

Table S6. Functional annotation analysis of the identified CAM protein constituents common to ED12 and ED19, and absent from EBS.

Cluster No.	GO term	No. of proteins	Official gene symbol
1	GO:0,000,166 Nucleotide binding	102	ACAD9, ACADL, ACTA2, AK1, AKT1, ARL8B, ASNS, ARF6, ATL1, ATP2A2, CAMK2D, CARS, CDC42, CDK5, CHTF18, CSK, CSNK2A1, DES, DLD, DNM1L, DYNC1H1, DYNC1LI1, EFTUD2, EHD3, ETFA, FMO3, GALK2, GARS, GLUD2, GMPS, GNA11, GNAI2, GNAI3, GNAS, GRPEL1, GSK3A, GSR, HARS, HIBADH, HK1, HRAS, HSP90AB1, HSP90B1, HYOU1, IARS2, IDH3A, IGF2BP1, IGF2BP3, ILF2, ILK, LONP1, MAPK3, MAPK14, MATR3, MCM6, MYLK, MYH11, MYO1B, MYO1C, MYO6, NARS, NDUFA10, NDUFV1, NDUFV2, NT5C1B, NT5C2, PC, POLQ, POR, PSMC5, RRAGA, PRKAR1A, PYGL, RAB5A, RAB6A, RAB10, RAB18, RAB22A, RAB32, RBM25, RHOA, RHOG, RRAS, SAR1A, SDHA, SEPHS1, SEPT2L, SEPT6, SEPT7, SEPTIN8, SEPTIN9, SEPTIN11, SIRT2, SIRT5, SRC, SUCLA2, SYNCRIP, TUBB2A, TUBB2B, UBA2, UBA7, VPS4B
2	GO:0,005,198 Structural molecule activity	41	ANXA1, ASL2, CLDN1, CLTB, COL1A1, COL1A2, COL3A1, COL4A1, COL4A2, COL11A1, COL12A1, COL18A1, COPG1, DES, KRT7, KRT14, LAMA1, LAMC1, MYH11, RPL3, RPL4, RPL6, RPL13, RPL14, RPL15, RPL17, RPL18A, RPL21, RPL26L1, RPL31, RPL36, RPS6, RPS11, RPS12, RPS14, RPS15A, RPS17, TUBB2A, TUBB2B, VAPA, VMO1
3	GO:0,008,104 Protein localization	32	AKAP12, AKT1, AP1M1, AP2A2, AP2M1, ARF6, CAV1, CDC42, CHMP6, CLTB, COPG1, CTNNB1, GRPEL1, HSPG2, KPNA4, MYO6, PCNA, RAB5A, RAB6A, RAB10, RAB18, RAB22A, RAB32, RRBP1, SAR1A, SEC61A1, STXBP1, VAMP7, VPS29, USO1, XPO1, YWHAH
4	GO:0,007,242 Intracellular signaling cascade	29	AKT1, ARF6, ARL8B, CAV1, CDC42, COL1A2, CSK, GNA11, GNAI2, GNAS, GNB1, HACD3, HRAS, MAPK3, MAPK14, MYO6, RRAS, RAB5A, RAB6A, RAB10, RAB18, RAB22A, RAB32, RPS6, RHOA, RHOG, STMN1, STAT3, YWHAH
5	GO:0,016,192 Vesicle-mediated transport	26	AP1M1, AP2A2, AP2M1, ARF6, CLTB, COLEC12, COPG1, CTNNB1, GARS, HRAS, ITGAV, MYH11, MYO6, RAB5A, RAB6A, RAB22A, RER1, SAR1A, SCFD1, SH3GL1, STXBP1, TMED10, TRAPPC3, USO1, VAMP7, VPS4B
6	GO:0,006,412 Translation	24	CARS, EIF1AD, GARS, HARS, IARS2, NARS, RPL3, RPL4, RPL6, RPL13, RPL14, RPL15, RPL17, RPL18A, RPL21, RPL26L1, RPL31, RPL36, RPS6, RPS11, RPS12, RPS15A, RPS17, RPS14
7	GO:0,006,091 Generation of precursor metabolites and energy	24	ACO2, AKT1, ATP5C1, ATP5PB, ATP5O, ATP6V1E1, CYCS, DLD, DLST, ETFDH, FH, GNAS, GNPDA1, HK1, IDH3A, NDUFA7, NDUFB8, NDUFS1, NDUFS4, PGAM1, PYGL, SDHA, SLC25A13, UQCRCF1
8	GO:0,046,907 Intracellular transport	22	AKAP12, AKT1, AP1M1, AP2A2, AP2M1, CLTB, COPG1, GRPEL1, KPNA4, MYO6, PCNA, RER1, SAR1A, SLC25A13, TMED10, TRAPPC3, UCHL1, USO1, VAMP7, VPS4B, XPO1, YWHAH
9	GO:0,003,735 Structural constituent of ribosome	18	RPL3, RPL4, RPL6, RPL13, RPL14, RPL15, RPL17, RPL18A, RPL21, RPL26L1, RPL31, RPL36, RPS6, RPS11, RPS12, RPS14, RPS15A, RPS17
10	GO:0,042,802 Identical protein binding	18	AKT1, ALDH1A3, CLDN1, COL1A2, GRPEL1, HDAC1, HINT2, HPRT1, HSPB1, ITGB3, LCP1, MCM6, MYO6, NRP1, PRRC1, OSTF1, S100A11, SNX32
11	GO:0,007,010 Cytoskeleton organization	15	ARF6, CAPZA2, CDC42, CNN1, CNN2, CTNNB1, EZR, HRAS, ITGB1, KRT14, LCP1, MYH11, PFN2, RHOA, THY1

