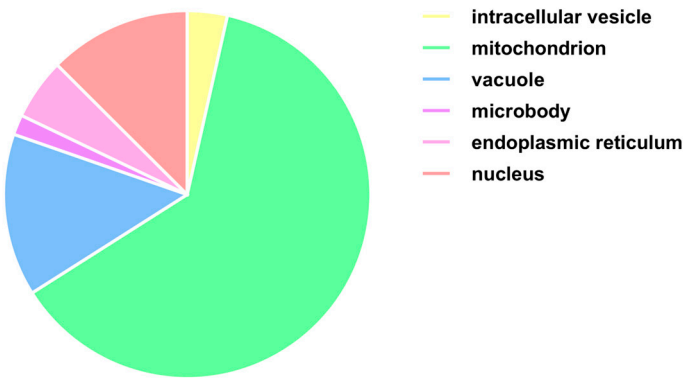


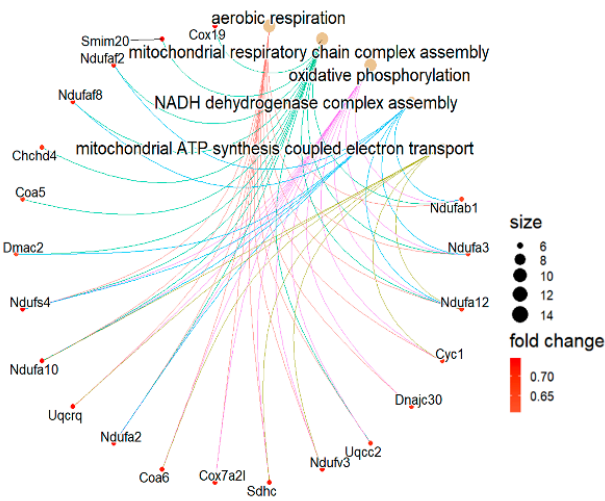
# Multidimensional Landscape of SA-AKI Revealed by Integrated Proteomics and Metabolomics Analysis

