein, 25kDa
35.5137	3.26E-26	-2.57222	1.30E-16	38.08592	CRYM	crystallin, mu
34.1107	7.52E-27	-1.66045	4.00E-07	35.77115	NRGN	neurogranin (protein kinase C substrate, RC3)
32.3611	7.24E-35	-2.12943	1.26E-11	34.49053	AK5	adenylate kinase 5
31.1015	1.85E-33	-2.45965	1.49E-14	33.56115	RGS4	regulator of G-protein signaling 4
25.0042	0	-2.42994	7.03E-12	27.43414	RIMBP2	RIMS binding protein 2
25.6378	1.85E-37	-1.72924	4.90E-15	27.36704	SYNGR3	synaptogyrin 3
24.3029	0	-2.12466	5.77E-10	26.42756	STYK1	serine/threonine/tyrosine kinase 1
22.4524	1.06E-18	-2.2731	7.26E-07	24.7255	FGF13	fibroblast growth factor 13
19.8853	6.38E-26	-4.11339	6.82E-17	23.99869	NMNAT2	nicotinamide nucleotide adenyltransferase 2
21.0659	3.89E-19	-2.61304	4.04E-08	23.67894	SERPINI1	serpin peptidase inhibitor, clade I (neuroserpin), member 1
20.4744	0	-2.98104	2.10E-12	23.45544	GABRG2	gamma-aminobutyric acid (GABA) A receptor, gamma 2
19.5019	1.06E-43	-3.64995	1.69E-16	23.15185	SNCA	synuclein, alpha (non A4 component of amyloid precursor)
17.6841	1.15E-21	-3.22699	1.17E-13	20.91109	DYNC111	dynein, cytoplasmic 1, intermediate chain 1
17.7008	0	-2.85475	3.98E-10	20.55555	SYN2	synapsin II
18.063	1.09E-42	-1.74732	7.51E-09	19.81032	KIAA0513	<i>KIAA0513 (uncharacterized protein KIAA051)</i>
15.4449	0	-1.94146	1.05E-08	17.38636	CPNE6	copine VI (neuronal)
14.1886	5.61E-45	-2.41781	4.25E-08	16.60641	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3
14.6089	8.23E-18	-1.76839	8.24E-12	16.37729	HSPB3	heat shock 27kDa protein 3
14.1951	7.36E-25	-1.93069	5.61E-08	16.12579	STXBP1	syntaxin binding protein 1
13.8307	1.30E-43	-2.16274	2.64E-10	15.99344	MAST3	microtubule associated serine/threonine kinase 3
12.22	0	-2.01739	7.06E-15	14.23739	CCKBR	cholecystokinin B receptor
11.7107	0	-2.23457	6.07E-12	13.94527	CNKSR2	connector enhancer of kinase suppressor of Ras 2
12.4551	1.56E-32	-1.43619	4.41E-07	13.89129	C6orf105	(now androgen-dependent TFPI-regulating protein (Previous name: chromosome 6 open reading frame 105)
11.6403	2.31E-17	-2.06788	1.25E-09	13.70818	NAV3	neuron navigator 3
11.7629	0	-1.92493	1.28E-21	13.68783	SLC30A3	solute carrier family 30 (zinc transporter), member 3

12.0352	8.90E-19	-1.64856	1.31E-12	13.68376	FXYP7	FXYP domain containing ion transport regulator 7
10.8876	2.41E-20	-2.72527	1.51E-11	13.61287	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
10.1852	8.17E-21	-3.09936	1.48E-10	13.28456	ENC1	ectodermal-neural cortex 1 (with BTB-like domain)
10.679	3.24E-41	-2.32297	6.37E-12	13.00197	SULT4A1	sulfotransferase family 4A, member 1
10.9362	0	-1.72639	1.73E-08	12.66259	GPR22	G protein-coupled receptor 22
9.6086	2.52E-24	-2.76907	2.18E-12	12.37767	GUCY1B3	guanylate cyclase 1, soluble, beta 3
8.78485	1.35E-35	-3.26765	3.03E-17	12.0525	GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)
8.80544	1.30E-21	-1.88344	1.24E-10	10.68888	EHD3	EH-domain containing 3
7.99811	5.75E-19	-1.9885	1.67E-10	9.98661	SLITRK5	SLIT and NTRK-like family, member 5
8.03525	2.42E-11	-1.81592	1.76E-07	9.85117	BASP1	brain abundant, membrane attached signal protein 1
7.16517	1.55E-26	-2.43205	1.50E-09	9.59722	PI4KA	phosphatidylinositol 4-kinase, catalytic, alpha
