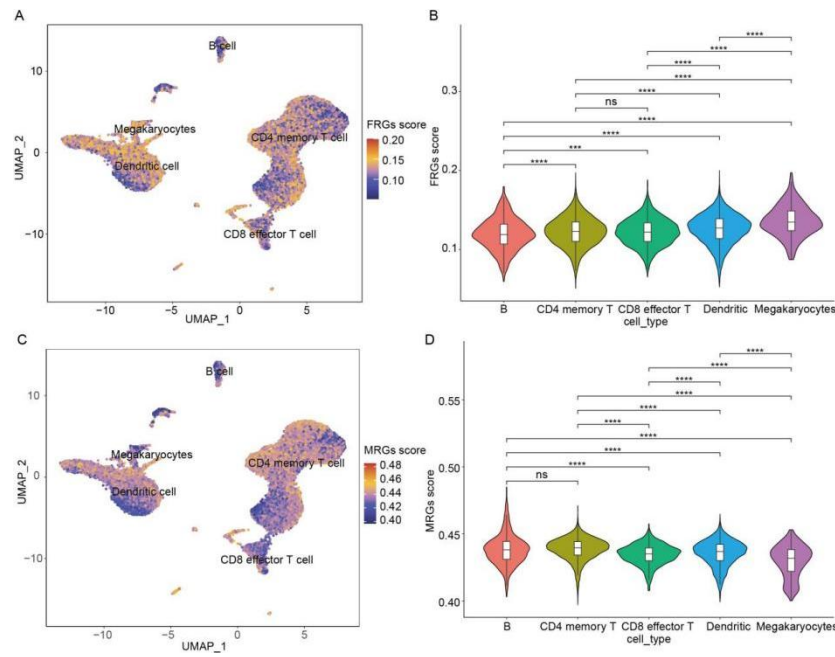
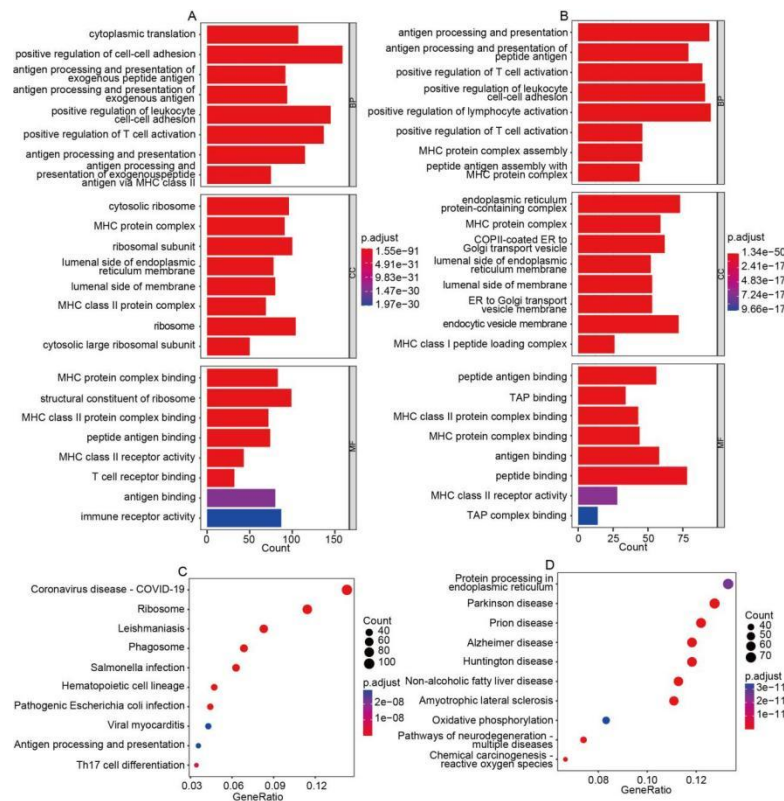
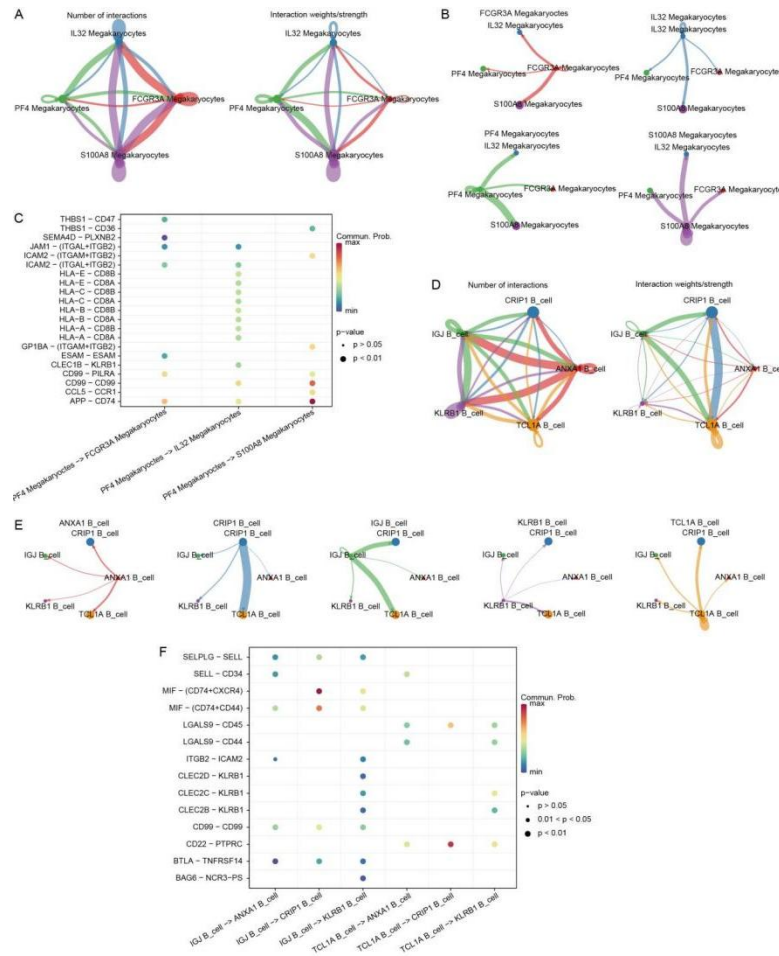




