Legends of Supplementary Figure

Supplementary Figure 1. The GO enrichment analysis of significantly differentially expressed proteins in the spinal cord of the SOD1 G93A transgenic mice compared the mice of progression stages with the age-matched WT mice. All GO entries associated with the differentially expressed proteins were marked in the orange frame in the cellular component of the GO enrichment analysis, the relationships between the all GO entries were linked using the black line.

Supplementary Figure 2. The GO enrichment analysis of significantly differentially expressed proteins in the spinal cord of the SOD1 G93A transgenic mice compared the mice of progression stages with the age-matched WT mice. All GO entries associated with the differentially expressed proteins were marked in the orange frame in the molecular function of the GO enrichment analysis, the relationships between the all GO entries were linked using the black line.

Supplementary Figure 3. The GO enrichment analysis of significantly differentially expressed proteins in the spinal cord of the SOD1 G93A transgenic mice compared the mice of progression stages with the age-matched WT mice. All GO entries associated with the differentially expressed proteins were marked in the orange frame in the biological process of the GO enrichment analysis, the relationships between the all GO entries were linked using the black line.

Supplementary figure 1

Supplementary figure 2

Supplementary figure 3

Feb 7, 2015

Supplementary Table 1. List of Significantly Up Regulated Proteins in Spinal Cord between a Pre-onset SOD1 G93A Mouse Vs an Age-Matched WT Mouse

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q3UHD1	Brain-specific angiogenesis inhibitor 1	3.433	Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	2.215
E9Q4M4	MICOS complex subunit Mic25	2.716	Q3UH86	Putative uncharacterized protein	2.204
Q91VN4	MICOS complex subunit Mic25	2.716	O08919	Numb-like protein	2.204
D3Z780	Translation initiation factor eIF-2B subunit delta	2.572	E9Q3M9	Protein 2010300C02Rik	2.192
Q61749	Translation initiation factor eIF-2B subunit delta	2.572	B0V2H4	V-type proton ATPase subunit G 2	2.184
Q9WVJ3	Carboxypeptidase Q	2.555	Q9WTT4	V-type proton ATPase subunit G 2	2.184
P43274	Histone H1.4	2.463	P68510	14-3-3 protein eta	2.167
Q3ULN5	Peptidyl-prolyl cis-trans isomerase	2.431	B2RPU8	MCG130675	2.15
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A	2.431	Q9D1L0	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	2.15
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	2.366	D3Z5B1	Protein Zbed5 (Fragment)	2.15
Q9DCT8	Cysteine-rich protein 2	2.35	Q8CEW7	Putative uncharacterized protein	2.15
Q71V06	Y box transcription factor (Fragment)	2.323	Q9CR57	60S ribosomal protein L14	2.129
Q810K5	Y box protein 1	2.323	Q9CWK0	Putative uncharacterized protein	2.129
P62960	Nuclease-sensitive element-binding protein 1	2.323	Q2Q7P0	ENH1	2.115
Q60951	MYB-1b	2.323	Q8CI51	PDZ and LIM domain protein 5	2.115
P60867	40S ribosomal protein S20	2.306	D9J300	ENH isoform 1c	2.115
D0VYV6	Erythrocyte protein band 4.1-like 3 isoform B	2.294	D9J2Z9	ENH isoform 1b	2.115
Q3UAC2	40S ribosomal protein S3a	2.274	D9J301	ENH isoform 1d	2.115
P97351	40S ribosomal protein S3a	2.274	D9J302	ENH isoform 1e	2.115
Q9D1S3	40S ribosomal protein S3a	2.274	Q3UHA5	Putative uncharacterized protein	2.07
Q8BY89	Choline transporter-like protein 2	2.238	Q8R5M7	CaV2.1	2.07
P63216	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-3	2.225	Q3UHN4	Putative uncharacterized protein	2.07
F6UP77	Putative N-acetylglucosamine-6-phosphate deacetylase (Fragment)	2.215	P97445	Voltage-dependent P/Q-type calcium channel subunit alpha-1A	2.07

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q8R5M6	CaV2.1	2.07	P67984	60S ribosomal protein L22	1.883
E9Q1R5	Voltage-dependent P/Q-type calcium channel subunit alpha-1A	2.07	Q3U0V1	Far upstream element-binding protein 2	1.867
Q2UY11	Collagen alpha-1(XXVIII) chain	2.059	A0JLV3	Histone H2B (Fragment)	1.866
Q71M36	Chondroitin sulfate proteoglycan 5	2.05	Q8CGP2	Histone H2B type 1-P	1.866
Q99JT9	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	2.033	Q64475	Histone H2B type 1-B	1.866
Q3TG58	Williams-Beuren syndrome chromosome region 1 homolog (Human), isoform CRA_b	2.024	Q921L4	Histone H2B	1.866
Q9WUK2	Eukaryotic translation initiation factor 4H	2.024	Q8CBB6	Histone H2B	1.866
Q80U88	MKIAA0038 protein (Fragment)	2.024	P10853	Histone H2B type 1-F/J/L	1.866
Q3V244	Putative uncharacterized protein	2.024	Q6ZWY9	Histone H2B type 1-C/E/G	1.866
Q3THJ0	60S ribosomal protein L18a	2	Q8CGP1	Histone H2B type 1-K	1.866
Q05CK2	60S ribosomal protein L18a	2	Q64525	Histone H2B type 2-B	1.866
P62717	60S ribosomal protein L18a	2	P10854	Histone H2B type 1-M	1.866
O35449	Proline-rich transmembrane protein 1	1.975	Q64478	Histone H2B type 1-H	1.866
Q9CWF2	Tubulin beta-2B chain	1.963	Q5NDA4	Fatty acid binding protein 7, brain	1.864
Q0VBF8	Protein stum homolog	1.956	P51880	Fatty acid-binding protein, brain	1.864
J3QP43	Protein 6330403A02Rik	1.956	P97855	Ras GTPase-activating protein-binding protein 1	1.863
Q3UBS0	Putative uncharacterized protein	1.955	Q8C6F4	Putative uncharacterized protein	1.863
P08226	Apolipoprotein E	1.955	Q8CAG6	Pleckstrin	1.863
Q4FK40	Apoe protein	1.955	Q9JHK5	Pleckstrin	1.863
Q6GTX3	Apoe protein	1.955	P62852	40S ribosomal protein S25	1.854
F8VQK3	Protein Gucy1a2	1.947	A1BN54	Alpha actinin 1a	1.845
Q8C6H6	Putative uncharacterized protein	1.921	Q3TLP8	RAS-related C3 botulinum substrate 1, isoform CRA_a	1.844
O70572	Sphingomyelin phosphodiesterase 2	1.921	Q8BPG5	Putative uncharacterized protein	1.844

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
P63001	Ras-related C3 botulinum toxin substrate 1	1.844	Q8R071	Inositol-trisphosphate 3-kinase A	1.756
Q9D859	Putative uncharacterized protein	1.844	G5E850	Cytochrome b-5, isoform CRA_a	1.754
Q8C4N8	Putative uncharacterized protein (Fragment)	1.844	P56395	Cytochrome b5	1.754
Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	1.841	P08228	Superoxide dismutase [Cu-Zn]	1.749
Q99L69	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	1.841	Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	1.735
Q6PJ18	Tpm2 protein	1.835	Q4FZL1	Eif4a1 protein (Fragment)	1.724
Q61344	Beta-tropomyosin	1.835	P60843	Eukaryotic initiation factor 4A-I	1.724
Q60972	Histone-binding protein RBBP4	1.834	Q8R366	Immunoglobulin superfamily member 8	1.719
Q8C1B7	Septin-11	1.832	P68372	Tubulin beta-4B chain	1.714
P97457	Myosin regulatory light chain 2, skeletal muscle isoform	1.821	P47911	60S ribosomal protein L6	1.714
Q9WU84	Copper chaperone for superoxide dismutase	1.819	Q3URD4	Putative uncharacterized protein	1.713
B2RWQ7	Arsb protein	1.814	P62812	Gamma-aminobutyric acid receptor subunit alpha-1	1.713
P50429	Arylsulfatase B	1.814	Q9JJI8	60S ribosomal protein L38	1.709
D3YYD5	Vacuolar protein sorting-associated protein 29 (Fragment)	1.808	Q3TZI7	Major prion protein	1.701
Q9QZ88	Vacuolar protein sorting-associated protein 29	1.808	Q3UBH0	Major prion protein	1.701
D3Z645	Vacuolar protein sorting-associated protein 29	1.808	P04925	Major prion protein	1.701
P05977	Myosin light chain 1/3, skeletal muscle isoform	1.803	Q9QYT9	Major prion protein	1.701
Q8BKZ9	Pyruvate dehydrogenase protein X component, mitochondrial	1.796	Q3UF68	Major prion protein	1.701
Q8K3Q4	Actinin alpha 2	1.79	Q3UG89	Major prion protein	1.701
Q9JI91	Alpha-actinin-2	1.79	Q9QY42	Prosaposin receptor GPR37	1.699
Q9JI95	CPN10-like protein	1.784	Q6NZB4	Transporter	1.697
Q64433	10 kDa heat shock protein, mitochondrial	1.784	Q8R2I2	Transporter	1.697
Q60829	Protein phosphatase 1 regulatory subunit 1B	1.757	O55192	Sodium-dependent noradrenaline transporter	1.697

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q3V471	Galectin (Fragment)	1.687	Q5CZY9	Rps16 protein	1.615
Q8C253	Galectin	1.687	Q641N3	Rps16 protein (Fragment)	1.615
P16110	Galectin-3	1.687	P14131	40S ribosomal protein S16	1.615
P62315	Small nuclear ribonucleoprotein Sm D1	1.67	B2RXS4	Plexin-B2	1.613
B1ASQ2	Apolipoprotein O	1.66	Q5XJV6	Serine/threonine-protein kinase LMTK3	1.613
Q9DCZ4	Apolipoprotein O	1.66	E9QNZ5	Serine/threonine-protein kinase LMTK3	1.613
Q3KNM9	Apoo protein	1.66	Q3UGX3	N-acetylaspartate synthetase	1.61
Q9D186	Apolipoprotein O	1.66	P0C0S6	Histone H2A.Z	1.598
P68134	Actin, alpha skeletal muscle	1.653	Q3THW5	Histone H2A.V	1.598
Q8R1N4	NudC domain-containing protein 3	1.651	Q3UEX4	Putative uncharacterized protein	1.596
Q9CZT8	Ras-related protein Rab-3B	1.65	O88741	Ganglioside-induced differentiation-associated protein 1 OS=Mus musculus GN=Gdap1 PE=1 SV=1	1.596
P16045	Galectin-1	1.637	Q3UTV3	Putative uncharacterized protein (Fragment)	1.596
Q3UUG6	TBC1 domain family member 24	1.633	Q5SX39	Myosin-4	1.595
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	1.632	Q3UJR8	Basic transcription factor 3, isoform CRA_b	1.589
B0R1E3	Histidine triad nucleotide-binding protein 1	1.624	Q64152	Transcription factor BTF3	1.589
P70349	Histidine triad nucleotide-binding protein 1	1.624	O35887	Calumenin	1.586
Q3TWG2	Putative uncharacterized protein	1.623	Q8BG39	Synaptic vesicle glycoprotein 2B	1.584
O08795	Glucosidase 2 subunit beta	1.623	D3Z0M9	MCG18410, isoform CRA_a	1.584
P97300	Neuroplastin	1.62	A2AVJ7	Ribosome-binding protein 1	1.57
Q4FJP8	Slc2a3 protein	1.616	Q6ZPS0	MKIAA1398 protein (Fragment)	1.57
P32037	Solute carrier family 2, facilitated glucose transporter member 3	1.616	Q99PL5	Ribosome-binding protein 1	1.57
Q8BLF7	Putative uncharacterized protein	1.616	Q9Z2A9	Gamma-glutamyltransferase 5	1.565

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q8C845	EF-hand domain-containing protein D2	1.562	Q9CQK2	40S ribosomal protein S24	1.534
P27048	Small nuclear ribonucleoprotein-associated protein B	1.559	Q9D7P1	40S ribosomal protein S24	1.534
P63163	Small nuclear ribonucleoprotein-associated protein N	1.559	Q9CY61	40S ribosomal protein S24	1.534
O70499	Small nuclear ribonucleoprotein-associated protein	1.559	P62849	40S ribosomal protein S24	1.534
Q3TXB1	Putative uncharacterized protein	1.557	P0C0A3	Charged multivesicular body protein 6	1.532
Q3UBX7	Putative uncharacterized protein	1.557	B1AZ42	Charged multivesicular body protein 6 (Fragment)	1.532
P98086	Complement C1q subcomponent subunit A	1.557	Q6PDY2	2-aminoethanethiol dioxygenase	1.53
D3Z3Z3	Voltage-dependent L-type calcium channel subunit beta-3	1.554	P62806	Histone H4	1.526
P54285	Voltage-dependent L-type calcium channel subunit beta-3	1.554	O35405	Phospholipase D3	1.524
Q8K5A7	Calcium channel beta 3 subunit	1.554	Q8BIW2	Putative uncharacterized protein	1.519
A0A087WR50	Fibronectin	1.552	Q8BJ13	Brain-specific angiogenesis inhibitor 3	1.519
A0A087WS56	Fibronectin	1.552	Q68FL1	Bai3 protein (Fragment)	1.519
Q3UHL6	Fibronectin	1.552	Q499E3	Brain-specific angiogenesis inhibitor 3	1.519
Q3UGY5	Putative uncharacterized protein	1.552	Q80ZF8	Brain-specific angiogenesis inhibitor 3	1.519
Q3UH17	Putative uncharacterized protein	1.552	Q8K0A3	Bai3 protein (Fragment)	1.519
Q3UHR1	Putative uncharacterized protein (Fragment)	1.552	P26645	Myristoylated alanine-rich C-kinase substrate	1.518
P11276	Fibronectin	1.552	P12658	Calbindin	1.517
P48678	Prelamin-A/C	1.545	E9Q3T0	Uncharacterized protein	1.514
Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5	1.545	P47955	60S acidic ribosomal protein P1	1.514
Q8BH58	TIP41-like protein	1.538	Q9EPL2	Calsyntenin-1	1.512
Q91VM2	Small nuclear ribonucleoprotein D3	1.535	G3X8X7	Vacuolar protein sorting 16 (Yeast)	1.511
P62320	Small nuclear ribonucleoprotein Sm D3	1.535	Q8BWV2	Putative uncharacterized protein	1.511
Q3TIF8	40S ribosomal protein S24	1.534	Q920Q4	Vacuolar protein sorting-associated protein 16 homolog	1.511

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q8QZV4	Serine/threonine-protein kinase 32C	1.511	Q61753	D-3-phosphoglycerate dehydrogenase	1.48
O35114	Lysosome membrane protein 2	1.51	Q8JZZ5	Pitpnb protein	1.48
Q53YX2	CD90.1	1.508	P53811	Phosphatidylinositol transfer protein beta isoform	1.48
P01831	Thy-1 membrane glycoprotein	1.508	O88737	Protein bassoon	1.477
Q9CQ75	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	1.508	Q3TT11	Putative uncharacterized protein	1.472
P0C192	Leucine-rich repeat-containing protein 4B	1.507	Q3UHW2	Putative uncharacterized protein	1.472
Q8K394	Inactive phospholipase C-like protein 2	1.502	P51660	Peroxisomal multifunctional enzyme type 2	1.472
Q8CGP0	Histone H2B type 3-B	1.5	Q6IRU5	Clathrin light chain B	1.471
Q9D2U9	Histone H2B type 3-A	1.5	P62264	40S ribosomal protein S14	1.468
Q64524	Histone H2B type 2-E	1.5	O70569	Ribosomal protein S14	1.468
Q9QYG0	Protein NDRG2	1.499	E9PZ41	Trafficking protein particle complex subunit 9	1.465
V9GX43	CUGBP Elav-like family member 2 (Fragment)	1.497	E9Q3T8	Trafficking protein particle complex subunit 9	1.465
Q8K1M3	Protein kinase, cAMP dependent regulatory, type II alpha	1.494	Q3U0M1	Trafficking protein particle complex subunit 9	1.465
Q3TWB8	Putative uncharacterized protein	1.492	Q8BGT8	Phytanoyl-CoA hydroxylase-interacting protein-like	1.464
E9PZ69	Transmembrane 9 superfamily member 2	1.492	Q9WV34	MAGUK p55 subfamily member 2	1.455
Q8C7F9	Putative uncharacterized protein	1.492	Q8QZY9	Splicing factor 3B subunit 4	1.454
P58021	Transmembrane 9 superfamily member 2	1.492	Q8BIF2	RNA binding protein fox-1 homolog 3	1.449
Q8C6H4	Putative uncharacterized protein	1.492	Q3UVX5	Metabotropic glutamate receptor 5	1.444
Q3V2C6	Putative uncharacterized protein	1.489	E9QMC2	Metabotropic glutamate receptor 5	1.444
P31001	Desmin	1.489	Q9R0N5	Synaptotagmin-5	1.442
Q8BPH1	Putative uncharacterized protein	1.487	D3YXH0	Immunoglobulin superfamily member 5	1.441
P62259	14-3-3 protein epsilon	1.487	P63054	Purkinje cell protein 4	1.441
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	1.482	Q78IK2	Up-regulated during skeletal muscle growth protein 5	1.44

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	1.438	Q91XV3	Brain acid soluble protein 1	1.42
Q8R1P3	Gpm6a protein	1.438	Q7TSJ2	Microtubule-associated protein 6	1.416
P35802	Neuronal membrane glycoprotein M6-a	1.438	Q8R429	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	1.415
Q3U8W4	Superoxide dismutase	1.436	F8WIE5	E3 ubiquitin-protein ligase HECTD1	1.409
P09671	Superoxide dismutase [Mn], mitochondrial	1.436	Q3TDT0	Tripartite motif-containing protein 3	1.408
Q91W50	Cold shock domain-containing protein E1	1.434	Q9R1R2	Tripartite motif-containing protein 3	1.408
Q3TGI6	Putative uncharacterized protein (Fragment)	1.429	Q9QXV0	ProSAAS	1.403
Q3UE53	Putative uncharacterized protein	1.429	G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a	1.401
P53810	Phosphatidylinositol transfer protein alpha isoform	1.429	Q8K3H0	DCC-interacting protein 13-alpha	1.396
Q8C522	Endonuclease domain-containing 1 protein	1.428	Q8BU33	Acetolactate synthase-like protein	1.396
Q69ZY2	MKIAA0830 protein (Fragment)	1.428	Q6PE15	Mycophenolic acid acyl-glucuronide esterase, mitochondrial	1.393
A2APM1	CD44 antigen	1.423	P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	1.39
E9QKM8	CD44 antigen	1.423	P62748	Hippocalcin-like protein 1	1.388
P15379	CD44 antigen	1.423	Q8BNA5	Putative uncharacterized protein	1.386
Q80X37	CD44 antigen	1.423	Q921L6	Cortactin, isoform CRA_a	1.386
Q3U8S1	CD44 antigen	1.423	Q60598	Src substrate cortactin	1.386
Q3TLT9	Putative uncharacterized protein	1.423	Q4V9X9	Rpl23a protein (Fragment)	1.386
A2APM5	CD44 antigen	1.423	Q91YK6	Rpl23a protein (Fragment)	1.386
A2APM2	CD44 antigen	1.423	P62751	60S ribosomal protein L23a	1.386
Q3U468	Putative uncharacterized protein	1.423	Q9ERD7	Tubulin beta-3 chain	1.384
Q3UNN2	Putative uncharacterized protein	1.423	Q3TIQ2	Putative uncharacterized protein	1.383
A2APM4	CD44 antigen	1.423	P35979	60S ribosomal protein L12	1.383
A2APM3	CD44 antigen	1.423	Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	1.382

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q9D2R0	Acetoacetyl-CoA synthetase	1.382	Q920W8	Fau protein (Fragment)	1.328
Q569Z6	Thyroid hormone receptor-associated protein 3	1.378	Q642K5	40S ribosomal protein S30	1.328
P62983	Ubiquitin-40S ribosomal protein S27a	1.377	Q91V99	Fau protein (Fragment)	1.328
Q9D1D4	Transmembrane emp24 domain-containing protein 10	1.373	P62862	40S ribosomal protein S30	1.328
Q9WVQ1	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2	1.373	Q8BGZ1	Hippocalcin-like protein 4	1.327
D3Z1M3	Malectin	1.371	Q3TA13	Putative uncharacterized protein	1.327
Q6ZQI3	Malectin	1.371	E9Q3E2	Synaptopodin	1.327
Q3U5K7	Putative uncharacterized protein (Fragment)	1.37	Q3URF1	MCG6023	1.327
P21460	Cystatin-C	1.37	Q3TY32	Putative uncharacterized protein (Fragment)	1.327
Q9EPX9	Cystatin C	1.37	Q3U336	Putative uncharacterized protein	1.327
G3UWG1	MCG115977	1.367	Q8CC35	Synaptopodin	1.327
P62897	Cytochrome c, somatic	1.367	Q6P5H2	Nestin	1.327
Q9CRB9	MICOS complex subunit Mic19	1.361	Q9CZP6	Putative uncharacterized protein	1.32
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	1.358	P62908	40S ribosomal protein S3	1.32
Q5D0A4	Stx1a protein (Fragment)	1.356	F8VQJ3	Laminin subunit gamma-1	1.318
O35526	Syntaxin-1A	1.356	Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial	1.315
P63318	Protein kinase C gamma type	1.352	Q8R1F1	Niban-like protein 1	1.313
P14602	Heat shock protein beta-1	1.348	Q3UXQ6	40S ribosomal protein S4	1.31
Q9CVB6	Actin-related protein 2/3 complex subunit 2	1.345	Q545F8	40S ribosomal protein S4	1.31
Q5XJY5	Coatomer subunit delta	1.344	P62702	40S ribosomal protein S4, X isoform	1.31
Q91YP2	Neurolysin, mitochondrial	1.332	Q9Z2D6	Methyl-CpG-binding protein 2	1.309
P97315	Cysteine and glycine-rich protein 1	1.328	Q3TAJ7	Putative uncharacterized protein (Fragment)	1.309
Q3THB2	Putative uncharacterized protein	1.328	Q920R0	Alsin	1.309

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
P51885	Lumican	1.305	Q5SQB0	Nucleophosmin	1.277
Q5EBG5	Ribosomal protein L7A	1.304	Q61937	Nucleophosmin	1.277
P12970	60S ribosomal protein L7a	1.304	Q5U438	Nucleophosmin 1	1.277
Q80UT7	Rpl7a protein (Fragment)	1.304	D3Z0B9	Aldehyde dehydrogenase family 16 member A1	1.276
Q6P1A9	Ribosomal protein L7A	1.304	Q571I9	Aldehyde dehydrogenase family 16 member A1	1.276
Q6PDM2	Serine/arginine-rich splicing factor 1	1.3	B2RWE8	Eif4b protein	1.274
H7BX95	Serine/arginine-rich-splicing factor 1	1.3	Q3TSY9	Putative uncharacterized protein	1.274
E6Y2W6	Coiled-coil domain-containing protein 136	1.295	Q3TDD8	Putative uncharacterized protein	1.274
D3Z165	Coiled-coil domain-containing protein 136	1.295	Q3UGC0	Putative uncharacterized protein	1.274
E6Y2W7	Coiled-coil domain-containing protein 136	1.295	Q8BGD9	Eukaryotic translation initiation factor 4B	1.274
Q3TVA9	Coiled-coil domain-containing protein 136	1.295	Q3THB0	Putative uncharacterized protein	1.274
E9QP94	Coiled-coil domain-containing protein 136	1.295	P17426	AP-2 complex subunit alpha-1	1.264
B1AZ46	Brain-specific angiogenesis inhibitor 1-associated protein 2	1.292	Q3UIB5	Putative uncharacterized protein	1.259
Q8BKX1	Brain-specific angiogenesis inhibitor 1-associated protein 2	1.292	Q99LB2	Dehydrogenase/reductase SDR family member 4	1.259
Q3UKP6	Putative uncharacterized protein	1.292	Q8K215	LYR motif-containing protein 4	1.258
P70202	Latexin	1.292	Q569Z5	Probable ATP-dependent RNA helicase DDX46	1.256
Q9CPY7	Cytosol aminopeptidase	1.282	Q3TUA8	Putative uncharacterized protein	1.253
O70310	Glycylpeptide N-tetradecanoyltransferase 1	1.282	Q6NZM8	3~-phosphoadenosine 5~-phosphosulfate synthase 1, isoform CRA_a	1.253
A7UQY4	Putative uncharacterized protein	1.278	Q60967	Bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 1	1.253
G8JL68	Myelin expression factor 2 (Fragment)	1.278	Q3UDM0	MOB kinase activator 1B	1.248
Q8C854	Myelin expression factor 2	1.278	Q921Y0	MOB kinase activator 1A	1.248
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta	1.278	Q8BPB0	MOB kinase activator 1B	1.248
Q3U536	Putative uncharacterized protein	1.277	Q3U741	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a	1.247

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q501J6	Probable ATP-dependent RNA helicase DDX17	1.247	B8JK32	Heterogeneous nuclear ribonucleoprotein M	1.237
P14733	Lamin-B1	1.245	Q570Z0	MKIAA4193 protein (Fragment)	1.237
A0A0A0MQA5	Tubulin alpha-4A chain (Fragment)	1.243	Q3TL61	Putative uncharacterized protein	1.237
P68368	Tubulin alpha-4A chain	1.243	Q8BRQ9	Sideroflexin-5	1.236
Q3V2R3	Beta-chimaerin	1.242	Q925N0	Sideroflexin-5	1.236
D3YYH0	PEX5-related protein	1.241	Q9JIS5	Synaptic vesicle glycoprotein 2A	1.235
F8SLQ1	Peroxisomal biogenesis factor 5-like protein transcript variant 6	1.241	Q6NZM3	Dctn1 protein	1.23
Q8C437	PEX5-related protein	1.241	O08788	Dynactin subunit 1	1.23
F8SLP9	PEX5-related protein	1.241	E9Q3M3	Dynactin subunit 1	1.23
F8SLP5	Peroxisomal biogenesis factor 5-like protein transcript variant 1	1.241	O35215	D-dopachrome decarboxylase	1.23
F8SLP8	Peroxin 2, isoform CRA_d	1.241	P99027	60S acidic ribosomal protein P2	1.229
F8SLP6	Peroxisomal biogenesis factor 5-like protein transcript variant 2	1.241	Q80X90	Filamin-B	1.225
F8SLQ4	Peroxisomal biogenesis factor 5-like protein transcript variant 10	1.241	Q3UE40	Putative uncharacterized protein	1.225
F8SLQ5	Peroxisomal biogenesis factor 5-like protein transcript variant 11	1.241	P27601	Guanine nucleotide-binding protein subunit alpha-13	1.225
F8SLQ3	PEX5-related protein	1.241	S4R255	Nitric oxide synthase	1.225
F8SLP7	Peroxisomal biogenesis factor 5-like protein transcript variant 3	1.241	Q9Z0J4	Nitric oxide synthase, brain	1.225
Q5M9L9	40S ribosomal protein S8	1.24	F8WGF2	Nitric oxide synthase, brain	1.225
P62242	40S ribosomal protein S8	1.24	Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1	1.22
Q3UZT7	Putative uncharacterized protein	1.238	Q9CWI9	Putative uncharacterized protein	1.219
Q02248	Catenin beta-1	1.238	P62267	40S ribosomal protein S23	1.219
Q3THB3	Putative uncharacterized protein	1.237	Q9CZI5	Putative uncharacterized protein	1.219
B8JK33	Heterogeneous nuclear ribonucleoprotein M	1.237	Q497E1	Ribosomal protein S23	1.219
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	1.237	Q91YM4	Protein TBRG4	1.217

Supplementary Table 1 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q3TI62	Putative uncharacterized protein	1.209	P80317	T-complex protein 1 subunit zeta	1.209
Q52KG9	Chaperonin containing Tcp1, subunit 6a (Zeta)	1.209	Q3TJ43	Vacuolar protein sorting-associated protein 35	1.207
Q3TIX8	Putative uncharacterized protein	1.209	Q9EQH3	Vacuolar protein sorting-associated protein 35	1.207

The comparison was performed in the spinal cord between a pre-onset SOD1 G93A mouse and an age-matched WT mouse, where the fold > 1.2 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 464 significantly up regulated proteins in the spinal cord between a pre-onset SOD1 G93A mouse vs an age-matched WT mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 2. List of Significantly Down Regulated Proteins in Spinal Cord between a Pre-onset SOD1 G93A Mouse Vs an Age-Matched WT Mouse

Accession No	Description	Fold Change (Pre-onset)
P31725	Protein S100-A9	0.431
Q5M8M3	Uncharacterized protein	0.445
Q9DCG9	Multifunctional methyltransferase subunit TRM112-like protein	0.445
Q8VCR4	0610038D11Rik protein	0.445
D3YX85	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	0.453
Q6A074	MKIAA0400 protein (Fragment)	0.453
Q3TS63	Putative uncharacterized protein (Fragment)	0.453
Q7SIG6	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	0.453
Q3UH05	Putative uncharacterized protein	0.453
E9PX52	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	0.453
Q3UH27	Putative uncharacterized protein	0.453
F6TQW2	Protein Ighg2c	0.476
P01864	Ig gamma-2A chain C region secreted form	0.476
Q9D8L4	Putative uncharacterized protein	0.476
Q58E56	Igh protein	0.476
Q3TIX9	U4/U6.U5 tri-snRNP-associated protein 2	0.494
Q3TCN2	Putative phospholipase B-like 2	0.497
Q62148	Retinal dehydrogenase 2	0.504
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	0.523
A2AG50	MAP7 domain-containing protein 2	0.525
Q3U6C5	Voltage-gated potassium channel subunit beta-1	0.526
Q9D5E9	Voltage-gated potassium channel subunit beta-1	0.526
P63143	Voltage-gated potassium channel subunit beta-1	0.526
A0A075DCA9	NADH-ubiquinone oxidoreductase chain 1	0.53
P03888	NADH-ubiquinone oxidoreductase chain 1	0.53
Q3TNL9	NADH-ubiquinone oxidoreductase chain 1 (Fragment)	0.53
G3EB90	NADH-ubiquinone oxidoreductase chain 1	0.53
F8VQ05	Protein Fryl	0.532
Q3UFY7	7-methylguanosine phosphate-specific 5~-nucleotidase	0.533
D3YYQ4	Carbonic anhydrase 1 (Fragment)	0.534
P13634	Carbonic anhydrase 1	0.534
Q8K097	Protein lifeguard 2	0.536
Q3UHW5	Putative uncharacterized protein	0.537
P55258	Ras-related protein Rab-8A	0.537
Q3U3Q7	Putative uncharacterized protein	0.538
Q8K233	Ace protein (Fragment)	0.538
P09470	Angiotensin-converting enzyme	0.538
Q5XK22	Ace protein (Fragment)	0.538
F6QCP8	Angiotensin-converting enzyme (Fragment)	0.538
Q3U3J9	Putative uncharacterized protein (Fragment)	0.54
Q80VQ0	Aldehyde dehydrogenase family 3 member B1	0.54
P50543	Protein S100-A11	0.542
B9EJA2	Cortactin-binding protein 2	0.542
Q8BXY4	Putative uncharacterized protein	0.548
P53994	Ras-related protein Rab-2A	0.548
Q5SRA0	Disintegrin and metalloproteinase domain-containing protein 23	0.552

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q9R1V7	Disintegrin and metalloproteinase domain-containing protein 23	0.552	Q6P1Y9	Exocyst complex component 1	0.594
Q5SVE1	Disintegrin and metalloproteinase domain-containing protein 23	0.552	Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	0.595
Q80ZX8	Sperm-associated antigen 1	0.552	Q50DZ7	LGI2B brain-derived splice form	0.595
Q3UFS0	Protein zyg-11 homolog B	0.557	Q3UG80	Putative uncharacterized protein	0.596
Q8BG40	Katanin p80 WD40 repeat-containing subunit B1	0.56	Q8CFS5	Vps18 protein	0.596
Q9EQX4	Allograft inflammatory factor 1-like	0.564	Q8R307	Vacuolar protein sorting-associated protein 18 homolog	0.596
Q9D4H1	Exocyst complex component 2	0.565	Q8BLK7	Putative uncharacterized protein	0.596
G3X9K3	Brefeldin A-inhibited guanine nucleotide-exchange protein 1	0.565	Q69ZI9	MKIAA1475 protein (Fragment)	0.596
Q3U4W5	RAB6, member RAS oncogene family, isoform CRA_c	0.567	Q3TU36	Putative uncharacterized protein	0.599
O35864	COP9 signalosome complex subunit 5	0.568	Q9JLC8	Sacsin	0.6
Q61646	Haptoglobin	0.569	E9QNY8	Sacsin	0.6
Q8BQX9	Putative uncharacterized protein	0.572	O35744	Chitinase-like protein 3	0.604
Q8C7S9	Putative uncharacterized protein	0.572	Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	0.614
Q8VD73	Potassium voltage-gated channel, shaker-related subfamily, beta member 3	0.572	Q0GNC1	Inverted formin-2	0.616
P97382	Voltage-gated potassium channel subunit beta-3	0.572	E9QLA5	Inverted formin-2	0.616
Q3TJB4	Putative uncharacterized protein	0.578	B1ATU4	COP9 signalosome complex subunit 1	0.616
Q3U3C4	Putative uncharacterized protein	0.578	Q99LD4	COP9 signalosome complex subunit 1	0.616
Q62419	Endophilin-A2	0.578	G3UXW9	COP9 signalosome complex subunit 1	0.616
G3X9A7	MCG49978	0.584	Q3MIA8	COP9 signalosome complex subunit 1	0.616
Q8BLJ3	PI-PLC X domain-containing protein 3	0.584	Q3TMH2	Secernin-3	0.617
Q3SXD3	HD domain-containing protein 2	0.588	Q3UUI3	Acyl-coenzyme A thioesterase THEM4	0.623
Q99M31	Heat shock 70 kDa protein 14	0.591	Q61081	Hsp90 co-chaperone Cdc37	0.624
Q8BLE7	Vesicular glutamate transporter 2	0.594	Q3TES0	IQ motif and SEC7 domain-containing protein 3	0.624

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q3UHJ6	Putative uncharacterized protein	0.624	A0A068WAZ7	Protein 4.1R (Fragment)	0.639
P45591	Cofilin-2	0.625	Q3UH12	Putative uncharacterized protein (Fragment)	0.639
Q3TST0	Putative uncharacterized protein	0.626	B6ZHC8	Erythrocyte protein band 4.1	0.639
Q8K1R3	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	0.626	A2AD32	Protein 4.1 (Fragment)	0.639
Q8BTG3	T-complex protein 11-like protein 1	0.627	A2A839	Protein 4.1	0.639
P62631	Elongation factor 1-alpha 2	0.628	Q8BIG7	Catechol O-methyltransferase domain-containing protein 1	0.64
Q8BHW2	Protein OSCP1	0.63	Q8BU21	Glutaminyl-tRNA synthetase, isoform CRA_a	0.641
Q3TWN8	Putative uncharacterized protein	0.633	Q3TN94	Putative uncharacterized protein	0.641
Q9Z110	Delta-1-pyrroline-5-carboxylate synthase	0.633	Q8BML9	Glutaminyl-tRNA synthetase	0.641
Q9JI78	Peptide-N(4)-(N-acetyl-beta-glucosaminyl)asparagine amidase	0.633	E9Q6L9	Leucine-rich repeat-containing protein 7	0.642
Q8BNU0	Armadillo repeat-containing protein 6	0.634	Q80TE7	Leucine-rich repeat-containing protein 7	0.642
A0PJL3	Sarm1 protein (Fragment)	0.636	A3KGU5	Spectrin alpha chain, non-erythrocytic 1	0.644
Q6PDS3	Sterile alpha and TIR motif-containing protein 1	0.636	Q99J77	N-acetylneuraminic acid synthase (Sialic acid synthase)	0.645
Q69ZK9	Neuroligin-2	0.637	Q8R151	NFX1-type zinc finger-containing protein 1	0.647
D3YYT1	Putative oxidoreductase GLYR1	0.638	Q9CPT3	N-acylneuraminate-9-phosphatase	0.648
Q922P9	Putative oxidoreductase GLYR1	0.638	B2RU82	Solute carrier family 30 (Zinc transporter), member 9	0.65
A0A068WAQ5	Protein 4.1R (Fragment)	0.639	F8WHL1	Zinc transporter 9	0.65
A2A838	Protein 4.1 (Fragment)	0.639	Q5IRJ6	Zinc transporter 9	0.65
A2A841	Protein 4.1	0.639	Q7TND9	Dihydrolipoamide branched chain transacylase E2	0.65
P48193	Protein 4.1	0.639	P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	0.65
A2A842	Protein 4.1	0.639	Q7TNL5	Protein phosphatase 2, regulatory subunit B (B56), delta isoform, isoform CRA_a	0.652

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q99PC9	Protein phosphatase 2 regulatory subunit B56 delta isoform	0.652	D3Z634	Latrophilin-3	0.661
Q91V89	Protein Ppp2r5d	0.652	D3Z6H7	Latrophilin-3	0.661
Q8K5D8	Protein phosphatase 2a regulatory b56-delta subunit (Fragment)	0.652	D3YU23	Latrophilin-3	0.661
P62830	60S ribosomal protein L23	0.652	D3Z3G4	Latrophilin-3	0.661
P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	0.653	D3Z4V0	Latrophilin-3	0.661
Q6PGG8	Tdrkh protein	0.654	D3Z5M6	Latrophilin-3	0.661
Q80VL1	Tudor and KH domain-containing protein	0.654	K3W4M8	Latrophilin-3	0.661
Q8BW41	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	0.654	D3Z6J2	Latrophilin-3	0.661
P16406	Glutamyl aminopeptidase	0.658	D3Z4S7	Latrophilin-3	0.661
Q3TBT0	Putative uncharacterized protein (Fragment)	0.658	D3YWB1	Latrophilin-3	0.661
F6YBY4	Integrin alpha-M (Fragment)	0.658	D3Z6H9	Latrophilin-3	0.661
Q3TD86	Putative uncharacterized protein	0.658	D3Z593	Latrophilin-3	0.661
Q3U3F0	Putative uncharacterized protein	0.658	D3YVT9	Latrophilin-3	0.661
E9Q5K8	Integrin alpha-M	0.658	D3YWR3	Latrophilin-3	0.661
P05555	Integrin alpha-M	0.658	P18894	D-amino-acid oxidase	0.668
Q3U1W4	Putative uncharacterized protein (Fragment)	0.658	Q9Z0R4	Intersectin-1	0.669
Q3U1U4	Integrin alpha-M	0.658	E9Q0N0	Intersectin-1	0.669
G5E8F1	Integrin alpha M, isoform CRA_a	0.658	Q8R0F8	Acylpyruvase FAHD1, mitochondrial	0.67
E9Q604	Integrin alpha-M	0.658	Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	0.67
Q3U4I5	Putative uncharacterized protein	0.658	Q3UVI9	Putative uncharacterized protein	0.671
D3YTW7	Latrophilin-3	0.661	Q99LE6	ATP-binding cassette sub-family F member 2	0.671
Q80TS3	Latrophilin-3	0.661	Q8CAQ8	MICOS complex subunit Mic60	0.676
D3Z3X6	Latrophilin-3	0.661	Q6A065	Centrosomal protein of 170 kDa	0.676

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
H7BX26	Centrosomal protein of 170 kDa	0.676	P33173	Kinesin-like protein KIF1A	0.688
P57722	Poly(rC)-binding protein 3	0.679	E9QAN4	Kinesin-like protein	0.688
Q3TQC7	Ectonucleoside triphosphate diphosphohydrolase 5	0.679	Q8BNU3	Putative uncharacterized protein	0.689
Q9WUZ9	Ectonucleoside triphosphate diphosphohydrolase 5	0.679	P50608	Fibromodulin	0.689
A3KGU7	Spectrin alpha chain, non-erythrocytic 1	0.68	Q80UW2	F-box only protein 2	0.692
B9EKJ1	Spna2 protein	0.68	P59325	Eukaryotic translation initiation factor 5	0.694
B2RXX6	Spna2 protein	0.68	Q0KL02	Triple functional domain protein	0.697
Q99JB8	Protein kinase C and casein kinase II substrate protein 3	0.682	Q80U19	Disheveled-associated activator of morphogenesis 2	0.699
Q3UGN9	Signal transducing adapter molecule 1	0.685	Q3T9P2	Putative uncharacterized protein	0.701
P70297	Signal transducing adapter molecule 1	0.685	O09172	Glutamate--cysteine ligase regulatory subunit	0.701
Q3UMC8	Putative uncharacterized protein	0.685	Q3UXP2	Putative uncharacterized protein	0.702
Q3TUQ5	Pinin	0.685	Q9WTM5	RuvB-like 2	0.702
Q9CV89	Putative uncharacterized protein (Fragment)	0.685	Q9CTY5	Calcium uptake protein 3, mitochondrial	0.702
O35691	Pinin	0.685	P97952	Sodium channel subunit beta-1	0.704
A2ADY9	Protein DDI1 homolog 2	0.686	Q9Z1Q2	Abhydrolase domain-containing protein 16A	0.706
Q8C6E0	Cilia- and flagella-associated protein 36	0.686	Q9D5T0	ATPase family AAA domain-containing protein 1	0.706
Q99JR9	Coiled-coil domain containing 104	0.686	Q7TMY2	Acyl-Coenzyme A dehydrogenase, short/branched chain	0.708
A0A087WQE8	Kinesin-like protein	0.688	Q9DBL1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	0.708
Q3UH16	Kinesin-like protein	0.688	B2RXR2	Phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	0.71
Q6P5H4	Kinesin-like protein	0.688	B2RY05	Pik3r4 protein	0.71
E9Q9G6	Kinesin-like protein	0.688	Q8VD65	Phosphoinositide 3-kinase regulatory subunit 4	0.71
G3UW47	Kinesin-like protein	0.688	F7C9N6	MMS19 nucleotide excision repair protein homolog (Fragment)	0.711
Q6TA13	Kinesin-like protein	0.688	Q9D071	MMS19 nucleotide excision repair protein homolog	0.711

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q9ESM3	Hyaluronan and proteoglycan link protein 2	0.714	P47941	Crk-like protein	0.73
O35344	Importin subunit alpha-4	0.715	Q8CHT1	Ephexin-1	0.73
Q9DB74	Phospholipase A2, group VII (Platelet-activating factor acetylhydrolase, plasma), isoform CRA_b	0.718	E9QK62	Ephexin-1	0.73
Q60963	Platelet-activating factor acetylhydrolase	0.718	P54731	FAS-associated factor 1	0.73
P56389	Cytidine deaminase	0.72	Q3TJT1	Putative uncharacterized protein	0.732
Q8VDQ1	Prostaglandin reductase 2	0.722	Q8CCB4	Vacuolar protein sorting-associated protein 53 homolog	0.732
Q80TB8	Synaptic vesicle membrane protein VAT-1 homolog-like	0.723	Q3TLZ3	Putative uncharacterized protein	0.732
A0A075B6D7	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A	0.723	Q3TX19	Putative uncharacterized protein	0.732
V9GXL7	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A (Fragment)	0.723	Q3UDN2	Putative uncharacterized protein	0.732
A0PJC0	Inpp5j protein (Fragment)	0.723	Q921S7	39S ribosomal protein L37, mitochondrial	0.735
Q3TBW1	Putative uncharacterized protein	0.723	Q5SQX6	Cytoplasmic FMR1-interacting protein 2	0.736
P59644	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A	0.723	Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	0.737
Q8C129	Leucyl-cystinyl aminopeptidase	0.725	Q3TGQ3	Putative uncharacterized protein	0.738
Q80WM4	Hyaluronan and proteoglycan link protein 4	0.726	P26231	Catenin alpha-1	0.738
Q3UEW2	Putative uncharacterized protein	0.727	Q9D4H8	Cullin-2	0.74
Q9WV69	Dematin	0.727	Q571A2	MKIAA4106 protein (Fragment)	0.74
Q8C1E4	Putative uncharacterized protein	0.728	Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	0.74
Q01405	Protein transport protein Sec23A	0.728	A0A087WQS2	Basic leucine zipper and W2 domain-containing protein 1	0.74
E9Q1S3	Protein transport protein Sec23A	0.728	Q9CQC6	Basic leucine zipper and W2 domain-containing protein 1	0.74
Q7TMI0	Psmd11 protein (Fragment)	0.729	D3YTP3	Protein Mtx3	0.742
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	0.729	Q8BTA2	Putative uncharacterized protein	0.744
Q8BK73	Putative uncharacterized protein	0.729	Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	0.744

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
P35235	Tyrosine-protein phosphatase non-receptor type 11	0.744	Q8BUV3	Gephyrin	0.757
Q3TMN1	Methionine aminopeptidase 2	0.744	Q3UIA5	Putative uncharacterized protein	0.757
Q3UI33	Methionine aminopeptidase 2	0.744	Q9WTX6	Cullin-1	0.757
O08663	Methionine aminopeptidase 2	0.744	Q4VA53	Sister chromatid cohesion protein PDS5 homolog B	0.757
Q7TMB8	Cytoplasmic FMR1-interacting protein 1	0.748	F8WHU5	Sister chromatid cohesion protein PDS5 homolog B	0.757
Q8CAA7	Glucose 1,6-bisphosphate synthase	0.749	Q8C140	Putative uncharacterized protein	0.758
Q03517	Secretogranin-2	0.749	Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	0.758
D3YVX4	Stromal membrane-associated protein 1	0.749	Q8CIE6	Coatomer subunit alpha	0.76
Q91VZ6	Stromal membrane-associated protein 1	0.749	Q8BTF0	Coatomer subunit alpha	0.76
O35409	Glutamate carboxypeptidase 2	0.75	F8WHL2	Coatomer subunit alpha	0.76
F8VPQ4	SLIT-ROBO Rho GTPase-activating protein 3	0.75	Q3US29	Putative uncharacterized protein	0.76
Q812A2	SLIT-ROBO Rho GTPase-activating protein 3	0.75	Q5M8R9	Farnesyl diphosphate synthetase	0.76
E9QN14	SLIT-ROBO Rho GTPase-activating protein 3	0.75	Q920E5	Farnesyl pyrophosphate synthase	0.76
Q9EPK7	Exportin-7	0.75	Q7TSQ8	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	0.76
E9PUW7	Exportin-7	0.75	B1AX58	Plastin-3	0.762
Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	0.751	Q3UDD5	Putative uncharacterized protein	0.762
Q8C076	Putative uncharacterized protein	0.752	Q99KK7	Dipeptidyl peptidase 3	0.762
P59016	Vacuolar protein sorting-associated protein 33B	0.752	Q3UDF3	Putative uncharacterized protein	0.762
P17563	Selenium-binding protein 1	0.754	Q6NXZ0	Dipeptidylpeptidase 3	0.762
O35685	Nuclear migration protein nudC	0.755	Q3UDQ7	Putative uncharacterized protein	0.765
A3KN68	Protein tyrosine phosphatase, receptor type, N polypeptide 2	0.756	Q8JZQ2	AFG3-like protein 2	0.765
P80560	Receptor-type tyrosine-protein phosphatase N2	0.756	P07759	Serine protease inhibitor A3K	0.766
A0JNY3	Gephyrin	0.757	Q61768	Kinesin-1 heavy chain	0.769

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q06138	Calcium-binding protein 39	0.769	Q3UJL7	Putative uncharacterized protein	0.785
Q9WU63	Heme-binding protein 2	0.771	Q64674	Spermidine synthase	0.785
Q4VBD2	Transmembrane anterior posterior transformation protein 1	0.771	Q8BSZ8	Putative uncharacterized protein	0.785
Q9CQV8	14-3-3 protein beta/alpha	0.772	Q9JLN9	Serine/threonine-protein kinase mTOR	0.787
Q3U1J4	DNA damage-binding protein 1	0.772	Q3TDD9	Protein phosphatase 1 regulatory subunit 21	0.789
Q9DD05	Delta-aminolevulinic acid dehydratase	0.773	P23591	GDP-L-fucose synthase	0.789
P10518	Delta-aminolevulinic acid dehydratase	0.773	D3Z0M6	Cytoplasmic dynein 1 intermediate chain 1	0.79
Q80ZI6	E3 ubiquitin-protein ligase LRSAM1	0.773	O88485	Cytoplasmic dynein 1 intermediate chain 1	0.79
Q6ZQ84	MKIAA0617 protein (Fragment)	0.774	Q3V1R3	Putative uncharacterized protein	0.79
Q9JLV5	Cullin-3	0.774	Q8K406	Leucine-rich repeat LGI family member 3	0.79
Q3TL79	Putative uncharacterized protein	0.774	P49442	Inositol polyphosphate 1-phosphatase	0.79
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	0.774	Q6ZWY7	Putative uncharacterized protein (Fragment)	0.791
Q9DB16	Calcium-binding protein 39-like	0.776	Q9WU28	Prefoldin subunit 5	0.791
A0A087WQF7	Zinc transporter ZIP10 (Fragment)	0.777	A2AGR0	MAP kinase-activating death domain protein	0.796
A0A087WRC8	Zinc transporter ZIP10 (Fragment)	0.777	Q80U28	MAP kinase-activating death domain protein	0.796
Q6P5F6	Zinc transporter ZIP10	0.777	A1L2Z3	C230096C10Rik protein	0.797
D3YUP9	Disintegrin and metalloproteinase domain-containing protein 22	0.778	Q8C7X2	ER membrane protein complex subunit 1	0.797
Q9R1V6	Disintegrin and metalloproteinase domain-containing protein 22	0.778	P51410	60S ribosomal protein L9	0.797
A4FUT9	Adam22 protein (Fragment)	0.778	P68404	Protein kinase C beta type	0.799
Q9JHU9	Inositol-3-phosphate synthase 1	0.78	Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	0.8
Q5EBJ4	Ermin	0.781	P62746	Rho-related GTP-binding protein RhoB	0.8
P16332	Methylmalonyl-CoA mutase, mitochondrial	0.783	H3BK65	Epidermal growth factor receptor substrate 15	0.8
D3YVV3	Protein Ankrd29	0.784	P42567	Epidermal growth factor receptor substrate 15	0.8

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q5JC28	Epidermal growth factor receptor pathway substrate 15 isoform B	0.8	A0A087WRE8	CLIP-associating protein 1	0.812
P28650	Adenylosuccinate synthetase isozyme 1	0.801	A0A087WQ31	CLIP-associating protein 1	0.812
Q9D6J5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	0.802	A0A087WQ95	CLIP-associating protein 1	0.812
B7ZCL8	55 kDa erythrocyte membrane protein	0.804	A5D6Q8	Clasp1 protein	0.812
Q684Q6	Membrane protein, palmitoylated (Fragment)	0.804	D3YWG2	Chitinase domain-containing protein 1 (Fragment)	0.812
P70290	55 kDa erythrocyte membrane protein	0.804	Q922Q9	Chitinase domain-containing protein 1	0.812
Q3TUI9	Proteasome subunit alpha type	0.805	Q9CRU8	Putative uncharacterized protein (Fragment)	0.812
Q9Z2U1	Proteasome subunit alpha type-5	0.805	G8JL55	Chitinase domain-containing protein 1 (Fragment)	0.812
Q3TUX3	Proteasome subunit alpha type	0.805	Q5F258	ARF GTPase-activating protein GIT1	0.815
P55264	Adenosine kinase	0.805	Q68FF6	ARF GTPase-activating protein GIT1	0.815
A2AJH3	Glycylpeptide N-tetradecanoyltransferase	0.805	Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	0.816
O70311	Glycylpeptide N-tetradecanoyltransferase 2	0.805	Q9WTQ5	A-kinase anchor protein 12	0.818
Q8CFK1	Glycylpeptide N-tetradecanoyltransferase	0.805	Q9WU78	Programmed cell death 6-interacting protein	0.82
Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	0.806	Q80Y09	Pdcd6ip protein	0.82
Q9JME5	AP-3 complex subunit beta-2	0.806	Q9DBL7	Bifunctional coenzyme A synthase	0.82
Q9CYT6	Adenylyl cyclase-associated protein 2	0.806	A2AN08	E3 ubiquitin-protein ligase UBR4	0.821
Q9DC63	F-box only protein 3	0.81	A6H5Z3	Exocyst complex component 6B	0.821
Q8BUR4	Dedicator of cytokinesis protein 1	0.81	Q9DBF1	Alpha-aminoadipic semialdehyde dehydrogenase	0.822
Q9D394	Protein RUFY3	0.812	Q9Z1L5	Voltage-dependent calcium channel subunit alpha-2/delta-3	0.822
A0A087WP42	CLIP-associating protein 1	0.812	Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	0.823
A0A087WRK0	CLIP-associating protein 1	0.812	Q05D14	Clmn protein (Fragment)	0.823
J3QP81	CLIP-associating protein 1	0.812	Q8C5W0	Calmin	0.823
A0A087WNW8	CLIP-associating protein 1	0.812	B9EJ15	Calmin	0.823

