

Figure S1

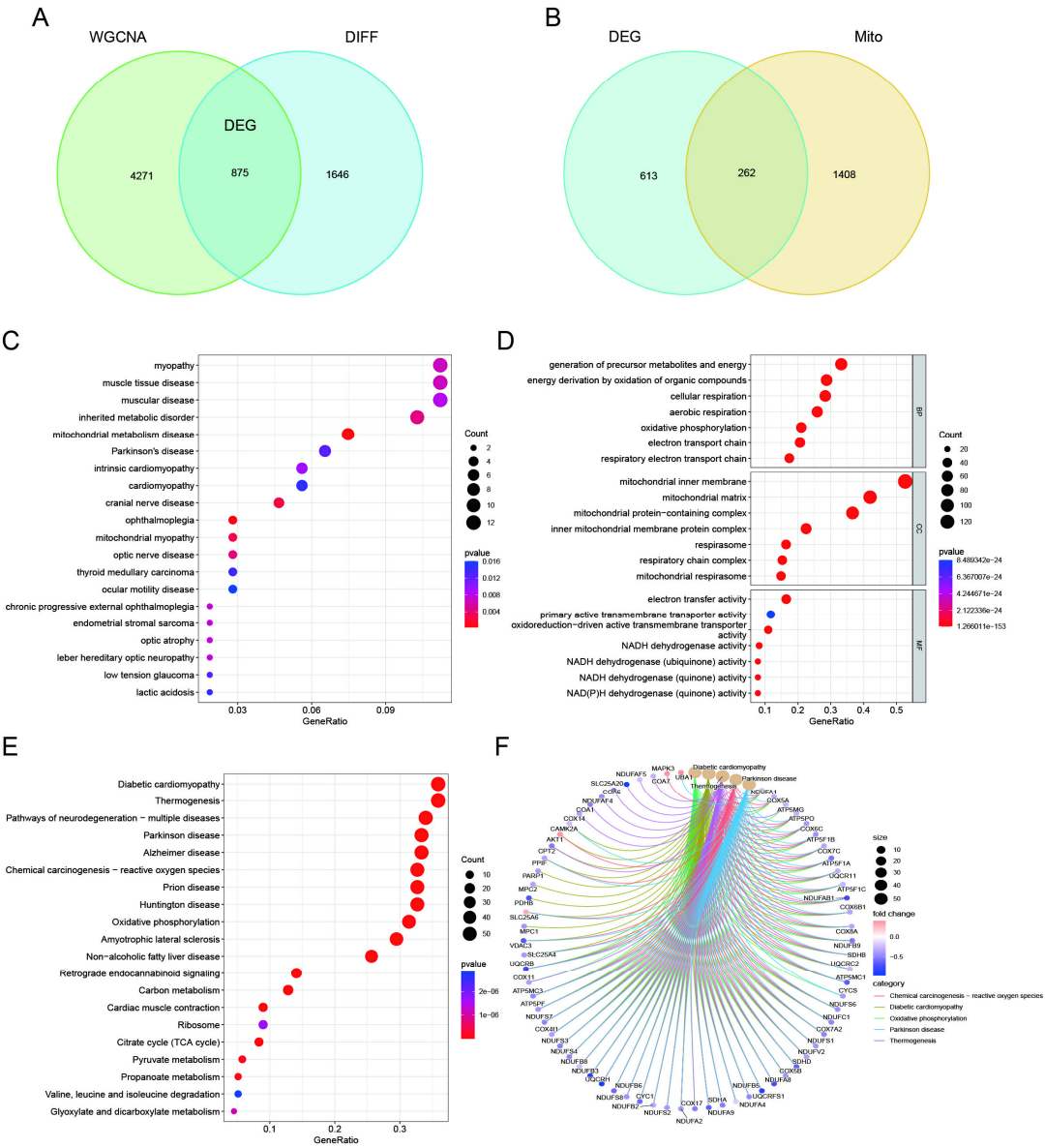


Figure S1. Identification and Functional Analysis of MitoDEGs in SCM.

(A) Venn diagram of key module genes versus differentially expressed genes. (B) Venn diagram of mitochondria-related genes versus DEGs. (C) DO analysis. (D) GO analysis. (E-F) KEGG analysis

