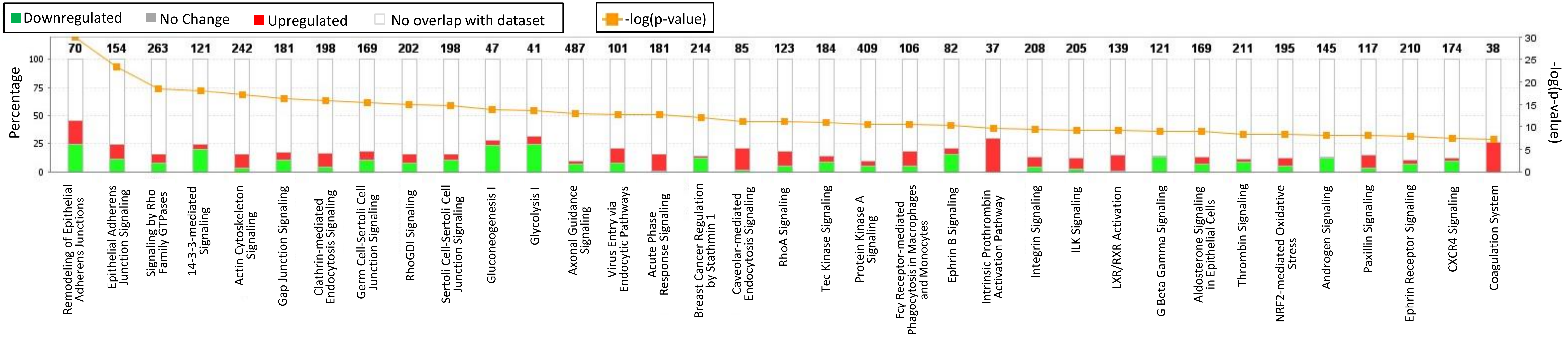
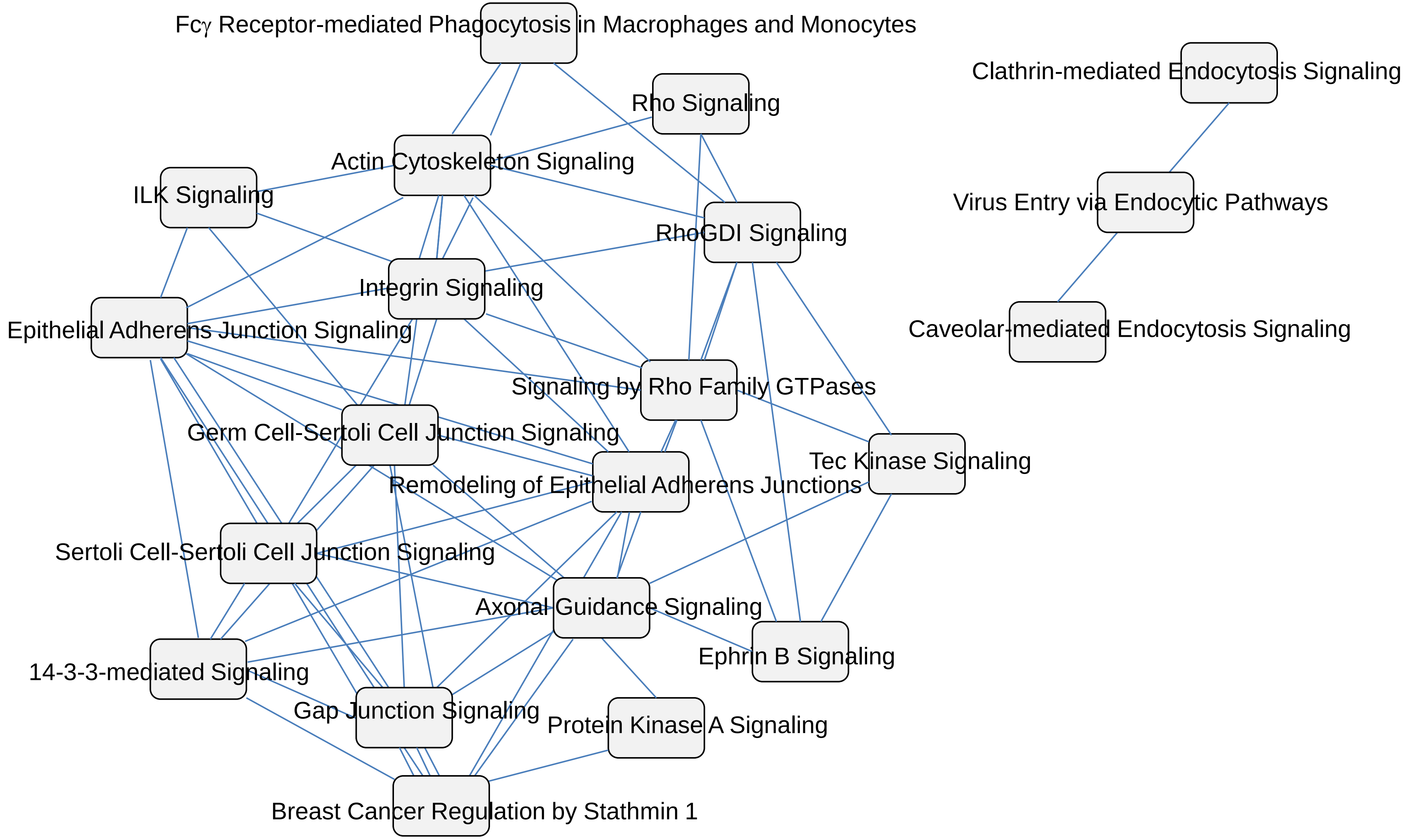
Supplemental Figure 1: The stack-bar chart of predominant canonical pathways of differentially expressed GBM proteins identified by IPA. The red and green color in each bar represent up- and down-regulated proteins, respectively



Supplemental Figure 2: Overlapping of canonical pathways of differentially expressed proteins in GBM as produced by IPA network analysis. A maximum of 25 pathways displayed with 12 common molecules overlapping is allowed in this network analysis



SDS-PAGE and Western Blotting Materials:

PBST: Gibco 70011-044 supplemented with 0.5% Tween-20.

TBST: 10 mM Tris-Cl pH 7.5, 150 mM NaCl, 0.8% Tween-20.

Ponceau S solution: Sigma-Aldrich P7170

3-8% Tris-Acetate gel (Life Technologies, Inc. P/N EA03755BOX)

4-12% Bis-Tris gel (Life Technologies, Inc. P/N NP0336BOX)

Tris-Acetate-SDS Running Buffer (20X) (Life Technologies, Inc. P/N LA0041)

MOPS-SDS Running Buffer (20X) (Life Technologies, Inc. P/N NP0001)

Nitrocellulose membrane, 0.45 μm pore size (Life Technologies, Inc. P/N LC2001)

PVDF membrane (Life Technologies, Inc. P/N LC2002)

NuPAGE Transfer Buffer (20X) (Life Technologies, Inc. P/N NP0006-1). (Transfer buffer was used at 2X and supplemented with 10% methanol.)

HRP-conjugated secondary antibodies were detected with Pierce Supersignal West chemiluminescent substrates, using Pico (P/N 34077), Dura (P/N 34075), or Femto (P/N 34095) reagents as required for optimum signal.

Autoradiography film (Midsci, Inc. P/N BX57)

Restore Western Blot Stripping Buffer (Thermo Scientific P/N 21059)

General protocol for western blotting:

1. Run gel according to manufacturer's specifications.
2. Transfer protein to membrane at 30V constant for 60 min at 4ºC.
3. Stain membrane in Ponceau S solution for 5 min. Rinse with milliQ H_2O until bands are visible to verify transfer.
4. Block as described for individual antibody.
5. Incubate in primary antibody.
6. Wash 4 x 5 min in TBST or PBST.
7. Incubate in secondary antibody.
8. Wash 4 x 5 min in TBST or PBST.
9. Incubate membrane for 5 min in Supersignal Detection Reagent.
10. Expose to film.
11. Develop film in Kodak X-Omat 2000 processor.
12. Image on Molecular Imager Gel Doc XR+ System (Biorad #170-8195).