Supplementary Table 2 (Continued)

Accession No	Description	Fold Change (Pre-onset)	Accession No	Description	Fold Change (Pre-onset)
Q3TPI3	Putative uncharacterized protein (Fragment)	0.824	Q3UKT3	Putative uncharacterized protein	0.828
Q9ESN6	Tripartite motif-containing protein 2	0.824	P29758	Ornithine aminotransferase, mitochondrial	0.828
Q3UHH4	Tripartite motif-containing protein 2	0.824	Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	0.828
E9QKC6	Tripartite motif-containing protein 2	0.824	B0V2P5	DmX-like protein 2	0.832
Q3URK9	Putative uncharacterized protein	0.824	Q8BPN8	DmX-like protein 2	0.832
E9PX29	Protein Sptbn4	0.825	P60766	Cell division control protein 42 homolog	0.833
P48036	Annexin A5	0.826			

The comparison was performed in the spinal cord between a pre-onset SOD1 G93A mouse and an age-matched WT mouse, where the fold < 0.833 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 421 significantly down regulated proteins in the spinal cord between a pre-onset SOD1 G93A mouse vs an age-matched WT mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 3. List of Significantly Up Regulated Proteins in the Spinal Cord between an Onset SOD1 G93A Mouse Vs an Age-Matched WT Mouse

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3TXB1	Putative uncharacterized protein	3.97	A2APM5	CD44 antigen	2.425
Q3UBX7	Putative uncharacterized protein	3.97	A2APM2	CD44 antigen	2.425
P98086	Complement C1q subcomponent subunit A	3.97	Q3U468	Putative uncharacterized protein	2.425
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a	3.505	Q3UNN2	Putative uncharacterized protein	2.425
P14602	Heat shock protein beta-1	3.471	A2APM4	CD44 antigen	2.425
P51910	Apolipoprotein D	3.145	A2APM3	CD44 antigen	2.425
Q6GQT1	Alpha-2-macroglobulin-P	3.09	Q3UHD1	Brain-specific angiogenesis inhibitor 1	2.312
Q3TWH2	Putative uncharacterized protein	3.006	M0QWA7	Integrin beta	2.279
Q61941	NAD(P) transhydrogenase, mitochondrial	3.006	P11835	Integrin beta-2	2.279
Q8C1W8	Nicotinamide nucleotide transhydrogenase, isoform CRA_a	3.006	Q542I8	Integrin beta	2.279
Q922E1	Nicotinamide nucleotide transhydrogenase	3.006	Q3UW40	Putative uncharacterized protein	2.272
Q8R422	CD109 antigen	2.831	Q8BP67	60S ribosomal protein L24	2.272
E9Q3H6	Protein Coq10a	2.734	Q9DAW9	Calponin-3	2.261
Q3V471	Galectin (Fragment)	2.723	Q9JKY7	Cytochrome P450 CYP2D22	2.193
Q8C253	Galectin	2.723	Q91W87	Cytochrome P450, family 2, subfamily d, polypeptide 22	2.193
P16110	Galectin-3	2.723	Q3UBS0	Putative uncharacterized protein	2.162
Q3TVU9	Putative uncharacterized protein	2.707	P08226	Apolipoprotein E	2.162
Q99L04	Dehydrogenase/reductase SDR family member 1	2.707	Q4FK40	Apoe protein	2.162
O88492	Perilipin-4	2.627	Q6GTX3	Apoe protein	2.162
A2APM1	CD44 antigen	2.425	Q5NDA4	Fatty acid binding protein 7, brain	2.154
E9QKM8	CD44 antigen	2.425	P51880	Fatty acid-binding protein, brain	2.154
P15379	CD44 antigen	2.425	B1B1A8	Myosin light chain kinase, smooth muscle	2.128
Q80X37	CD44 antigen	2.425	Q6PDN3	Myosin light chain kinase, smooth muscle	2.128
Q3U8S1	CD44 antigen	2.425	P15209	BDNF/NT-3 growth factors receptor	2.117
Q3TLT9	Putative uncharacterized protein	2.425	P05977	Myosin light chain 1/3, skeletal muscle isoform	2.115

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q06890	Clusterin	2.054	Q3TG58	Williams-Beuren syndrome chromosome region 1 homolog (Human), isoform CRA_b	1.81
Q3TWD0	Putative uncharacterized protein	2.008	Q3V244	Putative uncharacterized protein	1.81
Q3U7P0	Putative uncharacterized protein	2.008	Q8BRV5	Uncharacterized protein KIAA1671	1.796
P18242	Cathepsin D	2.008	P70232	Neural cell adhesion molecule L1-like protein	1.793
Q8C243	Putative uncharacterized protein	2.008	Q3ULL6	Protein Upf3b	1.782
Q3TWR6	Putative uncharacterized protein	2.008	F6Q8N5	Protein Upf3b (Fragment)	1.782
Q3U8W5	Putative uncharacterized protein	2.008	Q9CS15	Putative uncharacterized protein (Fragment)	1.782
B2RWQ7	Arsb protein	2	Q80UI8	Upf3b protein (Fragment)	1.782
P50429	Arylsulfatase B	2	Q80WS3	rRNA/tRNA 2~-O-methyltransferase fibrillarin-like protein 1	1.777
B2RXS4	Plexin-B2	1.954	Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	1.77
Q6P5H2	Nestin	1.948	O88990	Alpha-actinin-3	1.75
P70202	Latexin	1.936	Q3TVS6	Putative uncharacterized protein	1.747
P97457	Myosin regulatory light chain 2, skeletal muscle isoform	1.922	P10605	Cathepsin B	1.747
Q8R429	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	1.92	Q6GSS7	Histone H2A type 2-A	1.746
O09114	Prostaglandin-H2 D-isomerase	1.907	Q64523	Histone H2A type 2-C	1.746
P20060	Beta-hexosaminidase subunit beta	1.895	F8WIX8	Histone H2A	1.746
Q91V36	Nuclear receptor-binding protein 2	1.886	Q9CZT8	Ras-related protein Rab-3B	1.735
Q8QZY9	Splicing factor 3B subunit 4	1.82	P60867	40S ribosomal protein S20	1.733
J3QP71	Basigin (Fragment)	1.815	Q3TX26	Putative uncharacterized protein	1.732
O55108	Basigin (Fragment)	1.815	P97822	Acidic leucine-rich nuclear phosphoprotein 32 family member E	1.732
K3W4Q8	Basigin	1.815	E9PZF5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)	1.732
O55107	Basigin (Fragment)	1.815	E9Q5H2	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)	1.732
P18572	Basigin	1.815	E9Q3T0	Uncharacterized protein	1.728
Q9WUK2	Eukaryotic translation initiation factor 4H	1.81	P47955	60S acidic ribosomal protein P1	1.728
Q80U88	MKIAA0038 protein (Fragment)	1.81	Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	1.72

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q99L69	Branched chain ketoacid dehydrogenase E1, alpha polypeptide	1.72	P97352	Protein S100-A13	1.579
P26645	Myristoylated alanine-rich C-kinase substrate	1.707	B2ZRS5	DEP domain-containing mTOR-interacting protein	1.561
Q8BGU5	Cyclin-Y	1.7	B2ZRS7	Depdc6-003	1.561
P68134	Actin, alpha skeletal muscle	1.69	B2ZRS8	Depdc6-003	1.561
Q91X72	Hemopexin	1.685	B2ZRS6	Depdc6-002	1.561
Q3TFK4	Annexin	1.683	Q570Y9	DEP domain-containing mTOR-interacting protein	1.561
Q8C1X9	Annexin	1.683	Q3U7M5	Abhydrolase domain-containing protein 4	1.555
Q3U737	Annexin	1.683	Q8VD66	Abhydrolase domain-containing protein 4	1.555
O35639	Annexin A3	1.683	Q8C0M2	Abhydrolase domain-containing protein 4	1.555
Q3TLP8	RAS-related C3 botulinum substrate 1, isoform CRA_a	1.655	Q61503	5~-nucleotidase	1.555
Q8BPG5	Putative uncharacterized protein	1.655	Q3TZQ2	Putative uncharacterized protein	1.554
P63001	Ras-related C3 botulinum toxin substrate 1	1.655	P26041	Moesin	1.554
Q9D859	Putative uncharacterized protein	1.655	Q3T9U9	Putative uncharacterized protein	1.554
Q8C4N8	Putative uncharacterized protein (Fragment)	1.655	P27659	60S ribosomal protein L3	1.554
Q3UDM0	MOB kinase activator 1B	1.645	Q3UB15	Putative uncharacterized protein	1.554
Q921Y0	MOB kinase activator 1A	1.645	Q3UB67	Putative uncharacterized protein	1.554
Q8BPB0	MOB kinase activator 1B	1.645	Q3U9L3	Putative uncharacterized protein	1.554
P01027	Complement C3	1.63	Q3UB90	Putative uncharacterized protein	1.554
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	1.618	A0JLV3	Histone H2B (Fragment)	1.549
Q99KI3	ER membrane protein complex subunit 3	1.607	Q8CGP2	Histone H2B type 1-P	1.549
G3X8X7	Vacuolar protein sorting 16 (Yeast)	1.592	Q64475	Histone H2B type 1-B	1.549
Q8BWV2	Putative uncharacterized protein	1.592	Q921L4	Histone H2B	1.549
Q920Q4	Vacuolar protein sorting-associated protein 16 homolog	1.592	Q8CBB6	Histone H2B	1.549
Q80ZW2	Protein THEM6	1.587	P10853	Histone H2B type 1-F/J/L	1.549
A0A0A0MQ90	Protein S100-A13	1.579	Q6ZWY9	Histone H2B type 1-C/E/G	1.549

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q8CGP1	Histone H2B type 1-K	1.549	Q3TXM3	Amino acid transporter	1.486
Q64525	Histone H2B type 2-B	1.549	O35544	Excitatory amino acid transporter 4	1.486
P10854	Histone H2B type 1-M	1.549	D3YVC1	40S ribosomal protein S2 (Fragment)	1.483
Q64478	Histone H2B type 1-H	1.549	D3YWJ3	40S ribosomal protein S2	1.483
Q00915	Retinol-binding protein 1	1.548	Q3TXS9	Putative uncharacterized protein	1.483
Q3UEI6	Putative uncharacterized protein	1.534	Q9DC49	Putative uncharacterized protein	1.483
Q3UJK2	Putative uncharacterized protein	1.534	P25444	40S ribosomal protein S2	1.483
Q3UMP4	Putative uncharacterized protein	1.534	Q3UB36	Putative uncharacterized protein	1.483
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	1.534	E9Q1N8	Uncharacterized protein	1.483
Q3V274	Putative uncharacterized protein	1.534	P55088	Aquaporin-4	1.481
Q3TIP8	Putative uncharacterized protein	1.53	Q8VHK5	Membrane protein MLC1	1.48
Q9Z1Q5	Chloride intracellular channel protein 1	1.53	Q80U92	MKIAA0027 protein (Fragment)	1.48
Q5BKS2	Protein phosphatase 1B, magnesium dependent, beta isoform	1.505	E9QP87	Membrane protein MLC1	1.48
P36993	Protein phosphatase 1B	1.505	Q8BLR0	Putative uncharacterized protein	1.48
Q99NF7	Ppm1b protein	1.505	Q62000	Mimecan	1.479
D3Z2Y6	Protein S100a16 (Fragment)	1.505	Q80WJ7	Protein LYRIC	1.472
Q3TVE3	Putative uncharacterized protein	1.505	Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	1.47
Q9D708	Protein S100a16	1.505	A2A547	Ribosomal protein L19	1.467
A2AWT5	Nucleolar transcription factor 1	1.504	P84099	60S ribosomal protein L19	1.467
P25976	Nucleolar transcription factor 1	1.504	Q3UAC2	40S ribosomal protein S3a	1.457
A2AWT7	Nucleolar transcription factor 1	1.504	P97351	40S ribosomal protein S3a	1.457
Q9DBH1	Putative uncharacterized protein	1.504	Q9D1S3	40S ribosomal protein S3a	1.457
A2AWT6	Nucleolar transcription factor 1	1.504	Q6ZWZ6	40S ribosomal protein S12	1.455
B2RQ18	Peptidyl-prolyl cis-trans isomerase	1.49	Q2UY11	Collagen alpha-1(XXVIII) chain	1.448
Q6P9Q6	FK506-binding protein 15	1.49	Q9Z268	RasGAP-activating-like protein 1	1.442

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q9CPY7	Cytosol aminopeptidase	1.44	Q3TCP5	Putative uncharacterized protein	1.405
Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial	1.44	Q3UXR4	Putative uncharacterized protein	1.405
Q9QYG0	Protein NDRG2	1.437	P26040	Ezrin	1.405
Q9DBS1	Transmembrane protein 43	1.437	Q3UL48	Putative uncharacterized protein	1.405
Q8K010	5-oxoprolinase	1.433	Q91VM1	V-crk sarcoma virus CT10 oncogene homolog (Avian)	1.405
F6YB25	Regulation of nuclear pre-mRNA domain-containing protein 1B (Fragment)	1.427	Q64010	Adapter molecule crk	1.405
Q9CSU0	Regulation of nuclear pre-mRNA domain-containing protein 1B	1.427	P50543	Protein S100-A11	1.404
F8VQK3	Protein Gucy1a2	1.423	Q3TMX5	Arginine-rich, mutated in early stage tumors, isoform CRA_b	1.404
Q6P9S0	MTSS1-like protein	1.422	Q80ZP8	Armet protein	1.404
Q3THX5	Putative uncharacterized protein	1.42	A8C1V1	Putative uncharacterized protein (Fragment)	1.404
E9Q3X0	Major vault protein	1.42	Q9D6G9	CKLF-like MARVEL transmembrane domain-containing protein 5	1.402
Q3TVJ0	Putative uncharacterized protein	1.419	Q45TP8	Chemokine-like factor super family five variant 4	1.402
Q9D1Q3	Putative uncharacterized protein	1.419	A2AEG6	Glycoprotein m6b, isoform CRA_g	1.401
Q3UCT9	Putative uncharacterized protein	1.419	P35803	Neuronal membrane glycoprotein M6-b	1.401
O89051	Integral membrane protein 2B	1.419	Q3US81	Glycoprotein m6b, isoform CRA_f	1.401
B7FAU9	Filamin, alpha	1.417	Q3UF30	Putative uncharacterized protein	1.401
Q8BTM8	Filamin-A	1.417	P08207	Protein S100-A10	1.401
Q3UZE7	Catalase	1.412	Q61166	Microtubule-associated protein RP/EB family member 1	1.4
P24270	Catalase	1.412	Q3V1E0	Putative uncharacterized protein	1.4
Q8C6E3	Catalase	1.412	P52800	Ephrin-B2	1.4
Q60972	Histone-binding protein RBBP4	1.409	F6RSU6	Ephrin-B2 (Fragment)	1.4
Q6PEV0	Ephx1 protein	1.409	Q6ZQK2	MKIAA0051 protein (Fragment)	1.398
Q9D379	Epoxide hydrolase 1	1.409	Q9JKF1	Ras GTPase-activating-like protein IQGAP1	1.398
E9PWK1	Epoxide hydrolase 1	1.409	Q80UW7	IQ motif containing GTPase activating protein 1	1.398
Q8K2W5	Epoxide hydrolase 1, microsomal	1.409	Q3TWE1	Putative uncharacterized protein	1.394

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q9CZU7	Putative uncharacterized protein	1.394	Q9CZK0	Putative uncharacterized protein (Fragment)	1.368
Q8C876	Putative uncharacterized protein	1.394	Q91VH2	Sorting nexin-9	1.368
Q3UIW3	Putative uncharacterized protein	1.394	P57780	Alpha-actinin-4	1.362
P17047	Lysosome-associated membrane glycoprotein 2	1.394	Q7TMB8	Cytoplasmic FMR1-interacting protein 1	1.362
Q8C5K0	Lysosomal membrane glycoprotein 2, isoform CRA_a	1.394	P32020	Non-specific lipid-transfer protein	1.362
Q8BH58	TIP41-like protein	1.394	Q3TG93	Putative uncharacterized protein	1.359
Q8BH69	Selenide, water dikinase 1	1.392	Q8BTU4	Putative uncharacterized protein	1.359
Q8BL02	Putative uncharacterized protein (Fragment)	1.392	P32067	Lupus La protein homolog	1.359
O35295	Transcriptional activator protein Pur-beta	1.391	Q3ULN8	Putative uncharacterized protein (Fragment)	1.357
Q3TYF5	Serine/threonine-protein phosphatase (Fragment)	1.381	Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	1.357
Q3U8W0	Putative uncharacterized protein	1.381	Q3U0D9	E3 ubiquitin-protein ligase HACE1	1.355
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	1.381	H9KV09	E3 ubiquitin-protein ligase HACE1 (Fragment)	1.355
Q91VF2	Histamine N-methyltransferase	1.379	H9KV10	E3 ubiquitin-protein ligase HACE1 (Fragment)	1.355
Q5SX39	Myosin-4	1.378	A4GE64	Alpha-T-catenin	1.353
Q3TIF8	40S ribosomal protein S24	1.377	Q65CL1	Catenin alpha-3	1.353
Q9CQK2	40S ribosomal protein S24	1.377	Q14DP5	Catenin (Cadherin associated protein), alpha 3	1.353
Q9D7P1	40S ribosomal protein S24	1.377	Q9CR57	60S ribosomal protein L14	1.35
Q9CY61	40S ribosomal protein S24	1.377	Q9CWK0	Putative uncharacterized protein	1.35
P62849	40S ribosomal protein S24	1.377	G5E850	Cytochrome b-5, isoform CRA_a	1.348
Q91YP2	Neurolysin, mitochondrial	1.372	P56395	Cytochrome b5	1.348
F8VQA4	Peptidyl-glycine alpha-amidating monooxygenase	1.37	Q9WVA4	Transgelin-2	1.346
E9Q704	Peptidyl-glycine alpha-amidating monooxygenase	1.37	Q80X90	Filamin-B	1.343
Q8BQ31	Putative uncharacterized protein (Fragment)	1.37	Q3TJN6	Putative uncharacterized protein	1.342
P97467	Peptidyl-glycine alpha-amidating monooxygenase	1.37	Q9D8U8	Sorting nexin-5	1.342
Q3TZU7	Sorting nexin	1.368	Q8C5E7	Putative uncharacterized protein	1.342

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
E9Q1T1	Calcium/calmodulin-dependent protein kinase type II subunit delta	1.335	Q8C052	Microtubule-associated protein 1S	1.297
E9Q1V9	Calcium/calmodulin-dependent protein kinase type II subunit delta	1.335	Q6NS54	Na(+)/H(+) exchange regulatory cofactor NHE-RF	1.292
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	1.331	Q9JHL1	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	1.292
P28474	Alcohol dehydrogenase class-3	1.329	Q3TGI6	Putative uncharacterized protein (Fragment)	1.29
Q99PU5	Long-chain-fatty-acid--CoA ligase ACSBG1	1.327	Q3UE53	Putative uncharacterized protein	1.29
Q3UA32	Polypeptide N-acetylgalactosaminyltransferase (Fragment)	1.326	P53810	Phosphatidylinositol transfer protein alpha isoform	1.29
Q3UM52	Polypeptide N-acetylgalactosaminyltransferase (Fragment)	1.326	Q5F258	ARF GTPase-activating protein GIT1	1.289
Q6PB93	Polypeptide N-acetylgalactosaminyltransferase 2	1.326	Q68FF6	ARF GTPase-activating protein GIT1	1.289
P82198	Transforming growth factor-beta-induced protein ig-h3	1.325	Q9CQI6	Coactosin-like protein	1.286
Q3UYR3	Putative uncharacterized protein (Fragment)	1.318	Q62351	Transferrin receptor protein 1	1.286
Q08024	Core-binding factor subunit beta	1.318	Q8VCV3	ADP-ribosylation factor-like 6	1.285
Q920Y3	Glial cell line derived neurotrophic factor family receptor alpha 2	1.317	O88848	ADP-ribosylation factor-like protein 6	1.285
O08842	GDNF family receptor alpha-2	1.317	P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.284
Q3UJ44	Putative uncharacterized protein	1.313	Q02788	Collagen alpha-2(VI) chain	1.281
Q99LB4	Capping protein (Actin filament), gelsolin-like	1.313	Q3UNC0	Putative uncharacterized protein (Fragment)	1.276
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	1.31	Q922H4	Mannose-1-phosphate guanyltransferase alpha	1.276
P62983	Ubiquitin-40S ribosomal protein S27a	1.31	Q3U9P0	Putative uncharacterized protein	1.275
Q5D0A4	Stx1a protein (Fragment)	1.306	P63325	40S ribosomal protein S10	1.275
O35526	Syntaxin-1A	1.306	Q3UXQ6	40S ribosomal protein S4	1.275
Q4VA93	Protein kinase C	1.305	Q545F8	40S ribosomal protein S4	1.275
D3YYT0	Cadherin-2	1.298	P62702	40S ribosomal protein S4, X isoform	1.275
P15116	Cadherin-2	1.298	Q3TYK4	Putative uncharacterized protein	1.274
Q8BSI9	Putative uncharacterized protein	1.298	Q8C3Z4	Putative uncharacterized protein	1.274
Q3UIC2	Putative uncharacterized protein	1.298	Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	1.274
P54923	[Protein ADP-ribosylarginine] hydrolase	1.297	Q3TI99	L-lactate dehydrogenase	1.272

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
G5E8N5	L-lactate dehydrogenase	1.272	A0A0A0MQN4	Ubiquitin-like modifier-activating enzyme ATG7	1.247
P06151	L-lactate dehydrogenase A chain	1.272	Q3TAB9	Putative uncharacterized protein	1.247
Q3TFP8	Putative uncharacterized protein	1.272	Q9D906	Ubiquitin-like modifier-activating enzyme ATG7	1.247
Q3TH84	Putative uncharacterized protein	1.272	Q3TM87	Putative uncharacterized protein	1.247
O55022	Membrane-associated progesterone receptor component 1	1.272	S4R2D5	Ubiquitin-like modifier-activating enzyme ATG7	1.247
Q62348	Translin	1.271	Q9R1Q8	Transgelin-3	1.243
Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	1.269	Q3TE95	Putative uncharacterized protein	1.243
Q8R5J9	PRA1 family protein 3	1.268	Q8BP92	Reticulocalbin-2	1.243
Q3TEX8	Ubiquitin carboxyl-terminal hydrolase	1.268	Q3TW82	Beta-glucuronidase	1.243
P35123	Ubiquitin carboxyl-terminal hydrolase 4	1.268	P12265	Beta-glucuronidase	1.243
Q921M8	Ubiquitin carboxyl-terminal hydrolase	1.268	Q3TH46	Putative uncharacterized protein (Fragment)	1.241
Q3V1Q3	Adenylate cyclase type 2	1.267	Q3U111	Putative uncharacterized protein (Fragment)	1.241
Q80TL1	Adenylate cyclase type 2	1.267	P26043	Radixin	1.241
Q810U4	Neuronal cell adhesion molecule	1.266	Q60829	Protein phosphatase 1 regulatory subunit 1B	1.241
Q9CQE1	Protein NipSnap homolog 3B	1.265	B1ATI0	Aldehyde dehydrogenase	1.238
P48678	Prelamin-A/C	1.264	Q99PH3	Aldehyde dehydrogenase	1.238
Q8BMK4	Cytoskeleton-associated protein 4	1.262	Q3U7B5	Aldehyde dehydrogenase	1.238
Q3UHJ2	Dystrobrevin	1.262	P47740	Fatty aldehyde dehydrogenase	1.238
I6L9D6	Dystrobrevin	1.262	Q8C5J1	Aldehyde dehydrogenase	1.238
Q8CFR5	Dystrobrevin	1.262	Q8BQ93	Aldehyde dehydrogenase	1.238
Q3UHP1	Dystrobrevin	1.262	B1AV77	Aldehyde dehydrogenase	1.238
Q9D2N4	Dystrobrevin alpha	1.262	Q99PH4	Aldehyde dehydrogenase	1.238
Q9D8E6	60S ribosomal protein L4	1.257	Q8C3C9	Aldehyde dehydrogenase	1.238
Q3TFD9	Putative uncharacterized protein	1.255	Q3THQ0	Beta-hexosaminidase	1.236
O08600	Endonuclease G, mitochondrial	1.249	Q3U936	Beta-hexosaminidase	1.236

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3TXV7	Beta-hexosaminidase	1.236	Q8BM29	Putative uncharacterized protein (Fragment)	1.23
Q3TW10	Beta-hexosaminidase	1.236	Q05DT0	Add3 protein (Fragment)	1.23
Q3TKF6	Beta-hexosaminidase	1.236	Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	1.229
Q8BNS6	Beta-hexosaminidase	1.236	Q8VC94	Rpl11 protein	1.228
Q3TVI2	Beta-hexosaminidase	1.236	E9PYL9	Uncharacterized protein	1.228
Q3UCP6	Beta-hexosaminidase	1.236	Q9CXW4	60S ribosomal protein L11	1.228
P29416	Beta-hexosaminidase subunit alpha	1.236	E9PZB3	Protein Gm5093	1.228
B9EHJ3	Tight junction protein ZO-1	1.235	Q5FWB6	MCG17387, isoform CRA_a	1.227
P39447	Tight junction protein ZO-1	1.235	Q6GQT9	Nodal modulator 1	1.223
Q9WVA3	Mitotic checkpoint protein BUB3	1.235	Q99LR1	Monoacylglycerol lipase ABHD12	1.221
P24369	Peptidyl-prolyl cis-trans isomerase B	1.232	E9QMK2	Versican core protein	1.215
F8WGR0	Alpha-adducin	1.231	Q62059	Versican core protein	1.215
F8WHZ9	Alpha-adducin	1.231	E9PYH0	Versican core protein	1.215
Q9QYC0	Alpha-adducin	1.231	E9Q035	Protein Gm20425	1.215
Q8K232	Adducin 1 (Alpha)	1.231	Q3TGQ3	Putative uncharacterized protein	1.215
A0A087WR50	Fibronectin	1.231	P26231	Catenin alpha-1	1.215
A0A087WS56	Fibronectin	1.231	Q63810	Calcineurin subunit B type 1	1.215
Q3UHL6	Fibronectin	1.231	Q3TCT9	Putative uncharacterized protein	1.212
Q3UGY5	Putative uncharacterized protein	1.231	P35278	Ras-related protein Rab-5C	1.212
Q3UH17	Putative uncharacterized protein	1.231	Q8K0Z7	Translational activator of cytochrome c oxidase 1	1.211
Q3UHR1	Putative uncharacterized protein (Fragment)	1.231	Q3TF72	Protein disulfide-isomerase	1.208
P11276	Fibronectin	1.231	Q3TIM0	Protein disulfide-isomerase	1.208
Q3UNK1	Putative uncharacterized protein	1.23	Q3THC3	Protein disulfide-isomerase	1.208
Q05C56	Add3 protein (Fragment)	1.23	Q3UDR2	Protein disulfide-isomerase (Fragment)	1.208
Q9QYB5	Gamma-adducin	1.23	Q3URP6	Protein disulfide-isomerase	1.208

Supplementary Table 3 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P09103	Protein disulfide-isomerase	1.208	Q8CD23	Putative uncharacterized protein	1.206
Q3TWE3	Protein disulfide-isomerase	1.208	Q8BNS0	Putative uncharacterized protein	1.203
Q3TL52	Putative uncharacterized protein	1.206	Q8CHR8	Developmentally regulated GTP binding protein 1	1.203
P09405	Nucleolin	1.206	P32233	Developmentally-regulated GTP-binding protein 1	1.203

The comparison was performed in the spinal cord between an onset SOD1 G93A mouse and an age-matched WT mouse, where the fold > 1.2 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 458 significantly up regulated proteins in the spinal cord between an onset SOD1 G93A mouse vs an age-matched WT mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 4. List of Significantly Down Regulated Proteins in the Spinal Cord between an Onset SOD1 G93A Mouse Vs an Age-Matched WT Mouse

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P27573	Myelin protein P0	0.103	Q8BGD5	Carnitine O-palmitoyltransferase 1, brain isoform	0.572
A8DUK4	Beta-globin	0.227	Q1HL23	SorCS1a	0.578
A8DUK7	Beta-globin	0.227	E9PYT6	VPS10 domain-containing receptor SorCS1	0.578
Q9EQX4	Allograft inflammatory factor 1-like	0.405	E9QQ02	VPS10 domain-containing receptor SorCS1	0.578
A2AP78	High mobility group protein B3 (Fragment)	0.417	Q1HL25	SorCS1b	0.578
O54879	High mobility group protein B3	0.417	Q8BSV0	Putative uncharacterized protein	0.578
G5E920	MCG114640	0.417	Q1HL24	SorCS1c	0.578
Q3KQQ4	Serpina1a protein	0.474	Q9JLC4	VPS10 domain-containing receptor SorCS1	0.578
P22599	Alpha-1-antitrypsin 1-2	0.474	E9QQ63	VPS10 domain-containing receptor SorCS1	0.578
Q3TU64	Putative uncharacterized protein	0.486	Q3TCN2	Putative phospholipase B-like 2	0.58
Q01149	Collagen alpha-2(I) chain	0.486	Q8R357	Noelin	0.605
Q8BW41	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	0.491	O88998	Noelin	0.605
Q64676	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	0.507	A2A860	WW domain binding protein 2, isoform CRA_a	0.607
D3Z600	Peroxisomal targeting signal 1 receptor	0.511	P97765	WW domain-binding protein 2	0.607
O09012	Peroxisomal targeting signal 1 receptor	0.511	Q9DBP6	Putative uncharacterized protein	0.607
P31725	Protein S100-A9	0.519	Q3TRG5	Putative uncharacterized protein	0.607
Q3U3I1	Putative uncharacterized protein	0.53	Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	0.608
Q64444	Carbonic anhydrase 4	0.53	Q8K0C9	GDP-mannose 4,6 dehydratase	0.61
A2ADY9	Protein DDI1 homolog 2	0.536	Q62148	Retinal dehydrogenase 2	0.617
Q8CAV6	Protein kinase C theta type	0.558	Q3TDM2	Putative uncharacterized protein	0.62
Q02111	Protein kinase C theta type	0.558	Q3UH04	Putative uncharacterized protein	0.62
Q6XE40	MAGUK p55 subfamily member 3	0.564	Q8BW96	Calcium/calmodulin-dependent protein kinase type 1D	0.62
P07759	Serine protease inhibitor A3K	0.568	Q3U3J9	Putative uncharacterized protein (Fragment)	0.62

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q80VQ0	Aldehyde dehydrogenase family 3 member B1	0.62	Q8BHC1	Ras-related protein Rab-39B	0.649
Q6PCX2	Transporter	0.621	Q71RI9	Kynurenine--oxoglutarate transaminase 3	0.651
P31648	Sodium- and chloride-dependent GABA transporter 1	0.621	Q3UIA5	Putative uncharacterized protein	0.654
Q91W92	Cdc42 effector protein 1	0.625	Q9WTX6	Cullin-1	0.654
Q8BU88	39S ribosomal protein L22, mitochondrial	0.632	Q8BGH4	Receptor expression-enhancing protein 1	0.655
Q8C281	Putative uncharacterized protein	0.637	Q8VE70	Programmed cell death protein 10	0.657
Q8CE80	Calpastatin	0.637	F8WI55	Programmed cell death protein 10	0.657
Q921U7	Cast protein	0.637	Q8R2H9	Phosphoethanolamine/phosphocholine phosphatase	0.66
P51125	Calpastatin	0.637	Q3TFP0	Serine/arginine-rich-splicing factor 10	0.665
Q8CE04	Putative uncharacterized protein	0.637	Q3UA07	Putative uncharacterized protein	0.665
A2VDH5	Gnal1 protein (Fragment)	0.643	Q3UDH7	Putative uncharacterized protein	0.665
P36916	Guanine nucleotide-binding protein-like 1	0.643	Q3UYX6	Putative uncharacterized protein	0.665
Q52KE3	Gnal1 protein (Fragment)	0.643	Q9R0U0	Serine/arginine-rich splicing factor 10	0.665
Q3TQ86	Putative uncharacterized protein (Fragment)	0.645	B2KGR2	LanC-like protein 1 (Fragment)	0.675
B9EKC0	Magi1 protein	0.645	O89112	LanC-like protein 1	0.675
Q6RHR9	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	0.645	Q8VEH5	EPM2A-interacting protein 1	0.679
Q4H4B4	MAGI1c	0.645	E9Q706	Adenylate cyclase type 9	0.679
Q5DTM1	MKIAA4129 protein (Fragment)	0.645	P51830	Adenylate cyclase type 9	0.679
Q4H4B5	MAGI1a	0.645	Q3USC7	Ganglioside-induced differentiation-associated protein 1-like 1	0.682
E9PZ12	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	0.645	Q8VE33	Ganglioside-induced differentiation-associated protein 1-like 1	0.682
Q99K46	Ubiquitin carboxyl-terminal hydrolase 11	0.646	O35744	Chitinase-like protein 3	0.682
Q9QXS6	Drebrin	0.648	Q9JL26	Formin-like protein 1	0.683
Q99PL6	UBX domain-containing protein 6	0.648	A0PJL3	Sarm1 protein (Fragment)	0.684

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q6PDS3	Sterile alpha and TIR motif-containing protein 1	0.684	Q8R555	Cartilage acidic protein 1	0.696
A3KG00	Ephrin type-B receptor 2	0.685	Q3UHB1	5~-nucleotidase domain-containing protein 3	0.697
Q6P5F1	Ephb2 protein (Fragment)	0.685	Q8R0F8	Acylpyruvase FAHD1, mitochondrial	0.702
P54763	Ephrin type-B receptor 2	0.685	Q9DC51	Guanine nucleotide-binding protein G(k) subunit alpha	0.703
A3KG01	Eph receptor B2	0.685	Q3TH64	Putative uncharacterized protein	0.704
A3KG02	Ephrin type-B receptor 2	0.685	Q3TN44	Putative uncharacterized protein	0.704
Q3US29	Putative uncharacterized protein	0.686	Q9CQX2	Cytochrome b5 type B	0.704
Q5M8R9	Farnesyl diphosphate synthetase	0.686	Q3UZP4	Small VCP/p97-interacting protein	0.704
Q920E5	Farnesyl pyrophosphate synthase	0.686	Q6P5E8	Diacylglycerol kinase theta	0.707
Q9JMF3	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-13	0.686	Q80UW2	F-box only protein 2	0.708
Q8CC13	Putative uncharacterized protein	0.687	Q3U7K4	Putative uncharacterized protein (Fragment)	0.708
B7ZWF1	Ddx3x protein	0.687	Q8BH86	UPF0317 protein C14orf159 homolog, mitochondrial	0.708
Q62167	ATP-dependent RNA helicase DDX3X	0.687	E9QMK9	Protein 9030617O03Rik	0.708
B9EKE9	Ddx3x protein	0.687	P62631	Elongation factor 1-alpha 2	0.709
Q6NVG1	Lysophospholipid acyltransferase LPCAT4	0.687	Q3TKJ1	Branched-chain-amino-acid aminotransferase	0.709
Q8BXY4	Putative uncharacterized protein	0.688	P24288	Branched-chain-amino-acid aminotransferase, cytosolic	0.709
P53994	Ras-related protein Rab-2A	0.688	Q8CBC8	Branched-chain-amino-acid aminotransferase	0.709
Q04899	Cyclin-dependent kinase 18	0.689	Q9CXX6	Branched-chain-amino-acid aminotransferase	0.709
Q9JLC8	Sacsin	0.691	E9Q4K3	Branched-chain-amino-acid aminotransferase	0.709
E9QNY8	Sacsin	0.691	Q8BNY6	Neuronal calcium sensor 1	0.709
Q8R4V2	Dual specificity protein phosphatase 15	0.696	Q8CC88	von Willebrand factor A domain-containing protein 8	0.712
D3YXR8	RIMS-binding protein 2	0.696	Q8BTG7	Protein NDRG4	0.712
Q80U40	RIMS-binding protein 2	0.696	Q5SRX1	TOM1-like protein 2	0.713

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q9QY42	Prosaposin receptor GPR37	0.714	Q8C3W1	Uncharacterized protein C1orf198 homolog	0.724
Q8BLE7	Vesicular glutamate transporter 2	0.715	D3YWX2	YLP motif-containing protein 1	0.725
Q99JB2	Stomatin-like protein 2, mitochondrial	0.717	Q80XK6	Autophagy-related protein 2 homolog B	0.726
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	0.717	Q3THW7	Eukaryotic translation initiation factor 3 subunit H	0.726
P56389	Cytidine deaminase	0.717	Q91WK2	Eukaryotic translation initiation factor 3 subunit H	0.726
Q9JLN9	Serine/threonine-protein kinase mTOR	0.718	Q3TIK5	Eukaryotic translation initiation factor 3 subunit H	0.726
D3YUS7	Hydroxyacylglutathione hydrolase-like protein (Fragment)	0.718	Q3TII2	Eukaryotic translation initiation factor 3 subunit H	0.726
Q9DB32	Hydroxyacylglutathione hydrolase-like protein	0.718	Q8BTX5	Eukaryotic translation initiation factor 3 subunit H	0.726
P46414	Cyclin-dependent kinase inhibitor 1B	0.718	Q3UHE7	Kinesin-like protein	0.727
Q3UDD5	Putative uncharacterized protein	0.719	E9Q0J5	Kinesin-like protein	0.727
Q99KK7	Dipeptidyl peptidase 3	0.719	Q9QXL2	Kinesin-like protein KIF21A	0.727
Q3UDF3	Putative uncharacterized protein	0.719	F8WGN6	Kinesin-like protein	0.727
Q6NXZ0	Dipeptidylpeptidase 3	0.719	D3YU89	Citron Rho-interacting kinase	0.727
P70206	Plexin-A1	0.719	D3Z1U0	Citron Rho-interacting kinase	0.727
A2AHM4	Phosphatase and actin regulator	0.719	E9QL53	Citron Rho-interacting kinase	0.727
Q8BYK5	Phosphatase and actin regulator 3	0.719	F6SBR5	Citron Rho-interacting kinase (Fragment)	0.727
Q6KCA9	Phosphatase and actin regulator	0.719	P49025	Citron Rho-interacting kinase	0.727
Q5DTG6	Phosphatase and actin regulator (Fragment)	0.719	Q6A099	MKIAA0248 protein (Fragment)	0.729
Q7TNL5	Protein phosphatase 2, regulatory subunit B (B56), delta isoform, isoform CRA_a	0.72	Q6DFZ1	Golgi-specific brefeldin A-resistance factor 1	0.729
Q99PC9	Protein phosphatase 2 regulatory subunit B56 delta isoform	0.72	A3QM89	Reticulon (Fragment)	0.73
Q91V89	Protein Ppp2r5d	0.72	Q7M6W1	Reticulon	0.73
Q8K5D8	Protein phosphatase 2a regulatory b56-delta subunit (Fragment)	0.72	D3Z5P0	Serine/threonine-protein kinase BRSK1	0.731
Q99JB8	Protein kinase C and casein kinase II substrate protein 3	0.724	Q5RJI5	Serine/threonine-protein kinase BRSK1	0.731

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q5M8M3	Uncharacterized protein	0.731	Q8BTG3	T-complex protein 11-like protein 1	0.752
Q9DCG9	Multifunctional methyltransferase subunit TRM112-like protein	0.731	A2RSH4	Sv2c protein	0.755
Q8VCR4	0610038D11Rik protein	0.731	Q3UVQ0	Putative uncharacterized protein (Fragment)	0.755
Q80YV4	Pantothenate kinase 4	0.732	Q69ZS6	Synaptic vesicle glycoprotein 2C	0.755
Q9QZD8	Mitochondrial dicarboxylate carrier	0.734	Q9D154	Leukocyte elastase inhibitor A	0.758
Q8BU21	Glutaminyl-tRNA synthetase, isoform CRA_a	0.739	Q3UI39	Putative uncharacterized protein	0.76
Q3TN94	Putative uncharacterized protein	0.739	E9QLK9	Clathrin coat assembly protein AP180	0.76
Q8BML9	Glutaminyl-tRNA synthetase	0.739	E9Q9A3	Clathrin coat assembly protein AP180	0.76
Q9JJ59	ATP-binding cassette sub-family B member 9	0.743	Q61548	Clathrin coat assembly protein AP180	0.76
A2AJI0	MAP7 domain-containing protein 1	0.746	E9QQ05	Clathrin coat assembly protein AP180	0.76
A8Y5P4	MAP7 domain-containing protein 1	0.746	Q3U4W8	Ubiquitin carboxyl-terminal hydrolase	0.761
A2AJI1	MAP7 domain-containing protein 1	0.746	P56399	Ubiquitin carboxyl-terminal hydrolase 5	0.761
Q99JW2	Aminoacylase-1	0.747	Q6PCP5	Mitochondrial fission factor	0.763
Q3UH60	Disco-interacting protein 2 homolog B	0.75	Q9ESM3	Hyaluronan and proteoglycan link protein 2	0.763
Q9D6M3	Mitochondrial glutamate carrier 1	0.75	F8VPQ4	SLIT-ROBO Rho GTPase-activating protein 3	0.764
Q3TDA1	Oxysterol-binding protein	0.751	Q812A2	SLIT-ROBO Rho GTPase-activating protein 3	0.764
Q8BX94	Oxysterol-binding protein-related protein 2	0.751	E9QN14	SLIT-ROBO Rho GTPase-activating protein 3	0.764
Q3TGS9	ADP-ribosylation factor GTPase-activating protein 1	0.752	Q91YJ5	Translation initiation factor IF-2, mitochondrial	0.765
Q05DE0	ADP-ribosylation factor GTPase activating protein 1, isoform CRA_d (Fragment)	0.752	Q80XI4	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	0.766
V9GXM1	ADP-ribosylation factor GTPase-activating protein 1	0.752	A2AWI7	Endophilin-B2	0.767
Q9EPJ9	ADP-ribosylation factor GTPase-activating protein 1	0.752	Q8BKG0	Transporter (Fragment)	0.77
V9GWV1	ADP-ribosylation factor GTPase-activating protein 1	0.752	P31650	Sodium- and chloride-dependent GABA transporter 3	0.77
Q6PB94	Arfgap1 protein	0.752	Q9Z0R4	Intersectin-1	0.771

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
E9Q0N0	Intersectin-1	0.771	B1AQY2	Rho GTPase-activating protein 23	0.775
G3X9J1	Sodium/calcium exchanger 1	0.771	Q69ZH9	Rho GTPase-activating protein 23	0.775
G5E8Y0	Sodium/calcium exchanger 1	0.771	F8VQ11	Rho GTPase-activating protein 23	0.775
Q68FL0	Slc8a1 protein	0.771	P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	0.776
O35157	Sodium-calcium exchanger	0.771	D3YYH0	PEX5-related protein	0.778
Q8VD37	SH3-containing GRB2-like protein 3-interacting protein 1	0.772	F8SLQ1	Peroxisomal biogenesis factor 5-like protein transcript variant 6	0.778
Q6A4J8	Ubiquitin carboxyl-terminal hydrolase 7	0.772	Q8C437	PEX5-related protein	0.778
F8VPX1	Ubiquitin carboxyl-terminal hydrolase	0.772	F8SLP9	PEX5-related protein	0.778
E9PXY8	Ubiquitin carboxyl-terminal hydrolase	0.772	F8SLP5	Peroxisomal biogenesis factor 5-like protein transcript variant 1	0.778
Q3KQQ1	Nsfl1c protein (Fragment)	0.773	F8SLP8	Peroxin 2, isoform CRA_d	0.778
Q3UVN5	Putative uncharacterized protein	0.773	F8SLP6	Peroxisomal biogenesis factor 5-like protein transcript variant 2	0.778
Q9CZ44	NSFL1 cofactor p47	0.773	F8SLQ4	Peroxisomal biogenesis factor 5-like protein transcript variant 10	0.778
Q8C140	Putative uncharacterized protein	0.773	F8SLQ5	Peroxisomal biogenesis factor 5-like protein transcript variant 11	0.778
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	0.773	F8SLQ3	PEX5-related protein	0.778
O35551	Rab GTPase-binding effector protein 1	0.773	F8SLP7	Peroxisomal biogenesis factor 5-like protein transcript variant 3	0.778
P08122	Collagen alpha-2(IV) chain	0.773	P60229	Eukaryotic translation initiation factor 3 subunit E	0.779
Q9Z315	U4/U6.U5 tri-snRNP-associated protein 1	0.773	P11087	Collagen alpha-1(I) chain	0.78
Q80ZX0	Protein Sec24b	0.774	Q9DB27	Malignant T-cell-amplified sequence 1	0.78
Q3UDH4	Putative uncharacterized protein (Fragment)	0.774	A0A087WPR	Myelin-associated glycoprotein	0.782
Q9D0J4	ADP-ribosylation factor-like protein 2	0.774	P20917	Myelin-associated glycoprotein	0.782
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	0.774	Q9D394	Protein RUFY3	0.782
B9EKJ3	Mon2 protein	0.774	Q920I9	WD repeat-containing protein 7	0.783
Q80TL7	Protein MON2 homolog	0.774	Q99J77	N-acetylneuraminic acid synthase (Sialic acid synthase)	0.783

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
D3Z0M6	Cytoplasmic dynein 1 intermediate chain 1	0.785	Q8VC72	NADH dehydrogenase (Ubiquinone) Fe-S protein 8	0.789
O88485	Cytoplasmic dynein 1 intermediate chain 1	0.785	A2AMH4	Choline transporter-like protein 1	0.791
Q3TL79	Putative uncharacterized protein	0.785	Q6X893	Choline transporter-like protein 1	0.791
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	0.785	A2AMH5	Choline transporter-like protein 1	0.791
Q9DBS2	Tumor protein p63-regulated gene 1-like protein	0.785	Q9WU63	Heme-binding protein 2	0.792
Q3ULI3	Putative uncharacterized protein	0.785	P62482	Voltage-gated potassium channel subunit beta-2	0.793
Q9CR00	26S proteasome non-ATPase regulatory subunit 9	0.785	Q8VE47	Ubiquitin-like modifier-activating enzyme 5	0.794
Q9CZZ4	Putative uncharacterized protein	0.785	Q9ES97	Reticulon-3	0.795
B8QI35	Liprin-alpha 3	0.786	Q9CR95	Adaptin ear-binding coat-associated protein 1	0.795
D3YXZ3	Kinesin light chain 2	0.786	Q571F3E	MFLJ00061 protein (Fragment)	0.795
Q91YS4	Kinesin light chain 2	0.786	B1ARW4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 (Fragment)	0.795
Q80Y98	Phospholipase DDHD2	0.786	Q99LY9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	0.795
Q68EF0	Rab-3A-interacting protein	0.786	F2Z3X6	3-phosphoinositide-dependent protein kinase 1	0.795
Q6ZPQ6	Membrane-associated phosphatidylinositol transfer protein 2	0.787	Q810Z4	PDK1 (Fragment)	0.795
Q6NS55	Pitpnm2 protein	0.787	Q3UGN6	Putative uncharacterized protein	0.795
E9PYJ7	Membrane-associated phosphatidylinositol transfer protein 2	0.787	Q8K3L3	Phosphoinositide-dependent protein kinase-1 beta	0.795
D3YTS3	Protein D630045J12Rik	0.787	Q3UHZ0	Putative uncharacterized protein	0.795
Q68FD9	UPF0606 protein KIAA1549	0.787	Q9Z2A0	3-phosphoinositide-dependent protein kinase 1	0.795
F7ATU7	Protein D630045J12Rik (Fragment)	0.787	Q3TRL2	3-phosphoinositide-dependent protein kinase 1	0.795
Q9QXV0	ProSAAS	0.788	Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	0.796
P97300	Neuroplastin	0.788	D3YUP9	Disintegrin and metalloproteinase domain-containing protein 22	0.796
Q3UY05	Putative uncharacterized protein	0.789	Q9R1V6	Disintegrin and metalloproteinase domain-containing protein 22	0.796
Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	0.789	A4FUT9	Adam22 protein (Fragment)	0.796

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P21279	Guanine nucleotide-binding protein G(q) subunit alpha	0.797	Q78IK4	MICOS complex subunit Mic27	0.81
Q5EBI8	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	0.797	Q8BSX8	Putative uncharacterized protein	0.811
Q06185	ATP synthase subunit e, mitochondrial	0.797	Q9EQG9	Collagen type IV alpha-3-binding protein	0.811
Q9JMC3	DnaJ homolog subfamily A member 4	0.797	P68181	cAMP-dependent protein kinase catalytic subunit beta	0.812
P30275	Creatine kinase U-type, mitochondrial	0.798	Q9Z1Q2	Abhydrolase domain-containing protein 16A	0.813
Q5UE59	Kinesin light chain 1	0.798	Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial	0.814
E9Q7C9	Kinesin light chain 1	0.798	Q6PDL0	Cytoplasmic dynein 1 light intermediate chain 2	0.815
Q8CD76	Kinesin light chain 1	0.798	B1ASQ2	Apolipoprotein O	0.816
Q7TNF4	Kinesin light chain 1	0.798	Q9DCZ4	Apolipoprotein O	0.816
Q3V1R3	Putative uncharacterized protein	0.799	Q3KNM9	Apoo protein	0.816
Q8K406	Leucine-rich repeat LGI family member 3	0.799	Q9D186	Apolipoprotein O	0.816
Q5J7N1	Kras protein	0.799	O54984	ATPase Asna1	0.819
Q69Z26	Contactin-4	0.799	Q3U1J4	DNA damage-binding protein 1	0.82
Q9WVK8	Cholesterol 24-hydroxylase	0.802	Q8CAA7	Glucose 1,6-bisphosphate synthase	0.82
G3X9A7	MCG49978	0.803	Q80TB8	Synaptic vesicle membrane protein VAT-1 homolog-like	0.821
Q8BLJ3	PI-PLC X domain-containing protein 3	0.803	D3Z0Q6	Glycogen [starch] synthase, muscle	0.821
Q3UKD6	Putative uncharacterized protein	0.804	Q9Z1E4	Glycogen [starch] synthase, muscle	0.821
P05480	Neuronal proto-oncogene tyrosine-protein kinase Src	0.804	B1AX58	Plastin-3	0.822
Q80XU2	Neuronal proto-oncogene tyrosine-protein kinase Src	0.804	Q61644	Protein kinase C and casein kinase substrate in neurons protein 1	0.823
Q03517	Secretogranin-2	0.807	P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.823
Q0QEZ4	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (Fragment)	0.81	Q0VBR8	Growth arrest specific 7	0.823
Q3TE45	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	0.81	Q60780	Growth arrest-specific protein 7	0.823
Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	0.81	Q6A075	MKIAA0394 protein (Fragment)	0.823

