

Figure S1. PANTHER Gene Ontology overrepresented enrichment analysis of the 485 dysregulated proteins. The Cellular Component enrichments for (A) 192 up regulated, and (B) 293 down regulated proteins.

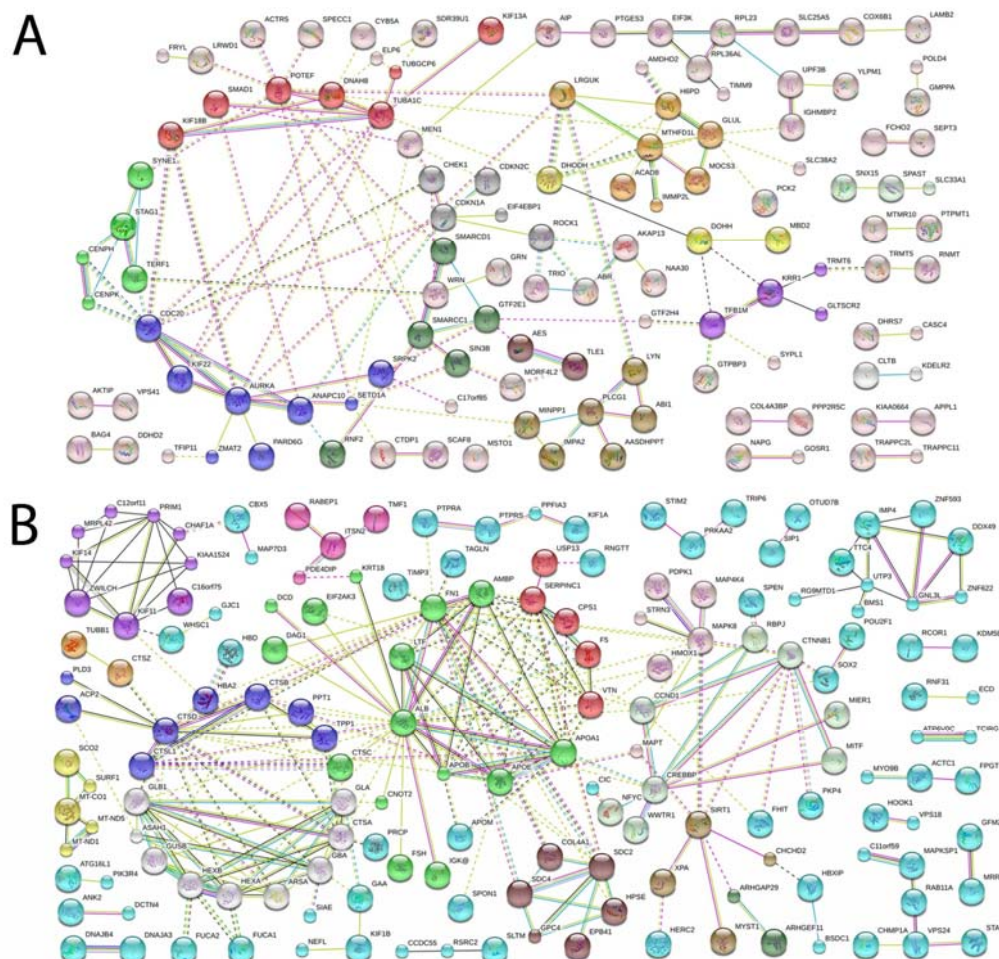


Figure S2. Protein-protein interactions were mapped using STRING database for (A) 192 up regulated proteins and (B) 293 down regulated proteins.