12	GO:0,032,989 Cellular component morphogenesis	15	<i>CDC42, CNP, CTNNB1, EZR, HPRT1, ILK, ITGB1, LAMA1, LAMC1, MAPK14, MYH11, NRP1, RHOA, STMN1, UCHL1</i>
13	GO:0,004,857 Enzyme inhibitor activity	14	<i>A2ML1, ANXA1, ANXA2, COL6A3, CST3, CSTB, OVALX, OVALY, OVST, RNH1, SERPINH1, SERPINB6, SPINK5, SPINK7</i>
14	GO:0,030,029 Actin filament-based process	13	<i>ARF6, CDC42, CNN1, CNN2, CAPZA2, EZR, HRAS, ITGB1, LCP1, MYH11, MYO6, PFN2, RHOA</i>
15	GO:0,005,996 Monosaccharide metabolic process	13	<i>AKT1, FUCA2, GALE, GALK2, GNPDA1, HIBADH, HK1, MAPK14, PC, PGAM1, PGM1, PMM2, PYGL</i>
16	GO:0,001,944 Vasculature development	13	<i>AKT1, ANXA2, CAV1, COL1A2, CTNNB1, ITGAV, MAPK14, MMP2, NRP1, POFUT1, QKI, RTN4, THY1</i>
17	GO:0,033,043 Regulation of organelle organization	11	<i>ARF6, ARPC1B, ARPC2, CAPZA2, CDC42, CTNNB1, HSPB1, MAP4, RHOA, STMN1, XPO1</i>
18	GO:0,030,030 Cell projection organization	11	<i>ARF6, CDC42, CNP, HPRT1, ITGA6, ITGA8, MYH11, MYO6, NRP1, STMN1, UCHL1</i>
19	GO:0,046,034 ATP metabolic process	10	<i>AK1, ATP1B1, ATP1B3, ATP2A2, ATP5C1, ATP5O, ATP5PB, ATP6V1E1, NDUFS1, VPS4B</i>
20	GO:0,016,044 Membrane organization	10	<i>COLEC12, ITGAV, HRAS, MYH11, MYO6, RAB5A, RAB22A, SH3GL1, USO1, VAMP7</i>
21	GO:0,051,186 Cofactor metabolic process	10	<i>ACO2, BAAT, COQ4, DBT, DLST, FH, HIBADH, HMOX2, IDH3A, SDHA</i>
22	GO:0,051,129 Negative regulation of cellular component organization	10	<i>CAPZA2, CDC42, CLU, HSPB1, MAP4, NRP1, RTN4, STMN1, THY1, YWHAH</i>
23	GO:0,045,596 Negative regulation of cell differentiation	10	<i>CAV1, CTNNB1, ITGAV, ITGB1, ITGB3, MAPK3, NRP1, RTN4, THY1, YWHAH</i>
24	GO:0,016,651 Oxidoreductase activity, acting on NADH or NADPH	9	<i>DLD, NDUFA7, NDUFA12, NDUFB8, NDUFS1, NDUFS3, NDUFS4, NDUFS8, NDUFV1</i>
25	GO:0,044,087 Regulation of cellular component biogenesis	9	<i>ARF6, ARPC1B, ARPC2, CAPZA2, CDC42, CLU, HSPB1, RHOA, STMN1</i>
26	GO:0,031,589 Cell-substrate adhesion	8	<i>CTNNB1, ITGA6, ITGB1, ITGB3, LAMC1, NID1, RHOA, THY1</i>
27	GO:0,006,631 Fatty acid metabolic process	7	<i>ETFDH, FASN, HADH, HADHA, MAPK14, QKI, RNPEP</i>
28	GO:0,008,238 Exopeptidase activity	7	<i>CTSA, ERAP1, LAP3, METAP2, PEPD, RNPEP, SCPEP1</i>
29	GO:0,051,539 4 iron, 4 sulfur cluster binding	5	<i>ACO2, ETFDH, NDUFS1, NDUFS8, NDUFV1</i>
30	GO:0,042,773 ATP synthesis coupled electron transport	4	<i>DLD, NDUFA7, NDUFB8, NDUFS1</i>
31	GO:0,034,330 Cell junction organization	4	<i>CDC42, ITGB3, LAMC1, THY1</i>

32	GO:0,016,620 Oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	4	<i>ALDH1A3, ALDH3A2, ALDH3B2, ALDH5A1</i>
33	GO:0,032,369 Negative regulation of lipid transport	3	<i>AKT1, ITGB3, ITGAV</i>
