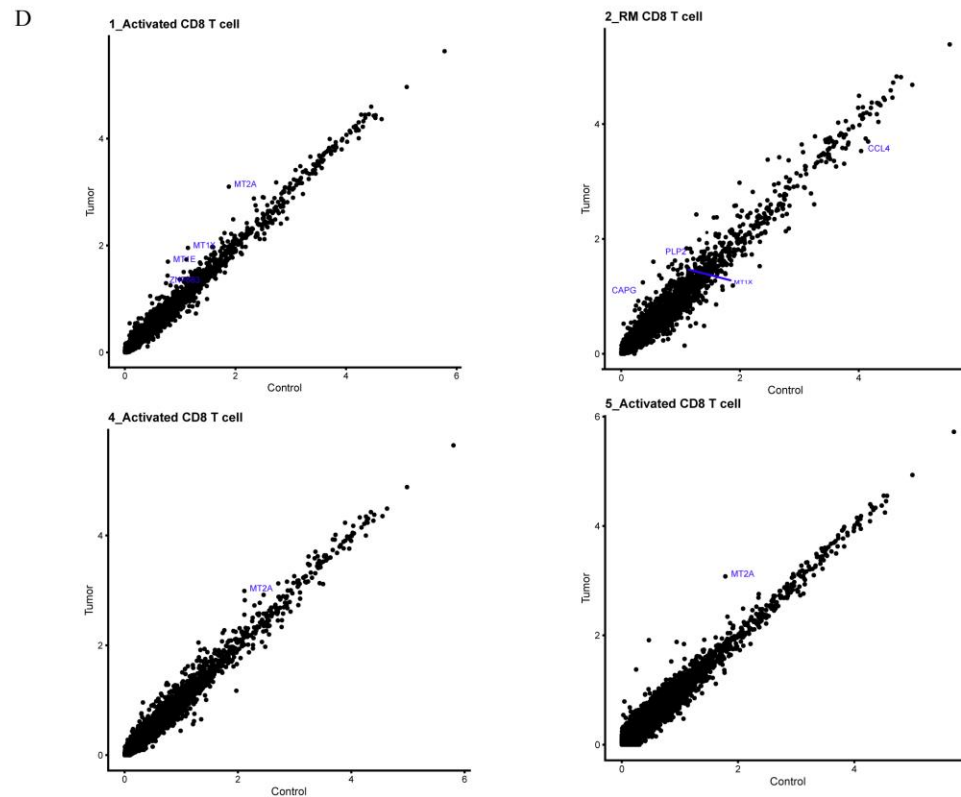
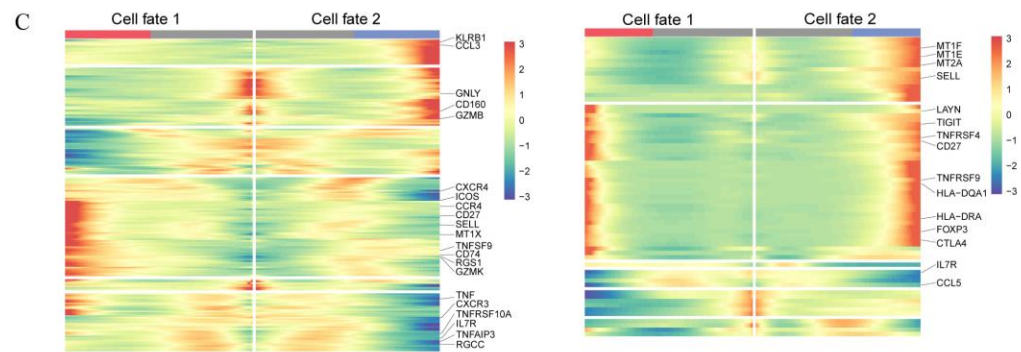
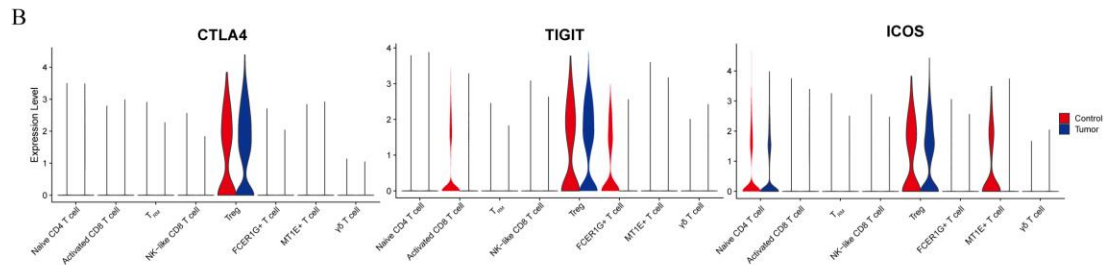
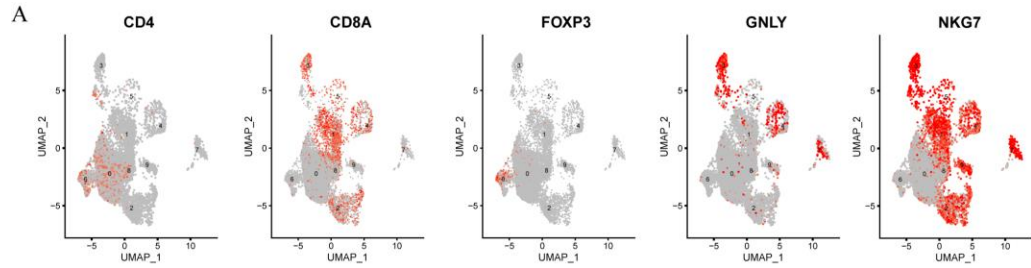


