

## Supplementary tables

**Table S1.** Peptide fraction separation liquid chromatography elution gradient table.

Time (min)	Flow rate (mL/min)	Mobile phase A (%)	Mobile phase B (%)
0	1	97	3
10	1	95	5
30	1	80	20
48	1	60	40
50	1	50	50
53	1	30	70
54	1	0	100

**Table S2.** Liquid chromatography elution gradient table.

<b>Time (min)</b>	<b>Flow rate (mL/min)</b>	<b>Mobile phase A (%)</b>	<b>Mobile phase B (%)</b>
0	600	94	6
2	600	85	15
48.5	600	60	40
50.5	600	50	50
51.5	600	45	55
60	600	0	100

**Table S3.** The analysis parameter of Proteome Discoverer 2.4.

Item	Value
Type of Quantification	Reporter Quantification (TMT)
Enzyme	Trypsin
Max. Missed Cleavage Sites	2
Precursor Mass Tolerance	10 ppm
Fragment Mass Tolerance	0.02 Da
Dynamic Modification	Oxidation/+15.995 Da (M) and TMT /+229.163 Da (K)
N-Terminal Modification	Acetyl/+42.011 Da (N-Terminal) and TMT 10plex/+229.163 Da (K, Y) and Met-loss/-131.040Da(M) and Met-loss+Acetyl/-89.030 Da(M)
Static Modification	Carbamidomethyl/+57.021 Da (C)

**Table S4.** The primer sequences from NCBI.

Target	Species	Forward	Reverse
Acot 1	Mouse	AGTGCTGATTCAAGGGCTGG	TTCTCGCAGCTGGATTGAAC
Mup 1	Mouse	CCAGGCCCCGAGAATGAAGAA	GGCCTCTCCATGAACACCAA
Mt 1	Mouse	CGACTTCAACGTCCTGAGTAC	GTCCATTCCGAGATCTGGTG
TPM 1	Mouse	ACAGAACCATTAACAGCCAGAG	TGAACAAAAGACCCCAGAGG
Actc 1	Mouse	AGGATGACCGTATTGTGCTTC	AACAAACTGCACTTGTGTAAACA