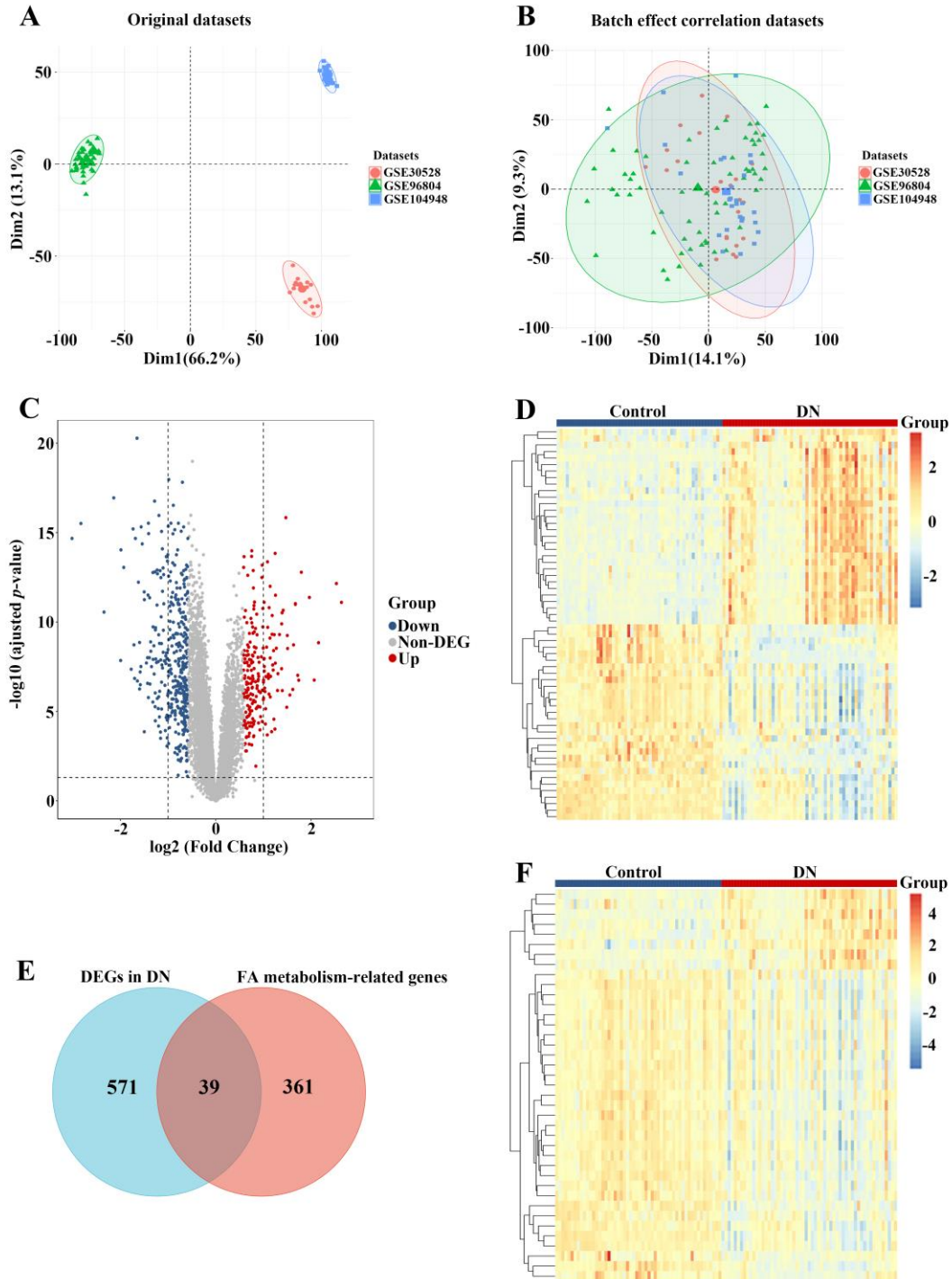


# Comprehensive analysis of fatty acid metabolism in diabetic nephropathy from the perspective of immune landscapes, diagnosis and precise therapy

