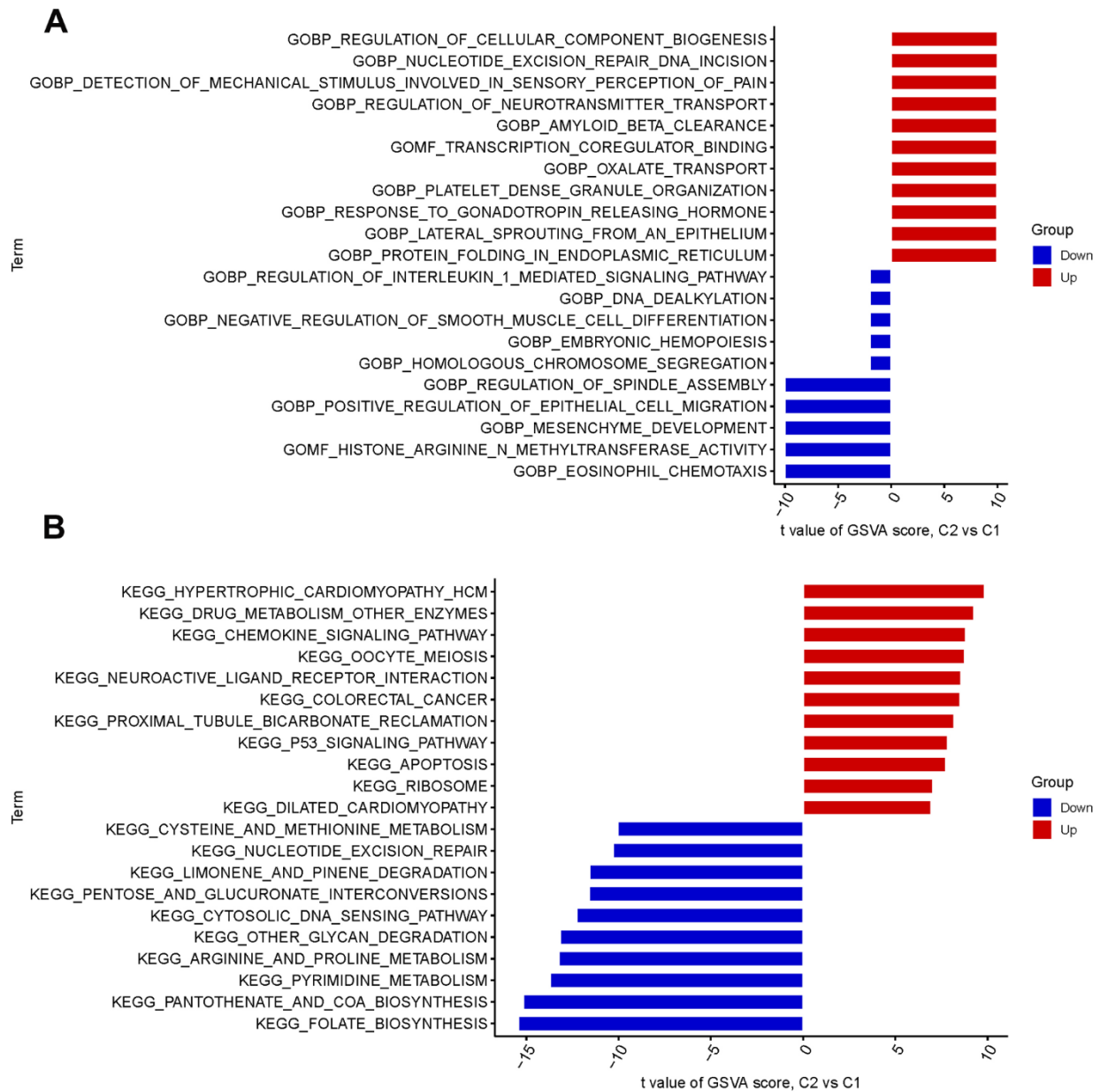
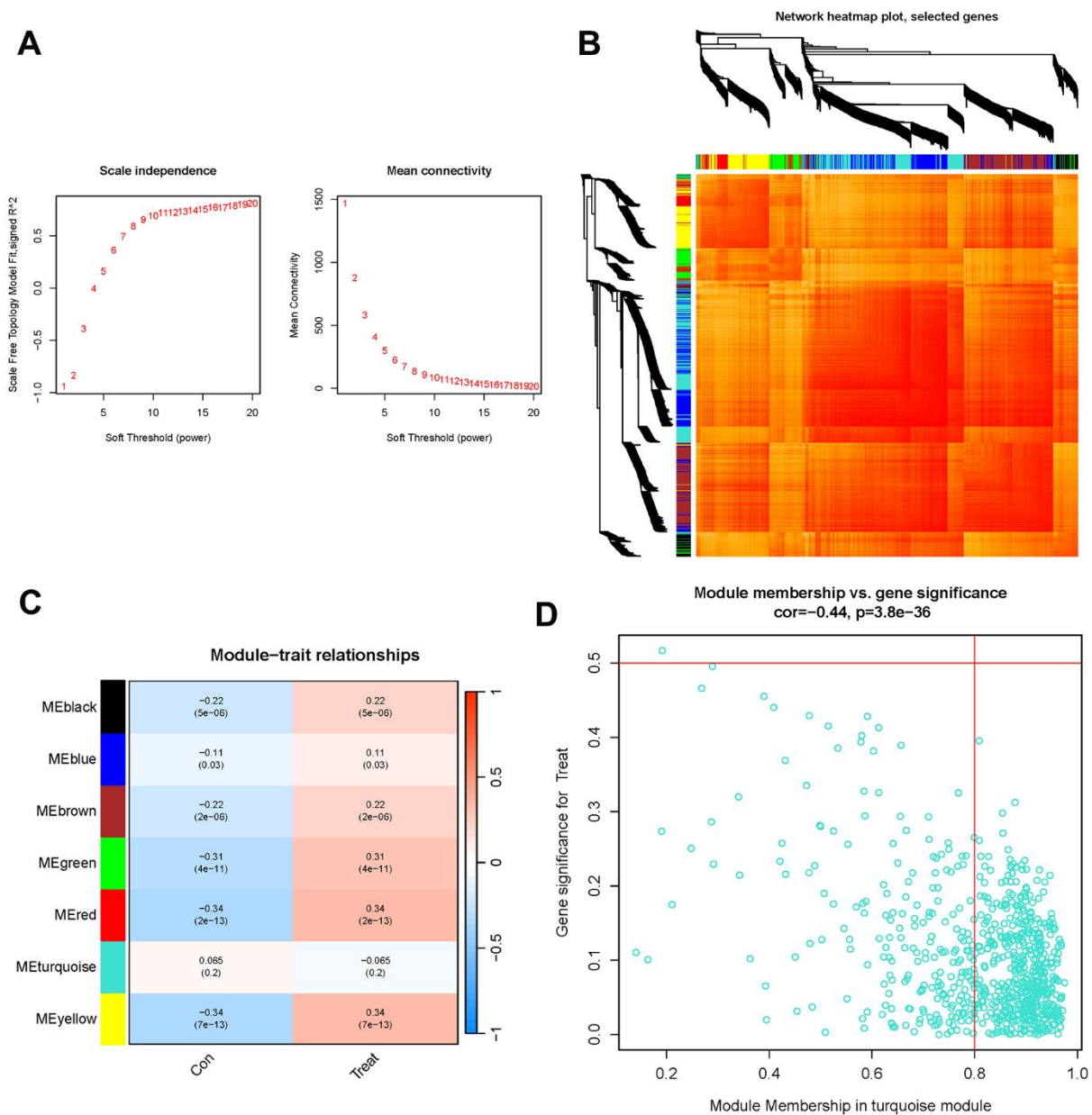


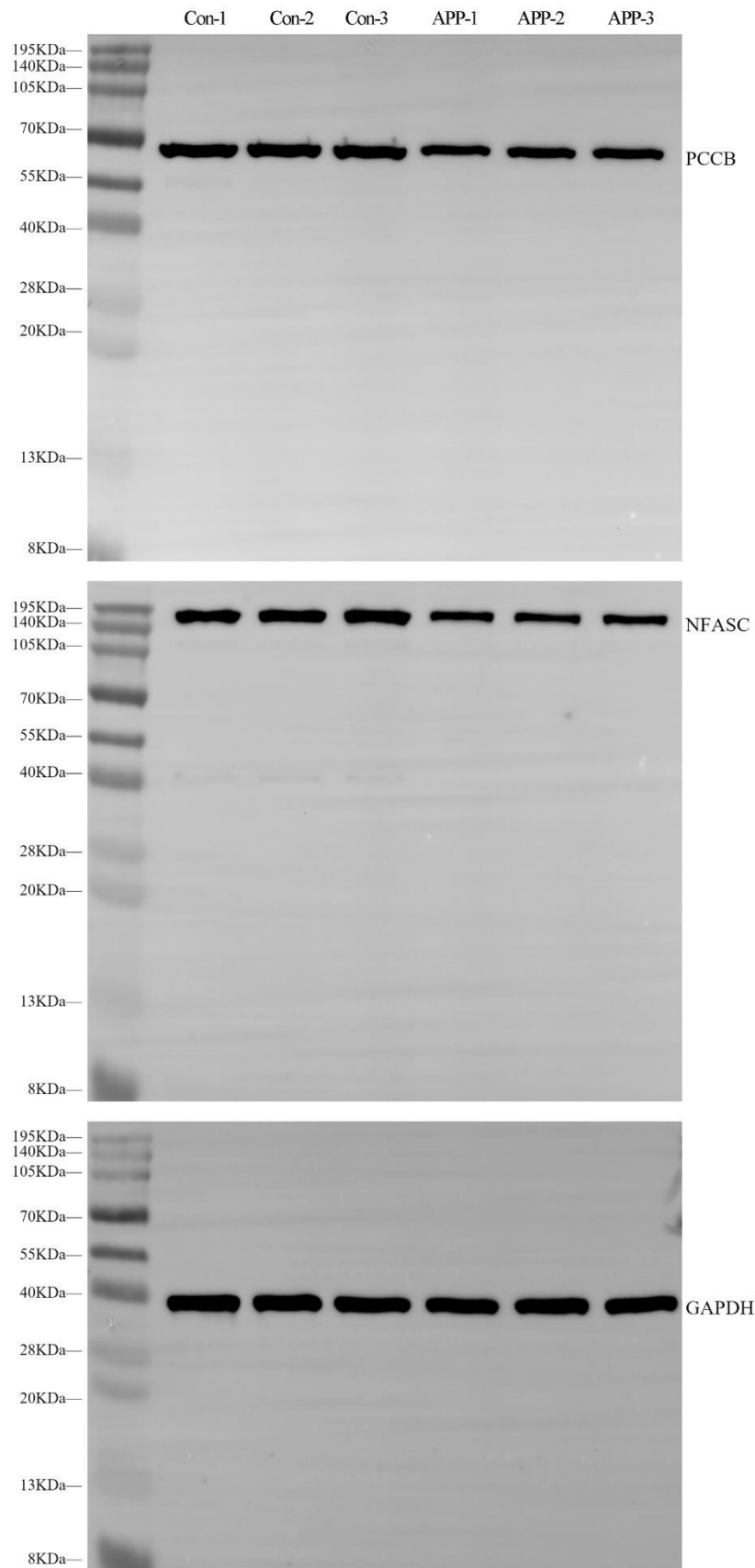
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Enrichment analysis for DEGs. (A) GO. (B) KEGG. (A) Barplot graph for GO enrichment (the longer bar means the more genes enriched; q-value: the adjusted p-value). **(B)** Barplot graph for KEGG pathways (the longer bar means the more genes enriched).



Supplementary Figure 2. Co-expression module construction. (A) Soft threshold power mean connection and scale-free fitting index analysis. (B) Clustering of dendrograms according to dynamic tree cutting, the genes were sorted into distinct modules using hierarchical clustering with a threshold of 0.25. Each color represents a separate module. (C) Heatmap of correlations between module eigengenes and clinical characteristics. (D) Gene scatterplot in the turquoise module.



Supplementary Figure 3. The original image of Western blotting.