Supplementary Information |

Gene	Log_2 MDA wt Air	Log_2 MDA wt Hyp	Log_2 MDA BT Air	Log_2 MDA BT Hyp
ACTA1	29.51	29.47	29.60	29.20
ACTN1	29.33	29.22	29.54	29.27
ACTN4	31.04	30.88	31.45	31.24
AGRN	28.25	28.23	29.32	29.79
ALDOA	31.12	31.25	31.76	31.92
ANXA1	26.83	26.75	27.07	26.56
ANXA2	29.22	29.21	29.25	29.09
ANXA5	27.04	27.08	26.92	26.56
APLP2	30.39	30.35	30.88	31.28
APP	30.88	30.91	30.39	30.70
AXL	29.94	30.10	30.45	31.01
B2M	31.02	31.09	32.13	32.48
C1QTNF3	27.94	27.76	27.49	27.61
CALRx	26.37	26.40	26.49	26.08
CAPZA1	27.12	26.87	27.11	27.21
CCDC80	26.08	25.78	27.35	27.98
CD44	29.37	29.25	29.99	30.57
CDH13	25.74	25.88	24.83	25.35
CDH4	26.80	26.68	25.33	25.54
CDK1	26.10	26.01	26.27	26.46
CLIC4	26.66	26.74	26.76	27.03
CLSTN1	29.73	29.89	29.76	30.16
CLTC	27.98	27.48	28.15	27.91
CNTN1	24.89	25.34	23.90	23.71
COL12A1	28.83	28.94	28.69	28.86
COL18A1	26.39	26.15	27.47	27.59
COL1A1	29.15	29.25	28.77	28.65
COL1A2	28.21	28.18	27.43	27.74
COL2A1	26.68	26.70	25.85	26.27
COL5A1	27.36	27.65	27.83	28.36
COL6A1	29.43	29.54	30.29	30.55
CPE	25.19	25.37	25.66	25.84
CSF1	26.88	27.40	28.09	28.72
CST3	31.07	31.30	32.38	32.83
CTGF	29.77	29.60	28.01	28.33
CTSB	27.99	28.03	28.97	29.42
CTSC	29.76	29.78	27.97	28.52
CTSD	31.46	31.65	32.59	32.68
CTSL	28.28	28.29	28.53	28.94
CTSZ	29.15	29.04	29.93	30.63
CYR61	28.52	28.03	28.94	29.07
DAG1	28.94	29.07	29.43	29.82
DKK1	27.82	27.71	28.39	29.06
ECM1	27.57	27.86	28.01	28.29

EDIL3	28.38	28.57	27.90	27.78
EHD1	26.14	26.31	27.62	27.57
ENO1	32.65	32.67	32.88	33.26
EZR	28.22	28.39	28.83	29.06
FAM3C	27.82	27.83	29.29	29.42
FKBP1A	27.69	27.96	28.59	28.97
FLNA	30.97	30.70	31.34	31.21
FLNC	28.39	28.20	28.45	28.56
FMOD	26.69	26.88	25.31	25.94
FN1	30.51	30.74	31.72	31.81
G6PD	26.26	25.59	28.06	27.97
GAPDH	31.87	31.81	32.01	32.08
GGH	28.60	28.78	28.37	28.73
GPI	29.17	29.27	29.47	29.64
HIST1H4A	27.47	27.68	27.49	27.19
HNRNPK	27.63	26.68	27.60	27.34
HSP90AA1	29.51	29.19	29.41	29.11
HSP90AB1	30.64	30.23	30.72	30.45
HSP90B1	27.33	27.03	27.04	27.07
HSPA8	31.62	31.32	31.64	31.77
HSPG2	27.95	27.92	28.60	29.22
HSPH1	26.26	26.34	25.82	26.02
HTRA1	26.29	26.48	26.80	27.01
IGF2R	27.91	28.00	27.27	27.40
IGFBP1	29.43	29.41	27.01	28.05
IGFBP4	30.21	30.28	30.36	30.46
IGFBP7	30.77	30.64	32.05	32.45
IL6ST	25.57	25.48	25.81	25.74
IQGAP1	26.96	26.42	27.17	27.11
ITGB1	26.72	26.69	27.15	27.16
KAL1	25.05	25.19	25.77	26.59
KPNB1	27.36	27.37	27.85	27.60
L1CAM	27.16	26.88	27.90	28.49
LAMA5	27.67	27.53	28.80	29.10
LAMB2	24.79	24.49	23.53	24.36
LAMC1	27.43	27.36	28.23	28.34
LASP1	28.09	27.87	28.74	28.94
LDHA	31.47	31.79	32.06	32.27
LDLR	26.28	26.52	26.02	26.55
LGALS1	29.00	28.99	30.35	30.20
LGALS3BP	32.15	32.15	32.24	32.48
LMNA	29.68	29.62	30.64	30.72
LOX	27.04	27.70	27.58	28.76
LOXL2	29.45	29.93	29.70	30.47
LOXL4	25.70	25.71	26.55	27.43
MATN2	26.63	26.67	27.17	27.83
MET	27.08	27.25	27.56	28.18
MFGE8	26.40	26.56	25.25	25.40