Figure S2

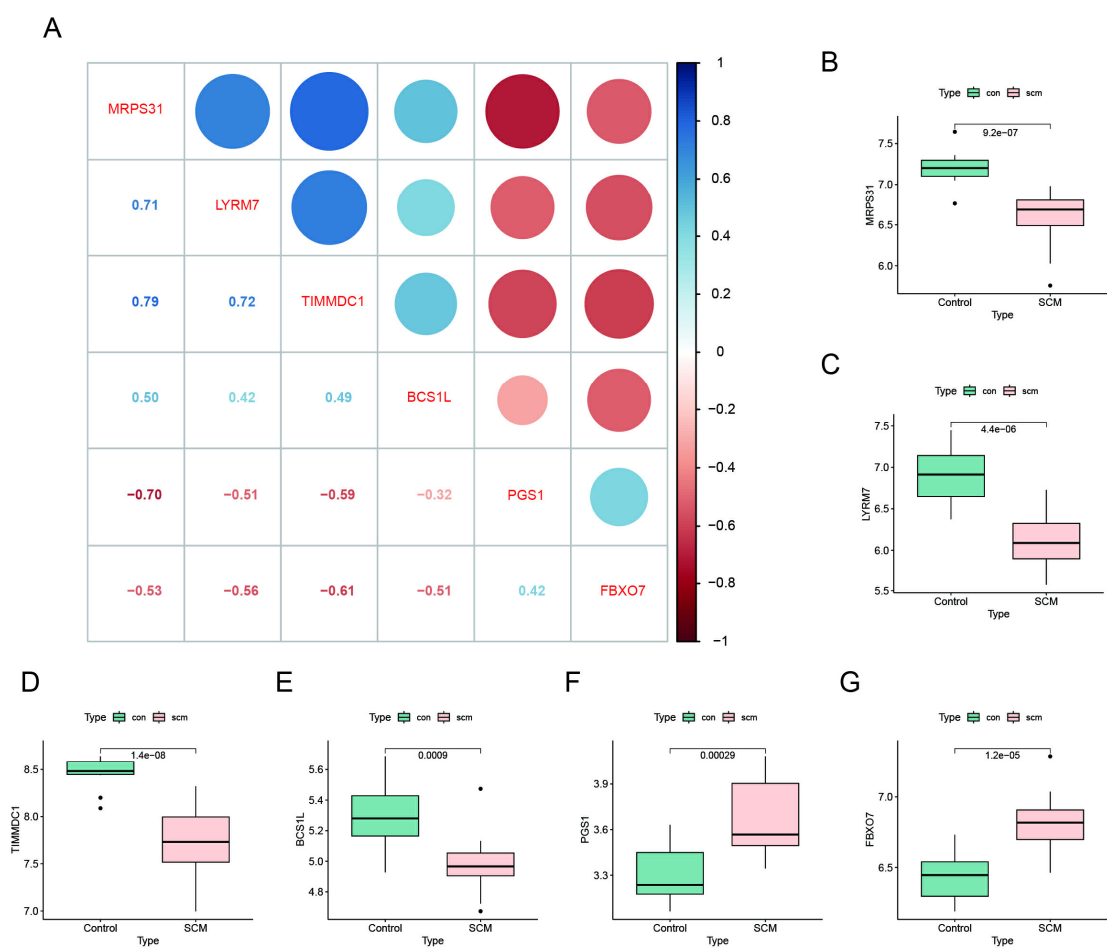


Figure S2. Expression analysis of hub genes.

(A) Correlation between hub genes. (B-G) Expression of six hub genes in SCM and control groups.

