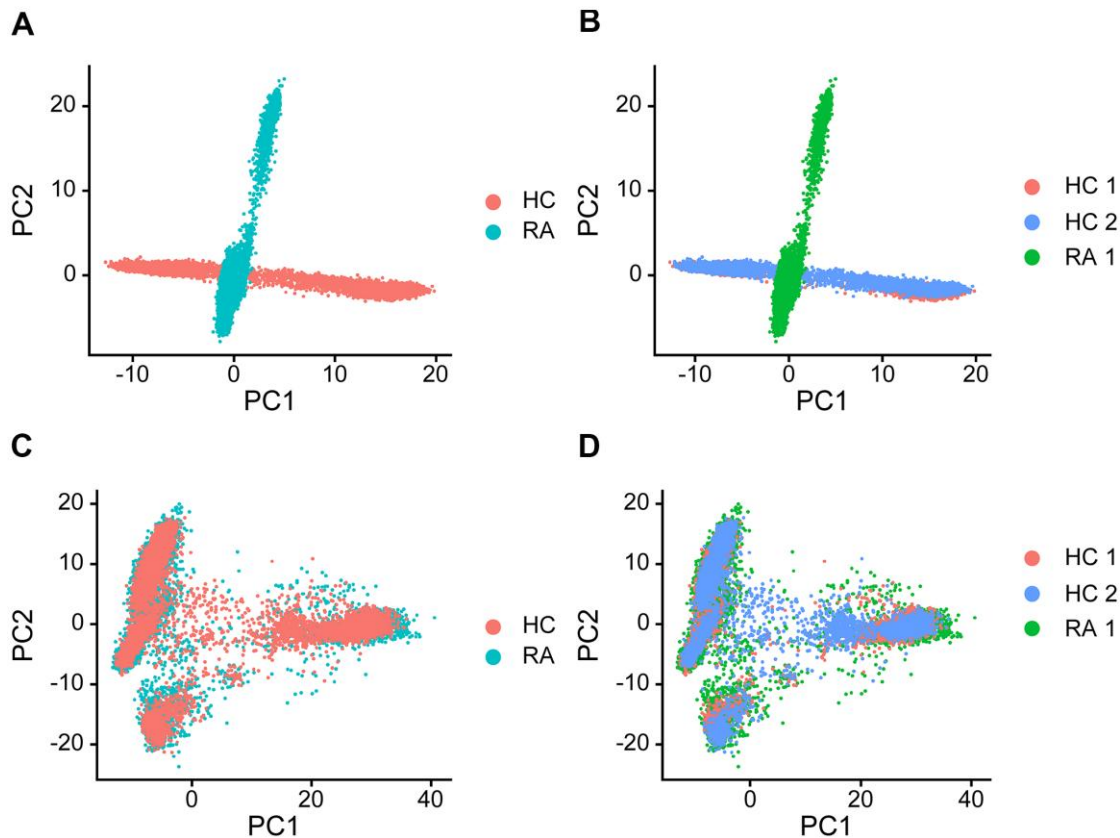
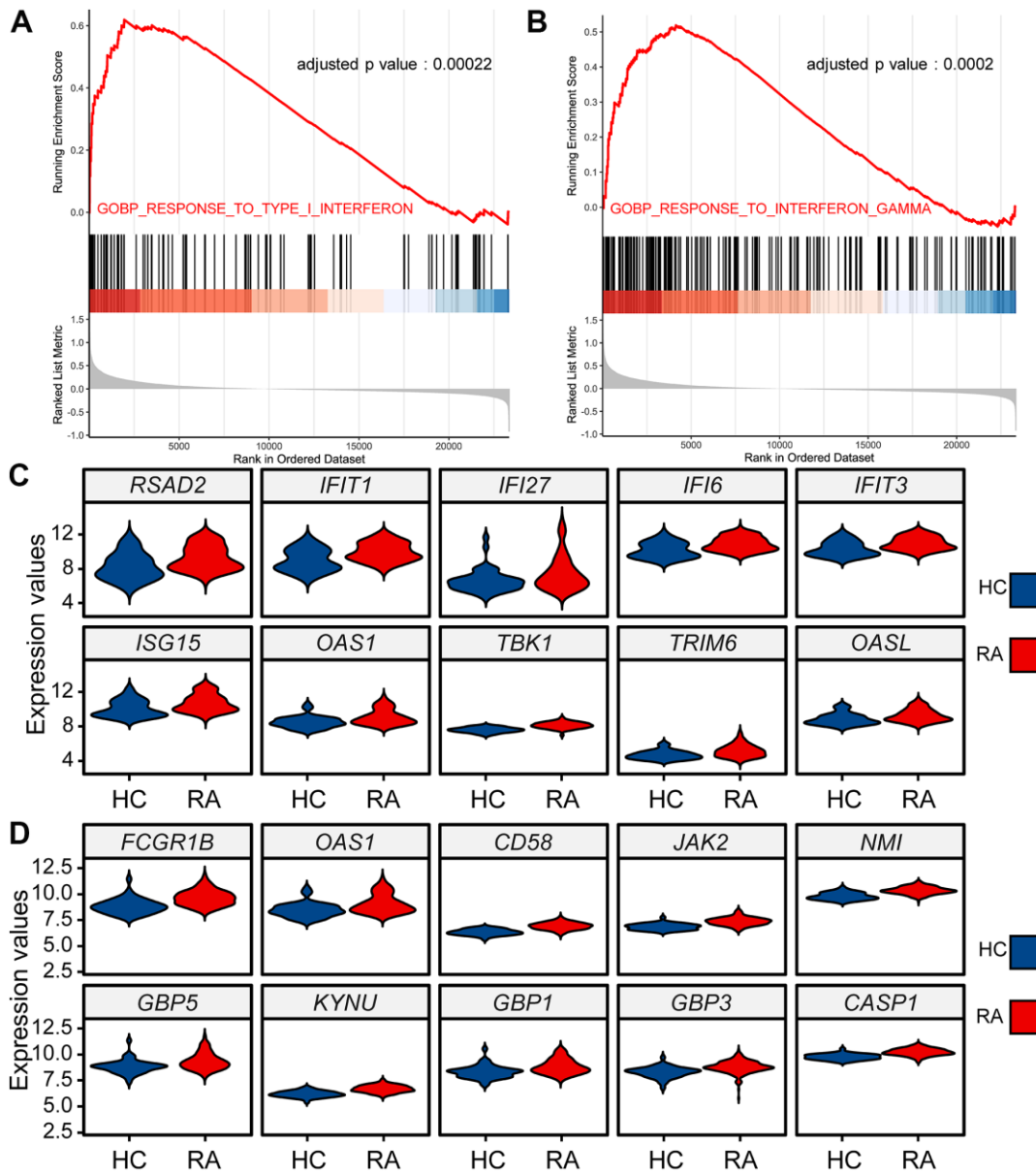