Western blotting protocols for individual antibodies:

Protein	**Nestin**				
SDS-PAGE	3-8% Tris-Acetate gel, Tris-Acetate-SDS running buffer, 150V constant, 70 min, 4ºC				
Transfer/membrane	0.45 um pore size Nitrocellulose, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% BSA in TBST	4ºC	5 hr
Primary Antibody	NB300-266 (Novus Biologicals)	1:5,000	1% BSA in TBST	4ºC	Overnight
Secondary Antibody	HAF007 (R&D Systems)	1:10,000	1% BSA in TBST	RT	1 hr

Protein	**IQGAP1**				
SDS-PAGE	3-8% Tris-Acetate gel, Tris-Acetate-SDS running buffer, 150V constant, 70 min, 4ºC				
Transfer/membrane	0.45 um pore size Nitrocellulose, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% NFDM in PBST	4ºC	Overnight
Primary Antibody	ab109292 (Abcam)	1:5,000	5% NFDM in PBST	4ºC	Overnight
Secondary Antibody	Ab97051 (Abcam)	1:10,000	5% NFDM in PBST	RT	1 hr

Protein	**NAMPT**				
SDS-PAGE	4-12% Bis-Tris gel, MOPS-SDS running buffer, 200V constant, 70 min, 4ºC				
Transfer/membrane	0.45 um pore size Nitrocellulose, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% NFDM in TBST	RT	1 hour
Primary Antibody	ab109292 (Abcam)	1:5,000	5% NFDM in TBST	4ºC	Overnight
Secondary Antibody	ab97051 (Abcam)	1:10,000	5% NFDM in TBST	RT	1 hr

Protein	**ANXA1**				
SDS-PAGE	4-12% Bis-Tris gel, MOPS-SDS running buffer, 200V constant, 70 min, 4ºC				
Transfer/membrane	Invitrolon PVDF, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% BSA in TBST	4ºC	Overnight
Primary Antibody	8691 (Cell Signaling Technologies)	1:5,000	5% BSA in TBST	4ºC	Overnight
Secondary Antibody	ab97051 (Abcam)	1:20,000	5% BSA in TBST	RT	1 hr

Protein	**Peripherin**				
SDS-PAGE	4-12% Bis-Tris gel, MOPS-SDS running buffer, 200V constant, 70 min, 4ºC				
Transfer/membrane	0.45 um pore size Nitrocellulose, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% NFDM in TBST	RT	1 hour
Primary Antibody	Sc-7604 (Santa Cruz Biotechnology, Inc.)	1:1,000	5% NFDM in TBST	4ºC	Overnight
Secondary Antibody	Sc-2020 (Santa Cruz Biotechnology, Inc.)	1:10,000	5% NFDM in TBST	RT	1 hr

Protein	**CATB**				
SDS-PAGE	4-12% Bis-Tris gel, MOPS-SDS running buffer, 200V constant, 70 min, 4ºC				
Transfer/membrane	Invitrolon PVDF, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% NFDM in PBST	RT	1 hour
Primary Antibody	Ab58802 (Abcam)	1:400	5% NFDM in PBST	4ºC	Overnight
Secondary Antibody	HAF007 (R&D Systems)	1:10,000	5% NFDM in PBST	RT	1 hr

Protein	**FETUA**				
SDS-PAGE	4-12% Bis-Tris gel, MOPS-SDS running buffer, 200V constant, 70 min, 4ºC				
Transfer/membrane	Invitrolon PVDF, 30V constant, 1 hr, 4ºC				
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% BSA in TBST	4ºC	Overnight
Primary Antibody	ab137125 (Abcam)	1:10,000	5% BSA in TBST	4ºC	Overnight
Secondary Antibody	ab97051 (Abcam)	1:50,000	5% BSA in TBST	RT	1 hr

Protein	**β-actin**				
Used as a loading control. Membranes were stripped with Restore Western Blot Stripping Buffer (Thermo Scientific) for 45 min at 37ºC and rinsed for 5 min in TBST before proceeding with β-actin blotting.					
	Antibody	**Dilution**	**Diluent**	**Temperature**	**Time**
Block	N/A	N/A	5% NFDM in TBST	4ºC	Overnight
Primary Antibody	A2228 (Sigma-Aldrich)	1:10,000	5% NFDM in TBST	4ºC	Overnight
Secondary Antibody	HAF007 (R&D Systems)	1:10,000	5% NFDM in TBST	RT	1 hr

Supplementary Table 1.

Symbol	Name	Total GBM Scans	Total EL Scans	Norm Log2 Ratio	*p* value
NEST	Nestin	1651	5	7.95	1.33E-35
CD14	Monocyte differentiation antigen	191	2	6.16	6.68E-10
LAC7	Ig lambda-7 chain C region IGLC7	612	10	5.52	1.32E-09
LAC6	Ig lambda-6 chain C region IGLC6	598	10	5.49	1.01E-08
ALS	Insulin-like growth factor-binding protein complex acid labile subunit IGFALS	176	4	5.04	1.42E-41
ITAM	Integrin alpha-M ITGAM	352	9	4.87	1.85E-19
VAT1	Synaptic vesicle membrane protein VAT-1 homolog	113	3	4.82	5.02E-18
IQGA1	Ras GTPase-activating-like protein IQGAP1	1207	37	4.61	1.15E-06
NAMPT	Nicotinamide phosphoribosyltransferase	1008	33	4.52	1.15E-06
STT3A	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit	86	3	4.43	1.17E-11
SERPH	Serpin H1 SERPINH1	187	7	4.32	4.39E-11
TAGL2	Transgelin-2	317	12	4.31	4.42E-06
VTNC	Vitronectin VTN	468	19	4.21	9.28E-14
LAMA4	Laminin subunit alpha-4	338	14	4.18	1.7E-05
LAC1	Ig lambda-1 chain C regions IGLC1	186	8	4.12	6.51E-13
IGHG2	Ig gamma-2 chain C region	1779	80	4.06	6.47E-05
SAMH1	SAM domain and HD domain-containing protein 1 SAMHD1	133	6	4.05	7.84E-19
A2AP	Alpha-2-antiplasmin SERPINF2	688	34	3.92	0.000126
ANXA1	Annexin A1	1388	69	3.91	3.12E-11
F13A	Coagulation factor XIII A chain F13A1	637	33	3.85	3.12E-11
CO5	Complement C5	459	24	3.84	1.13E-07
IGLL5	Immunoglobulin lambda-like polypeptide 5	200	11	3.77	1.13E-07
PERI	Peripherin PRPH	140	8	3.71	0.000245
LAMB1	Laminin subunit beta-1	172	10	3.69	0.000245
IGHG4	Ig gamma-4 chain C region	546	32	3.68	7.64E-10
CO3A1	Collagen alpha-1(III) chain COL3A1	136	8	3.67	7.46E-32
FLNC	Filamin-C	2792	168	3.64	5.66E-15
IGHG3	Ig gamma-3 chain C region	632	39	3.60	1.48E-06
TENA	Tenascin TNC	1926	126	3.52	3.48E-11
LUM	Lumican	235	16	3.46	2.81E-06
CLIC4	Chloride intracellular channel protein 4	101	7	3.44	2.42E-13
LAC3	Ig lambda-3 chain C regions IGLC3	991	71	3.39	1.22E-10
LAC2	Ig lambda-2 chain C regions IGLC2	990	71	3.39	4.4E-57
LAMP1	Lysosome-associated membrane glycoprotein 1	152	11	3.37	4.23E-10
NP1L1	Nucleosome assembly protein 1-like 1	151	11	3.36	4.23E-10
APOE	Apolipoprotein E	662	51	3.28	6.35E-08

PSME2	Proteasome activator complex subunit 2	227	18	3.24	6.35E-08
CPNS1	Calpain small subunit 1 CAPNS1	63	5	3.24	1E-05
IGKC	Ig kappa chain C region	2278	182	3.23	0.001792
DPYD	Dihydropyrimidine dehydrogenase [NADP(+)]	62	5	3.22	3.84E-29
ANT3	Antithrombin-III SERPINC1	859	70	3.20	5.24E-27
LTBP1	Latent-transforming growth factor β-binding protein 1	85	7	3.19	5.37E-12
LEG1	Galectin-1 LGALS1	779	69	3.08	1.19E-07
FINC	Fibronectin FN1	4060	362	3.07	2.02E-25
ROA1	Heterogeneous nuclear ribonucleoprotein A1 HNRNPA1	163	15	3.03	2.02E-25
COIA1	Collagen alpha-1(XVIII) chain COL18A1	194	18	3.01	1.84E-11
ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1	1156	111	2.96	6.26E-11
CLUS	Clusterin CLU	983	95	2.96	5E-09
PROS	Vitamin K-dependent protein S PROS1	81	8	2.92	3.56E-05
HRG	Histidine-rich glycoprotein	706	74	2.84	3.56E-05
CATB	Cathepsin B CTSB	180	19	2.83	0.003461
ANXA2	Annexin A2	790	86	2.78	9.24E-09
AFAM	Afamin AFM	211	23	2.78	1.99E-17
FCGBP	IgGFc-binding protein	100	11	2.77	1.7E-08
CR2	Complement receptor type 2	63	7	2.75	6.67E-05
ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2	1694	189	2.75	6.67E-05
FETUA	Alpha-2-HS-glycoprotein AHSG	133	15	2.73	1.94E-27
FIBB	Fibrinogen beta chain FGB	4833	578	2.65	0.000125
THRB	Prothrombin F2	165	20	2.63	0.006664
ANGT	Angiotensinogen AGT	488	60	2.61	0.006664
AKP13	A-kinase anchor protein 13 AKAP13	250	31	2.60	0.006664
RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	298	38	2.56	1.05E-07
AMPL	Cytosol aminopeptidase LAP3	405	53	2.52	4.81E-06
AXA2L	Putative annexin A2-like protein ANXA2P2	508	67	2.51	4.34E-09
VIME	Vimentin VIM	9652	1300	2.48	8.83E-06
CO6A3	Collagen alpha-3(VI) chain COL6A3	3034	419	2.44	8.83E-06
PDIA1	Protein disulfide-isomerase P4HB	724	100	2.44	2.71E-20
IGHG1	Ig gamma-1 chain C region	2335	325	2.43	1.16E-31
RLA1	60S acidic ribosomal protein P1 RPLP1	100	14	2.42	4.05E-24
GPX1	Glutathione peroxidase 1	85	12	2.41	3.7E-54
TSNAX	Translin-associated protein X	63	9	2.39	6.39E-07
SHOT1	Shootin-1 KIAA1598	278	40	2.38	1.62E-05
IC1	Plasma protease C1 inhibitor SERPING1	582	84	2.38	0.00043
ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4	567	88	2.27	0.012792
IGHA2	Ig alpha-2 chain C region	219	34	2.27	0.012792
RL6	60S ribosomal protein L6 RPL6	154	24	2.27	4.69E-08

