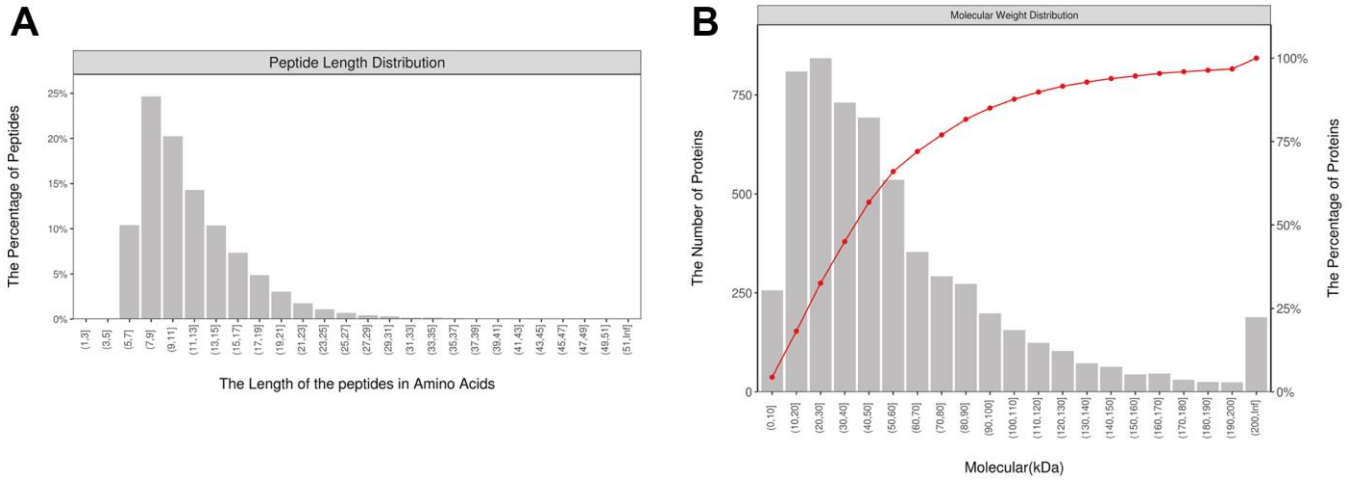
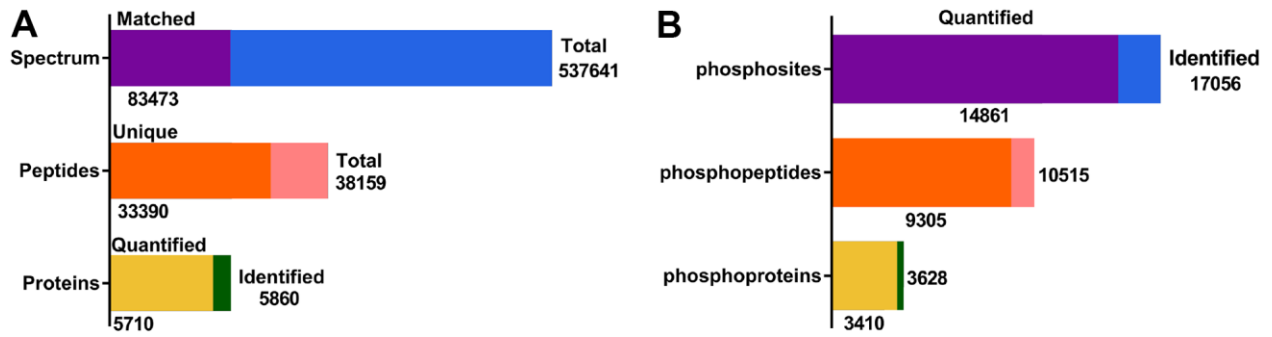


