

Table S8. Functional annotation analysis of the identified EBS protein constituents.

Cluster No.	GO term	No. of proteins	Official gene symbol
1	GO:0,000,166 Nucleotide binding	157	AARS1, ABCB10, ABCE1, ACSS1A, ACTBL2, ACTC1, ACTG1, ACTL6A, ACTR1A, ACTR2, ACTR3, ACLY, ADSS1, AK2, ALYREF, APAF1, ATP1A1, ATP5B, ATP6V1A, CAT, CCT2, CCT3, CCT4, CCT5, CCT6A, CCT7, CCT8, CKB, CMPK1, CPSF6, CTBP1, DARS, DAZAP1, DDX1, DDX3X, DDX6, DDX17, DDX19, DHX15, EEF1A1, EEF2, EFL1, EIF2S3, EIF4A2, EIF4A3, EIF4H, EIF5B, ELAVL1, EPRS, FARSB, FKBP4, FUS, G3BP1, GAPDH, GART, GNAL, GNA14, GPD1L, GSS, HK2, HAO2, HNRNPA1, HNRNPA2B1, HNRNPAB, HNRNPD, HNRNPDL, HNRNPH1, HNRNPH3, HNRNPM, HNRNPUL2, HSP90AA1, HSPA2, HSPA4L, HSPA5, HSPA8, HSPA9, HSPD1, HSPE1, IDH1, IDH2, KARS, LOC420368, MAST2, MOV10, MTHFD1, MYH1F, MYH9, MYH10, NACA, NCL, NME2, NONO, OLA1, PABPC1, PAICS, PGD, PKLR, PGK2, PFKP, PSMC1, PSMC2, PSMC3, PSMC6, PTBP1, PUF60, QARS, RAB1B, RAP1B, RAB8B, RAB9A, RAB11B, RAB14, RAB2A, RAB5C, RAB21, RAC1, RALY, RAN, RBM3, RARS, RAP1A, RBM12, RMB24, RBMXL1, RUVBL1, SARS1, SFPQ, SMC1A, SMC2, SMC3, SMC4, SNRNP200, SRSF1, SRSF2, SRSF3, SRSF6, SSB, STK26, TARS, TCP1, TOP2B, TUFM, TRA2A, TRA2B, TTN, TUBA1A, TUBA3E, TUBA8B, TUBB, TUBB1, TUBB4B, UBA3, UBE2I, UGDH, VCP, VRK1, YARS
2	GO:0,006,508 Proteolysis	45	APEH, BLMH, C3, CAPN1, CASP3, CNDP2, DDB1, DDI2, DNPEP, LTA4H, MYH9, NPEPL1, NPEPPS, PCNP, PLG, PM20D1, PREP, PSMA1, PSMA2, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB1, PSMB2, PSMB4, PSMB5, PSMB7, PSMC2, RAD23B, TPP2, UBE2H, UBE2I, UBE2L3, UBE2N, UBE2V2, UCHL3, UCHL5, UFD1L, UFSP2, USP7, USP9Y, USP47, XPNPEP1
3	GO:0,009,057 Macromolecule catabolic process	39	APOB, CASP3, DDB1, EIF3E, EIF4A3, FEN1, LYG2, MYH9, PCNP, PSMA1, PSMA2, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB1, PSMB2, PSMB4, PSMB5, PSMB7, PSMC1, PSMC2, PSMC3, PSMC6, RAD23B, SOD1, UBE2H, UBE2I, UBE2L3, UBE2N, UBE2V2, UCHL3, UCHL5, UFD1L, UFSP2, USP7, USP9Y, USP47
4	GO:0,008,104 Protein localization	33	ACTN4, APOB, ARCN1, BID, CLTC, COPA, COPB1, ERP29, GDI1, HSPA9, LIN7C, MYH9, NPM1, PLEK, RAB2A, RAB5C, RAB8B, RAB9A, RAB11B, RAB14, RAB21, RAN, RDX, SCAMP2, SNX2, SEC22B, TLN1, XPO7, YWHAB, YWHAE, YWHAG, YWHAQ, YWHAZ
