

Supplemental Information for “Peripheral immune landscape and natural killer-like B cells in human Vogt-Koyanagi-Harada disease”

Figure S1. Clusters of major immune cell types originated from scRNA-seq data.

(A) Heatmap showing scaled expression of discriminative gene sets for major immune cell types originated from scRNA-seq data. (B) *t*-SNE plots of canonical markers for major immune cell types originated from scRNA-seq data.

Figure S2. Clusters of immune cell subsets originated from scRNA-seq data.

(A) *t*-SNE plots of TC subsets originated from scRNA-seq data. (B) *t*-SNE plots of canonical markers for TC subsets originated from scRNA-seq data. (C) Heatmap showing scaled expression of discriminative gene sets for TC subsets originated from scRNA-seq data. (D) *t*-SNE plots of CD4 TC subsets originated from scRNA-seq data. (E) *t*-SNE plots of canonical markers for CD4 TC subsets originated from scRNA-seq data. (F) Heatmap showing scaled expression of discriminative gene sets for CD4 TC subsets originated from scRNA-seq data. (G) *t*-SNE plots of CD8 TC subsets originated from scRNA-seq data. (H) *t*-SNE plots of canonical markers for CD8 TC subsets originated from scRNA-seq data. (I) Heatmap showing scaled expression of discriminative gene sets for CD8 TC subsets originated from scRNA-seq data. (J) *t*-SNE plots of NK subsets originated from scRNA-seq data. (K) *t*-SNE plots of canonical markers for NK subsets originated from scRNA-seq data. (L) Heatmap showing scaled expression of discriminative gene sets for NK subsets originated from scRNA-seq data. (M) *t*-SNE plots of monocyte subsets originated from scRNA-seq data. (N) *t*-SNE plots of canonical markers for monocyte subsets originated from scRNA-seq data. (O) Heatmap showing scaled expression of discriminative gene sets for monocyte subsets originated from scRNA-seq data. (P) *t*-SNE plots of DC subsets

originated from scRNA-seq data. (Q) *t*-SNE plots of canonical markers for DC subsets originated from scRNA-seq data. (R) Heatmap showing scaled expression of discriminative gene sets for DC subsets originated from scRNA-seq data.

Figure S3. Clusters of major immune cell types and T cell subsets originated from CyTOF data.

(A) *t*-SNE plots of PBMCs of HC and VKH originated from mass cytometry (CyTOF) data. (B) *t*-SNE plots of canonical markers for major immune cell types originated from CyTOF data. (C) *t*-SNE plots of T cell subsets originated from CyTOF data. (D) *t*-SNE plots of canonical markers for T cell subsets originated from CyTOF data.

Figure S4. Clusters of immune cell subsets originated from CyTOF data.

(A) *t*-SNE plots of NK subsets originated from CyTOF data. (B) *t*-SNE plots of canonical markers for NK subsets originated from CyTOF data. (C) *t*-SNE plots of myeloid cell subsets originated from CyTOF data. (D) *t*-SNE plots of canonical markers for myeloid cell subsets originated from CyTOF data. (E) *t*-SNE plots of B cell subsets originated from CyTOF data. (F) *t*-SNE plots of canonical markers for B cell subsets originated from CyTOF data.

Figure S5. GO analysis of DEG.

(A) Heatmap showing representative GO terms enriched in downregulated DEGs of B cell subsets in the VKH/HC comparison group. (B) Heatmap showing representative GO terms enriched in upregulated DEGs of NK, MC, and DC in the VKH/HC comparison group. (C) Heatmap showing representative GO terms enriched in downregulated DEGs of NK, MC, and DC in the VKH/HC comparison group. (D) Bar plot showing representative GO terms enriched in up- and down-regulated DEGs of NK subsets in the VKH/HC comparison group. (E) Bar plot showing representative GO terms enriched in up- and down-regulated DEGs of MC subsets in the VKH/HC

comparison group. (F) Bar plot showing representative GO terms enriched in up-regulated DEGs of DC subsets in the VKH/HC comparison group.

Figure S6. Percentage of immune cell subsets from CyTOF data.