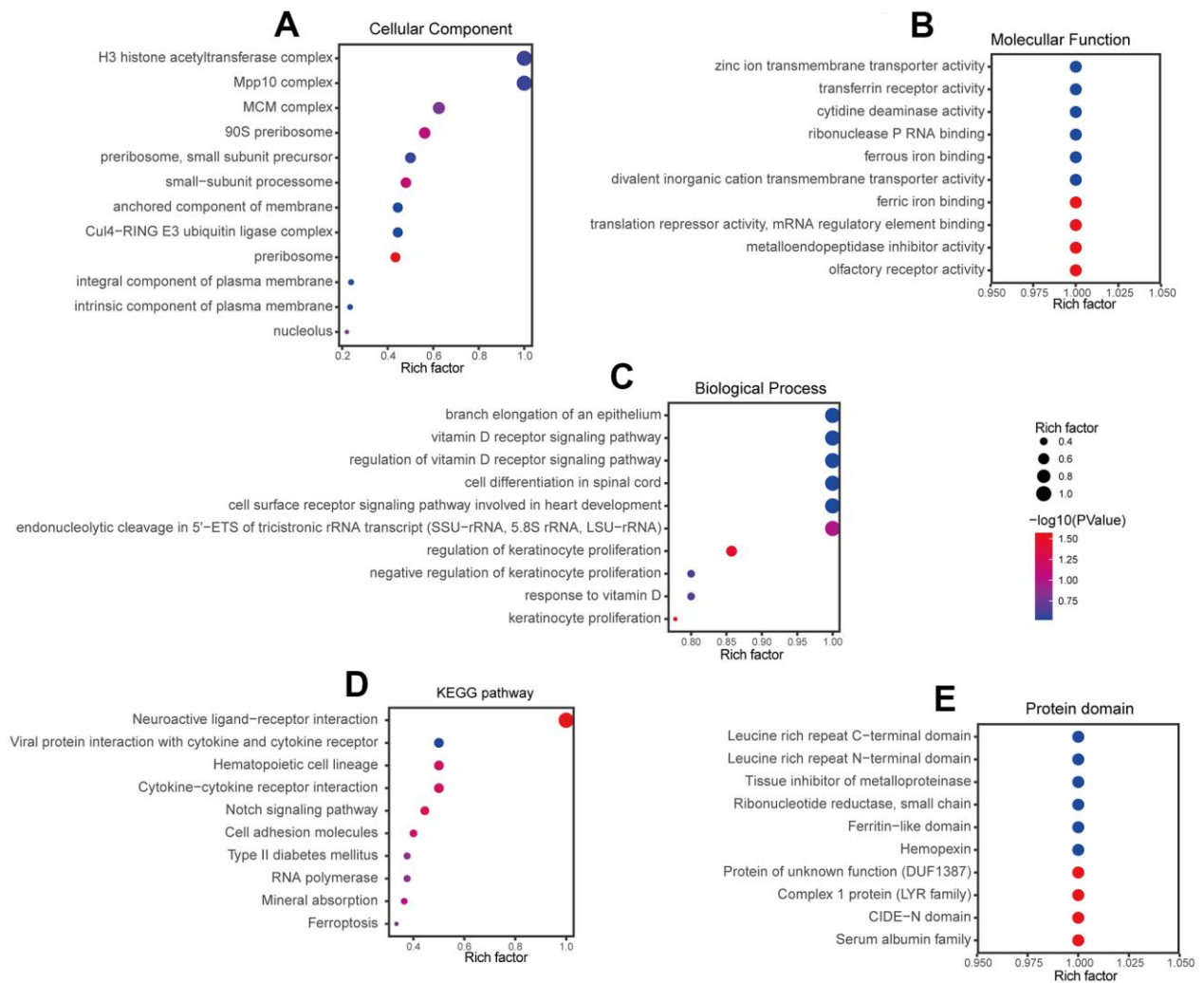
SUPPLEMENTARY FIGURES



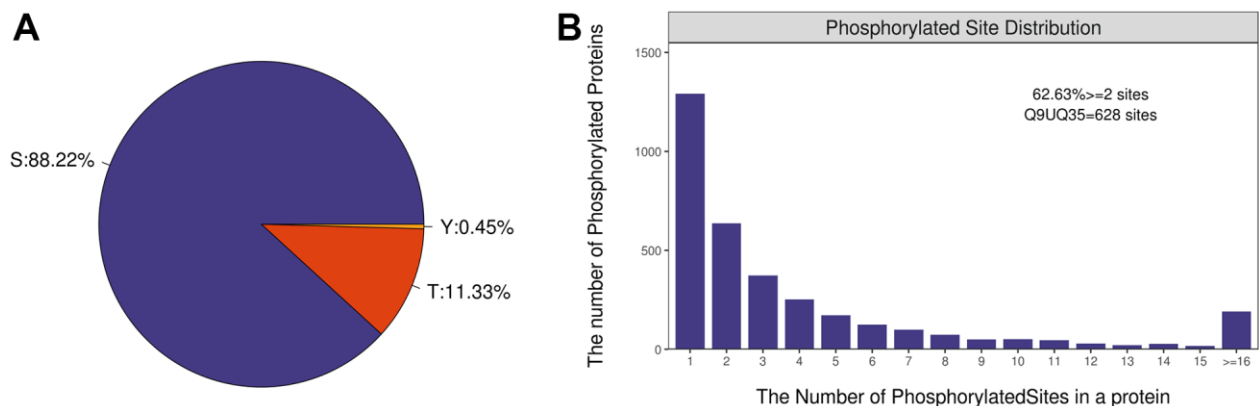
Supplementary Figure 1. (A) Distribution of peptide lengths identified by mass spectrometry. (B) Distribution