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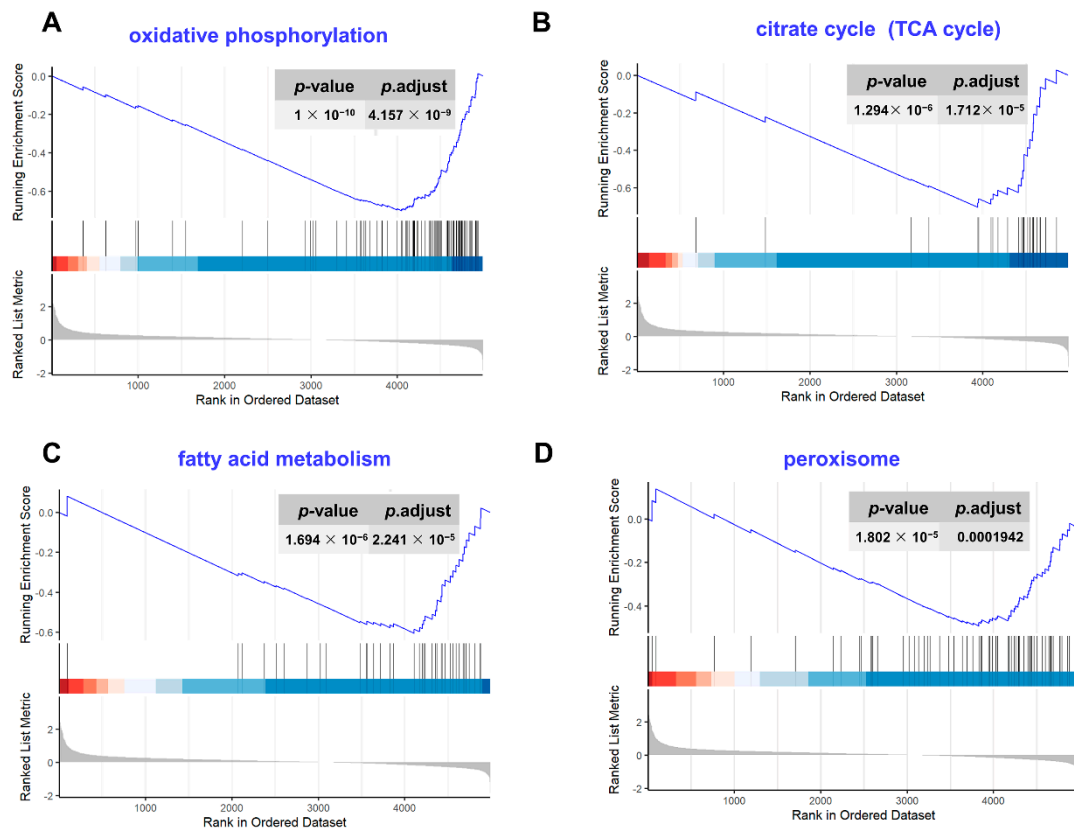
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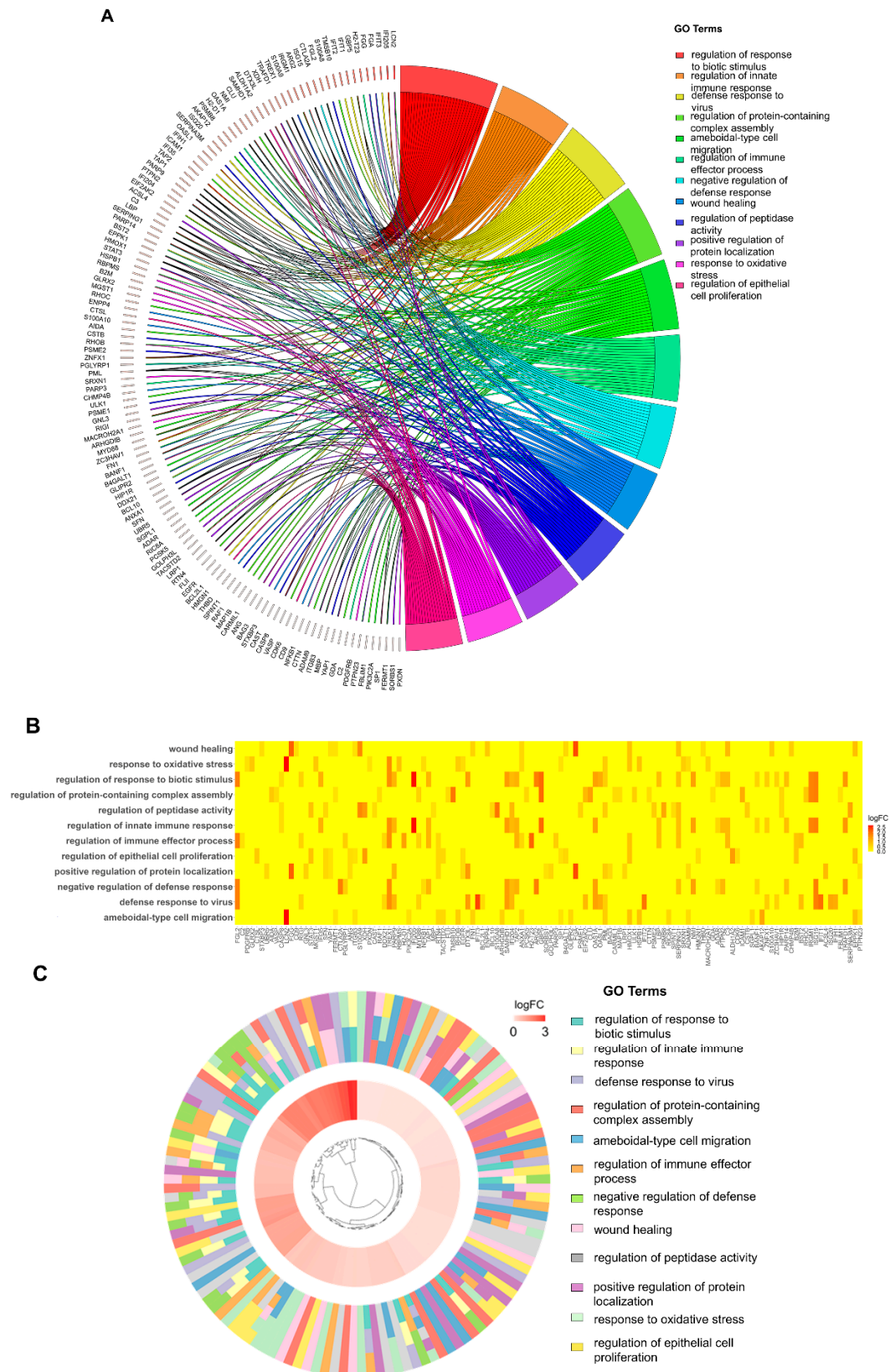
**Figure S1.** Cellular component enrichment analysis of downregulated proteins in SA-AKI kidneys analyzed by PANTHER 17.0 [59].