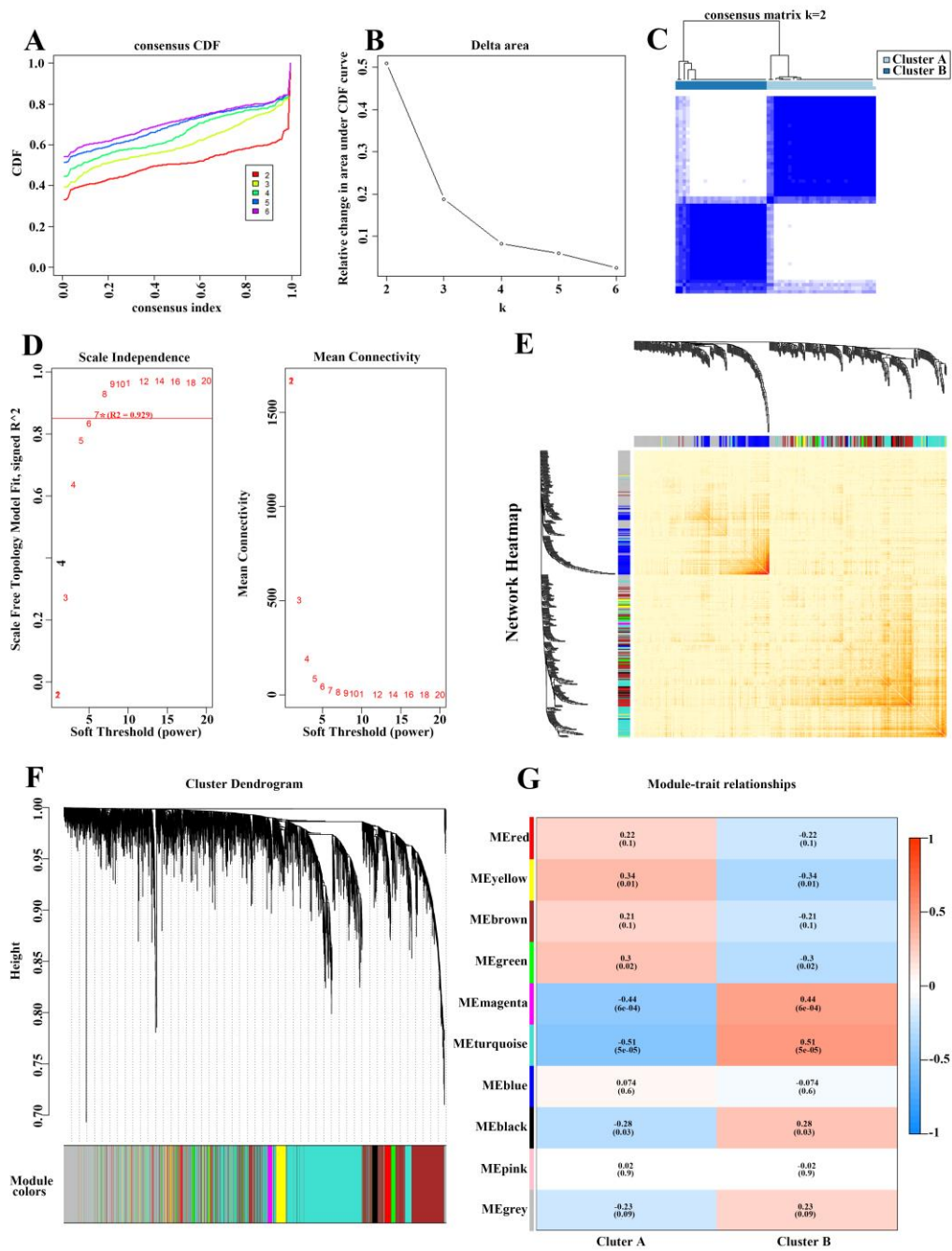
Additional file

Figure S1



**Figure S1. The integration of DN datasets and differential expression of FA metabolism-related genes in the combined DN dataset.** (A) The principal component analysis (PCA) for the obtained original DN datasets before batch-effect elimination. (B) PCA for the combined DN dataset after batch-effect elimination. (C) The volcano plot of the DEGs in the combined DN dataset. (D) The heatmap of the DEGs in the combined DN dataset. (E) The Venn diagram showing the differentially expressed FA metabolism-related genes in DN. (F) The heatmap of the differentially expressed FA metabolism-related genes in the combined DN dataset.