(A-D) Bar chart shows percentage of TC, BC, NK, and myeloid cell in total PBMCs from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. ns, not significant. (E-G) Bar chart shows percentage of CD4 T cell subsets in CD4 TC from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. ns, not significant. (H-J) Bar chart shows percentage of CD8 T cell subsets in CD8 TC from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. ns, not significant. (K-L) Bar chart shows percentage of B cell subsets in BC from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. ns, not significant. (M-O) Bar chart shows percentage of MC subsets in total PBMCs from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. ns, not significant. (P-Q) Bar chart shows percentage of DC subsets in total PBMCs from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. ns, not significant. (R-T) Bar chart shows percentage of NK subsets in total PBMCs from HC ($n = 10$) and VKH ($n = 5$) group originated from CyTOF data. The values represent the mean \pm SD. Significance was determined using unpaired student's t test. * $P < 0.05$. ns, not significant. (U) Gating strategy of NoBC.

Figure S7. Percentage of T-BCs and KT-BCs, and non-stimulated control of K-BCs.

(A) The percentage of T-BCs in BC from VKH patient in different stages (before treatment, after treatment for one month, and after treatment for three months). Each group contains six samples. The values represent the mean \pm SD. Significance was determined using ANOVA. ns, not significant. (B) The percentage of KT-BCs in BC from VKH patient in different stages (before treatment, after treatment for one month, and after treatment for three months). Each group contains six samples. The values represent the mean \pm SD. Significance was determined using ANOVA. ns, not significant. (C) Non-stimulated control of K-BCs in IL-12, IFN- γ , IL-18, IL-6, IL-21, IL-23, IL-1 β , and IL-2.

Figure S1

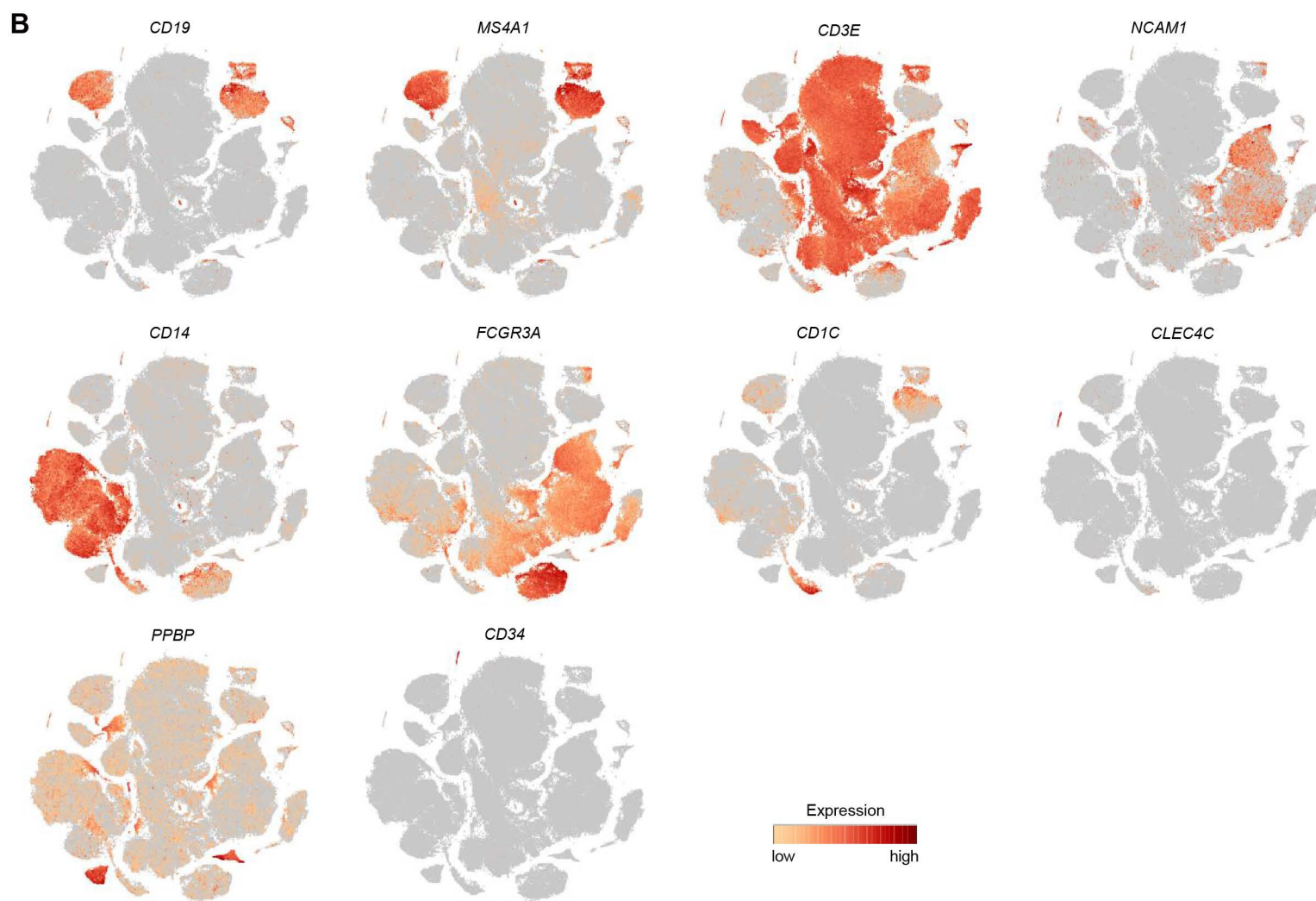
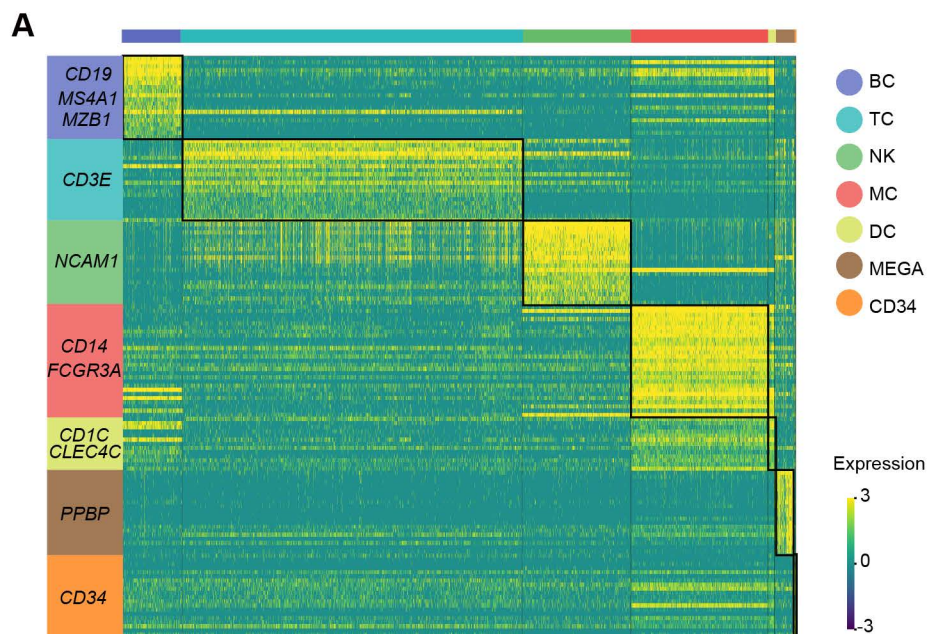