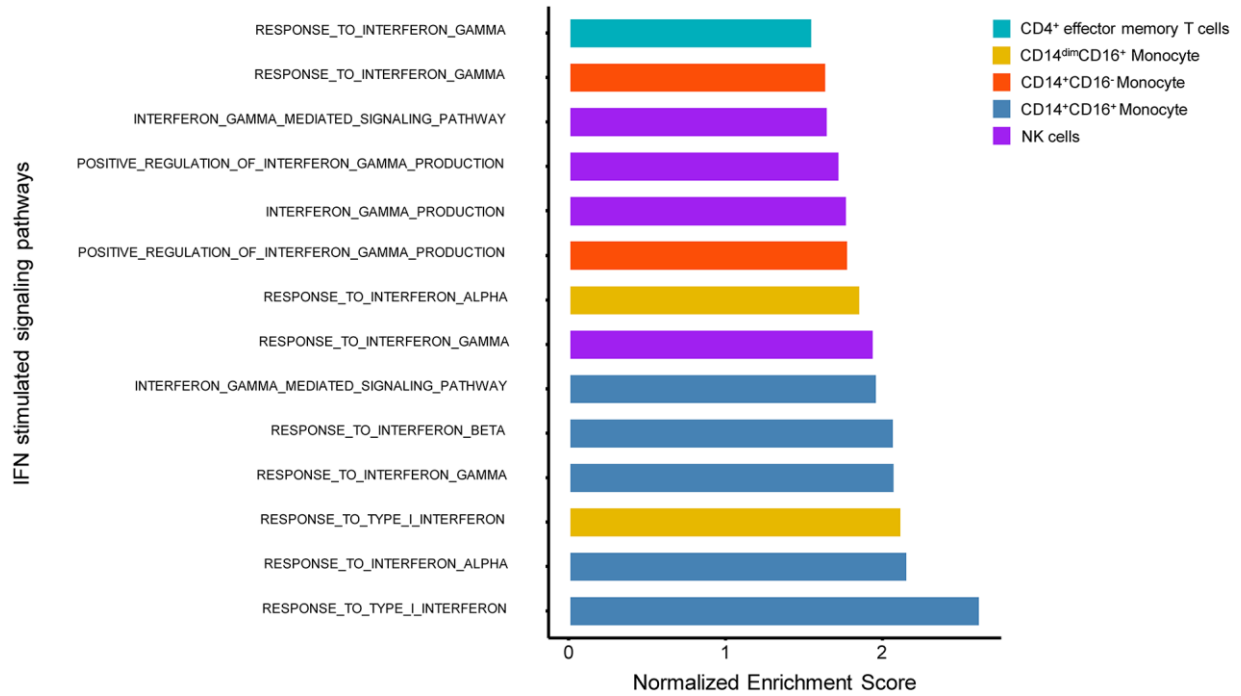
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Principal component analysis (PCA) visualization suggested that batch effects were removed between rheumatoid arthritis (RA) and healthy control individuals (HC) by canonical correlation analysis (CCA). (A) PCA visualization of cells before performing CCA, and cells are colored by batch. (B) PCA visualization of cells before performing CCA, and cells are colored by sample. (C) PCA visualization of cells after performing CCA, and cells are colored by batch. (D) PCA visualization of cells after performing CCA, and cells are colored by sample. PC: principal component.



Supplementary Figure 2. Upregulated interferon (IFN)-stimulated signaling pathways and genes in rheumatoid arthritis (RA) peripheral blood. (A, B) Bar plots of selected results of GSE93272 gene set enrichment analysis (GSEA) indicated upregulated Type I IFN (A) and IFN- γ (B) stimulated signaling pathways in RA. (C) Violin plots of the top 10 upregulated genes in the type I IFN-stimulated signaling pathway. (D) Violin plots of the top 10 upregulated genes in the IFN- γ -stimulated signaling pathway. Genes in (C, D) are ordered according to fold changes, and only genes satisfying adjusted p-value <0.05 are shown.



Supplementary Figure 3. Upregulated interferon (IFN)-stimulated signaling pathways in immune cells from rheumatoid arthritis (RA) peripheral blood. Bar plots of selected results of GSE93776 gene set enrichment analysis (GSEA) showing activated IFN-stimulated signaling pathways in RA peripheral blood. The horizontal axis represents the normalized enrichment score. Adjusted p-values of all pathways satisfied were less than 0.05.