6.33827	4.57E-23	-3.24359	1.44E-15	9.58186	YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
7.23834	2.42E-24	-2.32901	2.48E-08	9.56735	PDE1A	phosphodiesterase 1A, calmodulin-dependent
5.7499	1.57E-19	-3.22365	2.11E-15	8.97355	BSCL2	Berardinelli-Seip congenital lipodystrophy 2 (seipin)
6.82976	2.88E-26	-1.97198	3.46E-16	8.80174	ATP1A3	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide
6.72837	3.24E-32	-1.79005	4.49E-19	8.51842	PTPN3	protein tyrosine phosphatase, non-receptor type 3
6.37841	0	-1.98974	7.36E-07	8.36815	TRHDE	thyrotropin-releasing hormone degrading enzyme
5.13805	2.40E-16	-3.10573	9.16E-14	8.24378	TUBA4A	tubulin, alpha 4a
5.72132	3.63E-14	-2.49821	2.10E-10	8.21953	GABRA5	gamma-aminobutyric acid (GABA) A receptor, alpha 5
4.67008	1.33E-08	-3.54264	1.95E-13	8.21272	UCHL1	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
4.94632	4.84E-14	-3.2254	1.37E-12	8.17172	HPRT1	hypoxanthine phosphoribosyltransferase 1
6.16296	0	-1.92571	2.79E-12	8.08867	KCNV1	potassium channel, subfamily V, member 1
5.06232	2.40E-28	-3.01742	9.96E-13	8.07974	STAT4	signal transducer and activator of transcription 4
6.11517	7.69E-36	-1.7648	3.69E-16	7.87997	SYP	synaptophysin
5.06218	5.34E-07	-2.61984	5.83E-09	7.68202	SCG5	secretogranin V (7B2 protein)
4.2986	6.30E-33	-3.33084	2.20E-13	7.62944	ATP6V1H	ATPase, H ⁺ transporting, lysosomal 50/57kDa, V1 subunit H
5.04864	2.39E-23	-2.54492	4.16E-11	7.59356	SLC9A6	solute carrier family 9, subfamily A (NHE6, cation proton antiporter 6), member 6
5.61695	0	-1.9623	1.31E-08	7.57925	NEUROD6	neuronal differentiation 6
6.04564	9.56E-41	-1.51713	2.93E-10	7.56277	GREM2	gremlin 2
5.48298	3.85E-19	-2.06085	4.81E-11	7.54383	XK	X-linked Kx blood group (McLeod syndrome)
5.95235	6.88E-36	-1.49221	2.06E-08	7.44456	KIAA1324	<i>KIAA1324 (Estrogen-induced gene 121 protein)</i>
4.76908	1.40E-45	-2.67227	2.59E-15	7.44135	GLS	glutaminase
4.76053	7.03E-29	-2.57473	3.31E-14	7.33526	CALM3	calmodulin 3 (phosphorylase kinase, delta)
5.63535	7.18E-36	-1.61611	1.10E-11	7.25146	ZNF215	zinc finger protein 215
4.29683	3.80E-19	-2.90255	1.93E-13	7.19938	ACOT7	acyl-CoA thioesterase 7

5.21979	2.11E-24	-1.85222	9.93E-09	7.07201	MOAP1	modulator of apoptosis 1
5.5634	4.80E-22	-1.50696	8.86E-09	7.07036	STAR	steroidogenic acute regulatory protein
3.80472	1.40E-18	-3.2345	2.37E-14	7.03922	ATP6V1B2	ATPase, H ⁺ transporting, lysosomal 56/58kDa, V1 subunit B2
4.90147	0	-2.04443	8.33E-12	6.9459	CAMK1G	calcium/calmodulin-dependent protein kinase IG
3.14873	3.53E-36	-3.79134	5.89E-13	6.94007	MDH1	malate dehydrogenase 1, NAD (soluble)
4.7172	8.44E-23	-2.14686	1.92E-08	6.86406	WDR7	WD repeat domain 7
3.98513	1.35E-25	-2.76284	2.77E-14	6.74797	RGS7	regulator of G-protein signaling 7
4.67675	2.18E-08	-1.93327	9.49E-10	6.61002	LDOC1	leucine zipper, down-regulated in cancer 1
4.34982	8.26E-23	-2.21231	3.38E-06	6.56213	PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme
3.8003	4.38E-06	-2.69632	2.54E-14	6.49662	NRN1	neuritin 1
3.83026	2.47E-09	-2.45417	5.44E-09	6.28443	PLK2	polo-like kinase 2
3.65995	6.31E-17	-2.62392	4.94E-13	6.28387	NECAP1	NECAP endocytosis associated 1
4.49276	7.84E-42	-1.7659	5.71E-10	6.25866	CRH	corticotropin releasing hormone
