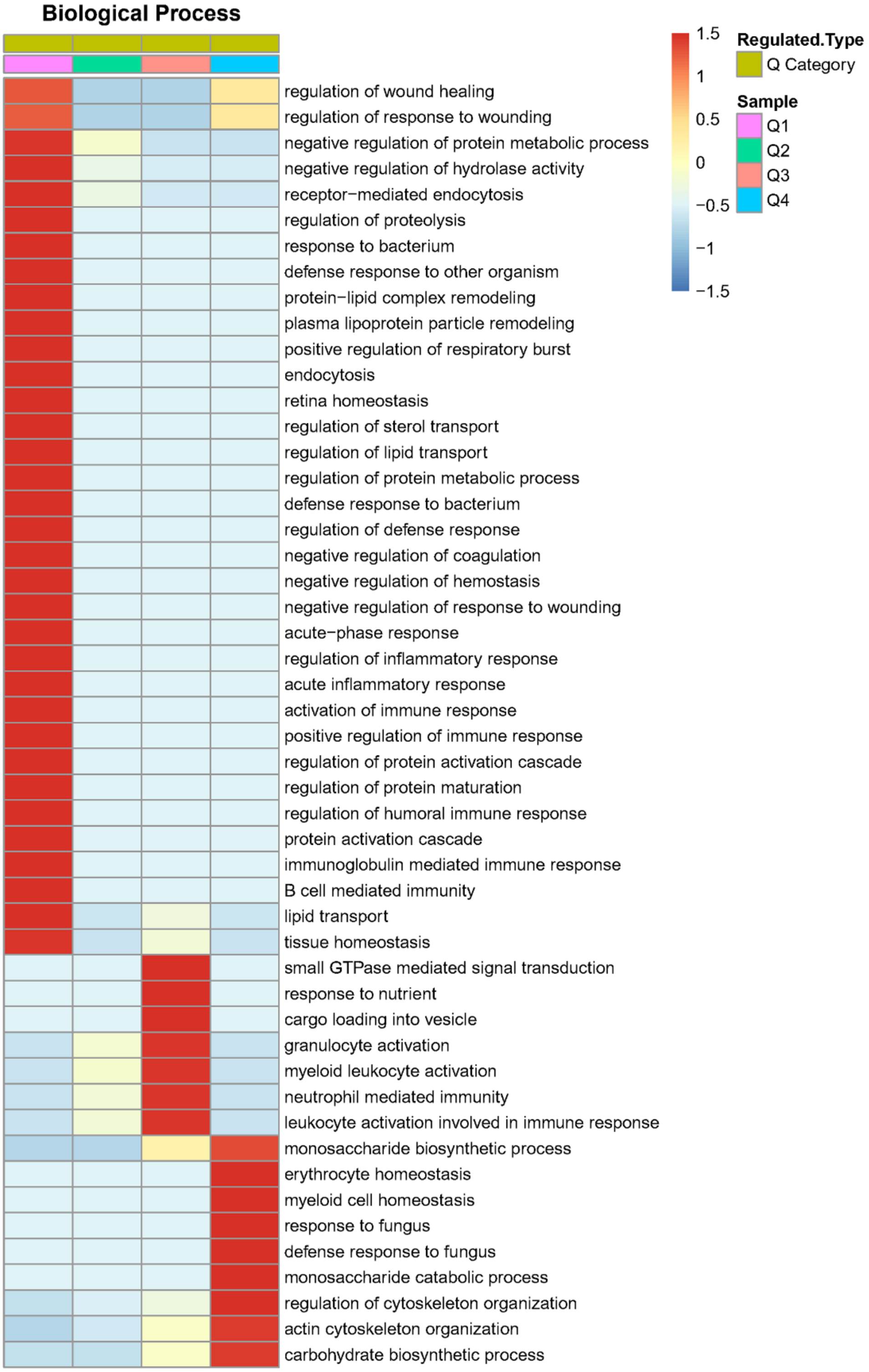
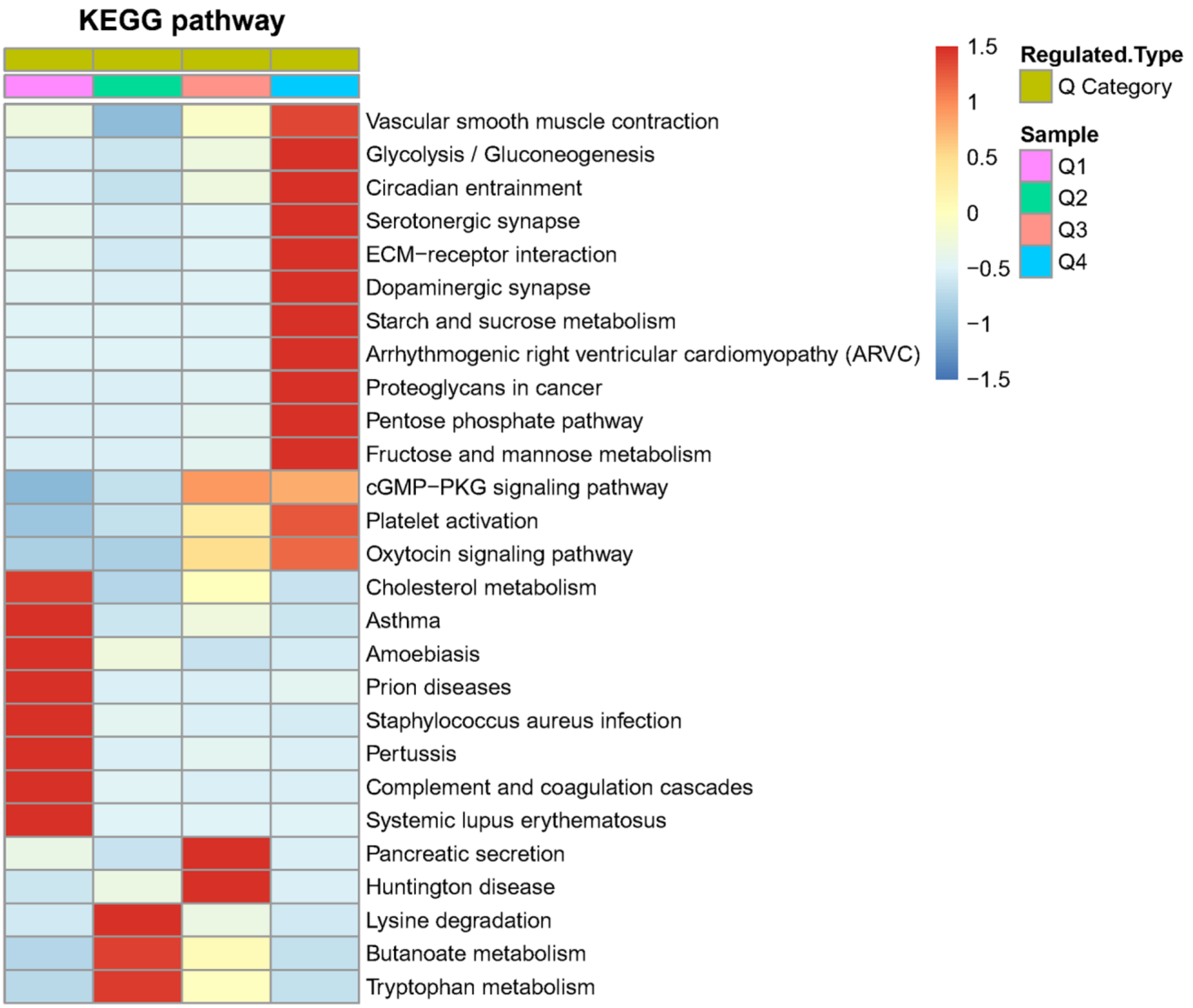
SUPPLEMENTARY FIGURES

