

Supplementary Table 1: Proteins identified in excised gels regions indicated in Figure 1C.

Gel region and proteins identified ¹	Protein entry names ²	Protein MW ³	Protein probability ⁴	# of unique peptides ⁵	# of unique spectra ⁶	# of total spectra ⁷	% sequence coverage ⁸
Gel region 1							
Myosin-9 (Q8VDD5)	MYH9_MOUSE	226,360	100.00%	20	20	23	14.40%
Gel region 2							
Caldesmon 1 (O8VCO8)	QBVCQ8_MOUSE	60,435	100.00%	36	45	54	53.80%
Heterogeneous nuclear ribonucleoprotein M (B8JK30)	B8JK30_MOUSE.HNRP1_MOUSE.Q3THB3_MOUSE.Q3TW40_MOUSE.Q570Z0_MOUSE	73,725	100.00%	32	33	43	47.50%
Heat shock cognate 71 kDa protein (P63017)	HSP7C_MOUSE.Q3TEK2_MOUSE.Q3TH56_MOUSE.Q3TQ13_MOUSE.Q3TJ3_MOUSE.Q3UBA6_MOUSE	70,767	100.00%	25	32	39	38.10%
Signal recognition particle 68 (A2AAN1)	A2AAN1_MOUSE.SRP68_MOUSE	70,559	100.00%	17	18	18	31.40%
Polyadenylate-binding protein 1 (P29341)	PABP1_MOUSE.Q3UBU8_MOUSE.Q8BN32_MOUSE.Q99L36_MOUSE	70,623	100.00%	13	14	15	22.60%
Probable ATP-dependent RNA helicase DDX17 (Q501J6)	DDX17_MOUSE.Q3U741_MOUSE	72,568	100.00%	11	11	11	19.60%
Insulin-like growth factor 2 mRNA-binding protein 3 (Q9CPN8)	IF2B3_MOUSE	63,558	100.00%	7	7	7	15.00%
Actin, cytoplasmic 2 (P63260)	ACTB_MOUSE.ACTG_MOUSE.B2RRX1_MOUSE.Q3TSB7_MOUSE.Q3U5R4_MOUSE.Q3UAF6_MOUSE.Q3UAF7_MOUSE.Q4KL81_MOUSE	41,794	100.00%	7	7	7	22.90%
Coronin, actin binding protein 1B (A2R522)	A2R522_MOUSE.COR1B_MOUSE	53,894	100.00%	6	6	6	12.20%
Ras GTPase-activating protein-binding protein 2 (P97379)	G3BP2_MOUSE.Q3U541_MOUSE.Q3U6B1_MOUSE	61,047	100.00%	5	5	5	9.45%
Gel region 3							
Cytoskeleton-associated protein 4 (B2RRB4)	B2RRB4_MOUSE.CKAP4_MOUSE	63,674	100.00%	24	31	33	42.80%
Calreticulin (B2MWM9)	B2MWM9_MOUSE.CALR_MOUSE.Q3UWP8_MOUSE	47,978	100.00%	17	21	34	45.40%
Coatomer subunit delta (Q5XJY5)	COPD_MOUSE.Q91W48_MOUSE	57,200	100.00%	17	19	20	32.90%
Eukaryotic translation initiation factor 3 subunit L (Q8QZY1)	EIF3L_MOUSE	66,597	100.00%	10	11	11	20.20%
26S proteasome non-ATPase regulatory subunit 3 (P14685)	PSMD3_MOUSE.Q3TP95_MOUSE.Q3ULJ5_MOUSE.Q8BK46_MOUSE	60,702	100.00%	9	9	9	19.10%
Putative uncharacterized protein (Q3THP2)	Q3THP2_MOUSE.Q3TM73_MOUSE.Q3UBR2_MOUSE.Q5SXA8_MOUSE.SYRC_MOUSE	75,676	100.00%	9	9	9	15.20%
Heterogeneous nuclear ribonucleoprotein K (B2M1R6)	B2M1R6_MOUSE.HNRPK_MOUSE.Q3TJ38_MOUSE.Q3TL71_MOUSE.Q3TUA1_MOUSE.Q5FWJ5_MOUSE	50,991	100.00%	9	9	9	25.10%
Chaperonin containing Tcp1, subunit fta (Zeta) (Q3TI05)	Q3TI05_MOUSE.Q3TI62_MOUSE.Q3TI19_MOUSE.Q3TIW97_MOUSE.Q52K69_MOUSE.TCP2_MOUSE	58,060	100.00%	8	8	8	17.70%
Eukaryotic translation initiation factor 3 subunit D (O70194)	EIF3D_MOUSE	63,972	100.00%	8	8	8	15.70%
Protein kinase C and casein kinase substrate in neurons protein 2 (Q9WVE8)	PACN2_MOUSE.Q3TDA7_MOUSE	55,815	100.00%	8	8	8	17.30%
Heterogeneous nuclear ribonucleoprotein Q (Q77MK9)	HNRPQ_MOUSE	69,616	100.00%	7	7	7	13.30%
THUMP domain-containing protein 3 (P97770)	THUM3_MOUSE	56,413	100.00%	7	8	8	15.80%
Putative uncharacterized protein (Q3UKQ2)	Q3UKQ2_MOUSE.Q3UL22_MOUSE.Q6A0F1_MOUSE.Q9WVS5_MOUSE.TCPQ_MOUSE	59,538	100.00%	7	7	7	15.30%