4.35707	1.70E-31	-1.81543	8.16E-18	6.1725	KIAA0319	<i>KIAA0319(dyslexia-associated protein KIAA0319)</i>
3.82589	7.98E-28	-2.29756	4.37E-15	6.12345	AP3M2	adaptor-related protein complex 3, mu 2 subunit
4.51085	1.10E-21	-1.61129	1.49E-13	6.12214	CABYR	calcium binding tyrosine-(Y)-phosphorylation regulated
4.45015	7.01E-45	-1.54321	1.05E-09	5.99336	CDKN2D	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)
2.05487	5.23E-08	-3.83289	2.22E-16	5.88776	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
3.54066	2.16E-18	-2.27991	2.41E-11	5.82057	TRIM37	tripartite motif containing 37
3.85136	6.31E-44	-1.9658	4.05E-23	5.81716	KALRN	kalirin, RhoGEF kinase
2.85905	3.73E-08	-2.94669	8.95E-13	5.80574	RTN3	reticulon 3
3.47879	1.01E-13	-2.31086	5.64E-13	5.78965	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein
3.05376	1.76E-26	-2.73506	3.85E-14	5.78882	PAK1	p21 protein (Cdc42/Rac)-activated kinase 1
3.90666	5.23E-13	-1.84946	9.56E-09	5.75612	B3GNT1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1
4.04744	3.00E-13	-1.68534	2.85E-10	5.73278	CDH9	cadherin 9, type 2 (T1-cadherin)
3.82825	7.45E-21	-1.84474	3.18E-08	5.67299	C1orf216	chromosome 1 open reading frame 216
3.59106	2.60E-14	-2.07887	1.06E-09	5.66993	SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1
2.90251	1.69E-13	-2.74628	3.86E-16	5.64879	GLRB	glycine receptor, beta
2.94701	4.28E-25	-2.68496	6.03E-16	5.63197	ATP6V1E1	ATPase, H ⁺ transporting, lysosomal 31kDa, V1 subunit E1
3.09872	7.87E-17	-2.51656	1.23E-11	5.61528	MAP2K4	mitogen-activated protein kinase kinase 4
3.6681	0	-1.9368	4.55E-11	5.6049	PRMT8	protein arginine methyltransferase 8
3.93153	1.19E-07	-1.65898	8.00E-07	5.59051	PPL	periplakin
3.40802	2.35E-25	-2.18015	5.77E-14	5.58817	LARGE	like-glycosyltransferase
3.86062	5.65E-24	-1.6762	6.44E-09	5.53682	ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 (putative)
3.48653	2.25E-13	-2.00889	7.19E-13	5.49542	FABP3	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)

2.24303	7.03E-09	-3.19185	1.37E-12	5.43488	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1
3.69969	7.12E-26	-1.70438	4.14E-08	5.40407	ARF3	ADP-ribosylation factor 3
3.83905	6.20E-17	-1.56395	7.60E-09	5.403	B4GALT6	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6
1.70996	4.18E-07	-3.68599	3.29E-19	5.39595	ATP5C1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
3.6658	0	-1.72318	2.47E-10	5.38898	KCNAB1	potassium voltage-gated channel, shaker-related subfamily, beta member 1
3.56936	7.29E-18	-1.79267	6.21E-12	5.36203	GABARAPL1	GABA(A) receptor-associated protein like 1
3.07958	2.41E-34	-2.26235	1.78E-10	5.34193	PPP3CB	protein phosphatase 3, catalytic subunit, beta isozyme
3.48592	4.49E-42	-1.84575	1.48E-09	5.33167	CDH12	cadherin 12, type 2 (N-cadherin 2)
2.86446	4.57E-06	-2.44715	2.05E-12	5.31161	CARTPT	CART prepropeptide
2.84323	1.77E-22	-2.40833	1.01E-09	5.25156	MAP2K1	mitogen-activated protein kinase kinase 1
2.99392	1.35E-13	-2.20323	2.73E-09	5.19715	OXCT1	3-oxoacid CoA transferase 1
3.59613	1.30E-13	-1.57784	1.26E-10	5.17397	PPP3R1	protein phosphatase 3, regulatory subunit B, alpha
