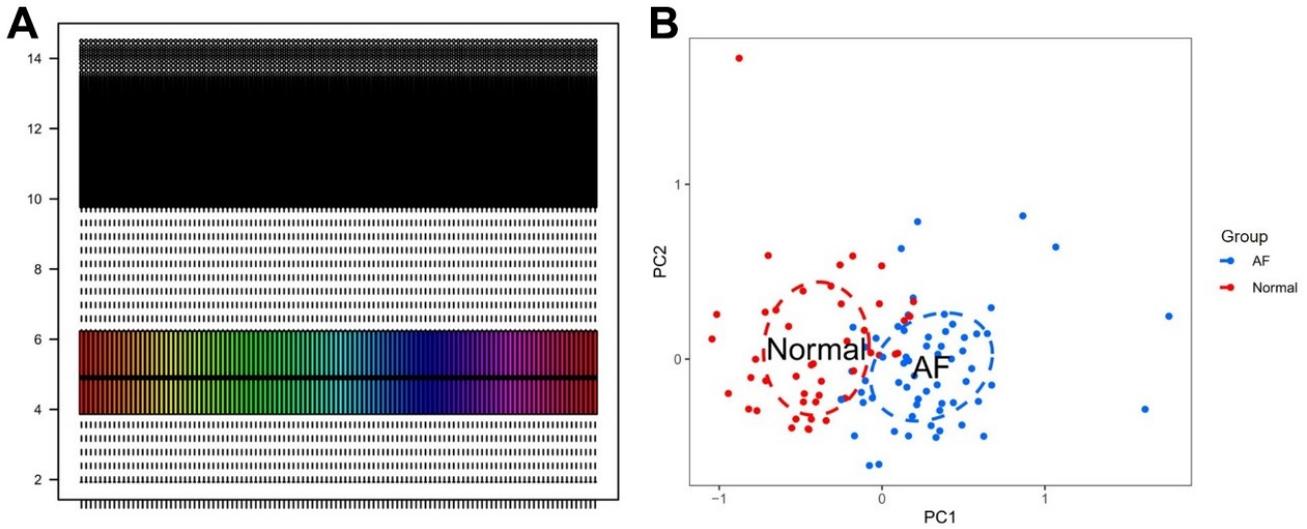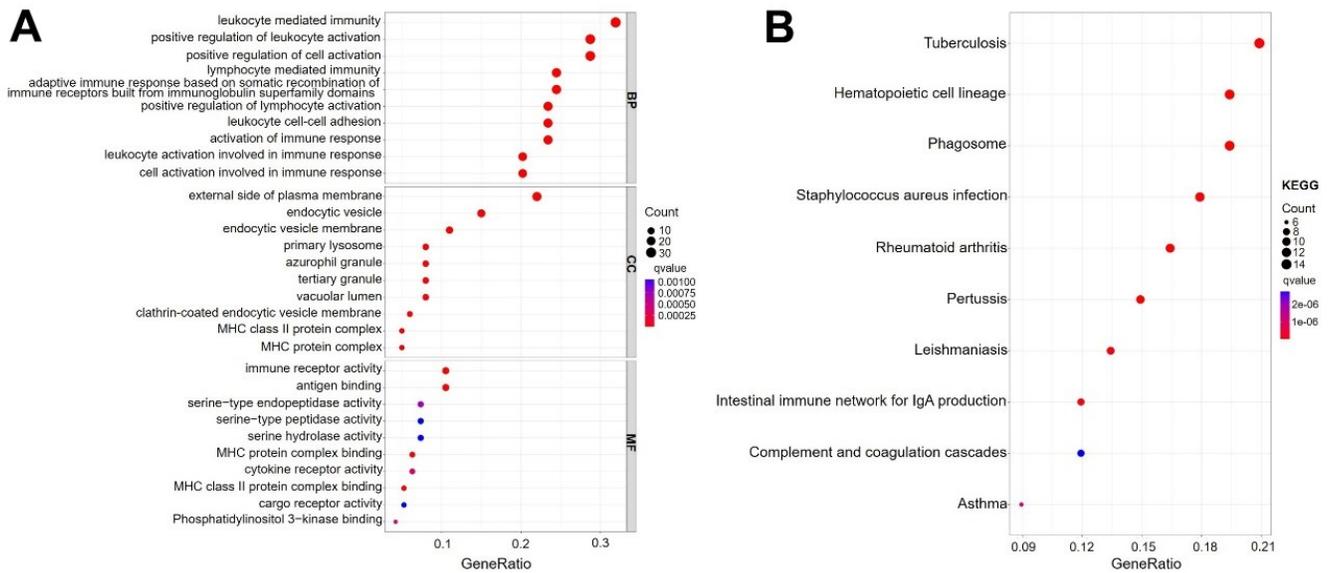**Supplementary Figure 1. Standardization and principal component analysis of all samples.** (**A**) Normalized for all samples. (**B**) Principal component analysis for all samples.