5	GO:0,065,003 Macromolecular complex assembly	31	APOA4, ALDOB, ARPC4, CAT, FGA, FGB, FGG, FKBP4, GSN, H1F0, H2AZ2, HIST1H111L, HIST1H111R, HIST1H2A4, HIST1H2B7, HIST1H2B8, HIST2H4B, HP1BP3, LOC769852, MYH10, NAP1L4, NPM1, SET, SOD2, TUBA1A, TUBA3E, TUBA8B, TUBB, TUBB1, TUBB4B, XPO7
6	GO:0,006,091 Generation of precursor metabolites and energy	30	ACO1, ATP5B, ATP5A1W, ATP6V1A, ATP6V1B2, ATP6V1H, ALDOB, ALDOC, BPGM, CAT, CYB5A, ENO1, GAPDH, GLRX, GOT1, GPI, HK2, LDHA, LDHB, MDH1, MDH2, OGDH, PDHA2, PFKP, PGK2, PKLR, PPP1CB, SOD2, TPI1, TXN
7	GO:0,070,011 Peptidase activity, acting on L-amino acid peptides	30	APEH, BLMH, CAPN1, CASP3, CNDP2, COPS5, DDI2, DNPEP, LTA4H, NPEPL1, NPEPPS, PLG, PM20D1, PREP, PSMA1, PSMA2, PSMA3, PSMA4, PSMA5, PSMA6, PSMA7, PSMB1, PSMB2, PSMB4, PSMB5, PSMB7, TPP2, UFSP2, USP7, XPNPEP1
8	GO:0,005,525 GTP binding	30	ADSS1, EEF1A1, EEF2, EFL1, EIF5B, EIF2S3, FKBP4, GNA14, GNAL, LOC420368, OLA1, RAB11B, RAB1B, RAB2A, RAB5C, RAB8B, RAB9A, RAB14, RAB21, RAC1, RAN, RAP1A, RAP1B, TUBA1A, TUBA3E, TUBA8B, TUBB, TUBB1, TUBB4B, TUFM
9	GO:0,042,592 Homeostatic process	30	ACO1, ADD1, APOA4, APOB, BCL2L1, CASP3, GCLM, GLRX, GLRX3, GOT1, FTH1, HBZ, NPM1, P4HB, PARK7, PDIA3, PDIA4, PDIA6, PLG, PRDX1, PRDX6, RHAG, RPA1, RBP4A, SOD1, SOD2,

			<i>TCEA1, TF, TMX4, TXN</i>
10	GO:0,044,271 Nitrogen compound biosynthetic process	28	<i>ADA, ADAL, ADK, ADSL, ADSS1, AMPD3, ATIC, ATP5B, ATP1A1, ATP5A1W, ATP6V1A, ATP6V1B2, ATP6V1H, CBSL, CMPK1, CPOX, FECH, GART, GOT1, GOT2, HMBS, NME2, PAICS, PRPS1L1, PRPSAP2, TMLHE, UMPS, UROD</i>
11	GO:0,051,276 Chromosome organization	25	<i>BRE, BUB3, H1FO, H2AZ2, HIST1H111L, HIST1H111R, HIST1H2A4, HIST1H2B7, HIST1H2B8, HIST2H4B, HP1BP3, LOC769852, NCAPD2, NAP1L4, NPM1, PDS5B, RPA1, RBBP4, RUVBL1, SET, SMC1A, SMC2, SMC3, SMC4, UBE2N</i>
12	GO:0,016,052 Carbohydrate catabolic process	23	<i>AKR1A1, ALDOB, ALDOC, BPGM, ENO1, GAPDH, GPD1L, GPI, HK2, LDHA, LDHB, LYG2, MDH1, MDH2, OGDH, PDHA2, PFKP, PGD, PGK2, PGLS, PKLR, TALDO1, TPI1</i>
