

Caveolin-1 Y14 phosphorylation suppresses tumor growth while promoting invasion

SUPPLEMENTARY MATERIALS

Supplementary Table 1: The Cav1-dependent MDA-MB-435 pseudopod proteome

Description	435 overexpressing Cav PS vs 435 WT Cav PS		
	Ratio	StDev	# peptides
empAI:0.17 Tax_Id=9606 Gene_Symbol=TCP1 T-complex protein 1 subunit alpha	13.256	10.83	3
empAI:0.57 Tax_Id=9606 Gene_Symbol=SFN Isoform 1 of 14-3-3 protein sigma	12.776	8.56	2
empAI:0.46 Tax_Id=9606 Gene_Symbol=HSP90AA1 Isoform 1 of Heat shock protein HSP 90-alpha	12.066	5.17	2
empAI:0.36 Tax_Id=9606 Gene_Symbol=PARK7 Protein DJ-1	9.797	7.79	9
empAI:0.88 Tax_Id=9606 Gene_Symbol=EEF1A1 Elongation factor 1-alpha	8.277	8.9	2
empAI:0.46 Tax_Id=9606 Gene_Symbol=SOD1 Superoxide dismutase [Cu-Zn]	8.219	6.22	6
empAI:0.13 Tax_Id=9606 Gene_Symbol=ASS1 Argininosuccinate synthase	8.074	1.39	2
empAI:0.41 Tax_Id=9606 Gene_Symbol=HSP90AB1 Heat shock protein HSP 90-beta	7.81	1.21	2
empAI:0.41 Tax_Id=9606 Gene_Symbol=LDHA Isoform 1 of L-lactate dehydrogenase A chain	6.117	6.62	2
empAI:0.13 Tax_Id=9606 Gene_Symbol=LGALS3 Galectin-3	5.295	3.65	2
empAI:0.98 Tax_Id=9606 Gene_Symbol=ACTB Actin, cytoplasmic 1	4.541	0.47	2
empAI:0.17 Tax_Id=9606 Gene_Symbol=ALDOA Fructose-bisphosphate aldolase A	4.482	7.71	6
empAI:0.55 Tax_Id=9606 Gene_Symbol=PKM2 Isoform M2 of Pyruvate kinase isozymes M1/M2	4.455	5.08	8
empAI:0.20 Tax_Id=9606 Gene_Symbol=HSPA8 Isoform 1 of Heat shock cognate 71 kDa protein	4.361	3.73	6
empAI:1.20 Tax_Id=9606 Gene_Symbol=GAPDH Glyceraldehyde-3-phosphate dehydrogenase	4.229	5.08	8
empAI:0.31 Tax_Id=9606 Gene_Symbol=PSAT1 Isoform 2 of Phosphoserine aminotransferase	3.675	1.93	2
empAI:0.21 Tax_Id=9606 Gene_Symbol=PPA1 Inorganic pyrophosphatase	3.652	1.59	4
empAI:0.03 Tax_Id=9606 Gene_Symbol=IARS IARS protein	3.635	0.49	2
empAI:0.05 Tax_Id=9606 Gene_Symbol=ACLY ATP-citrate synthase	3.618	2.46	3
empAI:0.17 Tax_Id=9606 Gene_Symbol=CCT5 T-complex protein 1 subunit epsilon	3.496	2.49	5
empAI:0.28 Tax_Id=9606 Gene_Symbol=AHSA1 Activator of 90 kDa heat shock protein ATPase homolog 1	3.469	3.25	3
empAI:0.15 Tax_Id=9606 Gene_Symbol=TKT Transketolase	3.456	0.04	3
empAI:0.57 Tax_Id=9606 Gene_Symbol=ARF1 ADP-ribosylation factor	3.363	0.16	2
empAI:0.11 Tax_Id=9606 Gene_Symbol=FASN Fatty acid synthase	3.275	1.09	3
empAI:0.07 Tax_Id=9606 Gene_Symbol=FDPS Putative uncharacterized protein	3.225	1.26	3
empAI:0.97 Tax_Id=9606 Gene_Symbol=UBC;UBB;RPS27A ubiquitin and ribosomal protein S27a precursor	3.073	1	3
empAI:0.07 Tax_Id=9606 Gene_Symbol=USP5 Isoform Long of Ubiquitin carboxyl-terminal hydrolase 5	2.716	0.64	2
empAI:0.67 Tax_Id=9606 Gene_Symbol=TUBB Tubulin beta chain	2.631	0.15	2
empAI:0.83 Tax_Id=9606 Gene_Symbol=ENO1 Isoform alpha-enolase of Alpha-enolase	2.605	0.71	2
empAI:0.36 Tax_Id=9606 Gene_Symbol=EIF5A Isoform 2 of Eukaryotic translation initiation factor 5A-1	2.57	1.9	2
empAI:0.28 Tax_Id=9606 Gene_Symbol=HSP90B1 Endoplasmic	2.568	0.27	2
empAI:0.06 Tax_Id=9606 Gene_Symbol=GANAB Isoform 2 of Neutral alpha-glucosidase AB	2.535	1.87	7
empAI:0.19 Tax_Id=9606 Gene_Symbol=UGDH UDP-glucose 6-dehydrogenase	2.419	0.49	2
empAI:1.86 Tax_Id=9606 Gene_Symbol=GSTM3 Glutathione S-transferase Mu 3	2.345	0.09	7

