

Supplementary Table 8.
Differential protein expression

protein accession	gene symbols	<i>p</i>	adjusted <i>p</i>	logFC	dysregulation
P52701	MSH6	1.79286E-10	3.90305E-07	1.51582523	UP
P49736	MCM2	8.03314E-08	4.37408E-05	1.74465747	UP
P04040	CAT	2.91509E-07	6.56876E-05	1.61861611	UP
Q8WW12	PCNP	7.35641E-07	0.000132955	1.10501624	UP
Q9UKA9	PTBP2	1.51098E-06	0.000173127	1.11510924	UP
Q8N1F7	NUP93	2.43776E-06	0.000230739	1.04347774	UP
Q8N1N4	KRT78	3.67218E-06	0.000280986	1.43218072	UP
Q96A72	MAGOHB	4.13497E-06	0.000291343	1.70001312	UP
P12270	TPR	8.81318E-06	0.000518548	1.13836153	UP
Q9P013	CWC15	9.69351E-06	0.000541096	1.71125384	UP
P35579	MYH9	1.06568E-05	0.000566985	1.03349928	UP
Q96EP5	DAZAP1	2.28906E-05	0.000889874	1.00422934	UP
Q9P258	RCC2	2.537E-05	0.000915205	1.00847416	UP
P00352	ALDH1A1	3.25034E-05	0.001028938	3.74121164	UP
Q4J6C6	PREPL	3.30848E-05	0.001028938	2.62338163	UP
Q15631	TSN	4.65948E-05	0.001284012	1.0418886	UP
Q16401	PSMD5	5.73675E-05	0.001504686	2.30911755	UP
P42166	TMPO	0.000104417	0.002198227	1.74039894	UP
Q5JSH3	WDR44	0.000107956	0.002238287	1.32669848	UP
Q15637	SF1	0.000114641	0.002314339	1.01235244	UP
O00267	SUPT5H	0.000215063	0.003657751	1.62552895	UP
Q9NYB0	TERF2IP	0.000303232	0.004715262	1.16220452	UP
P13807	GYS1	0.000365809	0.005608214	1.42026108	UP
O75155	CAND2	0.00053802	0.007320441	1.68331267	UP
Q8IX12	CCAR1	0.000548194	0.007396172	1.26030755	UP
P07741	APRT	0.000637939	0.008468252	1.14654647	UP
P48739	PITPNB	0.000804314	0.010005663	1.29907061	UP
Q96C90	PPP1R14B	0.000930368	0.010922569	1.19191428	UP
O15143	ARPC1B	0.001078203	0.012099214	1.67244458	UP

P42285	MTREX	0.001158857	0.012427747	1.55093484	UP
Q12996	CSTF3	0.001245967	0.013167334	1.74460711	UP
P53396	ACLY	0.001299217	0.013598053	1.14914008	UP
Q92600	CNOT9	0.001671227	0.01646523	1.31961028	UP
Q99700	ATXN2	0.001671482	0.01646523	1.19962645	UP
Q13724	MOGS	0.001737737	0.016771605	1.71500162	UP
P51513	NOVA1	0.001993312	0.018588736	1.45400689	UP
Q14677	CLINT1	0.002112386	0.019568784	1.1047739	UP
Q9BX40	LSM14B	0.002512265	0.02214251	1.09658956	UP
P57740	NUP107	0.002584254	0.022503682	1.65841561	UP
Q9BRF8	CPPED1	0.002849097	0.023494257	1.18960271	UP
O95479	H6PD	0.002885716	0.023706427	1.5302134	UP
P27482	CALML3	0.003071033	0.024579559	1.92221289	UP
Q8IZ83	ALDH16A1	0.003280256	0.025609336	1.93315187	UP
Q9Y2Y0	ARL2BP	0.003282042	0.025609336	1.0726697	UP
P35754	GLRX	0.003302177	0.025674426	1.0547667	UP
O15042	U2SURP	0.004126356	0.030198997	1.38029745	UP
O60341	KDM1A	0.004133808	0.030198997	1.13711638	UP
Q27J81	INF2	0.004396136	0.031901296	1.1735201	UP
O00159	MYO1C	0.0051035	0.03504833	2.01761905	UP
Q6P3W7	SCYL2	0.005135155	0.035154818	1.30867061	UP
P02786	TFRC	0.007121151	0.043425056	1.13950995	UP
Q6Y7W6	GIGYF2	0.007180122	0.043662365	1.21774159	UP
Q05519	SRSF11	0.007846168	0.046669692	1.13064981	UP
P19174	PLCG1	0.008572155	0.049109424	1.12650725	UP
Q9HCB6	SPON1	4.18474E-08	4.37408E-05	-2.13129684	DOWN
O75396	SEC22B	1.19415E-07	4.37408E-05	-1.78613299	DOWN
Q12860	CNTN1	1.38913E-07	4.37408E-05	-2.56693184	DOWN
Q9ULC4	MCTS1	1.40646E-07	4.37408E-05	-2.48073804	DOWN
P54578	USP14	1.80027E-07	4.89898E-05	-1.0277028	DOWN
P27338	MAOB	3.01734E-07	6.56876E-05	-2.44210286	DOWN
P61601	NCALD	1.03265E-06	0.000132955	-1.45524497	DOWN
P10515	DLAT	2.77473E-06	0.000247236	-2.41511072	DOWN