13	GO:0,005,996 Monosaccharide metabolic process	23	<i>AKR1A1, BPGM, ALDOB, ALDOC, ENO1, GAPDH, GPI, HK2, LDHA, LDHB, MDH1, MDH2, OGDH, PDHA2, PFKP, PGD, PGLS, PGK2, PKLR, RBP4A, TPI1, PPP1CB, TALDO1</i>
14	GO:0,046,907 Intracellular transport	23	<i>ACTBL2, ACTC1, ARCN1, BCL2L1, BID, CLTC, COPA, COPB1, HSPA9, MYH9, NPM1, NUP133, NUP155, BAFAH1B1, RAN, RANBP1, SNX2, XPO7, YWHAB, YWHAE, YWHAG, YWHAQ, YWHAZ</i>
15	GO:0,042,981 Regulation of apoptosis	23	<i>AARS1, ADA, ALB, API5, APAF1, BCL2L1, BID, CAT, CIAPIN1, EEF1A1, FADD, HSPA5, CASP3, GAPDH, GCLM, HSPD1, NME2, PDIA3, PGP, PLG, RPS3, SOD1, SOD2</i>
16	GO:0,016,887 ATPase activity	23	<i>ACTBL2, ABCB10, ABCE1, ACTC1, ATP1A1, ATP5A1W, ATP5B, ATP6V1A, ATP6V1B2, ATP6V1H, DDX1, DDX3X, DDX6, DDX17, DDX19, DHX15, EIF4A2, EIF4A3, HSPA8, MYH9, PSMC2, RBBP4, SNRNP200</i>
17	GO:0,042,802 Identical protein binding	21	<i>ACTG1, ADH4, ALDOB, APOA4, ARHGDI, BCL2L1, CAT, ELAVL1, FBP1, GPD1L, HSP90AA1, MYH9, NFS1, NONO, NPM1, PAFAH1B1, PLEK, PSMA7, TPD52, TRA2A, VAPB</i>
18	GO:0,006,396 RNA processing	20	<i>AARS1, CPSF6, CSTF3, EIFA3, HNRNPCL, MAGOH, MOV10, PRPF19, PTBP1, RPL10A, SF3A1, SNRNP200, SNRPE, SRSF1, SRSF2, SSB, STRAP, TRA2A, WBP4, YBX1</i>
19	GO:0,007,010 Cytoskeleton organization	20	<i>ACTBL2, ACTC1, ACTG1, ARPC4, CAPZA1, CAPZB, EPB41, GSN, KRT24, MYH9, MYH10, NPM1, PLEK, RAC1, BAFAH1B1, RANBP1, SMC3, SOD1, TLN1, TUBB1</i>
20	GO:0,033,554 Cellular response to stress	20	<i>AARS1, ALB, APOA4, BRE, CASP3, CAT, EIF2S1, DDB1, FEN1, HMGB2, HSPA5, PRPF19, RAD23B, RPA1, RPS3, SOD1, SOD2, UBE2N, UBE2V2, VAPB</i>
21	GO:0,016,071 mRNA metabolic process	18	<i>CPSF6, CSTF3, EIF3E, EIFA3, ELAVL1, HNRNPD, HNRNPCL, MAGOH, MOV10, PRPF19, PTBP1, SNRPE, SRSF1, SRSF2, STRAP, TRA2A, WBP4, YBX1</i>
22	GO:0,042,623 ATPase activity, coupled	18	<i>ABCB10, ATP1A1, ATP5A1W, ATP5B, ATP6V1A, ATP6V1B2, ATP6V1H, DDX1, DDX3X, DDX6, DDX17, DDX19, DHX15, EIF4A2, EIF4A3, HSPA8, RBBP4, SNRNP200</i>
23	GO:0,009,259 Ribonucleotide metabolic process	18	<i>ADA, ADAL, ADSL, AMPD3, ATIC, ATP5B, ATP1A1, ATP5A1W, ATP6V1A, ATP6V1B2, ATP6V1H, ENTPD1, GART, NME2, OLA1, PAICS, PRPS1L1, UMPS</i>