Figure S2

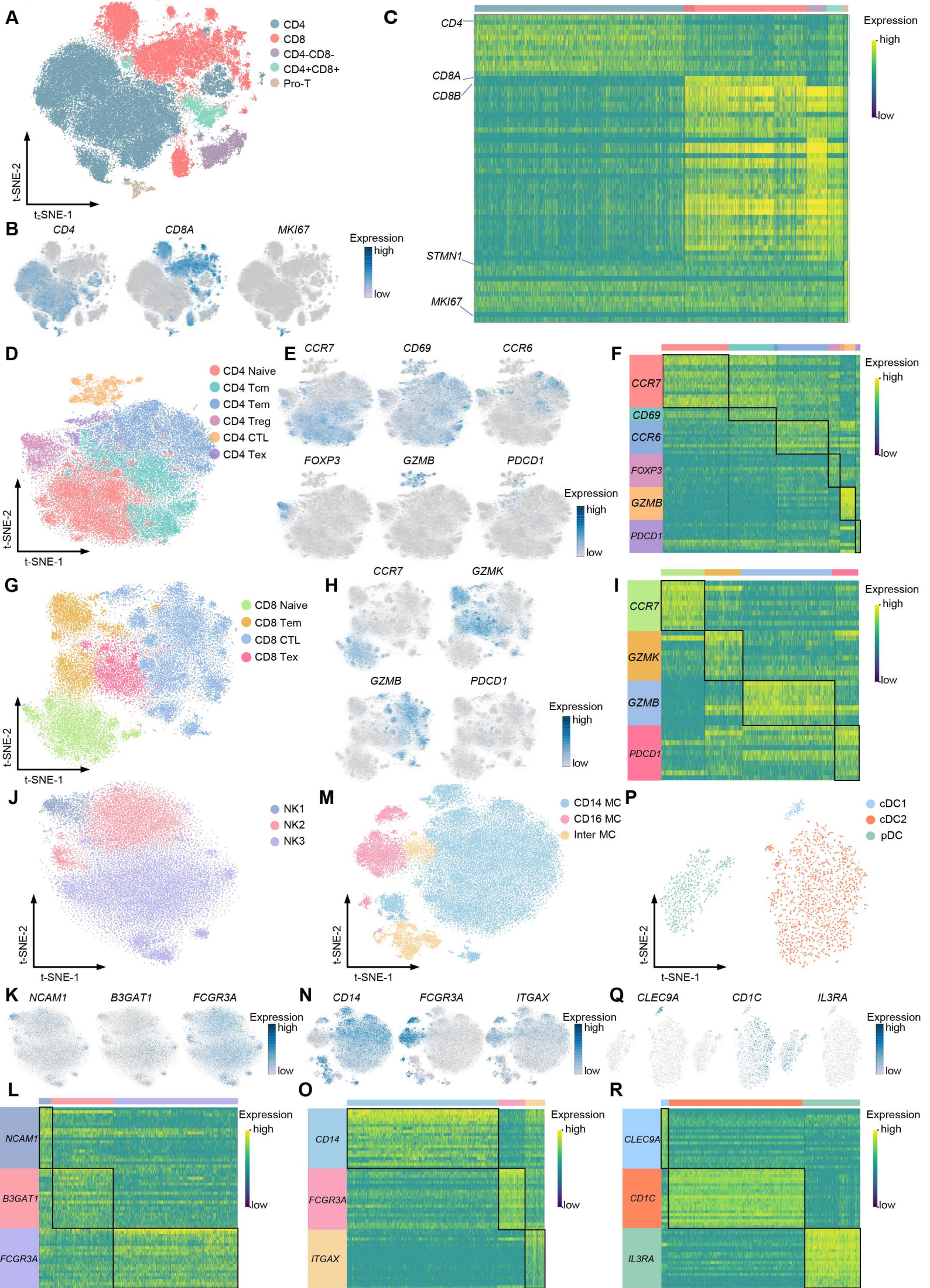
