Figure S1 EC infiltration promoted RCC progression through an immunosuppressive TME. (A) Distribution of EC infiltration in TNM classification and stage of RCC. (B) Heatmap of the TME components and scores in RCC with high and low EC infiltration. EC, endothelial cells; RCC, renal cell carcinoma; TME, tumor microenvironment.
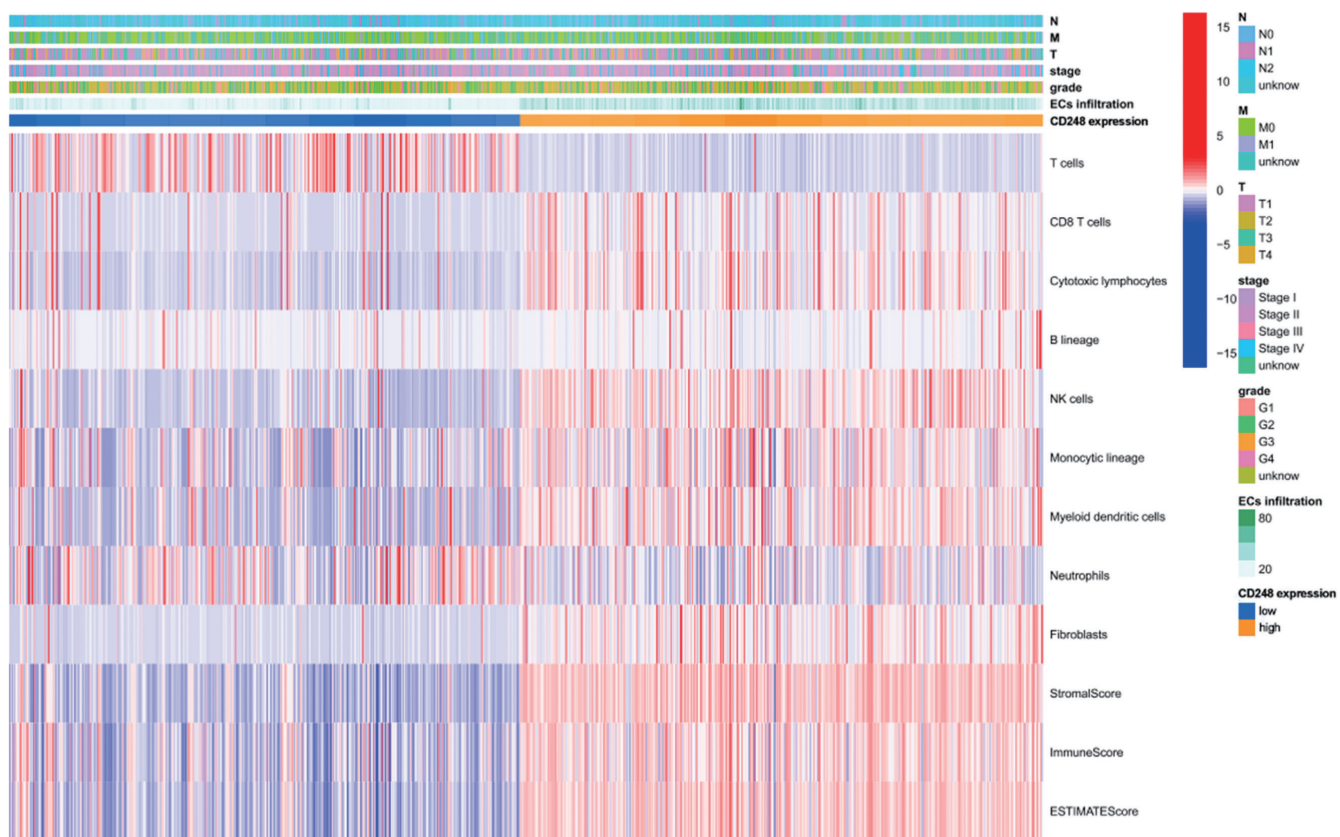
Figure S2 The heatmap of TME components and scores in RCC with high and low CD248 expression. TME, tumor microenvironment; RCC, renal cell carcinoma.