24	GO:0,006,163 Purine nucleotide metabolic process	18	<i>ADA, ADAL, ADK, ADSL, ADSS1, AMPD3, ATIC, ATP5B, ATP1A1, ATP5A1W, ATP6V1A, ATP6V1B2, ATP6V1H, ENTPD1, GART, NME2, OLA1, PAICS</i>
25	GO:0,008,135 Translation factor activity, nucleic acid binding	16	<i>EEF1A1, EEF1B2, EEF2, EIF1AX, EIF2S1, EIF2S2, EIF2S3, EIF3D, EIF3E, EIF3J, EIF3M, EIF4A2, EIF4E, EIF5, TCEA1, TUFM</i>

26	GO:0,003,924	GTPase activity	16	<i>EEF1A1, EEF2, EFL1, EIF5B, EIF2S3, RAC1, RAN, RAP1A, RAP1B, TUBA1A, TUBA3E, TUBA8B, TUBB, TUBB1, TUBB4B, TUFM</i>
27	GO:0,009,260	Ribonucleotide biosynthetic process	16	<i>ADA, ADAL, ADSL, AMPD3, ATIC, ATP1A1, ATP5A1W, ATP5B, ATP6V1A, ATP6V1B2, ATP6V1H, GART, NME2, PAICS, PRPS1L1, UMPS</i>
28	GO:0,016,879	Ligase activity, forming carbon-nitrogen bonds	16	<i>ADSS1, GART, GCLC, GCLM, GSS, MTHFD1, PAICS, PRPF19, UBA3, UBE2H, UBE2I, UBE2L3, UBE2N, UBE2V2, UBE2O, UBR4</i>
29	GO:0,033,043	Regulation of organelle organization	14	<i>ACTR3, ARPC1A, ARPC5, CAPZA1, CAPZB, DSTN, GSN, MAPRE1, NPM1, PLEK, RDX, RANBP1, SPTAN1, UBE2N</i>
30	GO:0,022,402	Cell cycle process	14	<i>BUB3, MARRE1, MYH10, NCAPD2, NPM1, PAFAH1B1, PDS5B, RANBP1, RPA1, SMC2, SMC3, SMC4, TUBB1, UBE2I</i>
31	GO:0,004,857	Enzyme inhibitor activity	14	<i>A2ML2, AGT, AMBP, ANP32E, C3, CASP3, CAST, FETUB, HSPA5, ITIH2, KNG1, OVAL, SERPINC1, SERPIND1</i>
32	GO:0,006,732	Coenzyme metabolic process	13	<i>ACO1, ALDOB, GCLC, GCLM, GSS, MDH1, MTHFD1, PGD, PGLS, SOD1, SOD2, TALDO1, TPI1</i>
33	GO:0,009,611	Response to wounding	13	<i>C3, CASP3, ENTPD1, F13A1, FGA, FGB, FGG, FN1, PLEK, PLG, MYH10, SOD1, SOD2</i>
34	GO:0,032,535	Regulation of cellular component size	12	<i>ACTR3, ARPC1A, ARPC5, CAPZA1, CAPZB, DSTN, ENO1, GSN, NPM1, PLEK, RDX, SPTAN1</i>
35	GO:0,001,701	In utero embryonic development	12	<i>ADA, ADD1, APOB, BCL2L1, GABPA, MYH10, PITPNB, PRPF19, PSMC3, RPA1, SRSF1, YBX1</i>
36	GO:0,051,258	Protein polymerization	11	<i>ARPC4, FGA, FGB, FGG, GSN, TUBA1A, TUBA5, TUBA8B, TUBB, TUBB1, TUBB4B</i>
37	GO:0,051,301	Cell division	11	<i>DSTN, MARRE1, MYH9, MYH10, PAFAH1B1, PDS5B, PPP1CB, RBP4A, SMC2, TOP1, UBE2I</i>