Supplementary Table 4 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3U432	Growth arrest-specific protein 7	0.823	Q9DB72	BTB/POZ domain-containing protein 17	0.83
Q3U8N2	Putative uncharacterized protein (Fragment)	0.823	Q9WTQ5	A-kinase anchor protein 12	0.831
B1ATI9	Growth arrest-specific protein 7	0.823	A0A0A0MQC7	Microtubule-associated protein tau	0.832
P46664	Adenylosuccinate synthetase isozyme 2	0.826	P10637	Microtubule-associated protein tau	0.832
Q3TQY2	Putative uncharacterized protein	0.826	A2A5Y6	Microtubule-associated protein	0.832
Q8CBY8	Dynactin subunit 4	0.826	Q61361	Brevican core protein	0.833
P28663	Beta-soluble NSF attachment protein	0.829			

The comparison was performed in the spinal cord between an onset SOD1 G93A mouse and an age-matched WT mouse, where the fold < 0.833 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 381 significantly down regulated proteins in the spinal cord between an onset SOD1 G93A mouse vs an age-matched WT mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 5. List of Significantly Up Regulated Proteins in the Spinal Cord between a Progression SOD1 G93A Mouse Vs an Age-Matched WT Mouse

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P51910	Apolipoprotein D	12	P62960	Nuclease-sensitive element-binding protein 1	2.858
Q3V471	Galectin (Fragment)	4.093	Q60951	MYB-1b	2.858
Q8C253	Galectin	4.093	Q3TVU9	Putative uncharacterized protein	2.81
P16110	Galectin-3	4.093	Q99L04	Dehydrogenase/reductase SDR family member 1	2.81
Q3UBS0	Putative uncharacterized protein	3.906	Q3TX84	Putative uncharacterized protein	2.797
P08226	Apolipoprotein E	3.906	P11438	Lysosome-associated membrane glycoprotein 1	2.797
Q4FK40	Apoe protein	3.906	Q9DC13	Lysosomal membrane glycoprotein 1, isoform CRA_a	2.797
Q6GTX3	Apoe protein	3.906	Q8VH34	LAMP-1	2.797
P14602	Heat shock protein beta-1	3.505	O88492	Perilipin-4	2.761
Q3TXB1	Putative uncharacterized protein	3.349	Q3U292	Putative uncharacterized protein	2.742
Q3UBX7	Putative uncharacterized protein	3.349	P43277	Histone H1.3	2.742
P98086	Complement C1q subcomponent subunit A	3.349	P15864	Histone H1.2	2.742
Q3TWH2	Putative uncharacterized protein	3.152	Q5NDA4	Fatty acid binding protein 7, brain	2.738
Q61941	NAD(P) transhydrogenase, mitochondrial	3.152	P51880	Fatty acid-binding protein, brain	2.738
Q8C1W8	Nicotinamide nucleotide transhydrogenase, isoform CRA_a	3.152	P20060	Beta-hexosaminidase subunit beta	2.638
Q922E1	Nicotinamide nucleotide transhydrogenase	3.152	F6UP77	Putative N-acetylglucosamine-6-phosphate deacetylase (Fragment)	2.63
Q99JT9	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	3.071	Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	2.63
Q8R422	CD109 antigen	3.043	Q3TVS6	Putative uncharacterized protein	2.623
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a	2.899	P10605	Cathepsin B	2.623
Q3ULL6	Protein Upf3b	2.884	Q8BY89	Choline transporter-like protein 2	2.623
F6Q8N5	Protein Upf3b (Fragment)	2.884	Q9CYL5	Golgi-associated plant pathogenesis-related protein 1	2.611
Q9CS15	Putative uncharacterized protein (Fragment)	2.884	Q3UW40	Putative uncharacterized protein	2.564
Q80UI8	Upf3b protein (Fragment)	2.884	Q8BP67	60S ribosomal protein L24	2.564
Q71V06	Y box transcription factor (Fragment)	2.858	Q6GQT1	Alpha-2-macroglobulin-P	2.498
Q810K5	Y box protein 1	2.858	A7YQ68	Prickle-like 2 (Drosophila)	2.481

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q80Y24	Prickle-like protein 2	2.481	Q64525	Histone H2B type 2-B	2.346
A0A087WNP6	Protein CDV3	2.438	P10854	Histone H2B type 1-M	2.346
Q4VAA2	Protein CDV3	2.438	Q64478	Histone H2B type 1-H	2.346
A2APM1	CD44 antigen	2.417	Q9CWF2	Tubulin beta-2B chain	2.345
E9QKM8	CD44 antigen	2.417	M0QWA7	Integrin beta	2.345
P15379	CD44 antigen	2.417	P11835	Integrin beta-2	2.345
Q80X37	CD44 antigen	2.417	Q542I8	Integrin beta	2.345
Q3U8S1	CD44 antigen	2.417	A2AQ87	SH2 domain-containing adapter protein F (Fragment)	2.337
Q3TLT9	Putative uncharacterized protein	2.417	A2AQ88	SH2 domain-containing adapter protein F (Fragment)	2.337
A2APM5	CD44 antigen	2.417	F7AIV2	SH2 domain-containing adapter protein F (Fragment)	2.337
A2APM2	CD44 antigen	2.417	P60867	40S ribosomal protein S20	2.306
Q3U468	Putative uncharacterized protein	2.417	Q3TFK4	Annexin	2.265
Q3UNN2	Putative uncharacterized protein	2.417	Q8C1X9	Annexin	2.265
A2APM4	CD44 antigen	2.417	Q3U737	Annexin	2.265
A2APM3	CD44 antigen	2.417	O35639	Annexin A3	2.265
P43274	Histone H1.4	2.411	Q3TJZ7	Putative uncharacterized protein	2.261
Q9DAW9	Calponin-3	2.37	Q6PGH2	Hematological and neurological expressed 1-like protein	2.261
A0JLV3	Histone H2B (Fragment)	2.346	Q3U7P4	Putative uncharacterized protein	2.261
Q8CGP2	Histone H2B type 1-P	2.346	P68510	14-3-3 protein eta	2.247
Q64475	Histone H2B type 1-B	2.346	G3X9G2	Misshapen-like kinase 1	2.233
Q921L4	Histone H2B	2.346	Q9JM52	Misshapen-like kinase 1	2.233
Q8CBB6	Histone H2B	2.346	P0C0S6	Histone H2A.Z	2.219
P10853	Histone H2B type 1-F/J/L	2.346	Q3THW5	Histone H2A.V	2.219
Q6ZWY9	Histone H2B type 1-C/E/G	2.346	Q3TLP8	RAS-related C3 botulinum substrate 1, isoform CRA_a	2.219
Q8CGP1	Histone H2B type 1-K	2.346	Q8BPG5	Putative uncharacterized protein	2.219

supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P63001	Ras-related C3 botulinum toxin substrate 1	2.219	Q60972	Histone-binding protein RBBP4	2.078
Q9D859	Putative uncharacterized protein	2.219	Q9JKY7	Cytochrome P450 CYP2D22	2.07
Q8C4N8	Putative uncharacterized protein (Fragment)	2.219	Q91W87	Cytochrome P450, family 2, subfamily d, polypeptide 22	2.07
Q9WU84	Copper chaperone for superoxide dismutase	2.21	P63216	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-3	2.048
Q9CR57	60S ribosomal protein L14	2.201	Q8K0G5	Protein TSSC1	2.039
Q9CWK0	Putative uncharacterized protein	2.201	G5E850	Cytochrome b-5, isoform CRA_a	1.991
Q3TWV0	Putative uncharacterized protein	2.195	P56395	Cytochrome b5	1.991
P20152	Vimentin	2.195	B1APX2	Protein 5031439G07Rik	1.989
Q3UHD1	Brain-specific angiogenesis inhibitor 1	2.164	Q69ZV3	MKIAA0930 protein (Fragment)	1.989
P70202	Latexin	2.151	Q3UE31	Uncharacterized protein KIAA0930 homolog	1.989
D3Z780	Translation initiation factor eIF-2B subunit delta	2.129	P26645	Myristoylated alanine-rich C-kinase substrate	1.984
Q61749	Translation initiation factor eIF-2B subunit delta	2.129	P23927	Alpha-crystallin B chain	1.971
B2RWQ7	Arsb protein	2.127	P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	1.961
P50429	Arylsulfatase B	2.127	P32020	Non-specific lipid-transfer protein	1.947
Q7TMM9	Tubulin beta-2A chain	2.097	P51885	Lumican	1.946
Q3TWD0	Putative uncharacterized protein	2.088	P48678	Prelamin-A/C	1.942
Q3U7P0	Putative uncharacterized protein	2.088	O35887	Calumenin	1.936
P18242	Cathepsin D	2.088	Q3TWG2	Putative uncharacterized protein	1.929
Q8C243	Putative uncharacterized protein	2.088	O08795	Glucosidase 2 subunit beta	1.929
Q3TWR6	Putative uncharacterized protein	2.088	B1AWD8	Clathrin light chain A	1.928
Q3U8W5	Putative uncharacterized protein	2.088	O08585	Clathrin light chain A	1.928
Q06890	Clusterin	2.083	B1AWD9	Clathrin light chain A	1.928
D3YW48	Calpain small subunit 1 (Fragment)	2.079	B2RXS4	Plexin-B2	1.924
O88456	Calpain small subunit 1	2.079	Q9DBS1	Transmembrane protein 43	1.917
O35449	Proline-rich transmembrane protein 1	2.079	Q3U5K7	Putative uncharacterized protein (Fragment)	1.914

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P21460	Cystatin-C	1.914	Q8C6F4	Putative uncharacterized protein	1.77
Q9EPX9	Cystatin C	1.914	Q8CAG6	Pleckstrin	1.77
Q8C1B7	Septin-11	1.882	Q9JHK5	Pleckstrin	1.77
Q8R2U6	Diphosphoinositol polyphosphate phosphohydrolase 2	1.868	P62806	Histone H4	1.764
D0VYV6	Erythrocyte protein band 4.1-like 3 isoform B	1.855	Q00915	Retinol-binding protein 1	1.764
Q3ULN5	Peptidyl-prolyl cis-trans isomerase	1.853	B2RPU8	MCG130675	1.76
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A	1.853	Q9D1L0	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	1.76
P11352	Glutathione peroxidase 1	1.839	D3Z5B1	Protein Zbed5 (Fragment)	1.76
Q3U0V1	Far upstream element-binding protein 2	1.836	Q8CEW7	Putative uncharacterized protein	1.76
Q91VM2	Small nuclear ribonucleoprotein D3	1.825	P67984	60S ribosomal protein L22	1.756
P62320	Small nuclear ribonucleoprotein Sm D3	1.825	Q9CPY7	Cytosol aminopeptidase	1.755
Q6P5H2	Nestin	1.823	Q3THA6	MCG17902, isoform CRA_a	1.739
Q8C845	EF-hand domain-containing protein D2	1.814	Q8BL97	Serine/arginine-rich splicing factor 7	1.739
Q9WVA4	Transgelin-2	1.809	Q8QZV4	Serine/threonine-protein kinase 32C	1.738
Q91YP2	Neurolysin, mitochondrial	1.803	P01027	Complement C3	1.734
Q3UVX5	Metabotropic glutamate receptor 5	1.799	Q8BNA5	Putative uncharacterized protein	1.733
E9QMC2	Metabotropic glutamate receptor 5	1.799	Q921L6	Cortactin, isoform CRA_a	1.733
Q8BX02	KN motif and ankyrin repeat domain-containing protein 2	1.799	Q60598	Src substrate cortactin	1.733
Q9QYG0	Protein NDRG2	1.789	Q80WJ7	Protein LYRIC	1.721
Q3UG34	Putative uncharacterized protein	1.778	B0R1E3	Histidine triad nucleotide-binding protein 1	1.715
Q6PDS4	Fxn protein	1.778	P70349	Histidine triad nucleotide-binding protein 1	1.715
O35943	Frataxin, mitochondrial	1.778	P08228	Superoxide dismutase [Cu-Zn]	1.707
A2AVJ7	Ribosome-binding protein 1	1.771	B7FAU9	Filamin, alpha	1.703
Q6ZPS0	MKIAA1398 protein (Fragment)	1.771	Q8BTM8	Filamin-A	1.703
Q99PL5	Ribosome-binding protein 1	1.771	O09114	Prostaglandin-H2 D-isomerase	1.701

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P11087	Collagen alpha-1(I) chain	1.696	P47911	60S ribosomal protein L6	1.63
P62774	Myotrophin	1.693	A2A9M5	Dedicator of cytokinesis protein 7	1.626
P70232	Neural cell adhesion molecule L1-like protein	1.682	E9PX48	Dedicator of cytokinesis protein 7	1.626
Q3TZQ2	Putative uncharacterized protein	1.663	Q8R1A4	Dedicator of cytokinesis protein 7	1.626
P26041	Moesin	1.663	Q80X90	Filamin-B	1.615
D3YYD5	Vacuolar protein sorting-associated protein 29 (Fragment)	1.663	P62852	40S ribosomal protein S25	1.607
Q9QZ88	Vacuolar protein sorting-associated protein 29	1.663	P82198	Transforming growth factor-beta-induced protein ig-h3	1.605
D3Z645	Vacuolar protein sorting-associated protein 29	1.663	Q3TFU8	Putative uncharacterized protein	1.603
Q3TSV1	Putative uncharacterized protein	1.662	Q3U7N8	Putative uncharacterized protein	1.603
P28654	Decorin	1.662	Q9CZL0	Putative uncharacterized protein	1.603
Q05816	Fatty acid-binding protein, epidermal	1.656	Q99KF1	Transmembrane emp24 domain-containing protein 9	1.603
Q4FZL1	Eif4a1 protein (Fragment)	1.648	O54983	Ketimine reductase mu-crystallin	1.599
P60843	Eukaryotic initiation factor 4A-I	1.648	Q3UAC2	40S ribosomal protein S3a	1.597
S4R281	60S ribosomal protein L13a	1.645	P97351	40S ribosomal protein S3a	1.597
E9Q5A0	60S ribosomal protein L13a	1.645	Q9D1S3	40S ribosomal protein S3a	1.597
P19253	60S ribosomal protein L13a	1.645	Q3U850	Putative uncharacterized protein	1.596
Q3THJ0	60S ribosomal protein L18a	1.644	P47962	60S ribosomal protein L5	1.596
Q05CK2	60S ribosomal protein L18a	1.644	Q3THX5	Putative uncharacterized protein	1.595
P62717	60S ribosomal protein L18a	1.644	E9Q3X0	Major vault protein	1.595
Q8C6H6	Putative uncharacterized protein	1.643	Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial	1.595
O70572	Sphingomyelin phosphodiesterase 2	1.643	Q3TWE1	Putative uncharacterized protein	1.59
Q3UJ44	Putative uncharacterized protein	1.638	Q9CZU7	Putative uncharacterized protein	1.59
Q99LB4	Capping protein (Actin filament), gelsolin-like	1.638	Q8C876	Putative uncharacterized protein	1.59
P0C0A3	Charged multivesicular body protein 6	1.631	Q3UIW3	Putative uncharacterized protein	1.59
B1AZ42	Charged multivesicular body protein 6 (Fragment)	1.631	P17047	Lysosome-associated membrane glycoprotein 2	1.59

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8C5K0	Lysosomal membrane glycoprotein 2, isoform CRA_a	1.59	Q05D44	Eukaryotic translation initiation factor 5B	1.549
Q3TX26	Putative uncharacterized protein	1.584	Q8BYY7	Putative uncharacterized protein (Fragment)	1.549
P97822	Acidic leucine-rich nuclear phosphoprotein 32 family member E	1.584	Q3TYK4	Putative uncharacterized protein	1.547
E9PZF5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)	1.584	Q8C3Z4	Putative uncharacterized protein	1.547
E9Q5H2	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)	1.584	Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	1.547
Q0VGU4	MCG18019	1.582	Q8VHY0	Chondroitin sulfate proteoglycan 4	1.544
F8VQK3	Protein Gucy1a2	1.577	P08122	Collagen alpha-2(IV) chain	1.536
Q80YX1	Tenascin	1.576	G3X9V4	Glutamate receptor ionotropic, NMDA 2B	1.532
Q148T5	Tenascin C, isoform CRA_a	1.576	Q01097	Glutamate receptor ionotropic, NMDA 2B	1.532
Q148T4	Tnc protein	1.576	Q8K010	5-oxoprolinase	1.531
B7ZNF6	Ctnnd2 protein	1.57	Q9WUR9	Adenylate kinase 4, mitochondrial	1.527
O35927	Catenin delta-2	1.57	Q9WV34	MAGUK p55 subfamily member 2	1.524
E9QKH8	Catenin delta-2	1.57	B0V2H4	V-type proton ATPase subunit G 2	1.524
Q8R071	Inositol-trisphosphate 3-kinase A	1.566	Q9WTT4	V-type proton ATPase subunit G 2	1.524
Q3UYQ4	Putative uncharacterized protein	1.565	P62264	40S ribosomal protein S14	1.52
O35841	Apoptosis inhibitor 5	1.565	O70569	Ribosomal protein S14	1.52
Q3UEI6	Putative uncharacterized protein	1.56	Q9CVB6	Actin-related protein 2/3 complex subunit 2	1.519
Q3UJK2	Putative uncharacterized protein	1.56	Q3UF30	Putative uncharacterized protein	1.519
Q3UMP4	Putative uncharacterized protein	1.56	P08207	Protein S100-A10	1.519
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	1.56	Q9JI95	CPN10-like protein	1.515
Q3V274	Putative uncharacterized protein	1.56	Q64433	10 kDa heat shock protein, mitochondrial	1.515
P68372	Tubulin beta-4B chain	1.559	P12658	Calbindin	1.513
Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5	1.557	P61982	14-3-3 protein gamma	1.511
Q8BH58	TIP41-like protein	1.553	P52760	Ribonuclease UK114	1.51
Q9DBG9	Tax1-binding protein 3	1.552	G3X8X7	Vacuolar protein sorting 16 (Yeast)	1.509

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8BWV2	Putative uncharacterized protein	1.509	Q9JJQ6	Factor 8-associated gene A	1.5
Q920Q4	Vacuolar protein sorting-associated protein 16 homolog	1.509	Q00558	Factor VIII intron 22 protein	1.5
Q5DTP7	MKIAA4075 protein (Fragment)	1.508	Q6PEV0	Ephx1 protein	1.495
E9QAS4	Chromodomain-helicase-DNA-binding protein 4	1.508	Q9D379	Epoxide hydrolase 1	1.495
E9QAS5	Chromodomain-helicase-DNA-binding protein 4	1.508	E9PWK1	Epoxide hydrolase 1	1.495
Q6PDQ2	Chromodomain-helicase-DNA-binding protein 4	1.508	Q8K2W5	Epoxide hydrolase 1, microsomal	1.495
D3Z2Y6	Protein S100a16 (Fragment)	1.507	F6RJ39	Apoptotic chromatin condensation inducer in the nucleus (Fragment)	1.49
Q3TVE3	Putative uncharacterized protein	1.507	Q80TU6	MKIAA0670 protein (Fragment)	1.49
Q9D708	Protein S100a16	1.507	Q9JIX8	Apoptotic chromatin condensation inducer in the nucleus	1.49
Q3THQ0	Beta-hexosaminidase	1.506	P21981	Protein-glutamine gamma-glutamyltransferase 2	1.487
Q3U936	Beta-hexosaminidase	1.506	Q6ZQK2	MKIAA0051 protein (Fragment)	1.485
Q3TXV7	Beta-hexosaminidase	1.506	Q9JKF1	Ras GTPase-activating-like protein IQGAP1	1.485
Q3TW10	Beta-hexosaminidase	1.506	Q80UW7	IQ motif containing GTPase activating protein 1	1.485
Q3TKF6	Beta-hexosaminidase	1.506	Q3TA13	Putative uncharacterized protein	1.48
Q8BNS6	Beta-hexosaminidase	1.506	E9Q3E2	Synaptopodin	1.48
Q3TVI2	Beta-hexosaminidase	1.506	Q3URF1	MCG6023	1.48
Q3UCP6	Beta-hexosaminidase	1.506	Q3TY32	Putative uncharacterized protein (Fragment)	1.48
P29416	Beta-hexosaminidase subunit alpha	1.506	Q3U336	Putative uncharacterized protein	1.48
Q5EBG5	Ribosomal protein L7A	1.505	Q8CC35	Synaptopodin	1.48
P12970	60S ribosomal protein L7a	1.505	J3QNT7	Epsin-2	1.479
Q80UT7	Rpl7a protein (Fragment)	1.505	Q69ZS5	MKIAA1065 protein (Fragment)	1.479
Q6P1A9	Ribosomal protein L7A	1.505	Q5NCM5	Epsin-2	1.479
Q70IV5	Synemin	1.505	Q9DBR7	Protein phosphatase 1 regulatory subunit 12A	1.478
Q3TLS9	Putative uncharacterized protein	1.5	Q7TMN7	Annexin	1.473
Q8CCG9	Putative uncharacterized protein	1.5	P97429	Annexin A4	1.473

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q3TT11	Putative uncharacterized protein	1.47	Q9D6B6	Putative uncharacterized protein	1.434
Q3UHW2	Putative uncharacterized protein	1.47	E9Q0V4	Mitochondrial pyruvate carrier 1	1.434
P51660	Peroxisomal multifunctional enzyme type 2	1.47	Q61753	D-3-phosphoglycerate dehydrogenase	1.431
Q8K354	Carbonyl reductase [NADPH] 3	1.467	Q9R069	Basal cell adhesion molecule	1.43
Q80ZW2	Protein THEM6	1.467	Q99K86	Bcam protein	1.43
F8VQJ3	Laminin subunit gamma-1	1.465	G3UXZ5	Proteasome activator complex subunit 1 (Fragment)	1.43
Q9QY42	Prosaposin receptor GPR37	1.463	P97371	Proteasome activator complex subunit 1	1.43
P07724	Serum albumin	1.462	Q3U8W4	Superoxide dismutase	1.429
Q3TFD9	Putative uncharacterized protein	1.46	P09671	Superoxide dismutase [Mn], mitochondrial	1.429
Q3TD08	Putative uncharacterized protein	1.46	Q3UKZ1	Syndecan	1.429
B7ZWC0	N-myc downstream regulated gene 1	1.46	O35988	Syndecan-4	1.429
Q62433	Protein NDRG1	1.46	Q3U3F4	Putative uncharacterized protein	1.428
Q3TSR4	Putative uncharacterized protein	1.46	P31938	Dual specificity mitogen-activated protein kinase kinase 1	1.428
Q9EPL2	Calsyntenin-1	1.45	Q9JJE1	Brain cDNA, clone MNCb-1208, similar to Mus musculus mitogen activated protein kinase kinase 1 (Map2k1), mRNA	1.428
O09131	Glutathione S-transferase omega-1	1.449	Q3UK05	Putative uncharacterized protein	1.428
Q6ZWZ6	40S ribosomal protein S12	1.449	P21619	Lamin-B2	1.425
Q9DB29	Isoamyl acetate-hydrolyzing esterase 1 homolog	1.447	D3YVF0	A-kinase anchor protein 5	1.425
Q91ZP9	N-terminal EF-hand calcium-binding protein 2	1.44	H3BIV5	A-kinase anchor protein 5	1.425
Q3UNZ8	Quinone oxidoreductase-like protein 2	1.44	Q3UZE7	Catalase	1.424
Q9WVA3	Mitotic checkpoint protein BUB3	1.439	P24270	Catalase	1.424
D3YWY6	Mitochondrial pyruvate carrier 1	1.434	Q8C6E3	Catalase	1.424
Q3TCV4	Putative uncharacterized protein	1.434	Q8R086	Sulfite oxidase, mitochondrial	1.424
P63030	Mitochondrial pyruvate carrier 1	1.434	P27048	Small nuclear ribonucleoprotein-associated protein B	1.423
D3Z5S0	Brain protein 44-like, isoform CRA_a	1.434	P63163	Small nuclear ribonucleoprotein-associated protein N	1.423

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
O70499	Small nuclear ribonucleoprotein-associated protein	1.423	P35980	60S ribosomal protein L18	1.404
Q3UNH4	G protein-regulated inducer of neurite outgrowth 1	1.421	Q642K1	60S ribosomal protein L18	1.404
A1L333	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.417	Q3TCP5	Putative uncharacterized protein	1.403
Q5U222	Ddx5 protein (Fragment)	1.417	Q3UXR4	Putative uncharacterized protein	1.403
Q61656	Probable ATP-dependent RNA helicase DDX5	1.417	P26040	Ezrin	1.403
Q8BTS0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.417	Q3UL48	Putative uncharacterized protein	1.403
Q3V0Z8	Putative uncharacterized protein (Fragment)	1.417	Q4VA93	Protein kinase C	1.403
Q9R0N5	Synaptotagmin-5	1.417	Q8BMK4	Cytoskeleton-associated protein 4	1.403
Q0VBF8	Protein stum homolog	1.417	P08030	Adenine phosphoribosyltransferase	1.403
J3QP43	Protein 6330403A02Rik	1.417	O88704	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1	1.402
A2VCP3	P2X purinoceptor (Fragment)	1.415	Q3TXX4	Vesicular glutamate transporter 1	1.401
Q3ULZ7	P2X purinoceptor	1.415	Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	1.4
Q3UN00	P2X purinoceptor	1.415	Q9DCN2	NADH-cytochrome b5 reductase 3	1.397
F8WI93	P2X purinoceptor	1.415	P57780	Alpha-actinin-4	1.396
C8YIX4	P2X purinoceptor	1.415	A4GE64	Alpha-T-catenin	1.396
Q3UM93	P2X purinoceptor	1.415	Q65CL1	Catenin alpha-3	1.396
Q9Z1M0	P2X purinoceptor 7	1.415	Q14DP5	Catenin (Cadherin associated protein), alpha 3	1.396
Q8CHP3	P2X purinoceptor	1.415	Q3UF75	Alpha-parvin	1.396
Q3TBP1	P2X purinoceptor	1.415	Q8C5R4	Putative uncharacterized protein	1.396
Q3UF03	Putative uncharacterized protein	1.412	Q9EPC1	Alpha-parvin	1.396
P24668	Cation-dependent mannose-6-phosphate receptor	1.412	Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	1.394
Q91VC3	Eukaryotic initiation factor 4A-III	1.412	P97492	Regulator of G-protein signaling 14	1.394
E0CYM8	Tyrosine-protein phosphatase non-receptor type substrate 1	1.404	Q9CPV4	Glyoxalase domain-containing protein 4	1.391
Q6P6I8	Signal-regulatory protein alpha	1.404	Q8C052	Microtubule-associated protein 1S	1.39
Q0QEW9	60S ribosomal protein L18 (Fragment)	1.404	Q91W50	Cold shock domain-containing protein E1	1.387

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P62315	Small nuclear ribonucleoprotein Sm D1	1.386	Q9WVS5	Chaperonin containing TCP-1 theta subunit	1.339
B9EHJ3	Tight junction protein ZO-1	1.372	P42932	T-complex protein 1 subunit theta	1.339
P39447	Tight junction protein ZO-1	1.372	Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	1.338
Q80VP0	Tectonin beta-propeller repeat-containing protein 1	1.372	P09528	Ferritin heavy chain	1.335
P97855	Ras GTPase-activating protein-binding protein 1	1.372	Q3UNK1	Putative uncharacterized protein	1.334
Q6IRU2	Tropomyosin alpha-4 chain	1.37	Q05C56	Add3 protein (Fragment)	1.334
Q3U0C4	Putative uncharacterized protein	1.369	Q9QYB5	Gamma-adducin	1.334
Q9R111	Guanine deaminase	1.369	Q8BM29	Putative uncharacterized protein (Fragment)	1.334
Q69ZN0	MKIAA1258 protein (Fragment)	1.369	Q05DT0	Add3 protein (Fragment)	1.334
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	1.364	Q9Z1X4	Interleukin enhancer-binding factor 3	1.334
Q8QZY9	Splicing factor 3B subunit 4	1.364	Q45VK6	Nuclear factor 90	1.334
B2RWE8	Eif4b protein	1.363	Q45VK5	Interleukin enhancer-binding factor 3	1.334
Q3TSY9	Putative uncharacterized protein	1.363	Q5DTY9	BTB/POZ domain-containing protein KCTD16	1.334
Q3TDD8	Putative uncharacterized protein	1.363	E9Q4M4	MICOS complex subunit Mic25	1.332
Q3UGC0	Putative uncharacterized protein	1.363	Q91VN4	MICOS complex subunit Mic25	1.332
Q8BGD9	Eukaryotic translation initiation factor 4B	1.363	Q3TEA8	Heterochromatin protein 1-binding protein 3	1.332
Q3THB0	Putative uncharacterized protein	1.363	Z4YKB8	Heterochromatin protein 1-binding protein 3	1.332
O54724	Polymerase I and transcript release factor	1.352	P10639	Thioredoxin	1.331
Q3TW51	Putative uncharacterized protein	1.352	Q3UTJ2	Sorbin and SH3 domain-containing protein 2	1.33
Q3UZI3	Putative uncharacterized protein	1.352	B9EKP8	Sorbin and SH3 domain-containing protein 2	1.33
Q78PY7	Staphylococcal nuclease domain-containing protein 1	1.352	E9Q0B0	Sorbin and SH3 domain-containing protein 2	1.33
Q9Z2Y3	Homer protein homolog 1	1.352	B7ZWM6	Sorbin and SH3 domain-containing protein 2	1.33
A0A087WRY3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	1.341	G3X8Q5	Ceruloplasmin	1.33
Q80XU3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	1.341	Q61147	Ceruloplasmin	1.33
Q6A0F1	MKIAA0002 protein (Fragment)	1.339	G3X9T8	Ceruloplasmin	1.33

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
E9PZD8	Ceruloplasmin	1.33	O89017	Legumain	1.316
Q8C9R8	Putative uncharacterized protein	1.33	P14733	Lamin-B1	1.315
O54781	SRSF protein kinase 2	1.33	E9PX70	Collagen alpha-1(XII) chain	1.313
Q8CBI1	Putative uncharacterized protein (Fragment)	1.33	Q60847	Collagen alpha-1(XII) chain	1.313
P52196	Thiosulfate sulfurtransferase	1.329	P55264	Adenosine kinase	1.313
Q9CRB9	MICOS complex subunit Mic19	1.329	E9PVU0	Unconventional myosin-VI	1.312
Q62348	Translin	1.328	E9Q175	Unconventional myosin-VI	1.312
Q3TFP8	Putative uncharacterized protein	1.328	P63318	Protein kinase C gamma type	1.312
Q3TH84	Putative uncharacterized protein	1.328	Q3TJN6	Putative uncharacterized protein	1.312
O55022	Membrane-associated progesterone receptor component 1	1.328	Q9D8U8	Sorting nexin-5	1.312
Q3UM23	Putative uncharacterized protein	1.325	Q8C5E7	Putative uncharacterized protein	1.312
Q91VI7	Ribonuclease inhibitor	1.325	P09055	Integrin beta-1	1.311
Q8K3H0	DCC-interacting protein 13-alpha	1.325	Q3TPN0	Putative uncharacterized protein	1.31
Q3UH68	LIM and calponin homology domains-containing protein 1	1.325	Q3US45	Putative uncharacterized protein	1.31
D3YU59	LIM and calponin homology domains-containing protein 1	1.325	Q8CFA3	Nidogen-2	1.31
Q3TEX8	Ubiquitin carboxyl-terminal hydrolase	1.324	O88322	Nidogen-2	1.31
P35123	Ubiquitin carboxyl-terminal hydrolase 4	1.324	Q3TIR3	Synembryn-A	1.31
Q921M8	Ubiquitin carboxyl-terminal hydrolase	1.324	Q3TBF1	Putative uncharacterized protein	1.306
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	1.323	Q08642	Protein-arginine deiminase type-2	1.306
P63040	Complexin-1	1.319	Q8R1F1	Niban-like protein 1	1.303
B2RUH8	6330439K17Rik protein	1.318	Q3U3A8	Putative uncharacterized protein	1.302
B7ZNV9	6330439K17Rik protein	1.318	Q3U8S5	Putative uncharacterized protein	1.302
E9Q4Z6	Double zinc ribbon and ankyrin repeat-containing protein 1	1.318	O08529	Calpain-2 catalytic subunit	1.302
Q8C008	Double zinc ribbon and ankyrin repeat-containing protein 1	1.318	Q3TJ21	Pyrroline-5-carboxylate reductase	1.301
Q3UE99	Putative uncharacterized protein (Fragment)	1.316	Q922Q4	Pyrroline-5-carboxylate reductase 2	1.301

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q6PAR5	GTPase-activating protein and VPS9 domain-containing protein 1	1.299	B9EIU1	Glutamyl-prolyl-tRNA synthetase	1.281
P63321	Ras-related protein Ral-A	1.297	Q3TWB8	Putative uncharacterized protein	1.279
Q9JHW2	Omega-amidase NIT2	1.297	E9PZ69	Transmembrane 9 superfamily member 2	1.279
Q8VIJ6	Splicing factor, proline- and glutamine-rich	1.293	Q8C7F9	Putative uncharacterized protein	1.279
P98203	Armadillo repeat protein deleted in velo-cardio-facial syndrome homolog	1.293	P58021	Transmembrane 9 superfamily member 2	1.279
P55066	Neurocan core protein	1.289	Q8C6H4	Putative uncharacterized protein	1.279
Q3U896	Putative uncharacterized protein	1.289	Q3TUA8	Putative uncharacterized protein	1.279
Q9Z2D0	Myotubularin-related protein 9	1.289	Q6NZM8	3~-phosphoadenosine 5~-phosphosulfate synthase 1, isoform CRA_a	1.279
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	1.288	Q60967	Bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 1	1.279
Q99PU5	Long-chain-fatty-acid--CoA ligase ACSBG1	1.286	Q3TF72	Protein disulfide-isomerase	1.278
Q3UE40	Putative uncharacterized protein	1.286	Q3TIM0	Protein disulfide-isomerase	1.278
P27601	Guanine nucleotide-binding protein subunit alpha-13	1.286	Q3THC3	Protein disulfide-isomerase	1.278
Q5RKP3	60S ribosomal protein L13	1.286	Q3UDR2	Protein disulfide-isomerase (Fragment)	1.278
P47963	60S ribosomal protein L13	1.286	Q3URP6	Protein disulfide-isomerase	1.278
B1ASQ2	Apolipoprotein O	1.285	P09103	Protein disulfide-isomerase	1.278
Q9DCZ4	Apolipoprotein O	1.285	Q3TWE3	Protein disulfide-isomerase	1.278
Q3KNM9	Apoo protein	1.285	Q3UXQ6	40S ribosomal protein S4	1.275
Q9D186	Apolipoprotein O	1.285	Q545F8	40S ribosomal protein S4	1.275
Q9QYX7	Protein piccolo	1.283	P62702	40S ribosomal protein S4, X isoform	1.275
Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1	1.282	Q8R2Y2	Cell surface glycoprotein MUC18	1.275
Q64727	Vinculin	1.281	F8WGR0	Alpha-adducin	1.273
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	1.281	F8WHZ9	Alpha-adducin	1.273
A2AMW0	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a	1.281	Q9QYC0	Alpha-adducin	1.273
Q923G3	Capping protein (Actin filament) muscle Z-line, beta	1.281	Q8K232	Adducin 1 (Alpha)	1.273
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	1.281	Q3TIK0	Platelet-activating factor acetylhydrolase IB subunit alpha	1.273

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q3TJG1	Platelet-activating factor acetylhydrolase IB subunit alpha	1.273	Q8BP16	Histone H2A	1.248
Q3UGR6	Platelet-activating factor acetylhydrolase IB subunit alpha	1.273	G5E829	Plasma membrane calcium-transporting ATPase 1	1.245
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	1.273	Q3UZT7	Putative uncharacterized protein	1.245
Q569Z5	Probable ATP-dependent RNA helicase DDX46	1.269	Q02248	Catenin beta-1	1.245
A2AS45	Plakophilin-4	1.265	Q8VC94	Rpl11 protein	1.244
Q68FH0	Plakophilin-4	1.265	E9PYL9	Uncharacterized protein	1.244
P10493	Nidogen-1	1.262	Q9CXW4	60S ribosomal protein L11	1.244
Q5CZY9	Rps16 protein	1.258	E9PZB3	Protein Gm5093	1.244
Q641N3	Rps16 protein (Fragment)	1.258	P28653	Biglycan	1.244
P14131	40S ribosomal protein S16	1.258	J3QNM3	Protein enabled homolog	1.244
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	1.257	Q03173	Protein enabled homolog	1.244
E9Q035	Protein Gm20425	1.257	E9QKR1	Protein enabled homolog	1.244
Q99KC8	von Willebrand factor A domain-containing protein 5A	1.255	E9QLZ9	Protein enabled homolog	1.244
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	1.254	E9QKQ9	Protein enabled homolog	1.244
Q3THB3	Putative uncharacterized protein	1.251	P62983	Ubiquitin-40S ribosomal protein S27a	1.243
B8JK33	Heterogeneous nuclear ribonucleoprotein M	1.251	Q3TP13	Putative uncharacterized protein (Fragment)	1.238
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	1.251	Q3TN26	Putative uncharacterized protein	1.238
B8JK32	Heterogeneous nuclear ribonucleoprotein M	1.251	Q60714	Long-chain fatty acid transport protein 1	1.238
Q570Z0	MKIAA4193 protein (Fragment)	1.251	Q9CZP6	Putative uncharacterized protein	1.23
Q3TL61	Putative uncharacterized protein	1.251	P62908	40S ribosomal protein S3	1.23
Q5M9L9	40S ribosomal protein S8	1.251	Q9D8E6	60S ribosomal protein L4	1.23
P62242	40S ribosomal protein S8	1.251	Q3TL52	Putative uncharacterized protein	1.227
Q3TIQ2	Putative uncharacterized protein	1.25	P09405	Nucleolin	1.227
P35979	60S ribosomal protein L12	1.25	Q8CD23	Putative uncharacterized protein	1.227
Q8CCK0	Core histone macro-H2A.2	1.248	Q6PDM2	Serine/arginine-rich splicing factor 1	1.227

Supplementary Table 5 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
H7BX95	Serine/arginine-rich-splicing factor 1	1.227	Q8C0M9	Isoaspartyl peptidase/L-asparaginase	1.214
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	1.227	Q3TI62	Putative uncharacterized protein	1.212
Q9QZQ8	Core histone macro-H2A.1	1.222	Q52KG9	Chaperonin containing Tcp1, subunit 6a (Zeta)	1.212
P16015	Carbonic anhydrase 3	1.222	Q3TIX8	Putative uncharacterized protein	1.212
Q7TSJ2	Microtubule-associated protein 6	1.221	P80317	T-complex protein 1 subunit zeta	1.212
D3Z396	Neurotrimin	1.219	Q62108	Disks large homolog 4	1.212
Q99PJ0	Neurotrimin	1.219	Q3UIB5	Putative uncharacterized protein	1.212
Q3TYC2	Putative uncharacterized protein	1.219	Q99LB2	Dehydrogenase/reductase SDR family member 4	1.212
Q8BG33	Neurotrimin	1.219	O70251	Elongation factor 1-beta	1.21
Q3TVF4	Geranylgeranyl transferase type-2 subunit beta	1.216	P16254	Signal recognition particle 14 kDa protein	1.209
P53612	Geranylgeranyl transferase type-2 subunit beta	1.216	Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	1.208
Q9JIF6	RAB geranylgeranyl transferase, b subunit, isoform CRA_c	1.216	Q8C1A5	Thimet oligopeptidase	1.208
Q6PFA1	Rabggtb protein	1.216	Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	1.204
Q99KZ1	Rabggtb protein (Fragment)	1.216	Q3UGX3	N-acetylaspartate synthetase	1.204

The comparison was performed in the spinal cord between a progression SOD1 G93A mouse and an age-matched WT mouse, where the fold > 1.2 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 676 significantly up regulated proteins in the spinal cord between a progression SOD1 G93A mouse vs an age-matched WT mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 6. List of Significantly Down Regulated Proteins in the Spinal Cord between a progression SOD1 G93A Mouse Vs an Age-Matched WT Mouse

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q00898	Alpha-1-antitrypsin 1-5	0.148	Q9JLC8	Sacsin	0.534
Q64018	Glycine receptor subunit alpha-1	0.383	E9QNY8	Sacsin	0.534
A2A6J8	Troponin I, fast skeletal muscle (Fragment)	0.428	Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	0.534
A2A6K0	Troponin I, fast skeletal muscle (Fragment)	0.428	O70250	Phosphoglycerate mutase 2	0.536
P13412	Troponin I, fast skeletal muscle	0.428	Q8R4V3	Acetyl CoA transferase-like protein	0.544
Q9EQX4	Allograft inflammatory factor 1-like	0.439	Q80X81	Acetyl-Coenzyme A acetyltransferase 3	0.544
Q3TRG0	Gene model 1604B, (NCBI)	0.441	Q3UEE0	Sphingomyelin phosphodiesterase	0.548
A2ADY9	Protein DDI1 homolog 2	0.469	Q8K011	Sphingomyelin phosphodiesterase	0.548
E0CX41	Leucine-rich repeat transmembrane neuronal protein 1 (Fragment)	0.472	Q3UG03	Sphingomyelin phosphodiesterase	0.548
Q8K377	Leucine-rich repeat transmembrane neuronal protein 1	0.472	Q04519	Sphingomyelin phosphodiesterase	0.548
Q5DTM2	Oxysterol-binding protein (Fragment)	0.48	Q80UW2	F-box only protein 2	0.551
F8WIZ7	Oxysterol-binding protein	0.48	Q8CEW9	Putative uncharacterized protein	0.562
Q8BXR9	Oxysterol-binding protein-related protein 6	0.48	Q923D4	Splicing factor 3B subunit 5	0.562
Q64676	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	0.484	F6TQW2	Protein Ighg2c	0.567
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.51	P01864	Ig gamma-2A chain C region secreted form	0.567
Q6PNC0	DmX-like protein 1	0.519	Q9D8L4	Putative uncharacterized protein	0.567
F8WGX5	DmX-like protein 1	0.519	Q58E56	Igh protein	0.567
D0U293	Beta-globin	0.522	Q9D154	Leukocyte elastase inhibitor A	0.568
Q9QUN8	Beta-2-globin (Fragment)	0.522	Q3UY05	Putative uncharacterized protein	0.571
A8DV41	Beta-globin	0.522	Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	0.571
P02089	Hemoglobin subunit beta-2	0.522	Q8VC72	NADH dehydrogenase (Ubiquinone) Fe-S protein 8	0.571
Q54AH9	Beta-2-globin (Fragment)	0.522	D3YZV2	Potassium voltage-gated channel subfamily C member 3	0.573
A8DV59	Beta-globin	0.522	Q63959	Potassium voltage-gated channel subfamily C member 3	0.573

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
E9QKI2	Potassium voltage-gated channel subfamily C member 3	0.573	Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	0.595
Q6XE40	MAGUK p55 subfamily member 3	0.578	Q8BJH1	Zinc finger C2HC domain-containing protein 1A	0.595
B2RY90	Isoc2a protein	0.581	Q6NVF0	Inositol polyphosphate 5-phosphatase OCRL-1	0.602
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	0.581	B2KGA7	Protein archease	0.602
Q8VCE6	5~(3~)-deoxyribonucleotidase, mitochondrial	0.581	Q505B7	Protein archease	0.602
Q8R2Y0	Monoacylglycerol lipase ABHD6	0.585	P62631	Elongation factor 1-alpha 2	0.605
Q9D375	Putative uncharacterized protein	0.585	Q3UUI3	Acyl-coenzyme A thioesterase THEM4	0.61
D5MCW4	Protein CutA	0.586	Q91X72	Hemopexin	0.61
Q9CQ89	Protein CutA	0.586	P47809	Dual specificity mitogen-activated protein kinase kinase 4	0.611
Q8C7Z5	Putative uncharacterized protein	0.587	P63248	cAMP-dependent protein kinase inhibitor alpha	0.611
Q499F6	Kcnj10 protein (Fragment)	0.587	Q7TNL5	Protein phosphatase 2, regulatory subunit B (B56), delta isoform, isoform CRA_a	0.613
Q9JM63	ATP-sensitive inward rectifier potassium channel 10	0.587	Q99PC9	Protein phosphatase 2 regulatory subunit B56 delta isoform	0.613
B9EIV1	Kcnj10 protein	0.587	Q91V89	Protein Ppp2r5d	0.613
Q8BUB3	Putative uncharacterized protein	0.588	Q8K5D8	Protein phosphatase 2a regulatory b56-delta subunit (Fragment)	0.613
O35083	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	0.588	O35744	Chitinase-like protein 3	0.615
Q91VJ9	1-acylglycerol-3-phosphate O-acyltransferase 1 (Lysophosphatidic acid acyltransferase, alpha)	0.588	Q8BTA2	Putative uncharacterized protein	0.618
Q9DB72	BTB/POZ domain-containing protein 17	0.591	Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	0.618
D3YTS3	Protein D630045J12Rik	0.591	Q8BLE7	Vesicular glutamate transporter 2	0.62
Q68FD9	UPF0606 protein KIAA1549	0.591	Q9EQZ6	Rap guanine nucleotide exchange factor 4	0.621
F7ATU7	Protein D630045J12Rik (Fragment)	0.591	Q571A8	MKIAA4040 protein (Fragment)	0.621
Q4FZG7	Putative mitochondrial import inner membrane translocase subunit Tim8 A-B	0.595	P56389	Cytidine deaminase	0.621

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
G5E814	MCG5603	0.623	Q921U7	Cast protein	0.646
Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0.623	P51125	Calpastatin	0.646
O35864	COP9 signalosome complex subunit 5	0.626	Q8CE04	Putative uncharacterized protein	0.646
Q8BNY6	Neuronal calcium sensor 1	0.629	Q8CBN6	Protein Gm9967	0.647
Q5SRA0	Disintegrin and metalloproteinase domain-containing protein 23	0.629	Q8BR63	Protein FAM177A1	0.65
Q9R1V7	Disintegrin and metalloproteinase domain-containing protein 23	0.629	P07759	Serine protease inhibitor A3K	0.652
Q5SVE1	Disintegrin and metalloproteinase domain-containing protein 23	0.629	Q8VHP7	Leukocyte elastase inhibitor B	0.654
Q62148	Retinal dehydrogenase 2	0.63	A3QM89	Reticulon (Fragment)	0.654
O88990	Alpha-actinin-3	0.631	Q7M6W1	Reticulon	0.654
Q8BRK8	5~-AMP-activated protein kinase catalytic subunit alpha-2	0.634	Q3U0E7	Putative uncharacterized protein	0.654
Q9D5T0	ATPase family AAA domain-containing protein 1	0.635	Q5DTI3	MKIAA4194 protein (Fragment)	0.656
Q9WVT6	Carbonic anhydrase 14	0.637	Q8BXY4	Putative uncharacterized protein	0.66
Q3US29	Putative uncharacterized protein	0.638	P53994	Ras-related protein Rab-2A	0.66
Q5M8R9	Farnesyl diphosphate synthetase	0.638	Q3TKJ1	Branched-chain-amino-acid aminotransferase	0.66
Q920E5	Farnesyl pyrophosphate synthase	0.638	P24288	Branched-chain-amino-acid aminotransferase, cytosolic	0.66
Q3TMH2	Secernin-3	0.64	Q8CBC8	Branched-chain-amino-acid aminotransferase	0.66
Q6ZQ74	MKIAA0666 protein (Fragment)	0.644	Q9CXX6	Branched-chain-amino-acid aminotransferase	0.66
Q8BPM0	Disheveled-associated activator of morphogenesis 1	0.644	E9Q4K3	Branched-chain-amino-acid aminotransferase	0.66
Q3TZE2	Putative uncharacterized protein (Fragment)	0.644	A2APX6	Sodium channel protein	0.661
Q9R1V4	Disintegrin and metalloproteinase domain-containing protein 11	0.644	A2APX8	Sodium channel protein	0.661
Q7TQG7	A disintegrin and metallopeptidase domain 11, isoform CRA_a	0.644	A2APX7	Sodium channel protein	0.661
Q8C281	Putative uncharacterized protein	0.646	Q91UZ1	Phosphoinositide phospholipase C	0.662
Q8CE80	Calpastatin	0.646	P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	0.667

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
A2AVR9	Dynein light chain roadblock-type 1	0.669	P18894	D-amino-acid oxidase	0.678
P62627	Dynein light chain roadblock-type 1	0.669	B2RU82	Solute carrier family 30 (Zinc transporter), member 9	0.682
Q3TP69	Putative uncharacterized protein	0.67	F8WHL1	Zinc transporter 9	0.682
Q8R3X6	Glypican 6	0.67	Q5IRJ6	Zinc transporter 9	0.682
Q9R087	Glypican-6	0.67	P50114	Protein S100-B	0.685
Q8BGD5	Carnitine O-palmitoyltransferase 1, brain isoform	0.671	A2AMH4	Choline transporter-like protein 1	0.686
B2RSH2	Guanine nucleotide-binding protein G(i) subunit alpha-1	0.672	Q6X893	Choline transporter-like protein 1	0.686
Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	0.672	A2AMH5	Choline transporter-like protein 1	0.686
Q9QUP5	Hyaluronan and proteoglycan link protein 1	0.672	B1AQY2	Rho GTPase-activating protein 23	0.686
H3BLL2	ATP synthase mitochondrial F1 complex assembly factor 1	0.673	Q69ZH9	Rho GTPase-activating protein 23	0.686
Q811I0	ATP synthase mitochondrial F1 complex assembly factor 1	0.673	F8VQ11	Rho GTPase-activating protein 23	0.686
G3X9J8	Prominin 1, isoform CRA_g	0.673	Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	0.687
G5E8G5	Prominin 1, isoform CRA_a	0.673	Q9DB16	Calcium-binding protein 39-like	0.687
O54990	Prominin-1	0.673	Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	0.688
Q8R056	Prom1 protein	0.673	A2BDX3	Adenylyltransferase and sulfurtransferase MOCS3	0.689
Q8CDK8	Prominin-1	0.673	Q9CQA1	Trafficking protein particle complex subunit 5	0.69
Q8R404	Protein QIL1	0.675	Q8R429	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	0.691
Q5M8M3	Uncharacterized protein	0.675	Q3V1R3	Putative uncharacterized protein	0.692
Q9DCG9	Multifunctional methyltransferase subunit TRM112-like protein	0.675	Q8K406	Leucine-rich repeat LGI family member 3	0.692
Q8VCR4	0610038D11Rik protein	0.675	Q8C078	Calcium/calmodulin-dependent protein kinase kinase 2	0.694
Q99J77	N-acetylneuraminic acid synthase (Sialic acid synthase)	0.675	Q80XD3	Rgs7 protein	0.695
P05977	Myosin light chain 1/3, skeletal muscle isoform	0.676	O54829	Regulator of G-protein signaling 7	0.695
Q5SX39	Myosin-4	0.677	D3Z2J6	Thioredoxin-related transmembrane protein 2	0.697