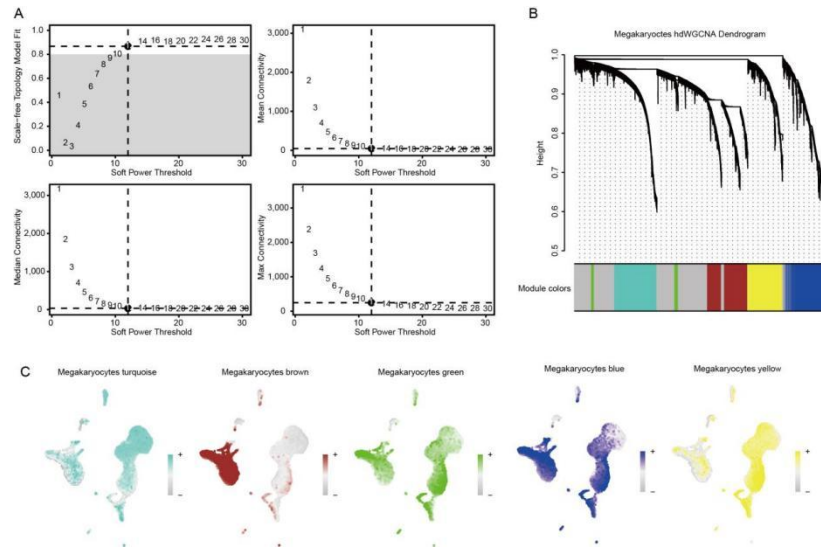
Supplementary Figure 1. Phenotype-related gene score analysis in single-cell data. (A) UMAP plot displaying the distribution of FRGs Scores across different cell types. (B) Violin plot illustrating the distribution of FRGs Scores. (C, D) UMAP and violin plots, respectively, showing the distribution of MRGs Scores within distinct cell types. FRGs: ferroptosis related genes; MRGs: mitochondrial related genes.



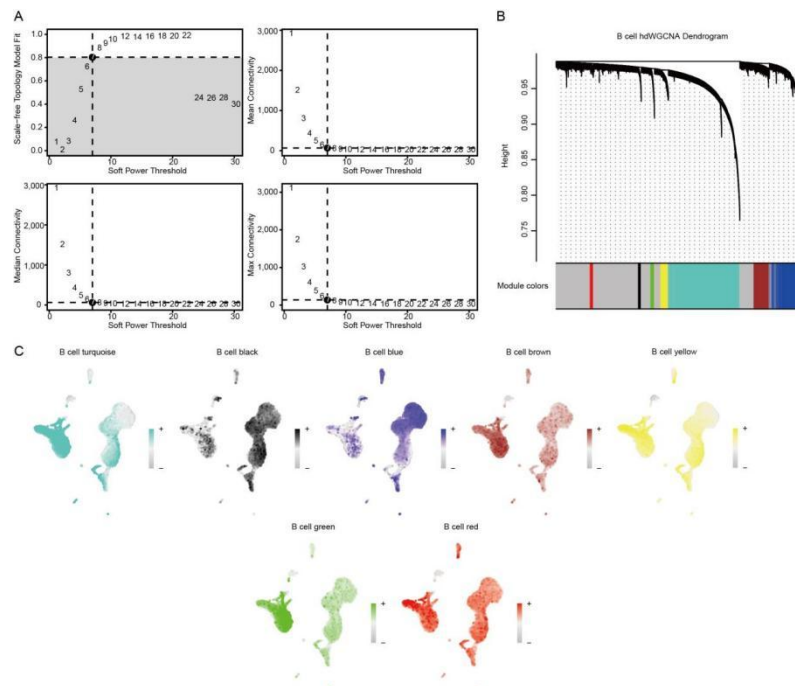
Supplementary Figure 2. Enrichment Analysis Results for DEGs. (A, C) GO and KEGG enrichment analysis results for Megakaryocytes subtypes; (B, D) GO and KEGG enrichment analysis results for B cell subtypes.



