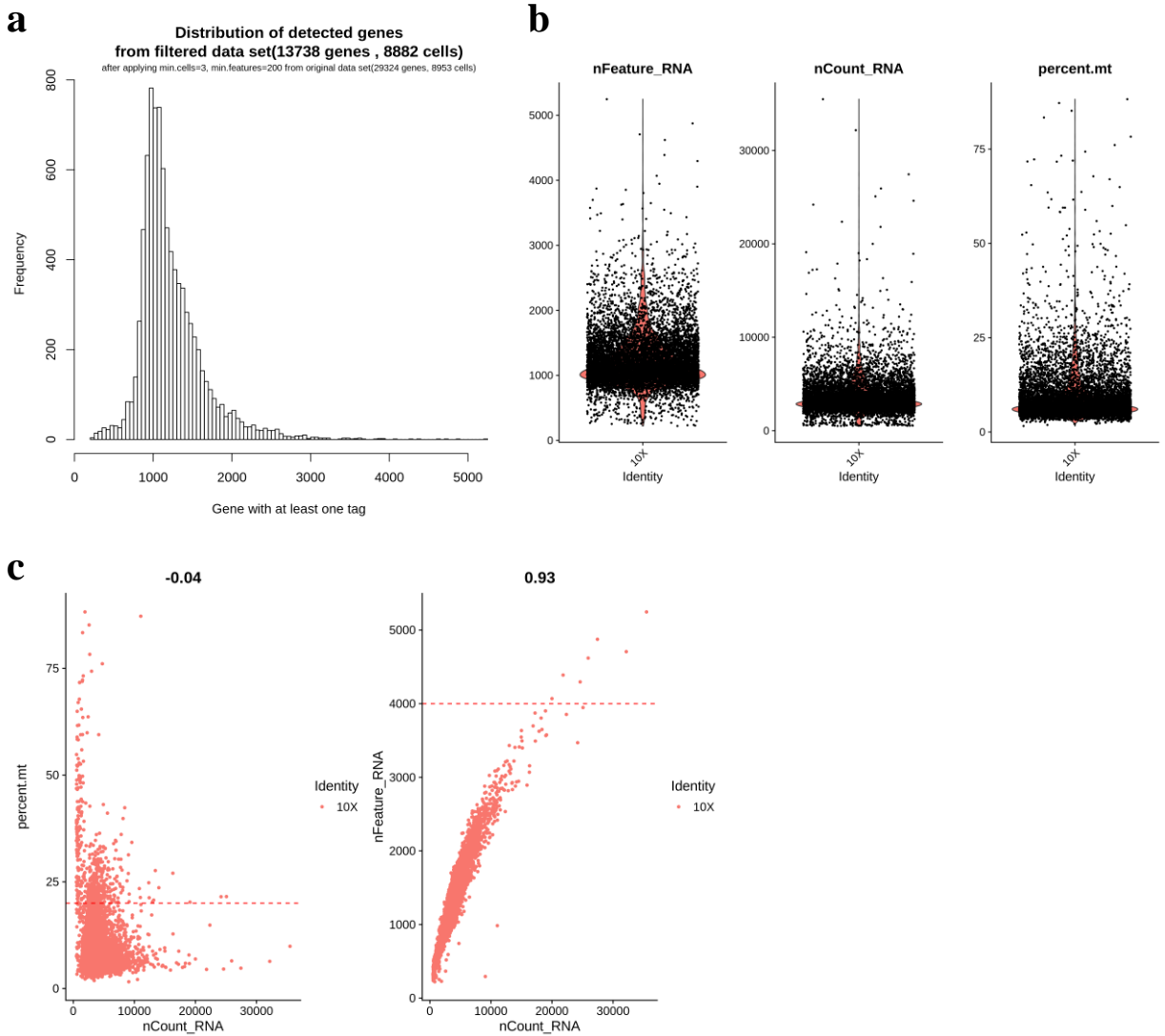


Cellular heterogeneity of circulating CD4⁺CD8⁺ double-positive T cells characterized by single-cell RNA sequencing