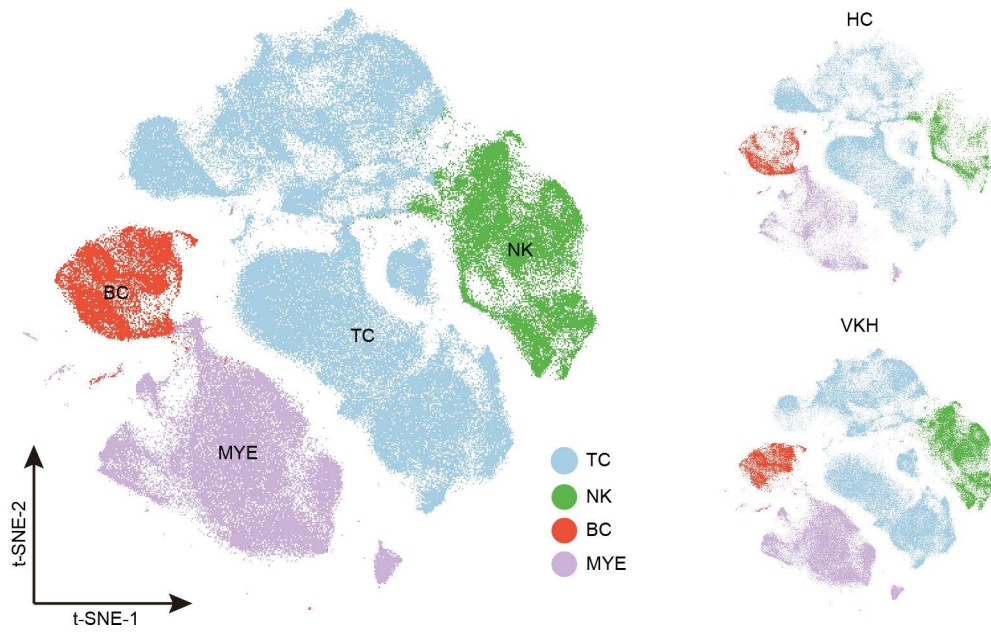
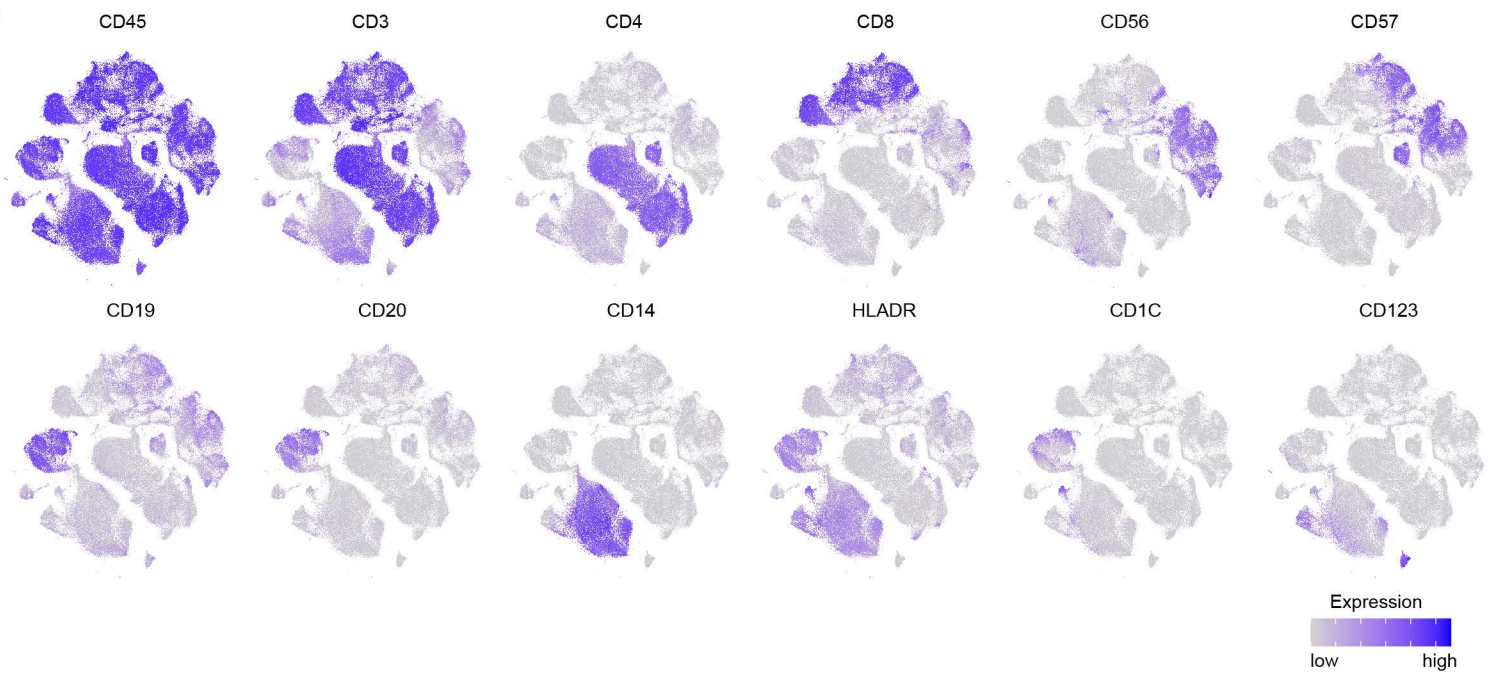


