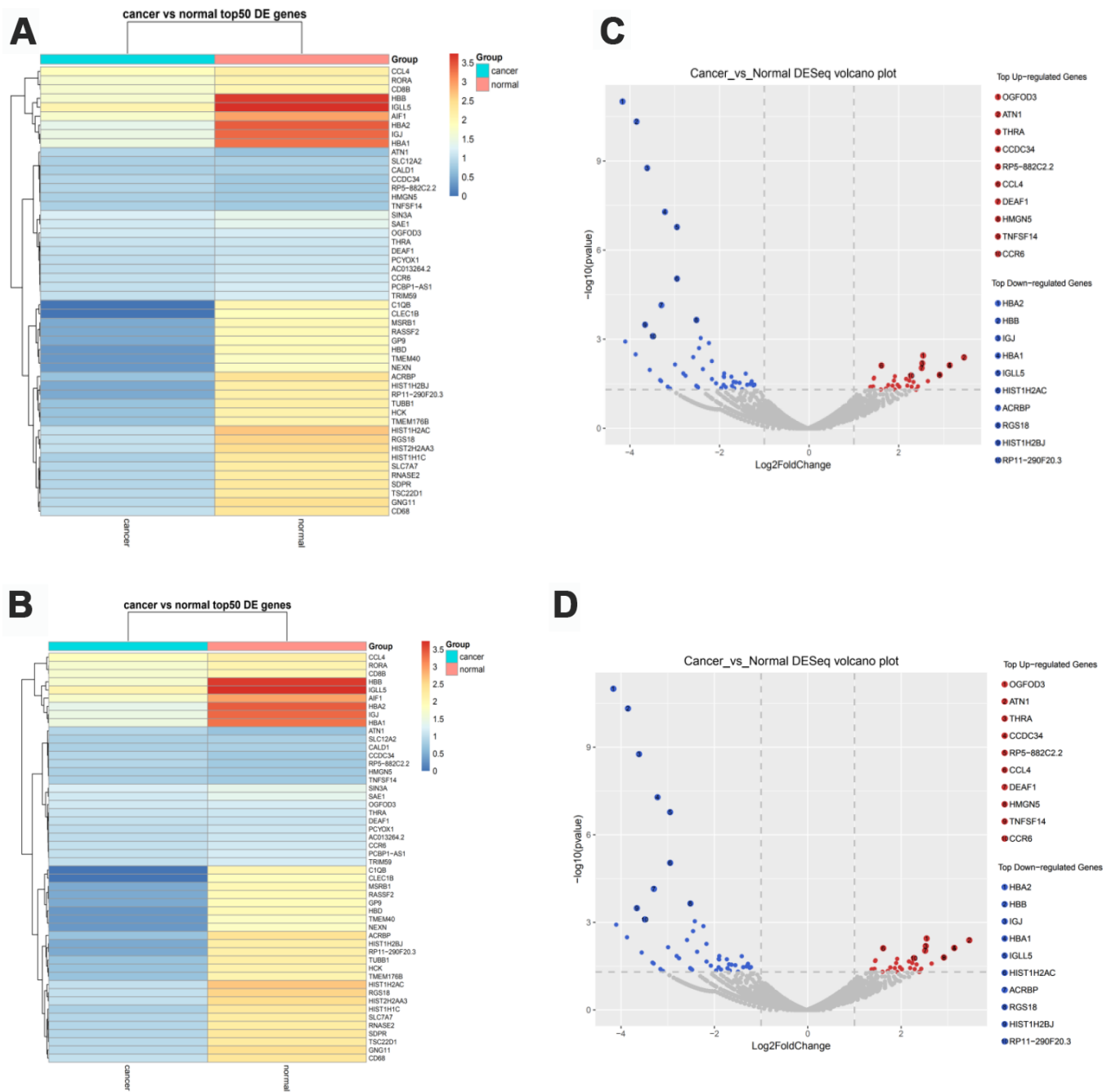
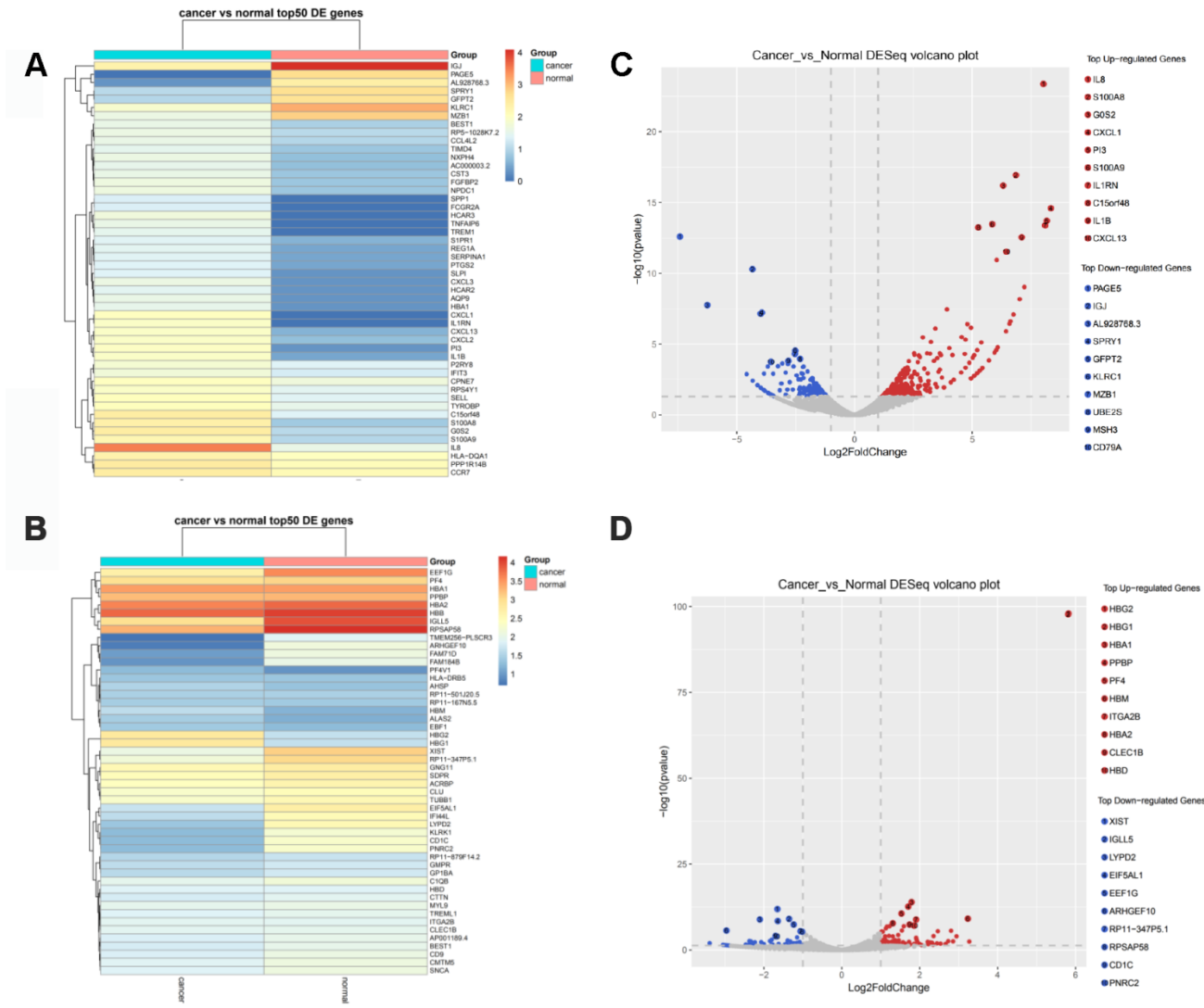


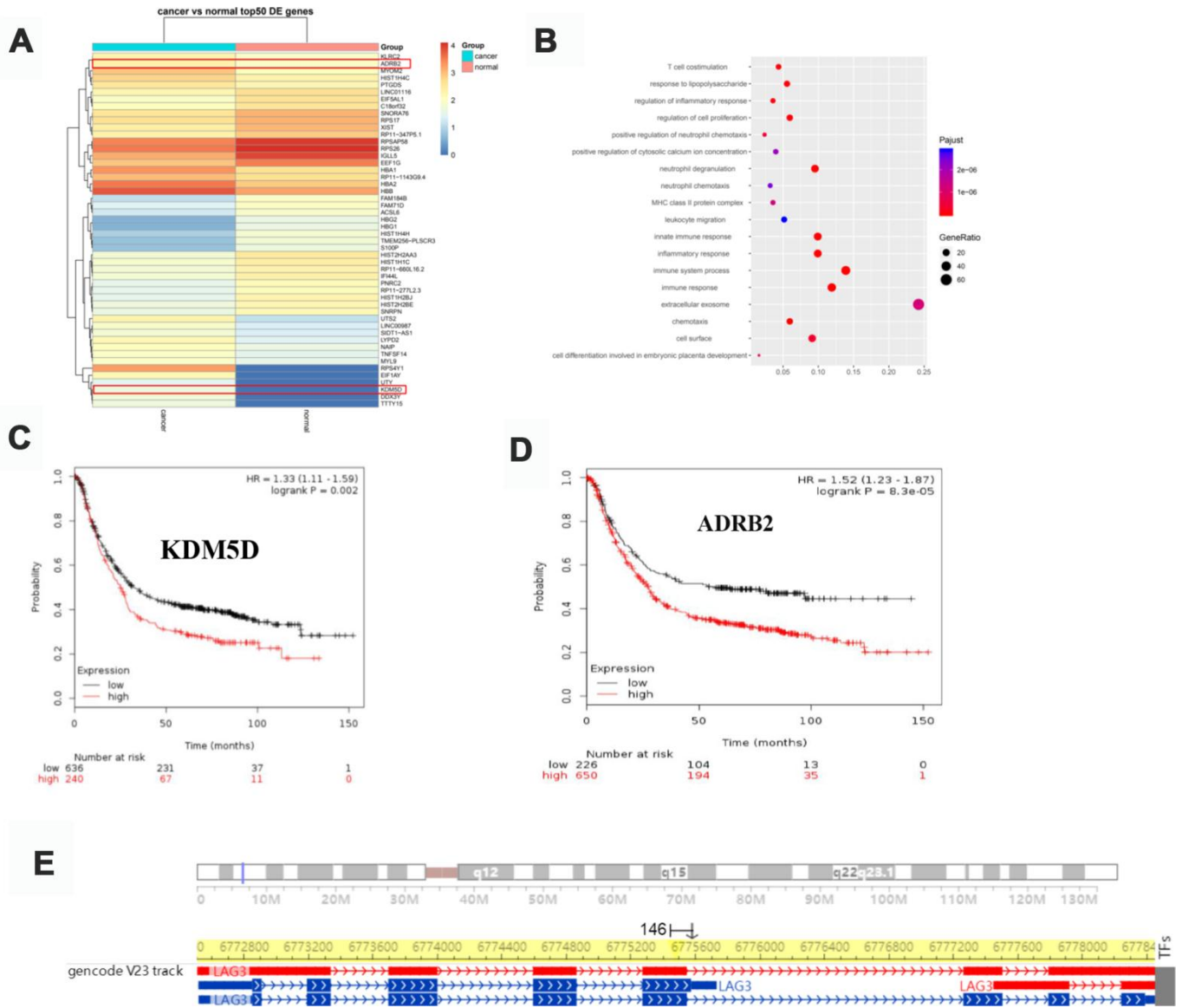
SUPPLEMENTARY FIGURES



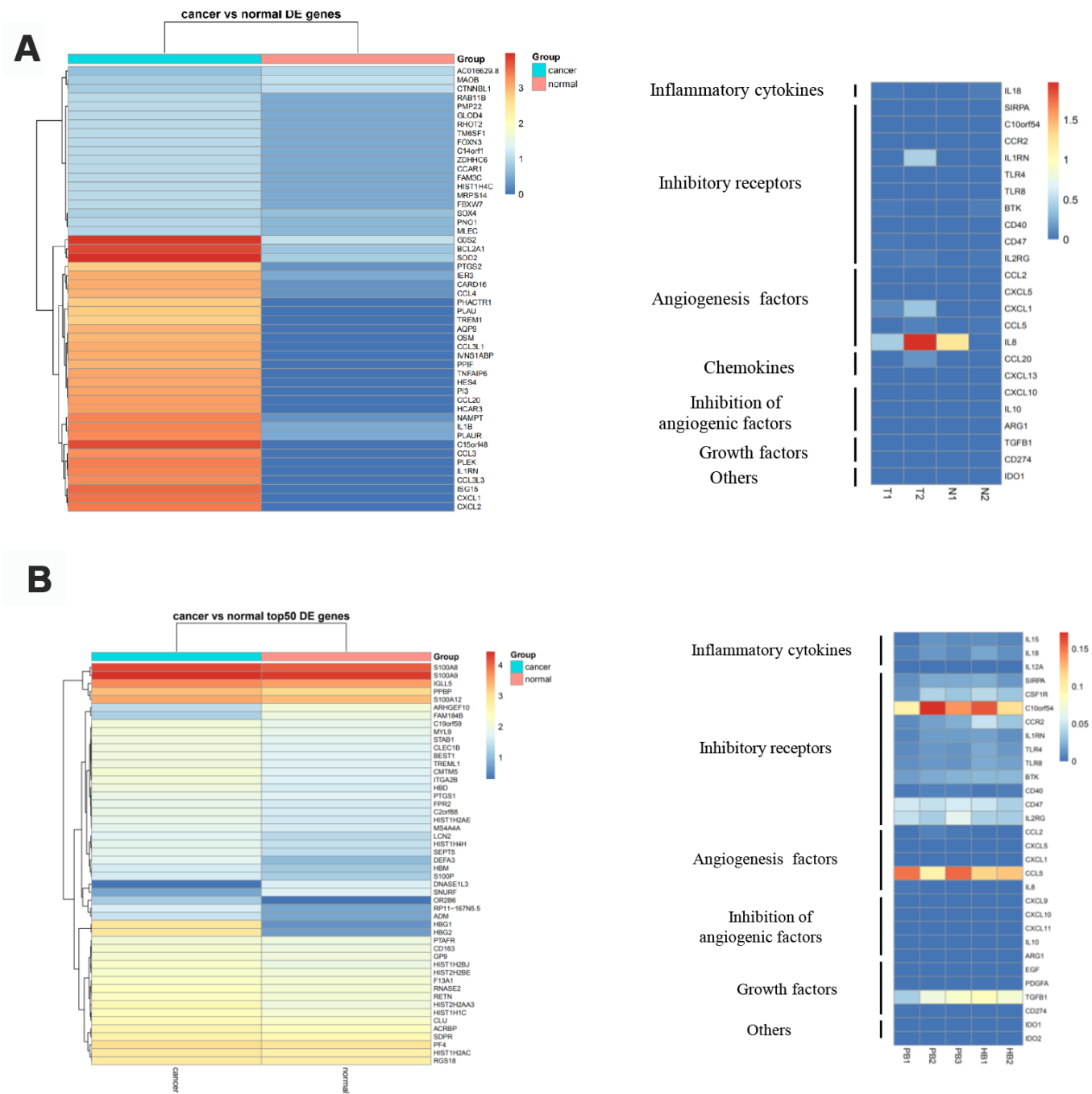
Supplementary Figure 1. Identification of CD8⁺ naive T cells in GC. (A) Heat map displaying the top 50 different genes in CD8⁺ naive T cells in T vs N. (B) Heat map displaying the top 50 different genes in CD8⁺ naive T cells in PB vs