

Description of Supplemental Data:

Supplementary Tables 1-5 list all of the proteins identified by tandem MS/MS in this project. The tables are organized by function: Table 1 Ribosomal and Ribosomal associated proteins, Table 2 RNA binding proteins, Table 3 Cytoskeletal proteins, Table 4 Novel and Other proteins, Table 5 CCV proteins. In this table the name, GI, molecular weight, number of peptides and the approximate abundance of the protein (Peptides/Mol WT) are given.

Peptidedetails.htm lists the same proteins as in supplemental tables 1-5, but includes all of the details about peptides requested in the guidelines for MCP. This includes masses of each peptide, MASCOT scores, mass error, charge, modifications, missed cleavages, sequence coverage and additional information. The job number each peptide came from is also given. At the end of this file there is a list to match each job number to the band excised from the gel and its approximate molecular weight. Finally, in the list of peptides, the peptide that an MS/MS spectrum is provided for is underlined.

MSMS.pdf is a file including one identifying tandem MS/MS profile for each protein in the supplementary tables. This peptide is underlined in the file peptidedetails.htm and is included as a comment in the PDF file.

TABLE S1

Ribosomal Proteins					
	MW	Peptides	Gi	Band App. MW	Peptide/MW ratio
P0	34	8	228176	36-39	0.24
P2	11	4	57676	14.5-15	0.36
L4	47	13	1363989	47-53	0.28
L5	35	17	13592051	35-36	0.49
L6	33	26	1490384	35-36	0.79
L7	30	13	27660180	31-32	0.43
L7A	30	2	4506661	31-32	0.07
L8	28	4	27685597	33-34	0.14
L9	22	6	133033	28-29	0.27
L10	25	11	2143959	28-29	0.44
L10a	24	3	2143564	30-31	0.13
L11	15	4	71106	19-21	0.27
L12	18	5	34864776	19-21	0.28
L13	24	4	510552	30-31	0.17
L13a	24	4	27545438	28-29	0.17
L14	24	6	2500360	29-30	0.25
L15	24	8	12846287	29-30	0.33
L17	21	6	132805	25-26	0.29
L18	22	8	132733	26-28	0.36
L18a	21	8	47059006	23-25	0.38
L19	23	5	1154899	29-30	0.22
L21	18	5	57686	25-26	0.28
L22	15	2	13938046	14.5-15	0.13
L23	15	2	27689189	14.5-15	0.13
L23A	17	9	404015	19-21	0.53
L24	18	3	11968096	23-25	0.17
L26	17	5	27729769	19-21	0.29
L27	16	9	11968094	15-17	0.56
L27A	16	3	34858914	15-17	0.19
L28	16	2	19353451	15-17	0.13
L30	13	4	28189753	≤14	0.31
L31	14	4	57115	14.5-15	0.29
L32	16	4	71335	15-17	0.25
L35A	12	2	71347	≤14	0.17
L35	14	5	71362	15-17	0.36
L36	12	2	730560	≤14	0.17
SA	33	17	466439	45-47	0.52

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S2	27	17	2920831	33-34	0.63
S3	29	22	70850	33-34	0.76
S3A	30	19	7441114	34-35	0.63
S4	27	13	70870	31-32	0.48
S5	25	5	34854534	26-28	0.20
S6	29	2	54010	33-34	0.07
S7	22	11	49065830	26-28	0.50
S8	22	11	57141	30-31	0.50
S9	22	14	20178311	25-26	0.64
S10	19	7	27669179	19-21	0.37
S11	20	6	13592071	19-21	0.30
S12	15	4	12805235	≤14	0.27
S13	17	8	15029927	15-17	0.47
S14	15	9	7440317	14.5-15	0.60
S15a	15	1	16758882	≤14	0.07
S16	16	5	200796	14.5-15	0.31
S17	17	2	34877956	15-17	0.12
S18	17	6	70965	15-17	0.35
S19	15	3	133857	14.5-15	0.20
S20	14	4	70925	14.5-15	0.29
S23	16	4	543449	≤14	0.25
S24	15	7	71038	≤14	0.47
S25	14	10	71047	≤14	0.71
S26	13	2	27666352	14.5-15	0.15
Translation Factors					
eIF3 subunit 2	36	5	6014677	39-41	0.14
eIF3 subunit 4	35	3	23503073	47-53	0.09
eIF3 subunit 5	37	6	23396621	53-55	0.16
eIF3 subunit 6	52	4	34866211	47-53	0.08
eIF3 subunit 7	65	5	2992164	65-68	0.08
eIF3 subunit 10	167	23	4503509	165-175	0.14
eIF3 subunit 11	25	2	23396620	28-29	0.08
eIF3 subunit 6 interacting protein	67	13	7705433	60-65	0.19
EF1 alpha	50	25	34862972	47-53	0.50
EF1 beta	47	3	5902663	33-35	0.06
EF1 gamma	50	7	51261278	47-53	0.14
EF1 delta	31	4	27662108	39-41	0.13
eEF2	96	6	56082	15-17	0.06
eIF5A	17	4	12847616	36-39	0.24
eIF2A	64	1	15080229	97-100	0.02