Prolyl 4-hydroxylase subunit alpha-1 (Q60715)	P4HA1_MOUSE.Q3TN84_MOUSE.Q3UF16_MOUSE	60,908	100.00%	7	8	8	16.10%
Ribophorin II (A2AC06)	A2AC06_MOUSE.A2AC57_MOUSE.Q3U505_MOUSE.Q61833_MOUSE.RPN2_MOUSE	67,485	100.00%	6	7	7	15.50%
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform (Q76M23)	A2AA_MOUSE.Q8C2E1_MOUSE	65,306	100.00%	6	6	6	12.60%
Myelin basic protein expression factor 2, repressor (A2ATP5)	A2ATP5_MOUSE.A2ATP6_MOUSE.A7UQY4_MOUSE.MYEF2_MOUSE	59,527	100.00%	6	6	6	11.60%
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 (A1L333)	A1L333_MOUSE.DDX5_MOUSE.Q3V0Z9_MOUSE.Q5UZZ2_MOUSE.Q8BT50_MOUSE	69,304	100.00%	6	6	6	15.00%
Putative uncharacterized protein (Fragment) (Q3TE06)	Q3TE06_MOUSE.Q3TJV2_MOUSE.Q8QZ19_MOUSE.Q9DBN6_MOUSE.Q8Q208_MOUSE.WDR1_MOUSE	66,388	100.00%	6	6	6	11.20%
Poly(U)-binding-splicing factor PUF60 (Q3UEB3)	PUF60_MOUSE	60,231	100.00%	5	5	5	11.30%
Ras GTPase-activating protein-binding protein 2 (P97379)	G3BP2_MOUSE.Q3U541_MOUSE.Q3U6B1_MOUSE	61,047	100.00%	5	6	6	9.64%
Putative adenosylhomocysteinase 2 (Q805W1)	SAHH2_MOUSE	58,934	100.00%	5	5	5	9.43%
Gel region 4							
Actin, cytoplasmic 2 (P63260)	ACTB_MOUSE.ACTG_MOUSE.B2RRX1_MOUSE.Q3TSB7_MOUSE.Q3U5R4_MOUSE.Q3UAF6_MOUSE.Q3UAF7_MOUSE.Q4KL81_MOUSE	41,794	100.00%	8	8	9	33.90%
Gel region 5							
Tropomyosin 1, alpha (Q564G1)	Q564G1_MOUSE	32,692	100.00%	27	37	45	51.40%
Ribosomal protein large, P0 (Q5M8R8)	Q5M8R8_MOUSE.RLA0_MOUSE	34,199	100.00%	12	16	18	50.20%
Ribosomal protein L5 (Q58EUE)	Q3U850_MOUSE.Q58EUE_MOUSE.RL5_MOUSE	34,339	100.00%	12	15	18	37.70%
Mitochondrial ribosomal protein L39 (A6X954)	A6X954_MOUSE.Q8CCX9_MOUSE.RM39_MOUSE	38,592	100.00%	6	6	6	18.20%
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (P62880)	GBB2_MOUSE.Q3U9V4_MOUSE	37,314	100.00%	6	6	6	17.90%

¹ Proteins identified by liquid chromatography-MS/MS analysis of in-gel tryptic digests. UniProtKB accession numbers for identified proteins are given in parenthesis. ² Entry names for the identified proteins from the UniProtKB database. Multiple names are provided for protein entries which, due to sequence homology, contained the same complement of identified peptides. ³ Calculated molecular weight, based on the identified protein's sequence. ⁴ Probability of a correct protein identification calculated by Scaffold software using the method of Nesvizhskii et al. (2003). The probability of correct identification was 100% for all identified proteins due to the conservative requirement of 5 unique peptide matches to each entry. ⁵ The number of unique peptide sequences matched to the given protein entry following interpretation of the MS/MS data. ⁶ The number of unique MS/MS spectra matched to the given protein entry following interpretation of MS/MS spectra. This number is often higher than the number of unique peptides due to the presence of multiple charge sites for each peptide. ⁷ The number of total spectra assigned to the given protein entry. This is often higher than the number of unique MS/MS spectra due to redundant generation of MS/MS spectra for each peptide ion. ⁸ The percentage of the total proteins sequence matched to assigned MS/MS spectra.

Table S1