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q9D710	Thioredoxin-related transmembrane protein 2	0.697	P62746	Rho-related GTP-binding protein RhoB	0.71
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	0.697	Q9R061	Cytosolic Fe-S cluster assembly factor NUBP2	0.71
A0A075DC90	Cytochrome c oxidase subunit 2	0.698	Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	0.711
P00405	Cytochrome c oxidase subunit 2	0.698	Q5SRX1	TOM1-like protein 2	0.713
Q8VE47	Ubiquitin-like modifier-activating enzyme 5	0.699	Q99JW2	Aminoacylase-1	0.714
P97379	Ras GTPase-activating protein-binding protein 2	0.699	Q3TIX9	U4/U6.U5 tri-snRNP-associated protein 2	0.715
D3YZP9	Coiled-coil domain-containing protein 6	0.7	S4R1M9	Oxysterol-binding protein	0.716
Q8BGB7	Enolase-phosphatase E1	0.701	S4R296	Oxysterol-binding protein	0.716
Q9D6K8	FUN14 domain-containing protein 2	0.701	Q8R2T7	Oxysterol-binding protein	0.716
Q61733	28S ribosomal protein S31, mitochondrial	0.701	D3YTU0	Vesicle-associated membrane protein 1	0.717
Q920I9	WD repeat-containing protein 7	0.702	Q9CXX2	Putative uncharacterized protein	0.717
Q80WM4	Hyaluronan and proteoglycan link protein 4	0.702	Q62442	Vesicle-associated membrane protein 1	0.717
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	0.702	Q9CQ54	NADH dehydrogenase [ubiquinone] 1 subunit C2	0.717
Q3UIA5	Putative uncharacterized protein	0.702	Q9D846	NADH dehydrogenase [ubiquinone] 1 subunit C2	0.717
Q9WTX6	Cullin-1	0.702	Q80TJ1	Calcium-dependent secretion activator 1	0.718
Q3UYC0	Protein phosphatase 1H	0.702	B1AX58	Plastin-3	0.719
Q80TB8	Synaptic vesicle membrane protein VAT-1 homolog-like	0.705	D3YVX4	Stromal membrane-associated protein 1	0.721
Q8BHW2	Protein OSCP1	0.705	Q91VZ6	Stromal membrane-associated protein 1	0.721
Q5SVL6	Rap1 GTPase-activating protein 2	0.707	P63141	Potassium voltage-gated channel subfamily A member 2	0.724
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	0.708	Q9CQ65	S-methyl-5~-thioadenosine phosphorylase	0.732
E0CZE0	NEDD8-activating enzyme E1 regulatory subunit	0.708	P63213	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2	0.732
Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit	0.708	Q6A4J8	Ubiquitin carboxyl-terminal hydrolase 7	0.733
P61329	Fibroblast growth factor 12	0.709	F8VPX1	Ubiquitin carboxyl-terminal hydrolase	0.733

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
E9PXY8	Ubiquitin carboxyl-terminal hydrolase	0.733	Q3UFD0	Putative uncharacterized protein	0.74
Q8CI71	Coiled-coil domain-containing protein 132	0.733	Q9D6K5	Synaptojanin-2-binding protein	0.74
Q8BQX9	Putative uncharacterized protein	0.734	E9PVN6	Protein Gm20498	0.74
Q8C7S9	Putative uncharacterized protein	0.734	Q6Y642	Activin receptor-interacting protein 2a	0.74
Q8VD73	Potassium voltage-gated channel, shaker-related subfamily, beta member 3	0.734	Q8VIM9	Immunity-related GTPase family Q protein	0.74
P97382	Voltage-gated potassium channel subunit beta-3	0.734	E9Q6P5	Protein Ttc7b	0.74
F8WIS9	Calcium/calmodulin-dependent protein kinase type II subunit alpha	0.735	G3XA48	Isopentenyl-diphosphate Delta-isomerase 1	0.74
Q80TN1	MKIAA0968 protein (Fragment)	0.735	P58044	Isopentenyl-diphosphate Delta-isomerase 1	0.74
P11798	Calcium/calmodulin-dependent protein kinase type II subunit alpha	0.735	E9PW07	Protein Dos	0.74
Q3TWN8	Putative uncharacterized protein	0.736	E9QP85	Protein Dos	0.74
Q9Z110	Delta-1-pyrroline-5-carboxylate synthase	0.736	Q66L44	Protein Dos	0.74
Q3TES0	IQ motif and SEC7 domain-containing protein 3	0.738	P46660	Alpha-internexin	0.741
Q3UHJ6	Putative uncharacterized protein	0.738	Q3TJB4	Putative uncharacterized protein	0.743
Q9WU63	Heme-binding protein 2	0.738	Q3U3C4	Putative uncharacterized protein	0.743
D3YUP9	Disintegrin and metalloproteinase domain-containing protein 22	0.739	Q62419	Endophilin-A2	0.743
Q9R1V6	Disintegrin and metalloproteinase domain-containing protein 22	0.739	Q3TD17	Putative uncharacterized protein	0.743
A4FUT9	Adam22 protein (Fragment)	0.739	Q3U2J2	Putative uncharacterized protein	0.743
P45591	Cofilin-2	0.739	P17809	Solute carrier family 2, facilitated glucose transporter member 1	0.743
Q8VED9	Galectin-related protein	0.739	Q8C0E1	Serine/threonine-protein phosphatase 2A activator	0.744
Q3UVI9	Putative uncharacterized protein	0.739	P58389	Serine/threonine-protein phosphatase 2A activator	0.744
Q99LE6	ATP-binding cassette sub-family F member 2	0.739	F8VPQ4	SLIT-ROBO Rho GTPase-activating protein 3	0.744
Q3TST0	Putative uncharacterized protein	0.739	Q812A2	SLIT-ROBO Rho GTPase-activating protein 3	0.744
Q8K1R3	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	0.739	E9QN14	SLIT-ROBO Rho GTPase-activating protein 3	0.744

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q9DB73	NADH-cytochrome b5 reductase 1	0.744	Q3TY51	Kinesin-like protein	0.758
A0JNY3	Gephyrin	0.745	P28738	Kinesin heavy chain isoform 5C	0.758
Q8BUV3	Gephyrin	0.745	Q8CHF1	Kinesin-like protein (Fragment)	0.758
Q8K2C9	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	0.745	P33175	Kinesin heavy chain isoform 5A	0.758
Q0KL02	Triple functional domain protein	0.745	E0CYV0	Protein-L-isoaspartate O-methyltransferase	0.758
Q80YV4	Pantothenate kinase 4	0.748	Q8BPI6	Protein-L-isoaspartate O-methyltransferase (Fragment)	0.758
P16390	Potassium voltage-gated channel subfamily A member 3	0.749	E9PWE0	Protein-L-isoaspartate O-methyltransferase	0.758
A6H5Z3	Exocyst complex component 6B	0.751	P23506	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	0.758
Q80TQ3	MKIAA0845 protein (Fragment)	0.752	F7D432	Protein-L-isoaspartate O-methyltransferase (Fragment)	0.758
P19246	Neurofilament heavy polypeptide	0.752	Q3UFF9	Putative uncharacterized protein	0.758
Q60737	Casein kinase II subunit alpha	0.752	Q8BM84	Putative uncharacterized protein	0.758
Q61177	Casein kinase II alpha subunit	0.752	P70372	ELAV-like protein 1	0.758
D3YVV3	Protein Ankrd29	0.752	Q8BW03	Putative uncharacterized protein	0.758
A0A087WNV1	Arf-GAP domain and FG repeat-containing protein 1	0.752	Q9CZX0	Elongator complex protein 3	0.758
A0A087WR52	Arf-GAP domain and FG repeat-containing protein 1 (Fragment)	0.752	Q5M8N4	Epimerase family protein SDR39U1	0.759
Q8K2K6	Arf-GAP domain and FG repeat-containing protein 1	0.752	Q8BZ98	Dynamin-3	0.76
A0A087WSR7	Arf-GAP domain and FG repeat-containing protein 1	0.752	Q8BUT2	Putative uncharacterized protein	0.76
B1ASU0	Interleukin-1 receptor accessory protein-like 1	0.753	E9QLL2	Dynamin-3	0.76
B9EKJ3	Mon2 protein	0.755	A3KGU7	Spectrin alpha chain, non-erythrocytic 1	0.761
Q80TL7	Protein MON2 homolog	0.755	B9EKJ1	Spna2 protein	0.761
Q3UNF6	Putative uncharacterized protein	0.757	B2RXX6	Spna2 protein	0.761
Q8BGE6	Cysteine protease ATG4B	0.757	Q9Z0P5	Twinfilin-2	0.762
Q9Z0E0	Neurochondrin	0.758	Q8BNU0	Armadillo repeat-containing protein 6	0.762

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q03517	Secretogranin-2	0.762	Q8K4Z3	NAD(P)H-hydrate epimerase	0.771
Q99JB8	Protein kinase C and casein kinase II substrate protein 3	0.762	Q9D1K2	V-type proton ATPase subunit F	0.772
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.763	Q3TL79	Putative uncharacterized protein	0.773
P08553	Neurofilament medium polypeptide	0.764	Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	0.773
Q8CHT1	Ephexin-1	0.764	Q8BU21	Glutaminyl-tRNA synthetase, isoform CRA_a	0.773
E9QK62	Ephexin-1	0.764	Q3TN94	Putative uncharacterized protein	0.773
Q9D4H8	Cullin-2	0.764	Q8BML9	Glutaminyl-tRNA synthetase	0.773
Q571A2	MKIAA4106 protein (Fragment)	0.764	D3YTP3	Protein Mtx3	0.774
Q9ERK4	Exportin-2	0.766	Q6A028	Switch-associated protein 70	0.776
Q5DTH1	MKIAA4216 protein (Fragment)	0.766	Q05BD4	Prpsap2 protein	0.777
Q8CE29	Ubiquitin protein ligase E3A	0.766	Q8R574	Phosphoribosyl pyrophosphate synthase-associated protein 2	0.777
E9QKT1	Ubiquitin-protein ligase E3A	0.766	Q8BK37	Putative uncharacterized protein	0.777
Q4VAF0	Acylphosphatase (Fragment)	0.767	Q8R146	Acylamino-acid-releasing enzyme	0.777
P56376	Acylphosphatase-1	0.767	Q9CPW0	Contactin-associated protein-like 2	0.778
E9QJT5	Acylphosphatase	0.767	E9QNF7	Contactin-associated protein-like 2	0.778
B1AZF3	Serine/threonine-protein kinase LMTK1	0.767	Q61151	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	0.778
B1AZF9	Apoptosis-associated tyrosine kinase	0.767	Q0VF59	Disks large-associated protein 2	0.778
Q80YE4	Serine/threonine-protein kinase LMTK1	0.767	Q8BJ42	Disks large-associated protein 2	0.778
Q7TMF3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	0.768	Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	0.779
Q8BME2	Putative uncharacterized protein	0.768	Q8K0U4	Heat shock 70 kDa protein 12A	0.781
G3X9F4	Transmembrane protein 143	0.769	Q69ZK9	Neuroligin-2	0.781
Q8VD26	Transmembrane protein 143	0.769	B2RQ71	Dip2c protein	0.781
Q91V41	Ras-related protein Rab-14	0.771	E9PWR4	Protein Dip2c	0.781

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q9Z0R4	Intersectin-1	0.782	Q78ZA7	Nucleosome assembly protein 1-like 4	0.791
E9Q0N0	Intersectin-1	0.782	P58281	Dynamin-like 120 kDa protein, mitochondrial	0.792
Q6P9J5	KN motif and ankyrin repeat domain-containing protein 4	0.782	Q3UHL8	Putative uncharacterized protein (Fragment)	0.795
D3YUM1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0.784	F6VG18	Leucine zipper transcription factor-like protein 1 (Fragment)	0.795
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0.784	Q9JHQ5	Leucine zipper transcription factor-like protein 1	0.795
G3UYW1	WD repeat and FYVE domain-containing protein 3	0.784	Q8CDG8	Putative uncharacterized protein	0.795
Q6VNB8	WD repeat and FYVE domain-containing protein 3	0.784	F6VTH5	Leucine zipper transcription factor-like protein 1 (Fragment)	0.795
P35585	AP-1 complex subunit mu-1	0.784	Q3UJ20	Putative uncharacterized protein	0.796
Q9DBL7	Bifunctional coenzyme A synthase	0.786	P17183	Gamma-enolase	0.796
Q9QXS6	Drebrin	0.787	Q9Z140	Copine-6	0.797
P61164	Alpha-centractin	0.788	Q80V42	Carboxypeptidase M	0.797
Q3UI39	Putative uncharacterized protein	0.788	Q3UGN9	Signal transducing adapter molecule 1	0.799
E9QLK9	Clathrin coat assembly protein AP180	0.788	P70297	Signal transducing adapter molecule 1	0.799
E9Q9A3	Clathrin coat assembly protein AP180	0.788	Q3UMC8	Putative uncharacterized protein	0.799
Q61548	Clathrin coat assembly protein AP180	0.788	P49442	Inositol polyphosphate 1-phosphatase	0.8
E9QQ05	Clathrin coat assembly protein AP180	0.788	Q9QXB9	Developmentally-regulated GTP-binding protein 2	0.8
D3Z0M6	Cytoplasmic dynein 1 intermediate chain 1	0.789	Q9CX34	Suppressor of G2 allele of SKP1 homolog	0.8
O88485	Cytoplasmic dynein 1 intermediate chain 1	0.789	Q8BKC5	Importin-5	0.802
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta	0.789	Q8BNU3	Putative uncharacterized protein	0.802
Q9D517	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	0.789	P50608	Fibromodulin	0.802
Q6NZL0	Protein SOGA3	0.79	Q3TSY8	DCN1-like protein	0.802
B7ZNL2	Nap1l4 protein	0.791	G5E8Q6	DCN1-like protein	0.802
Q8C1W9	Putative uncharacterized protein	0.791	G5E8Q5	DCN1-like protein	0.802

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8BZJ7	DCN1-like protein 2	0.802	Q02357	Ankyrin-1	0.812
Q9DBJ1	Phosphoglycerate mutase 1	0.804	B7ZW98	Ank1 protein	0.812
Q6ZQ84	MKIAA0617 protein (Fragment)	0.804	Q8BVE3	V-type proton ATPase subunit H	0.812
Q9JLV5	Cullin-3	0.804	Q9D394	Protein RUFY3	0.814
Q3TDK6	Protein rogdi homolog	0.804	P56379	6.8 kDa mitochondrial proteolipid	0.814
P42669	Transcriptional activator protein Pur-alpha	0.805	Q80TZ3	Putative tyrosine-protein phosphatase auxilin	0.816
Q5SQX6	Cytoplasmic FMR1-interacting protein 2	0.805	Q3U5V6	Putative uncharacterized protein	0.816
Q8BGH2	Sorting and assembly machinery component 50 homolog	0.805	P62838	Ubiquitin-conjugating enzyme E2 D2	0.816
Q3UHJ0	AP2-associated protein kinase 1	0.808	Q6ZWY6	Ubiquitin-conjugating enzyme E2 D2B	0.816
Q61699	Heat shock protein 105 kDa	0.808	P61079	Ubiquitin-conjugating enzyme E2 D3	0.816
E9PX29	Protein Sptbn4	0.808	Q9D7F5	Putative uncharacterized protein	0.816
Q7TQF7	Amphiphysin	0.808	Q9D1S1	Putative uncharacterized protein	0.816
Q8BH66	Atlastin-1	0.808	Q8C076	Putative uncharacterized protein	0.817
Q3UEW2	Putative uncharacterized protein	0.808	P59016	Vacuolar protein sorting-associated protein 33B	0.817
Q9WV69	Dematin	0.808	Q8VDQ8	NAD-dependent protein deacetylase sirtuin-2	0.818
Q5F2D0	Putative uncharacterized protein	0.809	Q3UDQ7	Putative uncharacterized protein	0.82
Q91WC3	Long-chain-fatty-acid--CoA ligase 6	0.809	Q8JZQ2	AFG3-like protein 2	0.82
A8IP90	Long-chain acyl-CoA synthetase	0.809	Q3TFF0	Putative uncharacterized protein	0.823
Q80U19	Disheveled-associated activator of morphogenesis 2	0.809	Q9QYJ0	DnaJ homolog subfamily A member 2	0.823
Q8C7R4	Ubiquitin-like modifier-activating enzyme 6	0.809	Q3U7R1	Extended synaptotagmin-1	0.825
D3YTV8	Ankyrin-1	0.812	A0A087WNZ9	Regulator of G-protein-signaling 6	0.825
E9QNT8	Ankyrin-1	0.812	A0A087WSJ9	Regulator of G-protein-signaling 6	0.825
G5E8J2	Ankyrin 1, erythroid	0.812	A0A087WRP8	Regulator of G-protein-signaling 6 (Fragment)	0.825

Supplementary Table 6 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
A0A087WPD1	Regulator of G-protein-signaling 6	0.825	B0V2P5	DmX-like protein 2	0.828
F6WDS8	Regulator of G-protein-signaling 6	0.825	Q8BPN8	DmX-like protein 2	0.828
A0A087WPC4	Regulator of G-protein-signaling 6 (Fragment)	0.825	E9Q3V0	Transporter	0.828
A0A087WRN0	Regulator of G-protein-signaling 6 (Fragment)	0.825	E9Q517	Transporter	0.828
A0A087WPW1	Regulator of G-protein-signaling 6	0.825	P28571	Sodium- and chloride-dependent glycine transporter 1	0.828
Q9Z2H2	Regulator of G-protein signaling 6	0.825	Q9ESM3	Hyaluronan and proteoglycan link protein 2	0.828
A0A087WQG6	Regulator of G-protein-signaling 6	0.825	Q9D7N3	28S ribosomal protein S9, mitochondrial	0.828
P11930	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	0.825	Q9EPN1	Neurobeachin	0.829
Z4YJV4	2-oxoglutarate dehydrogenase, mitochondrial	0.826	O54774	AP-3 complex subunit delta-1	0.83
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	0.826	Q8BTX9	Inactive hydroxysteroid dehydrogenase-like protein 1	0.83
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	0.827	Q3TMN1	Methionine aminopeptidase 2	0.83
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	0.827	Q3UI33	Methionine aminopeptidase 2	0.83

The comparison was performed in the spinal cord between a progression SOD1 G93A mouse and an age-matched WT mouse, where the fold < 0.833 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 480 significantly down regulated proteins in the spinal cord between a progression SOD1 G93A mouse vs an age-matched WT mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 7. List of Significantly Up Regulated Proteins in the Spinal Cord between the Onset Vs the Pre-onset of SOD1 G93A Mouse

Accession No	Description	Fold Change (Onset)
Q8R422	CD109 antigen	3.083
Q3TXB1	Putative uncharacterized protein	2.939
Q3UBX7	Putative uncharacterized protein	2.939
P98086	Complement C1q subcomponent subunit A	2.939
Q91X23	Alpha-1-acid glycoprotein	2.901
Q61613	Alpha-1-acid glycoprotein (AGP) (Fragment)	2.901
Q4FJY6	Ifit3 protein	2.852
E9PV48	Protein I830012O16Rik	2.852
Q64345	Interferon-induced protein with tetratricopeptide repeats 3	2.852
Q8BPC3	Putative uncharacterized protein	2.852
Q6GQT1	Alpha-2-macroglobulin-P	2.74
P14602	Heat shock protein beta-1	2.631
Q91X72	Hemopexin	2.608
P50543	Protein S100-A11	2.571
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a	2.543
Q3UN02	Lysocardiolipin acyltransferase 1	2.452
D3YX85	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	2.232
Q6A074	MKIAA0400 protein (Fragment)	2.232
Q3TS63	Putative uncharacterized protein (Fragment)	2.232
Q7SIG6	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	2.232
Q3UH05	Putative uncharacterized protein	2.232
E9PX52	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	2.232
Q3UH27	Putative uncharacterized protein	2.232
Q6GT24	Peroxiredoxin 6	2.209
B1B1A8	Myosin light chain kinase, smooth muscle	2.179
Q6PDN3	Myosin light chain kinase, smooth muscle	2.179
Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	2.145
Q0VGY8	Protein TANC1	2.106
Q8CHA0	MKIAA1728 protein (Fragment)	2.106
B9EJ77	Tanc1 protein	2.106
E9QAF9	Protein TANC1	2.106
P70232	Neural cell adhesion molecule L1-like protein	2.089
M0QWA7	Integrin beta	2.083
P11835	Integrin beta-2	2.083
Q542I8	Integrin beta	2.083
O09114	Prostaglandin-H2 D-isomerase	2.035
Q8BW44	Putative uncharacterized protein	1.988
Q91YN3	Acyl-CoA synthetase long-chain family member 4	1.988
Q9QUJ7	Long-chain-fatty-acid--CoA ligase 4	1.988
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	1.979
O88492	Perilipin-4	1.96
Q3TWH2	Putative uncharacterized protein	1.93
Q61941	NAD(P) transhydrogenase, mitochondrial	1.93
Q8C1W8	Nicotinamide nucleotide transhydrogenase, isoform CRA_a	1.93
Q922E1	Nicotinamide nucleotide transhydrogenase	1.93
Q9JMK2	Casein kinase I isoform epsilon	1.881
Q0GNC1	Inverted formin-2	1.877
E9QLA5	Inverted formin-2	1.877
A2AN81	H/ACA ribonucleoprotein complex subunit 4 (Fragment)	1.812
Q9ESX5	H/ACA ribonucleoprotein complex subunit 4	1.812

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3TI79	Putative uncharacterized protein	1.812	B2RRF1	B230339M05Rik protein	1.75
F6YUI5	H/ACA ribonucleoprotein complex subunit 4 (Fragment)	1.812	Q7TSH2	Phosphorylase b kinase regulatory subunit beta	1.75
B7ZCL7	H/ACA ribonucleoprotein complex subunit 4 (Fragment)	1.812	Q3TGQ3	Putative uncharacterized protein	1.747
Q3TM67	Putative uncharacterized protein	1.812	P26231	Catenin alpha-1	1.747
Q499D4	Dkc1 protein	1.812	O35864	COP9 signalosome complex subunit 5	1.747
Q3TXM3	Amino acid transporter	1.765	D0U293	Beta-globin	1.716
O35544	Excitatory amino acid transporter 4	1.765	Q9QUN8	Beta-2-globin (Fragment)	1.716
A2CG35	Ras-related protein Rab-12	1.756	A8DV41	Beta-globin	1.716
P35283	Ras-related protein Rab-12	1.756	P02089	Hemoglobin subunit beta-2	1.716
A2APM1	CD44 antigen	1.755	Q54AH9	Beta-2-globin (Fragment)	1.716
E9QKM8	CD44 antigen	1.755	A8DV59	Beta-globin	1.716
P15379	CD44 antigen	1.755	Q9JKY7	Cytochrome P450 CYP2D22	1.693
Q80X37	CD44 antigen	1.755	Q91W87	Cytochrome P450, family 2, subfamily d, polypeptide 22	1.693
Q3U8S1	CD44 antigen	1.755	Q3U645	Putative uncharacterized protein	1.689
Q3TLT9	Putative uncharacterized protein	1.755	Q9DBZ6	Putative uncharacterized protein	1.689
A2APM5	CD44 antigen	1.755	P55096	ATP-binding cassette sub-family D member 3	1.689
A2APM2	CD44 antigen	1.755	Q91VT3	ATP-binding cassette, sub-family D (ALD), member 3	1.689
Q3U468	Putative uncharacterized protein	1.755	Q3TWD0	Putative uncharacterized protein	1.685
Q3UNN2	Putative uncharacterized protein	1.755	Q3U7P0	Putative uncharacterized protein	1.685
A2APM4	CD44 antigen	1.755	P18242	Cathepsin D	1.685
A2APM3	CD44 antigen	1.755	Q8C243	Putative uncharacterized protein	1.685
A2ACC6	Ral GTPase-activating protein subunit beta	1.75	Q3TWR6	Putative uncharacterized protein	1.685
E9Q0J2	Ral GTPase-activating protein subunit beta	1.75	Q3U8W5	Putative uncharacterized protein	1.685
F8WHN4	Ral GTPase-activating protein subunit beta	1.75	Q3TWE1	Putative uncharacterized protein	1.679
Q8BQZ4	Ral GTPase-activating protein subunit beta	1.75	Q9CZU7	Putative uncharacterized protein	1.679

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q8C876	Putative uncharacterized protein	1.679	Q06890	Clusterin	1.626
Q3UIW3	Putative uncharacterized protein	1.679	Q3TDR0	Putative uncharacterized protein	1.614
P17047	Lysosome-associated membrane glycoprotein 2	1.679	Q6GV12	3-ketodihydrosphingosine reductase	1.614
Q8C5K0	Lysosomal membrane glycoprotein 2, isoform CRA_a	1.679	Q3TWV0	Putative uncharacterized protein	1.61
B2RXW7	Complement component 4B (Childo blood group)	1.677	P20152	Vimentin	1.61
P62331	ADP-ribosylation factor 6	1.676	Q3TCP5	Putative uncharacterized protein	1.61
Q3UDC0	Putative uncharacterized protein (Fragment)	1.673	Q3UXR4	Putative uncharacterized protein	1.61
Q3UDC7	Putative uncharacterized protein (Fragment)	1.673	P26040	Ezrin	1.61
Q9Z0E6	Interferon-induced guanylate-binding protein 2	1.673	Q3UL48	Putative uncharacterized protein	1.61
Q7TND9	Dihydrolipoamide branched chain transacylase E2	1.666	P20060	Beta-hexosaminidase subunit beta	1.601
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	1.666	Q3TJB4	Putative uncharacterized protein	1.601
A3KGU5	Spectrin alpha chain, non-erythrocytic 1	1.665	Q3U3C4	Putative uncharacterized protein	1.601
Q3V471	Galectin (Fragment)	1.664	Q62419	Endophilin-A2	1.601
Q8C253	Galectin	1.664	Q3UQ84	Threonine--tRNA ligase, mitochondrial	1.598
P16110	Galectin-3	1.664	Q922A3	Tars2 protein	1.598
Q9D3M4	Protein S100	1.656	E9Q7H6	Threonine--tRNA ligase, mitochondrial	1.598
Q91V77	Protein S100	1.656	Q3TP97	Threonine--tRNA ligase, mitochondrial	1.598
B2ZRS5	DEP domain-containing mTOR-interacting protein	1.649	D3Z2Y6	Protein S100a16 (Fragment)	1.595
B2ZRS7	Depdc6-003	1.649	Q3TVE3	Putative uncharacterized protein	1.595
B2ZRS8	Depdc6-003	1.649	Q9D708	Protein S100a16	1.595
B2ZRS6	Depdc6-002	1.649	Q9CQE5	Regulator of G-protein signaling 10	1.589
Q570Y9	DEP domain-containing mTOR-interacting protein	1.649	Q3TVS6	Putative uncharacterized protein	1.576
Q5SVR0	TBC1 domain family member 9B	1.646	P10605	Cathepsin B	1.576
Q9WVA4	Transgelin-2	1.641	F8WGT1	Adenosylhomocysteinase	1.566

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q68FL4	Putative adenosylhomocysteinase 3	1.566	Q3U6C5	Voltage-gated potassium channel subunit beta-1	1.493
Q3UF30	Putative uncharacterized protein	1.561	Q9D5E9	Voltage-gated potassium channel subunit beta-1	1.493
P08207	Protein S100-A10	1.561	P63143	Voltage-gated potassium channel subunit beta-1	1.493
E9QK82	Myelin protein P0	1.56	Q8BXZ1	Protein disulfide-isomerase TMX3	1.487
A2AL85	Aspartyl/asparaginyl beta-hydroxylase	1.559	Q62351	Transferrin receptor protein 1	1.482
Q8BSY0	Aspartyl/asparaginyl beta-hydroxylase	1.559	Q3T9U9	Putative uncharacterized protein	1.48
Q8BQK0	Putative uncharacterized protein	1.559	P27659	60S ribosomal protein L3	1.48
Q8CBM2	Aspartyl/asparaginyl beta-hydroxylase	1.559	Q3UB15	Putative uncharacterized protein	1.48
Q9EQ66	Aspartly beta-hydroxylase	1.559	Q3UB67	Putative uncharacterized protein	1.48
Q04690	Neurofibromin	1.543	Q3U9L3	Putative uncharacterized protein	1.48
M0QWP2	ER membrane protein complex subunit 8 (Fragment)	1.531	Q3UB90	Putative uncharacterized protein	1.48
Q8C988	Putative uncharacterized protein	1.531	Q9QYB1	Chloride intracellular channel protein 4	1.477
Q3TTC9	Putative uncharacterized protein	1.531	A0A087WPR9	Protein FAM134A (Fragment)	1.474
M0QWY0	ER membrane protein complex subunit 8 (Fragment)	1.531	Q6NS82	Protein FAM134A	1.474
O70378	ER membrane protein complex subunit 8	1.531	Q3UP03	Putative uncharacterized protein (Fragment)	1.465
E9PYB0	Protein Ahnak2 (Fragment)	1.516	B9EIV0	Ablim1 protein	1.465
Q9DB60	Prostamide/prostaglandin F synthase	1.516	Q8K4G5	Actin-binding LIM protein 1	1.465
Q9DAW9	Calponin-3	1.513	E9Q9C2	Actin-binding LIM protein 1	1.465
Q9CXD6	Mitochondrial calcium uniporter regulator 1	1.513	E9Q9C0	Actin-binding LIM protein 1	1.465
Q8QZY9	Splicing factor 3B subunit 4	1.502	E9Q9C4	Actin-binding LIM protein 1	1.465
P17156	Heat shock-related 70 kDa protein 2	1.501	E9QK41	Actin-binding LIM protein 1	1.465
D3YW87	Filamin-C	1.5	E9Q9C1	Actin-binding LIM protein 1	1.465
Q8VHX6	Filamin-C	1.5	E9Q9C7	Actin-binding LIM protein 1	1.465
D3Z576	Filamin-C	1.5	Q3UA32	Polypeptide N-acetylgalactosaminyltransferase (Fragment)	1.465
Q50DZ7	LGI2B brain-derived splice form	1.498	Q3UM52	Polypeptide N-acetylgalactosaminyltransferase (Fragment)	1.465

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q6PB93	Polypeptide N-acetylgalactosaminyltransferase 2	1.465	Q8CI22	2310005E10Rik protein	1.447
Q8C1D9	Putative uncharacterized protein	1.456	Q3U2B2	Putative uncharacterized protein	1.447
P63082	V-type proton ATPase 16 kDa proteolipid subunit	1.456	Q7TMD4	Niemann Pick type C1	1.447
E9Q9C5	V-type proton ATPase 16 kDa proteolipid subunit (Fragment)	1.456	O35604	Niemann-Pick C1 protein	1.447
Q80YP7	Atp6v0c protein (Fragment)	1.456	F6YB25	Regulation of nuclear pre-mRNA domain-containing protein 1B (Fragment)	1.445
Q3TSU7	Putative uncharacterized protein (Fragment)	1.456	Q9CSU0	Regulation of nuclear pre-mRNA domain-containing protein 1B	1.445
Q91YM2	Rho GTPase-activating protein 35	1.456	Q8BGU5	Cyclin-Y	1.443
Q3US35	Amino acid transporter	1.455	Q8BPU7	Engulfment and cell motility protein 1	1.442
O35874	Neutral amino acid transporter A	1.455	Q571D6	MKIAA0281 protein (Fragment)	1.442
Q9ESU8	Amino acid transporter	1.455	Q9D5T0	ATPase family AAA domain-containing protein 1	1.44
Q8BXT5	Amino acid transporter	1.455	O70503	Estradiol 17-beta-dehydrogenase 12	1.439
Q3TT06	Putative uncharacterized protein	1.455	Q3TFK4	Annexin	1.438
Q8BH74	Nuclear pore complex protein Nup107	1.455	Q8C1X9	Annexin	1.438
Q569X8	Nucleoporin 107	1.455	Q3U737	Annexin	1.438
E9Q4V9	Nuclear pore complex protein Nup107	1.455	O35639	Annexin A3	1.438
Q3TGN0	Putative uncharacterized protein (Fragment)	1.453	Q9CQU0	Thioredoxin domain-containing protein 12	1.436
Q8BL63	GPI-anchor transamidase	1.453	P16045	Galectin-1	1.424
Q8BXX3	GPI-anchor transamidase	1.453	Q3TTY6	Putative uncharacterized protein (Fragment)	1.424
Q9CXY9	GPI-anchor transamidase	1.453	O88952	Protein lin-7 homolog C	1.424
E9Q421	GPI-anchor transamidase	1.453	Q3TZQ2	Putative uncharacterized protein	1.416
Q8BGX2	Uncharacterized protein C19orf52 homolog	1.45	P26041	Moesin	1.416
Q91W86	Vacuolar protein sorting-associated protein 11 homolog	1.448	Q6PEV0	Ephx1 protein	1.416
D3Z494	MCG142264, isoform CRA_a	1.447	Q9D379	Epoxide hydrolase 1	1.416
Q8BIV6	Putative uncharacterized protein	1.447	E9PWK1	Epoxide hydrolase 1	1.416
G5E895	MCG142264, isoform CRA_b	1.447	Q8K2W5	Epoxide hydrolase 1, microsomal	1.416

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	1.414	Q3TPX4	Exocyst complex component 5	1.385
P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	1.41	Q3U8A5	Putative uncharacterized protein	1.385
Q3TIP8	Putative uncharacterized protein	1.409	P09528	Ferritin heavy chain	1.384
Q9Z1Q5	Chloride intracellular channel protein 1	1.409	F8VQ40	Laminin subunit alpha-1	1.382
Q9WTI7	Unconventional myosin-Ic	1.408	P19137	Laminin subunit alpha-1	1.382
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	1.406	Q6P3C3	Calsequestrin	1.381
K3W4R4	Collagen alpha-1(XIV) chain	1.405	O09165	Calsequestrin-1	1.381
B7ZNH7	Collagen alpha-1(XIV) chain	1.405	Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	1.378
Q80X19	Collagen alpha-1(XIV) chain	1.405	Q3TP13	Putative uncharacterized protein (Fragment)	1.377
D3YTT4	Isobutyryl-CoA dehydrogenase, mitochondrial	1.403	Q3TN26	Putative uncharacterized protein	1.377
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	1.403	Q60714	Long-chain fatty acid transport protein 1	1.377
Q7TMB8	Cytoplasmic FMR1-interacting protein 1	1.401	Q8BK72	28S ribosomal protein S27, mitochondrial	1.376
Q3TMH2	Secernin-3	1.401	Q80ZI4	Mrps27 protein	1.376
Q8BRF7	Sec1 family domain-containing protein 1	1.4	P28650	Adenylosuccinate synthetase isozyme 1	1.373
Q9D020	Cytosolic 5~-nucleotidase 3A	1.4	Q7TNV0	Protein DEK	1.372
P61226	Ras-related protein Rap-2b	1.399	Q9CVL7	Putative uncharacterized protein (Fragment)	1.372
Q8R4V3	Acetyl CoA transferase-like protein	1.398	Q9D023	Mitochondrial pyruvate carrier 2	1.372
Q80X81	Acetyl-Coenzyme A acetyltransferase 3	1.398	Q3THQ0	Beta-hexosaminidase	1.367
B2RY90	Isoc2a protein	1.397	Q3U936	Beta-hexosaminidase	1.367
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	1.397	Q3TXV7	Beta-hexosaminidase	1.367
Q02257	Junction plakoglobin	1.393	Q3TW10	Beta-hexosaminidase	1.367
Q05816	Fatty acid-binding protein, epidermal	1.387	Q3TKF6	Beta-hexosaminidase	1.367
O55222	Integrin-linked protein kinase	1.387	Q8BNS6	Beta-hexosaminidase	1.367
Q9CZS7	Putative uncharacterized protein	1.385	Q3TVI2	Beta-hexosaminidase	1.367
O70172	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	1.385	Q3UCP6	Beta-hexosaminidase	1.367

Supplementary Table 7. (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P29416	Beta-hexosaminidase subunit alpha	1.367	Q64010	Adapter molecule crk	1.349
Q3TJX0	Putative uncharacterized protein	1.366	G3X9N3	MCG16539	1.349
Q61233	Plastin-2	1.366	E0CXN5	Glycerol-3-phosphate dehydrogenase [NAD(+)]	1.348
Q3U6Z1	Putative uncharacterized protein	1.366	P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	1.348
Q3U6N7	Putative uncharacterized protein	1.366	Q91V76	Ester hydrolase C11orf54 homolog	1.348
Q3U8H8	Putative uncharacterized protein	1.366	Q6P8K4	AW551984 protein	1.346
P61971	Nuclear transport factor 2	1.366	Q8C1D4	Putative uncharacterized protein	1.346
Q3T9B4	Putative uncharacterized protein	1.365	Q8BGF0	Protein AW551984	1.346
Q3TAV0	Putative uncharacterized protein (Fragment)	1.365	Q9CZW4	Long-chain-fatty-acid--CoA ligase 3	1.345
Q9D8S4	Oligoribonuclease, mitochondrial	1.365	E9PUC2	Long-chain-fatty-acid--CoA ligase 3	1.345
Q78KL9	Rexo2 protein	1.365	Q3TBF1	Putative uncharacterized protein	1.344
Q3UD20	Putative uncharacterized protein (Fragment)	1.365	Q08642	Protein-arginine deiminase type-2	1.344
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	1.363	P52760	Ribonuclease UK114	1.341
Q0KL02	Triple functional domain protein	1.362	Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	1.339
Q9WTP6	Adenylate kinase 2, mitochondrial	1.36	P70202	Latexin	1.338
Q6PAR5	GTPase-activating protein and VPS9 domain-containing protein 1	1.359	Q8BH44	Coronin-2B	1.337
Q3U7V7	Profilin	1.357	P23927	Alpha-crystallin B chain	1.335
P62962	Profilin-1	1.357	Q80U19	Disheveled-associated activator of morphogenesis 2	1.334
P62830	60S ribosomal protein L23	1.357	O88533	Aromatic-L-amino-acid decarboxylase	1.334
Q8BHW2	Protein OSCP1	1.356	E9QL65	Conserved oligomeric Golgi complex subunit 3	1.334
Q3UXP2	Putative uncharacterized protein	1.351	Q3UA81	Elongation factor 1-alpha	1.332
Q9WTM5	RuvB-like 2	1.351	P10126	Elongation factor 1-alpha 1	1.332
Q8BIW1	Protein prune homolog	1.35	Q3UM23	Putative uncharacterized protein	1.332
F6RT34	Myelin basic protein (Fragment)	1.349	Q91VI7	Ribonuclease inhibitor	1.332
Q91VM1	V-crk sarcoma virus CT10 oncogene homolog (Avian)	1.349	Q3TB79	Putative uncharacterized protein (Fragment)	1.331

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q8C2J1	Putative uncharacterized protein	1.331	P16406	Glutamyl aminopeptidase	1.314
Q80Y25	Capn1 protein	1.331	P00920	Carbonic anhydrase 2	1.309
O35350	Calpain-1 catalytic subunit	1.331	Q8R404	Protein QIL1	1.309
Q3UDG8	Putative uncharacterized protein	1.331	P11930	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	1.309
Q8BZF8	Phosphoglucomutase-like protein 5	1.331	Q3TD78	Putative uncharacterized protein	1.306
Q7TMI0	Psmd11 protein (Fragment)	1.329	Q7TMG8	Glioblastoma amplified sequence	1.306
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	1.329	O55126	Protein NipSnap homolog 2	1.306
Q8BK73	Putative uncharacterized protein	1.329	Q8BVQ5	Protein phosphatase methylesterase 1	1.305
A3KGU7	Spectrin alpha chain, non-erythrocytic 1	1.328	Q3U2K1	Putative uncharacterized protein (Fragment)	1.303
B9EKJ1	Spna2 protein	1.328	Q8C1M0	Putative uncharacterized protein	1.303
B2RXX6	Spna2 protein	1.328	Q922H1	Protein arginine N-methyltransferase 3	1.303
P45591	Cofilin-2	1.328	Q3TFD9	Putative uncharacterized protein	1.302
P59325	Eukaryotic translation initiation factor 5	1.323	Q921S7	39S ribosomal protein L37, mitochondrial	1.301
Q8C1E4	Putative uncharacterized protein	1.322	Q3TVT6	Putative uncharacterized protein	1.298
Q01405	Protein transport protein Sec23A	1.322	Q9CQF9	Prenylcysteine oxidase	1.298
E9Q1S3	Protein transport protein Sec23A	1.322	Q3UYP2	Putative uncharacterized protein	1.298
P24369	Peptidyl-prolyl cis-trans isomerase B	1.319	Q3U214	Microtubule-associated serine/threonine-protein kinase 3	1.297
P09055	Integrin beta-1	1.318	E9Q8S5	Microtubule-associated serine/threonine-protein kinase 3	1.297
H3BK65	Epidermal growth factor receptor substrate 15	1.317	Q3UJN2	Putative uncharacterized protein	1.296
P42567	Epidermal growth factor receptor substrate 15	1.317	P60122	RuvB-like 1	1.296
Q5JC28	Epidermal growth factor receptor pathway substrate 15 isoform B	1.317	Q7TPM9	Myotubularin-related protein 10	1.296
A2AAN2	Signal recognition particle subunit SRP68	1.316	P97770	THUMP domain-containing protein 3	1.294
Q8BMA6	Signal recognition particle subunit SRP68	1.316	Q5HZJ8	Isocitrate dehydrogenase [NADP]	1.29
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	1.315	Q8C338	Isocitrate dehydrogenase [NADP]	1.29
P35235	Tyrosine-protein phosphatase non-receptor type 11	1.314	O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	1.29

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3UBZ3	Putative uncharacterized protein	1.29	P42227	Signal transducer and activator of transcription 3	1.275
P47754	F-actin-capping protein subunit alpha-2	1.29	Q6GU23	Signal transducer and activator of transcription	1.275
O35409	Glutamate carboxypeptidase 2	1.29	B7ZC18	Signal transducer and activator of transcription	1.275
P60766	Cell division control protein 42 homolog	1.29	Q3ULI4	Signal transducer and activator of transcription	1.275
P24549	Retinal dehydrogenase 1	1.286	Q3UEG9	Putative uncharacterized protein	1.274
Q9ESM3	Hyaluronan and proteoglycan link protein 2	1.282	Q5SS83	Flotillin 2, isoform CRA_a	1.274
A0JLN1	Srp72 protein (Fragment)	1.281	Q8CDE0	Putative uncharacterized protein	1.274
Q3UZL8	Putative uncharacterized protein (Fragment)	1.281	Q9DC36	Putative uncharacterized protein	1.274
F8VQC1	Signal recognition particle subunit SRP72	1.281	Q60634	Flotillin-2	1.274
Q99LF5	Me1 protein	1.28	Q9JLC8	Sacsin	1.274
Q921S3	Malic enzyme	1.28	E9QNY8	Sacsin	1.274
P06801	NADP-dependent malic enzyme	1.28	A2AP18	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2	1.271
P54923	[Protein ADP-ribosylarginine] hydrolase	1.28	F7C3A0	Phosphoinositide phospholipase C	1.271
Q8BR63	Protein FAM177A1	1.28	H3BIW6	Phosphoinositide phospholipase C	1.271
Q3TCT9	Putative uncharacterized protein	1.276	Q9D967	Magnesium-dependent phosphatase 1	1.27
P35278	Ras-related protein Rab-5C	1.276	P10649	Glutathione S-transferase Mu 1	1.268
Q3TI99	L-lactate dehydrogenase	1.276	D3Z315	Coatomer subunit epsilon (Fragment)	1.266
G5E8N5	L-lactate dehydrogenase	1.276	O89079	Coatomer subunit epsilon	1.266
P06151	L-lactate dehydrogenase A chain	1.276	P47941	Crk-like protein	1.265
Q3UVJ2	Adenylyl cyclase-associated protein	1.276	Q6IRU2	Tropomyosin alpha-4 chain	1.264
P40124	Adenylyl cyclase-associated protein 1	1.276	Q06138	Calcium-binding protein 39	1.263
Q3TMN1	Methionine aminopeptidase 2	1.276	Q9DBL7	Bifunctional coenzyme A synthase	1.258
Q3UI33	Methionine aminopeptidase 2	1.276	P63028	Translationally-controlled tumor protein	1.258
O08663	Methionine aminopeptidase 2	1.276	Q3UD53	Putative uncharacterized protein	1.257
Q3U5Q4	Signal transducer and activator of transcription	1.275	Q9CR86	Calcium-regulated heat stable protein 1	1.257

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3U7M5	Abhydrolase domain-containing protein 4	1.257	Q8BMK4	Cytoskeleton-associated protein 4	1.242
Q8VD66	Abhydrolase domain-containing protein 4	1.257	P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.241
Q8C0M2	Abhydrolase domain-containing protein 4	1.257	Q3TFF0	Putative uncharacterized protein	1.241
E9Q616	Protein Ahnak	1.255	Q9QYJ0	DnaJ homolog subfamily A member 2	1.241
Q8QZS1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	1.255	Q9D517	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	1.241
Q3U7D2	Ribosomal protein L15	1.255	E9Q8N8	Electrogenic sodium bicarbonate cotransporter 1	1.238
Q9CZM2	60S ribosomal protein L15	1.255	Q9D1A2	Cytosolic non-specific dipeptidase	1.236
E9QAZ2	Ribosomal protein L15	1.255	Q3U646	Putative uncharacterized protein	1.236
Q8R151	NFX1-type zinc finger-containing protein 1	1.25	Q9WV54	Acid ceramidase	1.236
Q91YP2	Neurolysin, mitochondrial	1.247	P16332	Methylmalonyl-CoA mutase, mitochondrial	1.236
Q9QUP5	Hyaluronan and proteoglycan link protein 1	1.246	Q3TES0	IQ motif and SEC7 domain-containing protein 3	1.232
Q7TMY2	Acyl-Coenzyme A dehydrogenase, short/branched chain	1.246	Q3UHJ6	Putative uncharacterized protein	1.232
Q9DBL1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	1.246	O08583	THO complex subunit 4	1.231
Q3TF72	Protein disulfide-isomerase	1.245	Q3UWG5	Tetraspanin	1.228
Q3TIM0	Protein disulfide-isomerase	1.245	P35762	CD81 antigen	1.228
Q3THC3	Protein disulfide-isomerase	1.245	Q9EPL8	Importin-7	1.226
Q3UDR2	Protein disulfide-isomerase (Fragment)	1.245	Q8BPF9	Putative uncharacterized protein	1.226
Q3URP6	Protein disulfide-isomerase	1.245	O54833	Casein kinase II subunit alpha~	1.226
P09103	Protein disulfide-isomerase	1.245	A2AIJ1	Tetraspanin (Fragment)	1.226
Q3TWE3	Protein disulfide-isomerase	1.245	P40237	CD82 antigen	1.226
P15532	Nucleoside diphosphate kinase A	1.245	Q8CIE6	Coatomer subunit alpha	1.224
P63239	Neuroendocrine convertase 1	1.243	Q8BTF0	Coatomer subunit alpha	1.224
Q3UGN9	Signal transducing adapter molecule 1	1.242	F8WHL2	Coatomer subunit alpha	1.224
P70297	Signal transducing adapter molecule 1	1.242	Q9QYG0	Protein NDRG2	1.222
Q3UMC8	Putative uncharacterized protein	1.242	P08003	Protein disulfide-isomerase A4	1.221

Supplementary Table 7 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P48036	Annexin A5	1.22	Q3TF41	Nucleosome assembly protein 1-like 1, isoform CRA_d	1.204
Q3TE95	Putative uncharacterized protein	1.22	Q8BSH9	Nucleosome assembly protein 1-like 1, isoform CRA_b	1.204
Q8BP92	Reticulocalbin-2	1.22	P28656	Nucleosome assembly protein 1-like 1	1.204
Q5SYD0	Unconventional myosin-Id	1.219	E9PW66	Nucleosome assembly protein 1-like 1	1.204
Q3TZZ7	Extended synaptotagmin-2	1.218	Q5RJV4	Phosphoglucomutase 2	1.203
Q3TJN6	Putative uncharacterized protein	1.218	Q9D0F9	Phosphoglucomutase-1	1.203
Q9D8U8	Sorting nexin-5	1.218	Q66JR7	Pgm2 protein (Fragment)	1.203
Q8C5E7	Putative uncharacterized protein	1.218	Q7TNU0	Pgm2 protein (Fragment)	1.203
Q3U3A8	Putative uncharacterized protein	1.217	Q99KC8	von Willebrand factor A domain-containing protein 5A	1.203
Q3U8S5	Putative uncharacterized protein	1.217	P55088	Aquaporin-4	1.202
O08529	Calpain-2 catalytic subunit	1.217	Q3UJW9	Putative uncharacterized protein	1.201
Q8BQP9	Regulator of G-protein signaling 7-binding protein	1.215	Q9JII6	Alcohol dehydrogenase [NADP(+)]	1.201
Q9R1Q8	Transgelin-3	1.214	E9QMK2	Versican core protein	1.201
Q9CYT6	Adenylyl cyclase-associated protein 2	1.21	Q62059	Versican core protein	1.201
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	1.205	E9PYH0	Versican core protein	1.201

The comparison was performed in the spinal cord between the onset and the pre-onset of SOD1 G93A mouse, where the fold > 1.2 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 528 significantly up regulated proteins in the spinal cord between the onset vs the pre-onset of SOD1 G93A mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 8. List of Significantly Down Regulated Proteins in the Spinal Cord between the Onset Vs the Pre-onset of SOD1 G93A Mouse

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P27573	Myelin protein P0	0.106	A8DUK4	Beta-globin	0.458
D0VYV6	Erythrocyte protein band 4.1-like 3 isoform B	0.32	A8DUK7	Beta-globin	0.458
Q9Z1K6	E3 ubiquitin-protein ligase ARIH2	0.349	Q9CSN1	SNW domain-containing protein 1	0.462
Q71M36	Chondroitin sulfate proteoglycan 5	0.371	P10630	Eukaryotic initiation factor 4A-II	0.464
Q3TZI7	Major prion protein	0.383	B1ASQ2	Apolipoprotein O	0.464
Q3UBH0	Major prion protein	0.383	Q9DCZ4	Apolipoprotein O	0.464
P04925	Major prion protein	0.383	Q3KNM9	Apoo protein	0.464
Q9QYT9	Major prion protein	0.383	Q9D186	Apolipoprotein O	0.464
Q3UF68	Major prion protein	0.383	A3KG38	NF-kappa-B essential modulator (Fragment)	0.465
Q3UG89	Major prion protein	0.383	E9Q2Y3	NF-kappa-B essential modulator	0.465
Q3U6D7	Synaptogyrin 1, isoform CRA_a	0.389	Q8VC91	Ikbkg protein	0.465
O55100	Synaptogyrin-1	0.389	Q3UG24	Putative uncharacterized protein (Fragment)	0.465
Q71V06	Y box transcription factor (Fragment)	0.43	A3KG41	NF-kappa-B essential modulator (Fragment)	0.465
Q810K5	Y box protein 1	0.43	O88522	NF-kappa-B essential modulator	0.465
P62960	Nuclease-sensitive element-binding protein 1	0.43	Q7TSS3	Inhibitor of kappaB kinase gamma	0.465
Q60951	MYB-1b	0.43	A3KG44	NF-kappa-B essential modulator (Fragment)	0.465
B1AWD8	Clathrin light chain A	0.434	A3KG40	NF-kappa-B essential modulator (Fragment)	0.465
O08585	Clathrin light chain A	0.434	F6UP77	Putative N-acetylglucosamine-6-phosphate deacetylase (Fragment)	0.478
B1AWD9	Clathrin light chain A	0.434	Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	0.478
Q8BK24	Putative uncharacterized protein (Fragment)	0.434	Q6I6G8	E3 ubiquitin-protein ligase HECW2	0.485
P06880	Somatotropin	0.434	Q1HL23	SorCS1a	0.494
Q9R2C3	Growth hormome	0.434	E9PYT6	VPS10 domain-containing receptor SorCS1	0.494
P68510	14-3-3 protein eta	0.437	E9QQ02	VPS10 domain-containing receptor SorCS1	0.494
P43274	Histone H1.4	0.438	Q1HL25	SorCS1b	0.494
Q7TMM9	Tubulin beta-2A chain	0.439	Q8BSV0	Putative uncharacterized protein	0.494