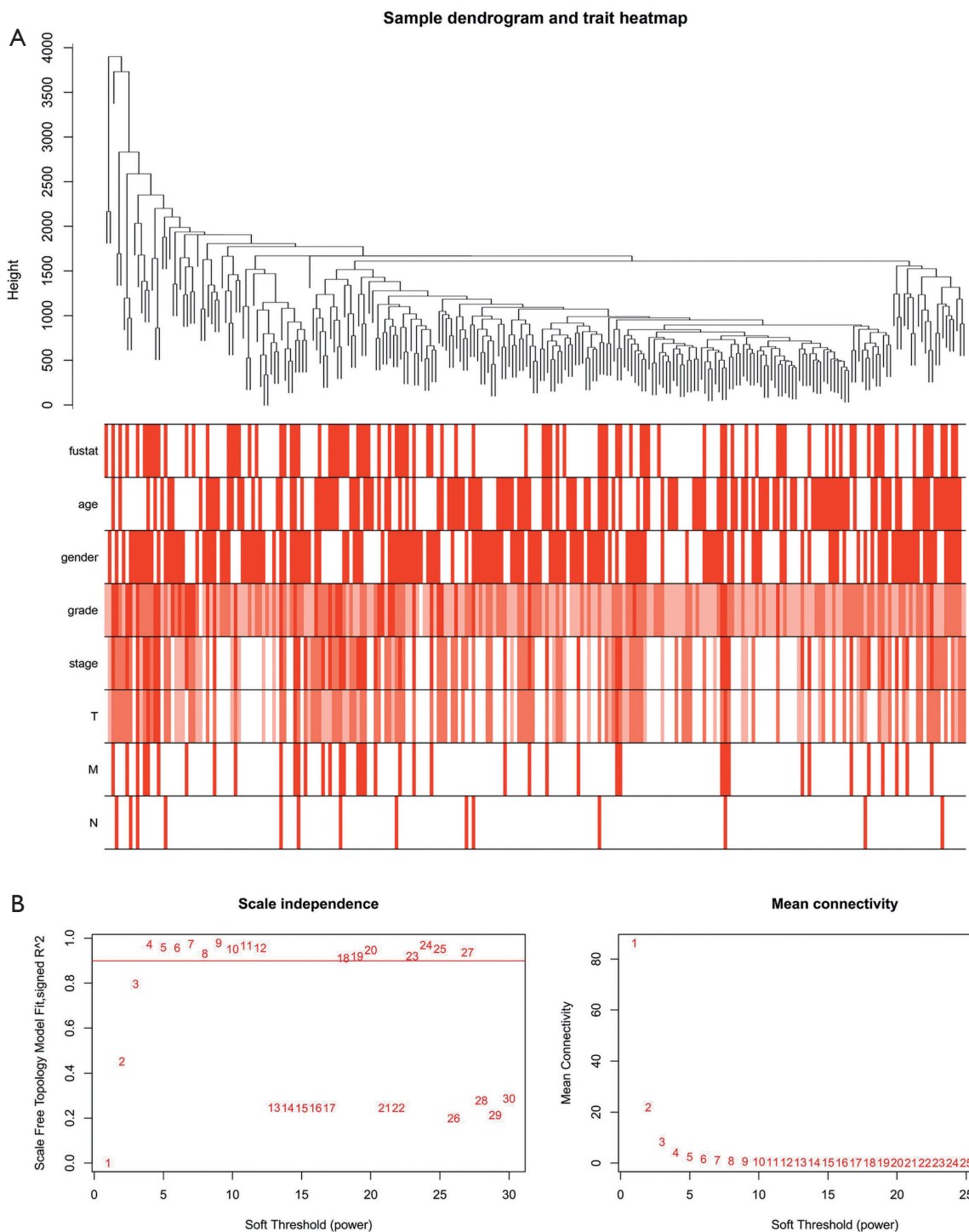
Figure S3 Analysis of the network topology for adjacency matrix weighting parameters (power). (A) Hierarchical average linkage clustering. Branches of the dendrogram represent genes with similar expression patterns. (B) The x-axis represents soft threshold (power), and the y-axis represents the scale-free fitting index and connectivity for each power. The soft-thresholding power for network construction was set at 0.9.