DYH5	Dynein heavy chain 5, axonemal DNAH5	526	82	2.27	6.13E-12
PGBM	Basement membrane-specific heparan sulfate proteoglycan core protein HSPG2	706	111	2.25	1.16E-06
PTN13	Tyrosine-protein phosphatase non-receptor type 13 PTPN13	76	12	2.25	2.95E-05
BAI2	Brain-specific angiogenesis inhibitor 2	1586	267	2.15	2.95E-05
TLR1	Toll-like receptor 1	59	10	2.14	2.73E-15
CERU	Ceruloplasmin CP	1458	249	2.13	6.35E-14
CLIP1	CAP-Gly domain-containing linker protein 1	138	24	2.11	1.96E-11
FLNB	Filamin-B	681	123	2.05	2.1E-06
SODM	Superoxide dismutase [Mn], mitochondrial SOD2	601	110	2.03	0.000795
COPB2	Coatomer subunit beta'	152	28	2.02	3.23E-45
AOFB	Amine oxidase [flavin-containing] B MAOB	1261	238	1.99	5.37E-05
1C18	HLA class I histocompatibility antigen, Cw-18 alpha chain HLA-C	90	17	1.99	2.73E-07
MAGI3	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3	116	22	1.98	2E-08
STOM	Erythrocyte band 7 integral membrane protein	427	81	1.98	2E-08
ZHX3	Zinc fingers and homeoboxes protein 3	219	42	1.97	6.8E-06
RBM27	RNA-binding protein 27	67	13	1.95	0.001464
AACT	Alpha-1-antichymotrypsin SERPINA3	1288	254	1.93	0.001464
FLNA	Filamin-A	5408	1096	1.89	0.024456
CFAH	Complement factor H CFH	330	67	1.88	0.024456
RAB5C	Ras-related protein Rab-5C	123	25	1.88	0.024456
APMAP	Adipocyte plasma membrane-associated protein	170	35	1.86	0.024456
IF5A1	Eukaryotic translation initiation factor 5A-1 EIF5A	165	34	1.86	2.08E-26
BIEA	Biliverdin reductase A BLVRA	82	17	1.85	8.16E-11
FKBP5	Peptidyl-prolyl cis-trans isomerase FKBP5	106	22	1.85	0.000176
FIBG	Fibrinogen gamma chain FGG	5122	1066	1.85	1.09E-09
PR14L	Protein PRR14L PRR14L	66	14	1.82	0.002679
MYH7	Myosin-7	146	31	1.82	0.002679
IGHA1	Ig alpha-1 chain C region	639	137	1.81	0.002679
PUR2	Trifunctional purine biosynthetic protein adenosine-3 GART	132	29	1.77	0.002679
SYWC	Tryptophan--tRNA ligase, cytoplasmic WARS	335	74	1.76	2.75E-06
TRFE	Serotransferrin TF	3428	759	1.76	8.31E-18
CO6A1	Collagen alpha-1(VI) chain COL6A1	1130	251	1.75	0.000316
SLIT3	Slit homolog 3 protein	252	56	1.75	4.23E-60
DAAM1	Disheveled-associated activator of morphogenesis 1	72	16	1.75	3.87E-05
NAGK	N-acetyl-D-glucosamine kinase	63	14	1.75	3.87E-05
ATAD2	ATPase family AAA domain-containing protein 2	54	12	1.75	3.87E-05
ECH1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	121	27	1.75	4.85E-06
APOA1	Apolipoprotein A-I	1425	319	1.74	4.85E-06

CPNE1	Copine-1	155	35	1.73	7.95E-08
A1AT	Alpha-1-antitrypsin SERPINA1	3461	793	1.71	7.95E-08
IGHM	Ig mu chain C region	1010	232	1.71	1.93E-21
ALBU	Serum albumin ALB	37159	8627	1.69	1.35E-09
APOB	Apolipoprotein B-100	2660	619	1.69	3.34E-21
DESM	Desmin DES	1194	278	1.69	4.11E-13
MVP	Major vault protein	334	78	1.68	3.02E-53
FIBA	Fibrinogen alpha chain FGA	7012	1646	1.68	1.03E-35
IF5A2	Eukaryotic translation initiation factor 5A-2 EIF5A2	97	23	1.66	8.54E-06
ITB1	Integrin beta-1 ITGB1	354	84	1.66	8.54E-06
DECR	2,4-dienoyl-CoA reductase, mitochondrial DECR1	188	45	1.65	0.000565
FEZF2	Fez family zinc finger protein 2	124	30	1.63	0.004876
PDIA6	Protein disulfide-isomerase A6	336	82	1.62	0.004876
MOGS	Mannosyl-oligosaccharide glucosidase	127	31	1.62	0.046526
GP179	Probable G-protein coupled receptor 179 GPR179	292	72	1.60	0.046526
ASAH1	Acid ceramidase	232	58	1.58	0.046526
H1T	Histone H1t HIST1H1T	104	26	1.58	2.92E-15
HSPB1	Heat shock protein beta-1	542	136	1.58	3.77E-14
HBE	Hemoglobin subunit epsilon HBE1	1418	357	1.57	8.72E-20
HBG1	Hemoglobin subunit gamma-1	1575	412	1.52	4.23E-60
HBG2	Hemoglobin subunit gamma-2	1550	406	1.52	5.43E-08
CO4A	Complement C4-A C4A	1508	404	1.48	0.000121
CO4B	Complement C4-B C4B	1480	397	1.48	2.56E-14
PRKDC	DNA-dependent protein kinase catalytic subunit	737	200	1.47	0.001005
DNMT1	DNA (cytosine-5)-methyltransferase 1	92	25	1.46	0.001005
PPIB	Peptidyl-prolyl cis-trans isomerase B	287	78	1.46	2.75E-09
RGS3	Regulator of G-protein signaling 3	91	25	1.45	0.000912
PIGS	GPI transamidase component PIG-S	79	22	1.43	5.72E-06
MCR	Mineralocorticoid receptor NR3C2	50	14	1.42	5.72E-06
G3P	Glyceraldehyde-3-phosphate dehydrogenase GAPDH	7935	2230	1.42	0.008818
ITPR2	Inositol 1,4,5-trisphosphate receptor type 2	64	18	1.41	0.008818
IF4A1	Eukaryotic initiation factor 4A-I EIF4A1	195	55	1.41	0.008818
GFAP	Glial fibrillary acidic protein	19103	5403	1.41	0.008818
ZA2G	Zinc-alpha-2-glycoprotein AZGP1	105	30	1.39	0.008818
FHR1	Complement factor H-related protein 1 CFHR1	80	23	1.38	1.86E-31
CO3	Complement C3 C3	5914	1704	1.38	9E-16
VINC	Vinculin VCL	1081	313	1.37	9.62E-13
H11	Histone H1.1 HIST1H1A	93	27	1.37	2.19E-13
DIAP2	Protein diaphanous homolog 2 DIAPH2	86	25	1.37	4.56E-05
ANXA5	Annexin A5	1754	517	1.35	4.56E-05
APC5	Anaphase-promoting complex subunit 5 ANAPC5	189	56	1.34	4.87E-35