of molecular weights of all proteins identified.



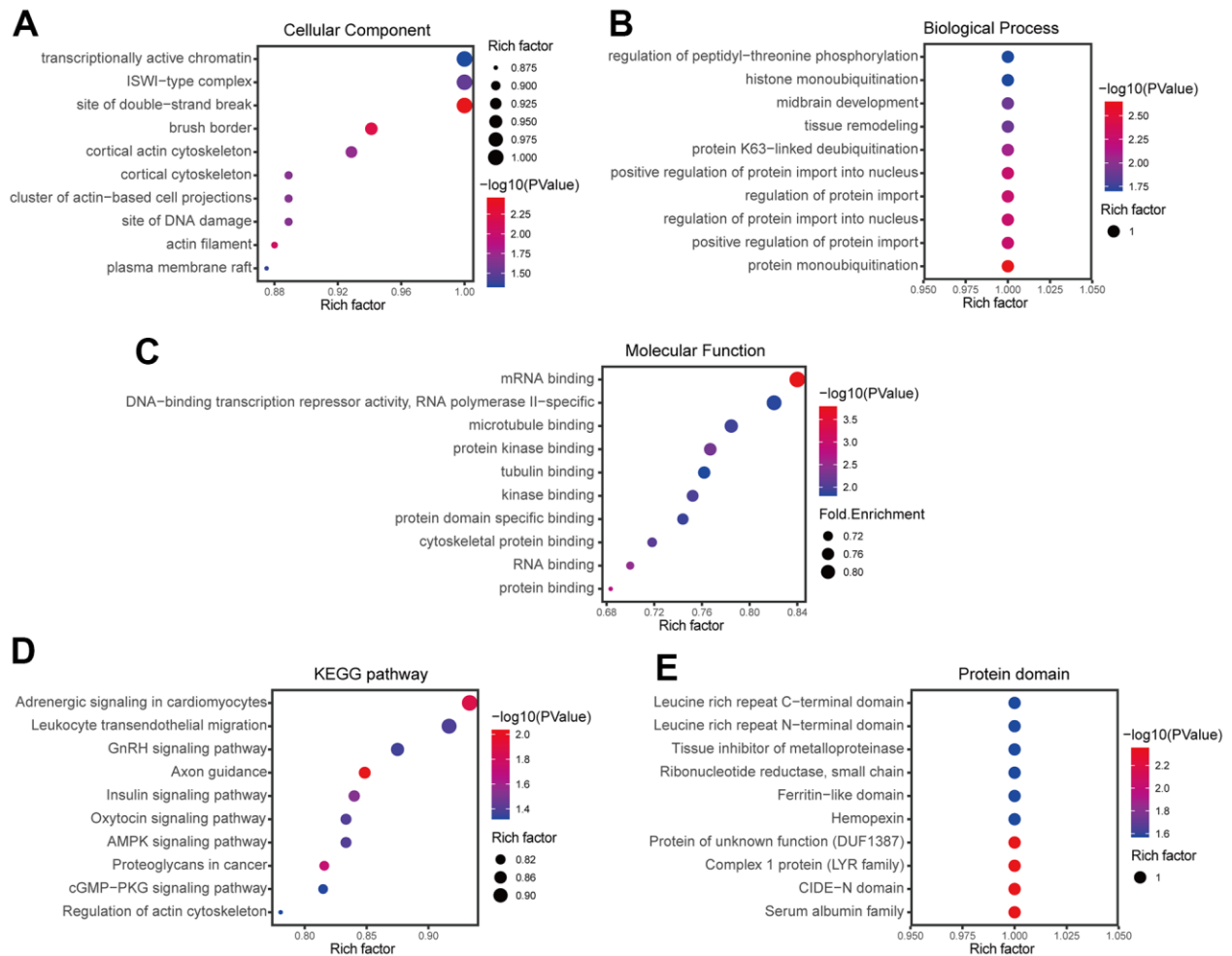
Supplementary Figure 2. (A) Results of proteome quantitation. (B) Results of phosphoproteome quantitation.



