

Supplemental Table 1: List of proteins exclusively identified in MCF-Exo.

**FINC\_HUMAN** Mass: 262622 **Score: 335** Matches: 9(8) Sequences: 9(8) emPAI: 0.13  
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

Query	Score	Peptide
628	37	R.FTNIGPDTMR.V
803	79	R.DLQFVEVTDVK.V
883	76	K.IYLYTLNDNAR.S
884	57	K.IAWESPQGQVSR.Y
898	86	K.GLAFTDVDVDSIK.I
929	96	R.VPGTSTSATLTGLTR.G
1007	71	R.SYTITGLQPGTDYK.I
1039	68	R.GDSPASSKPISINYR.T
1070	57	R.VDVIPVNLPGEHGQR.L

**ANXA1\_HUMAN** Mass: 38714 **Score: 322** Matches: 7(7) Sequences: 7(7) emPAI: 1.08  
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2

Query	Score	Peptide
554	55	R.SEIDMNDIK.A
709	75	K.DITSDTSGDFR.N
777	81	K.TPAQFDADEL.R.A
1028	82	K.GTDVNVFNTILTTR.S
1166	131	R.SEDFGVNEDLADSDAR.A
1330	50	K.AAYLQETGKPLDETLKK.A
1540	66	K.GPGSAVSPYPTFNPSSDVAALHK.A

**VIME\_HUMAN** Mass: 53651 **Score: 205** Matches: 7(6) Sequences: 7(6) emPAI: 0.58  
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Query	Score	Peptide
561	37	R.DNLAEDIMR.L
574	73	K.FADLSEAANR.N
588	50	K.VELQELNDR.F
598	52	R.EYQDLLNVK.M
844	65	R.EEAENTLQSFR.Q
1036	63	R.TNEKVELQELNDR.F
1159	93	R.LQDEIQNMKEEMAR.H

**ACTA\_HUMAN** Mass: 42009 **Score: 200** Matches: 11(10) Sequences: 5(4) emPAI: 0.97  
Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

Query	Score	Peptide
488	55	R.DLTDYLMK.I
508	-46	R.DLTDYLMK.I + Oxidation (M)
647	-48	K.EITALAPSTMK.I
648	67	K.EITALAPSTMK.I
667	-39	K.EITALAPSTMK.I + Oxidation (M)
668	-53	K.EITALAPSTMK.I + Oxidation (M)
670	-49	K.EITALAPSTMK.I + Oxidation (M)
688	37	R.AVFPSIVGRPR.H
1218	-58	K.SYELPDGQVITIGNER.F
1219	61	K.SYELPDGQVITIGNER.F
1380	60	K.YPIEHGIITNWDDMEK.I

**5NTD\_HUMAN** Mass: 63367 **Score: 158** Matches: 5(4) Sequences: 4(3) emPAI: 0.38  
5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1

Query	Score	Peptide
781	69	K.YPFIVTSDDGR.K
825	36	R.KVPVVQAYAFGK.Y
1152	40	K.VLPVGDEVVGIVGYTSK.E
1308	103	R.HDSGDQDINVVSTYISK.M
1313	-47	R.HDSGDQDINVVSTYISK.M

**1C07\_HUMAN** Mass: 40648 **Score: 137** Matches: 4(3) Sequences: 4(3) emPAI: 0.49  
HLA class I histocompatibility antigen, Cw-7 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=3

Query	Score	Peptide
879	38	R.YLENGKETLQR.A
921	60	K.WAAVVVPSGQEQR.Y
977	66	R.SWTAADTAAQITQR.K
1580	80	R.DGEDQTQDTELVETRPAGDGTFFQK.W

**GRP78\_HUMAN** Mass: 72332 **Score: 108** Matches: 5(3) Sequences: 4(3) emPAI: 0.18  
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2

Query	Score	Peptide
729	-38	R.VEIIANDQGNR.I
730	46	R.VEIIANDQGNR.I
839	38	R.NELESYAYSLK.N
922	53	R.TWNDPSVQQDIK.F
1094	84	K.NQLTSNPENTVFDK.R

**H2B1C\_HUMAN** Mass: 13906 **Score: 106** Matches: 2(2) Sequences: 2(2) emPAI: 0.76  
Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4

Query	Score	Peptide
780	39	R.KESYSVYVYK.V
1208	104	K.AMGIMNSFVNDIFER.I + 2 Oxidation (M)

**CD44\_HUMAN** Mass: 81537 **Score: 99** Matches: 2(2) Sequences: 2(2) emPAI: 0.11  
CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3

Query	Score	Peptide
875	60	K.LVINSNGNGAVEDR.K
1271	77	K.ESSETPDQFMTAETR.N

**MFGM\_HUMAN** Mass: 43122 **Score: 91** Matches: 1(1) Sequences: 1(1) emPAI: 0.10  
Lactadherin OS=Homo sapiens GN=MFG8 PE=1 SV=2

Query	Score	Peptide
619	91	K.EVTGIITQGAR.N

**LDHA\_HUMAN** Mass: 36688 **Score: 81** Matches: 3(3) Sequences: 3(3) emPAI: 0.39  
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Query	Score	Peptide
591	53	K.SADTLWGIQK.E