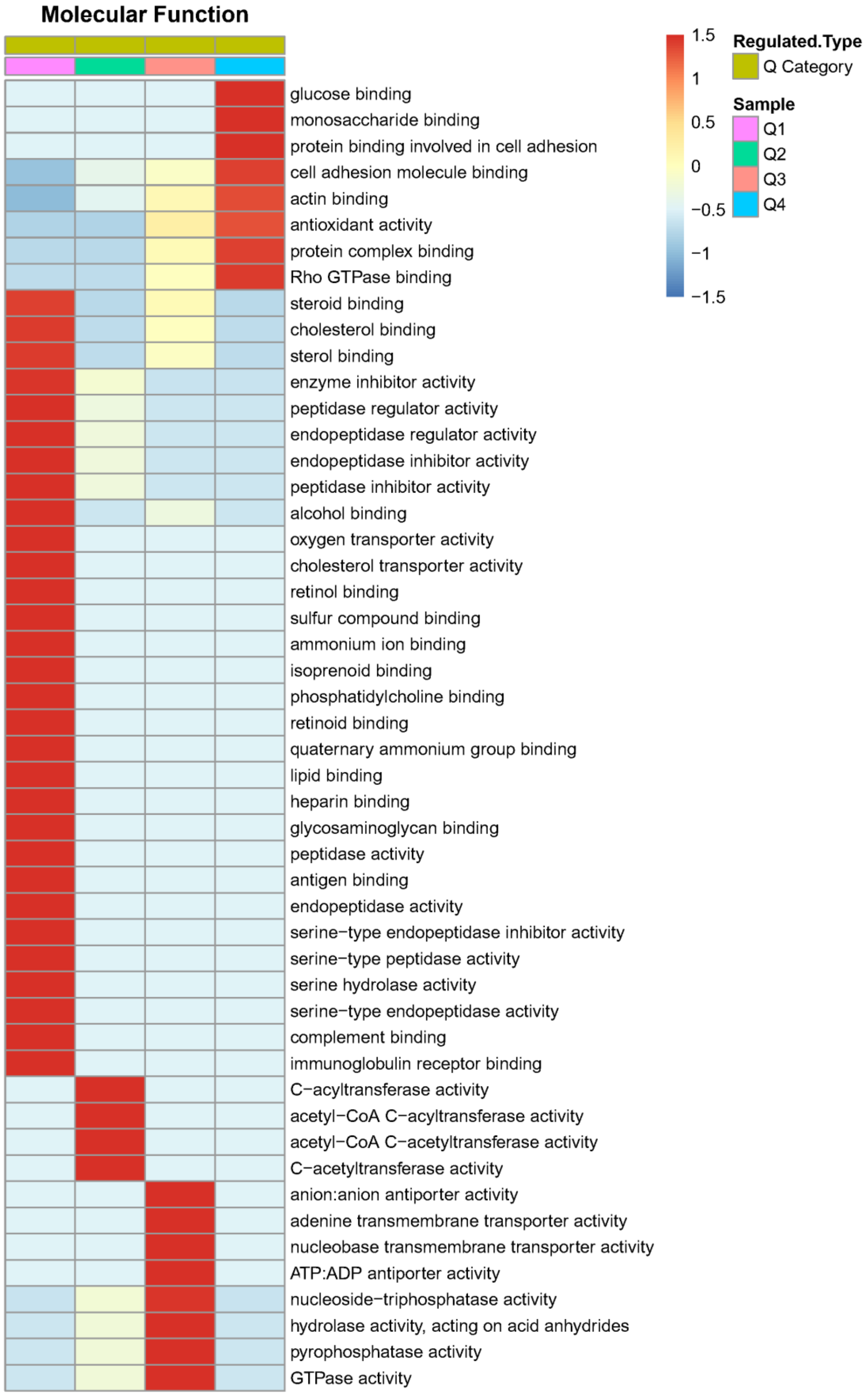


Supplementary Figure 1. Functional enrichment clustering analyses of differentially expressed proteins (DEPs) in four quantiles (Q1-Q4) based on biological process.