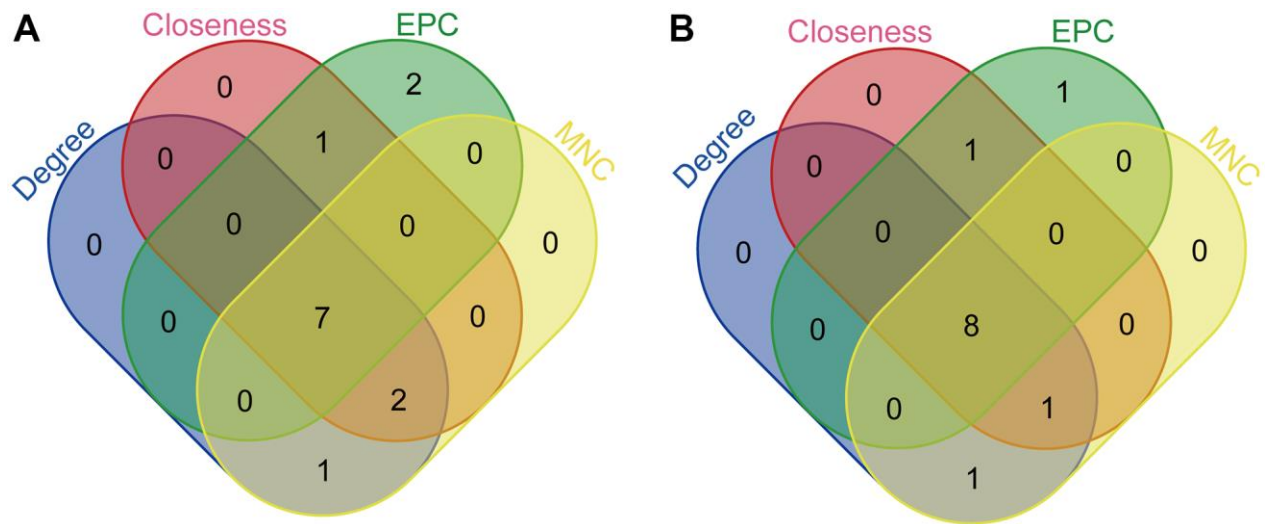
Supplementary Figure 3. (A) Clustering of differentially expressed proteins based on enrichment in Gene Ontology (GO) cellular components. (B) Clustering of differentially expressed proteins based on enrichment in GO molecular functions. (C) Clustering of differentially expressed proteins based on enrichment in GO biological processes. (D) Clustering of differentially expressed proteins based on enrichment in Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. (E) Clustering of differentially expressed proteins based on protein domains.



Supplementary Figure 4. (A) Distribution of serine (S), threonine (T) and tyrosine (Y) phosphorylation among all phosphoproteins identified by mass spectrometry. (B) Distribution of phosphoproteins based on number of phosphorylation sites per protein.



Supplementary Figure 5. (A) Clustering of differentially phosphorylated proteins based on enrichment in Gene Ontology (GO) cellular components. (B) Clustering of differentially phosphorylated proteins based on enrichment in Gene Ontology (GO) biological processes. (C) Clustering of differentially phosphorylated proteins based on enrichment in Gene Ontology (GO) molecular functions. (D) Clustering of differentially phosphorylated proteins based on enrichment in Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. (E) Clustering of differentially phosphorylated proteins based on enrichment in protein domains.



Supplementary Figure 6. (A) Venn diagram of differentially expressed proteins screened by four classification methods in order to identify hub proteins. (B) Venn diagram of differentially phosphorylated proteins screened by four classification methods in order to identify hub phosphorylated proteins.