Q8IWU5	SULF2	3.13126E-06	0.000262183	-2.61586381	DOWN
Q99714	HSD17B10	4.48359E-06	0.000291343	-1.40246571	DOWN
Q9BW30	TPPP3	4.49102E-06	0.000291343	-1.55683486	DOWN
P13637	ATP1A3	5.89031E-06	0.000366377	-1.40254941	DOWN
O76070	SNCG	9.44785E-06	0.000541096	-2.03269706	DOWN
Q15768	EFNB3	1.12671E-05	0.000579573	-2.01176087	DOWN
Q02252	ALDH6A1	1.19569E-05	0.000591596	-1.86603969	DOWN
P36776	LONP1	1.31247E-05	0.000621141	-1.82303623	DOWN
P38646	HSPA9	1.43278E-05	0.000649827	-1.07185827	DOWN
P08559	PDHA1	1.54198E-05	0.000671377	-1.28342567	DOWN
Q14194	CRMP1	1.82937E-05	0.000780889	-1.63135688	DOWN
P30038	ALDH4A1	2.16836E-05	0.000889874	-1.83598517	DOWN
Q4G0N4	NADK2	2.22121E-05	0.000889874	-1.68617734	DOWN
P49748	ACADVL	2.25285E-05	0.000889874	-1.53257805	DOWN
P55084	HADHB	2.74911E-05	0.000949971	-1.77644147	DOWN
Q9NVJ2	ARL8B	3.14462E-05	0.001028938	-1.56121056	DOWN
P14866	HNRNPL	3.16565E-05	0.001028938	-1.24247002	DOWN
Q8IWU6	SULF1	3.30438E-05	0.001028938	-2.82265067	DOWN
P41208	CETN2	3.75224E-05	0.001128501	-1.29042776	DOWN
P51649	ALDH5A1	3.79779E-05	0.001128501	-1.51843453	DOWN
P62136	PPP1CA	5.06421E-05	0.001378098	-1.43537174	DOWN
P62714	PPP2CB	5.30569E-05	0.001408596	-1.19079753	DOWN
P43003	SLC1A3	6.04053E-05	0.001565504	-2.7978545	DOWN
P26440	IVD	6.45755E-05	0.001615872	-2.07146086	DOWN
Q9Y2S2	CRYL1	7.08036E-05	0.001721539	-1.21182832	DOWN
P61020	RAB5B	7.11707E-05	0.001721539	-1.07515359	DOWN
P60033	CD81	7.60598E-05	0.001780454	-1.61473303	DOWN
P09543	CNP	7.78319E-05	0.001802553	-1.19707236	DOWN
P34897	SHMT2	8.9303E-05	0.002004253	-1.02342414	DOWN
P99999	CYCS	9.3564E-05	0.002078458	-1.30171179	DOWN
P36542	ATP5F1C	9.86831E-05	0.002169021	-1.12423431	DOWN
P21796	VDAC1	0.000113404	0.002314339	-1.44824709	DOWN
P21695	GPD1	0.000132185	0.002592497	-2.08989022	DOWN