Figure S3

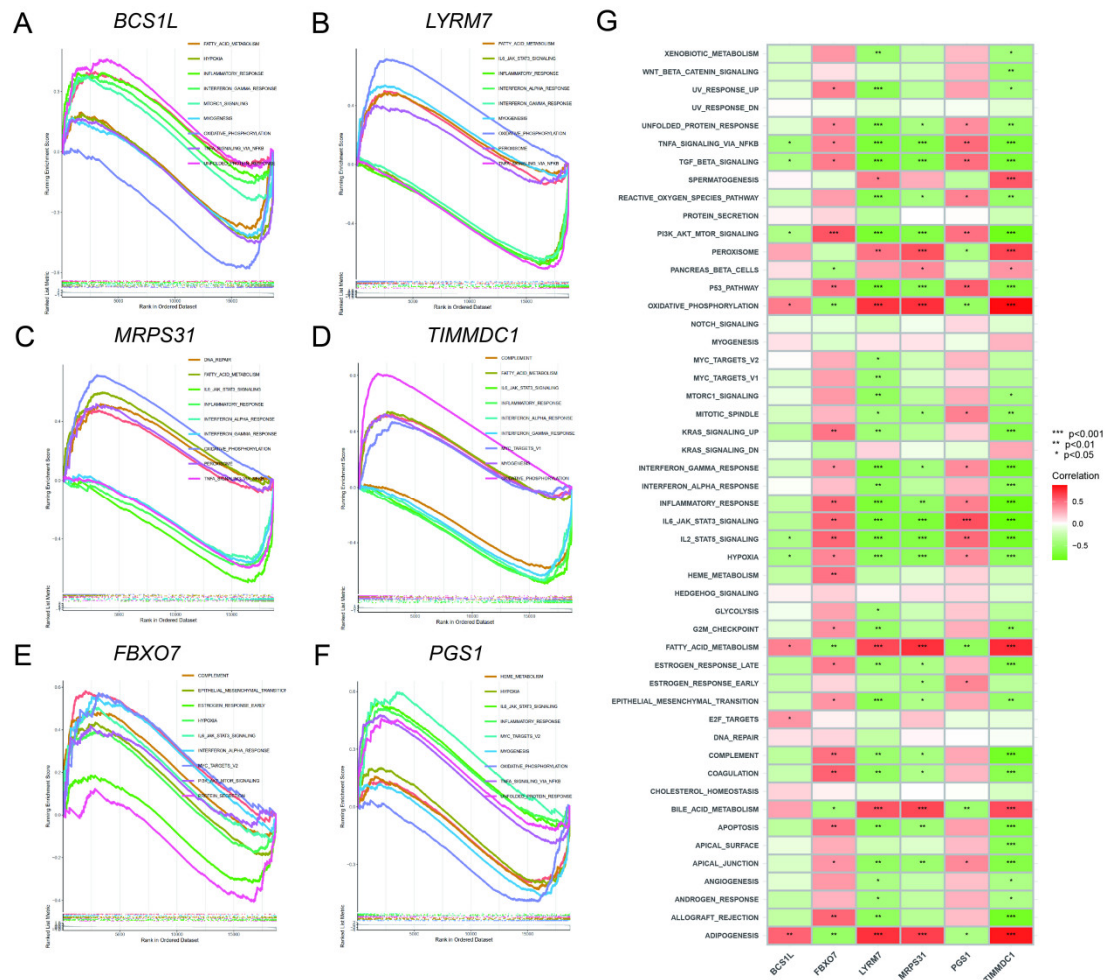


Figure S3. Correlation between hallmark pathways and hub genes.

(A-F) GSEA analysis of hub genes. Top 5 GSEA enrichment in the high and low expression group of (A) BCS1L, (B) LYRM7, (C) MRPS31, (D) TIMMDC1, (E) FBXO7, (F) PGS1. (G) Correlation between hub genes and hallmark pathways. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Figure S4

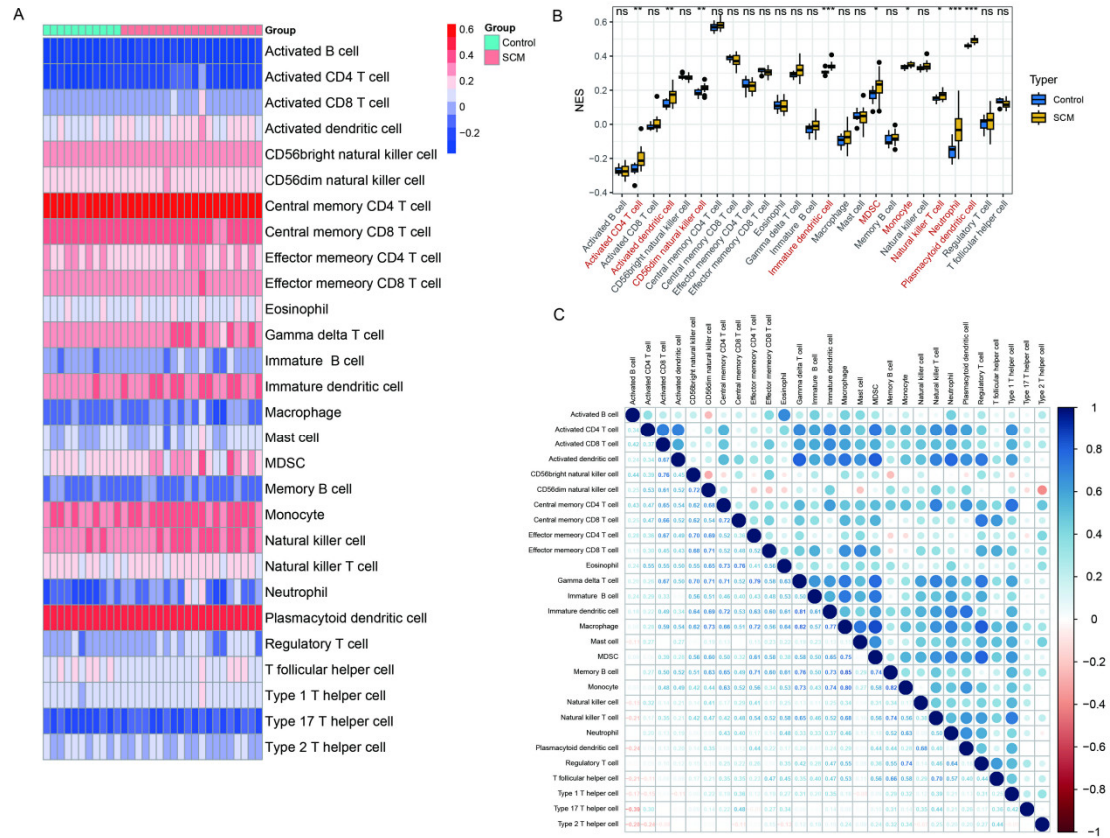


Figure S4. Infiltration of immune cell types compared between SCM and CON.

(A) Heatmap of the proportions of 28 immune cell types; (B) The boxplot of the immune cell proportions; (C) The correlation matrix of immune cell proportions. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.