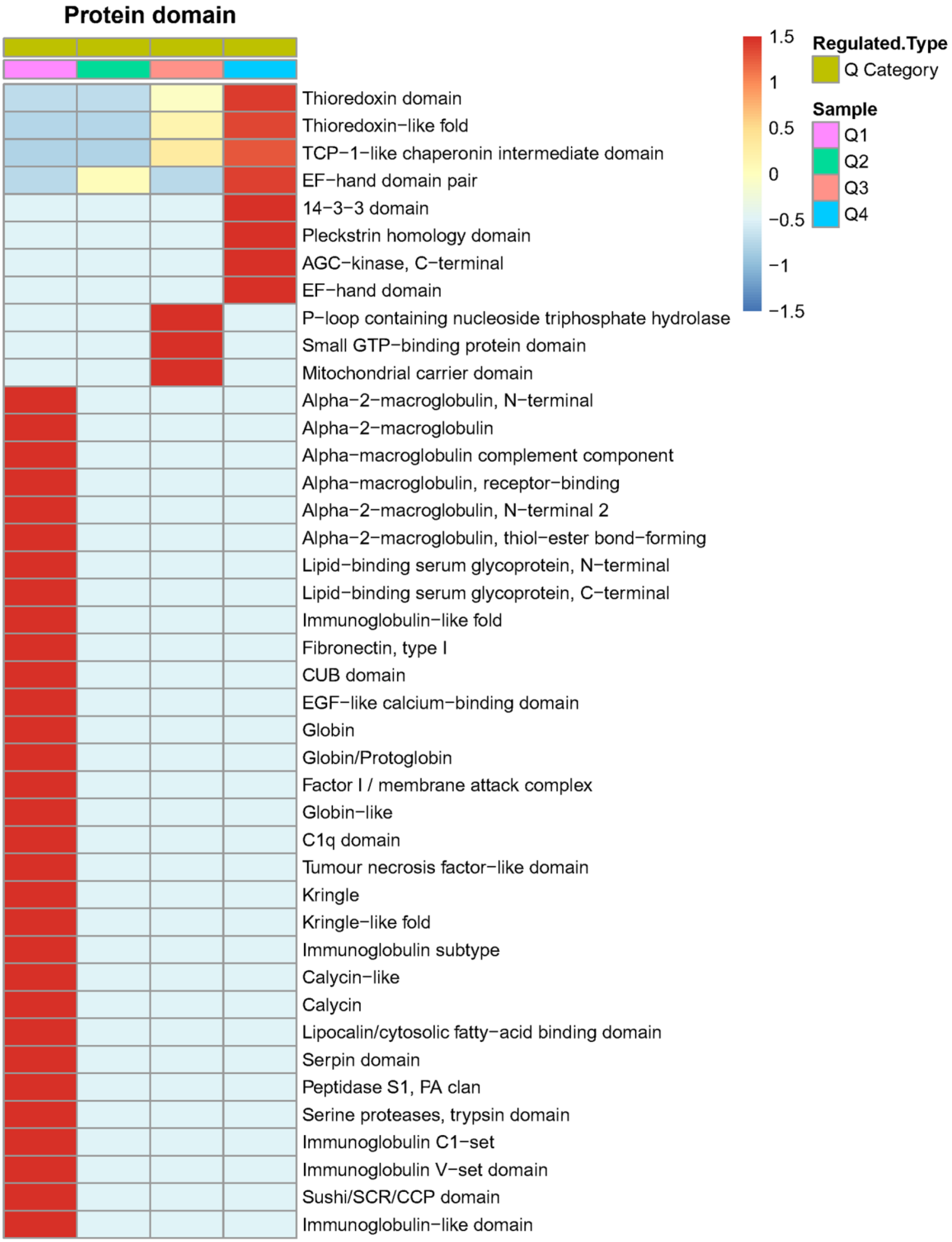
Supplementary Figure 2. Functional enrichment clustering analyses of differentially expressed proteins (DEPs) in four quantiles (Q1-Q4) based on cellular component.