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q1HL24	SorCS1c	0.494	Q01149	Collagen alpha-2(I) chain	0.573
Q9JLC4	VPS10 domain-containing receptor SorCS1	0.494	Q9CQ75	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	0.575
E9QQ63	VPS10 domain-containing receptor SorCS1	0.494	Q9CWF2	Tubulin beta-2B chain	0.58
Q9QY42	Prosaposin receptor GPR37	0.504	Q6PCX2	Transporter	0.582
O35449	Proline-rich transmembrane protein 1	0.507	P31648	Sodium- and chloride-dependent GABA transporter 1	0.582
Q05D16	Cd200 protein	0.517	A2AI14	Glutamate receptor ionotropic, NMDA 1	0.585
O54901	OX-2 membrane glycoprotein	0.517	A2AI21	Glutamate receptor ionotropic, NMDA 1	0.585
E9PZI9	OX-2 membrane glycoprotein	0.517	A2AI16	Glutamate receptor ionotropic, NMDA 1	0.585
E9QMY1	OX-2 membrane glycoprotein	0.517	A2AI20	Glutamate receptor ionotropic, NMDA 1	0.585
Q80VX2	CD200 antigen	0.517	A2AI19	Glutamate receptor ionotropic, NMDA 1	0.585
Q3U292	Putative uncharacterized protein	0.518	P35438	Glutamate receptor ionotropic, NMDA 1	0.585
P43277	Histone H1.3	0.518	A2AI17	Glutamate receptor ionotropic, NMDA 1	0.585
P15864	Histone H1.2	0.518	Q3TN10	Putative uncharacterized protein	0.585
D3Z780	Translation initiation factor eIF-2B subunit delta	0.531	Q3U2V0	Putative uncharacterized protein	0.585
Q61749	Translation initiation factor eIF-2B subunit delta	0.531	F8WJD4	Symplekin	0.585
Q9DCT8	Cysteine-rich protein 2	0.54	Q3U2B5	Putative uncharacterized protein	0.585
S0DHL8	RLTPR	0.542	Q80X82	Symplekin	0.585
P60879	Synaptosomal-associated protein 25	0.543	B2RQS1	Striatin-3	0.588
Q62277	Synaptophysin	0.562	Q9JJY3	Sphingomyelin phosphodiesterase 3	0.589
A0A087WQY4	Brain-enriched guanylate kinase-associated protein (Fragment)	0.562	Q3UF03	Putative uncharacterized protein	0.594
Q68EF6	Brain-enriched guanylate kinase-associated protein	0.562	P24668	Cation-dependent mannose-6-phosphate receptor	0.594
F8WIG2	Brain-enriched guanylate kinase-associated protein	0.562	P14115	60S ribosomal protein L27a	0.597
Q9QXV0	ProSAAS	0.565	Q9CR57	60S ribosomal protein L14	0.604
Q5Y5T1	Probable palmitoyltransferase ZDHHC20	0.572	Q9CWK0	Putative uncharacterized protein	0.604
Q3TU64	Putative uncharacterized protein	0.573	Q6PAL3	Adaptor-related protein complex 3, sigma 2 subunit	0.61

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q8BNE3	Putative uncharacterized protein	0.61	G3UYV7	40S ribosomal protein S28 (Fragment)	0.624
Q8BSZ2	AP-3 complex subunit sigma-2	0.61	P62858	40S ribosomal protein S28	0.624
A2AJA9	Uncharacterized protein C9orf172 homolog	0.613	Q3USC7	Ganglioside-induced differentiation-associated protein 1-like 1	0.628
Q8VBY2	Calcium/calmodulin-dependent protein kinase kinase 1	0.613	Q8VE33	Ganglioside-induced differentiation-associated protein 1-like 1	0.628
Q0VBR8	Growth arrest specific 7	0.613	Q9Z0Y1	Dynactin subunit 3	0.628
Q60780	Growth arrest-specific protein 7	0.613	E9Q919	Dynactin subunit 3	0.628
Q6A075	MKIAA0394 protein (Fragment)	0.613	P63040	Complexin-1	0.629
Q3U432	Growth arrest-specific protein 7	0.613	P63137	Gamma-aminobutyric acid receptor subunit beta-2	0.63
Q3U8N2	Putative uncharacterized protein (Fragment)	0.613	P47911	60S ribosomal protein L6	0.63
B1ATI9	Growth arrest-specific protein 7	0.613	Q3TCY0	Putative uncharacterized protein	0.635
G5E8T9	Hydroxyacyl glutathione hydrolase	0.615	Q3TQ93	Putative uncharacterized protein	0.635
Q99KB8	Hydroxyacylglutathione hydrolase, mitochondrial	0.615	O35963	Ras-related protein Rab-33B	0.635
E9PYA3	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)	0.615	A0A0A0MQA5	Tubulin alpha-4A chain (Fragment)	0.637
Q8K1L5	Protein phosphatase 1 regulatory subunit 11	0.615	P68368	Tubulin alpha-4A chain	0.637
P11404	Fatty acid-binding protein, heart	0.618	Q9D855	Cytochrome b-c1 complex subunit 7	0.637
K3W4S6	Glycogenin-1	0.618	Q9CQB4	Cytochrome b-c1 complex subunit 7	0.637
V9GX26	Glycogenin-1 (Fragment)	0.618	Q8BTI8	Serine/arginine repetitive matrix protein 2	0.645
Q9R062	Glycogenin-1	0.618	Q921W4	Quinone oxidoreductase-like protein 1	0.645
Q8C1B7	Septin-11	0.619	Q8QZV4	Serine/threonine-protein kinase 32C	0.648
Q53YX2	CD90.1	0.619	Q3UEX4	Putative uncharacterized protein	0.649
P01831	Thy-1 membrane glycoprotein	0.619	O88741	Ganglioside-induced differentiation-associated protein 1	0.649
Q9D358	Low molecular weight phosphotyrosine protein phosphatase	0.62	Q3UTV3	Putative uncharacterized protein (Fragment)	0.649
D3Z3Z3	Voltage-dependent L-type calcium channel subunit beta-3	0.62	Q60692	Proteasome subunit beta type-6	0.651
P54285	Voltage-dependent L-type calcium channel subunit beta-3	0.62	P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	0.652
Q8K5A7	Calcium channel beta 3 subunit	0.62	Q3TWB8	Putative uncharacterized protein	0.652

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
E9PZ69	Transmembrane 9 superfamily member 2	0.652	Q8K1M6	Dynamin-1-like protein	0.676
Q8C7F9	Putative uncharacterized protein	0.652	B9EIX2	AW555464 protein	0.676
P58021	Transmembrane 9 superfamily member 2	0.652	Q80U49	Centrosomal protein of 170 kDa protein B	0.676
Q8C6H4	Putative uncharacterized protein	0.652	D3YXZ3	Kinesin light chain 2	0.677
Q61411	GTPase HRas	0.655	Q91YS4	Kinesin light chain 2	0.677
Q8JZZ5	Pitpnb protein	0.656	P27048	Small nuclear ribonucleoprotein-associated protein B	0.678
P53811	Phosphatidylinositol transfer protein beta isoform	0.656	P63163	Small nuclear ribonucleoprotein-associated protein N	0.678
P70698	CTP synthase 1	0.657	O70499	Small nuclear ribonucleoprotein-associated protein	0.678
P62264	40S ribosomal protein S14	0.658	P67984	60S ribosomal protein L22	0.682
O70569	Ribosomal protein S14	0.658	Q9DCB8	Iron-sulfur cluster assembly 2 homolog, mitochondrial	0.682
Q08274	Dystrophia myotonica WD repeat-containing protein	0.658	Q80TH1	Discs, large homolog 3 (Drosophila), isoform CRA_c (Fragment)	0.683
P97300	Neuroplastin	0.66	P62869	Transcription elongation factor B polypeptide 2	0.683
P63216	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-3	0.661	Q61753	D-3-phosphoglycerate dehydrogenase	0.687
O35405	Phospholipase D3	0.663	Q4VAE8	Ndufb4 protein (Fragment)	0.689
E9PUD2	Dynamin-1-like protein	0.664	Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	0.689
Q5CZY9	Rps16 protein	0.664	Q80TL0	Protein phosphatase 1E	0.689
Q641N3	Rps16 protein (Fragment)	0.664	Q7TSJ2	Microtubule-associated protein 6	0.69
P14131	40S ribosomal protein S16	0.664	Q8R1P3	Gpm6a protein	0.69
P08228	Superoxide dismutase [Cu-Zn]	0.668	P35802	Neuronal membrane glycoprotein M6-a	0.69
Q60829	Protein phosphatase 1 regulatory subunit 1B	0.669	P07724	Serum albumin	0.694
Q3TYH2	Ras-related protein Rab-15	0.669	Q2UY11	Collagen alpha-1(XXVIII) chain	0.696
Q8K386	Ras-related protein Rab-15	0.669	Q3TDM2	Putative uncharacterized protein	0.697
P07759	Serine protease inhibitor A3K	0.672	Q3UH04	Putative uncharacterized protein	0.697
Q569Z6	Thyroid hormone receptor-associated protein 3	0.672	Q8BW96	Calcium/calmodulin-dependent protein kinase type 1D	0.697
Q3U4P3	Putative uncharacterized protein (Fragment)	0.676	P30275	Creatine kinase U-type, mitochondrial	0.699

supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q3TI34	Glutathione peroxidase	0.699	Q3USY4	Putative uncharacterized protein	0.714
Q76LV0	Glutathione peroxidase	0.699	P56959	RNA-binding protein FUS	0.714
O70325	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	0.699	Q9QXS6	Drebrin	0.715
Q5XJZ8	Glutathione peroxidase (Fragment)	0.699	Q9D1H7	Golgi to ER traffic protein 4 homolog	0.715
S4R1E5	Glutathione peroxidase	0.699	P46414	Cyclin-dependent kinase inhibitor 1B	0.715
Q3U8W4	Superoxide dismutase	0.705	Q91VC3	Eukaryotic initiation factor 4A-III	0.716
P09671	Superoxide dismutase [Mn], mitochondrial	0.705	Q8CIN4	Serine/threonine-protein kinase PAK 2	0.719
Q9Z2Y3	Homer protein homolog 1	0.705	Q8BW41	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	0.719
O35435	Dihydroorotate dehydrogenase (quinone), mitochondrial	0.705	Q8VBV7	COP9 signalosome complex subunit 8	0.72
Q4FJP8	Slc2a3 protein	0.706	D3Z5I6	IQ motif and SEC7 domain-containing protein 2	0.721
P32037	Solute carrier family 2, facilitated glucose transporter member 3	0.706	Q5DU25	IQ motif and SEC7 domain-containing protein 2	0.721
Q8BLF7	Putative uncharacterized protein	0.706	E9QAD8	IQ motif and SEC7 domain-containing protein 2	0.721
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta	0.708	A4GZ26	ARF6 guanine nucleotide exchange factor IQArfGEF	0.721
B0R1E3	Histidine triad nucleotide-binding protein 1	0.71	Q5EBG5	Ribosomal protein L7A	0.721
P70349	Histidine triad nucleotide-binding protein 1	0.71	P12970	60S ribosomal protein L7a	0.721
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	0.711	Q80UT7	Rpl7a protein (Fragment)	0.721
Q91XU3	Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma	0.711	Q6P1A9	Ribosomal protein L7A	0.721
Q3TIK0	Platelet-activating factor acetylhydrolase IB subunit alpha	0.713	B2RWE8	Eif4b protein	0.721
Q3TJG1	Platelet-activating factor acetylhydrolase IB subunit alpha	0.713	Q3TSY9	Putative uncharacterized protein	0.721
Q3UGR6	Platelet-activating factor acetylhydrolase IB subunit alpha	0.713	Q3TDD8	Putative uncharacterized protein	0.721
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	0.713	Q3UGC0	Putative uncharacterized protein	0.721
Q921M3	Splicing factor 3B subunit 3	0.714	Q8BGD9	Eukaryotic translation initiation factor 4B	0.721
G3UXT7	RNA-binding protein FUS (Fragment)	0.714	Q3THB0	Putative uncharacterized protein	0.721
Q8CFQ9	Fusion, derived from t(1216) malignant liposarcoma (Human)	0.714	Q3TV38	Putative uncharacterized protein	0.721
Q3UK30	Putative uncharacterized protein	0.714	Q9JJZ4	Ubiquitin-conjugating enzyme E2 J1	0.721

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
F6SPK0	Ubiquitin-conjugating enzyme E2 J1 (Fragment)	0.721	Q9ER00	Syntaxin-12	0.734
P08122	Collagen alpha-2(IV) chain	0.721	Q9D0M5	Dynein light chain 2, cytoplasmic	0.736
D3YU06	Abhydrolase domain-containing protein 3	0.721	Q3U3F4	Putative uncharacterized protein	0.737
D3Z6Y2	Abhydrolase domain-containing protein 3	0.721	P31938	Dual specificity mitogen-activated protein kinase kinase 1	0.737
Q91ZH7	Abhydrolase domain-containing protein 3	0.721	Q9JJE1	Brain cDNA, clone MNCb-1208, similar to Mus musculus mitogen activated protein kinase kinase 1 (Map2k1), mRNA	0.737
Q62425	Cytochrome c oxidase subunit NDUFA4	0.722	Q3UK05	Putative uncharacterized protein	0.737
Q61120	SHC-transforming protein 3	0.723	Q9WV34	MAGUK p55 subfamily member 2	0.741
G5E8A7	Serine/threonine-protein kinase PAK 4	0.723	Q91XV3	Brain acid soluble protein 1	0.745
Q80XS6	Protein Smaug homolog 2	0.723	Q3UPL0	Protein transport protein Sec31A	0.745
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.726	Q3TGI6	Putative uncharacterized protein (Fragment)	0.746
Z4YLI8	Clustered mitochondria protein homolog	0.728	Q3UE53	Putative uncharacterized protein	0.746
Q5SW19	Clustered mitochondria protein homolog	0.728	P53810	Phosphatidylinositol transfer protein alpha isoform	0.746
Q922Y1	UBX domain-containing protein 1	0.729	A2AKU9	ATP synthase subunit gamma	0.747
Q05BC3	Echinoderm microtubule-associated protein-like 1	0.731	Q91VR2	ATP synthase subunit gamma, mitochondrial	0.747
B9EKL9	Eml1 protein	0.731	Q9D9D7	ATP synthase subunit gamma	0.747
D6RII3	Echinoderm microtubule-associated protein-like 1	0.731	Q8C2Q8	ATP synthase subunit gamma	0.747
A2VCP7	Psmf1 protein (Fragment)	0.731	P0C0S6	Histone H2A.Z	0.747
Q8BHL8	Proteasome inhibitor PI31 subunit	0.731	Q3THW5	Histone H2A.V	0.747
Q6PDL0	Cytoplasmic dynein 1 light intermediate chain 2	0.732	A2AVJ7	Ribosome-binding protein 1	0.747
P11087	Collagen alpha-1(I) chain	0.733	Q6ZPS0	MKIAA1398 protein (Fragment)	0.747
Q3UF95	Large proline-rich protein BAG6	0.733	Q99PL5	Ribosome-binding protein 1	0.747
Q9Z1R2	Large proline-rich protein BAG6	0.733	Q3THM1	Putative uncharacterized protein	0.751
Q8K3H0	DCC-interacting protein 13-alpha	0.734	Q3TIC8	Putative uncharacterized protein	0.751
Q3TDG9	Putative uncharacterized protein	0.734	Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	0.751

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q4FZL1	Eif4a1 protein (Fragment)	0.751	Q61344	Beta-tropomyosin	0.76
P60843	Eukaryotic initiation factor 4A-I	0.751	E9QB02	Methionine--tRNA ligase, cytoplasmic	0.76
A0JLV3	Histone H2B (Fragment)	0.752	F6VW30	14-3-3 protein theta (Fragment)	0.761
Q8CGP2	Histone H2B type 1-P	0.752	P68254	14-3-3 protein theta	0.761
Q64475	Histone H2B type 1-B	0.752	F6YY69	14-3-3 protein theta (Fragment)	0.761
Q921L4	Histone H2B	0.752	Q6PER3	Microtubule-associated protein RP/EB family member 3	0.762
Q8CBB6	Histone H2B	0.752	Q9JM14	5~(3~)-deoxyribonucleotidase, cytosolic type	0.765
P10853	Histone H2B type 1-F/J/L	0.752	Q3TJ21	Pyrroline-5-carboxylate reductase	0.765
Q6ZWY9	Histone H2B type 1-C/E/G	0.752	Q922Q4	Pyrroline-5-carboxylate reductase 2	0.765
Q8CGP1	Histone H2B type 1-K	0.752	G3X9J1	Sodium/calcium exchanger 1	0.765
Q64525	Histone H2B type 2-B	0.752	G5E8Y0	Sodium/calcium exchanger 1	0.765
P10854	Histone H2B type 1-M	0.752	Q68FL0	Slc8a1 protein	0.765
Q64478	Histone H2B type 1-H	0.752	O35157	Sodium-calcium exchanger	0.765
Q8K298	Actin-binding protein anillin	0.752	Q0QEZ4	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (Fragment)	0.767
Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	0.753	Q3TE45	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	0.767
Q91VC7	Protein phosphatase 1 regulatory subunit 14A	0.754	Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	0.767
O35551	Rab GTPase-binding effector protein 1	0.755	Q3U741	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a	0.768
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	0.757	Q501J6	Probable ATP-dependent RNA helicase DDX17	0.768
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.758	Q9WVK8	Cholesterol 24-hydroxylase	0.77
E9Q6R3	Vesicle-trafficking protein SEC22b	0.758	P23242	Gap junction alpha-1 protein	0.772
O08547	Vesicle-trafficking protein SEC22b	0.758	Q7TMQ1	Gap junction protein	0.772
Q9DBS6	Putative uncharacterized protein	0.759	P97315	Cysteine and glycine-rich protein 1	0.772
Q01065	Calcium/calmodulin-dependent 3~,5~-cyclic nucleotide phosphodiesterase 1B	0.759	Q3UE40	Putative uncharacterized protein	0.773
Q6PJ18	Tpm2 protein	0.76	P27601	Guanine nucleotide-binding protein subunit alpha-13	0.773

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
D3Z5F7	Protein Gm20521	0.775	A2A6U3	Septin-9	0.783
Q3TK29	Putative uncharacterized protein	0.777	Q80UG5	Septin-9	0.783
Q3TSG8	Putative uncharacterized protein	0.777	A2AVX1	Breast carcinoma-amplified sequence 1 homolog	0.784
Q922Z3	Trap1 protein (Fragment)	0.777	Q14DK3	Bcas1 protein	0.784
Q9CQN1	Heat shock protein 75 kDa, mitochondrial	0.777	E9Q8Q5	Breast carcinoma-amplified sequence 1 homolog	0.784
Q3UPJ8	Putative uncharacterized protein	0.777	Q14CE2	Bcas1 protein	0.784
Q3TT11	Putative uncharacterized protein	0.777	F7BNZ5	Breast carcinoma-amplified sequence 1 homolog (Fragment)	0.784
Q3UHW2	Putative uncharacterized protein	0.777	Q80YN3	Breast carcinoma-amplified sequence 1 homolog	0.784
P51660	Peroxisomal multifunctional enzyme type 2	0.777	Q8C0B4	Putative uncharacterized protein (Fragment)	0.784
G5E850	Cytochrome b-5, isoform CRA_a	0.777	Q91W50	Cold shock domain-containing protein E1	0.786
P56395	Cytochrome b5	0.777	Q80YV4	Pantothenate kinase 4	0.786
Q9CQX8	28S ribosomal protein S36, mitochondrial	0.777	B2RQX9	Transporter	0.788
Q9D6T9	28S ribosomal protein S36, mitochondrial	0.777	B2RXV9	Transporter	0.788
P28663	Beta-soluble NSF attachment protein	0.778	E0CYT1	Serine/threonine-protein kinase WNK2	0.79
Q8BGD5	Carnitine O-palmitoyltransferase 1, brain isoform	0.778	E0CZE3	Serine/threonine-protein kinase WNK2	0.79
Q3U4W8	Ubiquitin carboxyl-terminal hydrolase	0.779	E9QJQ9	Serine/threonine-protein kinase WNK2	0.79
P56399	Ubiquitin carboxyl-terminal hydrolase 5	0.779	E9QMI9	Serine/threonine-protein kinase WNK2	0.79
Q3TK61	Putative uncharacterized protein	0.781	E9QMI8	Serine/threonine-protein kinase WNK2	0.79
P63037	DnaJ homolog subfamily A member 1	0.781	E9QM73	Serine/threonine-protein kinase WNK2	0.79
D3YYD5	Vacuolar protein sorting-associated protein 29 (Fragment)	0.782	E9Q6Q2	Serine/threonine-protein kinase WNK2	0.79
Q9QZ88	Vacuolar protein sorting-associated protein 29	0.782	Q3UF82	Mitogen-activated protein kinase	0.791
D3Z645	Vacuolar protein sorting-associated protein 29	0.782	P63085	Mitogen-activated protein kinase 1	0.791
Q78IK2	Up-regulated during skeletal muscle growth protein 5	0.782	Q9CXI0	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	0.791
Q3ULN5	Peptidyl-prolyl cis-trans isomerase	0.783	Q91WS0	CDGSH iron-sulfur domain-containing protein 1	0.793
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A	0.783	Q8C522	Endonuclease domain-containing 1 protein	0.795

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
Q69ZY2	MKIAA0830 protein (Fragment)	0.795	Q9WUB4	Dynactin subunit 6	0.812
D3YTU0	Vesicle-associated membrane protein 1	0.798	Q3TA13	Putative uncharacterized protein	0.813
Q9CXX2	Putative uncharacterized protein	0.798	E9Q3E2	Synaptopodin	0.813
Q62442	Vesicle-associated membrane protein 1	0.798	Q3URF1	MCG6023	0.813
A0A087WP80	Limbic system-associated membrane protein	0.799	Q3TY32	Putative uncharacterized protein (Fragment)	0.813
Q8BLK3	Limbic system-associated membrane protein	0.799	Q3U336	Putative uncharacterized protein	0.813
Q3TYE5	Limbic system-associated membrane protein	0.799	Q8CC35	Synaptopodin	0.813
G3UYF9	Prefoldin subunit 6	0.799	P46660	Alpha-internexin	0.815
Q03958	Prefoldin subunit 6	0.799	Q5M8N4	Epimerase family protein SDR39U1	0.815
P05202	Aspartate aminotransferase, mitochondrial	0.8	Q3UAS2	Putative uncharacterized protein	0.815
Q9D2R0	Acetoacetyl-CoA synthetase	0.801	Q5RKN9	Capping protein (Actin filament) muscle Z-line, alpha 1	0.815
S4R1F9	Ankyrin-2	0.802	P47753	F-actin-capping protein subunit alpha-1	0.815
S4R249	Ankyrin-2	0.802	Q3UJV2	Putative uncharacterized protein	0.815
Q9DB20	ATP synthase subunit O, mitochondrial	0.804	Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	0.817
Q9D6M3	Mitochondrial glutamate carrier 1	0.806	P50516	V-type proton ATPase catalytic subunit A	0.818
Q3TVK3	Aspartyl aminopeptidase	0.807	P48678	Prelamin-A/C	0.823
Q8CAJ7	Putative uncharacterized protein	0.807	Q8BFR5	Elongation factor Tu, mitochondrial	0.825
Q3U3I6	Putative uncharacterized protein	0.807	Q9DC07	LIM zinc-binding domain-containing Nebulette	0.825
Q9Z2W0	Aspartyl aminopeptidase	0.807	Q5M9L9	40S ribosomal protein S8	0.825
Q8VIJ6	Splicing factor, proline- and glutamine-rich	0.809	P62242	40S ribosomal protein S8	0.825
Q6P9K8	Caskin-1	0.811	Q3TEK2	Putative uncharacterized protein	0.826
B7ZNJ3	Caskin1 protein	0.811	Q3TQ13	Putative uncharacterized protein	0.826
Q9JMF3	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-13	0.811	Q3TH56	Putative uncharacterized protein	0.826
P08553	Neurofilament medium polypeptide	0.812	Q3UBA6	Putative uncharacterized protein	0.826
D3Z6H3	Dynactin 6, isoform CRA_b	0.812	P63017	Heat shock cognate 71 kDa protein	0.826

Supplementary Table 8 (Continued)

Accession No	Description	Fold Change (Onset)	Accession No	Description	Fold Change (Onset)
P62806	Histone H4	0.826	Q9DCL8	Protein phosphatase inhibitor 2	0.83
Q3UK68	Putative uncharacterized protein	0.826	Q9DBN7	Putative uncharacterized protein	0.831
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	0.826	P42125	Enoyl-CoA delta isomerase 1, mitochondrial	0.831
Q60817	Nascent polypeptide-associated complex subunit alpha	0.826	Q8VCE6	5~(3~)-deoxyribonucleotidase, mitochondrial	0.831
P35585	AP-1 complex subunit mu-1	0.826	P18872	Guanine nucleotide-binding protein G(o) subunit alpha	0.832
Q8R3P0	Aspartoacylase	0.827	G5E829	Plasma membrane calcium-transporting ATPase 1	0.832
Q3UM45	Protein phosphatase 1 regulatory subunit 7	0.828	D3YTV8	Ankyrin-1	0.832
B0QZN5	Vesicle-associated membrane protein 2	0.829	E9QNT8	Ankyrin-1	0.832
O35619	Vesicle associated membrane protein 2	0.829	G5E8J2	Ankyrin 1, erythroid	0.832
P63044	Vesicle-associated membrane protein 2	0.829	Q02357	Ankyrin-1	0.832
Q8K183	Pyridoxal kinase	0.829	B7ZW98	Ank1 protein	0.832
Q05DD2	Nefl protein (Fragment)	0.83	D3Z1Z8	Stathmin (Fragment)	0.833
P08551	Neurofilament light polypeptide	0.83	D3Z5N2	Stathmin	0.833
D3Z4B2	Gamma-soluble NSF attachment protein (Fragment)	0.83	Q91XT3	Stathmin	0.833
Q9CWZ7	Gamma-soluble NSF attachment protein	0.83	Q9DCP3	Stathmin	0.833
Q8C1T5	Putative uncharacterized protein	0.83	P54227	Stathmin	0.833
D3Z3A0	MCG126099, isoform CRA_b	0.83			

The comparison was performed in the spinal cord between the onset and the pre-onset of SOD1 G93A mouse, where the fold < 0.833 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 479 significantly down regulated proteins in the spinal cord between the onset vs the pre-onset of SOD1 G93A mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 9. List of Significantly Up Regulated Proteins in the Spinal Cord of a Progression SOD1 MouseVs a Pre-onset Mouse

AccessionNo	Desription	Fold Change (Progression)	AccessionNo	Desription	Fold Change (Progression)
P51910	Apolipoprotein D	4.155	Q3TVS6	Putative uncharacterized protein	2.023
Q8R422	CD109 antigen	3.303	P10605	Cathepsin B	2.023
P14602	Heat shock protein beta-1	2.926	Q3TVU9	Putative uncharacterized protein	1.963
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a	2.688	Q99L04	Dehydrogenase/reductase SDR family member 1	1.963
M0QWA7	Integrin beta	2.567	O09114	Prostaglandin-H2 D-isomerase	1.957
P11835	Integrin beta-2	2.567	P70232	Neural cell adhesion molecule L1-like protein	1.941
Q542I8	Integrin beta	2.567	Q3UBS0	Putative uncharacterized protein	1.94
Q3TWH2	Putative uncharacterized protein	2.54	P08226	Apolipoprotein E	1.94
Q61941	NAD(P) transhydrogenase, mitochondrial	2.54	Q4FK40	Apoe protein	1.94
Q8C1W8	Nicotinamide nucleotide transhydrogenase, isoform CRA_a	2.54	Q6GTX3	Apoe protein	1.94
Q922E1	Nicotinamide nucleotide transhydrogenase	2.54	D3YW87	Filamin-C	1.938
B1B1A8	Myosin light chain kinase, smooth muscle	2.45	Q8VHX6	Filamin-C	1.938
Q6PDN3	Myosin light chain kinase, smooth muscle	2.45	D3Z576	Filamin-C	1.938
P41233	ATP-binding cassette sub-family A member 1	2.295	Q3TWD0	Putative uncharacterized protein	1.873
Q3V471	Galectin (Fragment)	2.241	Q3U7P0	Putative uncharacterized protein	1.873
Q8C253	Galectin	2.241	P18242	Cathepsin D	1.873
P16110	Galectin-3	2.241	Q8C243	Putative uncharacterized protein	1.873
Q3UFY7	7-methylguanosine phosphate-specific 5~-nucleotidase	2.188	Q3TWR6	Putative uncharacterized protein	1.873
P20060	Beta-hexosaminidase subunit beta	2.127	Q3U8W5	Putative uncharacterized protein	1.873
Q3TXB1	Putative uncharacterized protein	2.123	P50543	Protein S100-A11	1.828
Q3UBX7	Putative uncharacterized protein	2.123	Q3TU16	Putative uncharacterized protein (Fragment)	1.819
P98086	Complement C1q subcomponent subunit A	2.123	Q61285	ATP-binding cassette sub-family D member 2	1.819
O88492	Perilipin-4	2.072	Q3UYE0	Putative uncharacterized protein	1.819

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
P20152	Vimentin	1.806	A2APM1	CD44 antigen	1.66
Q3UBR4	Putative uncharacterized protein	1.806	E9QKM8	CD44 antigen	1.66
O70370	Cathepsin S	1.806	P15379	CD44 antigen	1.66
F6WR04	Cathepsin S	1.806	Q80X37	CD44 antigen	1.66
Q3UD32	Putative uncharacterized protein	1.806	Q3U8S1	CD44 antigen	1.66
Q8BSZ5	Cathepsin S	1.806	Q3TLT9	Putative uncharacterized protein	1.66
Q99M14	Ctss protein	1.806	A2APM5	CD44 antigen	1.66
P11352	Glutathione peroxidase 1	1.778	A2APM2	CD44 antigen	1.66
A2A4J1	Proteasome activator complex subunit 3 (Fragment)	1.771	Q3U468	Putative uncharacterized protein	1.66
P61290	Proteasome activator complex subunit 3	1.771	Q3UNN2	Putative uncharacterized protein	1.66
Q3TX26	Putative uncharacterized protein	1.755	A2APM4	CD44 antigen	1.66
P97822	Acidic leucine-rich nuclear phosphoprotein 32 family member E	1.755	A2APM3	CD44 antigen	1.66
E9PZF5	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)	1.755	Q3TFD9	Putative uncharacterized protein	1.657
E9Q5H2	Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment)	1.755	B2RXW7	Complement component 4B (Childo blood group)	1.653
Q3UE99	Putative uncharacterized protein (Fragment)	1.746	E0CYM8	Tyrosine-protein phosphatase non-receptor type substrate 1	1.648
O89017	Legumain	1.746	Q6P6I8	Signal-regulatory protein alpha	1.648
Q6GQT1	Alpha-2-macroglobulin-P	1.741	Q3UF30	Putative uncharacterized protein	1.638
Q00915	Retinol-binding protein 1	1.713	P08207	Protein S100-A10	1.638
A2AWA9	RabGTPase-activating protein 1	1.713	P57722	Poly(rC)-binding protein 3	1.633
P23927	Alpha-crystallin B chain	1.709	Q8BWU8	Ethanolamine-phosphate phospho-lyase	1.625
Q9WVA4	Transgelin-2	1.702	E9PYH3	Ethanolamine-phosphate phospho-lyase	1.625
O88428	Bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 2	1.691	Q7TQK5	Coiled-coil domain-containing protein 93	1.624
P03995	Glial fibrillary acidic protein	1.672	E9QAD4	Coiled-coil domain-containing protein 93	1.624

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
D3Z2Y6	Protein S100a16 (Fragment)	1.616	Q3UDC0	Putative uncharacterized protein (Fragment)	1.576
Q3TVE3	Putative uncharacterized protein	1.616	Q3UDC7	Putative uncharacterized protein (Fragment)	1.576
Q9D708	Protein S100a16	1.616	Q9Z0E6	Interferon-induced guanylate-binding protein 2	1.576
Q9CU62	Structural maintenance of chromosomes protein 1A	1.616	Q6IRU2	Tropomyosin alpha-4 chain	1.575
Q5DTP7	MKIAA4075 protein (Fragment)	1.588	Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	1.57
E9QAS4	Chromodomain-helicase-DNA-binding protein 4	1.588	Q3UJ44	Putative uncharacterized protein	1.569
E9QAS5	Chromodomain-helicase-DNA-binding protein 4	1.588	Q99LB4	Capping protein (Actin filament), gelsolin-like	1.569
Q6PDQ2	Chromodomain-helicase-DNA-binding protein 4	1.588	Q6PEV0	Ephx1 protein	1.567
Q3THX5	Putative uncharacterized protein	1.587	Q9D379	Epoxide hydrolase 1	1.567
E9Q3X0	Major vault protein	1.587	E9PWK1	Epoxide hydrolase 1	1.567
B7ZWF1	Ddx3x protein	1.586	Q8K2W5	Epoxide hydrolase 1, microsomal	1.567
Q62167	ATP-dependent RNA helicase DDX3X	1.586	U5LGR7	Marshalin-La transcript variant 1	1.563
B9EKE9	Ddx3x protein	1.586	U5LHT8	Marshalin-La transcript variant 2	1.563
D3YX85	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	1.584	U5LHW1	Marshalin-Lc transcript variant 1	1.563
Q6A074	MKIAA0400 protein (Fragment)	1.584	U5LGS1	Marshalin-Lc transcript variant 2	1.563
Q3TS63	Putative uncharacterized protein (Fragment)	1.584	E9Q616	Protein Ahnak	1.558
Q7SIG6	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	1.584	Q9D4H1	Exocyst complex component 2	1.556
Q3UH05	Putative uncharacterized protein	1.584	A0A0A0MQ90	Protein S100-A13	1.551
E9PX52	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2	1.584	P97352	Protein S100-A13	1.551
Q3UH27	Putative uncharacterized protein	1.584	Q7TMN7	Annexin	1.547
D3YU80	Cold-inducible RNA-binding protein (Fragment)	1.583	P97429	Annexin A4	1.547
P60824	Cold-inducible RNA-binding protein	1.583	A3KGU5	Spectrin alpha chain, non-erythrocytic 1	1.546
K4DI65	Cold inducible RNA binding protein, isoform CRA_a	1.583	Q3TZQ2	Putative uncharacterized protein	1.545

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q9CXD6	Mitochondrial calcium uniporter regulator 1	1.529	Q91YP2	Neurolysin, mitochondrial	1.496
Q3UC80	Tetraspanin	1.528	A2CG35	Ras-related protein Rab-12	1.491
Q8BT06	Tetraspanin	1.528	P35283	Ras-related protein Rab-12	1.491
P41731	CD63 antigen	1.528	Q04690	Neurofibromin	1.488
G3X8Q5	Ceruloplasmin	1.525	Q8C3X2	Coiled-coil domain-containing protein 90B, mitochondrial	1.481
Q61147	Ceruloplasmin	1.525	Q3UM23	Putative uncharacterized protein	1.481
G3X9T8	Ceruloplasmin	1.525	Q91VI7	Ribonuclease inhibitor	1.481
E9PZD8	Ceruloplasmin	1.525	P21981	Protein-glutamine gamma-glutamyltransferase 2	1.474
Q0GNC1	Inverted formin-2	1.516	E0CXT5	Disabled homolog 2	1.472
E9QLA5	Inverted formin-2	1.516	E9PX84	Disabled homolog 2	1.472
Q5M8M3	Uncharacterized protein	1.515	Q3TRE6	Disabled homolog 2	1.472
Q9DCG9	Multifunctional methyltransferase subunit TRM112-like protein	1.515	Q3TRI2	Putative uncharacterized protein	1.472
Q8VCR4	0610038D11Rik protein	1.515	Q3TMQ2	Putative uncharacterized protein	1.472
P55264	Adenosine kinase	1.51	Q3TN55	Putative uncharacterized protein	1.472
Q3TCP5	Putative uncharacterized protein	1.509	E9QL31	Disabled homolog 2	1.472
Q3UXR4	Putative uncharacterized protein	1.509	P98078	Disabled homolog 2	1.472
P26040	Ezrin	1.509	Q9DCE6	Disabled homolog 2	1.472
Q3UL48	Putative uncharacterized protein	1.509	Q3UG80	Putative uncharacterized protein	1.471
Q9DC63	F-box only protein 3	1.507	Q8CFS5	Vps18 protein	1.471
P11087	Collagen alpha-1(I) chain	1.501	Q8R307	Vacuolar protein sorting-associated protein 18 homolog	1.471
P16045	Galectin-1	1.501	Q8BLK7	Putative uncharacterized protein	1.471
Q61133	Glutathione S-transferase theta-2	1.501	A2AL85	Aspartyl/asparaginyl beta-hydroxylase	1.46
Q6P5D8	Structural maintenance of chromosomes flexible hinge domain-containing protein 1	1.499	Q8BSY0	Aspartyl/asparaginyl beta-hydroxylase	1.46

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q8BQK0	Putative uncharacterized protein	1.46	Q9CV53	Putative uncharacterized protein (Fragment)	1.443
Q8CBM2	Aspartyl/asparaginyl beta-hydroxylase	1.46	Q91WK5	Glycine cleavage system H protein, mitochondrial	1.443
Q9EQ66	Aspartly beta-hydroxylase	1.46	Q3THQ0	Beta-hexosaminidase	1.443
P62774	Myotrophin	1.457	Q3U936	Beta-hexosaminidase	1.443
Q05186	Reticulocalbin-1	1.456	Q3TXV7	Beta-hexosaminidase	1.443
D3Z125	Tumor protein D52 (Fragment)	1.453	Q3TW10	Beta-hexosaminidase	1.443
F8WHQ1	Tumor protein D52	1.453	Q3TKF6	Beta-hexosaminidase	1.443
D3Z7X7	Tumor protein D52 (Fragment)	1.453	Q8BNS6	Beta-hexosaminidase	1.443
E9PUA7	Tumor protein D52	1.453	Q3TVI2	Beta-hexosaminidase	1.443
Q62393	Tumor protein D52	1.453	Q3UCP6	Beta-hexosaminidase	1.443
Q3U896	Putative uncharacterized protein	1.451	P29416	Beta-hexosaminidase subunit alpha	1.443
Q9Z2D0	Myotubularin-related protein 9	1.451	Q5M9L1	60S ribosomal protein L36	1.442
Q3TGQ3	Putative uncharacterized protein	1.451	Q6ZWZ4	60S ribosomal protein L36	1.442
P26231	Catenin alpha-1	1.451	Q3U6T2	Putative uncharacterized protein	1.441
Q3UF75	Alpha-parvin	1.449	Q9QWR8	Alpha-N-acetylgalactosaminidase	1.441
Q8C5R4	Putative uncharacterized protein	1.449	Q3TST0	Putative uncharacterized protein	1.439
Q9EPC1	Alpha-parvin	1.449	Q8K1R3	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	1.439
Q9D8X2	Coiled-coil domain-containing protein 124	1.449	B7FAU9	Filamin, alpha	1.439
Z4YJL4	182 kDa tankyrase-1-binding protein	1.449	Q8BTM8	Filamin-A	1.439
P58871	182 kDa tankyrase-1-binding protein	1.449	Q9D3M4	Protein S100	1.434
A2AFI3	RNA binding motif protein, X chromosome, isoform CRA_b	1.444	Q91V77	Protein S100	1.434
Q9WV02	RNA-binding motif protein, X chromosome	1.444	D3YTT4	Isobutyryl-CoA dehydrogenase, mitochondrial	1.432
A2AFI4	RNA-binding motif protein, X chromosome (Fragment)	1.444	Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	1.432

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
P08122	Collagen alpha-2(IV) chain	1.428	Q8BK73	Putative uncharacterized protein	1.372
P57780	Alpha-actinin-4	1.426	Q70IV5	Synemin	1.371
Q9CQE5	Regulator of G-protein signaling 10	1.425	P51885	Lumican	1.369
Q02788	Collagen alpha-2(VI) chain	1.422	Q6ZQK2	MKIAA0051 protein (Fragment)	1.366
Q62000	Mimecan	1.421	Q9JKF1	RasGTPase-activating-like protein IQGAP1	1.366
Q3TPN0	Putative uncharacterized protein	1.418	Q80UW7	IQ motif containing GTPase activating protein 1	1.366
Q3US45	Putative uncharacterized protein	1.418	B2RUD7	Psap protein	1.363
Q8CFA3	Nidogen-2	1.418	Q3TWE9	Putative uncharacterized protein	1.363
O88322	Nidogen-2	1.418	Q3U8C4	Putative uncharacterized protein	1.363
Q6P8K4	AW551984 protein	1.417	Q3UAS4	Putative uncharacterized protein	1.363
Q8C1D4	Putative uncharacterized protein	1.417	Q61207	Prosaposin	1.363
Q8BGF0	Protein AW551984	1.417	Q3UE29	Putative uncharacterized protein	1.363
Q6A0D9	Glucosamine-6-phosphate isomerase (Fragment)	1.391	Q3TWL8	Putative uncharacterized protein	1.363
O88958	Glucosamine-6-phosphate isomerase 1	1.391	E9PZ00	Prosaposin	1.363
Q02257	Junction plakoglobin	1.389	Q3U825	Putative uncharacterized protein	1.363
P52760	Ribonuclease UK114	1.384	Q3U5W2	Putative uncharacterized protein	1.363
Q3UBU0	Putative uncharacterized protein	1.382	J3QPG5	Prosaposin	1.363
G3UXZ5	Proteasome activator complex subunit 1 (Fragment)	1.379	Q8BFQ1	Prosaposin	1.363
Q04857	Collagen alpha-1(VI) chain	1.379	Q3TID4	Putative uncharacterized protein	1.363
A2AS45	Plakophilin-4	1.373	Q3TIT5	Putative uncharacterized protein	1.363
Q68FH0	Plakophilin-4	1.373	K3W4L3	Prosaposin	1.363
Q7TMI0	Psmd11 protein (Fragment)	1.372	Q3U897	Putative uncharacterized protein	1.363
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	1.372	Q3TWM9	Putative uncharacterized protein (Fragment)	1.363

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q3TXJ0	Putative uncharacterized protein	1.363	Q9D020	Cytosolic 5~-nucleotidase 3A	1.326
A2AIJ1	Tetraspanin (Fragment)	1.359	O35344	Importin subunit alpha-4	1.325
P40237	CD82 antigen	1.359	O54724	Polymerase I and transcript release factor	1.324
Q8R086	Sulfite oxidase, mitochondrial	1.355	Q3TP13	Putative uncharacterized protein (Fragment)	1.323
Q9R069	Basal cell adhesion molecule	1.353	Q3TN26	Putative uncharacterized protein	1.323
Q99K86	Bcam protein	1.353	Q60714	Long-chain fatty acid transport protein 1	1.323
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial	1.352	Q8BQX9	Putative uncharacterized protein	1.323
Q9ESM3	Hyaluronan and proteoglycan link protein 2	1.35	Q8C7S9	Putative uncharacterized protein	1.323
P32020	Non-specific lipid-transfer protein	1.348	Q8VD73	Potassium voltage-gated channel, shaker-related subfamily, beta member 3	1.323
Q3U9A8	SH3 domain-binding glutamic acid-rich-like protein	1.342	P97382	Voltage-gated potassium channel subunit beta-3	1.323
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	1.342	Q2PFD7	PH and SEC7 domain-containing protein 3	1.323
Q3TJL8	Putative uncharacterized protein	1.342	F6Z9E6	PH and SEC7 domain-containing protein 3	1.323
Q3TML0	Protein disulfide-isomerase A6	1.342	F8WIE1	Alpha-mannosidase	1.319
Q05816	Fatty acid-binding protein, epidermal	1.34	Q8BWY6	Alpha-mannosidase	1.319
Q6P5H2	Nestin	1.338	E9PZ88	Alpha-mannosidase	1.319
Q8R2K3	Single-stranded DNA-binding protein	1.335	Q8VDP4	Cell cycle and apoptosis regulator protein 2	1.318
A6H663	BCL2-associated athanogene 3	1.333	G3UYP0	SUMO-conjugating enzyme UBC9 (Fragment)	1.318
Q9JLV1	BAG family molecular chaperone regulator 3	1.333	Q8CFZ0	SUMO-conjugating enzyme UBC9	1.318
Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	1.331	P63280	SUMO-conjugating enzyme UBC9	1.318
Q3UA81	Elongation factor 1-alpha	1.33	Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	1.318
P10126	Elongation factor 1-alpha 1	1.33	Q3TSU7	Putative uncharacterized protein (Fragment)	1.317
Q8VHY0	Chondroitin sulfate proteoglycan 4	1.329	Q91YM2	Rho GTPase-activating protein 35	1.317
Q8R2Z5	von Willebrand factor A domain-containing protein 1	1.326	Q8K010	5-oxoprolinase	1.317

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q3TBF1	Putative uncharacterized protein	1.313	Q60951	MYB-1b	1.297
Q08642	Protein-arginine deiminase type-2	1.313	Q3TJG6	Putative uncharacterized protein	1.295
P28650	Adenylosuccinatesynthetaseisozyme 1	1.312	Q9R0Q7	Prostaglandin E synthase 3	1.295
A2AIW9	Mitochondrial-processing peptidase subunit alpha	1.309	Q80X90	Filamin-B	1.29
Q3UDE0	Putative uncharacterized protein (Fragment)	1.309	Q99JT9	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	1.29
Q3TY06	Putative uncharacterized protein (Fragment)	1.309	Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5	1.288
Q8BK51	Putative uncharacterized protein	1.309	Q9CQU0	Thioredoxin domain-containing protein 12	1.286
Q9DC61	Mitochondrial-processing peptidase subunit alpha	1.309	Q3TLX1	Putative uncharacterized protein	1.285
Q3TTM6	Putative uncharacterized protein	1.309	Q99KQ4	Nicotinamidephosphoribosyltransferase	1.285
E9Q2W9	Alpha-actinin-4 (Fragment)	1.309	Q8BXZ1	Protein disulfide-isomerase TMX3	1.285
Q8K354	Carbonyl reductase [NADPH] 3	1.308	E9PZF0	Nucleoside diphosphate kinase	1.282
Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase	1.308	D3YW48	Calpain small subunit 1 (Fragment)	1.281
Q3U3A8	Putative uncharacterized protein	1.307	O88456	Calpain small subunit 1	1.281
Q3U8S5	Putative uncharacterized protein	1.307	P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	1.281
P26645	Myristoylated alanine-rich C-kinase substrate	1.303	A2BE92	Protein SET (Fragment)	1.28
Q3TU36	Putative uncharacterized protein	1.303	A2BE93	Protein SET (Fragment)	1.28
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	1.302	Q9EQU5	Protein SET	1.28
Q7TMB8	Cytoplasmic FMR1-interacting protein 1	1.302	Q5U445	cDNA sequence BC085271	1.28
Q9CWF2	Tubulin beta-2B chain	1.302	Q3UD53	Putative uncharacterized protein	1.28
Q9D892	Inosine triphosphate pyrophosphatase	1.3	Q9CR86	Calcium-regulated heat stable protein 1	1.28
Q71V06	Y box transcription factor (Fragment)	1.297	Q8R2U6	Diphosphoinositol polyphosphate phosphohydrolase 2	1.279
Q810K5	Y box protein 1	1.297	P16332	Methylmalonyl-CoA mutase, mitochondrial	1.277
P62960	Nuclease-sensitive element-binding protein 1	1.297	D3Z4S6	Transmembrane protein 132A	1.277

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q922P8	Transmembrane protein 132A	1.277	P26043	Radixin	1.267
Q60675	Laminin subunit alpha-2	1.276	D3Z0U2	Chromobox protein homolog 5 (Fragment)	1.266
Q3TJN6	Putative uncharacterized protein	1.275	Q61686	Chromobox protein homolog 5	1.266
Q9D8U8	Sorting nexin-5	1.275	Q3TIP8	Putative uncharacterized protein	1.265
Q8C5E7	Putative uncharacterized protein	1.275	Q9Z1Q5	Chloride intracellular channel protein 1	1.265
D3YTP0	Metalloreductase STEAP3 (Fragment)	1.271	Q3TWI5	Putative uncharacterized protein (Fragment)	1.264
E9QN92	Metalloreductase STEAP3	1.271	Q3U9R7	Putative uncharacterized protein (Fragment)	1.264
Q8CI59	Metalloreductase STEAP3	1.271	Q91Z57	Gsr protein (Fragment)	1.264
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	1.271	Q3UB84	Putative uncharacterized protein (Fragment)	1.264
B9EIU1	Glutamyl-prolyl-tRNAsynthetase	1.271	Q3TXK9	Putative uncharacterized protein (Fragment)	1.264
Q3TSV1	Putative uncharacterized protein	1.27	P47791	Glutathione reductase, mitochondrial	1.264
P28654	Decorin	1.27	P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	1.263
Q3TUQ5	Pinin	1.269	Q8K0E9	Dhdh protein (Fragment)	1.262
Q9CV89	Putative uncharacterized protein (Fragment)	1.269	Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	1.262
O35691	Pinin	1.269	Q5F258	ARF GTPase-activating protein GIT1	1.262
Q9CPY7	Cytosol aminopeptidase	1.269	Q68FF6	ARF GTPase-activating protein GIT1	1.262
A0A4W9	Neuronal growth regulator 1	1.269	P37804	Transgelin	1.26
Q80Z24	Neuronal growth regulator 1	1.269	Q9CQZ1	Heat shock factor-binding protein 1	1.259
D3Z4T6	Neuronal growth regulator 1	1.269	Q8VDD5	Myosin-9	1.259
P52196	Thiosulfate sulfurtransferase	1.268	Q8C1E4	Putative uncharacterized protein	1.259
P17563	Selenium-binding protein 1	1.267	Q01405	Protein transport protein Sec23A	1.259
Q3TH46	Putative uncharacterized protein (Fragment)	1.267	E9Q1S3	Protein transport protein Sec23A	1.259
Q3U111	Putative uncharacterized protein (Fragment)	1.267	Q3TE95	Putative uncharacterized protein	1.259

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q8BP92	Reticulocalbin-2	1.259	Q3TSR4	Putative uncharacterized protein	1.244
Q8CIE6	Coatomer subunit alpha	1.256	Q8VHK5	Membrane protein MLC1	1.244
Q8BTF0	Coatomer subunit alpha	1.256	Q80U92	MKIAA0027 protein (Fragment)	1.244
F8WHL2	Coatomer subunit alpha	1.256	E9QP87	Membrane protein MLC1	1.244
Q61292	Laminin subunit beta-2	1.253	Q8BLR0	Putative uncharacterized protein	1.244
Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F	1.251	P16015	Carbonic anhydrase 3	1.243
P24549	Retinal dehydrogenase 1	1.251	B2RX09	Nrxn2 protein	1.243
Q3U646	Putative uncharacterized protein	1.25	E9PUM9	Protein Nrxn2	1.243
Q9WV54	Acid ceramidase	1.25	E9Q7X7	Protein Nrxn2	1.243
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	1.249	E9Q5N7	Protein Nrxn2	1.243
P09055	Integrin beta-1	1.249	Q6ZQ25	MKIAA0921 protein (Fragment)	1.243
Q8CFX3	Protein Pcdh1	1.249	Q3TEA8	Heterochromatin protein 1-binding protein 3	1.242
Q8QZT6	Pcdh1 protein (Fragment)	1.249	Z4YKB8	Heterochromatin protein 1-binding protein 3	1.242
P10493	Nidogen-1	1.248	B9EHJ3	Tight junction protein ZO-1	1.24
Q3TL95	Proteasome subunit alpha type (Fragment)	1.248	P39447	Tight junction protein ZO-1	1.24
E9PW69	Proteasome subunit alpha type (Fragment)	1.248	Q8K274	Ketosamine-3-kinase	1.24
Q9R1P0	Proteasome subunit alpha type-4	1.248	P40240	CD9 antigen	1.239
P48678	Prelamin-A/C	1.245	Q60770	Syntaxin-binding protein 3	1.237
O55029	Coatomer subunit beta~	1.245	Q9R1P4	Proteasome subunit alpha type-1	1.235
Q62426	Cystatin-B	1.244	F6UP77	Putative N-acetylglucosamine-6-phosphate deacetylase (Fragment)	1.233
Q3TD08	Putative uncharacterized protein	1.244	Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	1.233
B7ZWC0	N-myc downstream regulated gene 1	1.244	Q3TIP0	Putative uncharacterized protein	1.233
Q62433	Protein NDRG1	1.244	Q3TWL6	Putative uncharacterized protein	1.233

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	1.233	Q78KL9	Rexo2 protein	1.223
Q3U9Y8	Putative uncharacterized protein	1.233	Q3UD20	Putative uncharacterized protein (Fragment)	1.223
Q3TXV1	Putative uncharacterized protein	1.233	O88307	Sortilin-related receptor	1.223
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	1.233	Q3U7D2	Ribosomal protein L15	1.222
Q99KK2	N-acylneuraminatecytidylyltransferase	1.232	Q9CZM2	60S ribosomal protein L15	1.222
Q3TFE5	Putative uncharacterized protein	1.232	E9QAZ2	Ribosomal protein L15	1.222
O35286	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	1.232	P27546	Microtubule-associated protein 4	1.221
Q6PAR5	GTPase-activating protein and VPS9 domain-containing protein 1	1.229	A1L333	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.219
Q3TN94	Putative uncharacterized protein	1.229	Q5U222	Ddx5 protein (Fragment)	1.219
Q8BML9	Glutaminyl-tRNAsynthetase	1.229	Q61656	Probable ATP-dependent RNA helicase DDX5	1.219
Q3UP03	Putative uncharacterized protein (Fragment)	1.228	Q8BTS0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.219
B9EIV0	Ablim1 protein	1.228	Q3V0Z8	Putative uncharacterized protein (Fragment)	1.219
Q8K4G5	Actin-binding LIM protein 1	1.228	H3BK65	Epidermal growth factor receptor substrate 15	1.216
E9Q9C2	Actin-binding LIM protein 1	1.228	P42567	Epidermal growth factor receptor substrate 15	1.216
E9Q9C0	Actin-binding LIM protein 1	1.228	Q5JC28	Epidermal growth factor receptor pathway substrate 15 isoform B	1.216
E9Q9C4	Actin-binding LIM protein 1	1.228	Q3UGN9	Signal transducing adapter molecule 1	1.213
E9QK41	Actin-binding LIM protein 1	1.228	P70297	Signal transducing adapter molecule 1	1.213
E9Q9C1	Actin-binding LIM protein 1	1.228	Q3UMC8	Putative uncharacterized protein	1.213
E9Q9C7	Actin-binding LIM protein 1	1.228	Q91VK4	Integral membrane protein 2C	1.212
O35409	Glutamate carboxypeptidase 2	1.228	Q8BFZ9	Erlin-2	1.212
Q3T9B4	Putative uncharacterized protein	1.223	Q3UJN2	Putative uncharacterized protein	1.212
Q3TAV0	Putative uncharacterized protein (Fragment)	1.223	P60122	RuvB-like 1	1.212
Q9D8S4	Oligoribonuclease, mitochondrial	1.223	Q8QZY9	Splicing factor 3B subunit 4	1.211

Supplementary Table 9 (Continued)

Accession No	Desription	Fold Change (Progression)	Accession No	Desription	Fold Change (Progression)
Q921L6	Cortactin, isoform CRA_a	1.209	Q3U5L3	Putative uncharacterized protein	1.207
Q60598	Src substrate cortactin	1.209	Q91VZ1	Snx2 protein	1.207
Q9QYG0	Protein NDRG2	1.209	Q9CWK8	Sorting nexin-2	1.207
Q3U5K7	Putative uncharacterized protein (Fragment)	1.208	Q99LD8	N(G),N(G)-dimethylargininedimethylaminohydrolase 2	1.206
P21460	Cystatin-C	1.208	Q91WS8	Acyl-Coenzyme A dehydrogenase, medium chain	1.204
Q9EPX9	Cystatin C	1.208	P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	1.204
Q9D2V7	Coronin-7	1.208	Q9JKK7	Tropomodulin-2	1.203
Q9CPV4	Glyoxalase domain-containing protein 4	1.207			

The comparison was made between the spinal cord of a progression SOD1 mouse and the spinal cord of an preonset mouse,where fold changes of >1.2 and p-value < 0.05 were taken into consideration. This table contains the 521 proteins that upregulated significantly in the spinal cord of a progression SOD1 mousevs an preonset mouse. The accession number of UniProt Knowledgebase, description, and fold change of each protein are provided here. The proteins are listed according to the level of the fold changes. The top 30 proteins are highlighted with gray.