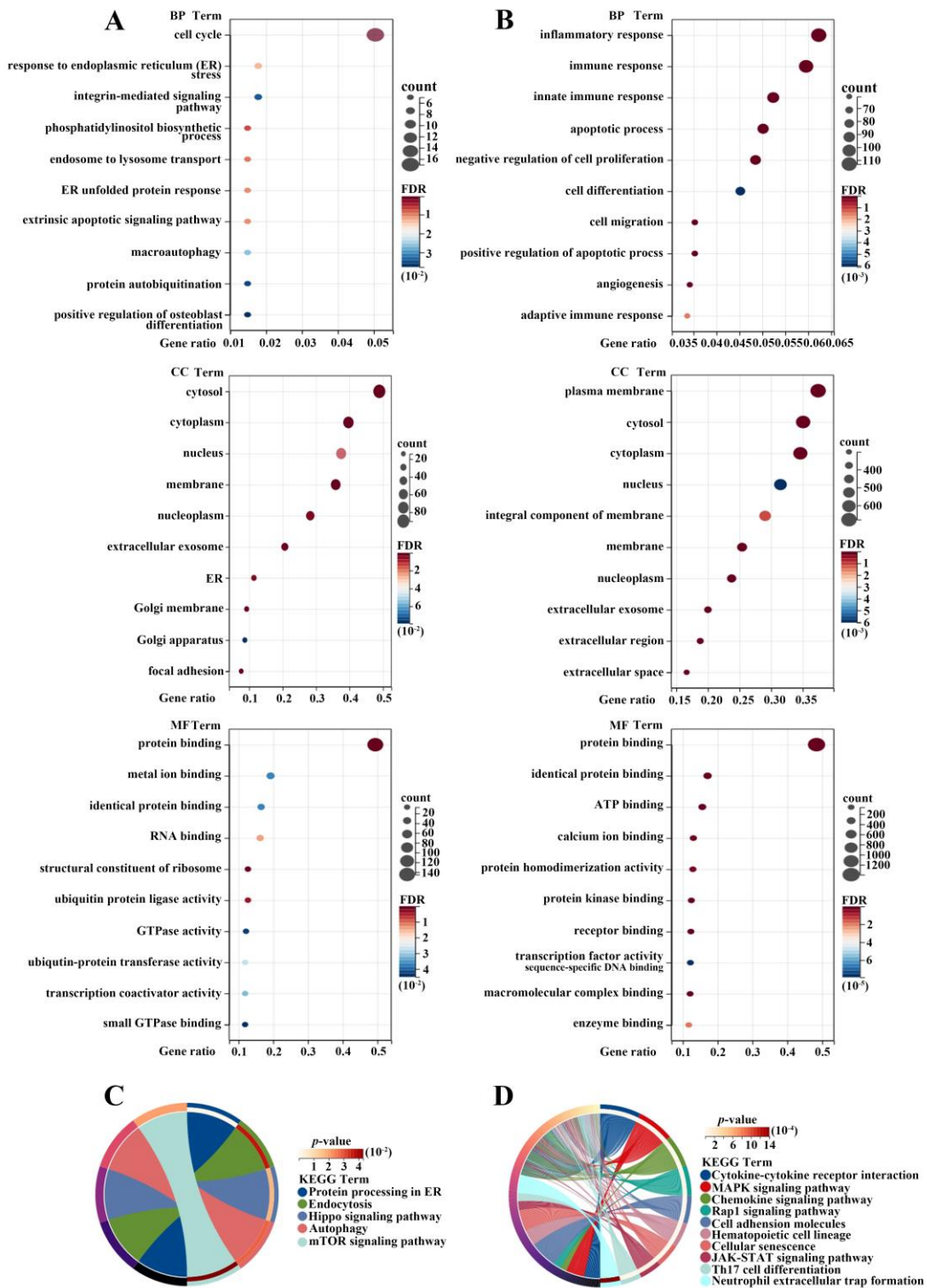
**Figure S2**



**Figure S2. Molecular grouping recognition of FA metabolism-related genes and key modules identification for DN subtypes via WGCNA.** (A) The cumulative distributive function (CDF) for  $k = 2$  to 6. (B) The delta diagram presenting the relative change in the area under the CDF curve for  $k = 2$  to 6. (C) The consistency matrix heatmap showing the two molecular subtypes of DN patients

with  $k = 2$ . (D) The network topology exhibiting a series of soft-threshold powers, and  $\beta = 7$  ( $R^2 = 0.929$ ) was selected as the soft threshold for further analysis. (E) The network heatmap for the gene dendrogram and module eigengenes. (F) Dendrogram clustered based on a dissimilarity measure (1-TOM), and various colors under the gene tree illustrate the co-expressed gene modules. (G) The heatmap displaying the relationship between different modules and molecular subtypes.

**Figure S3**



**Figure S3. The functional enrichment analysis of molecular subtypes-associated key module**

**genes. (A) The gene ontology (GO) annotation of genes included in Cluster A-associated key**

modules, including biological process (BP), cellular component (CC), and molecular function (MF).

(B) The BP, CC, and MF annotations of genes included in Cluster B-associated key modules. (C)

The KEGG analysis of genes included in Cluster A-associated key modules. (D) The KEGG analysis

of genes included in Cluster B-correlated key modules.