P46976	GYG1	0.000141831	0.002702529	-1.00684638	DOWN
P40939	HADHA	0.000156871	0.002824717	-1.60778583	DOWN
O75521	ECI2	0.000235639	0.003886265	-2.47028778	DOWN
Q16698	DECR1	0.00027586	0.004351796	-1.22291897	DOWN
Q96I99	SUCLG2	0.000417764	0.006186886	-2.60456624	DOWN
O60313	OPA1	0.00043951	0.006378753	-1.11850647	DOWN
P51572	BCAP31	0.000442737	0.006383034	-1.20913085	DOWN
Q12955	ANK3	0.000459263	0.006534747	-2.21778945	DOWN
Q00325	SLC25A3	0.000465601	0.0065819	-2.55364765	DOWN
P45954	ACADSB	0.000550381	0.007396172	-1.3545549	DOWN
Q96FJ2	DYNLL2	0.000598797	0.007997432	-1.80117775	DOWN
P61764	STXBP1	0.00065719	0.008618696	-1.75962628	DOWN
P20711	DDC	0.000670988	0.008643433	-1.74803981	DOWN
Q7L099	RUFY3	0.000676804	0.008667068	-1.99894138	DOWN
O95631	NTN1	0.000787528	0.009853146	-1.86284307	DOWN
P48147	PREP	0.000866664	0.010445539	-1.60712699	DOWN
P05026	ATP1B1	0.000893343	0.010630529	-1.04900648	DOWN
Q12926	ELAVL2	0.00093321	0.010922569	-1.01885789	DOWN
Q9H4G4	GLIPR2	0.001089139	0.012123672	-1.67345033	DOWN
P45880	VDAC2	0.00109152	0.012123672	-1.50760737	DOWN
Q01650	SLC7A5	0.001119668	0.01219155	-1.76879814	DOWN
P83881	RPL36A	0.001127868	0.012215762	-1.61271228	DOWN
Q13228	SELENBP1	0.001368217	0.014116623	-1.29336499	DOWN
P17252	PRKCA	0.00139429	0.014250561	-1.66873768	DOWN
Q7Z6G3	NECAB2	0.001690441	0.016576987	-1.63634318	DOWN
Q9UI30	TRMT112	0.001732918	0.016771605	-2.33002983	DOWN
P11177	PDHB	0.001756512	0.016771605	-1.03787768	DOWN
P53597	SUCLG1	0.001947538	0.018354066	-2.02014507	DOWN
P35613	BSG	0.002304299	0.021077555	-1.9520005	DOWN
Q9H313	TTYH1	0.00231956	0.021128377	-1.58507523	DOWN
P59768	GNG2	0.002397311	0.021655374	-1.05857602	DOWN
Q9BQ69	MACROD1	0.002428084	0.02184272	-1.78675596	DOWN
Q16836	HADH	0.002475524	0.021907378	-1.03649485	DOWN

P04899	GNAI2	0.00263813	0.022751331	-1.42532148	DOWN
Q13541	EIF4EBP1	0.002664947	0.022751331	-1.41612923	DOWN
O75093	SLIT1	0.002695875	0.022925469	-1.58076534	DOWN
Q5SSJ5	HP1BP3	0.002848702	0.023494257	-1.06566903	DOWN
Q9NRW1	RAB6B	0.003040948	0.024428572	-2.41695989	DOWN
P21741	MDK	0.003876294	0.028792105	-1.48706005	DOWN
Q9Y277	VDAC3	0.003996191	0.029490537	-2.32361708	DOWN
P06753	TPM3	0.004658661	0.033206557	-1.21305301	DOWN
P22695	UQCRC2	0.004856874	0.03388915	-1.39328628	DOWN
Q5VTU8	ATP5F1EP2	0.005011784	0.034636999	-1.02213092	DOWN
Q99523	SORT1	0.0054301	0.036150851	-1.51001627	DOWN
A6NHL2	TUBAL3	0.005585805	0.036984157	-2.40593036	DOWN
Q7L0J3	SV2A	0.006153263	0.0395152	-1.61597766	DOWN
P61513	RPL37A	0.006350686	0.040423224	-1.04340117	DOWN
Q9HAV7	GRPEL1	0.006647693	0.041586288	-1.5299544	DOWN
P11498	PC	0.007062045	0.043185593	-2.60208395	DOWN
P62877	RBX1	0.007780409	0.046567158	-1.00076909	DOWN
Q96FN4	CPNE2	0.007807539	0.046567158	-1.97063693	DOWN
P14136	GFAP	0.008320155	0.048172812	-1.97031377	DOWN
Q15382	RHEB	0.008474622	0.048781282	-1.35551809	DOWN
P07196	NEFL	0.008695716	0.049540194	-1.0982261	DOWN
Q02218	OGDH	0.008715615	0.049540194	-1.1398314	DOWN