609 44 K.VTLTSEEEAR.L  
778 55 K.QVVESAYEVIK.L

**K22E\_HUMAN** Mass: 65432 **Score: 78** Matches: 1(1) Sequences: 1(1) emPAI: 0.06  
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

Query Score Peptide  
934 78 R.FLEQQNQVLQTK.W

**EDIL3\_HUMAN** Mass: 53764 **Score: 77** Matches: 2(1) Sequences: 2(1) emPAI: 0.08  
EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1

Query Score Peptide  
645 36 K.NVIDPPIYAR.H  
1383 77 R.GNIDNNTPYANSFTPIK.A

**PGK1\_HUMAN** Mass: 44614 **Score: 69** Matches: 2(2) Sequences: 2(2) emPAI: 0.20  
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3

Query Score Peptide  
577 53 K.VLPGVDALSNI.-  
892 49 R.AHSSMVGVNLPQK.A

**CH10\_HUMAN** Mass: 10932 **Score: 67** Matches: 1(1) Sequences: 1(1) emPAI: 0.43  
10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2

Query Score Peptide  
836 67 K.VLQATVVAVGSGSK.G

**MYOF\_HUMAN** Mass: 234706 **Score: 65** Matches: 1(1) Sequences: 1(1) emPAI: 0.02  
Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1

Query Score Peptide  
798 65 K.GPVGTVSEAQLAR.R

**GTR1\_HUMAN** Mass: 54083 **Score: 61** Matches: 1(1) Sequences: 1(1) emPAI: 0.08  
Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2

Query Score Peptide  
617 61 R.TFDEIASGFR.Q

**BASI\_HUMAN** Mass: 42200 **Score: 59** Matches: 2(2) Sequences: 2(2) emPAI: 0.21  
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2

Query Score Peptide  
510 39 R.FFVSSSQGR.S  
915 54 K.GGVVLKEDALPGQK.T

**MYH9\_HUMAN** Mass: 226530 **Score: 58** Matches: 1(1) Sequences: 1(1) emPAI: 0.02  
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

Query Score Peptide

683 58 K.ALELDSNLYR.I

**COF1\_HUMAN** Mass: 18502 **Score: 57** Matches: 1(1) Sequences: 1(1) emPAI: 0.24

Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3

Query	Score	Peptide
869	57	R.YALYDATYETK.E

**HMGA1\_HUMAN** Mass: 11676 **Score: 57** Matches: 3(2) Sequences: 2(2) emPAI: 1.72

High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3

Query	Score	Peptide
1040	47	R.KQPPVSPGTALVGSQK.E
1511	-36	K.KLEKEEEEEEGISQESSEEEQ.-
1512	42	K.KLEKEEEEEEGISQESSEEEQ.-

**PPIA\_HUMAN** Mass: 18012 **Score: 56** Matches: 1(1) Sequences: 1(1) emPAI: 0.25

Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2

Query	Score	Peptide
638	56	K.FEDENFILK.H

**MYL6B\_HUMAN** Mass: 22764 **Score: 56** Matches: 1(1) Sequences: 1(1) emPAI: 0.19

Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1

Query	Score	Peptide
882	56	R.ALGQNPTNAEVLK.V

**S10AA\_HUMAN** Mass: 11203 **Score: 50** Matches: 1(1) Sequences: 1(1) emPAI: 0.41

Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2

Query	Score	Peptide
1357	50	K.EFPGFLENQKDPLAVDK.I

**PLP2\_HUMAN** Mass: 16691 **Score: 48** Matches: 1(1) Sequences: 1(1) emPAI: 0.27

Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1

Query	Score	Peptide
763	48	R.HTAAPTDPADGPV.-

**THIO\_HUMAN** Mass: 11737 **Score: 47** Matches: 1(1) Sequences: 1(1) emPAI: 0.39

Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3

Query	Score	Peptide
864	47	K.TAFQEALDAAGDK.L

**LMNA\_HUMAN** Mass: 74139 **Score: 43** Matches: 1(1) Sequences: 1(1) emPAI: 0.06

Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1

Query	Score	Peptide
651	43	K.AAYEAELGDAR.K

**RL7\_HUMAN** Mass: 29225 **Score: 41** Matches: 1(1) Sequences: 1(1) emPAI: 0.15

60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1

Query	Score	Peptide
659	41	R.IALTDNALIAR.S

**GNAO\_HUMAN** Mass: 40050 **Score: 41** Matches: 1(1) Sequences: 1(1) emPAI: 0.11

Guanine nucleotide-binding protein G(o) subunit alpha OS=Homo sapiens GN=GNAO1 PE=1 SV=4

Query	Score	Peptide
900	41	K.TTGIVETHFTFK.N

**AHNK\_HUMAN** Mass: 629094 **Score: 41** Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2

Query	Score	Peptide
767	41	K.GEGPEVDVNLPK.A

**TCPH\_HUMAN** Mass: 59366 **Score: 39** Matches: 1(1) Sequences: 1(1) emPAI: 0.07

T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2

Query	Score	Peptide
697	39	K.ATISNDGATILK.L

**TMSL3\_HUMAN** Mass: 5063 **Score: 39** Matches: 1(1) Sequences: 1(1) emPAI: 1.03

Thymosin beta-4-like protein 3 OS=Homo sapiens GN=TMSL3 PE=2 SV=1

Query	Score	Peptide
964	39	K.NPLPSKETIEQEK.Q