GPTC8	G patch domain-containing protein 8 GPATCH8	87	26	1.33	2.49E-18
UGGG1	UDP-glucose:glycoprotein glucosyltransferase 1 UGGT1	218	66	1.31	4.09E-21
PZP	Pregnancy zone protein	579	176	1.30	4.11E-10
PROF1	Profilin-1 PFN1	455	139	1.29	4.11E-10
RLA0L	60S acidic ribosomal protein P0-like RPLP0P6	121	37	1.29	0.001778
SYCP1	Synaptonemal complex protein 1	85	26	1.29	0.001778
ARHGB	Rho guanine nucleotide exchange factor 11 ARHGEF11	127	39	1.29	0.001778
FBW10	F-box/WD repeat-containing protein 10 FBXW10	292	90	1.28	0.001778
GCN1L	Translational activator GCN1 GCN1L1	152	47	1.28	1.72E-30
NDRG1	Protein NDRG1	106	33	1.27	2.1E-11
TAF1	Transcription initiation factor TFIID subunit 1	99	31	1.26	0.000371
TPP1	Tripeptidyl-peptidase 1	185	58	1.26	0.000371
LAMC1	Laminin subunit gamma-1	604	190	1.25	1.58E-10
A2MG	Alpha-2-macroglobulin A2M	4032	1282	1.24	8.06E-12
H2B3B	Histone H2B type 3-B HIST3H2BB	1107	353	1.23	7.89E-05
DOCK4	Dedicator of cytokinesis protein 4	47	15	1.23	1.71E-05
MLL1	Histone-lysine N-methyltransferase MLL MLL	75	24	1.23	6.04E-11
MOES	Moesin MSN	2303	737	1.23	1.82E-32
MYO1E	Unconventional myosin-Ie	228	73	1.23	1.73E-10
TIGD1	Tigger transposable element-derived protein 1	618	198	1.23	7.67E-10
CO1A1	Collagen alpha-1(I) chain COL1A1	783	253	1.21	1.52E-08
VP33A	Vacuolar protein sorting-associated protein 33A VPS33A	83	27	1.20	6.36E-06
PRDX4	Peroxiredoxin-4	193	63	1.20	2.92E-05
CRYAB	Alpha-crystallin B chain	1150	377	1.19	0.000136
H2BFS	Histone H2B type F-S	1180	387	1.19	0.000644
H2B1K	Histone H2B type 1-K HIST1H2BK	1179	387	1.19	0.015826
H2B1L	Histone H2B type 1-L HIST1H2BL	1181	389	1.19	0.015826
ATR	Serine/threonine-protein kinase ATR	197	65	1.18	0.015826
KIF4A	Chromosome-associated kinesin KIF4A	178	59	1.18	0.015826
SETX	Probable helicase senataxin	235	78	1.18	0.015826
LAMP2	Lysosome-associated membrane glycoprotein 2	241	80	1.18	0.015826
VIGLN	Vigilin HDLBP	108	36	1.17	0.015826
KI16B	Kinesin-like protein KIF16B KIF16B	54	18	1.17	0.015826
FRIL	Ferritin light chain FTL	1425	477	1.16	0.015826
H2B1B	Histone H2B type 1-B HIST1H2BB	1150	387	1.16	0.015826
H2B1J	Histone H2B type 1-J HIST1H2BJ	1149	387	1.15	0.087976
DIC	Mitochondrial dicarboxylate carrier SLC25A10	86	29	1.15	0.087976
SND1	Staphylococcal nuclease domain-containing protein 1	184	63	1.13	0.087976
RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	294	101	1.13	0.087976

ROA2	Heterogeneous nuclear ribonucleoproteins A2/B1 HNRNPA2B1	293	101	1.12	0.087976
SPG17	Sperm-associated antigen 17 SPAG17	75	26	1.11	1.67E-34
RDH12	Retinol dehydrogenase 12	137	48	1.10	8.4E-63
MYH9	Myosin-9	5235	1838	1.09	2.17E-09
SSX2	Protein SSX2	981	348	1.08	2.14E-12
HBB	Hemoglobin subunit beta	10162	3616	1.07	4.99E-05
GOGA4	Golgin subfamily A member 4 GOLGA4	59	21	1.07	0.000233
MYH8	Myosin-8	140	50	1.07	0.000233
PYGL	Glycogen phosphorylase, liver form	355	127	1.07	8.2E-10
YES	Tyrosine-protein kinase Yes YES1	117	42	1.06	8.81E-07
PININ	Pinin PNN	242	87	1.06	0.000912
KDIS	Kinase D-interacting substrate of 220 kDa KIDINS220	69	25	1.05	2.91E-20
ENAM	Enamelin	66	24	1.04	4.01E-06
6PGL	6-phosphogluconolactonase PGLS	90	33	1.03	0.001112
PDIA3	Protein disulfide-isomerase A3	408	150	1.03	0.001112
C8AP2	CASP8-associated protein 2 CASP8AP2	151	56	1.02	1.36E-12
IRPL1	Interleukin-1 receptor accessory protein-like 1 IL1RAPL1	102	38	1.01	1.05E-17
GSTP1	Glutathione S-transferase P	539	202	1.00	0.000912
RADI	Radixin RDX	1745	655	1.00	1.01E-14
H13	Histone H1.3 HIST1H1D	239	91	0.98	8.49E-05
NIN	Ninein	42	16	0.98	0.005452
HBD	Hemoglobin subunit delta	3706	1423	0.97	8.54E-13
PLSL	Plastin-2 LCP1	304	117	0.96	6.36E-15
TLN1	Talin-1	2654	1024	0.96	6.75E-06
ASPD	Putative L-aspartate dehydrogenase ASPDH	399	154	0.96	4.56E-08
NB5R3	NADH-cytochrome b5 reductase 3 CYB5R3	229	89	0.95	3.1E-05
TM236	Transmembrane protein 236 TMEM236	72	28	0.95	1.43E-38
HEMO	Hemopexin HPX	303	119	0.93	1.13E-05
PYR1	CAD protein CAD	180	71	0.93	1.13E-05
CO1A2	Collagen alpha-2(I) chain COL1A2	685	273	0.91	0.001908
LMBL3	Lethal(3)malignant brain tumor-like protein 3 L3MBTL3	303	121	0.91	0.001908
PCBP1	Poly(rC)-binding protein 1	120	48	0.91	0.001908
MDN1	Midasin	120	48	0.91	0.001908
CO6A2	Collagen alpha-2(VI) chain COL6A2	585	236	0.89	0.028161
EIF3A	Eukaryotic translation initiation factor 3 subunit A	270	109	0.89	0.028161
6PGD	6-phosphogluconate dehydrogenase, decarboxylating PGD	435	177	0.88	0.028161
ARPC3	Actin-related protein 2/3 complex subunit 3	221	91	0.86	0.028161
H4	Histone H4 HIST1H4A	570	235	0.86	0.028161
TRIPB	Thyroid receptor-interacting protein 11 TRIP11	80	33	0.86	0.028161

HPT	Haptoglobin HP	379	157	0.86	0.028161
COPA	Coatomer subunit alpha	328	137	0.84	0.028161
MUCB	Ig mu heavy chain disease protein	215	90	0.84	0.028161
SF3B3	Splicing factor 3B subunit 3	143	60	0.84	0.028161
SVEP1	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1	40	17	0.82	0.028161
KI67	Antigen KI-67 MKI67	215	92	0.81	0.028161
PCX1	Pecanex-like protein 1 PCNX	259	111	0.81	1.91E-28
KAD7	Adenylate kinase 7 AK7	330	142	0.80	2.8E-25
PGM1	Phosphoglucomutase-1	545	235	0.80	8.16E-17
CANB2	Calcineurin subunit B type 2 PPP3R2	88	38	0.80	4.16E-06
CDC42	Cell division control protein 42 homolog	395	171	0.79	0.000676
CAP1	Adenylyl cyclase-associated protein 1	736	319	0.79	0.000676
TAF1L	Transcription initiation factor TFIID subunit 1-like	117	51	0.78	1.48E-68
H2AV	Histone H2A.V H2AFV	342	151	0.76	6.92E-06
GANAB	Neutral alpha-glucosidase AB	543	240	0.76	6.92E-06
ADHX	Alcohol dehydrogenase class-3 ADH5	95	42	0.76	0.000242
H2AZ	Histone H2A.Z H2AFZ	341	151	0.76	0.000242
FNTA	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	88	39	0.76	0.000242
H14	Histone H1.4 HIST1H1E	200	89	0.75	0.009437
RN213	E3 ubiquitin-protein ligase RNF213 RNF213	193	86	0.75	0.009437
XPO5	Exportin-5	105	47	0.74	0.009437
MINT	Msx2-interacting protein SPEN	58	26	0.74	7.62E-11
RLA0	60S acidic ribosomal protein P0 RPLP0	185	84	0.72	8.7E-05
GELS	Gelsolin GSN	2736	1244	0.72	5.63E-13
AOFA	Amine oxidase [flavin-containing] A MAOA	268	122	0.72	3.15E-05
ASML	N-acetylserotonin O-methyltransferase-like protein ASMTL	449	205	0.72	3.15E-05
HBA	Hemoglobin subunit alpha HBA1	10762	4920	0.71	0.003249
AL4A1	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial ALDH4A1	480	220	0.71	2.75E-46
HNRDL	Heterogeneous nuclear ribonucleoprotein D-like HNRPDL	133	61	0.71	1.27E-07
CO4A2	Collagen alpha-2(IV) chain COL4A2	218	100	0.71	1.15E-05
UB2L3	Ubiquitin-conjugating enzyme E2 L3 UBE2L3	137	63	0.70	0.000912
R3HD2	R3H domain-containing protein 2 R3HDM2	374	172	0.70	2.41E-09
PLXB1	Plexin-B1 PLXNB1	50	23	0.70	3.8E-39
FYN	Tyrosine-protein kinase Fyn	89	41	0.70	5.66E-07
DJC13	DnaJ homolog subfamily C member 13 DNAJC13	78	36	0.70	0.000145
GBRL3	Gamma-aminobutyric acid receptor-associated protein-like 3 GABARAPL3	171	79	0.70	2.85E-08
EZRI	Ezrin EZR	1725	797	0.70	1E-22
MYL6	Myosin light polypeptide 6	380	177	0.69	1.06E-08