3.0434	1.62E-14	-2.06185	3.74E-09	5.10525	TERF2IP	telomeric repeat binding factor 2, interacting protein
3.4688	2.39E-14	-1.5222	3.65E-09	4.991	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)
2.60617	2.01E-10	-2.38449	1.05E-14	4.99066	CDK5	cyclin-dependent kinase 5
3.00758	2.38E-06	-1.97344	1.34E-09	4.98102	SOSTDC1	sclerostin domain containing 1
3.01014	6.61E-07	-1.96743	1.41E-11	4.97757	C16orf45	chromosome 16 open reading frame 45
3.31278	1.10E-15	-1.61039	6.11E-10	4.92317	SEC61A2	Sec61 alpha 2 subunit (<i>S. cerevisiae</i>)
2.15416	9.93E-09	-2.75425	1.72E-10	4.90841	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase
2.52009	1.13E-30	-2.38795	1.83E-10	4.90804	RBP4	retinol binding protein 4, plasma
3.38625	2.79E-27	-1.49393	2.63E-05	4.88018	PTPRM	protein tyrosine phosphatase, receptor type, M
3.21011	7.31E-16	-1.66511	1.97E-05	4.87522	ATP6V1A	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A
2.22031	1.64E-33	-2.62559	1.10E-16	4.8459	GHITM	growth hormone inducible transmembrane protein
2.39675	7.15E-12	-2.40925	1.84E-16	4.806	FIG4	<i>FIG4</i> homolog, SAC1 lipid phosphatase domain containing (<i>S. cerevisiae</i>)
2.72271	1.67E-11	-2.05103	2.74E-09	4.77374	FKBP1B	FK506 binding protein 1B, 12.6 kDa
2.85278	1.12E-24	-1.90495	2.28E-11	4.75773	PTPRN2	protein tyrosine phosphatase, receptor type, N polypeptide 2
2.40482	2.62E-08	-2.28991	3.39E-11	4.69473	KIAA1279	<i>KIAA1279 (KIF1-binding protein)</i>
2.5088	3.05E-07	-2.18237	1.27E-09	4.69117	EPHA5	EPH receptor A5
2.94933	2.35E-16	-1.71572	9.44E-09	4.66505	FBXO34	F-box protein 34
2.9362	8.66E-12	-1.71891	1.44E-07	4.65511	HERC1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 1
3.27604	7.81E-18	-1.37666	8.90E-06	4.6527	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1
2.37296	6.79E-08	-2.2596	1.99E-10	4.63256	MAPK1	mitogen-activated protein kinase 1
2.72567	0	-1.88605	2.87E-10	4.61172	DLGAP2	discs, large (<i>Drosophila</i>) homolog-associated protein 2
2.58637	3.70E-14	-2.02299	1.16E-15	4.60936	CISD1	CDGSH iron sulfur domain 1
2.20801	2.04E-11	-2.39773	3.43E-11	4.60574	SERINC3	serine incorporator 3

2.00009	9.57E-15	-2.56213	5.55E-11	4.56222	AP2M1	adaptor-related protein complex 2, mu 1 subunit
2.50768	2.40E-09	-2.02606	7.89E-08	4.53374	DMXL2	Dmx-like 2
2.44852	6.83E-15	-2.0249	7.49E-10	4.47342	PGRMC1	progesterone receptor membrane component 1
2.5435	5.39E-17	-1.89831	2.56E-14	4.44181	IDS	iduronate 2-sulfatase
2.37597	1.26E-13	-2.0509	2.99E-09	4.42687	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D
2.4622	4.05E-15	-1.93761	1.40E-06	4.39981	TM2D3	TM2 domain containing 3
2.24835	3.69E-12	-2.11609	2.42E-14	4.36444	GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
2.65351	4.69E-14	-1.70547	2.65E-14	4.35898	DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24
2.56141	1.72E-08	-1.75816	6.01E-16	4.31957	FAM49A	family with sequence similarity 49, member A
1.97392	2.54E-06	-2.3439	9.32E-11	4.31782	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
2.31326	1.89E-12	-1.99237	1.16E-12	4.30563	PPME1	protein phosphatase methylesterase 1
1.81134	3.04E-06	-2.47869	4.12E-15	4.29003	RRAGA	Ras-related GTP binding A
2.26972	4.06E-21	-2.01132	1.06E-10	4.28104	ATPIF1	ATPase inhibitory factor 1