Enrichment of Down-regulated genes in proteomic data

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> -value	gene ID	count
GO:0016054	organic acid catabolic process	14/96	3.62E-11	3.40065E-08	2.88E-08	HSD17B10/ALDH6A1/ALDH4A1/ACADVL/HADHB/ALDH5A1/IVD/CRYL1/SHMT2/HADHA/ECI2/DECR1/ACADSB/HADH	14
GO:0046395	carboxylic acid catabolic process	14/96	3.62E-11	3.40065E-08	2.88E-08	HSD17B10/ALDH6A1/ALDH4A1/ACADVL/HADHB/ALDH5A1/IVD/CRYL1/SHMT2/HADHA/ECI2/DECR1/ACADSB/HADH	14
GO:0015980	energy derivation by oxidation of organic compounds	15/96	1.56E-10	9.76212E-08	8.27E-08	DLAT/PDHA1/ACADVL/PPP1CA/SHMT2/CYCS/ATP5F1C/GPD1/GYG1/SUCLG2/PDHB/SUCLG1/UQCRC2/ATP5F1EP2/OGDH	15
GO:0045333	cellular respiration	12/96	3.81E-09	1.5491E-06	1.31E-06	DLAT/PDHA1/SHMT2/CYCS/ATP5F1C/GPD1/SUCLG2/PDHB/SUCLG1/UQCRC2/ATP5F1EP2/OGDH	12
GO:0009060	aerobic respiration	11/96	4.94E-09	1.5491E-06	1.31E-06	DLAT/PDHA1/SHMT2/CYCS/ATP5F1C/SUCLG2/PDHB/SUCLG1/UQCRC2/ATP5F1EP2/OGDH	11

GO:0006635	fatty acid beta-oxidation	8/96	4.73E-09	1.5491E-06	1.31E-06	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8
GO:0044282	small molecule catabolic process	14/96	6.44E-09	1.73037E-06	1.47E-06	HSD17B10/ALDH6A1/ALDH4A1/ACADVL/HADHB/ALDH5A1/IVD/CRYL1/SHMT2/HADHA/ECI2/DECR1/ACADSB/HADH	14
GO:0006099	tricarboxylic acid cycle	6/96	1.47E-08	3.44979E-06	2.92E-06	DLAT/PDHA1/SUCLG2/PDHB/SUCLG1/OGDH	6
GO:0072329	monocarboxylic acid catabolic process	9/96	2.21E-08	4.62126E-06	3.91E-06	HSD17B10/ACADVL/HADHB/IVD/CRYL1/HADHA/ECI2/DECR1/HADH	9
GO:0072521	purine-containing compound metabolic process	15/96	2.74E-08	5.15022E-06	4.36E-06	DLAT/PDHA1/NADK2/SHMT2/ATP5F1C/GPD1/SUCLG2/OPA1/ATP1B1/PDHB/SUCLG1/MACROD1/ATP5F1EP2/PC/OGDH	15
GO:0009062	fatty acid catabolic process	8/96	6.69E-08	1.1279E-05	9.55E-06	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8

GO:0019395	fatty acid oxidation	8/96	7.2E-08	1.1279E-05	9.55E-06	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8
GO:0034440	lipid oxidation	8/96	1.18E-07	1.70751E-05	1.45E-05	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8
GO:0006163	purine nucleotide metabolic process	13/96	6.26E-07	8.40509E-05	7.12E-05	DLAT/PDHA1/NADK2/ATP5F1C/GPD1/SUCLG2/OPA1/ATP1B1/PDHB/SUCLG1/ATP5F1EP2/PC/OGDH	13
GO:0009063	amino acid catabolic process	7/96	1.76E-06	0.000220613	0.000187	HSD17B10/ALDH6A1/ALDH4A1/ALDH5A1/IVD/SHMT2/ACADSB	7
GO:0006090	pyruvate metabolic process	7/96	2.35E-06	0.000276579	0.000234	DLAT/PDHA1/VDAC1/GPD1/PDHB/PC/OGDH	7
GO:0009083	branched-chain amino acid catabolic process	4/96	3.52E-06	0.000389788	0.00033	HSD17B10/ALDH6A1/IVD/ACADSB	4