Figure S3

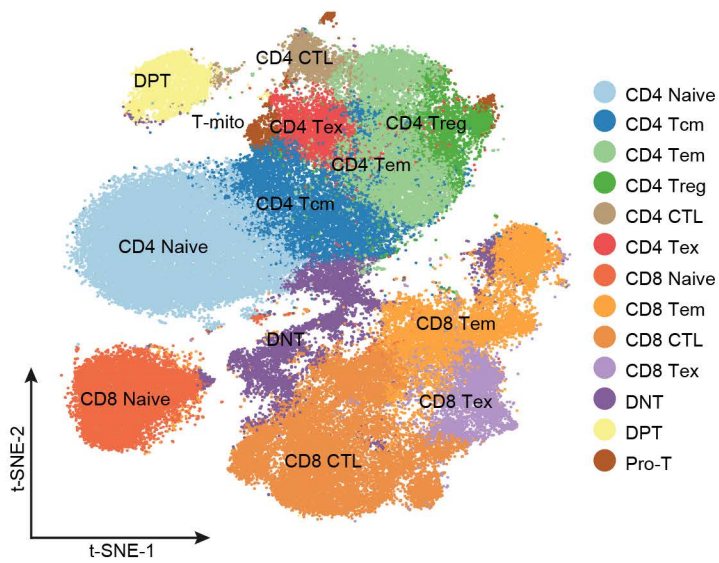
A



B



C



D

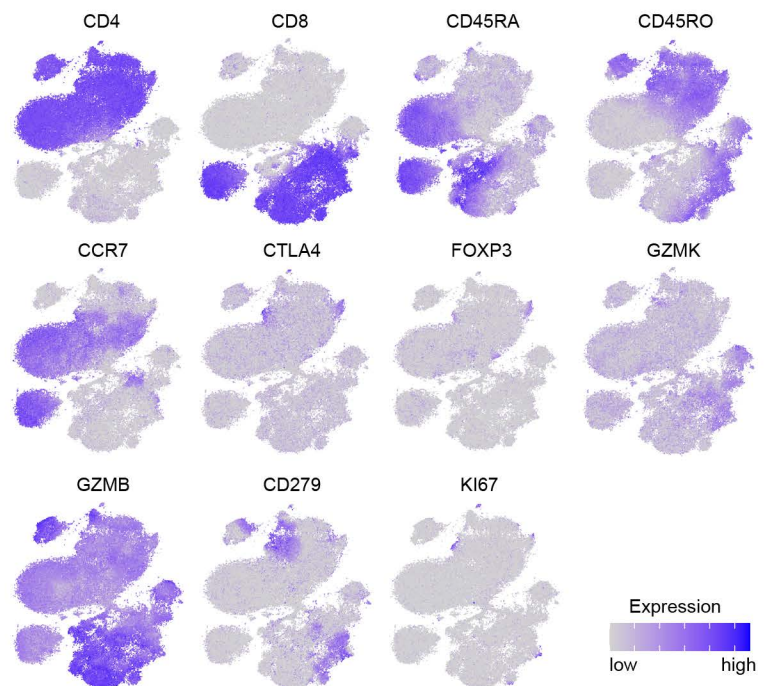


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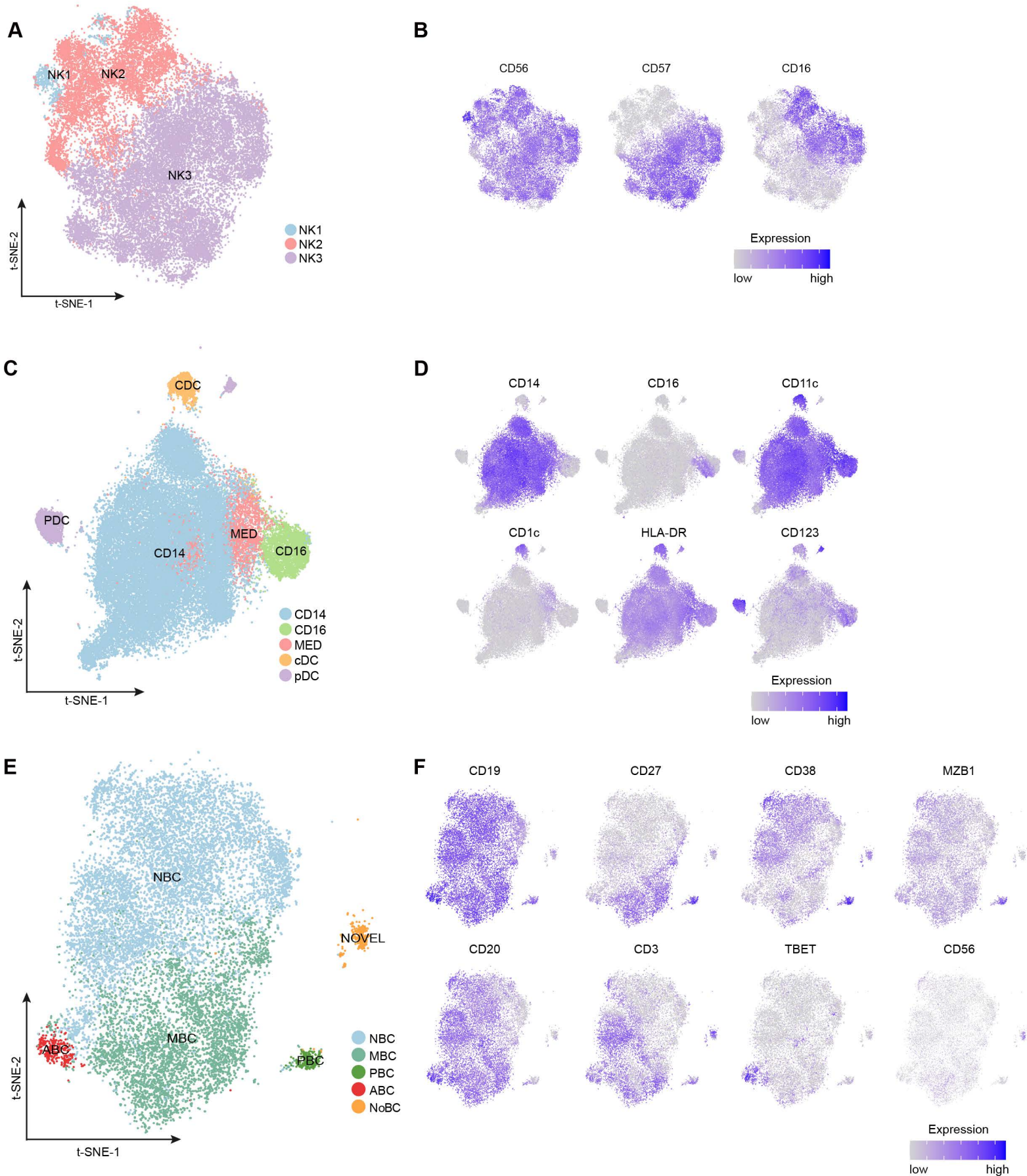