MMP1	30.45	30.49	26.52	26.55
MMP14	28.11	28.33	27.85	28.54
MSN	30.92	30.86	31.37	31.48
MYH9	29.32	29.18	30.38	30.11
NME2	30.58	30.42	31.05	31.21
NPC2	26.36	26.47	26.78	26.65
NRP1	28.58	28.54	27.98	28.55
NUCB1	28.55	28.67	29.13	29.62
P4HB	27.15	26.80	27.36	27.47
PAM	25.97	26.08	26.74	27.30
PDIA3	27.33	27.01	27.60	27.95
PKM	32.20	32.23	32.53	32.49
PLAT	28.23	28.75	29.54	29.83
PLEC	29.18	28.50	29.58	29.60
PLOD1	27.63	27.97	28.10	28.56
PLTP	26.48	26.96	26.09	26.45
PPIA	31.84	31.93	32.39	32.73
PPIB	27.51	27.30	27.73	27.71
PPT1	27.28	27.33	25.69	25.96
PRKCSH	27.26	26.91	26.78	27.28
PSAP	27.13	27.46	28.08	27.93
PSMA2	26.38	26.34	26.71	26.89
PSMA3	25.13	24.97	25.55	25.36
PSMA5	26.56	26.26	26.70	26.74
PSMA7	26.46	26.40	26.77	26.48
PSMD11	25.51	25.22	25.35	25.10
PSMD14	25.02	24.63	25.12	24.91
PSMD2	25.97	25.87	25.93	25.73
PSME1	26.59	26.65	27.27	27.39
PSME2	26.49	26.42	26.97	26.97
PTPRF	27.39	27.63	26.35	26.94
PTPRK	27.19	27.45	28.19	28.52
PTPRS	25.66	25.83	25.55	25.95
PTX3	29.12	29.15	28.27	28.65
PVR	27.60	27.94	27.54	27.96
PXDN	28.79	29.00	27.44	27.89
QSOX1	31.52	31.54	31.23	31.38
SDC4	26.55	26.95	27.39	27.97
SEMA7A	27.43	27.43	25.57	26.38
SERPINB6	24.94	24.96	24.88	25.33
SERPINE1	30.88	31.12	32.34	32.75
SERPINE2	27.58	27.64	26.44	26.92
SERPINH1	25.56	25.25	25.51	25.67
SFN	27.44	27.54	29.26	29.04
SOD1	28.19	28.03	28.71	28.83
SPTAN1	26.30	26.17	26.52	26.40
STC1	26.47	26.92	26.99	28.02
TCP1	26.73	26.64	26.47	26.29

TFRC	27.82	27.66	27.26	27.55
TGFBI	27.47	27.52	29.46	29.76
THBS1	33.64	33.66	33.99	34.29
TIMP1	30.33	30.40	31.44	31.70
TIMP2	29.51	29.63	30.29	30.67
TINAGL1	26.89	27.09	27.45	28.19
TLN1	29.73	29.75	29.75	29.79
TMSB4X	29.59	29.74	30.95	30.74
TNC	28.64	28.68	26.90	27.31
TPT1	28.19	27.72	28.07	28.08
VASN	25.63	25.95	26.90	27.15
VCL	30.43	30.45	30.62	30.77
VCP	28.79	28.54	29.27	29.14
VIM	32.58	32.17	32.43	32.36
WDR1	28.89	28.77	29.83	29.99
YWHAB	28.94	28.95	29.58	29.89
YWHAE	29.69	29.60	30.04	30.02
YWHAG	27.48	27.44	28.42	28.42
YWHAH	26.28	26.24	27.12	26.71
YWHAQ	27.91	27.80	28.99	28.48
YWHAZ	31.54	31.55	32.12	32.12

Average Log_2 secretome expression values from global differential quantitative mass spectrometry based proteomics. Raw data was processed using MaxQuant v1.5 and Perseus v1.4 and results analysed using scripts written in-house in Python, and statistically tested for significance using the quantile function in the R statistical framework. To ensure high confidence identifications and quantitation, a MaxQuant score of >50 and a minimum of 3 unique peptides per protein seen by MS/MS in all repeats was required. Initial analysis was undertaken using a label-free approach (2x repeats), and data subsequently validated in a standard- and reverse-label SILAC approach (2x repeats). Intracellular contaminants were removed and secreted proteins retained by using the cellular compartment annotations in Ensembl and PantherDB and Gene Ontology annotation enrichment for extracellular associated terms.