



## Supplementary Figure S1

(A) The mass error of the whole identified peptides.

(B) Statistic analyses of the whole identified peptide length.

(C) Statistic analyses of the number of modified site per crotonylated proteins.

(D) Motif analysis of all the identified sites.

(E-G) The identified crotonylated proteins were classified according to Gene Ontology annotation, including the distribution of proteins in cellular component (E), the molecular function characterization (F) and the biological process characterization (G).

- (H) KEGG pathway-based enrichment analysis of the crotonylation proteins.
- (I) Pfam domain analysis of the crotonylation proteins.
- (J) Protein complex enrichment analysis of the crotonylation proteins.
- (K) The interaction network of crotonylated proteins were listed in gene names, based on STRING database, and visualized in Cytoscape.