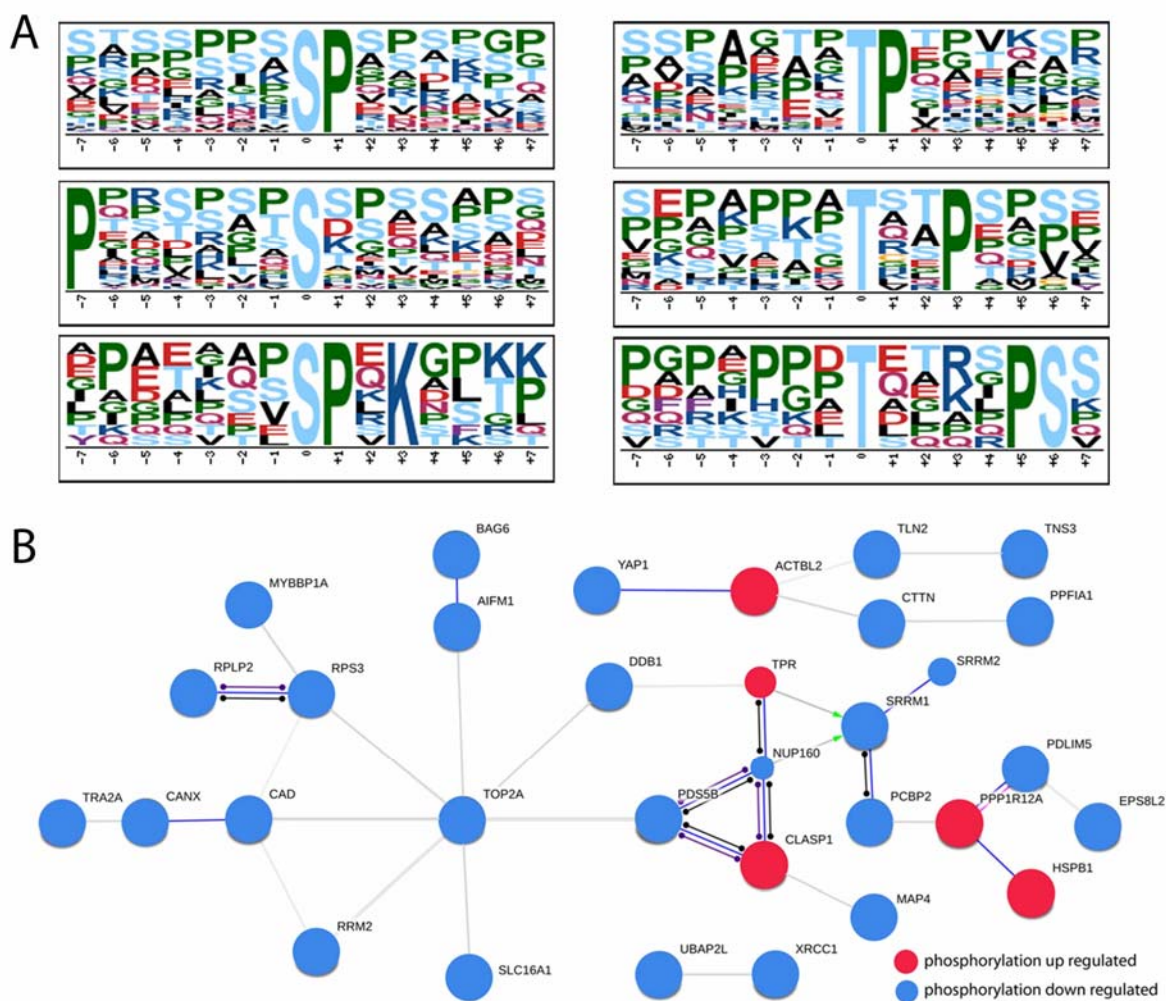


Figure S3. (A) Phosphor- peptides were subjected to motif-x (<http://motif-x.med.harvard.edu>) tool to extract the overrepresented sequence patterns. Six sequence patterns were identified. (B) Protein-protein interaction network of the dysregulated phosphoproteins were established from the STRING database (<http://www.string-db.org>).