GO:0030258	lipid modification	8/96	6.13E-06	0.000640473	0.000542	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8
GO:1901606	alpha-amino acid catabolic process	6/96	7.9E-06	0.000782215	0.000662	HSD17B10/ALDH6A1/ALDH4A1/IVD/SHMT2/ACADSB	6
GO:0006637	acyl-CoA metabolic process	6/96	9.49E-06	0.000850255	0.00072	DLAT/PDHA1/SUCLG2/PDHB/SUCLG1/OGDH	6
GO:0035383	thioester metabolic process	6/96	9.49E-06	0.000850255	0.00072	DLAT/PDHA1/SUCLG2/PDHB/SUCLG1/OGDH	6
GO:0009081	branched-chain amino acid metabolic process	4/96	1.01E-05	0.000862793	0.000731	HSD17B10/ALDH6A1/IVD/ACADSB	4
GO:0006104	succinyl-CoA metabolic process	3/96	1.49E-05	0.001220297	0.001033	SUCLG2/SUCLG1/OGDH	3

GO:0009150	purine ribonucleotide metabolic process	10/96	1.67E-05	0.001309356	0.001109	DLAT/PDHA1/ATP5F1C/SUCLG2/OPA1/ATP1B1/PDHB/SUCLG1/ATP5F1EP2/OGDH	10
GO:0006520	amino acid metabolic process	9/96	1.75E-05	0.001315853	0.001114	HSD17B10/ALDH6A1/ALDH4A1/ALDH5A1/SLC1A3/IVD/SHMT2/ACADSB/DDC	9
GO:0044242	cellular lipid catabolic process	8/96	1.82E-05	0.001318268	0.001116	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8
GO:0006086	acetyl-CoA biosynthetic process from pyruvate	3/96	2.04E-05	0.001424053	0.001206	DLAT/PDHA1/PDHB	3
GO:0009259	ribonucleotide metabolic process	10/96	2.64E-05	0.001771829	0.0015	DLAT/PDHA1/ATP5F1C/SUCLG2/OPA1/ATP1B1/PDHB/SUCLG1/ATP5F1EP2/OGDH	10
GO:0019693	ribose phosphate metabolic process	10/96	3.14E-05	0.002037375	0.001725	DLAT/PDHA1/ATP5F1C/SUCLG2/OPA1/ATP1B1/PDHB/SUCLG1/ATP5F1EP2/OGDH	10

GO:0014015	positive regulation of gliogenesis	5/96	3.28E-05	0.002055776	0.001741	NTN1/SLC7A5/MDK/GFAP/RHEB	5
GO:0006631	fatty acid metabolic process	10/96	3.73E-05	0.002260237	0.001914	HSD17B10/ACADVL/HADHB/IVD/CRYL1/HADHA/ECI2/DECR1/ACADSB/HADH	10
GO:0033865	nucleoside bisphosphate metabolic process	6/96	4.27E-05	0.002360708	0.001999	DLAT/PDHA1/SUCLG2/PDHB/SUCLG1/OGDH	6
GO:0033875	ribonucleoside bisphosphate metabolic process	6/96	4.27E-05	0.002360708	0.001999	DLAT/PDHA1/SUCLG2/PDHB/SUCLG1/OGDH	6
GO:0034032	purine nucleoside bisphosphate metabolic process	6/96	4.27E-05	0.002360708	0.001999	DLAT/PDHA1/SUCLG2/PDHB/SUCLG1/OGDH	6
GO:0010977	negative regulation of neuron projection development	6/96	8.03E-05	0.004314796	0.003653	EFNB3/CRMP1/RUFY3/NTN1/SLIT1/GFAP	6

GO:1901605	alpha-amino acid metabolic process	7/96	9.02E-05	0.00471151	0.003989	HSD17B10/ALDH6A1/ALDH4A1/ALDH5A1/IVD/SHMT2/ACADSB	7
GO:0006085	acetyl-CoA biosynthetic process	3/96	9.85E-05	0.005007952	0.00424	DLAT/PDHA1/PDHB	3
GO:0043648	dicarboxylic acid metabolic process	5/96	0.000118	0.005830251	0.004936	ALDH4A1/ALDH5A1/SHMT2/SUCLG2/OGDH	5
GO:0050767	regulation of neurogenesis	9/96	0.000167	0.008047112	0.006813	EFNB3/RUFY3/NTN1/SLC7A5/SLIT1/MDK/GFAP/RHEB/NEFL	9
GO:0006883	intracellular sodium ion homeostasis	3/96	0.000183	0.008614307	0.007294	ATP1A3/SLC1A3/ATP1B1	3
GO:0060252	positive regulation of glial cell proliferation	3/96	0.00021	0.009629243	0.008153	NTN1/SLC7A5/GFAP	3