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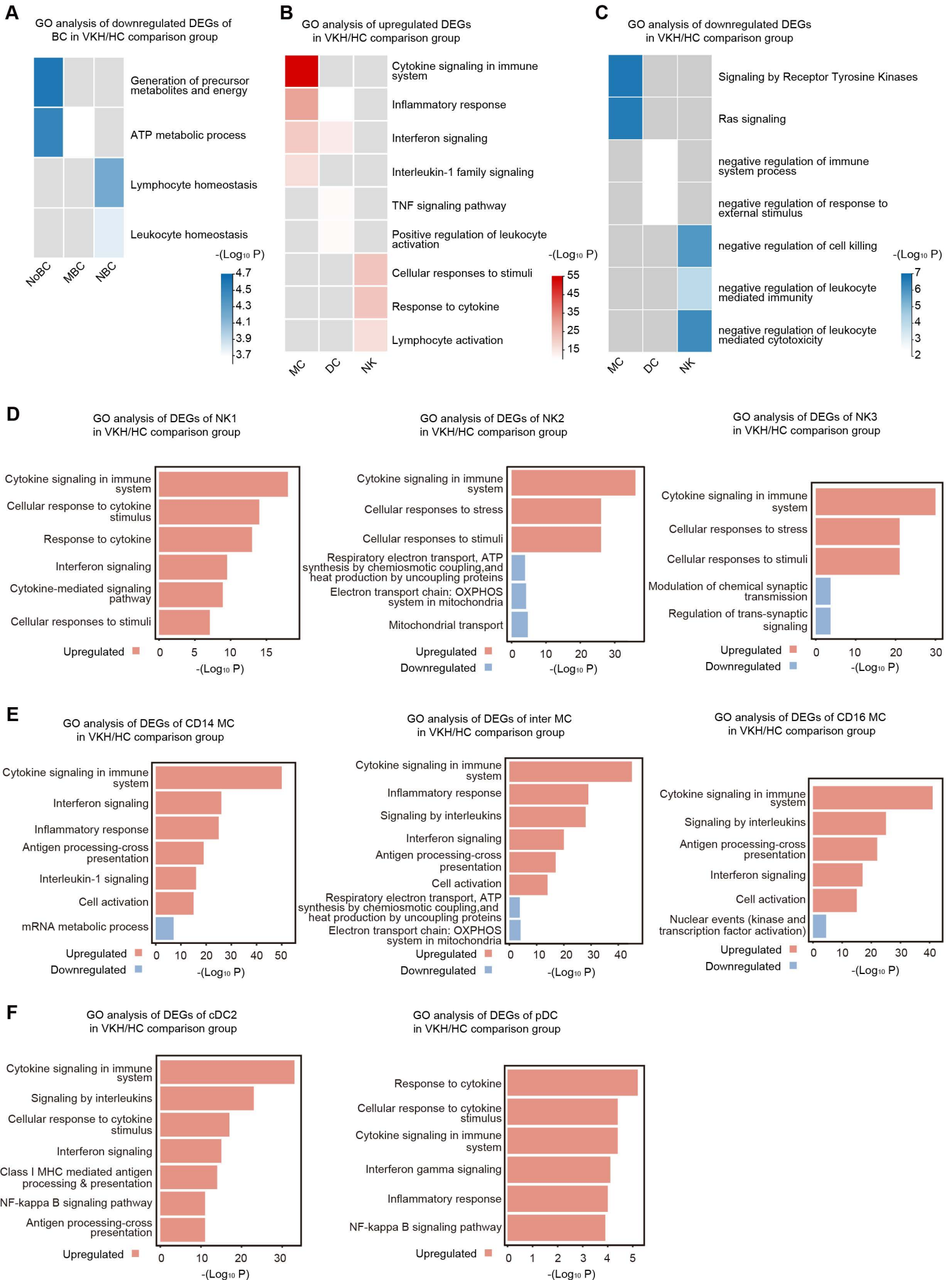


