

Supplemental Material: 4T1 Exosomes Proteomic Analysis

Supplemental Table 1. Results of 4T1 Exosome Proteomic Analysis

UniProt ID	Protein	Symbol/Entrez Gene ID	Scores	#Peptides	Subcellular Localization	Function	XO GO mouse	XO GO human	Vesiclepedia
Q8BTM8	Filamin-A	Flna	132.0 (M:132.0)	4	membrane	transporter	Y	Y	Y
P61982	14-3-3 protein gamma	Ywhag	114.7 (M:114.7)	2	membrane	receptor	N	Y	Y
P10852	4F2 cell-surface antigen heavy chain	Slc3a2	212.9 (M:212.9)	4	membrane	transporter	N	Y	Y
P51912	Neutral amino acid transporter B(0)	Slc1a5	159.8 (M:159.8)	3	membrane	transporter	Y	Y	Y
P60710	Actin, cytoplasmic 1	Actb	166.4 (M:166.4)	4	cytoplasm	cytoskeleton	N	Y	Y
P97384	Annexin A11	Anxa11	62.1 (M:62.1)	2	cytoplasm, nucleus	scaffold	Y	Y	Y
P10107	Annexin A1	Anxa1	222.8 (M:222.8)	4	membrane	scaffold	Y	Y	Y
P07356	Annexin A2	Anxa2	111.4 (M:111.4)	2	membrane, extracellular	scaffold	Y	Y	Y
P48036	Annexin A5	Anxa5	399.4 (M:399.4)	7	extracellular	coagulation	Y	Y	Y
P14824	Annexin A6	Anxa6	84.1 (M:84.1)	2	cytoplasm	scaffold	N	Y	Y
P61205	ADP-ribosylation factor 3	Arf3	183.8 (M:183.8)	3	cytoplasm, Golgi	enzyme (GTPase)	N	Y	Y
P61750	ADP-ribosylation factor 4	Arf4	77.5 (M:77.5)	2	cytoplasm, Golgi	enzyme (GTPase)	N	Y	Y
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	Atp1a1	275.8 (M:275.8)	6	membrane	transporter	N	Y	Y
P18572	Basigin	Bsg	64.3 (M:64.3)	2	membrane	receptor	N	Y	Y
Q9Z1Q5	Chloride intracellular channel protein 1	Clic1	101.9 (M:101.9)	3	membrane	transporter	N	Y	Y
P10126	Elongation factor 1-alpha 1	Eef1a1	111.7 (M:111.7)	3	cytoplasm, nucleus	translation regulator	N	Y	Y
P58252	Elongation factor 2	Eef2	59.4 (M:59.4)	2	cytoplasm	translation regulator	N	Y	Y
Q9WVK4	EH domain-containing protein 1	Ehd1	149.1 (M:149.1)	4	membrane	membrane fusion	N	Y	Y

Supplemental Table 1. Continued

UniProt ID	Protein	Symbol/Entrez Gene ID	Scores	#Peptides	Subcellular Localization	Function	XO GO mouse	XO GO human	Vesiclepedia
P10404	MLV-related proviral Env polyprotein OS=Mus musculus	N/A	70.3 (M:70.3)	2	membrane	membrane fusion	N	N/A	N/A
Q03145	Ephrin type-A receptor 2	Epha2	96.6 (M:96.6)	3	membrane	adhesion	N	N	Y
O88783	Coagulation factor V	F5	64.3 (M:64.3)	2	extracellular	coagulation	N	N	Y
Q9WV91	Prostaglandin F2 receptor negative regulator	Ptgfrn	432.3 (M:432.3)	7	cytoplasm, Golgi	inhibitor	N	N	Y
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	Gnai2	213.0 (M:213.0)	4	cytoplasm	translation regulator	N	Y	Y
Q8CGP6	Histone H2A type 1-H	Hist1h2ah	106.1 (M:106.1)	2	nucleus	DNA binding	N	Y	Y
Q6ZWW9	Histone H2B type 1-C/E/G	Hist1h2bc	95.0 (M:95.0)	2	nucleus	DNA binding	N	Y	Y
P62806	Histone H4	Hist1h4a	90.5 (M:90.5)	2	nucleus	DNA binding	N	Y	Y
P11499	Heat shock protein HSP 90-beta	Hsp90ab1	214.2 (M:214.2)	4	cytoplasm	chaperone	N	Y	Y
P63017	Heat shock cognate 71 kDa protein	Hspa8	307.4 (M:307.4)	5	cytoplasm	chaperone	Y	Y	Y
Q62469	Integrin alpha-2	Itga2	76.2 (M:76.2)	2	membrane	adhesion	N	N	Y
Q62470	Integrin alpha-3	Itga3	101.9 (M:101.9)	2	membrane	adhesion	N	Y	Y
P09055	Integrin beta-1	Itgb1	358.6 (M:358.6)	7	membrane	adhesion	N	Y	Y
P52480	Pyruvate kinase PKM	Pkm	327.1 (M:327.1)	6	cytoplasm, nucleus	enzyme (metabolism)	Y	Y	Y
P16045	Galectin-1	Lgals1	87.4 (M:87.4)	2	extracellular	receptor	N	N	Y
P26041	Moesin	Msn	330.4 (M:330.4)	7	cytoplasm, membrane	cytoskeleton	Y	Y	Y
P53986	Monocarboxylate transporter 1	Slc16a1	101.9 (M:101.9)	2	membrane	transporter	N	Y	Y
Q9CQ65	S-methyl-5'-thioadenosine phosphorylase	Mtap	77.1 (M:77.1)	2	cytoplasm, nucleus	enzyme (metabolism)	N	Y	Y
Q9WU77	Unconventional myosin-1c	Myo1c	217.9 (M:217.9)	4	cytoplasm, nucleus, membrane	transporter	Y	Y	Y
Q9WU78	Programmed cell death 6-interacting protein (Alix)	Pdcd6ip	478.0 (M:478.0)	8	cytoplasm	transporter	N	Y	Y

