

**Table S4.** The parameters used for mass spectrum analysis and peptides identification.

Mass Spectrum Parameters				The Peptides Parameters	
Name	Setting	Name	Setting	Name	Setting
Use lock masses	No	Fixed first mass	100	Enzyme digestion method	Trypsin/P
Peptide match	Yes	NCE/stepped NCE	32	Number of missed cuts	2
MS AGC target	2.00E+05	Isolation window	1.6	mass tolerance for the precursor ion	10.0 ppm
MS Maximum IT	50 ms	Intensity threshold	2.00E+04	mass tolerance for fragment ion	0.02 Da
MS Scan range	400-1500	Charge exclusion	1, $\geq 6$	fixed modification	Carbamidomethyl(C)
MS Resolution	60,000	ddMS2 TopN	20	variable modification	Oxidation(M), Acetyl (Protein N-term), NQ
MS2 Resolution	15,000	MS2 AGC target	5.00E+04	quantitative method	TMT 6plex
Dynamic exclusion	30s	MS2 Maximum IT	70 ms	Peptide scoring threshold	Aug-40