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eIF2 alpha	44	2	9506571	65-68	0.05
GCN1	255	5	34872627	200-210	0.02
Ribosomal Chaperones					
Chaperonin TCP1 alpha	61	5	220915	68-70	0.08
Chaperonin TCP1 beta	57	3	6671700	55-60	0.05
Chaperonin TCP1 gamma	61	9	40018616	65-68	0.15
Chaperonin TCP1 delta	58	4	6753322	68-70	0.07
Chaperonin TCP1 epsilon	51	3	603955	68-70	0.06
Chaperonin TCP1 theta	50	3	9988062	68-70	0.06
Chaperonin TCP1 zeta	58	5	5295933	68-70	0.09
NAC alpha	23	4	7513740	36-39	0.17
Other Ribosome-Associated					
Receptor for Activated C Kinase (RACK)	35	10	1083582	33-34	0.29

TABLE S2

a) RNA-binding proteins					
hnRNPs					
	MW	Peptides	Gi	Bands App MW	Peptides/ MW ratio
hnRNP D (Auf 1)	38	14	9588096	45-47	0.42
hnRNP A1	34	12	70819	36-39	0.35
SYNCRIP/hnRNP Q1/Gry-RBP	53	14	6576815	68-70	0.30
hnRNP A/B	38	5	5052976	35-33	0.29
hnRNP A2/B1	35	9	6647752	35-33	0.26
hnRNP K	51	8	16923998	65-68	0.16
hnRNP A0	31	5	12859567	36-39	0.16
hnRNP R	71	11	28212266	84-90	0.13
hnRNP U	89	12	284156	120-125	0.09
hnRNP C	32	3	34869692	41-45	0.09
TAR DNA binding	45	4	26350443	45-47	0.09
hnRNP L	64	7	34855641	60-65	0.08
hnRNP X(E2)	37	6	495128	39-41	0.08
hnRNP H	49	3	26353116	53-55	0.06
hnRNPA3	38	3	34327779	39-41	0.05
hnRNP M	78	4	34862395	70-75	0.04
DEAD Box Helicases					
DEAD box 3	73	16	6753620	80-82	0.23
DEAD box 1/DDX1	83	12	26390412	84-90	0.12
DEAD box 6	55	5	34879288	55-60	0.07
NORP1 (regulator of nonsense)	124	7	11993646	125-140	0.05
DEAD box 5/17	69	5	27690065	65-68	0.04
DEAD box 9	142	4	34880497	140-160	0.03
eIF4A	46	2	34869306	47-53	0.02
DEAD box BAT-1	49	1	19773876	53-55	0.02
Other RNA-binding proteins					
Poly-A Binding Protein	70	15	19705459	70-80	0.21
G3BP1	52	12	1902907	68-70	0.23
Zip-code Binding Protein IMP-1	54	8	61967	68-70	0.15
Zip code Binding protein/IMP-2	54	4	27464838	68-70	0.07
Nucleophosmin	33	7	205786	39-41	0.21
PAI-1 RNA binding	45	6	12836024	55-60	0.13
Activator of dsRNA kinase	35	5	12849779	35-36	0.14
nucleolin	77	7	92559	110-115	0.09
interleukin enhancer binding factor 2	45	3	26346897	45-47	0.07

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interleukin enhancer binding factor 3	98	7	6911241	90-97	0.07
G3BP2	54	4	34876568	65-68	0.07
PTB	75	5	17136071	100-110	0.07
RNA granule protein 105	130	6	2137361	110-115	0.05
CYFIP2	147	5	19526988	125-140	0.03
Y box binding protein 1(mYB-1b)	59	4	9653686	47-53	0.07
Matrin 3	95	2	111944	120-125	0.02
Zip code Binding Protein 2/MART	74	2	19424312	84-90	0.03
Staufen2	62	1	19526444	68-70	0.02
ELAV-like proteins					
ELAV-like 2 (Hu-B)	40	5	6754264	39-41	0.13
ELAV-like 4 (Hu-D)	43	3	2500580	39-41	0.07
ELAV-like 3 (Hu-C)	40	5	27229298	36-39	0.13
ETR-R3b	52	2	3451291	53-55	0.04