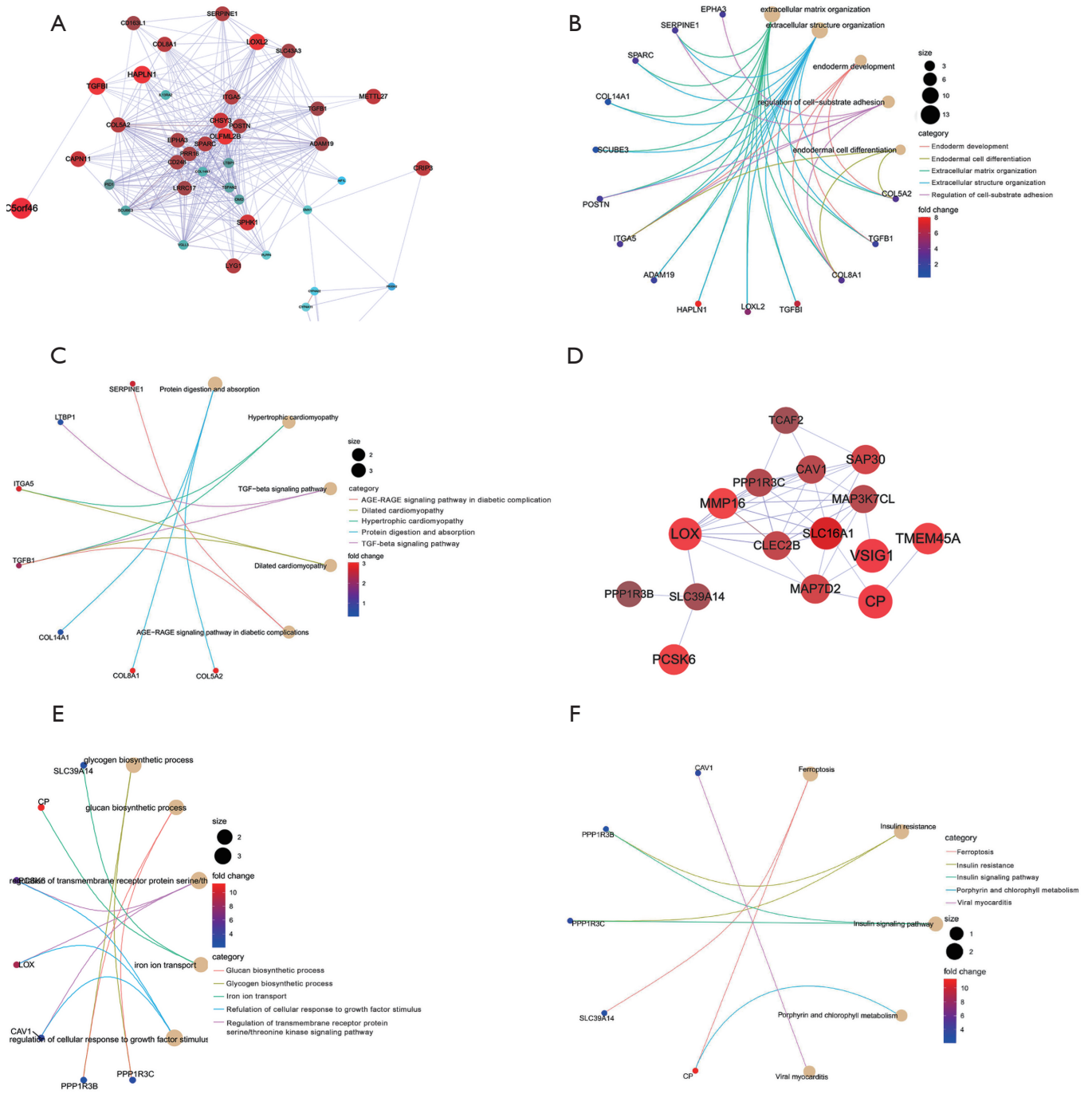
Figure S4 The WGCNA and enrichment analysis of the shared DEGs by EC infiltration and CD248 expression. (A) The coexpressed network of the black module annotated with stroma. (B,C) GO (B) and KEGG (C) enrichment analysis of the black module. (D) The coexpressed network of the green-yellow module. (E,F) GO (E) and KEGG (F) enrichment analysis of the green-yellow module. WGCNA, weighted gene coexpression network analysis; DEGs, differentially expressed genes; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.