SAHH	Adenosylhomocysteinase AHCY	241	113	0.68	5.22E-05
GLU2B	Glucosidase 2 subunit beta PRKCSH	260	122	0.68	1.19E-17
CP135	Centrosomal protein of 135 kDa CEP135	104	49	0.67	3.41E-07
ZN638	Zinc finger protein 638 ZNF638	61	29	0.66	1.26E-07
DMD	Dystrophin	84	40	0.65	2.08E-20
AHNK	Neuroblast differentiation-associated protein AHNAK	1516	727	0.64	2.24E-27
POTEE	POTE ankyrin domain family member E	2073	1002	0.63	4.13E-15
POTEF	POTE ankyrin domain family member F	2071	1002	0.63	1.91E-32
MYH13	Myosin-13	93	45	0.63	2.77E-11
YJ005	Uncharacterized protein FLJ45252	156	76	0.62	3.86E-09
RS16	40S ribosomal protein S16 RPS16	152	75	0.60	3.11E-05
SRC	Proto-oncogene tyrosine-protein kinase Src	85	42	0.60	8.61E-05
HNRPD	Heterogeneous nuclear ribonucleoprotein D0 HNRNPD	220	109	0.60	0.000672
HCK	Tyrosine-protein kinase HCK	111	55	0.60	0.001907
PSA2	Proteasome subunit alpha type-2 PSMA2	115	57	0.60	0.005492
KPYM	Pyruvate kinase isozymes M1/M2 PKM	5573	2764	0.60	0.005492
AGRIN	Agrin AGRN	195	97	0.59	0.005492
ACTB	Actin, cytoplasmic 1	8991	4489	0.59	0.016188
ACTG	Actin, cytoplasmic 2 ACTG1	8991	4489	0.59	0.016188
DYH11	Dynein heavy chain 11, axonemal DNAH11	378	190	0.58	0.016188
S100B	Protein S100-B	584	294	0.57	0.049601
HNRPK	Heterogeneous nuclear ribonucleoprotein K	403	204	0.57	0.049601
H2A1C	Histone H2A type 1-C HIST1H2AC	612	312	0.56	0.049601
H2A3	Histone H2A type 3 HIST3H2A	612	312	0.56	0.049601
POTEI	POTE ankyrin domain family member I	1315	672	0.55	0.049601
H2A1H	Histone H2A type 1-H HIST1H2AH	609	312	0.55	0.049601
CBR3	Carbonyl reductase [NADPH] 3	231	119	0.54	0.049601
B3AT	Band 3 anion transport protein SLC4A1	922	475	0.54	0.049601
CALX	Calnexin CANX	874	451	0.54	3.87E-26
CAH2	Carbonic anhydrase 2 CA2	495	256	0.54	8.76E-13
TANC1	Protein TANC1	109	57	0.52	3.95E-41
TCPE	T-complex protein 1 subunit epsilon CCT5	258	135	0.52	3.26E-27
XRCC5	X-ray repair cross-complementing protein 5	378	198	0.52	4.53E-32
H2AJ	Histone H2A.J H2AFJ	616	323	0.52	1.01E-08
UBB	Polyubiquitin-B	4899	2584	0.51	4.6E-17
KC1E	Casein kinase I isoform epsilon CSNK1E	618	327	0.50	5.41E-30
RL40	Ubiquitin-60S ribosomal protein L40 UBA52	1652	885	0.48	0.000394
ARP3	Actin-related protein 3 ACTR3	202	109	0.47	1.54E-32
CATD	Cathepsin D CTSD	519	281	0.47	0.001111
ASXL3	Putative Polycomb group protein ASXL3	120	65	0.47	2.18E-12
SYNE2	Nesprin-2	549	299	0.46	2.89E-81

ZC3HD	Zinc finger CCCH domain-containing protein 13 ZC3H13	402	219	0.46	1.09E-05
RS27A	Ubiquitin-40S ribosomal protein S27a RPS27A	1658	905	0.46	1.18E-07
TALDO	Transaldolase TALDO1	152	83	0.46	1.34E-09
DYH8	Dynein heavy chain 8, axonemal DNAH8	119	65	0.46	3E-05
KC1D	Casein kinase I isoform delta CSNK1D	617	338	0.45	0.003169
UBC	Polyubiquitin-C	11628	6379	0.45	0.003169
K1614	Uncharacterized protein KIAA1614 KIAA1614	134	74	0.44	0.003169
FERM2	Fermitin family homolog 2 FERMT2	278	154	0.44	3.81E-43
H2A2C	Histone H2A type 2-C HIST2H2AC	652	362	0.43	1.87E-16
H2A2A	Histone H2A type 2-A HIST2H2AA3	652	362	0.43	5.17E-63
POTEJ	POTE ankyrin domain family member J	1069	599	0.42	8.29E-05
H2A2B	Histone H2A type 2-B HIST2H2AB	326	183	0.42	2.98E-16
LMNA	Prelamin-A/C	518	291	0.42	0.009204
PLCE1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1	245	138	0.41	5.15E-07
ESYT1	Extended synaptotagmin-1	314	177	0.41	0.000645
H2AX	Histone H2A.x H2AFX	408	230	0.41	2.83E-10
SEPTIN2	Septin-2 SEPT2	434	245	0.41	1.1E-61
H2A1A	Histone H2A type 1-A HIST1H2AA	364	206	0.41	4.86E-05
DYH10	Dynein heavy chain 10, axonemal DNAH10	189	107	0.40	4.86E-05
H31	Histone H3.1 HIST1H3A	263	150	0.39	2.51E-23
PRS6B	26S protease regulatory subunit 6B PSMC4	176	101	0.39	2.48E-68
EF1A1	Elongation factor 1-alpha 1 EEF1A1	1568	901	0.38	6.67E-08
EF1A3	Putative elongation factor 1-alpha-like 3 EEF1A1P5	1560	902	0.37	0.001823
H3C	Histone H3.3C H3F3C	247	143	0.37	0.027488
KTN1	Kinectin	302	175	0.37	0.027488
ATPK	ATP synthase subunit f, mitochondrial ATP5J2	391	227	0.37	0.027488
H2B1A	Histone H2B type 1-A HIST1H2BA	268	156	0.36	0.027488
CENPF	Centromere protein F	211	123	0.36	0.027488
H32	Histone H3.2 HIST2H3A	250	146	0.36	0.027488
H33	Histone H3.3 H3F3A	249	146	0.35	0.027488
H31T	Histone H3.1t HIST3H3	252	148	0.35	0.027488
RAB7A	Ras-related protein Rab-7a	278	164	0.35	0.027488
CPNE7	Copine-7	242	143	0.34	2.68E-10
ENPL	Endoplasmin HSP90B1	1538	909	0.34	3.23E-09
TCPG	T-complex protein 1 subunit gamma CCT3	244	145	0.33	2.84E-05
ACTBM	Putative beta-actin-like protein 3 POTEKP	384	231	0.32	3.94E-08
CPNE2	Copine-2	236	142	0.32	0.000374
CAH1	Carbonic anhydrase 1 CA1	593	358	0.31	0.000374
LRP1	Prolow-density lipoprotein receptor-related protein 1	512	310	0.31	6.09E-06
PRDX1	Peroxiredoxin-1	598	363	0.30	7.83E-05

