

Supplementary Materials

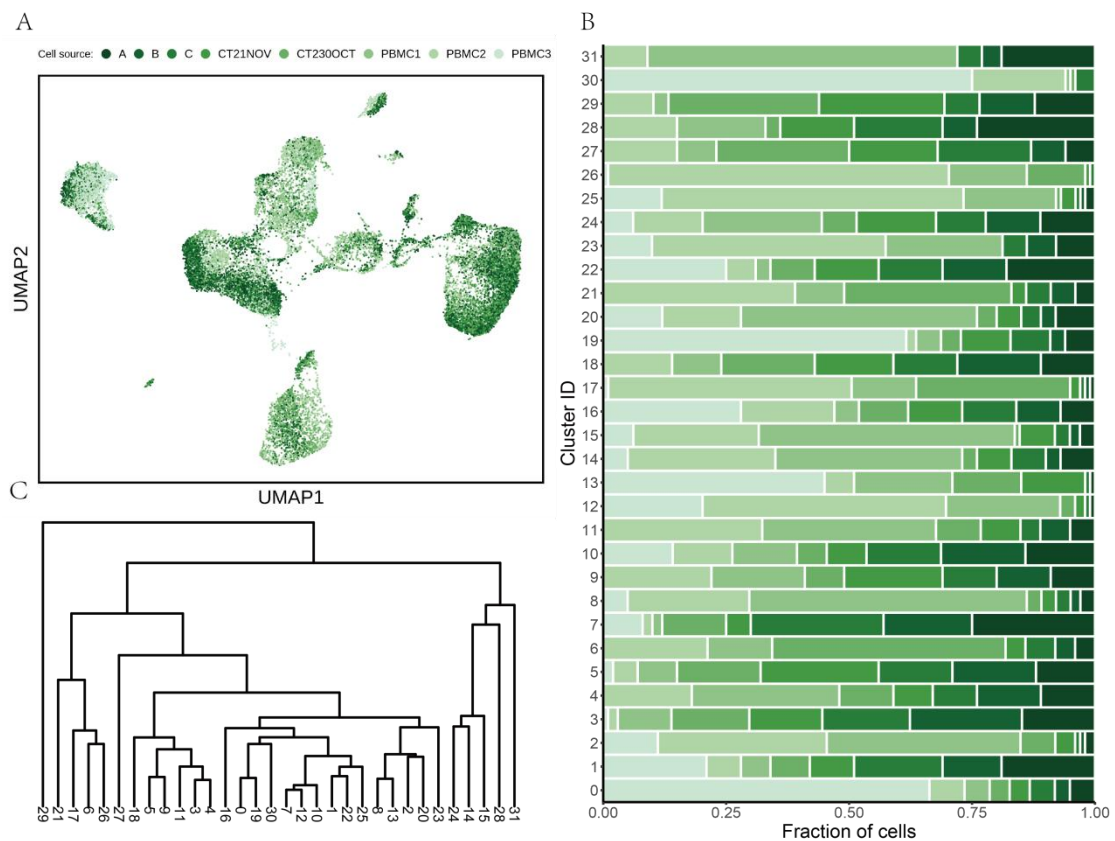


Figure S1. 32 cell clusters in porcine peripheral blood mononuclear cells obtained by unsupervised clustering. **(A)** The UMAP plot of integrated transcriptome of 34,220 single cells derived from all 8 PBMC samples. Color brightness represents sample source of cells. **(B)** Stacked bars of 32 cell clusters. The bar size represents the percentage of 8 PBMC samples in each cluster. **(C)** Hierarchical clustering trees of the relationships among cell clusters.

the CD2⁻γδ cluster, respectively. (F) GO analysis of up-regulated and down-regulated DEGs obtained by pseudobulk conversion (Supplemental Table III). Blue and orange bars denote the pathways enriched with up-regulated and down-regulated DEGs, respectively.