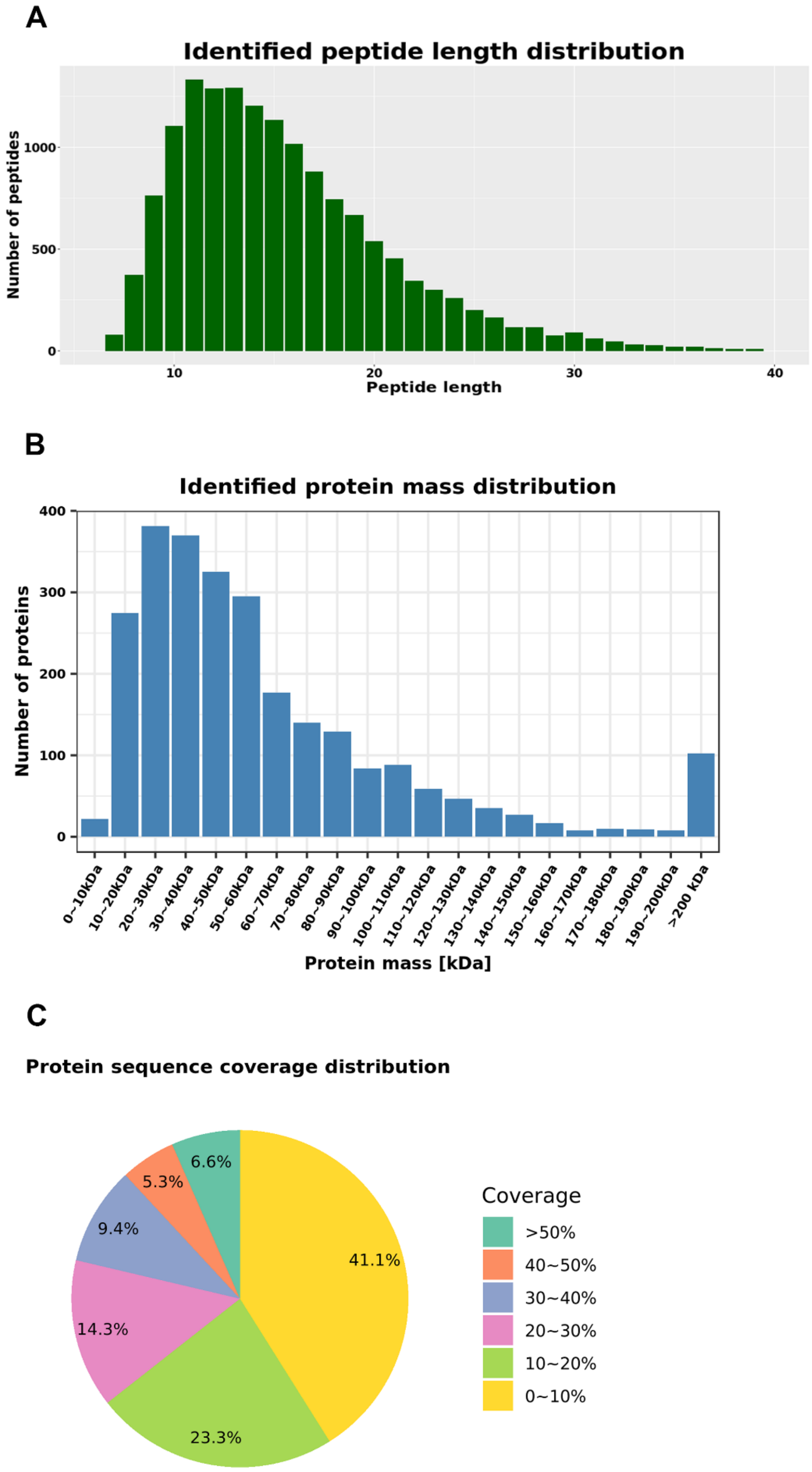
Supplementary Figure 3. Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment clustering analyses of differentially expressed proteins (DEPs) in four quantiles (Q1-Q4).