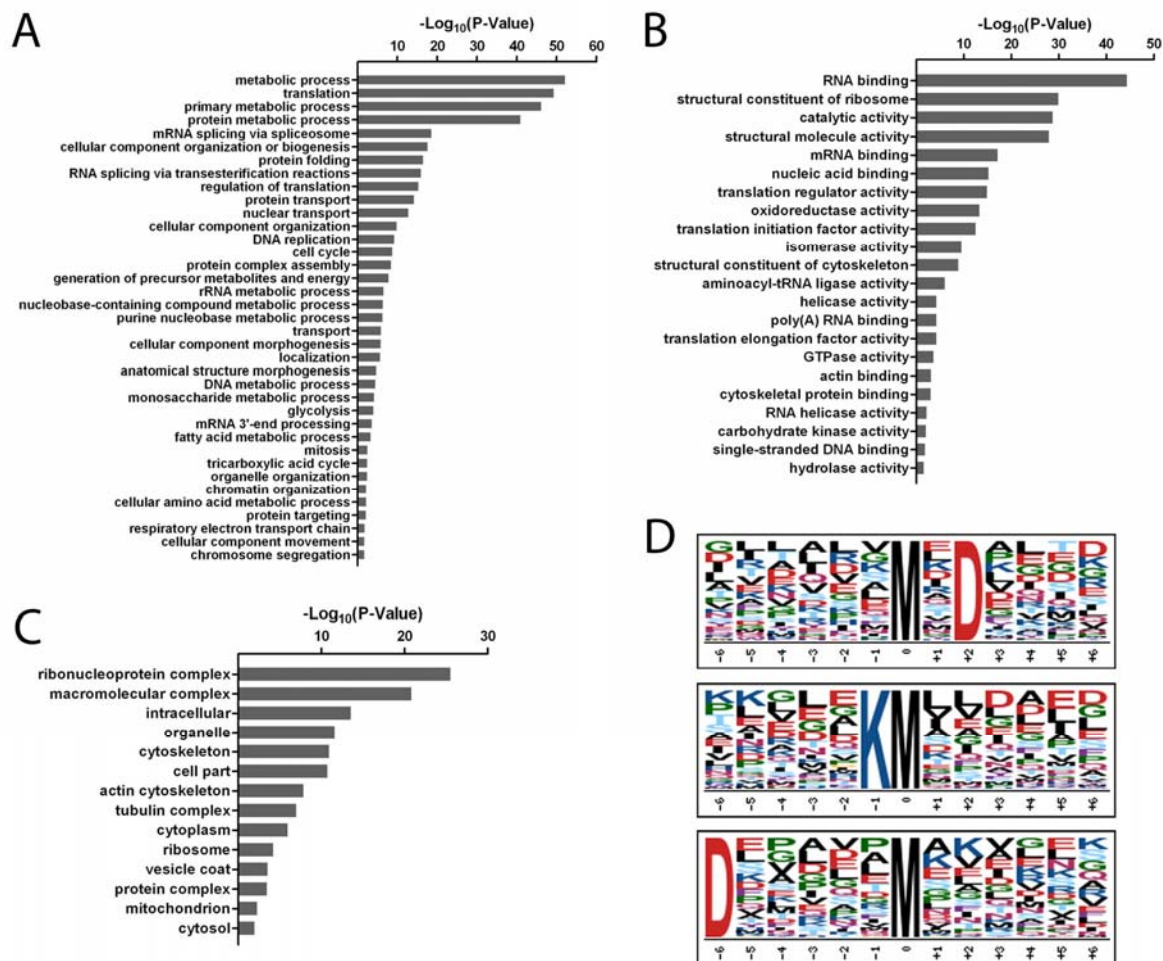


Figure S4. Classifications of the oxidized proteins and identifications of the conserved sequence patterns for oxidation. PANTHER Gene Ontology (GO) over-representative enrichment test of the 1050 oxidized proteins for (A) the GO-Slim biological process, (B) the GO-Slim molecular function, (C) the GO-Slim cellular component classifications. (D) Motif-x analysis revealed the conserved sequence patterns for protein oxidation.