Supplementary Table 10. List of Significantly Down Regulated Proteins in the Spinal Cord of a Progression SOD1 MouseVs a Pre-onset Mouse

Accession No	Description	Fold Change (Progression)
Q00898	Alpha-1-antitrypsin 1-5	0.191
P05977	Myosin light chain 1/3, skeletal muscle isoform	0.379
Q5SX39	Myosin-4	0.398
O88990	Alpha-actinin-3	0.398
P97457	Myosin regulatory light chain 2, skeletal muscle isoform	0.489
A2A6J8	Troponin I, fast skeletal muscle (Fragment)	0.501
A2A6K0	Troponin I, fast skeletal muscle (Fragment)	0.501
P13412	Troponin I, fast skeletal muscle	0.501
P56391	Cytochrome c oxidase subunit 6B1	0.502
Q8R429	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	0.516
P20801	Troponin C, skeletal muscle	0.519
Q9D6U7	Putative uncharacterized protein	0.547
P07310	Creatine kinase M-type	0.547
P68134	Actin, alpha skeletal muscle	0.562
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	0.577
Q62425	Cytochrome c oxidase subunit NDUFA4	0.584
P28666	Murinoglobulin-2	0.602
Q3UHH0	Calcium-transporting ATPase	0.613
D5L240	Calcium-transporting ATPase	0.613
Q9R0K7	Plasma membrane calcium-transporting ATPase 2	0.613
F8WHB1	Calcium-transporting ATPase	0.613
A2AJI0	MAP7 domain-containing protein 1	0.617
A8Y5P4	MAP7 domain-containing protein 1	0.617
A2AJI1	MAP7 domain-containing protein 1	0.617
Q9WTR1	Transient receptor potential cation channel subfamily V member 2	0.624
Q9D6J9	Putative uncharacterized protein	0.63
P62761	Visinin-like protein 1	0.637
Q3TG58	Williams-Beuren syndrome chromosome region 1 homolog (Human), isoform CRA_b	0.641
Q9WUK2	Eukaryotic translation initiation factor 4H	0.641
Q80U88	MKIAA0038 protein (Fragment)	0.641
Q3V244	Putative uncharacterized protein	0.641
U3M993	NAD(P)-dependent steroid dehydrogenase-like protein	0.642
Q7TPY3	NAD(P) dependent steroid dehydrogenase-like	0.642
Q9R1J0	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	0.642
Q8VE30	NAD(P) dependent steroid dehydrogenase-like	0.642
Q8BGB7	Enolase-phosphatase E1	0.657
Q9D2R6	Cytochrome c oxidase assembly factor 3 homolog, mitochondrial	0.661
Q9CQ75	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	0.665
O55125	Protein NipSnap homolog 1	0.665
Q6P3C3	Calsequestrin	0.667
O09165	Calsequestrin-1	0.667
G5E814	MCG5603	0.67
Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0.67
E0CX32	Coiled-coil domain-containing protein 85A	0.673
Q5SP85	Coiled-coil domain-containing protein 85A	0.673
P97855	RasGTPase-activating protein-binding protein 1	0.673

Supplementary Table 10 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
D3Z079	Syntaxin-binding protein 5	0.674	Q9D0M5	Dynein light chain 2, cytoplasmic	0.706
D3Z2Q2	Syntaxin-binding protein 5	0.674	D3YXH0	Immunoglobulin superfamily member 5	0.707
Q8K400	Syntaxin-binding protein 5	0.674	P63054	Purkinje cell protein 4	0.707
Q60829	Protein phosphatase 1 regulatory subunit 1B	0.677	P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	0.71
Q5DTI3	MKIAA4194 protein (Fragment)	0.682	Q4VAE8	Ndufb4 protein (Fragment)	0.71
Q9ME04	NADH-ubiquinone oxidoreductase chain 4	0.683	Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	0.71
P03911	NADH-ubiquinone oxidoreductase chain 4	0.683	Q9JIS5	Synaptic vesicle glycoprotein 2A	0.711
Q9QXV0	ProSAAS	0.688	Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	0.711
Q8BG39	Synaptic vesicle glycoprotein 2B	0.688	Q9DB20	ATP synthase subunit O, mitochondrial	0.713
P63137	Gamma-aminobutyric acid receptor subunit beta-2	0.689	Q8BG67	Protein EFR3 homolog A	0.714
Q9D1H7	Golgi to ER traffic protein 4 homolog	0.689	Q9WVT6	Carbonic anhydrase 14	0.714
Q8VI75	Importin-4	0.69	G3XA48	Isopentenyl-diphosphate Delta-isomerase 1	0.717
Q4FJP8	Slc2a3 protein	0.69	P58044	Isopentenyl-diphosphate Delta-isomerase 1	0.717
P32037	Solute carrier family 2, facilitated glucose transporter member 3	0.69	B1ATS4	Calcium-transporting ATPase	0.719
Q8BLF7	Putative uncharacterized protein	0.69	B1ATS5	Calcium-transporting ATPase	0.719
F8WHP8	ATP synthase subunit f, mitochondrial	0.7	Q8R0X5	Calcium-transporting ATPase	0.719
P56135	ATP synthase subunit f, mitochondrial	0.7	E9Q559	Calcium-transporting ATPase	0.719
Q9D6L8	Peptidyl-prolylcis-trans isomerase-like 3	0.704	Q3U1K2	Putative uncharacterized protein (Fragment)	0.719
P97450	ATP synthase-coupling factor 6, mitochondrial	0.705	Q64518	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	0.719
Q561M1	Acp1 protein	0.705	Q8C213	Putative uncharacterized protein (Fragment)	0.719
Q05BD4	Prpsap2 protein	0.705	D3Z3Z3	Voltage-dependent L-type calcium channel subunit beta-3	0.721
Q8R574	Phosphoribosyl pyrophosphate synthase-associated protein 2	0.705	P54285	Voltage-dependent L-type calcium channel subunit beta-3	0.721
Q8BK37	Putative uncharacterized protein	0.705	Q8K5A7	Calcium channel beta 3 subunit	0.721

Supplementary Table 10 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8VIM9	Immunity-related GTPase family Q protein	0.721	P48320	Glutamate decarboxylase 2	0.736
O35857	Mitochondrial import inner membrane translocase subunit TIM44	0.722	Q8C281	Putative uncharacterized protein	0.738
Q8K3Q4	Actinin alpha 2	0.722	Q8CE80	Calpastatin	0.738
Q9JI91	Alpha-actinin-2	0.722	Q921U7	Cast protein	0.738
Q04899	Cyclin-dependent kinase 18	0.722	P51125	Calpastatin	0.738
Q3U484	Putative uncharacterized protein	0.723	Q8CE04	Putative uncharacterized protein	0.738
Q62095	ATP-dependent RNA helicase DDX3Y	0.723	Q3TCY0	Putative uncharacterized protein	0.74
Q3UTI4	Putative uncharacterized protein (Fragment)	0.724	Q3TQ93	Putative uncharacterized protein	0.74
O54865	Guanylatecyclase soluble subunit beta-1	0.724	O35963	Ras-related protein Rab-33B	0.74
Q53YX2	CD90.1	0.724	Q8R1N4	NudC domain-containing protein 3	0.74
P01831	Thy-1 membrane glycoprotein	0.724	Q8K2C9	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	0.74
Q6PJ18	Tpm2 protein	0.726	Q3UI39	Putative uncharacterized protein	0.741
Q61344	Beta-tropomyosin	0.726	E9QLK9	Clathrin coat assembly protein AP180	0.741
Q8BKG0	Transporter (Fragment)	0.727	E9Q9A3	Clathrin coat assembly protein AP180	0.741
P31650	Sodium- and chloride-dependent GABA transporter 3	0.727	Q61548	Clathrin coat assembly protein AP180	0.741
Q8CFA2	Aminomethyltransferase, mitochondrial	0.728	E9QQ05	Clathrin coat assembly protein AP180	0.741
P30275	Creatine kinase U-type, mitochondrial	0.728	Q3TYH2	Ras-related protein Rab-15	0.75
O35239	Tyrosine-protein phosphatase non-receptor type 9	0.729	Q8K386	Ras-related protein Rab-15	0.75
P62823	Ras-related protein Rab-3C	0.73	Q99JW2	Aminoacylase-1	0.751
Q8C050	Ribosomal protein S6 kinase alpha-5	0.73	B1ASQ2	Apolipoprotein O	0.752
Q9QYS2	Metabotropic glutamate receptor 3	0.732	Q9DCZ4	Apolipoprotein O	0.752
Q2NL51	Glycogen synthase kinase-3 alpha	0.735	Q3KNM9	Apoo protein	0.752
D3Z7E5	Glycogen synthase kinase-3 alpha	0.735	Q9D186	Apolipoprotein O	0.752

Supplementary Table 10 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q9CRD0	OCIA domain-containing protein 1	0.756	F6VTH5	Leucine zipper transcription factor-like protein 1 (Fragment)	0.771
P14231	Sodium/potassium-transporting ATPase subunit beta-2	0.756	Q8JZU2	Tricarboxylate transport protein, mitochondrial	0.772
B0V2H4	V-type proton ATPase subunit G 2	0.758	Q9D5T0	ATPase family AAA domain-containing protein 1	0.772
Q9WTT4	V-type proton ATPase subunit G 2	0.758	Q3TDG9	Putative uncharacterized protein	0.773
Q6NZL0	Protein SOGA3	0.761	Q9ER00	Syntaxin-12	0.773
P60879	Synaptosomal-associated protein 25	0.762	G3X8U3	MCG6895	0.774
P21550	Beta-enolase	0.763	Q8C7K6	Prenylcysteine oxidase-like	0.774
D3YWF6	Ubiquitin thioesterase OTUB1	0.764	B0QZN5	Vesicle-associated membrane protein 2	0.776
Q7TQI3	Ubiquitin thioesterase OTUB1	0.764	O35619	Vesicle associated membrane protein 2	0.776
B1AWV9	Sodium-driven chloride bicarbonate exchanger	0.765	P63044	Vesicle-associated membrane protein 2	0.776
R4H243	Na-coupled HCO3-cotransporter splice variant NBCn2-D	0.765	D3Z6H3	Dynactin 6, isoform CRA_b	0.776
Q8C943	Putative uncharacterized protein (Fragment)	0.765	Q9WUB4	Dynactin subunit 6	0.776
E9NX85	Sodium bicarbonate cotransporter member 10 variant NBCn2-C	0.765	P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	0.776
Q5DTL9	Sodium-driven chloride bicarbonate exchanger	0.765	Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	0.777
F1DFN1	Na-coupled HCO3-cotransporter splice variant NBCn2	0.765	Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	0.777
Q99M71	Mammalian ependymin-related protein 1	0.767	Q78IK2	Up-regulated during skeletal muscle growth protein 5	0.778
Q3US29	Putative uncharacterized protein	0.768	A2ALS5	Rap1 GTPase-activating protein 1	0.778
Q5M8R9	Farnesyldiphosphatesynthetase	0.768	Q3TN35	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha, isoform CRA_b	0.779
Q920E5	Farnesyl pyrophosphate synthase	0.768	Q8BJU0	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	0.779
Q3UHL8	Putative uncharacterized protein (Fragment)	0.771	Q7TSE6	Serine/threonine-protein kinase 38-like	0.779
F6VG18	Leucine zipper transcription factor-like protein 1 (Fragment)	0.771	A2AP32	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	0.78
Q9JHQ5	Leucine zipper transcription factor-like protein 1	0.771	Q3UIU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	0.78
Q8CDG8	Putative uncharacterized protein	0.771	Q80TQ3	MKIAA0845 protein (Fragment)	0.781

Supplementary Table 10 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P19246	Neurofilament heavy polypeptide	0.781	Q9D997	N-acetyl-D-glucosamine kinase	0.791
Q8R2R9	AP-3 complex subunit mu-2	0.781	Q9CYG7	Mitochondrial import receptor subunit TOM34	0.791
Q3TDM2	Putative uncharacterized protein	0.783	Q9JJ43	RNA binding protein fox-1 homolog 1	0.791
Q3UH04	Putative uncharacterized protein	0.783	Q9JIA1	Leucine-rich glioma-inactivated protein 1	0.792
Q8BW96	Calcium/calmodulin-dependent protein kinase type 1D	0.783	Q8R059	UDP-glucose 4-epimerase	0.792
A3QM89	Reticulon (Fragment)	0.785	P05202	Aspartate aminotransferase, mitochondrial	0.792
Q7M6W1	Reticulon	0.785	P47809	Dual specificity mitogen-activated protein kinase kinase 4	0.793
Q9CPQ1	Cytochrome c oxidase subunit 6C	0.785	B2RSH2	Guanine nucleotide-binding protein G(i) subunit alpha-1	0.794
Q64288	Olfactory marker protein	0.787	Q9CPQ3	Mitochondrial import receptor subunit TOM22 homolog	0.796
P07759	Serine protease inhibitor A3K	0.788	Q8CBN6	Protein Gm9967	0.798
E0CZ72	Kinesin-like protein	0.79	Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	0.798
P28740	Kinesin-like protein KIF2A	0.79	S4R1M9	Oxysterol-binding protein	0.798
F8VQ42	Kinesin-like protein (Fragment)	0.79	S4R296	Oxysterol-binding protein	0.798
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.79	Q8R2T7	Oxysterol-binding protein	0.798
Q6PB99	Ena-vasodilator stimulated phosphoprotein	0.79	Q8K3H0	DCC-interacting protein 13-alpha	0.799
P70429	Ena/VASP-like protein	0.79	Q3UEX4	Putative uncharacterized protein	0.799
F8WJB9	Ena/VASP-like protein	0.79	O88741	Ganglioside-induced differentiation-associated protein 1	0.799
E9PVP4	Ena/VASP-like protein	0.79	Q3UTV3	Putative uncharacterized protein (Fragment)	0.799
Q5DTM9	MKIAA4112 protein (Fragment)	0.79	G3UWG1	MCG115977	0.802
B8QI34	Liprin-alpha 2	0.79	P62897	Cytochrome c, somatic	0.802
Q8BSS9	Liprin-alpha-2	0.79	Q3THU8	Putative uncharacterized protein	0.804
D3YXG2	N-acetyl-D-glucosamine kinase	0.791	G5E902	MCG10343, isoform CRA_b	0.804
Q9QZ08	N-acetyl-D-glucosamine kinase	0.791	Q8VEM8	Phosphate carrier protein, mitochondrial	0.804

Supplementary Table 10 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q3UB63	Putative uncharacterized protein	0.804	Q6GQV6	Nbas protein (Fragment)	0.814
Q3U995	Putative uncharacterized protein	0.804	E9Q411	Protein Nbas	0.814
Q99JR1	Sideroflexin-1	0.805	Q8BX70	Vacuolar protein sorting-associated protein 13C	0.815
A3KGQ6	Actin-related protein 2/3 complex subunit 5	0.808	Q80TJ1	Calcium-dependent secretion activator 1	0.815
Q9D898	Actin-related protein 2/3 complex subunit 5-like protein	0.808	Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	0.815
A2AWI7	Endophilin-B2	0.808	Q99J09	Methylosome protein 50	0.818
P62075	Mitochondrial import inner membrane translocase subunit Tim13	0.81	P17665	Cytochrome c oxidase subunit 7C, mitochondrial	0.818
P62748	Hippocalcin-like protein 1	0.81	D3YYK8	Microtubule-associated protein RP/EB family member 2 (Fragment)	0.82
P32848	Parvalbumin alpha	0.81	Q8R001	Microtubule-associated protein RP/EB family member 2	0.82
Q8R3X4	Timm44 protein (Fragment)	0.811	E9Q6X0	Microtubule-associated protein RP/EB family member 2	0.82
Q3U536	Putative uncharacterized protein	0.811	H3BLL2	ATP synthase mitochondrial F1 complex assembly factor 1	0.822
Q5SQB0	Nucleophosmin	0.811	Q811I0	ATP synthase mitochondrial F1 complex assembly factor 1	0.822
Q61937	Nucleophosmin	0.811	Q08331	Calretinin	0.822
Q5U438	Nucleophosmin 1	0.811	Q8C7Z5	Putative uncharacterized protein	0.822
B2RQX9	Transporter	0.811	Q499F6	Kcnj10 protein (Fragment)	0.822
B2RXV9	Transporter	0.811	Q9JM63	ATP-sensitive inward rectifier potassium channel 10	0.822
P26516	26S proteasome non-ATPase regulatory subunit 7	0.812	B9EIV1	Kcnj10 protein	0.822
Q8C8P2	Putative uncharacterized protein	0.813	Q3THM1	Putative uncharacterized protein	0.823
E9PV14	Band 4.1-like protein 1 (Fragment)	0.813	Q3TIC8	Putative uncharacterized protein	0.823
O54774	AP-3 complex subunit delta-1	0.813	Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	0.823
A2ALV3	Endophilin-A1	0.813	P48722	Heat shock 70 kDa protein 4L	0.825
Q62420	Endophilin-A1	0.813	E9Q3V0	Transporter	0.825
Q8R146	Acylamino-acid-releasing enzyme	0.813	E9Q517	Transporter	0.825

Supplementary Table 10 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P28571	Sodium- and chloride-dependent glycine transporter 1	0.825	Q91XF0	Pyridoxine-5~-phosphate oxidase	0.827
Q3UA17	Putative uncharacterized protein	0.825	Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	0.829
Q791V5	Mitochondrial carrier homolog 2	0.825	Q9D154	Leukocyte elastase inhibitor A	0.83
B8QI35	Liprin-alpha 3	0.826	G3UW70	MCG21719	0.83
Q3TGI6	Putative uncharacterized protein (Fragment)	0.826	Q9D1L9	Ragulator complex protein LAMTOR5	0.83
Q3UE53	Putative uncharacterized protein	0.826	P61087	Ubiquitin-conjugating enzyme E2 K	0.83
P53810	Phosphatidylinositol transfer protein alpha isoform	0.826	P46660	Alpha-internexin	0.831
Q3TK29	Putative uncharacterized protein	0.826	G5E8R4	SAPS domain family, member 3, isoform CRA_c	0.832
Q3TSG8	Putative uncharacterized protein	0.826	Q922D4	Serine/threonine-protein phosphatase 6 regulatory subunit 3	0.832
Q922Z3	Trap1 protein (Fragment)	0.826	Q920I9	WD repeat-containing protein 7	0.832
Q9CQN1	Heat shock protein 75 kDa, mitochondrial	0.826	Q9CZU6	Citrate synthase, mitochondrial	0.833
Q3UPJ8	Putative uncharacterized protein	0.826			

The comparison was made between the spinal cord of a progression SOD1 mouse and the spinal cord of anpreonset mouse,where fold changes of < 0.833(1/1.2) and p-value < 0.05 were taken into consideration. This table contains the 299 proteins that downregulated significantly in the spinal cord of a progression SOD1 mousevsa anpreonset mouse. The accession number of UniProt Knowledgebase, description, and fold change of each protein are provided here. The proteins are listed according to the level of the fold changes.The top 30 proteins are highlighted with gray.

Supplementary Table 11. List of Significantly Up Regulated Proteins in the Spinal Cord between the Progression Vs the Onset of SOD1 G93A Mouse

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P27573	Myelin protein P0	11.343	Q3KQQ4	Serpina1a protein	2.228
P51910	Apolipoprotein D	4.061	P22599	Alpha-1-antitrypsin 1-2	2.228
Q9D114	Guanosine-3~,5~-bis(diphosphate) 3~-pyrophosphohydrolase MESH1	3.351	D3Z0B9	Aldehyde dehydrogenase family 16 member A1	2.176
Q71V06	Y box transcription factor (Fragment)	3.065	Q571I9	Aldehyde dehydrogenase family 16 member A1	2.176
Q810K5	Y box protein 1	3.065	P43274	Histone H1.4	2.171
P62960	Nuclease-sensitive element-binding protein 1	3.065	Q3UDJ2	Putative uncharacterized protein	2.128
Q60951	MYB-1b	3.065	Q69ZN1	MKIAA1252 protein (Fragment)	2.128
A8DUK4	Beta-globin	2.699	Q4FK38	Sgpl1 protein	2.128
A8DUK7	Beta-globin	2.699	Q8R0X7	Sphingosine-1-phosphate lyase 1	2.128
Q9CSN1	SNW domain-containing protein 1	2.658	Q3UVX5	Metabotropic glutamate receptor 5	2.124
F6UP77	Putative N-acetylglucosamine-6-phosphate deacetylase (Fragment)	2.615	E9QMC2	Metabotropic glutamate receptor 5	2.124
Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	2.615	P11087	Collagen alpha-1(I) chain	2.108
Q3U292	Putative uncharacterized protein	2.537	Q8QZV4	Serine/threonine-protein kinase 32C	2.106
P43277	Histone H1.3	2.537	B2RPU8	MCG130675	2.063
P15864	Histone H1.2	2.537	Q9D1L0	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	2.063
B7ZWF1	Ddx3x protein	2.371	D3Z5B1	Protein Zbed5 (Fragment)	2.063
Q62167	ATP-dependent RNA helicase DDX3X	2.371	Q8CEW7	Putative uncharacterized protein	2.063
B9EKE9	Ddx3x protein	2.371	P68510	14-3-3 protein eta	2.042
Q7TMM9	Tubulin beta-2A chain	2.366	P08122	Collagen alpha-2(IV) chain	2.011
Q9CWF2	Tubulin beta-2B chain	2.281	Q9D3D9	ATP synthase subunit delta, mitochondrial	2
E9QPX1	Collagen alpha-1(XVIII) chain	2.274	Q9D0J2	Putative uncharacterized protein	2
P39061	Collagen alpha-1(XVIII) chain	2.274	P0C0S6	Histone H2A.Z	1.996
B1AWD8	Clathrin light chain A	2.244	Q3THW5	Histone H2A.V	1.996
O08585	Clathrin light chain A	2.244	Q8C1B7	Septin-11	1.992
B1AWD9	Clathrin light chain A	2.244	A2AUE1	DnaJ homolog subfamily C member 5 (Fragment)	1.951

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P60904	DnaJ homolog subfamily C member 5	1.951	O35449	Proline-rich transmembrane protein 1	1.713
Q921J3	Dnajc5 protein	1.951	Q3TR90	Putative uncharacterized protein	1.712
G5E8T0	DnaJ (Hsp40) homolog, subfamily C, member 5, isoform CRA_b	1.951	Q9JMG7	Hepatoma-derived growth factor-related protein 3	1.712
Q7TQ95	Protein lunapark	1.884	Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	1.705
Q8K1L5	Protein phosphatase 1 regulatory subunit 11	1.868	Q8BNA5	Putative uncharacterized protein	1.699
Q9QY42	Prosaposin receptor GPR37	1.858	Q921L6	Cortactin, isoform CRA_a	1.699
Q3TU64	Putative uncharacterized protein	1.839	Q60598	Src substrate cortactin	1.699
Q01149	Collagen alpha-2(I) chain	1.839	Q9Z315	U4/U6.U5 tri-snRNP-associated protein 1	1.696
Q3U449	Bisphosphate 3~-nucleotidase 1, isoform CRA_a	1.825	P08775	DNA-directed RNA polymerase II subunit RPB1	1.692
Q3TX84	Putative uncharacterized protein	1.813	O08847	DNA-directed RNA polymerase	1.692
P11438	Lysosome-associated membrane glycoprotein 1	1.813	D3YWQ0	Diacylglycerol kinase	1.69
Q9DC13	Lysosomal membrane glycoprotein 1, isoform CRA_a	1.813	D3Z2W1	Diacylglycerol kinase	1.69
Q8VH34	LAMP-1	1.813	P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	1.688
Q8BTI8	Serine/arginine repetitive matrix protein 2	1.767	Q8R2K3	Single-stranded DNA-binding protein	1.687
Q62277	Synaptophysin	1.766	Q8VCS3	Glycosaminoglycan xylosylkinase	1.681
Q3TWG2	Putative uncharacterized protein	1.739	P51885	Lumican	1.674
O08795	Glucosidase 2 subunit beta	1.739	Q9CR57	60S ribosomal protein L14	1.669
Q5SWP3	NAC-alpha domain-containing protein 1	1.731	Q9CWK0	Putative uncharacterized protein	1.669
B7ZNF6	Ctnnd2 protein	1.729	A0JLV3	Histone H2B (Fragment)	1.665
O35927	Catenin delta-2	1.729	Q8CGP2	Histone H2B type 1-P	1.665
E9QKH8	Catenin delta-2	1.729	Q64475	Histone H2B type 1-B	1.665
Q3U3I1	Putative uncharacterized protein	1.726	Q921L4	Histone H2B	1.665
Q64444	Carbonic anhydrase 4	1.726	Q8CBB6	Histone H2B	1.665
A0A087WNP6	Protein CDV3	1.725	P10853	Histone H2B type 1-F/J/L	1.665
Q4VAA2	Protein CDV3	1.725	Q6ZWY9	Histone H2B type 1-C/E/G	1.665

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8CGP1	Histone H2B type 1-K	1.665	B7ZNM3	Art3 protein	1.626
Q64525	Histone H2B type 2-B	1.665	E9Q7Q8	Ecto-ADP-ribosyltransferase 3	1.626
P10854	Histone H2B type 1-M	1.665	Q8R2G4	Ecto-ADP-ribosyltransferase 3	1.626
Q64478	Histone H2B type 1-H	1.665	E9Q1U7	Ecto-ADP-ribosyltransferase 3 (Fragment)	1.626
J3QNT7	Epsin-2	1.66	E9QNU1	Ecto-ADP-ribosyltransferase 3	1.626
Q69ZS5	MKIAA1065 protein (Fragment)	1.66	G5E8T9	Hydroxyacyl glutathione hydrolase	1.613
Q5NCM5	Epsin-2	1.66	Q99KB8	Hydroxyacylglutathione hydrolase, mitochondrial	1.613
Q3ULL6	Protein Upf3b	1.656	E9PYA3	Hydroxyacylglutathione hydrolase, mitochondrial (Fragment)	1.613
F6Q8N5	Protein Upf3b (Fragment)	1.656	Q3UBS0	Putative uncharacterized protein	1.597
Q9CS15	Putative uncharacterized protein (Fragment)	1.656	P08226	Apolipoprotein E	1.597
Q80UI8	Upf3b protein (Fragment)	1.656	Q4FK40	Apoe protein	1.597
D3YW48	Calpain small subunit 1 (Fragment)	1.651	Q6GTX3	Apoe protein	1.597
O88456	Calpain small subunit 1	1.651	Q61753	D-3-phosphoglycerate dehydrogenase	1.595
Q9ERB0	Synaptosomal-associated protein 29	1.647	P0C0A3	Charged multivesicular body protein 6	1.592
Q8BW41	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	1.645	B1AZ42	Charged multivesicular body protein 6 (Fragment)	1.592
Q02105	Complement C1q subcomponent subunit C	1.642	B9EIX2	AW555464 protein	1.587
Q9CWM4	Prefoldin subunit 1	1.634	Q80U49	Centrosomal protein of 170 kDa protein B	1.587
Q9CQF7	Prefoldin 1	1.634	A2ALS5	Rap1 GTPase-activating protein 1	1.58
E9PZ58	Spermine synthase	1.632	Q8C5Q4	G-rich sequence factor 1	1.579
P97355	Spermine synthase	1.632	E9Q179	G-rich sequence factor 1	1.579
P23242	Gap junction alpha-1 protein	1.628	B1AZS9	Peroxiredoxin-4 (Fragment)	1.576
Q7TMQ1	Gap junction protein	1.628	O08807	Peroxiredoxin-4	1.576
Q3THJ0	60S ribosomal protein L18a	1.627	G5E850	Cytochrome b-5, isoform CRA_a	1.574
Q05CK2	60S ribosomal protein L18a	1.627	P56395	Cytochrome b5	1.574
P62717	60S ribosomal protein L18a	1.627	D3Z5I6	IQ motif and SEC7 domain-containing protein 2	1.573

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q5DU25	IQ motif and SEC7 domain-containing protein 2	1.573	P67984	60S ribosomal protein L22	1.534
E9QAD8	IQ motif and SEC7 domain-containing protein 2	1.573	P08228	Superoxide dismutase [Cu-Zn]	1.53
A4GZ26	ARF6 guanine nucleotide exchange factor IQArfGEF	1.573	P60867	40S ribosomal protein S20	1.53
A7YQ68	Prickle-like 2 (Drosophila)	1.573	Q8BHC1	Ras-related protein Rab-39B	1.525
Q80Y24	Prickle-like protein 2	1.573	Q8K2C6	NAD-dependent protein deacylase sirtuin-5, mitochondrial	1.522
P48678	Prelamin-A/C	1.569	Q3TDT0	Tripartite motif-containing protein 3	1.517
Q3U3F4	Putative uncharacterized protein	1.569	Q9R1R2	Tripartite motif-containing protein 3	1.517
P31938	Dual specificity mitogen-activated protein kinase kinase 1	1.569	A0A087WQY4	Brain-enriched guanylate kinase-associated protein (Fragment)	1.517
Q9JJE1	Brain cDNA, clone MNCb-1208, similar to Mus musculus mitogen activated protein kinase kinase 1 (Map2k1), mRNA	1.569	Q68EF6	Brain-enriched guanylate kinase-associated protein	1.517
Q3UK05	Putative uncharacterized protein	1.569	F8WIG2	Brain-enriched guanylate kinase-associated protein	1.517
Q5EBG5	Ribosomal protein L7A	1.56	Q3U4P3	Putative uncharacterized protein (Fragment)	1.513
P12970	60S ribosomal protein L7a	1.56	Q8K1M6	Dynamin-1-like protein	1.513
Q80UT7	Rpl7a protein (Fragment)	1.56	Q8BX02	KN motif and ankyrin repeat domain-containing protein 2	1.513
Q6P1A9	Ribosomal protein L7A	1.56	P10639	Thioredoxin	1.508
Q62000	Mimecan	1.557	Q3UF75	Alpha-parvin	1.506
D3YU06	Abhydrolase domain-containing protein 3	1.552	Q8C5R4	Putative uncharacterized protein	1.506
D3Z6Y2	Abhydrolase domain-containing protein 3	1.552	Q9EPC1	Alpha-parvin	1.506
Q91ZH7	Abhydrolase domain-containing protein 3	1.552	P27048	Small nuclear ribonucleoprotein-associated protein B	1.505
P47911	60S ribosomal protein L6	1.55	P63163	Small nuclear ribonucleoprotein-associated protein N	1.505
Q8CGP0	Histone H2B type 3-B	1.547	O70499	Small nuclear ribonucleoprotein-associated protein	1.505
Q9D2U9	Histone H2B type 3-A	1.547	Q8K354	Carbonyl reductase [NADPH] 3	1.501
Q64524	Histone H2B type 2-E	1.547	P14115	60S ribosomal protein L27a	1.5
O35551	Rab GTPase-binding effector protein 1	1.543	Q9JI95	CPN10-like protein	1.499
Q60692	Proteasome subunit beta type-6	1.538	Q64433	10 kDa heat shock protein, mitochondrial	1.499

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
B1ASQ2	Apolipoprotein O	1.499	Q3TH64	Putative uncharacterized protein	1.476
Q9DCZ4	Apolipoprotein O	1.499	Q3TN44	Putative uncharacterized protein	1.476
Q3KNM9	Apoo protein	1.499	Q9CQX2	Cytochrome b5 type B	1.476
Q9D186	Apolipoprotein O	1.499	Q3UZP4	Small VCP/p97-interacting protein	1.475
Q3UJ44	Putative uncharacterized protein	1.496	A2AVJ7	Ribosome-binding protein 1	1.472
Q99LB4	Capping protein (Actin filament), gelsolin-like	1.496	Q6ZPS0	MKIAA1398 protein (Fragment)	1.472
Q1WWJ8	Pdap1 protein (Fragment)	1.495	Q99PL5	Ribosome-binding protein 1	1.472
Q3UHX2	28 kDa heat- and acid-stable phosphoprotein	1.495	P61982	14-3-3 protein gamma	1.469
Q6A0A9	Constitutive coactivator of PPAR-gamma-like protein 1	1.492	P21619	Lamin-B2	1.467
F8VPM7	ELKS/Rab6-interacting/CAST family member 1	1.491	D3YYD5	Vacuolar protein sorting-associated protein 29 (Fragment)	1.463
Q99MI1	ELKS/Rab6-interacting/CAST family member 1	1.491	Q9QZ88	Vacuolar protein sorting-associated protein 29	1.463
V9GXF0	ELKS/Rab6-interacting/CAST family member 1	1.491	D3Z645	Vacuolar protein sorting-associated protein 29	1.463
V9GXP8	ELKS/Rab6-interacting/CAST family member 1	1.491	D3Z4B0	Protein Srsf11 (Fragment)	1.462
V9GWT6	ELKS/Rab6-interacting/CAST family member 1	1.491	Q8C0Z3	Putative uncharacterized protein (Fragment)	1.462
V9GXH3	ELKS/Rab6-interacting/CAST family member 1	1.491	Q9CT17	Putative uncharacterized protein (Fragment)	1.462
P29595	NEDD8	1.49	Q8CGI3	Sfrs11 protein (Fragment)	1.462
D3YXK2	Scaffold attachment factor B1	1.489	Q6NSR2	Sfrs11 protein (Fragment)	1.462
S4R1M2	Scaffold attachment factor B1	1.489	Q3UIX4	Protein Srsf11	1.462
Q9WU84	Copper chaperone for superoxide dismutase	1.482	E9Q6E5	Protein Srsf11	1.462
A2AIW9	Mitochondrial-processing peptidase subunit alpha	1.477	Q8CFF2	Sfrs11 protein (Fragment)	1.462
Q3UDE0	Putative uncharacterized protein (Fragment)	1.477	Q6I6G8	E3 ubiquitin-protein ligase HECW2	1.461
Q3TY06	Putative uncharacterized protein (Fragment)	1.477	B0R1E3	Histidine triad nucleotide-binding protein 1	1.457
Q8BK51	Putative uncharacterized protein	1.477	P70349	Histidine triad nucleotide-binding protein 1	1.457
Q9DC61	Mitochondrial-processing peptidase subunit alpha	1.477	Q04857	Collagen alpha-1(VI) chain	1.446
Q3TTM6	Putative uncharacterized protein	1.477	Q3TJ49	Annexin	1.446

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q922A2	Annexin	1.446	P01831	Thy-1 membrane glycoprotein	1.431
Q8BP75	Annexin	1.446	Q61361	Brevican core protein	1.429
Q07076	Annexin A7	1.446	Q3TPN0	Putative uncharacterized protein	1.427
Q5H8C4	Vacuolar protein sorting-associated protein 13A	1.446	Q3US45	Putative uncharacterized protein	1.427
Q3UDE9	Protein-tyrosine kinase 2-beta	1.445	Q8CFA3	Nidogen-2	1.427
E9Q2A6	Protein-tyrosine kinase 2-beta	1.445	O88322	Nidogen-2	1.427
Q9QVP9	Protein-tyrosine kinase 2-beta	1.445	Q5EBI8	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	1.426
Q8C2G0	Putative uncharacterized protein	1.445	Q06185	ATP synthase subunit e, mitochondrial	1.426
Q5Y5T1	Probable palmitoyltransferase ZDHHC20	1.441	Q3TUA8	Putative uncharacterized protein	1.426
Q80ZI8	Itga6 protein (Fragment)	1.435	Q6NZM8	3~-phosphoadenosine 5~-phosphosulfate synthase 1, isoform CRA_a	1.426
Q8CC06	Putative uncharacterized protein	1.435	Q60967	Bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 1	1.426
Q61739	Integrin alpha-6	1.435	P62264	40S ribosomal protein S14	1.424
Q6PEE8	Itga6 protein	1.435	O70569	Ribosomal protein S14	1.424
Q3UP61	Putative uncharacterized protein	1.434	Q3TCJ1	BRISC complex subunit Abro1	1.422
E9Q9H0	Disks large homolog 1	1.434	D3Z4D8	BRISC complex subunit Abro1 (Fragment)	1.422
H7BWY4	Disks large homolog 1	1.434	Z4YJY0	BRISC complex subunit Abro1	1.422
Q811D0	Disks large homolog 1	1.434	Q5NDA4	Fatty acid binding protein 7, brain	1.419
Q3TI34	Glutathione peroxidase	1.433	P51880	Fatty acid-binding protein, brain	1.419
Q76LV0	Glutathione peroxidase	1.433	Q8R555	Cartilage acidic protein 1	1.418
O70325	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	1.433	Q9QXS6	Drebrin	1.416
Q5XJZ8	Glutathione peroxidase (Fragment)	1.433	Q9QXV0	ProSAAS	1.416
S4R1E5	Glutathione peroxidase	1.433	Q3V471	Galectin (Fragment)	1.413
O09164	Extracellular superoxide dismutase [Cu-Zn]	1.433	Q8C253	Galectin	1.413
O88592	Superoxide dismutase [Cu-Zn]	1.433	P16110	Galectin-3	1.413
Q53YX2	CD90.1	1.431	J3QNM3	Protein enabled homolog	1.412

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q03173	Protein enabled homolog	1.412	Q3TSY9	Putative uncharacterized protein	1.389
E9QKR1	Protein enabled homolog	1.412	Q3TDD8	Putative uncharacterized protein	1.389
E9QLZ9	Protein enabled homolog	1.412	Q3UGC0	Putative uncharacterized protein	1.389
E9QKQ9	Protein enabled homolog	1.412	Q8BGD9	Eukaryotic translation initiation factor 4B	1.389
Q93092	Transaldolase	1.411	Q3THB0	Putative uncharacterized protein	1.389
Q3UNH4	G protein-regulated inducer of neurite outgrowth 1	1.409	Q02788	Collagen alpha-2(VI) chain	1.386
P60879	Synaptosomal-associated protein 25	1.408	A0A068WAQ5	Protein 4.1R (Fragment)	1.386
A2A6U3	Septin-9	1.408	A2A838	Protein 4.1 (Fragment)	1.386
Q80UG5	Septin-9	1.408	A2A841	Protein 4.1	1.386
Q8CIP4	MAP/microtubule affinity-regulating kinase 4	1.407	P48193	Protein 4.1	1.386
Q3TSV1	Putative uncharacterized protein	1.407	A2A842	Protein 4.1	1.386
P28654	Decorin	1.407	A0A068WAZ7	Protein 4.1R (Fragment)	1.386
D3YXZ3	Kinesin light chain 2	1.405	Q3UH12	Putative uncharacterized protein (Fragment)	1.386
Q91YS4	Kinesin light chain 2	1.405	B6ZHC8	Erythrocyte protein band 4.1	1.386
Q3TG02	Putative uncharacterized protein	1.404	A2AD32	Protein 4.1 (Fragment)	1.386
Q3UA28	Putative uncharacterized protein	1.404	A2A839	Protein 4.1	1.386
Q3TUR1	Putative uncharacterized protein	1.404	Q9WUN2	Serine/threonine-protein kinase TBK1	1.385
Q3U9H4	Putative uncharacterized protein	1.404	Q61001	Laminin subunit alpha-5	1.379
P46978	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	1.404	Q3TVM1	Putative uncharacterized protein	1.377
Q8BMP9	Putative uncharacterized protein	1.404	Q8K4Z5	Splicing factor 3A subunit 1	1.377
Q5U412	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	1.404	Q70IV5	Synemin	1.376
Q3U547	Putative uncharacterized protein	1.404	Q8R1P3	Gpm6a protein	1.376
P14733	Lamin-B1	1.402	P35802	Neuronal membrane glycoprotein M6-a	1.376
Q3UHD9	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 2	1.394	Q3TA13	Putative uncharacterized protein	1.37
B2RWE8	Eif4b protein	1.389	E9Q3E2	Synaptopodin	1.37

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q3URF1	MCG6023	1.37	D3Z379	Synaptic vesicle 2-related protein (Fragment)	1.352
Q3TY32	Putative uncharacterized protein (Fragment)	1.37	Q8BFT9	Synaptic vesicle 2-related protein	1.352
Q3U336	Putative uncharacterized protein	1.37	F6VW30	14-3-3 protein theta (Fragment)	1.351
Q8CC35	Synaptopodin	1.37	P68254	14-3-3 protein theta	1.351
Q3U0V1	Far upstream element-binding protein 2	1.368	F6YY69	14-3-3 protein theta (Fragment)	1.351
O54724	Polymerase I and transcript release factor	1.368	Q9Z2Y3	Homer protein homolog 1	1.35
Q8VBZ3	Cleft lip and palate transmembrane protein 1 homolog	1.365	Q3UIH7	Putative uncharacterized protein	1.35
Q3U3A1	Putative uncharacterized protein	1.365	Q9JHK4	Geranylgeranyl transferase type-2 subunit alpha	1.35
Q3T9A3	Serine/threonine-protein kinase MARK2	1.365	B2RQS1	Striatin-3	1.35
Q571J8	MKIAA4207 protein (Fragment)	1.365	A2AU89	Tumor suppressor p53-binding protein 1	1.35
E9PYX3	Serine/threonine-protein kinase MARK2	1.365	P70399	Tumor suppressor p53-binding protein 1	1.35
F6ZS70	Serine/threonine-protein kinase MARK2 (Fragment)	1.365	A2AU91	Tumor suppressor p53-binding protein 1	1.35
E9Q9N6	Serine/threonine-protein kinase MARK2	1.365	P28651	Carbonic anhydrase-related protein	1.349
Q05512	Serine/threonine-protein kinase MARK2	1.365	A0A0A0MQA5	Tubulin alpha-4A chain (Fragment)	1.348
E9QMP6	Serine/threonine-protein kinase MARK2	1.365	P68368	Tubulin alpha-4A chain	1.348
P63216	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-3	1.364	E0CYM8	Tyrosine-protein phosphatase non-receptor type substrate 1	1.345
O55234	Proteasome subunit beta type-5	1.363	Q6P6I8	Signal-regulatory protein alpha	1.345
Q3U8W4	Superoxide dismutase	1.359	Q61292	Laminin subunit beta-2	1.342
P09671	Superoxide dismutase [Mn], mitochondrial	1.359	Q3UNZ8	Quinone oxidoreductase-like protein 2	1.342
B9EKC3	Rho GTPase activating protein 5	1.356	Q9CR26	Vacuolar protein sorting-associated protein VTA1 homolog	1.339
P97393	Rho GTPase-activating protein 5	1.356	Q9DCN2	NADH-cytochrome b5 reductase 3	1.335
E9PYT0	Rho GTPase-activating protein 5	1.356	Q91YP2	Neurolysin, mitochondrial	1.335
Q91VC3	Eukaryotic initiation factor 4A-III	1.354	Q3UGY8	Brefeldin A-inhibited guanine nucleotide-exchange protein 3	1.328
Q5M9L1	60S ribosomal protein L36	1.353	P97492	Regulator of G-protein signaling 14	1.326
Q6ZWZ4	60S ribosomal protein L36	1.353	O55042	Alpha-synuclein	1.325

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8BZW8	NHL repeat-containing protein 2	1.321	Q3TL96	Putative uncharacterized protein	1.309
Q3TT11	Putative uncharacterized protein	1.32	Q8C252	Putative uncharacterized protein	1.309
Q3UHW2	Putative uncharacterized protein	1.32	Q6PB52	Lrpap1 protein (Fragment)	1.309
P51660	Peroxisomal multifunctional enzyme type 2	1.32	Q8K295	Lrpap1 protein (Fragment)	1.309
Q05BC3	Echinoderm microtubule-associated protein-like 1	1.32	Q6PEM5	Lrpap1 protein (Fragment)	1.309
B9EKL9	Eml1 protein	1.32	P55302	Alpha-2-macroglobulin receptor-associated protein	1.309
D6RII3	Echinoderm microtubule-associated protein-like 1	1.32	Q6ZY49	Low density lipoprotein receptor-associated protein 1	1.309
P62774	Myotrophin	1.319	Q5D0B0	Lrpap1 protein (Fragment)	1.309
Q0QEW9	60S ribosomal protein L18 (Fragment)	1.317	Q9D832	DnaJ homolog subfamily B member 4	1.309
P35980	60S ribosomal protein L18	1.317	Q3UF95	Large proline-rich protein BAG6	1.306
Q642K1	60S ribosomal protein L18	1.317	Q9Z1R2	Large proline-rich protein BAG6	1.306
Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	1.317	Q3UHJ2	Dystrobrevin	1.302
A2AVR6	Acyl-coenzyme A thioesterase 11	1.317	I6L9D6	Dystrobrevin	1.302
Q80TT9	MKIAA0707 protein (Fragment)	1.317	Q8CFR5	Dystrobrevin	1.302
Q8VHQ9	Acyl-coenzyme A thioesterase 11	1.317	Q3UHP1	Dystrobrevin	1.302
Q8CAL6	Putative uncharacterized protein	1.317	Q9D2N4	Dystrobrevin alpha	1.302
A3KMJ8	Vbp1 protein (Fragment)	1.315	O55029	Coatomer subunit beta~	1.301
P61759	Prefoldin subunit 3	1.315	Q5RKP3	60S ribosomal protein L13	1.301
P47199	Quinone oxidoreductase	1.315	P47963	60S ribosomal protein L13	1.301
Q9R1T2	SUMO-activating enzyme subunit 1	1.313	Q5M9L9	40S ribosomal protein S8	1.3
P55264	Adenosine kinase	1.311	P62242	40S ribosomal protein S8	1.3
Q3TIK0	Platelet-activating factor acetylhydrolase IB subunit alpha	1.309	P20060	Beta-hexosaminidase subunit beta	1.3
Q3TJG1	Platelet-activating factor acetylhydrolase IB subunit alpha	1.309	E9PVU0	Unconventional myosin-VI	1.299
Q3UGR6	Platelet-activating factor acetylhydrolase IB subunit alpha	1.309	E9Q175	Unconventional myosin-VI	1.299
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	1.309	Q3UHB1	5~-nucleotidase domain-containing protein 3	1.299