GO:0050769	positive regulation of neurogenesis	7/96	0.000237	0.010594814	0.008971	RUFY3/NTN1/SLC7A5/MDK/GFAP/RHEB/NEFL	7
GO:0014013	regulation of gliogenesis	5/96	0.000246	0.010776271	0.009124	NTN1/SLC7A5/MDK/GFAP/RHEB	5
GO:0016042	lipid catabolic process	8/96	0.000304	0.012995208	0.011003	HSD17B10/ACADVL/HADHB/IVD/HADHA/ECI2/DECR1/HADH	8
GO:0050771	negative regulation of axonogenesis	4/96	0.000356	0.014884796	0.012603	EFNB3/RUFY3/NTN1/SLIT1	4
GO:0072522	purine-containing compound biosynthetic process	7/96	0.000428	0.017337251	0.014679	DLAT/PDHA1/NADK2/SHMT2/ATP5F1C/PDHB/ATP5F1EP2	7
GO:0031099	regeneration	6/96	0.000433	0.017337251	0.014679	SULF2/CD81/SLC7A5/MDK/GFAP/NEFL	6

GO:0031345	negative regulation of cell projection organization	6/96	0.000445	0.017452637	0.014777	EFNB3/CRMP1/RUFY3/NTN1/SLIT1/GFAP	6
GO:0007409	axonogenesis	9/96	0.000462	0.017740753	0.015021	CNTN1/EFNB3/CNP/ANK3/STXBP1/RUFY3/NTN1/SLIT1/NEFL	9
GO:0010975	regulation of neuron projection development	9/96	0.000501	0.01883413	0.015947	CNTN1/EFNB3/CRMP1/RUFY3/NTN1/SLIT1/MDK/GFAP/NEFL	9
GO:0010644	cell communication by electrical coupling	3/96	0.000569	0.020569862	0.017416	ATP1A3/ANK3/ATP1B1	3
GO:0010765	positive regulation of sodium ion transport	3/96	0.000569	0.020569862	0.017416	CNTN1/ANK3/ATP1B1	3
GO:0051960	regulation of nervous system development	9/96	0.000613	0.021708752	0.018381	EFNB3/RUFY3/NTN1/SLC7A5/SLIT1/MDK/GFAP/RHEB/NEFL	9

GO:0006084	acetyl-CoA metabolic process	3/96	0.000623	0.021708752	0.018381	DLAT/PDHA1/PDHB	3
GO:0051962	positive regulation of nervous system development	7/96	0.000699	0.023920153	0.020253	RUFY3/NTN1/SLC7A5/MDK/GFAP/RHEB/NEFL	7
GO:0098656	monoatomic anion transmembrane transport	5/96	0.000927	0.031149153	0.026374	SLC1A3/VDAC1/VDAC2/TTYH1/VDAC3	5
GO:0006119	oxidative phosphorylation	5/96	0.000956	0.031546801	0.02671	SHMT2/CYCS/ATP5F1C/UQCRC2/ATP5F1EP2	5
GO:0006865	amino acid transport	5/96	0.001015	0.0329223	0.027875	SLC1A3/STXBP1/SLC7A5/SV2A/GFAP	5
GO:0042135	neurotransmitter catabolic process	2/96	0.001122	0.035783268	0.030297	MAOB/ALDH5A1	2

GO:0006790	sulfur compound metabolic process	7/96	0.001175	0.036458912	0.03087	DLAT/HSPA9/PDHA1/SUCLG2/PDHB/ SUCLG1/OGDH	7
GO:0060251	regulation of glial cell proliferation	3/96	0.001182	0.036458912	0.03087	NTN1/SLC7A5/GFAP	3
GO:0050770	regulation of axonogenesis	5/96	0.001244	0.037738384	0.031953	EFNB3/RUFY3/NTN1/SLIT1/NEFL	5
GO:1902600	proton transmembrane transport	5/96	0.001353	0.037820984	0.032023	ATP1A3/ATP5F1C/SLC25A3/ATP1B1/ ATP5F1EP2	5
GO:0019674	NAD metabolic process	3/96	0.001269	0.037820984	0.032023	NADK2/GPD1/PC	3
GO:0051955	regulation of amino acid transport	3/96	0.001359	0.037820984	0.032023	STXBP1/SLC7A5/SV2A	3