Supplementary Figure 2. Enrichment analysis of the genes in the meaningful modules. (**A**) GO functional enrichment analysis. (**B**) KEGG pathways analysis. The gene number was represented at x-axis, the KEGG pathway and GO terms were presented at y-axis.
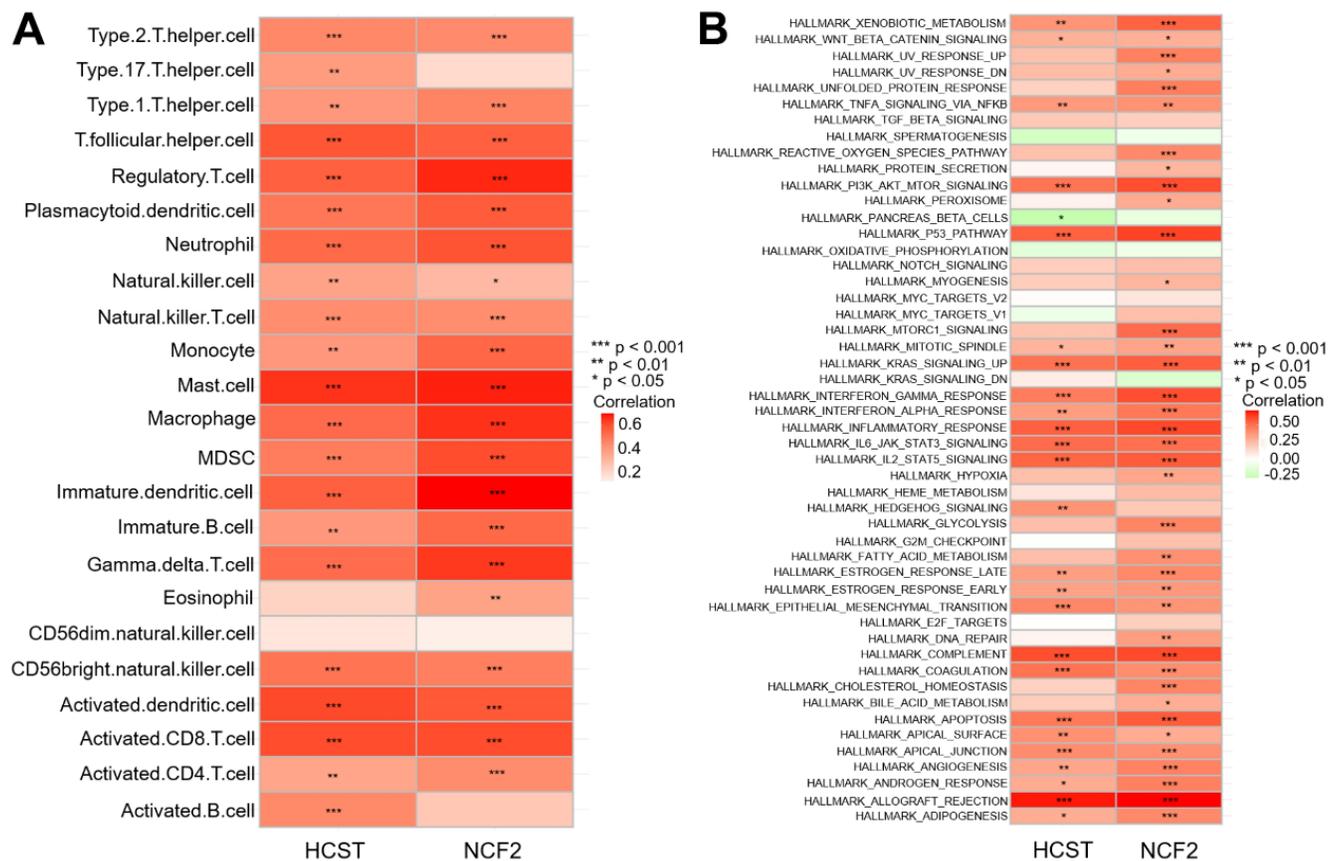
Supplementary Figure 3. Heatmap of correlations between *NCF2* as well as *HCST* genes and infiltrating immune cells and 50 HALLMARKS pathways. (**A**) The relationship between infiltrating immune cells and the *NCF2* and *HCST* genes. (**B**) The relationship between 50 HALLMARKS pathways and the *NCF2* and *HCST* genes. *$P < 0.05$; **$P < 0.01$; ***$P < 0.001$.