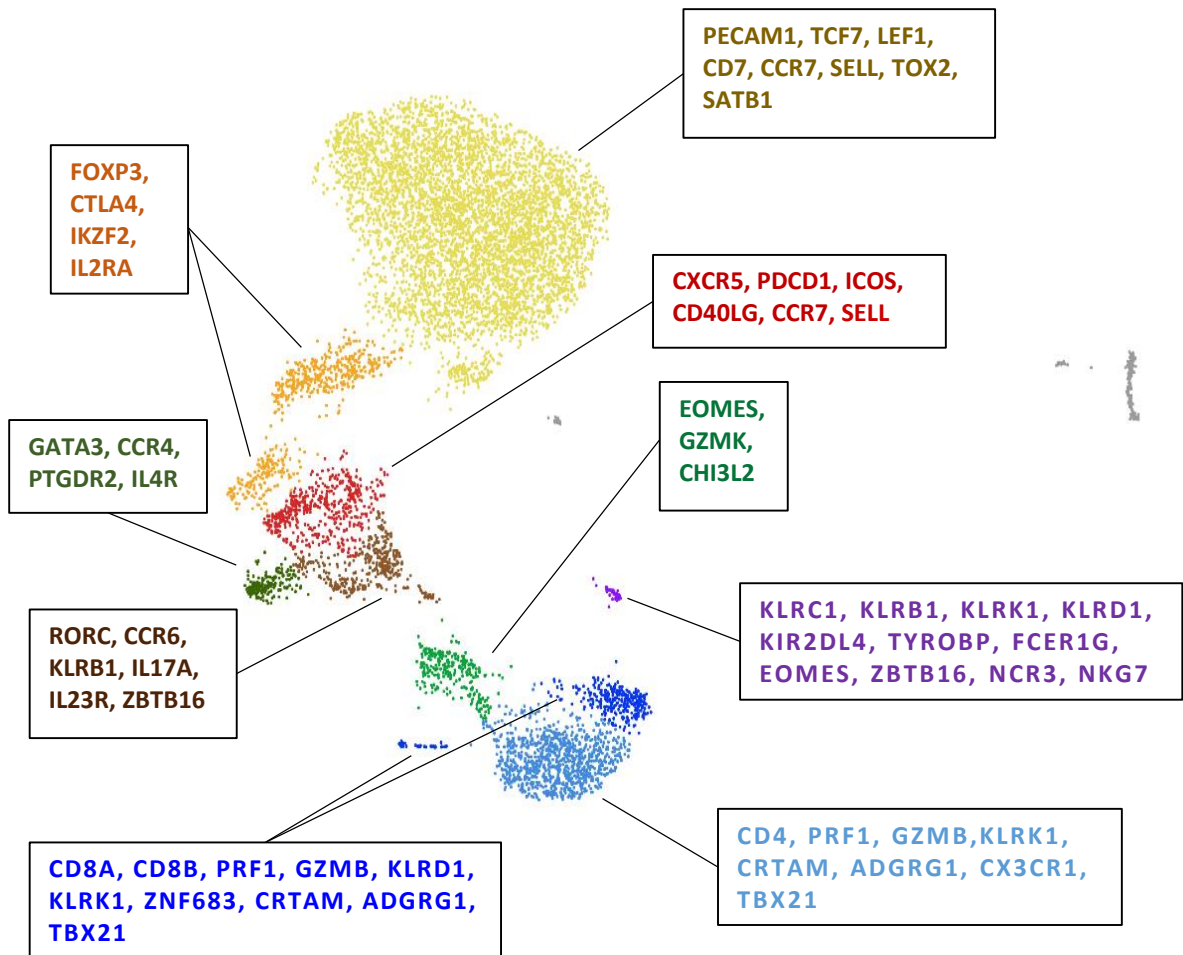
Sung Min Choi¹, Hi Jung Park¹, Eun A Choi¹,
Kyeong Cheon Jung^{2,3,4}, and Jae Il Lee^{2,5,*}

Supplementary Figure S1



S1. Quality control result for scRNA-seq analysis. (a) The histogram showing the frequency of cells containing genes with at least one UMI after filtering out cells/features from original data set. (b) The violin plots representing the distribution of nGene/nUMI/percentage of mitochondrial gene for each cell. (c) The scatter plots representing relationships of mitochondrial percentage-molecule counts and genes-molecule counts for each cell.

Supplementary Figure S2



S2. Differential expression of genes that define heterogeneous clusters of CD4⁺CD8⁺ DP T cells.

Supplementary Figure S3



S3. (a) UMAP representing *CD8 α* . (b) UMAP representing T and B cell-associated genes.