GO:0006734	NADH metabolic process	2/96	0.001367	0.037820984	0.032023	GPD1/PC	2
GO:0010248	establishment or maintenance of transmembrane electrochemical gradient	2/96	0.001367	0.037820984	0.032023	ATP1A3/ATP1B1	2
GO:0032836	glomerular basement membrane development	2/96	0.001367	0.037820984	0.032023	SULF2/SULF1	2
GO:0043434	response to peptide hormone	8/96	0.001572	0.039863783	0.033752	LONP1/HADHA/PRKCA/BSG/HADH/GNAI2/SORT1/NEFL	8
GO:0051952	regulation of amine transport	4/96	0.001518	0.039863783	0.033752	SNCG/STXBP1/SLC7A5/SV2A	4
GO:0055078	sodium ion homeostasis	3/96	0.001653	0.039863783	0.033752	ATP1A3/SLC1A3/ATP1B1	3

GO:0001973	G protein-coupled adenosine receptor signaling pathway	2/96	0.001635	0.039863783	0.033752	NECAB2/GNAI2	2
GO:0014831	gastro-intestinal system smooth muscle contraction	2/96	0.001635	0.039863783	0.033752	SULF2/SULF1	2
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	2/96	0.001635	0.039863783	0.033752	ACADVL/IVD	2
GO:0033869	nucleoside bisphosphate catabolic process	2/96	0.001635	0.039863783	0.033752	SUCLG2/SUCLG1	2
GO:0034031	ribonucleoside bisphosphate catabolic process	2/96	0.001635	0.039863783	0.033752	SUCLG2/SUCLG1	2
GO:0034034	purine nucleoside bisphosphate catabolic process	2/96	0.001635	0.039863783	0.033752	SUCLG2/SUCLG1	2

GO:0035588	G protein-coupled purinergic receptor signaling pathway	2/96	0.001635	0.039863783	0.033752	NECAB2/GNAI2	2
GO:0042063	gliogenesis	7/96	0.001696	0.0403813	0.034191	CNTN1/CNP/NTN1/SLC7A5/MDK/GFAP/RHEB	7
GO:0035384	thioester biosynthetic process	3/96	0.001759	0.040854446	0.034591	DLAT/PDHA1/PDHB	3
GO:0071616	acyl-CoA biosynthetic process	3/96	0.001759	0.040854446	0.034591	DLAT/PDHA1/PDHB	3
GO:0006820	monoatomic anion transport	5/96	0.00186	0.042663427	0.036123	SLC1A3/VDAC1/VDAC2/TTYH1/VDAC3	5
GO:0010720	positive regulation of cell development	8/96	0.001921	0.043542261	0.036867	RUFY3/NTN1/SLC7A5/PRKCA/MDK/GFAP/RHEB/NEFL	8

GO:0006164	purine nucleotide biosynthetic process	6/96	0.002048	0.045474133	0.038503	DLAT/PDHA1/NADK2/ATP5F1C/PDH B/ATP5F1EP2	6
GO:0022900	electron transport chain	5/96	0.002056	0.045474133	0.038503	MAOB/ALDH4A1/CYCS/GPD1/UQCR C2	5
GO:0048709	oligodendrocyte differentiation	4/96	0.002103	0.045474133	0.038503	CNTN1/CNP/MDK/RHEB	4
GO:0089718	amino acid import across plasma membrane	3/96	0.002103	0.045474133	0.038503	SLC1A3/SLC7A5/GFAP	3
GO:0015837	amine transport	4/96	0.002251	0.046019112	0.038964	SNCG/STXBP1/SLC7A5/SV2A	4
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	2/96	0.00224	0.046019112	0.038964	CYCS/UQCRC2	2