Supplemental Table 1. Continued

UniProt ID	Protein	Symbol/Entrez Gene ID	Scores	#Peptides	Subcellular Localization	Function	XO GO mouse	XO GO human	Vescilepedia
P17742	Peptidyl-prolyl cis-trans isomerase A	Ppia	211.1 (M:211.1)	4	cytoplasm, extracellular	enzyme (isomerization)	N	Y	Y
P35700	Peroxiredoxin-1	Prdx1	115.0 (M:115.0)	2	cytoplasm	enzyme (peroxidase)	N	Y	Y
P62962	Profilin-1	Pfn1	245.3 (M:245.3)	5	cytoplasm	cytoskeleton	N	Y	Y
P61027	Ras-related protein Rab-10	Rab10	115.1 (M:115.1)	2	membrane	enzyme (GTPase)	N	Y	Y
P62821	Ras-related protein Rab-1A	Rab1A	75.8 (M:75.8)	2	membrane	enzyme (GTPase)	N	Y	Y
Q6PHN9	Ras-related protein Rab-35	Rab35	96.7 (M:96.7)	2	membrane	enzyme (GTPase)	N	Y	Y
P26043	Radixin	Rdx	203.8 (M:203.8)	5	membrane, cytoplasm	receptor	N	Y	Y
P62984	Ubiquitin-60S ribosomal protein L40	Uba52	101.4 (M:101.4)	2	cytoplasm	regulatory	N	N	Y
P10833	Ras-related protein R-Ras	Rras	142.1 (M:142.1)	3	membrane	enzyme (GTPase)	N	Y	Y
P50543	Protein S100-A11	S100a11	77.6 (M:77.6)	2	cytoplasm, nucleus	receptor	N	Y	Y
O35874	Neutral amino acid transporter A	Slc1a4	73.9 (M:73.9)	2	membrane	transporter	N	Y	Y
P54116	Erythrocyte band 7 integral membrane protein	Stom	111.6 (M:111.6)	3	membrane	transporter	Y	Y	Y
P68373	Tubulin alpha-1C chain	Tuba1c	200.0 (M:200.0)	4	cytoplasm	cytoskeleton	N	N	Y
P68368	Tubulin alpha-4A chain	Tuba4a	211.0 (M:211.0)	4	cytoplasm	cytoskeleton	N	Y	Y
P99024	Tubulin beta-5 chain	Tubb5	196.5 (M:196.5)	4	cytoplasm	cytoskeleton	Y	Y	Y
P20152	Vimentin	Vim	171.9 (M:171.9)	3	cytoplasm	cytoskeleton	Y	Y	Y

Supplemental Table 1. UniProt numbers were gathered from the UniProt Knowledgebase (<http://www.uniprot.org/>). Subcellular Localization, Functions, and Gene Ontology (GO) of exosomes were assembled from the UniProt website. All proteins identified were searched in Vesiclepedia (<http://microvesicles.org/>) for literary examples of their association with exosomes. One hundred micrograms of exosomes, based on total protein content, was subjected to in-solution digestion using performic acid. To separate tryptic digests, a 5-50% ACN gradient over 120 minutes on a C18 column (Michrocom, Agilent) was used. MS/MS spectra were collected by an Amazon Speed ion ETD trap equipped with CaptiveSpray nanoBooster ionization source. Data was processed using ProteinScape 3.1. Database searches were performed against all mouse entries in the Swiss Prot database using the Mascot Server using 0.6Da peptide mass tolerance and 0.5Da MS/MS tolerance allowing for 1 missed cleavage and modifications for dioxidation of Methionine and trioxidation of cysteine. Identification of proteins was considered significant if at least 2 unique peptides were used for identification.