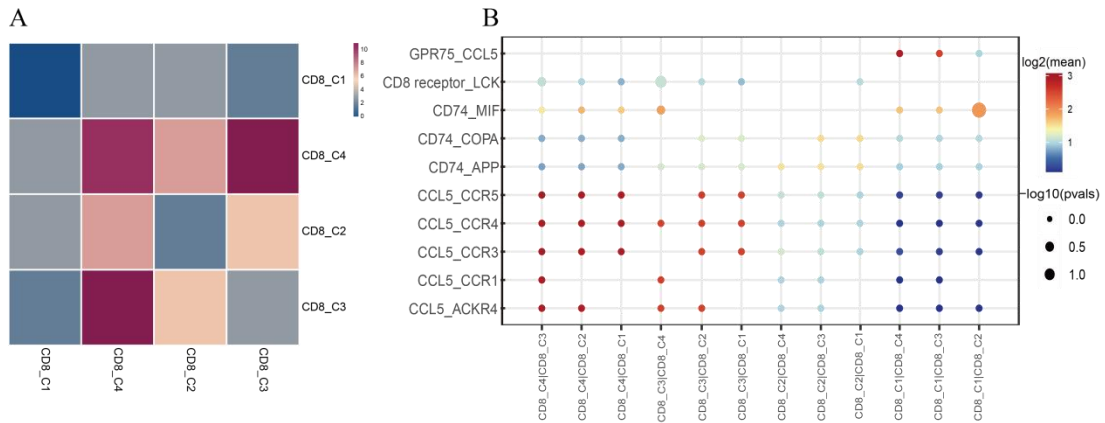


Figure S4. Cell communication among CD8 T cells subtypes. (A) Heatmap of the number of significant ligand-receptor interactions among different CD8 T cell subtypes. CD8_C1 represents CD8_naive cell; CD8_C2 represents CD8_memory cell; CD8_C3 represents CD8_effector cell; and CD8_C4 represents CD8_terminal_effector cell. (B) Dot plot of the significant ligand-receptor pairs involved in the interaction among CD8 T cell subtypes. Dot size represents the significance level ($-\log_{10}(\text{p-value})$), while colors indicate the expression levels ($\log_2 \text{mean (molecule 1-molecule 2)}$).

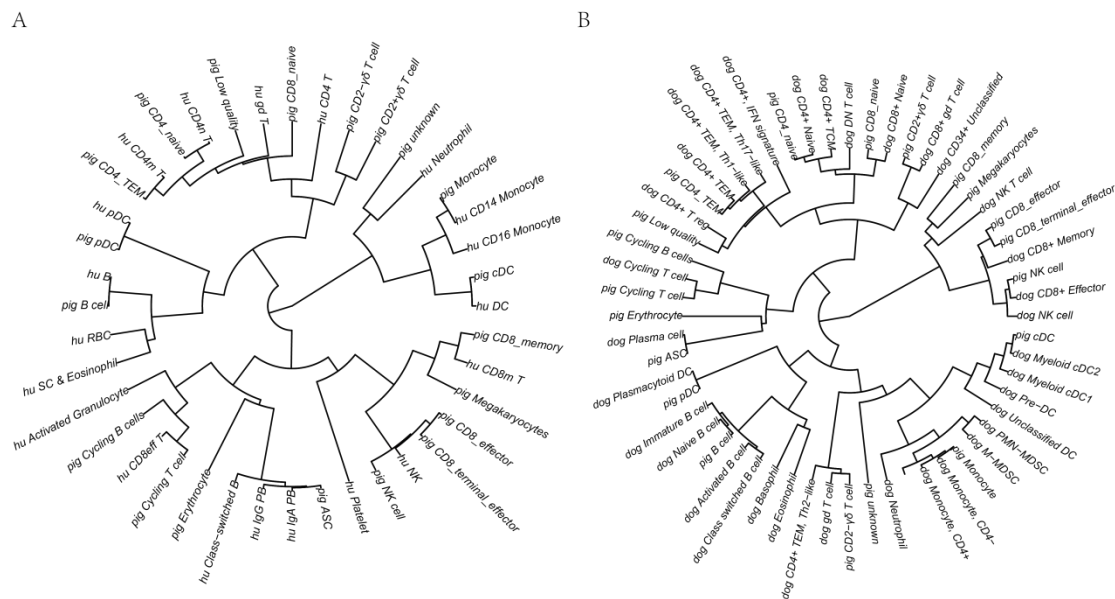


Figure S5. Comparison between porcine PBMCs and human PBMCs or dog PBMCs. (A) Hierarchical clustering of human and pig cell types using the top 2000 variable features after SCT normalization. (B) Hierarchical clustering of pig and dog cell types using the top 2000 variable features after SCT normalization. The prefix "hu_" represents human cell types.