GO:0051412	response to corticosterone	2/96	0.00224	0.046019112	0.038964	MAOB/NEFL	2
GO:0070262	peptidyl-serine dephosphorylation	2/96	0.00224	0.046019112	0.038964	PPP1CA/PPP2CB	2
GO:0106070	regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway	2/96	0.00224	0.046019112	0.038964	PRKCA/GNAI2	2
GO:0010038	response to metal ion	7/96	0.002382	0.048175175	0.04079	MAOB/LONP1/PPP1CA/PPP2CB/ANK3/BSG/CPNE2	7
GO:0030007	intracellular potassium ion homeostasis	2/96	0.002576	0.049950552	0.042293	ATP1A3/ATP1B1	2
GO:0036376	sodium ion export across plasma membrane	2/96	0.002576	0.049950552	0.042293	ATP1A3/ATP1B1	2

GO:0070863	positive regulation of protein exit from endoplasmic reticulum	2/96	0.002576	0.049950552	0.042293	CD81/BCAP31	2
GO:2000651	positive regulation of sodium ion transmembrane transporter activity	2/96	0.002576	0.049950552	0.042293	ANK3/ATP1B1	2

Enrichment of Up-regulated genes in proteomic data

pathway ID	description	GeneRatio	<i>p</i>	adjusted <i>p</i>	<i>q</i> - value	gene ID	count
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	8/50	2.381E-06	0.000972406	0.0008474	PTBP2/MAGOHB/CWC15/D AZAP1/SF1/MTREX/NOVA1/ KDM1A	8
GO:0000398	mRNA splicing, via spliceosome	8/50	2.381E-06	0.000972406	0.0008474	PTBP2/MAGOHB/CWC15/D AZAP1/SF1/MTREX/NOVA1/ KDM1A	8
GO:0000375	RNA splicing, via transesterification reactions	8/50	2.602E-06	0.000972406	0.0008474	PTBP2/MAGOHB/CWC15/D AZAP1/SF1/MTREX/NOVA1/ KDM1A	8
GO:0008380	RNA splicing	9/50	3.965E-06	0.001111283	0.0009684	PTBP2/MAGOHB/CWC15/D AZAP1/SF1/MTREX/NOVA1/ KDM1A/SRSF11	9
GO:0006999	nuclear pore organization	3/50	7.788E-06	0.001746088	0.0015215	NUP93/TPR/NUP107	3
GO:0006406	mRNA export from nucleus	4/50	3.515E-05	0.006212758	0.0054138	NUP93/MAGOHB/TPR/NUP1 07	4

GO:0006997	nucleus organization	5/50	3.88E-05	0.006212758	0.0054138	NUP93/TPR/SF1/PITPNB/NUP107	5
GO:0050657	nucleic acid transport	5/50	6.038E-05	0.007400952	0.0064492	NUP93/MAGOHB/TPR/ATX N2/NUP107	5
GO:0050658	RNA transport	5/50	6.038E-05	0.007400952	0.0064492	NUP93/MAGOHB/TPR/ATX N2/NUP107	5
GO:0051236	establishment of RNA localization	5/50	6.602E-05	0.007400952	0.0064492	NUP93/MAGOHB/TPR/ATX N2/NUP107	5
GO:0006405	RNA export from nucleus	4/50	0.0001026	0.010459819	0.0091147	NUP93/MAGOHB/TPR/NUP107	4
GO:0006403	RNA localization	5/50	0.0001706	0.015932747	0.0138838	NUP93/MAGOHB/TPR/ATX N2/NUP107	5
GO:0006310	DNA recombination	6/50	0.0002667	0.023000219	0.0200424	MSH6/MCM2/TSN/TERF2IP/KDM1A/TFRC	6

GO:0051292	nuclear pore complex assembly	2/50	0.0003055	0.023437692	0.0204237	NUP93/NUP107	2
GO:0015931	nucleobase-containing compound transport	5/50	0.0003156	0.023437692	0.0204237	NUP93/MAGOHB/TPR/ATX N2/NUP107	5
GO:0051028	mRNA transport	4/50	0.0003547	0.023437692	0.0204237	NUP93/MAGOHB/TPR/NUP107	4
GO:1903311	regulation of mRNA metabolic process	6/50	0.0003728	0.023437692	0.0204237	MAGOHB/DAZAP1/SF1/CNOT9/NOVA1/GIGYF2	6
GO:0050684	regulation of mRNA processing	4/50	0.0003763	0.023437692	0.0204237	MAGOHB/DAZAP1/SF1/NOVA1	4
GO:0000018	regulation of DNA recombination	4/50	0.0004598	0.027125886	0.0236376	MSH6/TERF2IP/KDM1A/TFR C	4