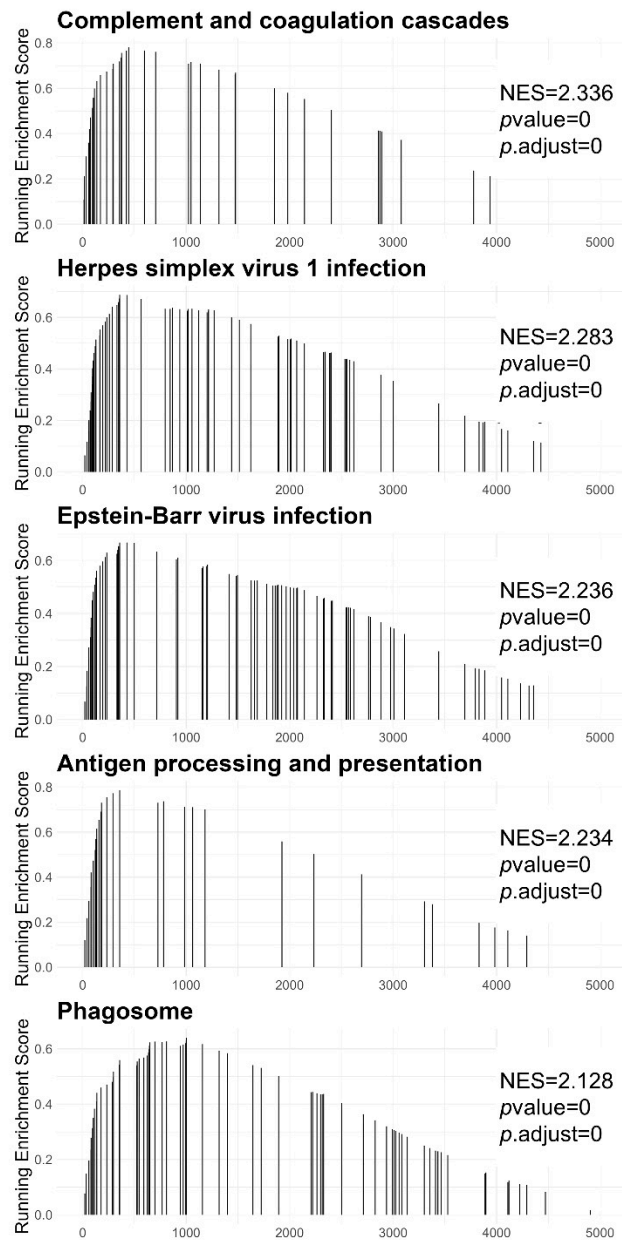
**Figure S2.** Cneplot representing shared genes between the top five enrichment pathways in GSEA analysis of all identified proteins based on the GO database.



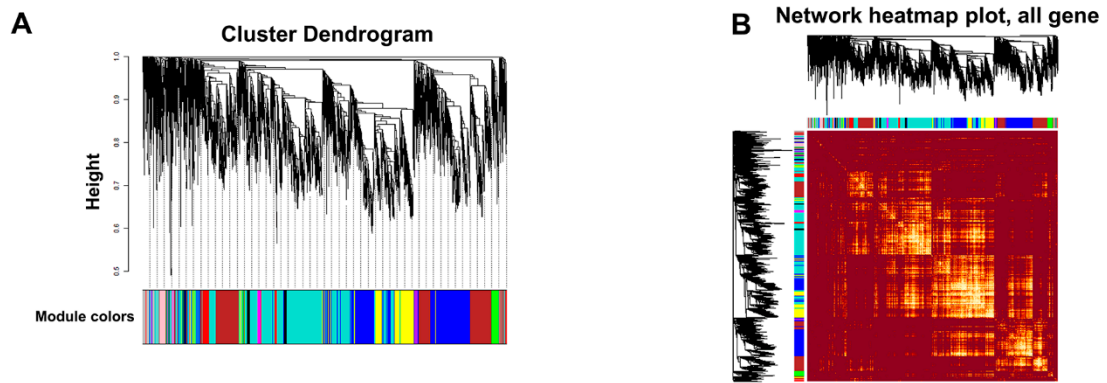
**Figure S3.** GSEA analysis of all identified proteins in proteomics analysis of SA-AKI kidneys compared with the control group based on the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. (A-D) GSEA plots showed oxidative phosphorylation, citrate cycle, fatty acid metabolism, and peroxisome metabolism were significantly downregulated in the KEGG database.



**Figure S4.** GO plots of upregulated proteins in SA-AKI kidneys. (A) GOChord plot visualized the interaction between the top 12 terms and proteins. GOChord plot was visualized with the R package GOpot [28]. (B) GOHeat plot visualized the interaction between the top 12 terms and proteins. (C) The cluster results of the top 12 terms were visualized by GOCluster plot.



**Figure S5.** The top five upregulated pathways according to the GSEA normalized enrichment score in the KEGG database.



**Figure S6.** The co-expression network of proteins in SA-AKI kidneys constructed by weighted gene co-expression network analysis (WGCNA). (A) The clustering dendrogram showed 12 protein co-expression modules with dissimilarity based on the topological overlap. (B) The network heatmap plot visualized the protein network and depicted the Topological Overlap Matrix among all proteins.