TABLE S3

Cytoskeletal					
	MW	Peptides	Gi	Bands App MW	Peptides/ MW ratio
Tubulin-related					
Tubulin (beta) ¹	50	48	2665736	55-60	0.96
Tubulin (alpha) ¹	50	20	71574	55-60	0.40
MAPs					
MAP 1A light chain 3	15	5	1083715	15-17	0.33
MAP-1B	250	74	1083716	≥250	0.30
Doublecortin	40	6	28913279	28-29	0.15
Doublecortin-kinase	85	9	20137987	84-90	0.11
MAP-2	199	13	57620	240-250	0.07
Hook3	84	2	14165274	84-90	0.02
Dynein complex					
Centractin ¹	42	2	256178	45-47	0.05
Dynactin-2	50	2	13435486	53-55	0.04
Dynactin	142	7	1743380	140-160	0.05
Dynein (MAP-1C) ¹	524	26	402528	>250	0.05
Actin-related					
Actin ¹	42	22	71620	45-47	0.52
Marcks	30	9	111322	80-82	0.30
MacMarcks	19	4	13540687	41-45	0.21
Septin	42	5	16924010	45-47	0.12
VAT 1	33	2	26330206	53-55	0.06
Sec 23 hom	87	4	21961650	82-84	0.05
Ezrin/Moesin ¹	60	3	17902245	82-84	0.05
CRUMP-2 (TOAD64) ¹	52	6	599966	65-68	0.12
Spectrin-alpha fodrin	285	5	31543764	210-230	0.02

1. Also identified in adult CCV preparation (Blondeau et al., 2004)

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TABLE S4

Other	MW	Peptides	Gi	Bands App MW	Peptides/ MW ratio
Novel					
CGI-99 (Megagranin)	28	6	27722175	29-30	0.21
FLJ13110	22	2	34855979	23-68	0.09
K1AA014	115	4	1469870	140-160	0.03
similar to SD08037p	58	1	34856672	45-47	0.03
hypothetical protein	75	1	34860217	60-65	0.03
KIAA0982(WD 40 repeat)	52	1	34876297	68-70	0.02
FLJ12890	84	1	13123772	84-90	0.01
Other Proteins					
N-acetyltransferase like	52	8	34856912	97-100	0.15
EBP-1 (proliferation associated p38-2G4)	38	8	51948384	47-53	0.13
PDGF associated phosphoprotein	20	2	1136586	29-30	0.1
progesterone receptor component	25	2	6572674	29-30	0.08
GTP binding (DRG)	40	3	346685	41-45	0.08
Glucose related protein 78 (BiP)	72	5	109893	80-82	0.07
protein disulfide isomerase	48	3	2501206	53-55	0.06
RNASE L inhibitor	68	3	7657518	65-68	0.04
IKAP, IKK Inhibitor	150	3	18266706	140-160	0.02

TABLE S5

Clathrin-Coated Vesicles					
	MW	Peptides	Gi	Bands App MW	Peptides/ MW ratio
Coats					
Clathrin heavy chain	193	92	71564	200-210	0.48
Hsc70	71	14	347019	70-80	0.20
Clathrin light chain A	27	6	71562	35-36	0.22
AP2 beta	105	3	34876358	110-115	0.03
Signaling					
G-alpha o 2	40	10	71907	39-41	0.25
G protein beta 1	38	8	51338711	36-39	0.21
G-alpha i 2	41	3	204440	39-41	0.07
Integral Plasma Membrane					
Reticulon 3	25	4	17066677	28-29	0.16
NCAM ¹	180	28	72067	230-240	0.16
Reticulon 1 ¹	30	6	456550	23-25	0.20
Na/K ATPase alpha 3	113	10	29839750	100-109	0.09
Na/K ATPase beta	36	4	6978549	47-53	0.11
NOGO A receptor ¹	126	5	13929188	175-180	0.04
thioredoxin containing ¹	28	2	34865352	31-32	0.07
Adaptors					
FK506 Binding protein 3	24	8	27664664	31-32	0.33
Cyclophilin A	18	3	68405	14.5-15	0.17
14-3-3 (undefined subtype)	30	3	477448	31-32	0.10
Cyclophilin B	23	2	11968126	19-21	0.09
14-3-3 zeta	28	1	13487931	31-32	0.04
Synaptic Vesicle					
Munc-18 (Nsec-1)	58	10	1944322	68-70	0.17
syntaxin 7	30	2	3152727	39-41	0.07
NSF	84	4	13489067	80-82	0.05
SCAMP	38	2	487057	35-36	0.05
Metabolic Enzymes					
Glyceraldehyde-3-phosphate dehydrogenase	36	7	56188	36-39	0.19
Aldolase A	40	3	6978487	39-41	0.08
Phosphofructokinase	85	6	400095	80-82	0.07
Trafficking					

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Rab 14	24	4	420272	29-30	0.17
Rab 2	23	5	10946940	25-26	0.22
Rab 5-C	23	3	27689505	29-30	0.13
Rab 11B	24	3	14249144	29-30	0.13
Rab 10	23	1	420269	29-30	0.04
Rab 7	23	4	92022	29-30	0.17
VSP35	87	2	1354050	82-84	0.02

1. These proteins were not found in adult CCVs, but they are integral membrane proteins that are likely to be cargo of E18 CCVs.