LDHA	L-lactate dehydrogenase A chain	1010	617	0.30	0.005225
CPNE9	Copine-9	338	207	0.29	0.005225
ACTS	Actin, alpha skeletal muscle ACTA1	4538	2804	0.28	5.13E-09
ACTH	Actin, gamma-enteric smooth muscle ACTG2	4397	2718	0.28	2.86E-07
ACTC	Actin, alpha cardiac muscle 1 ACTC1	4549	2819	0.27	1.38E-22
ACTN4	Alpha-actinin-4	1544	971	0.25	0.001048
HCDH	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial HADH	329	207	0.25	0.001048
TCPZ	T-complex protein 1 subunit zeta CCT6A	405	255	0.25	2.09E-06
PRDX6	Peroxiredoxin-6	571	363	0.24	2.17E-08
PRDX2	Peroxiredoxin-2	942	606	0.22	1.63E-20
GRP78	78 kDa glucose-regulated protein HSPA5	1915	1287	0.16	6.85E-12
TITIN	Titin TTN	1002	676	0.15	5.68E-06
ENOA	Alpha-enolase ENO1	1940	1326	0.13	0.000603
ACTN1	Alpha-actinin-1	2670	1833	0.13	0.000603
CH60	60 kDa heat shock protein, mitochondrial HSPD1	2628	1809	0.12	0.01528
PLEC	Plectin	8441	5914	0.10	0.01528
ANXA6	Annexin A6	1891	1518	-0.10	0.086307
HS71L	Heat shock 70 kDa protein 1-like HSPA1L	1530	1252	-0.13	0.086307
TBB8	Tubulin beta-8 chain TUBB8	2596	2152	-0.15	0.086307
TBB3	Tubulin beta-3 chain TUBB3	5613	4738	-0.17	0.086307
TBB5	Tubulin beta chain TUBB	6498	5491	-0.17	0.086307
TBB4A	Tubulin beta-4A chain TUBB4A	6762	5715	-0.17	0.086307
ENOG	Gamma-enolase ENO2	1479	1268	-0.19	0.086307
TBB1	Tubulin beta-1 chain TUBB1	981	842	-0.20	0.086307
TBB4B	Tubulin beta-4B chain TUBB4B	6970	5999	-0.20	0.086307
TBB2B	Tubulin beta-2B chain TUBB2B	6997	6038	-0.20	0.086307
1433G	14-3-3 protein gamma YWHAG	1456	1260	-0.21	0.086307
TBB2A	Tubulin beta-2A chain TUBB2A	7091	6160	-0.21	0.086307
MYPR	Myelin proteolipid protein PLP1	5459	4752	-0.22	0.086307
CBR1	Carbonyl reductase [NADPH] 1	398	348	-0.22	0.086307
FSCN1	Fascin	466	408	-0.22	0.086307
UBA1	Ubiquitin-like modifier-activating enzyme 1	1734	1520	-0.23	0.086307
H90B2	Putative heat shock protein HSP 90-beta 2 HSP90AB2P	571	503	-0.23	0.086307
VDAC1	Voltage-dependent anion-selective channel protein 1	387	342	-0.24	0.086307
YI016	Putative tubulin beta chain-like protein ENSP00000290377	2759	2446	-0.24	2.65E-05
HS90A	Heat shock protein HSP 90-alpha HSP90AA1	2885	2570	-0.25	0.00297
ADT4	ADP/ATP translocase 4 SLC25A31	708	633	-0.25	1.15E-82
1433E	14-3-3 protein epsilon YWHAE	1408	1270	-0.27	4.82E-11
SEPTIN7	Septin-7 SEPT7	522	471	-0.27	1.16E-79

1433T	14-3-3 protein theta YWHAQ	1014	915	-0.27	6.14E-25
KINH	Kinesin-1 heavy chain KIF5B	309	280	-0.27	1.94E-06
NFH	Neurofilament heavy polypeptide NEFH	874	793	-0.28	0.001692
HSP7C	Heat shock cognate 71 kDa protein HSPA8	3732	3391	-0.28	2.46E-07
CALM1	Calmodulin	632	575	-0.28	2.46E-07
HACD3	Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 PTPLAD1	296	272	-0.29	6.96E-09
IMB1	Importin subunit beta-1 KPNB1	596	548	-0.29	4.21E-05
HSP71	Heat shock 70 kDa protein 1A/1B HSPA1A	1565	1461	-0.32	2E-10
MAP1B	Microtubule-associated protein 1B	3165	2964	-0.32	2.7E-59
HSP72	Heat shock-related 70 kDa protein 2 HSPA2	1828	1712	-0.32	0.0002
PEBP1	Phosphatidylethanolamine-binding protein 1	487	458	-0.33	9.12E-12
1433B	14-3-3 protein beta/alpha YWHAB	1293	1219	-0.33	0.000966
DYHC1	Cytoplasmic dynein 1 heavy chain 1 DYNC1H1	6203	5867	-0.34	0.000115
LDHB	L-lactate dehydrogenase B chain	1034	982	-0.34	0.000115
TCPD	T-complex protein 1 subunit delta CCT4	272	263	-0.37	1.04E-06
CAZA1	F-actin-capping protein subunit alpha-1 CAPZA1	123	120	-0.38	6.66E-05
DPYL3	Dihydropyrimidinase-related protein 3 DPYSL3	1837	1795	-0.38	0.004801
PRC2C	Protein PRRC2C PRRC2C	136	133	-0.38	0.004801
2AAA	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform PPP2R1A	624	611	-0.39	0.004801
KCRB	Creatine kinase B-type CKB	2183	2138	-0.39	0.046139
PCNT	Pericentrin	111	109	-0.39	0.046139
AP3D1	AP-3 complex subunit delta-1	382	377	-0.40	0.046139
GNAO	Guanine nucleotide-binding protein G(o) subunit alpha GNAO1	935	923	-0.40	0.046139
G6PI	Glucose-6-phosphate isomerase GPI	1137	1127	-0.40	0.046139
MATR3	Matrin-3	469	467	-0.41	0.046139
G3PT	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific GAPDHS	237	236	-0.41	0.046139
IDHP	Isocitrate dehydrogenase [NADP], mitochondrial IDH2	633	631	-0.41	0.046139
NEBU	Nebulin NEB	208	211	-0.44	0.046139
1433Z	14-3-3 protein zeta/delta YWHAZ	1663	1688	-0.44	0.046139
GRP75	Stress-70 protein, mitochondrial HSPA9	1207	1235	-0.45	0.046139
1433F	14-3-3 protein eta YWHAH	855	875	-0.45	0.046139
CLH1	Clathrin heavy chain 1 CLTC	6849	7061	-0.46	0.046139
CDKL5	Cyclin-dependent kinase-like 5	145	150	-0.46	0.046139
GNA12	Guanine nucleotide-binding protein subunit alpha-12	113	117	-0.47	3.85E-05
TLL1	Tolloid-like protein 1	141	146	-0.47	8.11E-16
PP1R7	Protein phosphatase 1 regulatory subunit 7 PPP1R7	135	140	-0.47	2.64E-08
DPYL2	Dihydropyrimidinase-related protein 2 DPYSL2	4651	4826	-0.47	0.002711
WDR1	WD repeat-containing protein 1	381	396	-0.47	0.002711
NDKB	Nucleoside diphosphate kinase B NME2	249	259	-0.47	1.18E-09

SFPQ	Splicing factor, proline- and glutamine-rich	377	393	-0.48	6.7E-16
PYGB	Glycogen phosphorylase, brain form	1242	1301	-0.48	5.49E-07
BPIB3	BPI fold-containing family B member 3 BPIFB3	177	186	-0.49	7.48E-06
THIL	Acetyl-CoA acetyltransferase, mitochondrial ACAT1	235	247	-0.49	0.001537
TBA3C	Tubulin alpha-3C/D chain TUBA3C	5953	6264	-0.49	0.000105
ALDOC	Fructose-bisphosphate aldolase C	659	698	-0.50	6.46E-14
AINX	Alpha-internexin INA	1693	1797	-0.50	5.66E-88
SCRN1	Secernin-1	353	375	-0.50	0.013832
CISY	Citrate synthase, mitochondrial CS	320	340	-0.50	0.013832
SEPTIN8	Septin-8 SEPT8	326	348	-0.51	0.013832
ARP2	Actin-related protein 2 ACTR2	102	109	-0.51	1.16E-05
H90B3	Putative heat shock protein HSP 90-beta-3 HSP90AB3P	638	682	-0.51	0.000286
EAA1	Excitatory amino acid transporter 1 SLC1A3	895	961	-0.52	6.74E-06
TBA3E	Tubulin alpha-3E chain TUBA3E	5537	5946	-0.52	6.74E-06
CAND1	Cullin-associated NEDD8-dissociated protein 1	1160	1246	-0.52	0.000164
MAP4	Microtubule-associated protein 4	493	531	-0.52	0.007694
IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	466	502	-0.52	0.007694
TERA	Transitional endoplasmic reticulum ATPase VCP	1151	1245	-0.53	3.59E-47
NFM	Neurofilament medium polypeptide NEFM	2883	3135	-0.54	5.42E-05
MDHM	Malate dehydrogenase, mitochondrial MDH2	867	943	-0.54	0.004311
ZN195	Zinc finger protein 195 ZNF195	79	86	-0.54	0.004311
PHB	Prohibitin	214	234	-0.54	3.12E-05
BRWD1	Bromodomain and WD repeat-containing protein 1	156	171	-0.55	0.002429
GSTM2	Glutathione S-transferase Mu 2	112	123	-0.55	0.001375
TBA1A	Tubulin alpha-1A chain TUBA1A	7208	7925	-0.55	0.001375
PGK2	Phosphoglycerate kinase 2	100	110	-0.55	5.97E-21
GMFB	Glia maturation factor beta	53	59	-0.57	0.000446
NFL	Neurofilament light polypeptide NEFL	2550	2847	-0.57	3.12E-69
ARF1	ADP-ribosylation factor 1	382	429	-0.58	0.000255
ARF3	ADP-ribosylation factor 3	382	429	-0.58	0.000255
ALDOA	Fructose-bisphosphate aldolase A	1059	1195	-0.59	8.94E-35
MRCKB	Serine/threonine-protein kinase MRCK beta CDC42BPB	68	77	-0.60	9.99E-17
NUCL	Nucleolin NCL	352	399	-0.60	3.46E-17
HSP76	Heat shock 70 kDa protein 6 HSPA6	703	797	-0.60	4.78E-11
41528	Septin-11 SEPT11	328	373	-0.60	8.39E-05
COR1A	Coronin-1A CORO1A	381	439	-0.62	6.2E-10
COX2	Cytochrome c oxidase subunit 2 MT-CO2	147	170	-0.63	5.38E-06
EIF3B	Eukaryotic translation initiation factor 3 subunit B	57	66	-0.63	1.38E-08
H90B4	Putative heat shock protein HSP 90-beta 4 HSP90AB4P	169	196	-0.63	9.48E-54