1.95662	9.81E-06	-2.28408	2.79E-08	4.2407	ANKMY2	ankyrin repeat and MYND domain containing 2
1.51064	7.86E-06	-2.7225	4.59E-18	4.23314	SARS	seryl-tRNA synthetase
2.59055	1.00E-11	-1.64234	4.35E-05	4.23289	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)
2.37026	2.48E-13	-1.8603	8.62E-11	4.23056	MGST3	microsomal glutathione S-transferase 3
2.01046	3.07E-10	-2.16675	1.30E-08	4.17721	NDUFA8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa
2.32039	1.32E-12	-1.85253	1.40E-09	4.17292	AUH	AU RNA binding protein/enoyl-CoA hydratase
2.17178	6.63E-19	-1.99969	7.51E-11	4.17147	R3HDM1	R3H domain containing 1
1.99891	5.26E-30	-2.14352	6.87E-14	4.14243	CHP	calcineurin-like EF hand protein 1
1.94678	2.37E-20	-2.16239	3.39E-11	4.10917	ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
2.50412	4.92E-13	-1.59157	7.27E-09	4.09569	STOML1	stomatin (EPB72)-like 1
2.22021	3.34E-08	-1.80698	1.56E-17	4.02719	TUBG2	tubulin, gamma 2
2.50834	2.33E-14	-1.51235	3.26E-07	4.02069	PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta
2.05954	1.96E-10	-1.9381	4.25E-22	3.99764	C14orf2	chromosome 14 open reading frame 2
1.8637	1.68E-07	-2.1296	6.06E-12	3.9933	PEX11B	peroxisomal biogenesis factor 11 beta
1.87393	2.96E-12	-2.09782	6.95E-12	3.97175	STS	steroid sulfatase (microsomal), isozyme S
2.2572	1.12E-15	-1.71262	6.05E-08	3.96982	ARPC5L	actin related protein 2/3 complex, subunit 5-like
2.3608	7.29E-36	-1.60822	1.84E-11	3.96902	SYT5	synaptotagmin V
1.81686	4.63E-08	-2.13809	2.36E-13	3.95495	NDUFV1	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
2.19475	7.96E-12	-1.74289	4.32E-11	3.93764	SLC25A14	solute carrier family 25 (mitochondrial carrier, brain), member 14
1.84692	8.33E-14	-2.08499	1.11E-10	3.93191	ACTR10	actin-related protein 10 homolog (<i>S. cerevisiae</i>)
2.10551	7.42E-14	-1.81318	9.70E-18	3.91869	KCNB2	potassium voltage-gated channel, Shab-related subfamily, member 2
2.0264	3.75E-14	-1.88738	1.21E-09	3.91378	LCMT1	leucine carboxyl methyltransferase 1

1.92876	1.43E-23	-1.96901	5.66E-11	3.89777	TPM3	tropomyosin 3
2.13207	3.98E-11	-1.74687	1.27E-16	3.87894	ADAM23	ADAM metallopeptidase domain 23
2.36226	2.73E-31	-1.45684	1.46E-07	3.8191	DTNB	dystrobrevin, beta
2.32084	1.52E-11	-1.49225	2.22E-09	3.81309	RBM9 (now RE RNA binding protein, fox-1 homolog (C. elegans) 2 / (Previous name: RNA binding motif protein 9)	
2.12735	4.53E-10	-1.67807	8.59E-09	3.80542	PIN1	peptidylprolyl cis/trans isomerase, NIMA-interacting 1
1.90303	1.26E-08	-1.88079	2.09E-08	3.78382	REEP5	receptor accessory protein 5
2.17498	1.25E-12	-1.51105	6.99E-09	3.68603	PITPNB	phosphatidylinositol transfer protein, beta
1.84473	1.26E-09	-1.8039	1.62E-07	3.64863	ARL8B	ADP-ribosylation factor-like 8B
1.51257	2.92E-07	-2.1149	1.68E-12	3.62747	VPS35	vacuolar protein sorting 35 homolog (S. cerevisiae)
1.88876	3.09E-09	-1.6864	1.00E-13	3.57516	KATNB1	katanin p80 (WD repeat containing) subunit B 1
1.50024	9.11E-11	-1.95141	1.87E-06	3.45165	LMTK2	lemur tyrosine kinase 2
1.87163	1.06E-07	-1.46592	5.39E-07	3.33755	SLC41A3	solute carrier family 41, member 3
1.35474	6.18E-07	-1.38804	5.12E-06	2.74278	ALOX12B	arachidonate 12-lipoxygenase, 12R type