Supplementary Figure 3. Cell communication analysis. (A, B) Interactions among Megakaryocyte subtypes; (D, E) Interactions among B cell subtypes; (C, F) The bubble chart shows receptor-ligand interaction for Megakaryocyte subpopulations and B cell subtypes, respectively. Bubble color gradient from blue to red represents interaction strength from weak to strong, and bubble size from small to large indicates significance from weak to strong.

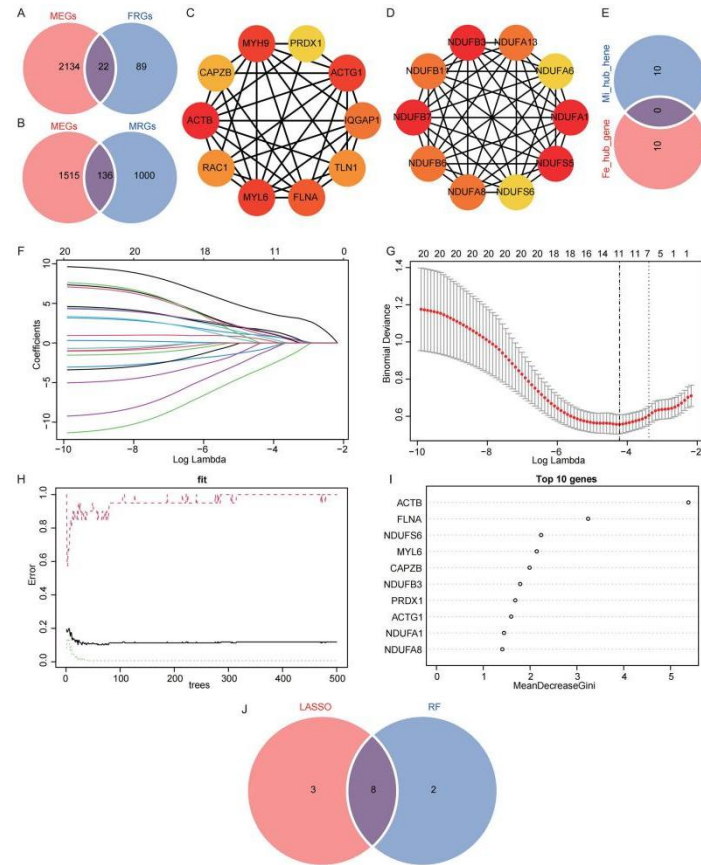


Supplementary Figure 5. *hdWGCNA* results for Megakaryocytes. (A) Soft power = 11 was selected to construct the scale-free network. (B) Dendrogram was utilized to visualize the hierarchical clustering based on gene expression patterns. (C) The UMAP plots respectively depicted the expression distribution of module genes across four subpopulations of Megakaryocytes.