XRCC6	X-ray repair cross-complementing protein 6	309	359	-0.63	1.62E-51
ATPA	ATP synthase subunit alpha, mitochondrial ATP5A1	1425	1657	-0.63	6.19E-08
GNA11	Guanine nucleotide-binding protein subunit alpha-11	141	165	-0.64	9.29E-07
ACON	Aconitate hydratase, mitochondrial ACO2	1756	2060	-0.65	0.000692
EFTU	Elongation factor Tu, mitochondrial TUFM	255	300	-0.65	0.006798
SLN14	Schlafen family member 14 SLFN14	56	66	-0.65	0.006798
SPTB2	Spectrin beta chain, non-erythrocytic 1 SPTBN1	6403	7559	-0.66	0.022169
SEPTIN6	Septin-6 SEPT6	327	387	-0.66	0.022169
GSTM5	Glutathione S-transferase Mu 5	103	123	-0.67	0.022169
ATPB	ATP synthase subunit beta, mitochondrial ATP5B	2446	2923	-0.67	1.07E-36
SPTN1	Spectrin alpha chain, non-erythrocytic 1 SPTAN1	9273	11153	-0.68	4.28E-05
ACTN2	Alpha-actinin-2	817	983	-0.68	0.003811
MTCH2	Mitochondrial carrier homolog 2	113	137	-0.69	0.012218
GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	141	171	-0.69	0.04076
UN13A	Protein unc-13 homolog A UNC13A	79	96	-0.70	0.04076
MARCS	Myristoylated alanine-rich C-kinase substrate MARCKS	999	1214	-0.70	0.04076
HS904	Putative heat shock protein HSP 90-alpha A4 HSP90AA4P	255	314	-0.72	0.04076
MPCP	Phosphate carrier protein, mitochondrial SLC25A3	643	803	-0.74	0.04076
MDHC	Malate dehydrogenase, cytoplasmic MDH1	359	449	-0.74	0.04076
PGAM2	Phosphoglycerate mutase 2	98	123	-0.74	0.076418
VATH	V-type proton ATPase subunit H ATP6V1H	278	349	-0.74	0.076418
GSTO1	Glutathione S-transferase omega-1	131	165	-0.75	0.076418
ANO2	Anoctamin-2	65	82	-0.75	0.076418
RAB6B	Ras-related protein Rab-6B	57	72	-0.75	0.076418
RAB35	Ras-related protein Rab-35	110	139	-0.75	0.076418
ANK1	Ankyrin-1	415	526	-0.76	0.076418
MYH10	Myosin-10	1534	1949	-0.76	0.076418
GTR3	Solute carrier family 2, facilitated glucose transporter member 3 SLC2A3	228	292	-0.77	0.076418
ARF5	ADP-ribosylation factor 5	192	248	-0.79	0.076418
TBA1B	Tubulin alpha-1B chain TUBA1B	6994	9067	-0.79	0.076418
IF4G3	Eukaryotic translation initiation factor 4 gamma 3 EIF4G3	97	126	-0.79	0.076418
TBA1C	Tubulin alpha-1C chain TUBA1C	6996	9092	-0.79	0.076418
CYFP1	Cytoplasmic FMR1-interacting protein 1 CYFIP1	513	669	-0.80	2.52E-26
COX41	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial COX4I1	150	196	-0.80	1.86E-08
GTR14	Solute carrier family 2, facilitated glucose transporter member 14 SLC2A14	224	293	-0.80	8.12E-21
ACTZ	Alpha-centractin ACTR1A	116	153	-0.82	1.15E-32
PGAM4	Probable phosphoglycerate mutase 4	112	148	-0.82	1.41E-06
GNAT3	Guanine nucleotide-binding protein G(t) subunit alpha-3	79	105	-0.83	1.12E-16

ODO1	2-oxoglutarate dehydrogenase, mitochondrial OGDH	541	720	-0.83	4.2E-06
KIF5A	Kinesin heavy chain isoform 5A	213	286	-0.84	1.07E-48
HNRPR	Heterogeneous nuclear ribonucleoprotein R HNRNPR	140	188	-0.84	9.61E-30
GNAL	Guanine nucleotide-binding protein G(olf) subunit alpha	72	97	-0.85	6.54E-05
NDKA	Nucleoside diphosphate kinase A NME1	255	344	-0.85	2.82E-08
UNC80	Protein unc-80 homolog	80	108	-0.85	4.65E-20
AT5F1	ATP synthase subunit b, mitochondrial ATP5F1	388	526	-0.85	1.81E-81
STIP1	Stress-induced-phosphoprotein 1	408	554	-0.86	2.44E-07
AP1B1	AP-1 complex subunit beta-1	726	986	-0.86	4.13E-12
HS902	Putative heat shock protein HSP 90-alpha A2 HSP90AA2	511	695	-0.86	2.88E-09
ADT3	ADP/ATP translocase 3 SLC25A6	640	872	-0.86	0.000607
ADT2	ADP/ATP translocase 2 SLC25A5	563	777	-0.88	0.000607
GNAT1	Guanine nucleotide-binding protein G(t) subunit alpha-1	78	108	-0.89	6.38E-06
MRCKA	Serine/threonine-protein kinase MRCK alpha CDC42BPA	306	427	-0.90	6.38E-06
AKA12	A-kinase anchor protein 12 AKAP12	570	801	-0.91	2.13E-12
RHOB	Rho-related GTP-binding protein RhoB	83	117	-0.91	1.48E-09
HSP77	Putative heat shock 70 kDa protein 7 HSPA7	354	504	-0.93	4.33E-09
MK01	Mitogen-activated protein kinase 1 MAPK1	276	394	-0.93	7.42E-09
ANR12	Ankyrin repeat domain-containing protein 12 ANKRD12	112	160	-0.93	3.58E-63
HXK3	Hexokinase-3 HK3	262	375	-0.93	5.73E-05
KNTC1	Kinetochore-associated protein 1	96	138	-0.94	0.005929
PGAM1	Phosphoglycerate mutase 1	347	503	-0.95	0.005929
PDC6I	Programmed cell death 6-interacting protein PDCD6IP	269	390	-0.95	0.000173
TBA4A	Tubulin alpha-4A chain TUBA4A	4960	7223	-0.96	0.000173
VDAC2	Voltage-dependent anion-selective channel protein 2	259	378	-0.96	2.44E-36
VPS35	Vacuolar protein sorting-associated protein 35	505	750	-0.99	0.010626
GNAT2	Guanine nucleotide-binding protein G(t) subunit alpha-2	70	104	-0.99	0.010626
KIF5C	Kinesin heavy chain isoform 5C	219	327	-0.99	6.67E-10
LPPRC	Leucine-rich PPR motif-containing protein, mitochondrial LRPPRC	602	899	-0.99	5.55E-07
SPTB1	Spectrin beta chain, erythrocytic SPTB	620	933	-1.01	3.26E-08
AP2A1	AP-2 complex subunit alpha-1	1049	1581	-1.01	1.77E-62
DPYL1	Dihydropyrimidinase-related protein 1 CRMP1	1151	1735	-1.01	2.89E-05
PI4KA	Phosphatidylinositol 4-kinase alpha	189	285	-1.01	5E-05
AP2A2	AP-2 complex subunit alpha-2	824	1251	-1.02	5E-05
DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	201	306	-1.02	0.000929
GNAI1	Guanine nucleotide-binding protein G(i) subunit alpha-1	168	256	-1.02	0.019209
PDXK	Pyridoxal kinase	325	496	-1.03	0.019209