HB. (C) Volcano plot showing the top 10 upregulated and 10 downregulated genes in CD8⁺ naive T cells in T vs N. (D) Volcano plot showing the top 10 upregulated and 10 downregulated genes in CD8⁺ naive T cells in PB vs HB.



Supplementary Figure 2. Identification of CD8⁺ cytotoxic T cells in GC. (A) Heat map displaying the top 50 differentially expressed genes in CD8⁺ cytotoxic T cells in T vs N. (B) Heat map displaying the top 50 differentially expressed genes in CD8⁺ cytotoxic T cells in PB vs HB. (C) Volcano plot showing the top 10 upregulated and 10 downregulated genes in CD8⁺ cytotoxic T cells in T vs N. (D) Volcano plot showing the top 10 up-regulated and 10 down-regulated genes in CD8⁺ cytotoxic T cells in PB vs HB.



Supplementary Figure 3. Identification of Tregs in GC blood. (A) Heat map displaying the top 50 differential genes in Tregs from blood. (B) Pathway analysis for different genes in Tregs. (C and D) KM-plotter database analysis of KDM5D and ADRB2 in GC. (E) RBPJ regulates the locus of LAG3.



Supplementary Figure 4. Gene signature of macrophages and pathway analysis. (A) The expression analysis of functional molecules in macrophages cell cluster in T vs N. **(B)** The expression analysis of functional molecules in macrophages cell cluster in PB vs HB