38	GO:0,006,418	tRNA aminoacylation for protein translation	10	<i>AARS1, DARS, EPRS, FARSB, KARS, PARS, QARS, SARS1, TARS, YARS</i>
39	GO:0,006,979	Response to oxidative stress	9	<i>APOA4, CAT, GCLM, GPX3, GPX4, PARK7, PRDX6, SOD1, SOD2</i>
40	GO:0,070,647	Protein modification by small protein conjugation or removal	9	<i>COPS5, PCNP, PRPF19, RPS27A, UBA3, UBE2H, UBE2N, UBI, USP7</i>
41	GO:0,016,209	Antioxidant activity	8	<i>APOA4, CAT, GPX3, GPX4, PRDX1, PRDX6, SOD1, SOD2</i>
42	GO:0,051,188	Cofactor biosynthetic process	8	<i>CPOX, FECH, GCLC, GCLM, GSS, MTHFD1, NFS1, UROD</i>
43	GO:0,015,669	Gas transport	8	<i>CA2, HBA1, HBAD, HBBA, HBBR, HBE1, HBZ, RHAG</i>
44	GO:0,016,860	Intramolecular oxidoreductase activity	7	<i>GPI, HPGDS, NACA, P4HB, PDIA3, PDIA4, TPI1</i>

45	GO:0,010,035 Response to inorganic substance	7	<i>APOA4, CAT, FGA, FGB, PARK7, SOD1, SOD2</i>
46	GO:0,016,051 Carbohydrate biosynthetic process	7	<i>GAPDH, GPI, GOT1, NANS, PGD, RBP4A, TPI1</i>
47	GO:0,019,748 Secondary metabolic process	7	<i>ADH4, ALDOB, PGD, PGLS, RBP4A, TALDO1, TPI1</i>
48	GO:0,006,790 Sulfur metabolic process	7	<i>CBSL, GCLC, GCLM, GSS, NFS1, SOD1, SOD2</i>
49	GO:0,019,825 Oxygen binding	7	<i>ALB, HBA1, HBAD, HBBA, HBBR, HBE1, HBZ</i>
50	GO:0,050,657 Nucleic acid transport	6	<i>EIF4A3, HNRNPA2B1, KHSRP, MAGOH, NPM1, NUP133</i>
51	GO:0,018,130 Heterocycle biosynthetic process	6	<i>ADA, ADK, CPOX, FECH, HMBS, UROD</i>
52	GO:0,010,927 Cellular component assembly involved in morphogenesis	6	<i>ACTBL2, ACTC1, ACTG1, KRT24, MYH10, PAFAH1B1</i>
53	GO:0,016,125 Sterol metabolic process	6	<i>APOA1, APOA4, APOB, CAT, FDPS, LCAT</i>
54	GO:0,033,013 Tetrapyrrole metabolic process	5	<i>BLVRA, CPOX, FECH, HMBS, UROD</i>
55	GO:0,046,961 Proton-transporting ATPase activity, rotational mechanism	5	<i>ATP5B, ATP5A1W, ATP6V1A, ATPV1B2, ATP6V1H</i>
56	GO:0,043,498 Cell surface binding	4	<i>APOA4, FGA, FGB, HSPD1</i>
57	GO:0,030,261 Chromosome condensation	4	<i>H1FO, NCAPD2, SMC2, SMC4</i>
58	GO:0,046,890 Regulation of lipid biosynthetic process	4	<i>APOA4, APOB, ATP1A1, SOD1</i>
59	GO:0,008,637 Apoptotic mitochondrial changes	4	<i>BCL2L1, BID, CASP3, SOD2</i>