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
P63040	Complexin-1	1.298	P27601	Guanine nucleotide-binding protein subunit alpha-13	1.282
Q3UYQ4	Putative uncharacterized protein	1.298	Q3TFK4	Annexin	1.282
O35841	Apoptosis inhibitor 5	1.298	Q8C1X9	Annexin	1.282
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	1.297	Q3U737	Annexin	1.282
P40240	CD9 antigen	1.295	O35639	Annexin A3	1.282
Q3TWB8	Putative uncharacterized protein	1.294	P11404	Fatty acid-binding protein, heart	1.281
E9PZ69	Transmembrane 9 superfamily member 2	1.294	Q9WVH9	Fibulin-5	1.28
Q8C7F9	Putative uncharacterized protein	1.294	D3YXR8	RIMS-binding protein 2	1.279
P58021	Transmembrane 9 superfamily member 2	1.294	Q80U40	RIMS-binding protein 2	1.279
Q8C6H4	Putative uncharacterized protein	1.294	Q61133	Glutathione S-transferase theta-2	1.276
Q78IK4	MICOS complex subunit Mic27	1.293	Q6PCX2	Transporter	1.27
Q9D0J4	ADP-ribosylation factor-like protein 2	1.292	P31648	Sodium- and chloride-dependent GABA transporter 1	1.27
S4R255	Nitric oxide synthase	1.29	Q8VCC9	Spondin-1	1.27
Q9Z0J4	Nitric oxide synthase, brain	1.29	Q69ZZ7	MKIAA0762 protein (Fragment)	1.27
F8WGF2	Nitric oxide synthase, brain	1.29	P60521	Gamma-aminobutyric acid receptor-associated protein-like 2	1.259
Q9Z2M7	Phosphomannomutase 2	1.29	Q6P9K8	Caskin-1	1.256
Q9DCE3	Phosphomannomutase	1.29	B7ZNJ3	Caskin1 protein	1.256
B1AUX2	Host cell factor 1	1.29	Q3TXJ4	Putative uncharacterized protein	1.255
Q61191	Host cell factor 1	1.29	Q99JZ4	GTP-binding protein SAR1a	1.255
P26645	Myristoylated alanine-rich C-kinase substrate	1.289	Q2PFD7	PH and SEC7 domain-containing protein 3	1.252
G3X9N6	Oxysterol-binding protein	1.289	F6Z9E6	PH and SEC7 domain-containing protein 3	1.252
B9EJ86	Oxysterol-binding protein	1.289	Q8BPH1	Putative uncharacterized protein	1.243
Q9WV34	MAGUK p55 subfamily member 2	1.288	P62259	14-3-3 protein epsilon	1.243
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	1.283	E0CYT1	Serine/threonine-protein kinase WNK2	1.242
Q3UE40	Putative uncharacterized protein	1.282	E0CZE3	Serine/threonine-protein kinase WNK2	1.242

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
E9QJQ9	Serine/threonine-protein kinase WNK2	1.242	Q8VEH5	EPM2A-interacting protein 1	1.226
E9QMI9	Serine/threonine-protein kinase WNK2	1.242	P62806	Histone H4	1.225
E9QMI8	Serine/threonine-protein kinase WNK2	1.242	Q80TH1	Discs, large homolog 3 (Drosophila), isoform CRA_c (Fragment)	1.224
E9QM73	Serine/threonine-protein kinase WNK2	1.242	Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	1.221
E9Q6Q2	Serine/threonine-protein kinase WNK2	1.242	B9EIU1	Glutamyl-prolyl-tRNA synthetase	1.221
E9PX70	Collagen alpha-1(XII) chain	1.241	Q91W50	Cold shock domain-containing protein E1	1.221
Q60847	Collagen alpha-1(XII) chain	1.241	Q3UZT7	Putative uncharacterized protein	1.22
Q8VHL1	Histone-lysine N-methyltransferase SETD7	1.24	Q02248	Catenin beta-1	1.22
Q7TSJ2	Microtubule-associated protein 6	1.238	A0A068BGR9	NADH dehydrogenase	1.219
G5E846	Peripherin	1.238	Q9Z1P6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	1.219
G3X8Y3	N-alpha-acetyltransferase 15, NatA auxiliary subunit	1.238	Q8R3P0	Aspartoacylase	1.218
Q80UM3	N-alpha-acetyltransferase 15, NatA auxiliary subunit	1.238	E9Q6R3	Vesicle-trafficking protein SEC22b	1.217
P12658	Calbindin	1.236	O08547	Vesicle-trafficking protein SEC22b	1.217
Q3TYA4	Syntaxin-binding protein 6	1.236	P21981	Protein-glutamine gamma-glutamyltransferase 2	1.217
Q8R3T5	Syntaxin-binding protein 6	1.236	Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	1.216
B8JJ84	Syntaxin-binding protein 6 (Fragment)	1.236	Q3TWH2	Putative uncharacterized protein	1.216
Q3TVU9	Putative uncharacterized protein	1.235	Q61941	NAD(P) transhydrogenase, mitochondrial	1.216
Q99L04	Dehydrogenase/reductase SDR family member 1	1.235	Q8C1W8	Nicotinamide nucleotide transhydrogenase, isoform CRA_a	1.216
A2AJY2	Collagen alpha-1(XV) chain	1.233	Q922E1	Nicotinamide nucleotide transhydrogenase	1.216
O35206	Collagen alpha-1(XV) chain	1.233	Q4FJP8	Slc2a3 protein	1.214
P28663	Beta-soluble NSF attachment protein	1.231	P32037	Solute carrier family 2, facilitated glucose transporter member 3	1.214
Q80X90	Filamin-B	1.23	Q8BLF7	Putative uncharacterized protein	1.214
P60229	Eukaryotic translation initiation factor 3 subunit E	1.23	B1AXW5	Peroxiredoxin-1 (Fragment)	1.213
P04117	Fatty acid-binding protein, adipocyte	1.23	P35700	Peroxiredoxin-1	1.213
P10493	Nidogen-1	1.226	B1AXW6	Peroxiredoxin-1 (Fragment)	1.213

Supplementary Table 11 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q8K021	Secretory carrier-associated membrane protein 1	1.213	Q9DB05	Alpha-soluble NSF attachment protein	1.207
Q8R2Z5	von Willebrand factor A domain-containing protein 1	1.211	Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial	1.207
G5E829	Plasma membrane calcium-transporting ATPase 1	1.21	Q3TIQ2	Putative uncharacterized protein	1.207
D3YUG3	40S ribosomal protein S19 (Fragment)	1.208	P35979	60S ribosomal protein L12	1.207
D3YUT3	40S ribosomal protein S19 (Fragment)	1.208	Q9DBG9	Tax1-binding protein 3	1.207
Q5M9P3	Rps19 protein (Fragment)	1.208	Q60675	Laminin subunit alpha-2	1.205
D3Z722	40S ribosomal protein S19	1.208	G3UXT7	RNA-binding protein FUS (Fragment)	1.205
D3Z5R8	40S ribosomal protein S19 (Fragment)	1.208	Q8CFQ9	Fusion, derived from t(1216) malignant liposarcoma (Human)	1.205
Q9CZX8	40S ribosomal protein S19	1.208	Q3UK30	Putative uncharacterized protein	1.205
Q3UH31	Putative uncharacterized protein	1.208	Q3USY4	Putative uncharacterized protein	1.205
Q99MU3	Double-stranded RNA-specific adenosine deaminase	1.208	P56959	RNA-binding protein FUS	1.205

The comparison was performed in the spinal cord between the progression and the onset of SOD1 G93A mouse, where the fold > 1.2 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 570 significantly up regulated proteins in the spinal cord between the progression vs the onset of SOD1 G93A mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 12. List of Significantly Down Regulated Proteins in the Spinal Cord between the Progression Vs the Onset of SOD1 G93A Mouse

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q61646	Haptoglobin	0.231	B2RWX0	Myosin, heavy polypeptide 1, skeletal muscle, adult	0.58
Q00898	Alpha-1-antitrypsin 1-5	0.254	Q5SX40	Myosin-1	0.58
O88990	Alpha-actinin-3	0.325	P62761	Visinin-like protein 1	0.594
P05977	Myosin light chain 1/3, skeletal muscle isoform	0.351	Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	0.6
Q91X72	Hemopexin	0.401	Q63739	Protein tyrosine phosphatase type IVA 1	0.617
P97457	Myosin regulatory light chain 2, skeletal muscle isoform	0.448	E9PYG6	Protein Rasa1	0.618
P28666	Murinoglobulin-2	0.483	Q91YX7	RAS p21 protein activator 1	0.618
Q8R429	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	0.492	Q4FZG7	Putative mitochondrial import inner membrane translocase subunit Tim8 A-B	0.621
Q4FJY6	Ifit3 protein	0.521	Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	0.621
E9PV48	Protein I830012O16Rik	0.521	Q9D5T0	ATPase family AAA domain-containing protein 1	0.625
Q64345	Interferon-induced protein with tetratricopeptide repeats 3	0.521	P61961	Ubiquitin-fold modifier 1	0.637
Q8BPC3	Putative uncharacterized protein	0.521	Q8BJH1	Zinc finger C2HC domain-containing protein 1A	0.638
Q5SX39	Myosin-4	0.539	B0R091	Calcineurin B homologous protein 1	0.644
D0U293	Beta-globin	0.544	P61022	Calcineurin B homologous protein 1	0.644
Q9QUN8	Beta-2-globin (Fragment)	0.544	Q8R4V3	Acetyl CoA transferase-like protein	0.649
A8DV41	Beta-globin	0.544	Q80X81	Acetyl-Coenzyme A acetyltransferase 3	0.649
P02089	Hemoglobin subunit beta-2	0.544	Q3SXD3	HD domain-containing protein 2	0.651
Q54AH9	Beta-2-globin (Fragment)	0.544	P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	0.652
A8DV59	Beta-globin	0.544	Q3UUI3	Acyl-coenzyme A thioesterase THEM4	0.658
G5E814	MCG5603	0.55	Q9D6U7	Putative uncharacterized protein	0.659
Q9D8B4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0.55	P07310	Creatine kinase M-type	0.659
P68134	Actin, alpha skeletal muscle	0.555	Q0VBD0	Integrin beta	0.659
Q60936	Chaperone activity of bc1 complex-like, mitochondrial	0.556	Q3V1A7	Putative uncharacterized protein	0.662

Supplementary Table 12 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q99JA0	Calcitonin gene-related peptide 1	0.662	F8VQ05	Protein Fryl	0.704
P70160	Calcitonin	0.662	Q61733	28S ribosomal protein S31, mitochondrial	0.705
D3YW52	Alpha-2-macroglobulin	0.662	Q9CWD8	Iron-sulfur protein NUBPL	0.706
Q61838	Alpha-2-macroglobulin	0.662	Q9JMK2	Casein kinase I isoform epsilon	0.71
Q6GQT1	Alpha-2-macroglobulin-P	0.67	Q61923	Potassium voltage-gated channel subfamily A member 6	0.716
Q9D517	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	0.675	F6RT34	Myelin basic protein (Fragment)	0.719
Q6ZWS7	Putative uncharacterized protein	0.689	D3YZV2	Potassium voltage-gated channel subfamily C member 3	0.719
Q923T9	Calcium/calmodulin-dependent protein kinase type II subunit gamma	0.689	Q63959	Potassium voltage-gated channel subfamily C member 3	0.719
Q8CI71	Coiled-coil domain-containing protein 132	0.692	E9QKI2	Potassium voltage-gated channel subfamily C member 3	0.719
Q3TG58	Williams-Beuren syndrome chromosome region 1 homolog (Human), isoform CRA_b	0.693	Q80W54	CAAX prenyl protease 1 homolog	0.72
Q9WUK2	Eukaryotic translation initiation factor 4H	0.693	P0C7M9	C-type lectin domain family 2 member L	0.72
Q80U88	MKIAA0038 protein (Fragment)	0.693	Q91VM5	RNA binding motif protein, X-linked-like-1	0.723
Q3V244	Putative uncharacterized protein	0.693	Q3TAD4	Putative uncharacterized protein	0.726
Q5RJG7	Isoprenoid synthase domain-containing protein	0.693	Q91YN5	UDP-N-acetylhexosamine pyrophosphorylase	0.726
Q3UFD0	Putative uncharacterized protein	0.698	Q3UHZ7	UDP-N-acetylhexosamine pyrophosphorylase	0.726
Q9D6K5	Synaptojanin-2-binding protein	0.698	Q9CRD0	OCIA domain-containing protein 1	0.727
E9PVN6	Protein Gm20498	0.698	D3YWG2	Chitinase domain-containing protein 1 (Fragment)	0.727
Q6Y642	Activin receptor-interacting protein 2a	0.698	Q922Q9	Chitinase domain-containing protein 1	0.727
Q8BR63	Protein FAM177A1	0.699	Q9CRU8	Putative uncharacterized protein (Fragment)	0.727
P50543	Protein S100-A11	0.7	G8JL55	Chitinase domain-containing protein 1 (Fragment)	0.727
B2RY90	Isoc2a protein	0.703	Q8BX70	Vacuolar protein sorting-associated protein 13C	0.728
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	0.703	D3YZ98	Phosphatidylinositol 3-kinase	0.729
A2BDX3	Adenylyltransferase and sulfurtransferase MOCS3	0.703	Q6PF93	Phosphatidylinositol 3-kinase catalytic subunit type 3	0.729

Supplementary Table 12 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
E9QLS6	Phosphatidylinositol 3-kinase	0.729	F8WHP8	ATP synthase subunit f, mitochondrial	0.745
Q8R2Y0	Monoacylglycerol lipase ABHD6	0.731	P56135	ATP synthase subunit f, mitochondrial	0.745
Q9D375	Putative uncharacterized protein	0.731	Q99J08	SEC14-like protein 2	0.746
P62331	ADP-ribosylation factor 6	0.732	Q9CZS7	Putative uncharacterized protein	0.754
Q8CIQ7	Dedicator of cytokinesis protein 3	0.732	O70172	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	0.754
F8VPQ1	Dedicator of cytokinesis protein 3	0.732	F6U329	Sodium channel protein	0.755
Q9DB41	Mitochondrial glutamate carrier 2	0.733	Q9WTU3	Sodium channel protein type 8 subunit alpha	0.755
Q8C0L8	Conserved oligomeric Golgi complex subunit 5	0.733	F7D6H8	Sodium channel protein	0.755
P97855	Ras GTPase-activating protein-binding protein 1	0.737	F7D6K4	Sodium channel protein	0.755
Q8VHP7	Leukocyte elastase inhibitor B	0.738	F7D6J5	Sodium channel protein	0.755
Q3TBT0	Putative uncharacterized protein (Fragment)	0.74	Q8C1D9	Putative uncharacterized protein	0.757
F6YBY4	Integrin alpha-M (Fragment)	0.74	P63082	V-type proton ATPase 16 kDa proteolipid subunit	0.757
Q3TD86	Putative uncharacterized protein	0.74	E9Q9C5	V-type proton ATPase 16 kDa proteolipid subunit (Fragment)	0.757
Q3U3F0	Putative uncharacterized protein	0.74	Q80YP7	Atp6v0c protein (Fragment)	0.757
E9Q5K8	Integrin alpha-M	0.74	Q8R404	Protein QIL1	0.757
P05555	Integrin alpha-M	0.74	Q9WUB3	Glycogen phosphorylase, muscle form	0.758
Q3U1W4	Putative uncharacterized protein (Fragment)	0.74	Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	0.758
Q3U1U4	Integrin alpha-M	0.74	Q8JZU2	Tricarboxylate transport protein, mitochondrial	0.758
G5E8F1	Integrin alpha M, isoform CRA_a	0.74	Q91UZ1	Phosphoinositide phospholipase C	0.761
E9Q604	Integrin alpha-M	0.74	Q8QZY9	Splicing factor 3B subunit 4	0.766
Q3U4I5	Putative uncharacterized protein	0.74	Q3TVQ3	Putative uncharacterized protein	0.766
P97450	ATP synthase-coupling factor 6, mitochondrial	0.742	P28798	Granulins	0.766
Q9Z0E0	Neurochondrin	0.743	Q3U9K2	Putative uncharacterized protein (Fragment)	0.766

Supplementary Table 12 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q3TW77	Putative uncharacterized protein	0.766	D3YUV1	Nuclear receptor-binding protein	0.782
Q3TX66	Putative uncharacterized protein	0.766	Q3TCW5	Putative uncharacterized protein	0.782
Q3U8W3	Putative uncharacterized protein	0.766	Q99J45	Nuclear receptor-binding protein	0.782
Q3U9N4	Granulins	0.766	Q8BWY4	Metallo-beta-lactamase domain-containing protein 1	0.783
Q3TWT4	Putative uncharacterized protein	0.766	Q3TD17	Putative uncharacterized protein	0.785
Q3UC19	Putative uncharacterized protein	0.766	Q3U2J2	Putative uncharacterized protein	0.785
Q9D2V3	Putative uncharacterized protein	0.766	P17809	Solute carrier family 2, facilitated glucose transporter member 1	0.785
Q3UDD6	Putative uncharacterized protein (Fragment)	0.766	Q4VAF0	Acylphosphatase (Fragment)	0.786
Q3UAJ3	Putative uncharacterized protein	0.766	P56376	Acylphosphatase-1	0.786
Q3UD85	Putative uncharacterized protein	0.766	E9QJT5	Acylphosphatase	0.786
A2AKW0	Solute carrier family 25 member 51	0.768	Q9DB27	Malignant T-cell-amplified sequence 1	0.787
Q5HZI9	Solute carrier family 25 member 51	0.768	Q6PDI5	Proteasome-associated protein ECM29 homolog	0.788
Q3TMH2	Secernin-3	0.769	O35239	Tyrosine-protein phosphatase non-receptor type 9	0.79
Q3TZU7	Sorting nexin	0.772	P48320	Glutamate decarboxylase 2	0.791
Q9CZK0	Putative uncharacterized protein (Fragment)	0.772	O35864	COP9 signalosome complex subunit 5	0.793
Q91VH2	Sorting nexin-9	0.772	A2AVR9	Dynein light chain roadblock-type 1	0.793
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	0.773	P62627	Dynein light chain roadblock-type 1	0.793
Q8R1I1	Cytochrome b-c1 complex subunit 9	0.774	A2AMH4	Choline transporter-like protein 1	0.795
Q64310	Surfeit locus protein 4	0.774	Q6X893	Choline transporter-like protein 1	0.795
Q3UVH2	Putative uncharacterized protein	0.774	A2AMH5	Choline transporter-like protein 1	0.795
P41241	Tyrosine-protein kinase CSK	0.774	Q9CQE8	UPF0568 protein C14orf166 homolog	0.797
P62743	AP-2 complex subunit sigma	0.775	Q8BRF7	Sec1 family domain-containing protein 1	0.797
O70503	Estradiol 17-beta-dehydrogenase 12	0.779	Q9JLC8	Sacsin	0.797

Supplementary Table 12 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
E9QNY8	Sacsin	0.797	P61021	Ras-related protein Rab-5B	0.812
Q3T9U9	Putative uncharacterized protein	0.797	Q9WVT6	Carbonic anhydrase 14	0.812
P27659	60S ribosomal protein L3	0.797	D3Z568	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 5, isoform CRA_e	0.813
Q3UB15	Putative uncharacterized protein	0.797	Q9CQH3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	0.813
Q3UB67	Putative uncharacterized protein	0.797	Q8BU20	Putative uncharacterized protein	0.813
Q3U9L3	Putative uncharacterized protein	0.797	Q62425	Cytochrome c oxidase subunit NDUFA4	0.813
Q3UB90	Putative uncharacterized protein	0.797	Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	0.817
Q3U8H8	Putative uncharacterized protein	0.799	A0A075DC90	Cytochrome c oxidase subunit 2	0.818
P61971	Nuclear transport factor 2	0.799	P00405	Cytochrome c oxidase subunit 2	0.818
B1AQZ2	Kinesin-like protein	0.801	Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.82
P28741	Kinesin-like protein KIF3A	0.801	A6H5Z3	Exocyst complex component 6B	0.82
Q3TET1	Kinesin-like protein	0.801	Q8CBN6	Protein Gm9967	0.82
Q3UI47	Kinesin-like protein	0.801	Q9CQ65	S-methyl-5~-thioadenosine phosphorylase	0.822
Q3TL44	NLR family member X1	0.803	Q8BIW1	Protein prune homolog	0.822
Q8R5H1	Ubiquitin carboxyl-terminal hydrolase 15	0.806	F8WGT1	Adenosylhomocysteinase	0.824
Q3U7R1	Extended synaptotagmin-1	0.808	Q68FL4	Putative adenosylhomocysteinase 3	0.824
Q3U621	Putative uncharacterized protein	0.808	Q8R2Y8	Peptidyl-tRNA hydrolase 2, mitochondrial	0.824
P61027	Ras-related protein Rab-10	0.808	Q8K2C9	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	0.825
D3YVA2	Neurocalcin-delta (Fragment)	0.809	P62075	Mitochondrial import inner membrane translocase subunit Tim13	0.825
Q91X97	Neurocalcin-delta	0.809	Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	0.825
Q3TFF0	Putative uncharacterized protein	0.809	Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	0.826
Q9QYJ0	DnaJ homolog subfamily A member 2	0.809	Q3V2D0	Lon protease homolog, mitochondrial	0.828
Q0PD56	Rab5B	0.812	Q8CGK3	Lon protease homolog, mitochondrial	0.828

Supplementary Table 12 (Continued)

Accession No	Description	Fold Change (Progression)	Accession No	Description	Fold Change (Progression)
Q9QUP5	Hyaluronan and proteoglycan link protein 1	0.828	Q8VC72	NADH dehydrogenase (Ubiquinone) Fe-S protein 8	0.829
Q3UY05	Putative uncharacterized protein	0.829	G3XA48	Isopentenyl-diphosphate Delta-isomerase 1	0.829
Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	0.829	P58044	Isopentenyl-diphosphate Delta-isomerase 1	0.829

The comparison was performed in the spinal cord between the progression and the onset of SOD1 G93A mouse, where the fold < 0.833 and p-value < 0.05 were considered as the significantly differentially expressed proteins. This table listed 236 significantly down regulated proteins in the spinal cord between the progression vs the onset of SOD1 G93A mouse. The accession number of UniProt Knowledgebase, description and fold of each protein were provided here. The proteins were presented according to the level of fold changes. Top 30 of proteins were highlighted with gray.

Supplementary Table 13. List of the overlapped proteins in the three independent comparisons of the pre-onset, onset and progression of the SOD1 G93A transgenic mice vs the SOD1 wild mice

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/WT)	Fold Change (Progression/WT)
Q921L4	Histone H2B	1.866	1.549	2.346
F8VQK3	Protein Gucy1a2	1.947	1.423	1.577
Q9D859	Putative uncharacterized protein	1.844	1.655	2.219
Q9JLC8	Sacsin	0.6	0.691	0.534
Q9DCG9	Multifunctional methyltransferase subunit TRM112-like protein	0.445	0.731	0.675
Q7TNL5	Protein phosphatase 2, regulatory subunit B (B56), delta isoform, isoform CRA_a	0.652	0.72	0.613
P62702	40S ribosomal protein S4, X isoform	1.31	1.275	1.275
Q8CGP2	Histone H2B type 1-P	1.866	1.549	2.346
O35744	Chitinase-like protein 3	0.604	0.682	0.615
Q9ESM3	Hyaluronan and proteoglycan link protein 2	0.714	0.763	0.828
Q920E5	Farnesyl pyrophosphate synthase	0.76	0.686	0.638
Q99JB8	Protein kinase C and casein kinase II substrate protein 3	0.682	0.724	0.762
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	0.774	0.785	0.773
P10853	Histone H2B type 1-F/J/L	1.866	1.549	2.346
Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	0.74	0.608	0.534
Q3TL79	Putative uncharacterized protein	0.774	0.785	0.773
Q3UXQ6	40S ribosomal protein S4	1.31	1.275	1.275
Q6GTX3	Apoe protein	1.955	2.162	3.906
Q3UIA5	Putative uncharacterized protein	0.757	0.654	0.702
Q9D394	Protein RUFY3	0.812	0.782	0.814
P15379	CD44 antigen	1.423	2.425	2.417
Q8CGP1	Histone H2B type 1-K	1.866	1.549	2.346

Supplementary Table 13 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/WT)	Fold Change (Progression/WT)
Q3UBS0	Putative uncharacterized protein	1.955	2.162	3.906
Q9WTX6	Cullin-1	0.757	0.654	0.702
Q6P5H2	Nestin	1.327	1.948	1.823
Q62148	Retinal dehydrogenase 2	0.504	0.617	0.63
Q9DCZ4	Apolipoprotein O	1.66	0.816	1.285
Q8K406	Leucine-rich repeat LGI family member 3	0.79	0.799	0.692
P97351	40S ribosomal protein S3a	2.274	1.457	1.597
Q8VCR4	0610038D11Rik protein	0.445	0.731	0.675
P08226	Apolipoprotein E	1.955	2.162	3.906
P60867	40S ribosomal protein S20	2.306	1.733	2.306
Q8BXY4	Putative uncharacterized protein	0.548	0.688	0.66
G5E850	Cytochrome b-5, isoform CRA_a	1.754	1.348	1.991
E9Q0N0	Intersectin-1	0.669	0.771	0.782
Q8BWV2	Putative uncharacterized protein	1.511	1.592	1.509
B1AX58	Plastin-3	0.762	0.822	0.719
Q920Q4	Vacuolar protein sorting-associated protein 16 homolog	1.511	1.592	1.509
B2RXS4	Plexin-B2	1.613	1.954	1.924
Q3TN94	Putative uncharacterized protein	0.641	0.739	0.773
Q9CR57	60S ribosomal protein L14	2.129	1.35	2.201
Q5NDA4	Fatty acid binding protein 7, brain	1.864	2.154	2.738
P51880	Fatty acid-binding protein, brain	1.864	2.154	2.738
P50429	Arylsulfatase B	1.814	2	2.127
Q03517	Secretogranin-2	0.749	0.807	0.762

Supplementary Table 13 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/WT)	Fold Change (Progression/WT)
E9QNY8	Sacsin	0.6	0.691	0.534
D3Z0M6	Cytoplasmic dynein 1 intermediate chain 1	0.79	0.785	0.789
Q3V1R3	Putative uncharacterized protein	0.79	0.799	0.692
Q80X90	Filamin-B	1.225	1.343	1.615
Q3KNM9	Apoo protein	1.66	0.816	1.285
P10854	Histone H2B type 1-M	1.866	1.549	2.346
Q812A2	SLIT-ROBO Rho GTPase-activating protein 3	0.75	0.764	0.744
P07759	Serine protease inhibitor A3K	0.766	0.568	0.652
B1ASQ2	Apolipoprotein O	1.66	0.816	1.285
Q8R429	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	1.415	1.92	0.691
A2APM1	CD44 antigen	1.423	2.425	2.417
Q64525	Histone H2B type 2-B	1.866	1.549	2.346
A4FUT9	Adam22 protein (Fragment)	0.778	0.796	0.739
Q64478	Histone H2B type 1-H	1.866	1.549	2.346
Q8BML9	Glutaminyl-tRNAsynthetase	0.641	0.739	0.773
Q5M8R9	Farnesyldiphosphatesynthetase	0.76	0.686	0.638
Q3US29	Putative uncharacterized protein	0.76	0.686	0.638
Q64475	Histone H2B type 1-B	1.866	1.549	2.346
Q80UW2	F-box only protein 2	0.692	0.708	0.551
P56389	Cytidinedeaminase	0.72	0.717	0.621
P16110	Galectin-3	1.687	2.723	4.093
Q8QZY9	Splicing factor 3B subunit 4	1.454	1.82	1.364
Q3V471	Galectin (Fragment)	1.687	2.723	4.093

Supplementary Table 13 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/WT)	Fold Change (Progression/WT)
O88485	Cytoplasmic dynein 1 intermediate chain 1	0.79	0.785	0.789
Q5SX39	Myosin-4	1.595	1.378	0.677
Q9D186	Apolipoprotein O	1.66	0.816	1.285
Q8BPG5	Putative uncharacterized protein	1.844	1.655	2.219
Q9R1V6	Disintegrin and metalloproteinase domain-containing protein 22	0.778	0.796	0.739
P62631	Elongation factor 1-alpha 2	0.628	0.709	0.605
Q3UBX7	Putative uncharacterized protein	1.557	3.97	3.349
Q80TB8	Synaptic vesicle membrane protein VAT-1 homolog-like	0.723	0.821	0.705
P48678	Prelamin-A/C	1.545	1.264	1.942
Q8BLE7	Vesicular glutamate transporter 2	0.594	0.715	0.62
A2APM4	CD44 antigen	1.423	2.425	2.417
Q9WTP7	GTP:AMP phosphotransferase AK3, mitochondrial	1.315	1.44	1.595
Q91YP2	Neurolysin, mitochondrial	1.332	1.372	1.803
P62983	Ubiquitin-40S ribosomal protein S27a	1.377	1.31	1.243
P53994	Ras-related protein Rab-2A	0.548	0.688	0.66
P70202	Latexin	1.292	1.936	2.151
Q4FK40	Apoe protein	1.955	2.162	3.906
P56395	Cytochrome b5	1.754	1.348	1.991
Q8BU21	Glutaminyl-tRNAsynthetase, isoform CRA_a	0.641	0.739	0.773
Q9QY42	Prosaposin receptor GPR37	1.699	0.714	1.463
Q9QYG0	Protein NDRG2	1.499	1.437	1.789
Q8C253	Galectin	1.687	2.723	4.093
Q8CBB6	Histone H2B	1.866	1.549	2.346

Supplementary Table 13 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/WT)	Fold Change (Progression/WT)
P26645	Myristoylated alanine-rich C-kinase substrate	1.518	1.707	1.984
E9QKM8	CD44 antigen	1.423	2.425	2.417
Q3UAC2	40S ribosomal protein S3a	2.274	1.457	1.597
Q3U468	Putative uncharacterized protein	1.423	2.425	2.417
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	0.523	0.717	0.702
Q99PC9	Protein phosphatase 2 regulatory subunit B56 delta isoform	0.652	0.72	0.613
P98086	Complement C1q subcomponent subunit A	1.557	3.97	3.349
Q9WU63	Heme-binding protein 2	0.771	0.792	0.738
Q3UNN2	Putative uncharacterized protein	1.423	2.425	2.417
Q9CPY7	Cytosol aminopeptidase	1.282	1.44	1.755
Q9D1S3	40S ribosomal protein S3a	2.274	1.457	1.597
Q3UHD1	Brain-specific angiogenesis inhibitor 1	3.433	2.312	2.164
Q99J77	N-acetylneuraminic acid synthase (Sialic acid synthase)	0.645	0.783	0.675
E9QN14	SLIT-ROBO Rho GTPase-activating protein 3	0.75	0.764	0.744
Q91V89	Protein Ppp2r5d	0.652	0.72	0.613
Q3TLP8	RAS-related C3 botulinum substrate 1, isoform CRA_a	1.844	1.655	2.219
A2APM5	CD44 antigen	1.423	2.425	2.417
Q9EQX4	Allograft inflammatory factor 1-like	0.564	0.405	0.439
Q80X37	CD44 antigen	1.423	2.425	2.417
G3X8X7	Vacuolar protein sorting 16 (Yeast)	1.511	1.592	1.509
P63001	Ras-related C3 botulinum toxin substrate 1	1.844	1.655	2.219
P14602	Heat shock protein beta-1	1.348	3.471	3.505
G3X8T9	Serine (Or cysteine) peptidase inhibitor, clade A, member 3N, isoform CRA_a	1.401	3.505	2.899

Supplementary Table 13 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/WT)	Fold Change (Progression/WT)
F8VPQ4	SLIT-ROBO Rho GTPase-activating protein 3	0.75	0.764	0.744
A2APM3	CD44 antigen	1.423	2.425	2.417
B2RWQ7	Arsb protein	1.814	2	2.127
Q60972	Histone-binding protein RBBP4	1.834	1.409	2.078
Q8BH58	TIP41-like protein	1.538	1.394	1.553
Q3TXB1	Putative uncharacterized protein	1.557	3.97	3.349
Q3U8S1	CD44 antigen	1.423	2.425	2.417
Q3TLT9	Putative uncharacterized protein	1.423	2.425	2.417
A2ADY9	Protein DDI1 homolog 2	0.686	0.536	0.469
P05977	Myosin light chain 1/3, skeletal muscle isoform	1.803	2.115	0.676
Q8K5D8	Protein phosphatase 2a regulatory b56-delta subunit (Fragment)	0.652	0.72	0.613
Q5M8M3	Uncharacterized protein	0.445	0.731	0.675
Q545F8	40S ribosomal protein S4	1.31	1.275	1.275
Q8C4N8	Putative uncharacterized protein (Fragment)	1.844	1.655	2.219
A0JLV3	Histone H2B (Fragment)	1.866	1.549	2.346
D3YUP9	Disintegrin and metalloproteinase domain-containing protein 22	0.778	0.796	0.739
A2APM2	CD44 antigen	1.423	2.425	2.417
Q9Z0R4	Intersectin-1	0.669	0.771	0.782
Q9CWK0	Putative uncharacterized protein	2.129	1.35	2.201
Q6ZWY9	Histone H2B type 1-C/E/G	1.866	1.549	2.346

The comparison was made between the spinal cord of the pre-onset, onset and progression of the SOD1 G93A transgenic mice vs the SOD1 wild mice,where fold changes of < 0.833(1/1.2) or ＞1.2 and p-value < 0.05 were taken into consideration. This table contains 134 overlapped proteins in the three independent comparisons. The accession number of UniProt Knowledgebase, description, and fold change of each protein are provided here. Top 30 of proteins were highlighted with gray.

Supplementary Table 14.List of the overlapped proteins in the three independent comparisons of the pre-onset vs the SOD1 wild , onset vs pre-onset and progression vs onset of the SOD1 G93A transgenic mice

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/Pre-onset)	Fold Change (Progression/Onset)
P68368	Tubulin alpha-4A chain	1.243	0.637	1.348
Q921L4	Histone H2B	1.866	0.752	1.665
Q3TY32	Putative uncharacterized protein (Fragment)	1.327	0.813	1.37
Q9D186	Apolipoprotein O	1.66	0.464	1.499
Q9JLC8	Sacsin	0.6	1.274	0.797
Q8BLF7	Putative uncharacterized protein	1.616	0.706	1.214
D3YYD5	Vacuolar protein sorting-associated protein 29 (Fragment)	1.808	0.782	1.463
O35864	COP9 signalosome complex subunit 5	0.568	1.747	0.793
P48678	Prelamin-A/C	1.545	0.823	1.569
Q8BW41	Protein O-linked-mannose beta-1,4-N-acetylglucosaminyltransferase 2	0.654	0.719	1.645
Q6P1A9	Ribosomal protein L7A	1.304	0.721	1.56
Q8CGP2	Histone H2B type 1-P	1.866	0.752	1.665
Q91YP2	Neurolysin, mitochondrial	1.332	1.247	1.335
Q9QXV0	ProSAAS	1.403	0.565	1.416
Q3TWB8	Putative uncharacterized protein	1.492	0.652	1.294
P67984	60S ribosomal protein L22	1.883	0.682	1.534
P08228	Superoxide dismutase [Cu-Zn]	1.749	0.668	1.53
A0A0A0MQA5	Tubulin alpha-4A chain (Fragment)	1.243	0.637	1.348
Q8CC35	Synaptopodin	1.327	0.813	1.37
Q3U8W4	Superoxide dismutase	1.436	0.705	1.359
P12970	60S ribosomal protein L7a	1.304	0.721	1.56
P56395	Cytochrome b5	1.754	0.777	1.574

Supplementary Table 14 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/Pre-onset)	Fold Change (Progression/Onset)
P01831	Thy-1 membrane glycoprotein	1.508	0.619	1.431
P10853	Histone H2B type 1-F/J/L	1.866	0.752	1.665
Q3U336	Putative uncharacterized protein	1.327	0.813	1.37
A2AVJ7	Ribosome-binding protein 1	1.57	0.747	1.472
Q9QY42	Prosaposin receptor GPR37	1.699	0.504	1.858
P70349	Histidine triad nucleotide-binding protein 1	1.624	0.71	1.457
P58021	Transmembrane 9 superfamily member 2	1.492	0.652	1.294
Q8C253	Galectin	1.687	1.664	1.413
P35802	Neuronal membrane glycoprotein M6-a	1.438	0.69	1.376
Q8CGP1	Histone H2B type 1-K	1.866	0.752	1.665
P0C0S6	Histone H2A.Z	1.598	0.747	1.996
Q3UGC0	Putative uncharacterized protein	1.274	0.721	1.389
Q8CBB6	Histone H2B	1.866	0.752	1.665
P62242	40S ribosomal protein S8	1.24	0.825	1.3
P47911	60S ribosomal protein L6	1.714	0.63	1.55
P27601	Guanine nucleotide-binding protein subunit alpha-13	1.225	0.773	1.282
Q9DCZ4	Apolipoprotein O	1.66	0.464	1.499
P68510	14-3-3 protein eta	2.167	0.437	2.042
Q99PL5	Ribosome-binding protein 1	1.57	0.747	1.472
D3Z645	Vacuolar protein sorting-associated protein 29	1.808	0.782	1.463
P51660	Peroxisomal multifunctional enzyme type 2	1.472	0.777	1.32
Q3TMH2	Secernin-3	0.617	1.401	0.769
Q8C1B7	Septin-11	1.832	0.619	1.992

Supplementary Table 14 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/Pre-onset)	Fold Change (Progression/Onset)
P63216	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-3	2.225	0.661	1.364
G5E850	Cytochrome b-5, isoform CRA_a	1.754	0.777	1.574
Q8BGD9	Eukaryotic translation initiation factor 4B	1.274	0.721	1.389
Q3UHW2	Putative uncharacterized protein	1.472	0.777	1.32
Q3TDD8	Putative uncharacterized protein	1.274	0.721	1.389
P27048	Small nuclear ribonucleoprotein-associated protein B	1.559	0.678	1.505
Q91W50	Cold shock domain-containing protein E1	1.434	0.786	1.221
B2RWE8	Eif4b protein	1.274	0.721	1.389
Q9D5T0	ATPase family AAA domain-containing protein 1	0.706	1.44	0.625
Q810K5	Y box protein 1	2.323	0.43	3.065
Q9CR57	60S ribosomal protein L14	2.129	0.604	1.669
Q3THW5	Histone H2A.V	1.598	0.747	1.996
P09671	Superoxide dismutase [Mn], mitochondrial	1.436	0.705	1.359
P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	0.653	1.41	0.652
F6UP77	Putative N-acetylglucosamine-6-phosphate deacetylase (Fragment)	2.215	0.478	2.615
B0R1E3	Histidine triad nucleotide-binding protein 1	1.624	0.71	1.457
Q3TSY9	Putative uncharacterized protein	1.274	0.721	1.389
Q61753	D-3-phosphoglycerate dehydrogenase	1.48	0.687	1.595
Q3TA13	Putative uncharacterized protein	1.327	0.813	1.37
E9PZ69	Transmembrane 9 superfamily member 2	1.492	0.652	1.294
E9QNY8	Sacsin	0.6	1.274	0.797
P43274	Histone H1.4	2.463	0.438	2.171
Q3KNM9	Apoo protein	1.66	0.464	1.499

Supplementary Table 14 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/Pre-onset)	Fold Change (Progression/Onset)
P10854	Histone H2B type 1-M	1.866	0.752	1.665
P62264	40S ribosomal protein S14	1.468	0.658	1.424
Q9CWF2	Tubulin beta-2B chain	1.963	0.58	2.281
O35449	Proline-rich transmembrane protein 1	1.975	0.507	1.713
Q8QZV4	Serine/threonine-protein kinase 32C	1.511	0.648	2.106
Q6ZPS0	MKIAA1398 protein (Fragment)	1.57	0.747	1.472
B1ASQ2	Apolipoprotein O	1.66	0.464	1.499
Q8C6H4	Putative uncharacterized protein	1.492	0.652	1.294
Q64525	Histone H2B type 2-B	1.866	0.752	1.665
P50543	Protein S100-A11	0.542	2.571	0.7
Q53YX2	CD90.1	1.508	0.619	1.431
Q3URF1	MCG6023	1.327	0.813	1.37
Q4FJP8	Slc2a3 protein	1.616	0.706	1.214
O70569	Ribosomal protein S14	1.468	0.658	1.424
Q8R1P3	Gpm6a protein	1.438	0.69	1.376
Q80UT7	Rpl7a protein (Fragment)	1.304	0.721	1.56
P62806	Histone H4	1.526	0.826	1.225
E9Q3E2	Synaptopodin	1.327	0.813	1.37
Q64478	Histone H2B type 1-H	1.866	0.752	1.665
Q9WV34	MAGUK p55 subfamily member 2	1.455	0.741	1.288
Q3THB0	Putative uncharacterized protein	1.274	0.721	1.389
Q8JZV7	Putative N-acetylglucosamine-6-phosphate deacetylase	2.215	0.478	2.615
Q3UE40	Putative uncharacterized protein	1.225	0.773	1.282

Supplementary Table 14 (Continued)

Accession NO	Desription	Fold Change (Pre-onset/WT)	Fold Change (Onset/Pre-onset)	Fold Change (Progression/Onset)
P62960	Nuclease-sensitive element-binding protein 1	2.323	0.43	3.065
P63163	Small nuclear ribonucleoprotein-associated protein N	1.559	0.678	1.505
Q71V06	Y box transcription factor (Fragment)	2.323	0.43	3.065
Q64475	Histone H2B type 1-B	1.866	0.752	1.665
Q5EBG5	Ribosomal protein L7A	1.304	0.721	1.56
Q3TT11	Putative uncharacterized protein	1.472	0.777	1.32
Q5M9L9	40S ribosomal protein S8	1.24	0.825	1.3
P16110	Galectin-3	1.687	1.664	1.413
Q7TSJ2	Microtubule-associated protein 6	1.416	0.69	1.238
Q8C7F9	Putative uncharacterized protein	1.492	0.652	1.294
Q8QZY9	Splicing factor 3B subunit 4	1.454	1.502	0.766
Q60951	MYB-1b	2.323	0.43	3.065
Q3V471	Galectin (Fragment)	1.687	1.664	1.413
A0JLV3	Histone H2B (Fragment)	1.866	0.752	1.665
Q9QZ88	Vacuolar protein sorting-associated protein 29	1.808	0.782	1.463
P32037	Solute carrier family 2, facilitated glucose transporter member 3	1.616	0.706	1.214
O70499	Small nuclear ribonucleoprotein-associated protein	1.559	0.678	1.505
Q9CYW4	Haloaciddehalogenase-like hydrolase domain-containing protein 3	1.735	0.753	1.317
Q9CWK0	Putative uncharacterized protein	2.129	0.604	1.669
Q6ZWY9	Histone H2B type 1-C/E/G	1.866	0.752	1.665

The comparison was made between the spinal cord of the pre-onset vsthe SOD1 wild , onset vs pre-onset and progression vs onset of the SOD1 G93A transgenic mice,where fold changes of $< 0.833(1/1.2)$ or ＞1.2 and p-value < 0.05 were taken into consideration. This table contains 111 overlapped proteins in the three independent comparisons. The accession number of UniProt Knowledgebase, description, and fold change of each protein are provided here. Top 30 of proteins were highlighted with gray.

Supplementary Table 15. Terms for WT spinal cord VS Progression spinal cord of Cellular Component

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Cell projection	123 out of 562 genes, 21.9%	733 out of 4862 genes, 15.1%	2.86638E-06
Cytosolic ribosome	24 out of 562 genes, 4.3%	79 out of 4862 genes, 1.6%	4.78114E-06
Extracellular region	77 out of 562 genes, 13.7%	413 out of 4862 genes, 8.5%	6.77875E-06
Neuron part	101 out of 562 genes, 18.0%	588 out of 4862 genes, 12.1%	9.92893E-06
Neuron projection	92 out of 562 genes, 16.4%	524 out of 4862 genes, 10.8%	1.0736E-05
Extracellular region part	56 out of 562 genes, 10.0%	281 out of 4862 genes, 5.8%	1.93881E-05
Extracellular matrix	30 out of 562 genes, 5.3%	129 out of 4862 genes, 2.7%	0.000108378
Axon	45 out of 562 genes, 8.0%	225 out of 4862 genes, 4.6%	0.000120688
Proteinaceous extracellular matrix	25 out of 562 genes, 4.4%	102 out of 4862 genes, 2.1%	0.000167681
Extracellular space	43 out of 562 genes, 7.7%	216 out of 4862 genes, 4.4%	0.000190814
Cell projection part	63 out of 562 genes, 11.2%	366 out of 4862 genes, 7.5%	0.000540095
Cytosolic large ribosomal subunit	13 out of 562 genes, 2.3%	43 out of 4862 genes, 0.9%	0.000778699
Cytosolic part	29 out of 562 genes, 5.2%	138 out of 4862 genes, 2.8%	0.000861152
Endocytic vesicle membrane	12 out of 562 genes, 2.1%	40 out of 4862 genes, 0.8%	0.001330037
Ribosomal subunit	24 out of 562 genes, 4.3%	110 out of 4862 genes, 2.3%	0.001372135
Contractile fiber	22 out of 562 genes, 3.9%	98 out of 4862 genes, 2.0%	0.001453753
Dendrite cytoplasm	5 out of 562 genes, 0.9%	9 out of 4862 genes, 0.2%	0.001715633
Cytosol	176 out of 562 genes, 31.3%	1279 out of 4862 genes, 26.3%	0.002724861
U12-type spliceosomal complex	6 out of 562 genes, 1.1%	14 out of 4862 genes, 0.3%	0.003081736
Dendrite	46 out of 562 genes, 8.2%	269 out of 4862 genes, 5.5%	0.003492347
Myofibril	20 out of 562 genes, 3.6%	93 out of 4862 genes, 1.9%	0.004002903
Cell junction	61 out of 562 genes, 10.9%	381 out of 4862 genes, 7.8%	0.004063853
Ruffle membrane	9 out of 562 genes, 1.6%	29 out of 4862 genes, 0.6%	0.004099638
Extrinsic to plasma membrane	13 out of 562 genes, 2.3%	51 out of 4862 genes, 1.0%	0.004246846
Extracellular matrix part	17 out of 562 genes, 3.0%	75 out of 4862 genes, 1.5%	0.004392264
Microvillus membrane	4 out of 562 genes, 0.7%	7 out of 4862 genes, 0.1%	0.004640842
Nucleosome	6 out of 562 genes, 1.1%	15 out of 4862 genes, 0.3%	0.004641268
Cytosolic small ribosomal subunit	10 out of 562 genes, 1.8%	35 out of 4862 genes, 0.7%	0.004902921
Leading edge membrane	13 out of 562 genes, 2.3%	52 out of 4862 genes, 1.1%	0.005081026
Cytoskeletal part	84 out of 562 genes, 14.9%	560 out of 4862 genes, 11.5%	0.005162233
Vacuolar lumen	9 out of 562 genes, 1.6%	30 out of 4862 genes, 0.6%	0.005270271
Lysosomal lumen	9 out of 562 genes, 1.6%	30 out of 4862 genes, 0.6%	0.005270271
Protein-DNA complex	8 out of 562 genes, 1.4%	25 out of 4862 genes, 0.5%	0.005464244
Contractile fiber part	18 out of 562 genes, 3.2%	83 out of 4862 genes, 1.7%	0.005630465
Cell body	45 out of 562 genes, 8.0%	269 out of 4862 genes, 5.5%	0.005866823
Cell leading edge	30 out of 562 genes, 5.3%	163 out of 4862 genes, 3.4%	0.005988463
Intercalated disc	9 out of 562 genes, 1.6%	32 out of 4862 genes, 0.7%	0.008371119
Organelle part	325 out of 562 genes, 57.8%	2578 out of 4862 genes, 53.0%	0.008493931
Endocytic vesicle	16 out of 562 genes, 2.8%	74 out of 4862 genes, 1.5%	0.009059008
Intermediate filament	10 out of 562 genes, 1.8%	38 out of 4862 genes, 0.8%	0.009182325
Postsynaptic membrane	20 out of 562 genes, 3.6%	100 out of 4862 genes, 2.1%	0.00930178

Supplementary Table 15 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Excitatory synapse	7 out of 562 genes, 1.2%	22 out of 4862 genes, 0.5%	0.00955324
Extrinsic to membrane	17 out of 562 genes, 3.0%	81 out of 4862 genes, 1.7%	0.009842252
Cell projection membrane	17 out of 562 genes, 3.0%	81 out of 4862 genes, 1.7%	0.009842252
Cell surface	33 out of 562 genes, 5.9%	190 out of 4862 genes, 3.9%	0.009935668
Cytoplasm	459 out of 562 genes, 81.7%	3783 out of 4862 genes, 77.8%	0.009987886
Sarcomere	16 out of 562 genes, 2.8%	75 out of 4862 genes, 1.5%	0.01032457
Cell-cell contact zone	9 out of 562 genes, 1.6%	33 out of 4862 genes, 0.7%	0.01036318
Synapse	55 out of 562 genes, 9.8%	353 out of 4862 genes, 7.3%	0.010938
Basement membrane	11 out of 562 genes, 2.0%	45 out of 4862 genes, 0.9%	0.011468
Mitochondrial respiratory chain	12 out of 562 genes, 2.1%	51 out of 4862 genes, 1.0%	0.01154364
Vacuolar part	20 out of 562 genes, 3.6%	102 out of 4862 genes, 2.1%	0.01157107
X chromosome	3 out of 562 genes, 0.5%	5 out of 4862 genes, 0.1%	0.0128406
Barr body	3 out of 562 genes, 0.5%	5 out of 4862 genes, 0.1%	0.0128406
Lamin filament	3 out of 562 genes, 0.5%	5 out of 4862 genes, 0.1%	0.0128406
Respiratory chain	13 out of 562 genes, 2.3%	58 out of 4862 genes, 1.2%	0.0132097
Axon part	22 out of 562 genes, 3.9%	117 out of 4862 genes, 2.4%	0.01354271
Intracellular organelle part	319 out of 562 genes, 56.8%	2543 out of 4862 genes, 52.3%	0.01361871
Striated muscle thin filament	4 out of 562 genes, 0.7%	9 out of 4862 genes, 0.2%	0.01381839
Neuronal cell body	40 out of 562 genes, 7.1%	248 out of 4862 genes, 5.1%	0.01651035
Golgi lumen	5 out of 562 genes, 0.9%	14 out of 4862 genes, 0.3%	0.01665554
Peroxisome	16 out of 562 genes, 2.8%	79 out of 4862 genes, 1.6%	0.01684171
Microbody	16 out of 562 genes, 2.8%	79 out of 4862 genes, 1.6%	0.01684171
Large ribosomal subunit	13 out of 562 genes, 2.3%	60 out of 4862 genes, 1.2%	0.017444
Extrinsic to internal side of plasma membrane	8 out of 562 genes, 1.4%	30 out of 4862 genes, 0.6%	0.01759995
Mitochondrial respiratory chain complex I	9 out of 562 genes, 1.6%	36 out of 4862 genes, 0.7%	0.01848218
NADH dehydrogenase complex	9 out of 562 genes, 1.6%	36 out of 4862 genes, 0.7%	0.01848218
Respiratory chain complex I	9 out of 562 genes, 1.6%	36 out of 4862 genes, 0.7%	0.01848218
Actin filament	10 out of 562 genes, 1.8%	42 out of 4862 genes, 0.9%	0.01873384
Cell periphery	176 out of 562 genes, 31.3%	1341 out of 4862 genes, 27.6%	0.02069537
Juxtaparanode region of axon	4 out of 562 genes, 0.7%	10 out of 4862 genes, 0.2%	0.02095918
Actin cytoskeleton	36 out of 562 genes, 6.4%	223 out of 4862 genes, 4.6%	0.02197789
Organelle envelope	69 out of 562 genes, 12.3%	476 out of 4862 genes, 9.8%	0.02323918
F-actin capping protein complex	3 out of 562 genes, 0.5%	6 out of 4862 genes, 0.1%	0.02349282
Paraspeckles	3 out of 562 genes, 0.5%	6 out of 4862 genes, 0.1%	0.02349282
Inhibitory synapse	3 out of 562 genes, 0.5%	6 out of 4862 genes, 0.1%	0.02349282
Envelope	70 out of 562 genes, 12.5%	485 out of 4862 genes, 10.0%	0.02442816
Spindle pole	8 out of 562 genes, 1.4%	32 out of 4862 genes, 0.7%	0.02573874
Microvillus	9 out of 562 genes, 1.6%	38 out of 4862 genes, 0.8%	0.02598437
Non-membrane-bounded organelle	190 out of 562 genes, 33.8%	1468 out of 4862 genes, 30.2%	0.02722717
Intracellular non-membrane-bounded organelle	190 out of 562 genes, 33.8%	1468 out of 4862 genes, 30.2%	0.02722717
Small ribosomal subunit	11 out of 562 genes, 2.0%	51 out of 4862 genes, 1.0%	0.02847194

Supplementary Table 15 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Ribosome	26 out of 562 genes, 4.6%	154 out of 4862 genes, 3.2%	0.02877632
Synaptic membrane	23 out of 562 genes, 4.1%	133 out of 4862 genes, 2.7%	0.02984069
NuRD complex	4 out of 562 genes, 0.7%	11 out of 4862 genes, 0.2%	0.02998713
Neurofilament cytoskeleton	4 out of 562 genes, 0.7%	11 out of 4862 genes, 0.2%	0.02998713
CHD-type complex	4 out of 562 genes, 0.7%	11 out of 4862 genes, 0.2%	0.02998713
Nuclear matrix	9 out of 562 genes, 1.6%	39 out of 4862 genes, 0.8%	0.03044715
Mitochondrial intermembrane space	8 out of 562 genes, 1.4%	33 out of 4862 genes, 0.7%	0.03065892
Cell cortex	21 out of 562 genes, 3.7%	120 out of 4862 genes, 2.5%	0.03281387
Cortical cytoskeleton	10 out of 562 genes, 1.8%	46 out of 4862 genes, 0.9%	0.03410797
Collagen	6 out of 562 genes, 1.1%	22 out of 4862 genes, 0.5%	0.0343103
Cytoskeleton	104 out of 562 genes, 18.5%	768 out of 4862 genes, 15.8%	0.03683232
I band	11 out of 562 genes, 2.0%	53 out of 4862 genes, 1.1%	0.03690225
Fibrillar collagen	2 out of 562 genes, 0.4%	3 out of 4862 genes, 0.1%	0.036946
Troponin complex	2 out of 562 genes, 0.4%	3 out of 4862 genes, 0.1%	0.036946
Histone pre-mRNA 3'end processing complex	2 out of 562 genes, 0.4%	3 out of 4862 genes, 0.1%	0.036946
Z disc	10 out of 562 genes, 1.8%	47 out of 4862 genes, 1.0%	0.03902727
Cytoplasmic part	374 out of 562 genes, 66.5%	3068 out of 4862 genes, 63.1%	0.03911425
Fascia adherens	4 out of 562 genes, 0.7%	12 out of 4862 genes, 0.2%	0.04097268
Organelle envelope lumen	8 out of 562 genes, 1.4%	35 out of 4862 genes, 0.7%	0.0423502
Lytic vacuole	23 out of 562 genes, 4.1%	139 out of 4862 genes, 2.9%	0.04665262
Lysosome	23 out of 562 genes, 4.1%	139 out of 4862 genes, 2.9%	0.04665262
Adherens junction	19 out of 562 genes, 3.4%	111 out of 4862 genes, 2.3%	0.04981595

Gene Ontology term was the entry of GO. Cluster frequency was the number and ratio of the differential proteins annotated to the differential proteins of the entry and all GO entries. Protein frequency of use was the number and ratio of all proteins annotated to all proteins of the entry and all entries of GO. P-value was calculated by the hypergeometric test, $P < 0.05$ considered for the statistical significance.