PSA	Puromycin-sensitive aminopeptidase NPEPPS	828	1277	-1.04	0.019209
AT1A1	Sodium/potassium-transporting ATPase subunit alpha-1 ATP1A1	3343	5167	-1.04	2.44E-22
AT1A3	Sodium/potassium-transporting ATPase subunit alpha-3 ATP1A3	3354	5193	-1.05	1.7E-09
NCAM1	Neural cell adhesion molecule 1	906	1424	-1.07	0.001634
PRDX5	Peroxiredoxin-5, mitochondrial	167	263	-1.07	0.001634
MAP1A	Microtubule-associated protein 1A	1569	2506	-1.09	4.88E-08
AP2B1	AP-2 complex subunit beta	1317	2106	-1.09	4.04E-45
RTN4	Reticulon-4	701	1133	-1.11	2.4E-32
KPCA	Protein kinase C alpha type PRKCA	270	440	-1.12	0.002887
ARI4B	AT-rich interactive domain-containing protein 4B ARID4B	64	105	-1.13	0.035129
PYGM	Glycogen phosphorylase, muscle form	339	560	-1.14	0.035129
ENPLL	Putative endoplasmin-like protein HSP90B2P	118	196	-1.15	0.035129
NSF	Vesicle-fusing ATPase	1431	2402	-1.16	0.035129
ATP4A	Potassium-transporting ATPase alpha chain 1	564	954	-1.17	0.000263
ADT1	ADP/ATP translocase 1 SLC25A4	518	877	-1.18	8.1E-84
HSP74	Heat shock 70 kDa protein 4 HSPA4	421	716	-1.18	1.15E-27
C170B	Centrosomal protein of 170 kDa protein B CEP170B	55	94	-1.19	7.58E-10
KCC2D	Calcium/calmodulin-dependent protein kinase type II subunit delta CAMK2D	324	554	-1.19	4.35E-05
GBB3	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 GNB3	222	382	-1.20	0.000459
AT1A2	Sodium/potassium-transporting ATPase subunit alpha-2 ATP1A2	2855	4961	-1.21	0.000459
HXK1	Hexokinase-1 HK1	1543	2687	-1.22	0.005124
GBB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 GNB2	425	743	-1.22	0.005124
GBB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 GNB1	423	742	-1.23	0.000804
TBA8	Tubulin alpha-8 chain TUBA8	3377	5926	-1.23	1.91E-29
UBE3B	Ubiquitin-protein ligase E3B	192	338	-1.23	1.2E-36
AATC	Aspartate aminotransferase, cytoplasmic GOT1	379	673	-1.24	5.6E-09
FRM4B	FERM domain-containing protein 4B FRMD4B	73	130	-1.25	3.22E-08
GBB4	Guanine nucleotide-binding protein subunit beta-4 GNB4	380	681	-1.26	0.000228
CD47	Leukocyte surface antigen CD47	139	250	-1.26	0.009147
KPCB	Protein kinase C beta type PRKCB	266	482	-1.27	0.009147
SYG	Glycine--tRNA ligase GARS	193	350	-1.27	0.065317
QCR2	Cytochrome b-c1 complex subunit 2, mitochondrial UQCRC2	314	570	-1.28	0.065317
SYAC	Alanine--tRNA ligase, cytoplasmic AARS	368	671	-1.28	0.065317
AN30A	Ankyrin repeat domain-containing protein 30A ANKRD30A	284	520	-1.29	0.065317
TRAP1	Heat shock protein 75 kDa, mitochondrial	217	405	-1.32	0.065317
HXK2	Hexokinase-2 HK2	326	624	-1.35	0.065317

SPTN4	Spectrin beta chain, non-erythrocytic 4 SPTBN4	91	175	-1.36	0.065317
CAC1E	Voltage-dependent R-type calcium channel subunit alpha-1E CACNA1E	54	104	-1.36	0.065317
ALDOB	Fructose-bisphosphate aldolase B	59	114	-1.37	0.065317
FAS	Fatty acid synthase FASN	656	1278	-1.38	0.065317
TLN2	Talin-2	705	1421	-1.43	0.065317
AT1A4	Sodium/potassium-transporting ATPase subunit alpha-4 ATP1A4	1097	2258	-1.46	1.67E-09
AT12A	Potassium-transporting ATPase alpha chain 2 ATP12A	375	794	-1.50	0.002486
4F2	4F2 cell-surface antigen heavy chain SLC3A2	346	737	-1.51	0.002486
NNTM	NAD(P) transhydrogenase, mitochondrial NNT	535	1155	-1.53	2.79E-55
CALL3	Calmodulin-like protein 3 CALML3	67	146	-1.54	0.000693
CSPG2	Versican core protein VCAN	221	506	-1.61	0.000693
IMMT	Mitochondrial inner membrane protein	394	921	-1.64	0.016451
K6PF	6-phosphofructokinase, muscle type PFKM	338	803	-1.66	0.016451
TBA4B	Putative tubulin-like protein alpha-4B TUBA4B	1771	4284	-1.69	0.016451
MD1L1	Mitotic spindle assembly checkpoint protein MAD1 MAD1L1	94	232	-1.72	0.016451
AP2M1	AP-2 complex subunit mu	245	629	-1.78	0.004398
CSKI1	Caskin-1 CASKIN1	134	375	-1.90	3.95E-30
RTN3	Reticulon-3	214	631	-1.98	1.3E-27
LETM1	LETM1 and EF-hand domain-containing protein 1, mitochondrial	176	557	-2.08	0.001213
SPTN2	Spectrin beta chain, non-erythrocytic 2 SPTBN2	408	1606	-2.39	0.000341
ANK3	Ankyrin-3	133	584	-2.55	9.74E-05

Supplemental Table 2

A. Top Diseases and Bio Functions of Up-regulated Proteins

Diseases and Disorders

Name	p-value	# Molecules
Cancer	1.72E-12 - 2.56E-04	160
Neurological Disease	1.81E-13 - 2.95E-04	74
Psychological Disorders	1.81E-13 - 1.65E-04	58
Metabolic Disease	1.61E-12 - 2.12E-04	59
Cardiovascular Disease	5.88E-14 - 2.12E-04	64

Molecular and Cellular Functions

Name	p-value	# Molecules
Cellular Movement	5.94E-15 - 3.16E-04	78
Cell Death and Survival	6.91E-15 - 2.71E-04	106
Cell-To-Cell Signaling and Interaction	2.32E-12 - 2.95E-04	77
Free Radical Scavenging	1.03E-11 - 1.04E-04	30
Cell Morphology	8.85E-11 - 3.12E-04	82

Physiological System Development and Function

Name	p-value	# Molecules
Immune Cell Trafficking	6.98E-13 - 2.78E-04	56
Nervous System Development and Function	1.26E-10 - 2.84E-04	46
Tissue Development	1.62E-10 - 2.95E-04	76
Hematological System Development and Function	1.77E-10 - 2.95E-04	71
Organismal Survival	4.59E-10 - 1.08E-06	77

Top Canonical Pathways

Name	p-value	Ratio .
Acute Phase Response Signaling	2.1E-19	24/181(0.133)
LXR/RXR Activation	5.44E-14	17/139(0.122)
Intrinsic Prothrombin Activation Pathway	4.11E-13	10/37(0.27)
Coagulation System	5.35E-12	10/38(0.263)
Extrinsic Prothrombin Activation Pathway	2.78E-10	7/22(0.318)

Top Upstream Regulators

Upstream Regulator	p-value of overlap	Predicted Activation State*
MYC	1.11E-18	
TGFB1	1.18E-17	
lipopolysaccharide	6.47E-17	
TP53	8.28E-17	
IL6	2.22E-15	

*Predicted activation state results are not provided as this analysis will give biased results due to either only up- or down-regulated proteins in each list.

B. Top Diseases and Bio Functions of Down-regulated Proteins

Diseases and Disorders

Name	p-value	# Molecules
Neurological Disease	2.09E-07 - 2.78E-02	28
Psychological Disorders	2.09E-07 - 1.75E-02	16
Hereditary Disorder	2.09E-07 - 1.75E-02	28
Immunological Disease	1.36E-07 - 2.44E-02	7
Organismal Injury and Abnormalities	1.36E-07 - 2.67E-02	16

Molecular and Cellular Functions

Name	p-value	# Molecules
Molecular Transport	8.85E-09 - 2.87E-02	35
Carbohydrate Metabolism	9.42E-06 - 2.78E-02	15
Cell Morphology	1.16E-05 - 2.86E-02	28
Cellular Assembly and Organization	1.16E-05 - 3.01E-02	29
Cellular Compromise	1.22E-05 - 2.44E-02	10

Physiological System Development and Function

Name	p-value	# Molecules
Behavior	4.27E-06 - 2.09E-02	15
Cardiovascular System Development	1.04E-05 - 1.66E-02	13
Organ Morphology	3.34E-05 - 2.78E-02	13
Organismal Development	3.65E-05 - 2.78E-02	11
Skeletal and Muscular System Development	1.92E-04 - 2.78E-02	14

Top Canonical Pathways

Name	p-value	Ratio .
a-Adrenergic Signaling	7.73E-10	8/109(0.073)
CCR5 Signaling in Macrophages	4.81E-09	7/97(0.072)
Androgen Signaling	5.35E-09	8/145(0.055)
Breast Cancer Regulation by Stathmin1	2.37E-08	9/214(0.042)
G Beta Gamma Signaling	2.63E-08	7/121(0.058)

Top Upstream Regulators

Upstream Regulator	p-value of overlap	Predicted Activation State*
MAPT	1.03E-10	
PSEN1	5.91E-10	
APP	1.29E-09	
D-glucose	7.80E-08	
Ins1	3.14E-06	

*Predicted activation state results are not provided as this analysis will give biased results due to either only up- or down-regulated proteins in each list.