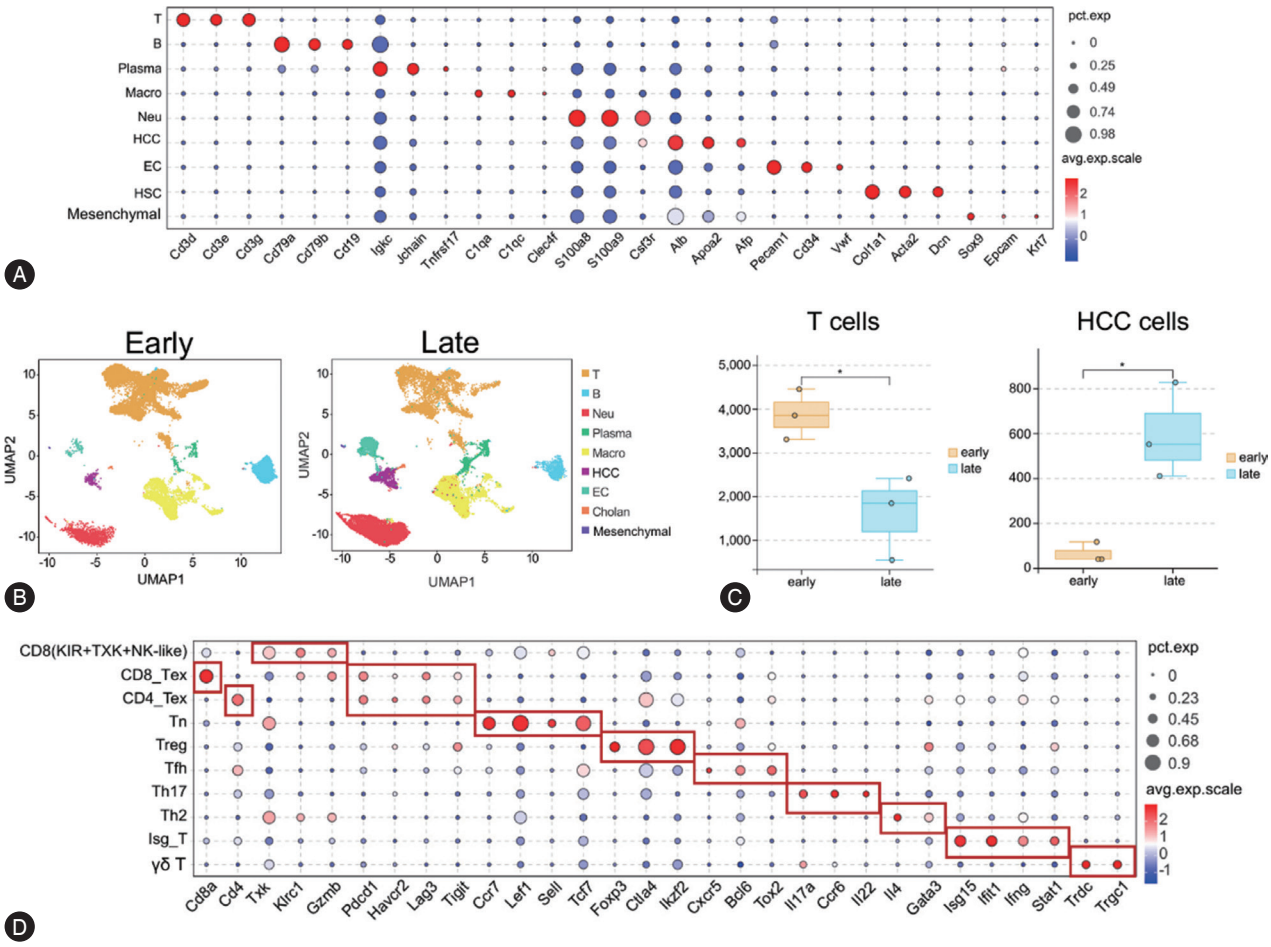

Supplementary Figure 4. Single-cell RNA sequencing of murine HTVi HCC tumors at early and late stages. (A) Dot plot showing the expression of top three most highly expressed genes in each cell type. The color and size indicate the effect size. (B) UMAP visualization of subclusters of HTVi HCC model tumor tissue formation at early or late stage. (C) Box plots comparing the number of T cells and HCC cells between early and late HCC stages. Statistical analysis was performed using unpaired two-tailed *t*-tests. (D) Dot plot depicting expression levels of selected immune-related genes in each T cell subcluster. The color and size indicate the effect size.