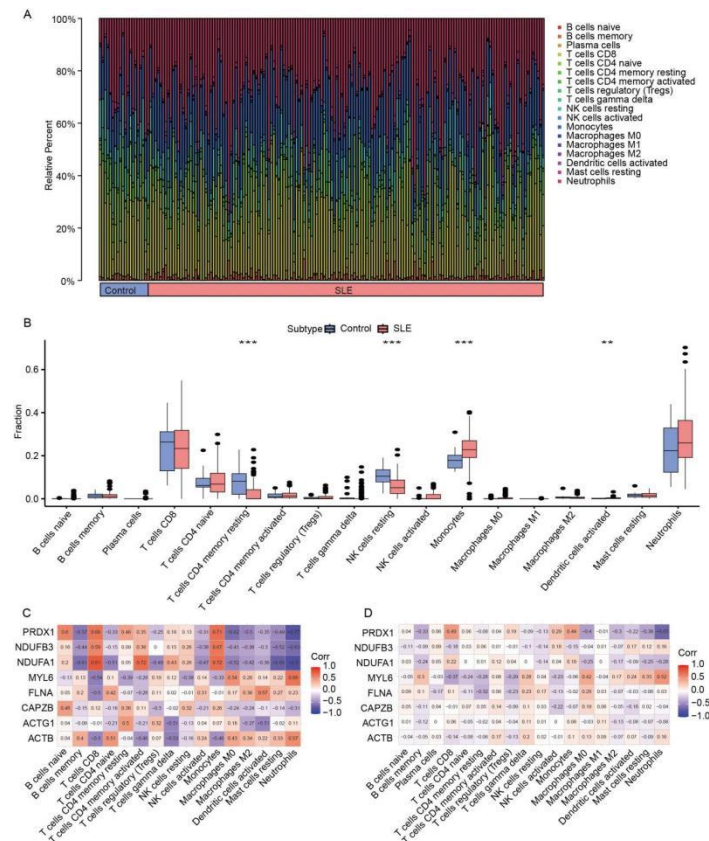


Supplementary Figure 6. *hdWGCNA* results for B cells. (A) Soft power = 7 was selected to construct the scale-free network. (B) Dendrogram was utilized to visualize the hierarchical clustering. (C) The

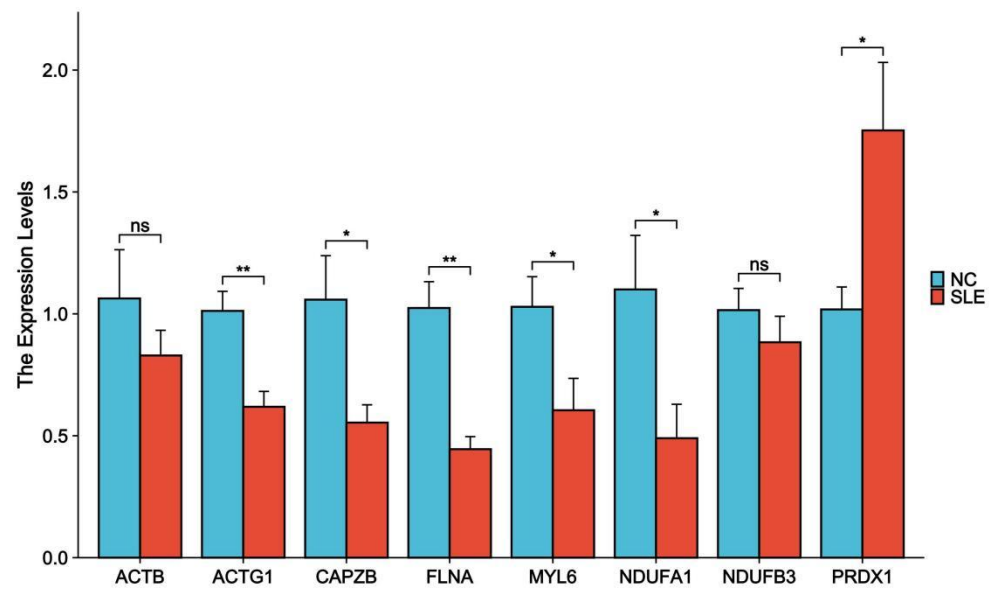
UMAP plots respectively depicted the expression distribution of module genes across five subpopulations of B cells.



Supplementary Figure 7. Selection of potential diagnostic genes. (A) The Venn diagram illustrates the intersection of module genes from Megakaryocytes and FRGs. (B) The Venn diagram shows the intersection of module genes from B cells and MRGs. (C,D) The MCC algorithm in cytoHubba is used to identify the top 10 genes as hub genes for both sets. (E) The Venn diagram illustrates the union of the hub genes identified, resulting in a set of 20 key genes. (F,G) LASSO coefficient profiles and the optimal tuning parameter selection map for SLE showed the final parameter selection λ (lambda). (H,I) Top10 genes according to their discriminant ability in the RF algorithm. (J) The Venn diagram showed eight candidate diagnostic genes in SLE by intersecting the results of LASSO and RF algorithms.



Supplementary Figure 8. The immune infiltration analysis between SLE patients and controls. (A) The relative percent of immune cell subsets in a bar plot. (B) Infiltrating difference of immune cells between SLE patients and controls in the box plot. (C, D) Heatmaps illustrate the correlations between immune cells and the eight diagnostic biomarkers in both the control and SLE groups, respectively. Statistical significance at the level of * <0.05, ** <0.01 and *** <0.001.



Supplementary Figure 9 The expression levels of the potential diagnostic markers in patients with SLE

*and controls. Statistical significance at the level of ns ≥ 0.05 , * < 0.05 , ** < 0.01 . NC: Negative control.*