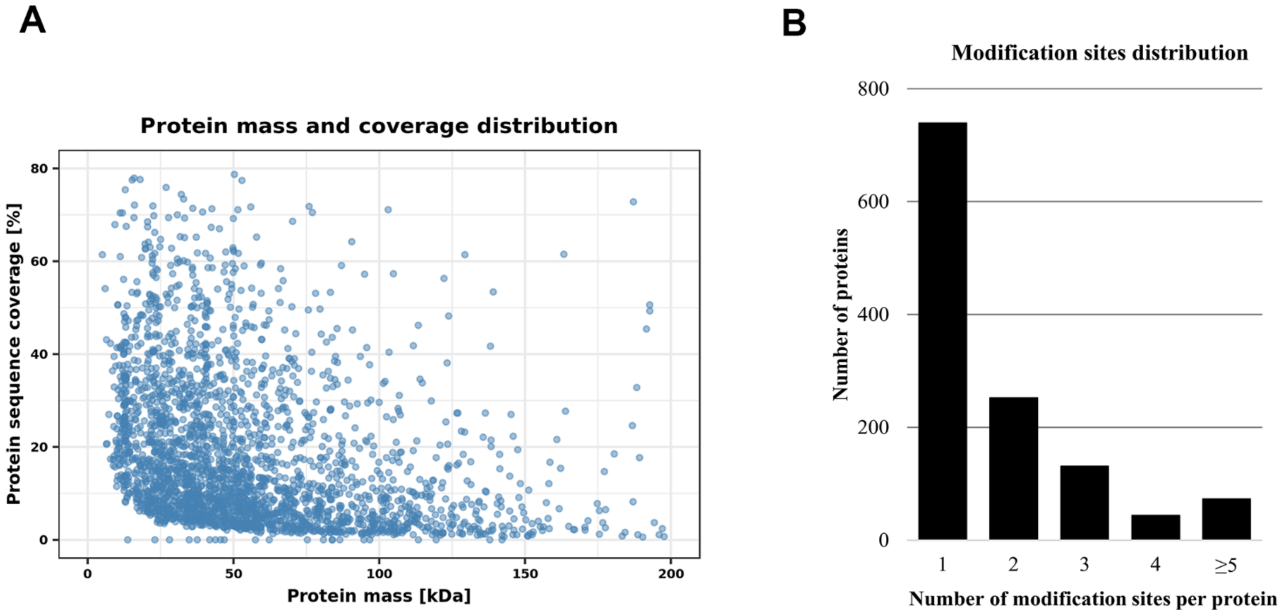
Supplementary Figure 4. Functional enrichment clustering analyses of differentially expressed proteins (DEPs) in four quantiles (Q1-Q4) based on molecular function.



Supplementary Figure 5. Functional enrichment clustering analyses of differentially expressed proteins (DEPs) in four quantiles (Q1-Q4) based on protein domain.



Supplementary Figure 6. (**A**) The length distribution of peptides identified by mass spectrometry. (**B**) Molecular weight distribution of all identified proteins. (**C**) Protein sequence coverage distribution.



Supplementary Figure 7. (**A**) The relationship between the molecular weight of the protein and the coverage determined by mass spectrometry. (**B**) The number of modification sites of each corresponding protein.