empAI:0.23 Tax_Id=9606 Gene_Symbol=EIF4A1 Eukaryotic initiation factor 4A-I	1.483	0.09	2
empAI:0.32 Tax_Id=9606 Gene_Symbol=SGTA Small glutamine-rich tetratricopeptide repeat-containing protein alpha	2.058	1.18	2
empAI:0.12 Tax_Id=9606 Gene_Symbol=LAP3 Isoform 1 of Cytosol aminopeptidase	2.055	0.19	2
empAI:0.07 Tax_Id=9606 Gene_Symbol=VCP Transitional endoplasmic reticulum ATPase	2.028	0.61	3
empAI:0.14 Tax_Id=9606 Gene_Symbol=PSMD11 Proteasome 26S non-ATPase subunit 11 variant (Fragment)	1.865	0.3	3
empAI:3.93 Tax_Id=9606 Gene_Symbol=GSTP1 Glutathione S-transferase P	1.567	0.42	10
empAI:0.10 Tax_Id=9606 Gene_Symbol=EZR Ezrin	1.328	0.57	2
empAI:0.09 Tax_Id=9606 Gene_Symbol=STRAP Serine-threonine kinase receptor-associated protein	1.285	0.59	8
empAI:0.33 Tax_Id=9606 Gene_Symbol=TPT1 Tumor protein, translationally-controlled 1	1.196	0.25	3
empAI:0.20 Tax_Id=9606 Gene_Symbol=ARPC2 Actin-related protein 2/3 complex subunit 2	1.189	0.23	2
empAI:0.40 Tax_Id=9606 Gene_Symbol=ACTR3 Actin-related protein 3	1.098	0.78	4
empAI:0.90 Tax_Id=9606 Gene_Symbol=RPLP0 60S acidic ribosomal protein P0	0.993	0.06	3
empAI:0.25 Tax_Id=9606 Gene_Symbol=P4HB Protein disulfide-isomerase precursor	0.979	0.24	3
empAI:0.19 Tax_Id=9606 Gene_Symbol=ANXA5 Annexin A5	0.816	0.12	2
empAI:0.22 Tax_Id=9606 Gene_Symbol=EEF1A1 Elongation factor 1-alpha	0.778	0.22	2
empAI:0.19 Tax_Id=9606 Gene_Symbol=HSPA5 HSPA5 protein	0.774	0.17	3
empAI:0.06 Tax_Id=9606 Gene_Symbol=MAP4 Isoform 2 of Microtubule-associated protein	0.729	0.14	2
empAI:0.52 Tax_Id=9606 Gene_Symbol=PRDX5 Isoform Mitochondrial of Peroxiredoxin-5, mitochondrial precursor	0.724	0.12	2
empAI:0.05 Tax_Id=9606 Gene_Symbol=TLN1 Talin-1	0.684	0.31	3
empAI:0.13 Tax_Id=9606 Gene_Symbol=MTHFD1 C-1-tetrahydrofolate synthase, cytoplasmic	0.659	0.15	2
empAI:0.46 Tax_Id=9606 Gene_Symbol=PRDX6 Peroxiredoxin-6	0.661	0.34	2
empAI:0.56 Tax_Id=9606 Gene_Symbol=CCT2 T-complex protein 1 subunit beta	0.654	0.24	7
empAI:0.09 Tax_Id=9606 Gene_Symbol=MYH9 Myosin-9	0.65	0.28	5
empAI:0.31 Tax_Id=9606 Gene_Symbol=EEF2 Elongation factor 2	0.639	0.31	5
empAI:0.22 Tax_Id=9606 Gene_Symbol=GPI Glucose-6-phosphate isomerase	0.642	0.1	2
empAI:1.77 Tax_Id=9606 Gene_Symbol=PPIA;PPIAL3;LOC654188 Peptidyl-prolyl cis-trans isomerase A	0.607	0.24	3
empAI:0.38 Tax_Id=9606 Gene_Symbol=YWHAE 14-3-3 protein epsilon	0.578	0.01	2
empAI:1.24 Tax_Id=9606 Gene_Symbol=PFN1 Profilin-1	0.581	0.13	3
empAI:0.64 Tax_Id=9606 Gene_Symbol=CCT6A T-complex protein 1 subunit zeta	0.573	0.08	7
empAI:0.08 Tax_Id=9606 Gene_Symbol=SERPINB1 Leukocyte elastase inhibitor	0.542	0.2	2
empAI:0.56 Tax_Id=9606 Gene_Symbol=TUBB2C Tubulin beta-2C chain	0.508	0.3	2
empAI:0.46 Tax_Id=9606 Gene_Symbol=TUBA1C Tubulin alpha-1C chain	0.475	0.12	5
empAI:0.21 Tax_Id=9606 Gene_Symbol=PAICS Multifunctional protein ADE2	0.451	0.09	2
empAI:0.29 Tax_Id=9606 Gene_Symbol=EEF1G Elongation factor 1-gamma	0.427	0.04	2
empAI:0.52 Tax_Id=9606 Gene_Symbol=PRDX1 Peroxiredoxin-1	0.395	0.01	2
empAI:0.11 Tax_Id=9606 Gene_Symbol=DPYSL2 Dihydropyrimidinase-related protein 2	0.384	0.05	2
empAI:0.20 Tax_Id=9606 Gene_Symbol=CORO1A Coronin-1A	0.381	0.18	3
empAI:0.05 Tax_Id=9606 Gene_Symbol=CLTC Isoform 1 of Clathrin heavy chain 1	0.345	1.04	3

Complete list of proteins identified by quantitative mass spectroscopy showing enrichment in purified pseudopodia of Cav1 WT-expressing MDA-MB-435 cells relative to pseudopodia of control MDA-MB-435 cells. Data represent 3 independent experiments. 3/1: ratio of detected protein in pseudopodia of Cav1 WT vs control MDA-MB-435 cells; StDev: standard deviation over 3 experiments; # peptides: number of detected peptides that match the protein.