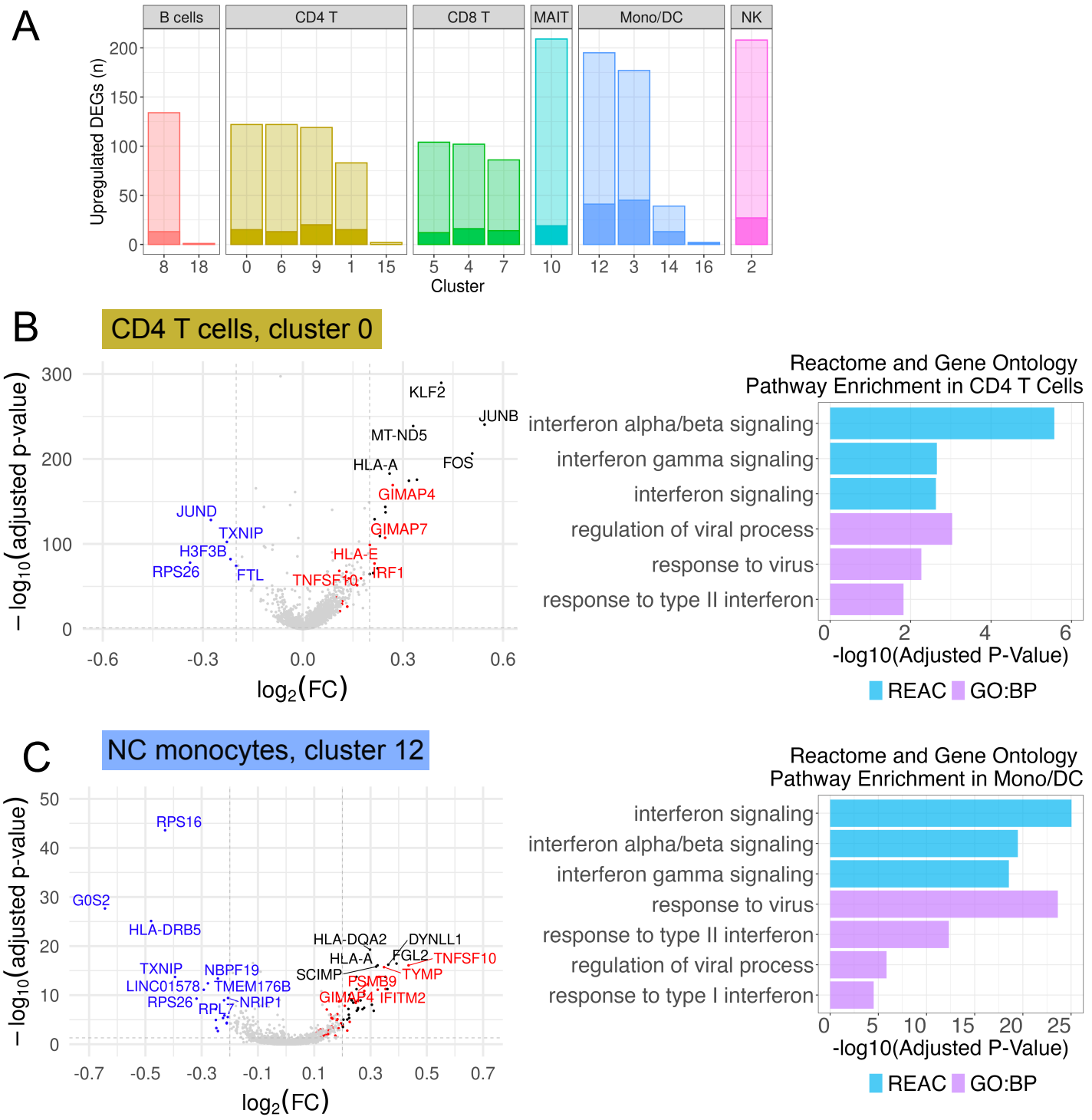

Figure S5. Differential expression analysis identifies dysregulation of ISAG^{hi} T-cell marker genes in additional PBMC types in EOAD.

A, Significantly upregulated genes are displayed across clusters, which are organized by PBMC type. The darker portion of each bar indicates the fraction of upregulated genes that are also ISAG^{hi} T-cell marker genes. **B**, **C** (left), Volcano plots for CD4 T cells and NC monocytes (clusters 0 and 12, respectively) display downregulated (blue) and upregulated (black) differentially expressed genes (DEGs); a subset of those with P_{FDR} < 0.05 and absolute LFC > 0.25 are labeled on the plots. In addition, a subset of upregulated genes with P_{FDR} < 0.05 and LFC > 0.1 that are also ISAG^{hi} T-cell marker genes are labeled in red. A maximum of 5 genes are labeled for each category to improve readability. **B**, **C** (right), Functional enrichment analysis of the upregulated genes (P_{FDR} < 0.05 and LFC > 0.1) in CD4 T cell clusters **(B)** and in monocyte/dendritic cell clusters **(C).** There was significant enrichment of IFN and antiviral response pathways in the CD4 T cell clusters (0, 1, 6, 9, and 15) and the monocyte/dendritic cell clusters (3, 12, 14, and 16) as sourced from the GO BP and reactome databases.