Supplementary Table 16. Terms for WT spinal cord VS Progression spinal cord of Molecular Function

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Structural molecule activity	63 out of 538 genes, 11.7%	323 out of 4617 genes, 7.0%	1.46337E-05
Enzyme inhibitor activity	28 out of 538 genes, 5.2%	119 out of 4617 genes, 2.6%	0.000168196
Enzyme binding	89 out of 538 genes, 16.5%	569 out of 4617 genes, 12.3%	0.001360774
Ferroxidase activity	3 out of 538 genes, 0.6%	3 out of 4617 genes, 0.1%	0.001574432
Oxidoreductase activity, oxidizing metal ions, Oxygen as acceptor	3 out of 538 genes, 0.6%	3 out of 4617 genes, 0.1%	0.001574432
Protein kinase C binding	10 out of 538 genes, 1.9%	32 out of 4617 genes, 0.7%	0.002516117
Structural constituent of ribosome	24 out of 538 genes, 4.5%	117 out of 4617 genes, 2.5%	0.003631265
Endopeptidase inhibitor activity	14 out of 538 genes, 2.6%	56 out of 4617 genes, 1.2%	0.003972892
Endopeptidase regulator activity	15 out of 538 genes, 2.8%	62 out of 4617 genes, 1.3%	0.004083646
Peptidase inhibitor activity	14 out of 538 genes, 2.6%	57 out of 4617 genes, 1.2%	0.004719122
Hyaluronic acid binding	4 out of 538 genes, 0.7%	7 out of 4617 genes, 0.2%	0.004779685
Antioxidant activity	10 out of 538 genes, 1.9%	35 out of 4617 genes, 0.8%	0.00518771
Oxidoreductase activity, oxidizing metal ions	3 out of 538 genes, 0.6%	4 out of 4617 genes, 0.1%	0.005750056
Protein kinase binding	35 out of 538 genes, 6.5%	196 out of 4617 genes, 4.2%	0.005820805
Actin binding	35 out of 538 genes, 6.5%	199 out of 4617 genes, 4.3%	0.007426908
Protein heterodimerization activity	25 out of 538 genes, 4.6%	131 out of 4617 genes, 2.8%	0.008024017
Glycoprotein binding	8 out of 538 genes, 1.5%	27 out of 4617 genes, 0.6%	0.009544036
Hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	11 out of 538 genes, 2.0%	45 out of 4617 genes, 1.0%	0.0121327
Collagen binding	7 out of 538 genes, 1.3%	23 out of 4617 genes, 0.5%	0.01292599
Fibronectin binding	3 out of 538 genes, 0.6%	5 out of 4617 genes, 0.1%	0.01313275
Beta-N-acetylhexosaminidase activity	3 out of 538 genes, 0.6%	5 out of 4617 genes, 0.1%	0.01313275
Superoxide dismutase activity	3 out of 538 genes, 0.6%	5 out of 4617 genes, 0.1%	0.01313275
Oxidoreductase activity, acting on superoxide Radicals as acceptor	3 out of 538 genes, 0.6%	5 out of 4617 genes, 0.1%	0.01313275
Telomeric DNA binding	3 out of 538 genes, 0.6%	5 out of 4617 genes, 0.1%	0.01313275
Choline transmembrane transporter activity	2 out of 538 genes, 0.4%	2 out of 4617 genes, 0.0%	0.01355598
Purinergic receptor activity	2 out of 538 genes, 0.4%	2 out of 4617 genes, 0.0%	0.01355598
Nucleoside triphosphate adenylate kinase activity	2 out of 538 genes, 0.4%	2 out of 4617 genes, 0.0%	0.01355598
Histone pre-mRNA DCP binding	2 out of 538 genes, 0.4%	2 out of 4617 genes, 0.0%	0.01355598
Small protein activating enzyme activity	4 out of 538 genes, 0.7%	9 out of 4617 genes, 0.2%	0.01420997
Isoprenoid binding	4 out of 538 genes, 0.7%	9 out of 4617 genes, 0.2%	0.01420997
Oxidoreductase activity, acting on NAD(P)H	12 out of 538 genes, 2.2%	52 out of 4617 genes, 1.1%	0.01429666
Calcium ion binding	39 out of 538 genes, 7.2%	237 out of 4617 genes, 5.1%	0.01463937
Kinase binding	37 out of 538 genes, 6.9%	223 out of 4617 genes, 4.8%	0.0151699
Serine-type endopeptidase inhibitor activity	8 out of 538 genes, 1.5%	30 out of 4617 genes, 0.6%	0.01839723
Cysteine-type endopeptidase activity	7 out of 538 genes, 1.3%	25 out of 4617 genes, 0.5%	0.02063725
C-acyltransferase activity	4 out of 538 genes, 0.7%	10 out of 4617 genes, 0.2%	0.02153679
Metallopeptidase activity	12 out of 538 genes, 2.2%	55 out of 4617 genes, 1.2%	0.02200353
Extracellular matrix binding	6 out of 538 genes, 1.1%	20 out of 4617 genes, 0.4%	0.02254293
Protein binding	373 out of 538 genes, 69.3%	3020 out of 4617 genes, 65.4%	0.02286228
Cell adhesion molecule binding	10 out of 538 genes, 1.9%	43 out of 4617 genes, 0.9%	0.02309893
Enzyme regulator activity	62 out of 538 genes, 11.5%	419 out of 4617 genes, 9.1%	0.02394574
Structural constituent of eye lens	3 out of 538 genes, 0.6%	6 out of 4617 genes, 0.1%	0.02400991

Supplementary Table 16 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Retinoid binding	3 out of 538 genes, 0.6%	6 out of 4617 genes, 0.1%	0.02400991
Dopamine receptor binding	3 out of 538 genes, 0.6%	6 out of 4617 genes, 0.1%	0.02400991
Peptidase regulator activity	15 out of 538 genes, 2.8%	75 out of 4617 genes, 1.6%	0.02407535
Kinase regulator activity	13 out of 538 genes, 2.4%	63 out of 4617 genes, 1.4%	0.02714204
G-protein coupled receptor binding	13 out of 538 genes, 2.4%	64 out of 4617 genes, 1.4%	0.03058054
Heme binding	9 out of 538 genes, 1.7%	39 out of 4617 genes, 0.8%	0.03185405
Oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	6 out of 538 genes, 1.1%	22 out of 4617 genes, 0.5%	0.03551158
NADH dehydrogenase activity	7 out of 538 genes, 1.3%	28 out of 4617 genes, 0.6%	0.03742139
3-keto sterol reductase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Bisphosphoglycerate mutase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Bisphosphoglycerate 2-phosphatase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Cytochrome-b5 reductase activity, acting on NAD(P)H	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Phosphoglycerate mutase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Phosphoserine phosphatase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Calcium-dependent protein kinase C activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Glutamate-tRNA ligase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Proline-tRNA ligase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Galactosyltransferase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Calcium-dependent protein serine/threonine kinase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Calcium-dependent protein kinase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Monosaccharide transmembrane transporter activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Hexose transmembrane transporter activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Long-chain-enoyl-CoA hydratase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Metallochaperone activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Troponin T binding	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Adenosine receptor binding	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
UDP-galactosyltransferase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Platelet-activating factor acetyltransferase activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Sugar transmembrane transporter activity	2 out of 538 genes, 0.4%	3 out of 4617 genes, 0.1%	0.03751907
Acetyl-CoA C-acyltransferase activity	3 out of 538 genes, 0.6%	7 out of 4617 genes, 0.2%	0.03843257
Insulin-like growth factor receptor binding	3 out of 538 genes, 0.6%	7 out of 4617 genes, 0.2%	0.03843257
Ferric iron binding	3 out of 538 genes, 0.6%	7 out of 4617 genes, 0.2%	0.03843257
Hexosaminidase activity	3 out of 538 genes, 0.6%	7 out of 4617 genes, 0.2%	0.03843257
Protein serine/threonine kinase activator activity	3 out of 538 genes, 0.6%	7 out of 4617 genes, 0.2%	0.03843257
Actin filament binding	11 out of 538 genes, 2.0%	53 out of 4617 genes, 1.1%	0.03879071
Oxidoreductase activity	51 out of 538 genes, 9.5%	345 out of 4617 genes, 7.5%	0.03925892

Supplementary Table 16 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Spectrin binding	4 out of 538 genes, 0.7%	12 out of 4617 genes, 0.3%	0.04203912
Cation binding	144 out of 538 genes, 26.8%	1094 out of 4617 genes, 23.7%	0.04319123
Metalloendopeptidase activity	6 out of 538 genes, 1.1%	23 out of 4617 genes, 0.5%	0.04348297
Calmodulin binding	17 out of 538 genes, 3.2%	95 out of 4617 genes, 2.1%	0.04555686
Glycosaminoglycan binding	10 out of 538 genes, 1.9%	48 out of 4617 genes, 1.0%	0.04650437
Tetrapyrrole binding	9 out of 538 genes, 1.7%	42 out of 4617 genes, 0.9%	0.04902364
Protein kinase regulator activity	11 out of 538 genes, 2.0%	55 out of 4617 genes, 1.2%	0.04926616
Calcium-dependent phospholipid binding	5 out of 538 genes, 0.9%	18 out of 4617 genes, 0.4%	0.04981259
Cadherin binding	5 out of 538 genes, 0.9%	18 out of 4617 genes, 0.4%	0.04981259

Gene Ontology term was the entry of GO. Cluster frequency was the number and ratio of the differential proteins annotated to the differential proteins of the entry and all GO entries. Protein frequency of use was the number and ratio of all proteins annotated to all proteins of the entry and all entries of GO. P-value was calculated by the hypergeometric test, $P < 0.05$ considered for the statistical significance.

Supplementary Table 17. Terms for WT spinal cord VS Progression spinal cord of Biological Process

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Cellular component disassembly	30 out of 542 genes, 5.5%	122 out of 4647 genes, 2.6%	4.17597E-05
Intermediate filament-based process	8 out of 542 genes, 1.5%	15 out of 4647 genes, 0.3%	9.91783E-05
Intermediate filament cytoskeleton organization	8 out of 542 genes, 1.5%	15 out of 4647 genes, 0.3%	9.91783E-05
Viral genome expression	19 out of 542 genes, 3.5%	66 out of 4647 genes, 1.4%	0.000119113
Viral transcription	19 out of 542 genes, 3.5%	66 out of 4647 genes, 1.4%	0.000119113
Translational termination	19 out of 542 genes, 3.5%	67 out of 4647 genes, 1.4%	0.000148577
Single-organism behavior	38 out of 542 genes, 7.0%	183 out of 4647 genes, 3.9%	0.000218463
Translational initiation	23 out of 542 genes, 4.2%	93 out of 4647 genes, 2.0%	0.000299013
Nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	22 out of 542 genes, 4.1%	88 out of 4647 genes, 1.9%	0.000342016
Protein complex disassembly	19 out of 542 genes, 3.5%	73 out of 4647 genes, 1.6%	0.00049916
Cellular protein complex disassembly	19 out of 542 genes, 3.5%	73 out of 4647 genes, 1.6%	0.00049916
Macromolecular complex subunit organization	94 out of 542 genes, 17.3%	594 out of 4647 genes, 12.8%	0.000679431
SRP-dependent cotranslational protein targeting to membrane	20 out of 542 genes, 3.7%	81 out of 4647 genes, 1.7%	0.00074838
Protein targeting to ER	20 out of 542 genes, 3.7%	81 out of 4647 genes, 1.7%	0.00074838
Establishment of protein localization to endoplasmic reticulum	20 out of 542 genes, 3.7%	81 out of 4647 genes, 1.7%	0.00074838
Chondroitin sulfate catabolic process	5 out of 542 genes, 0.9%	8 out of 4647 genes, 0.2%	0.000878107
Cotranslational protein targeting to membrane	20 out of 542 genes, 3.7%	82 out of 4647 genes, 1.8%	0.000884679
Positive regulation of angiogenesis	9 out of 542 genes, 1.7%	24 out of 4647 genes, 0.5%	0.000969707
Translational elongation	21 out of 542 genes, 3.9%	89 out of 4647 genes, 1.9%	0.001053541
Aminoglycan catabolic process	8 out of 542 genes, 1.5%	20 out of 4647 genes, 0.4%	0.001139582
Regulation of angiogenesis	13 out of 542 genes, 2.4%	45 out of 4647 genes, 1.0%	0.001355828
Regulation of B cell mediated immunity	3 out of 542 genes, 0.6%	3 out of 4647 genes, 0.1%	0.001578893
Positive regulation of B cell mediated immunity	3 out of 542 genes, 0.6%	3 out of 4647 genes, 0.1%	0.001578893
Regulation of immunoglobulin mediated immune response	3 out of 542 genes, 0.6%	3 out of 4647 genes, 0.1%	0.001578893
Positive regulation of immunoglobulin mediated immune response	3 out of 542 genes, 0.6%	3 out of 4647 genes, 0.1%	0.001578893
Positive regulation of humoral immune response	3 out of 542 genes, 0.6%	3 out of 4647 genes, 0.1%	0.001578893
Response to organic cyclic compound	52 out of 542 genes, 9.6%	300 out of 4647 genes, 6.5%	0.00171297
Anatomical structure development	187 out of 542 genes, 34.5%	1347 out of 4647 genes, 29.0%	0.001731566
Response to selenium ion	5 out of 542 genes, 0.9%	9 out of 4647 genes, 0.2%	0.001786952
Response to vitamin D	5 out of 542 genes, 0.9%	9 out of 4647 genes, 0.2%	0.001786952
Intermediate filament organization	5 out of 542 genes, 0.9%	9 out of 4647 genes, 0.2%	0.001786952
Single-multicellular organism process	234 out of 542 genes, 43.2%	1736 out of 4647 genes, 37.4%	0.001802548
System development	170 out of 542 genes, 31.4%	1210 out of 4647 genes, 26.0%	0.001803573
Behavior	39 out of 542 genes, 7.2%	210 out of 4647 genes, 4.5%	0.001814569
Positive regulation of NF-kappa B transcription factor activity	9 out of 542 genes, 1.7%	26 out of 4647 genes, 0.6%	0.001870338

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Protein localization to endoplasmic reticulum	20 out of 542 genes, 3.7%	87 out of 4647 genes, 1.9%	0.001932086
Locomotory behavior	19 out of 542 genes, 3.5%	81 out of 4647 genes, 1.7%	0.001938331
Regulation of molecular function	115 out of 542 genes, 21.2%	776 out of 4647 genes, 16.7%	0.002056485
Regulation of vasculature development	13 out of 542 genes, 2.4%	47 out of 4647 genes, 1.0%	0.002097358
Viral infectious cycle	20 out of 542 genes, 3.7%	88 out of 4647 genes, 1.9%	0.00223543
Macromolecular complex disassembly	19 out of 542 genes, 3.5%	82 out of 4647 genes, 1.8%	0.002256098
Regulation of humoral immune response	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
L-methionine salvage from methylthioadenosine	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
Amino acid salvage	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
Nucleoside salvage	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
Neurofilament cytoskeleton organization	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
L-methionine biosynthetic process	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
L-methionine salvage	4 out of 542 genes, 0.7%	6 out of 4647 genes, 0.1%	0.00226373
Sulfur compound catabolic process	8 out of 542 genes, 1.5%	22 out of 4647 genes, 0.5%	0.002340395
Protein complex subunit organization	78 out of 542 genes, 14.4%	496 out of 4647 genes, 10.7%	0.002457264
Chromatin assembly	9 out of 542 genes, 1.7%	27 out of 4647 genes, 0.6%	0.002521042
Aminoglycan metabolic process	10 out of 542 genes, 1.8%	32 out of 4647 genes, 0.7%	0.00253446
Regulation of intracellular protein kinase cascade	43 out of 542 genes, 7.9%	242 out of 4647 genes, 5.2%	0.002633506
Glycosaminoglycan catabolic process	7 out of 542 genes, 1.3%	18 out of 4647 genes, 0.4%	0.002832163
Adult locomotory behavior	12 out of 542 genes, 2.2%	43 out of 4647 genes, 0.9%	0.002842328
Multicellular organismal development	184 out of 542 genes, 33.9%	1338 out of 4647 genes, 28.8%	0.003099396
Cellular process involved in reproduction	33 out of 542 genes, 6.1%	175 out of 4647 genes, 3.8%	0.003109451
Cyclic-nucleotide-mediated signaling	5 out of 542 genes, 0.9%	10 out of 4647 genes, 0.2%	0.00323346
Ribosomal large subunit biogenesis	5 out of 542 genes, 0.9%	10 out of 4647 genes, 0.2%	0.00323346
Cellular iron ion homeostasis	9 out of 542 genes, 1.7%	28 out of 4647 genes, 0.6%	0.003339049
Response to axon injury	9 out of 542 genes, 1.7%	28 out of 4647 genes, 0.6%	0.003339049
Multicellular organismal process	237 out of 542 genes, 43.7%	1781 out of 4647 genes, 38.3%	0.003578364
Regulation of multicellular organismal process	94 out of 542 genes, 17.3%	626 out of 4647 genes, 13.5%	0.003785577
Chondroitin sulfate metabolic process	7 out of 542 genes, 1.3%	19 out of 4647 genes, 0.4%	0.004040707
Chondroitin sulfate proteoglycan metabolic process	7 out of 542 genes, 1.3%	19 out of 4647 genes, 0.4%	0.004040707
mRNA catabolic process	24 out of 542 genes, 4.4%	118 out of 4647 genes, 2.5%	0.004126407
metal ion homeostasis	24 out of 542 genes, 4.4%	118 out of 4647 genes, 2.5%	0.004126407
Regulation of MAPK cascade	30 out of 542 genes, 5.5%	158 out of 4647 genes, 3.4%	0.004248714
Negative regulation of MAPK cascade	12 out of 542 genes, 2.2%	45 out of 4647 genes, 1.0%	0.004285998
Glycosaminoglycan metabolic process	9 out of 542 genes, 1.7%	29 out of 4647 genes, 0.6%	0.004352108
Response to nutrient levels	28 out of 542 genes, 5.2%	145 out of 4647 genes, 3.1%	0.004427247
Humoral immune response mediated by circulating immunoglobulin	4 out of 542 genes, 0.7%	7 out of 4647 genes, 0.2%	0.004796443
Complement activation, classical pathway	4 out of 542 genes, 0.7%	7 out of 4647 genes, 0.2%	0.004796443
Auditory receptor cell differentiation	4 out of 542 genes, 0.7%	7 out of 4647 genes, 0.2%	0.004796443
Skeletal muscle tissue regeneration	4 out of 542 genes, 0.7%	7 out of 4647 genes, 0.2%	0.004796443
Neuromuscular process controlling posture	4 out of 542 genes, 0.7%	7 out of 4647 genes, 0.2%	0.004796443
Anatomical structure morphogenesis	91 out of 542 genes, 16.8%	608 out of 4647 genes, 13.1%	0.004851563
Tissue regeneration	6 out of 542 genes, 1.1%	15 out of 4647 genes, 0.3%	0.004853622
Cellular metal ion homeostasis	23 out of 542 genes, 4.2%	113 out of 4647 genes, 2.4%	0.004888356

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Negative regulation of multicellular organismal process	22 out of 542 genes, 4.1%	107 out of 4647 genes, 2.3%	0.005159369
Regulation of protein serine/threonine kinase activity	24 out of 542 genes, 4.4%	120 out of 4647 genes, 2.6%	0.005160019
DNA packaging	10 out of 542 genes, 1.8%	35 out of 4647 genes, 0.8%	0.005223769
Protein activation cascade	5 out of 542 genes, 0.9%	11 out of 4647 genes, 0.2%	0.005365114
Maintenance of location	13 out of 542 genes, 2.4%	52 out of 4647 genes, 1.1%	0.005476244
Cellular metabolic compound salvage	7 out of 542 genes, 1.3%	20 out of 4647 genes, 0.4%	0.005602851
RNA biosynthetic process	31 out of 542 genes, 5.7%	168 out of 4647 genes, 3.6%	0.005731627
Purine ribonucleoside salvage	3 out of 542 genes, 0.6%	4 out of 4647 genes, 0.1%	0.005765816
Regulation of vascular endothelial growth factor production	3 out of 542 genes, 0.6%	4 out of 4647 genes, 0.1%	0.005765816
Terpenoid biosynthetic process	3 out of 542 genes, 0.6%	4 out of 4647 genes, 0.1%	0.005765816
Hyaluronan metabolic process	3 out of 542 genes, 0.6%	4 out of 4647 genes, 0.1%	0.005765816
Nucleosome assembly	8 out of 542 genes, 1.5%	25 out of 4647 genes, 0.5%	0.005768659
Response to lipid	41 out of 542 genes, 7.6%	238 out of 4647 genes, 5.1%	0.005796554
Response to wounding	53 out of 542 genes, 9.8%	325 out of 4647 genes, 7.0%	0.005906335
Nuclear-transcribed mRNA catabolic process	23 out of 542 genes, 4.2%	115 out of 4647 genes, 2.5%	0.006116119
Negative regulation of cellular component organization	30 out of 542 genes, 5.5%	162 out of 4647 genes, 3.5%	0.006183752
DNA conformation change	12 out of 542 genes, 2.2%	47 out of 4647 genes, 1.0%	0.006265202
Sulfur compound biosynthetic process	10 out of 542 genes, 1.8%	36 out of 4647 genes, 0.8%	0.006497484
Response to extracellular stimulus	29 out of 542 genes, 5.4%	156 out of 4647 genes, 3.4%	0.00666798
Maternal process involved in female pregnancy	6 out of 542 genes, 1.1%	16 out of 4647 genes, 0.3%	0.00701297
RNA catabolic process	24 out of 542 genes, 4.4%	123 out of 4647 genes, 2.6%	0.007107559
Developmental process	196 out of 542 genes, 36.2%	1462 out of 4647 genes, 31.5%	0.007399879
Regulation of actin filament depolymerization	8 out of 542 genes, 1.5%	26 out of 4647 genes, 0.6%	0.007501246
Iron ion homeostasis	10 out of 542 genes, 1.8%	37 out of 4647 genes, 0.8%	0.00799983
Immunoglobulin mediated immune response	5 out of 542 genes, 0.9%	12 out of 4647 genes, 0.3%	0.008326845
B cell mediated immunity	5 out of 542 genes, 0.9%	12 out of 4647 genes, 0.3%	0.008326845
Vasodilation	5 out of 542 genes, 0.9%	12 out of 4647 genes, 0.3%	0.008326845
Complement activation	4 out of 542 genes, 0.7%	8 out of 4647 genes, 0.2%	0.008714779
Positive regulation of cardiac muscle hypertrophy	4 out of 542 genes, 0.7%	8 out of 4647 genes, 0.2%	0.008714779
Peripheral nervous system axon regeneration	4 out of 542 genes, 0.7%	8 out of 4647 genes, 0.2%	0.008714779
Positive regulation of muscle hypertrophy	4 out of 542 genes, 0.7%	8 out of 4647 genes, 0.2%	0.008714779
Ceramide biosynthetic process	4 out of 542 genes, 0.7%	8 out of 4647 genes, 0.2%	0.008714779
Regulation of catalytic activity	96 out of 542 genes, 17.7%	660 out of 4647 genes, 14.2%	0.008831032
Nucleosome organization	9 out of 542 genes, 1.7%	32 out of 4647 genes, 0.7%	0.008861945
Neuromuscular process	12 out of 542 genes, 2.2%	49 out of 4647 genes, 1.1%	0.008905296
Steroid metabolic process	14 out of 542 genes, 2.6%	61 out of 4647 genes, 1.3%	0.008985164
Negative regulation of protein serine/threonine kinase activity	10 out of 542 genes, 1.8%	38 out of 4647 genes, 0.8%	0.009755971

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Proteoglycan metabolic process	7 out of 542 genes, 1.3%	22 out of 4647 genes, 0.5%	0.01001994
Response to nutrient	18 out of 542 genes, 3.3%	87 out of 4647 genes, 1.9%	0.01018778
Sulfur compound metabolic process	20 out of 542 genes, 3.7%	100 out of 4647 genes, 2.2%	0.01020713
Maintenance of location in cell	11 out of 542 genes, 2.0%	44 out of 4647 genes, 0.9%	0.01027804
Protein targeting to membrane	21 out of 542 genes, 3.9%	107 out of 4647 genes, 2.3%	0.01067671
Response to stimulus	261 out of 542 genes, 48.2%	2019 out of 4647 genes, 43.4%	0.01069779
Cellular component disassembly involved in execution phase of apoptosis	9 out of 542 genes, 1.7%	33 out of 4647 genes, 0.7%	0.01096071
Execution phase of apoptosis	9 out of 542 genes, 1.7%	33 out of 4647 genes, 0.7%	0.01096071
Cellular component biogenesis	95 out of 542 genes, 17.5%	658 out of 4647 genes, 14.2%	0.01130753
Response to chemical stimulus	149 out of 542 genes, 27.5%	1090 out of 4647 genes, 23.5%	0.01142493
Negative regulation of biological process	137 out of 542 genes, 25.3%	993 out of 4647 genes, 21.4%	0.01148915
Response to external stimulus	64 out of 542 genes, 11.8%	419 out of 4647 genes, 9.0%	0.01161864
Negative regulation of peptidase activity	15 out of 542 genes, 2.8%	69 out of 4647 genes, 1.5%	0.01162823
Multi-organism reproductive process	47 out of 542 genes, 8.7%	292 out of 4647 genes, 6.3%	0.01181952
Positive regulation of intracellular protein kinase cascade	27 out of 542 genes, 5.0%	149 out of 4647 genes, 3.2%	0.01216203
Adult behavior	13 out of 542 genes, 2.4%	57 out of 4647 genes, 1.2%	0.01224481
Exocytosis	22 out of 542 genes, 4.1%	115 out of 4647 genes, 2.5%	0.012246
Inner mitochondrial membrane organization	5 out of 542 genes, 0.9%	13 out of 4647 genes, 0.3%	0.01225473
Cellular response to fatty acid	5 out of 542 genes, 0.9%	13 out of 4647 genes, 0.3%	0.01225473
Regeneration	12 out of 542 genes, 2.2%	51 out of 4647 genes, 1.1%	0.01234055
System process	92 out of 542 genes, 17.0%	637 out of 4647 genes, 13.7%	0.01256468
Response to inorganic substance	36 out of 542 genes, 6.6%	213 out of 4647 genes, 4.6%	0.01268364
Organic cyclic compound biosynthetic process	57 out of 542 genes, 10.5%	368 out of 4647 genes, 7.9%	0.01285616
Adult walking behavior	7 out of 542 genes, 1.3%	23 out of 4647 genes, 0.5%	0.0129911
Citrulline metabolic process	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Circadian sleep/wake cycle process	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Regulation of complement activation	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Cellular response to nutrient	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Keratan sulfate metabolic process	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Keratan sulfate catabolic process	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Apoptotic cell clearance	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Decidualization	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Regulation of protein activation cascade	3 out of 542 genes, 0.6%	5 out of 4647 genes, 0.1%	0.01316755
Cellular component assembly	88 out of 542 genes, 16.2%	607 out of 4647 genes, 13.1%	0.01327983
Reactive oxygen species metabolic process	9 out of 542 genes, 1.7%	34 out of 4647 genes, 0.7%	0.01341105
Regulation of type IIa hypersensitivity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Positive regulation of type IIa hypersensitivity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of inflammatory response to antigenic stimulus	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of acute inflammatory response to antigenic stimulus	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Regulation of hypersensitivity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of hypersensitivity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of myeloid leukocyte mediated immunity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Regulation of type II hypersensitivity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of type II hypersensitivity	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Choline transport	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Antibiotic metabolic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Carbon tetrachloride metabolic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Citrulline biosynthetic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Hyaluronan catabolic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Regulation of heat generation	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of heat generation	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Copper ion transmembrane transport	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Chlorinated hydrocarbon metabolic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Halogenated hydrocarbon metabolic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Superoxide anion generation	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
AMP salvage	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Negative regulation of cholesterol biosynthetic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of complement activation	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Hydrogen peroxide biosynthetic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Trabecula formation	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Cellular response to vitamin	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Cellular response to vitamin D	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Negative regulation of cholesterol metabolic process	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Regulation of platelet-derived growth factor production	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Regulation of Schwann cell migration	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Positive regulation of protein activation cascade	2 out of 542 genes, 0.4%	2 out of 4647 genes, 0.0%	0.0135814
Cellular response to nutrient levels	10 out of 542 genes, 1.8%	40 out of 4647 genes, 0.9%	0.0141322
Maternal placenta development	4 out of 542 genes, 0.7%	9 out of 4647 genes, 0.2%	0.01425704
Humoral immune response	4 out of 542 genes, 0.7%	9 out of 4647 genes, 0.2%	0.01425704
Neuroblast proliferation	4 out of 542 genes, 0.7%	9 out of 4647 genes, 0.2%	0.01425704
Methionine biosynthetic process	4 out of 542 genes, 0.7%	9 out of 4647 genes, 0.2%	0.01425704
Response to prostaglandin stimulus	4 out of 542 genes, 0.7%	9 out of 4647 genes, 0.2%	0.01425704
Cellular component organization	206 out of 542 genes, 38.0%	1567 out of 4647 genes, 33.7%	0.01449255
Platelet degranulation	8 out of 542 genes, 1.5%	29 out of 4647 genes, 0.6%	0.0150541
Axon cargo transport	8 out of 542 genes, 1.5%	29 out of 4647 genes, 0.6%	0.0150541

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Anatomical structure formation involved in morphogenesis	32 out of 542 genes, 5.9%	187 out of 4647 genes, 4.0%	0.01532817
Wound healing	37 out of 542 genes, 6.8%	223 out of 4647 genes, 4.8%	0.01539577
Negative regulation of molecular function	48 out of 542 genes, 8.9%	304 out of 4647 genes, 6.5%	0.01553021
Regulation of protein metabolic process	83 out of 542 genes, 15.3%	572 out of 4647 genes, 12.3%	0.01577645
Neurogenesis	80 out of 542 genes, 14.8%	549 out of 4647 genes, 11.8%	0.01604504
Chromatin assembly or disassembly	9 out of 542 genes, 1.7%	35 out of 4647 genes, 0.8%	0.01624511
Regulation of protein depolymerization	10 out of 542 genes, 1.8%	41 out of 4647 genes, 0.9%	0.01680368
Cellular response to chemical stimulus	88 out of 542 genes, 16.2%	613 out of 4647 genes, 13.2%	0.01702834
Regulation of acute inflammatory response	5 out of 542 genes, 0.9%	14 out of 4647 genes, 0.3%	0.01727088
Nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	5 out of 542 genes, 0.9%	14 out of 4647 genes, 0.3%	0.01727088
Response to growth factor stimulus	33 out of 542 genes, 6.1%	196 out of 4647 genes, 4.2%	0.01752076
heart contraction	6 out of 542 genes, 1.1%	19 out of 4647 genes, 0.4%	0.01752877
Regulation of cytokine production	14 out of 542 genes, 2.6%	66 out of 4647 genes, 1.4%	0.01790218
Regulation of synaptic plasticity	16 out of 542 genes, 3.0%	79 out of 4647 genes, 1.7%	0.01818531
Negative regulation of cellular process	128 out of 542 genes, 23.6%	934 out of 4647 genes, 20.1%	0.01834186
Cytoskeleton organization	52 out of 542 genes, 9.6%	337 out of 4647 genes, 7.3%	0.0183777
Regulation of I-kappaB kinase/NF-kappaB cascade	12 out of 542 genes, 2.2%	54 out of 4647 genes, 1.2%	0.01928967
Response to vitamin	9 out of 542 genes, 1.7%	36 out of 4647 genes, 0.8%	0.01949432
Liver development	11 out of 542 genes, 2.0%	48 out of 4647 genes, 1.0%	0.01971408
Regulation of protein complex disassembly	11 out of 542 genes, 2.0%	48 out of 4647 genes, 1.0%	0.01971408
Response to oxidative stress	24 out of 542 genes, 4.4%	134 out of 4647 genes, 2.9%	0.0199878
Cellular component organization or biogenesis	209 out of 542 genes, 38.6%	1604 out of 4647 genes, 34.5%	0.02029599
Generation of neurons	74 out of 542 genes, 13.7%	508 out of 4647 genes, 10.9%	0.02051111
Negative regulation of catalytic activity	41 out of 542 genes, 7.6%	257 out of 4647 genes, 5.5%	0.02077279
Positive regulation of cell communication	45 out of 542 genes, 8.3%	287 out of 4647 genes, 6.2%	0.02110003
Negative regulation of intracellular protein kinase cascade	13 out of 542 genes, 2.4%	61 out of 4647 genes, 1.3%	0.02128193
Long-chain fatty acid metabolic process	8 out of 542 genes, 1.5%	31 out of 4647 genes, 0.7%	0.02246559
Actin filament capping	6 out of 542 genes, 1.1%	20 out of 4647 genes, 0.4%	0.02263988
Hepaticobiliary system development	11 out of 542 genes, 2.0%	49 out of 4647 genes, 1.1%	0.02284294
Positive regulation of I-kappa B kinase/NF-kappa B cascade	9 out of 542 genes, 1.7%	37 out of 4647 genes, 0.8%	0.02318898
Regulation of phosphorylation	50 out of 542 genes, 9.2%	327 out of 4647 genes, 7.0%	0.02403522
Regulation of inflammatory response to antigenic stimulus	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Proline metabolic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Mitochondrial fusion	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Negative regulation of platelet-derived growth factor receptor signaling pathway	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Regulation of epithelial to mesenchymal transition	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
L-ascorbic acid metabolic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Optic nerve development	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Dermatan sulfate metabolic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Dermatan sulfate biosynthetic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Negative regulation of phosphoprotein phosphatase activity	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Alpha-linolenic acid metabolic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Dermatan sulfate proteoglycan biosynthetic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Dermatan sulfate proteoglycan metabolic process	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Regulation of transcription from RNA Polymerase II promoter in response to hypoxia	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Cellular response to prostaglandin stimulus	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Regulation of cell aging	3 out of 542 genes, 0.6%	6 out of 4647 genes, 0.1%	0.02407137
Regulation of response to stress	37 out of 542 genes, 6.8%	230 out of 4647 genes, 4.9%	0.02421483
Microtubule-based movement	15 out of 542 genes, 2.8%	75 out of 4647 genes, 1.6%	0.02426477
Response to organic substance	108 out of 542 genes, 19.9%	782 out of 4647 genes, 16.8%	0.0248686
Energy derivation by oxidation of organic compounds	27 out of 542 genes, 5.0%	158 out of 4647 genes, 3.4%	0.02511103
Cellular membrane organization	40 out of 542 genes, 7.4%	253 out of 4647 genes, 5.4%	0.02542181
Ceramide metabolic process	7 out of 542 genes, 1.3%	26 out of 4647 genes, 0.6%	0.02561322
Striated muscle contraction	7 out of 542 genes, 1.3%	26 out of 4647 genes, 0.6%	0.02561322
Cellular response to external stimulus	14 out of 542 genes, 2.6%	69 out of 4647 genes, 1.5%	0.02580298
Regulation of multicellular organismal development	54 out of 542 genes, 10.0%	359 out of 4647 genes, 7.7%	0.02604168
Regulation of cell proliferation	50 out of 542 genes, 9.2%	329 out of 4647 genes, 7.1%	0.02663131
Protein-DNA complex assembly	8 out of 542 genes, 1.5%	32 out of 4647 genes, 0.7%	0.02700014
negative regulation of endopeptidase activity	13 out of 542 genes, 2.4%	63 out of 4647 genes, 1.4%	0.02733386
Transition metal ion transport	9 out of 542 genes, 1.7%	38 out of 4647 genes, 0.8%	0.02735784
Cellular response to reactive oxygen species	9 out of 542 genes, 1.7%	38 out of 4647 genes, 0.8%	0.02735784
Regulation of defense response	21 out of 542 genes, 3.9%	117 out of 4647 genes, 2.5%	0.02776638
Cellular developmental process	120 out of 542 genes, 22.1%	882 out of 4647 genes, 19.0%	0.02777436
Cell differentiation	116 out of 542 genes, 21.4%	850 out of 4647 genes, 18.3%	0.02806555
Heart process	6 out of 542 genes, 1.1%	21 out of 4647 genes, 0.5%	0.02866525
Regulation of action potential in neuron	12 out of 542 genes, 2.2%	57 out of 4647 genes, 1.2%	0.0288109
Cellular cation homeostasis	23 out of 542 genes, 4.2%	132 out of 4647 genes, 2.8%	0.03014329
Positive regulation of signaling	44 out of 542 genes, 8.1%	286 out of 4647 genes, 6.2%	0.03014646
Regulation of hydrolase activity	55 out of 542 genes, 10.1%	370 out of 4647 genes, 8.0%	0.03055034
Sulfur amino acid biosynthetic process	4 out of 542 genes, 0.7%	11 out of 4647 genes, 0.2%	0.03088665
Methionine metabolic process	4 out of 542 genes, 0.7%	11 out of 4647 genes, 0.2%	0.03088665
Phospholipase C-activating G-protein coupled receptor signaling pathway	5 out of 542 genes, 0.9%	16 out of 4647 genes, 0.3%	0.0309643
Single-organism developmental process	152 out of 542 genes, 28.0%	1147 out of 4647 genes, 24.7%	0.03128538
Cell-matrix adhesion	10 out of 542 genes, 1.8%	45 out of 4647 genes, 1.0%	0.03128979
Regulation of cell communication	107 out of 542 genes, 19.7%	781 out of 4647 genes, 16.8%	0.03150774
Protein-DNA complex subunit organization	9 out of 542 genes, 1.7%	39 out of 4647 genes, 0.8%	0.03202774
Regulation of phosphate metabolic process	73 out of 542 genes, 13.5%	511 out of 4647 genes, 11.0%	0.03207599
Regulation of cellular component organization	82 out of 542 genes, 15.1%	582 out of 4647 genes, 12.5%	0.03214955

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Striated muscle cell differentiation	14 out of 542 genes, 2.6%	71 out of 4647 genes, 1.5%	0.0323438
Heterocycle biosynthetic process	50 out of 542 genes, 9.2%	333 out of 4647 genes, 7.2%	0.03248855
Membrane organization	40 out of 542 genes, 7.4%	258 out of 4647 genes, 5.6%	0.03373977
Response to endogenous stimulus	69 out of 542 genes, 12.7%	481 out of 4647 genes, 10.4%	0.03387282
Cellular response to extracellular stimulus	11 out of 542 genes, 2.0%	52 out of 4647 genes, 1.1%	0.034394
Response to hormone stimulus	51 out of 542 genes, 9.4%	342 out of 4647 genes, 7.4%	0.03466675
Regulation of developmental process	67 out of 542 genes, 12.4%	466 out of 4647 genes, 10.0%	0.03477744
Circadian rhythm	6 out of 542 genes, 1.1%	22 out of 4647 genes, 0.5%	0.03565724
Negative regulation of actin filament depolymerization	6 out of 542 genes, 1.1%	22 out of 4647 genes, 0.5%	0.03565724
Microtubule-based transport	10 out of 542 genes, 1.8%	46 out of 4647 genes, 1.0%	0.03597541
Secretion by cell	30 out of 542 genes, 5.5%	185 out of 4647 genes, 4.0%	0.03625253
Nervous system development	107 out of 542 genes, 19.7%	786 out of 4647 genes, 16.9%	0.03705477
Alternative mRNA splicing, via spliceosome	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Acrosome assembly	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Response to dietary excess	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Retinoic acid biosynthetic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Regulation of acute inflammatory response to antigenic stimulus	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
UDP-glucose metabolic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Glutamyl-tRNA aminoacylation	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Prolyl-tRNA aminoacylation	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Ganglioside catabolic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Phospholipase C-activating G-protein coupled glutamate receptor signaling pathway	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Positive regulation vascular endothelial growth factor production	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Positive regulation of cholesterol efflux	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Negative regulation of steroid biosynthetic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Positive regulation of protein processing	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Diterpenoid biosynthetic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Nucleosome positioning	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Axon transport of mitochondrion	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Hemoglobin metabolic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Actin rod assembly	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Positive regulation of sterol transport	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Positive regulation of cholesterol transport	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Positive regulation of interleukin-1 beta production	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
RNA import into mitochondrion	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
rRNA import into mitochondrion	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
cristae formation	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Intermediate filament bundle assembly	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Negative regulation of steroid metabolic process	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Maintenance of mitochondrion location	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Regulation of chromosome segregation	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Bergmann glial cell differentiation	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Angiogenesis involved in wound healing	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Cellular response to ATP	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Regulation of nephron tubule epithelial cell differentiation	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Regulation of epithelial cell differentiation involved in kidney development	2 out of 542 genes, 0.4%	3 out of 4647 genes, 0.1%	0.03758643
Phagocytosis	7 out of 542 genes, 1.3%	28 out of 4647 genes, 0.6%	0.0375907
Cell activation	28 out of 542 genes, 5.2%	171 out of 4647 genes, 3.7%	0.03774238
Placenta development	8 out of 542 genes, 1.5%	34 out of 4647 genes, 0.7%	0.03789329
Response to superoxide	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Positive regulation of acute inflammatory response	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Cytoskeletal anchoring at plasma membrane	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Adenylate cyclase-activating dopamine receptor signaling pathway	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Retrograde axon cargo transport	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Bile acid metabolic process	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Positive regulation of phosphatase activity	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Removal of superoxide radicals	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Circadian sleep/wake cycle	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Positive regulation of oxidoreductase activity	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Elevation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Cellular response to superoxide	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Positive regulation of protein depolymerization	3 out of 542 genes, 0.6%	7 out of 4647 genes, 0.2%	0.03852757
Aminoglycan biosynthetic process	5 out of 542 genes, 0.9%	17 out of 4647 genes, 0.4%	0.03978679
Glycosaminoglycan biosynthetic process	5 out of 542 genes, 0.9%	17 out of 4647 genes, 0.4%	0.03978679
Hydrogen peroxide metabolic process	5 out of 542 genes, 0.9%	17 out of 4647 genes, 0.4%	0.03978679
Response to reactive oxygen species	14 out of 542 genes, 2.6%	73 out of 4647 genes, 1.6%	0.04001333
Regulation of signal transduction	87 out of 542 genes, 16.1%	628 out of 4647 genes, 13.5%	0.0402766
Response to oxygen-containing compound	66 out of 542 genes, 12.2%	462 out of 4647 genes, 9.9%	0.04058524
Reproduction	75 out of 542 genes, 13.8%	533 out of 4647 genes, 11.5%	0.04077277
Cellular response to oxygen-containing compound	39 out of 542 genes, 7.2%	254 out of 4647 genes, 5.5%	0.04081872
Regulation of signaling	106 out of 542 genes, 19.6%	781 out of 4647 genes, 16.8%	0.04083958
Regulation of sequence-specific DNA binding transcription factor activity	15 out of 542 genes, 2.8%	80 out of 4647 genes, 1.7%	0.04099282
Oxidation-reduction process	68 out of 542 genes, 12.5%	478 out of 4647 genes, 10.3%	0.04106747
Cytoskeleton-dependent intracellular transport	10 out of 542 genes, 1.8%	47 out of 4647 genes, 1.0%	0.04112722

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Positive regulation of sequence-specific DNA binding transcription factor activity	10 out of 542 genes, 1.8%	47 out of 4647 genes, 1.0%	0.04112722
Multi-organism process	69 out of 542 genes, 12.7%	486 out of 4647 genes, 10.5%	0.04128617
Multi-multicellular organism process	12 out of 542 genes, 2.2%	60 out of 4647 genes, 1.3%	0.04134205
Muscle system process	16 out of 542 genes, 3.0%	87 out of 4647 genes, 1.9%	0.04165193
Regulation of MAP kinase activity	16 out of 542 genes, 3.0%	87 out of 4647 genes, 1.9%	0.04165193
Macromolecule catabolic process	51 out of 542 genes, 9.4%	346 out of 4647 genes, 7.4%	0.041746
Cellular ion homeostasis	40 out of 542 genes, 7.4%	262 out of 4647 genes, 5.6%	0.04179563
Positive regulation of MAPK cascade	17 out of 542 genes, 3.1%	94 out of 4647 genes, 2.0%	0.04204632
Regulation of cardiac muscle hypertrophy	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Regulation of muscle hypertrophy	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Axon regeneration	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Positive regulation of lipid transport	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Protein localization to synapse	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Regulation of DNA-dependent transcription in response to stress	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Positive regulation of cell division	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Positive regulation of amine transport	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Cardiac muscle contraction	4 out of 542 genes, 0.7%	12 out of 4647 genes, 0.3%	0.04216656
Regulation of protein phosphorylation	46 out of 542 genes, 8.5%	308 out of 4647 genes, 6.6%	0.0425303
Striated muscle cell development	9 out of 542 genes, 1.7%	41 out of 4647 genes, 0.9%	0.04296621
Response to fibroblast growth factor stimulus	13 out of 542 genes, 2.4%	67 out of 4647 genes, 1.4%	0.04306248
Neurological system process	72 out of 542 genes, 13.3%	511 out of 4647 genes, 11.0%	0.04346219
Lymphocyte mediated immunity	6 out of 542 genes, 1.1%	23 out of 4647 genes, 0.5%	0.04365706
Cell fate commitment	6 out of 542 genes, 1.1%	23 out of 4647 genes, 0.5%	0.04365706
Positive regulation of cell proliferation	30 out of 542 genes, 5.5%	188 out of 4647 genes, 4.0%	0.04375279
Sterol metabolic process	8 out of 542 genes, 1.5%	35 out of 4647 genes, 0.8%	0.04430756
Positive regulation of signal transduction	38 out of 542 genes, 7.0%	248 out of 4647 genes, 5.3%	0.04430865
Positive regulation of protein serine/threonine kinase activity	15 out of 542 genes, 2.8%	81 out of 4647 genes, 1.7%	0.04513888
Positive regulation of biological process	154 out of 542 genes, 28.4%	1177 out of 4647 genes, 25.3%	0.0452366
Regulation of phosphorus metabolic process	73 out of 542 genes, 13.5%	520 out of 4647 genes, 11.2%	0.04526348
Cation homeostasis	25 out of 542 genes, 4.6%	152 out of 4647 genes, 3.3%	0.04566864
Negative regulation of hydrolase activity	19 out of 542 genes, 3.5%	109 out of 4647 genes, 2.3%	0.04580592
Rhythmic process	12 out of 542 genes, 2.2%	61 out of 4647 genes, 1.3%	0.04625474
Regulation of response to stimulus	105 out of 542 genes, 19.4%	777 out of 4647 genes, 16.7%	0.04635878
Activation of MAPK activity	10 out of 542 genes, 1.8%	48 out of 4647 genes, 1.0%	0.04676225
Regulation of G-protein coupled receptor protein signaling pathway	10 out of 542 genes, 1.8%	48 out of 4647 genes, 1.0%	0.04676225
Cellular response to oxidative stress	10 out of 542 genes, 1.8%	48 out of 4647 genes, 1.0%	0.04676225
Muscle cell development	10 out of 542 genes, 1.8%	48 out of 4647 genes, 1.0%	0.04676225
Regulation of transmission of nerve impulse	26 out of 542 genes, 4.8%	160 out of 4647 genes, 3.4%	0.04785631
Regulation of kinase activity	37 out of 542 genes, 6.8%	242 out of 4647 genes, 5.2%	0.04809614

Supplementary Table 17 (Continued)

Gene Ontology term	Cluster frequency	Protein frequency of use	P-value
Response to steroid hormone stimulus	25 out of 542 genes, 4.6%	153 out of 4647 genes, 3.3%	0.04884005
Innate immune response	14 out of 542 genes, 2.6%	75 out of 4647 genes, 1.6%	0.04889599
Regulation of transferase activity	38 out of 542 genes, 7.0%	250 out of 4647 genes, 5.4%	0.04919678
Sensory perception of sound	9 out of 542 genes, 1.7%	42 out of 4647 genes, 0.9%	0.04927577
Regulation of inflammatory response	11 out of 542 genes, 2.0%	55 out of 4647 genes, 1.2%	0.04955388
Terpenoid metabolic process	5 out of 542 genes, 0.9%	18 out of 4647 genes, 0.4%	0.04998579
Positive regulation of inflammatory response	5 out of 542 genes, 0.9%	18 out of 4647 genes, 0.4%	0.04998579
Regulation of cell division	5 out of 542 genes, 0.9%	18 out of 4647 genes, 0.4%	0.04998579
Neural precursor cell proliferation	5 out of 542 genes, 0.9%	18 out of 4647 genes, 0.4%	0.04998579

Gene Ontology term was the entry of GO. Cluster frequency was the number and ratio of the differential proteins annotated to the differential proteins of the entry and all GO entries. Protein frequency of use was the number and ratio of all proteins annotated to all proteins of the entry and all entries of GO. P-value was calculated by the hypergeometric test, $P < 0.05$ considered for the statistical significance.