Figure S6

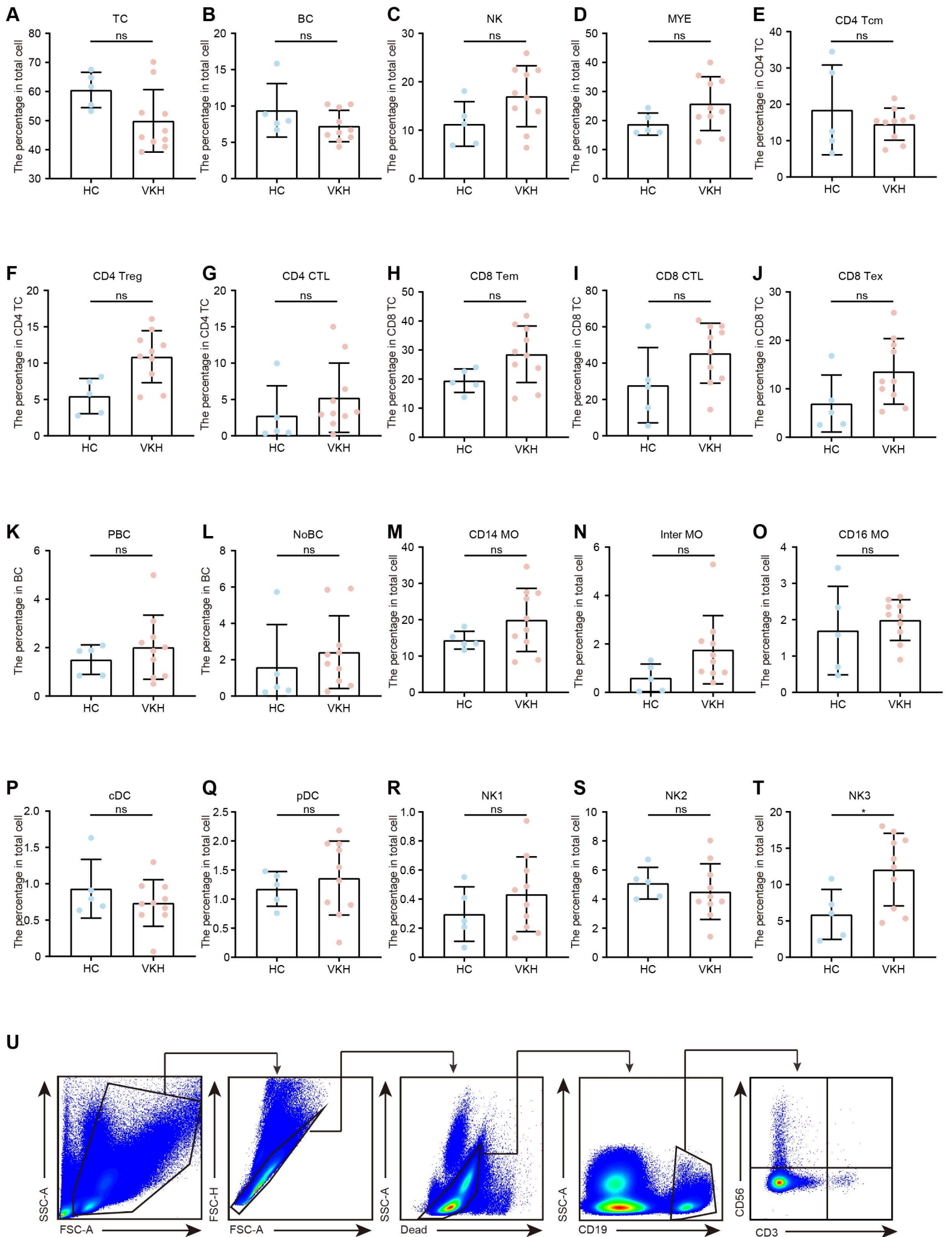


Figure S7