Supplementary Table 1 Clinical information of patient in the study

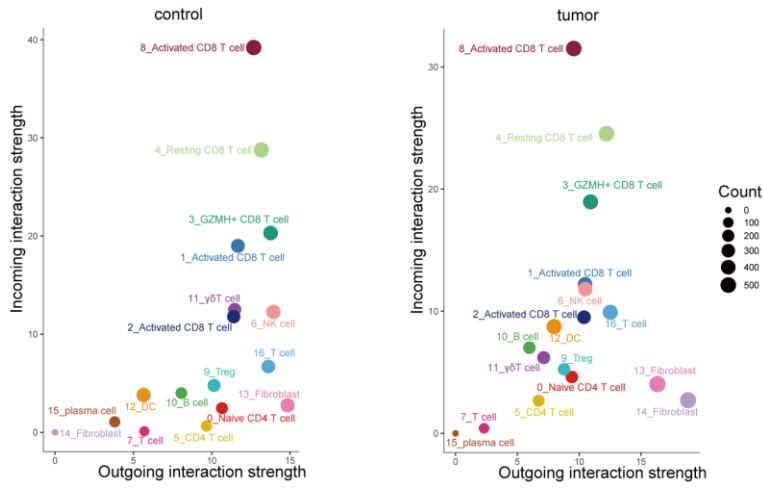
Patient ID	Age	Gender	Tumor type	Tissue	Types of viral hepatitis	Child-Pugh	BCLC stage	TMN stage
P0301	52	M	Primary HCC	tumor tissues/adjacent normal	HBV	A	A	T1N0M0
P0302	69	F	Primary HCC	tumor tissues/adjacent normal	HCV	A	A	T1N0M0



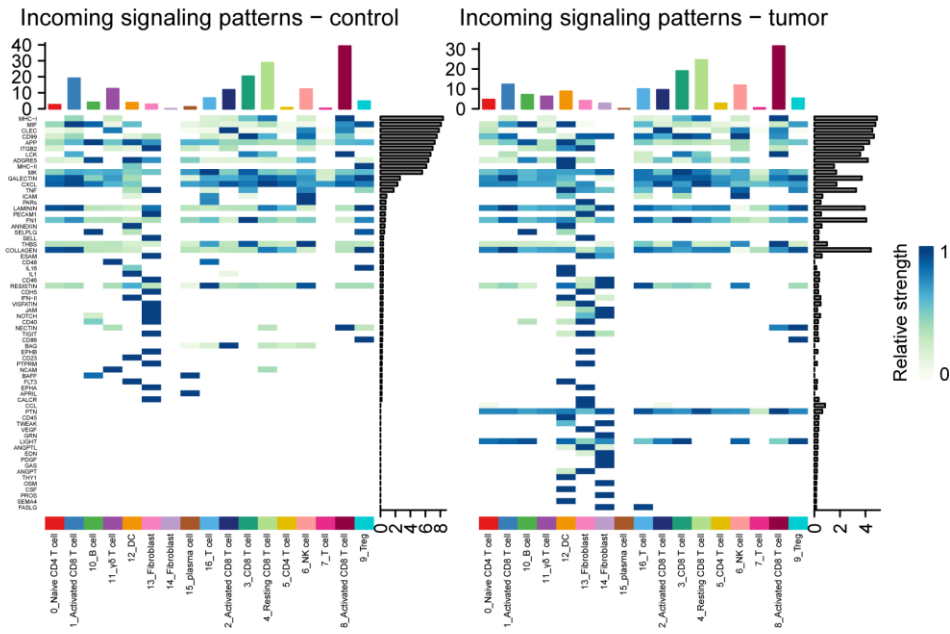
Supplementary Figure 1 Partial classical gene expression and BEAM analysis of P0302.

A: The UMAP plot shows the expression of five marker genes (CD4, CD8A, FOXP3, GNLY and NKG7) in T cells; B: Highly Expressed Genes in Tregs; C: Heat map of differential gene expression by branch point expression analysis comparing different cell fates of CD8 T and CD4 T cells in P0302. D: Scatter plot of differentially expressed genes (DEGs) showing genes highly expressed in tumor 1_Activated CD8 T cells, 2_TRM, 4_Activated CD8 T cells and 5_Activated CD8 T cells in P0302. Each dot represents a gene;

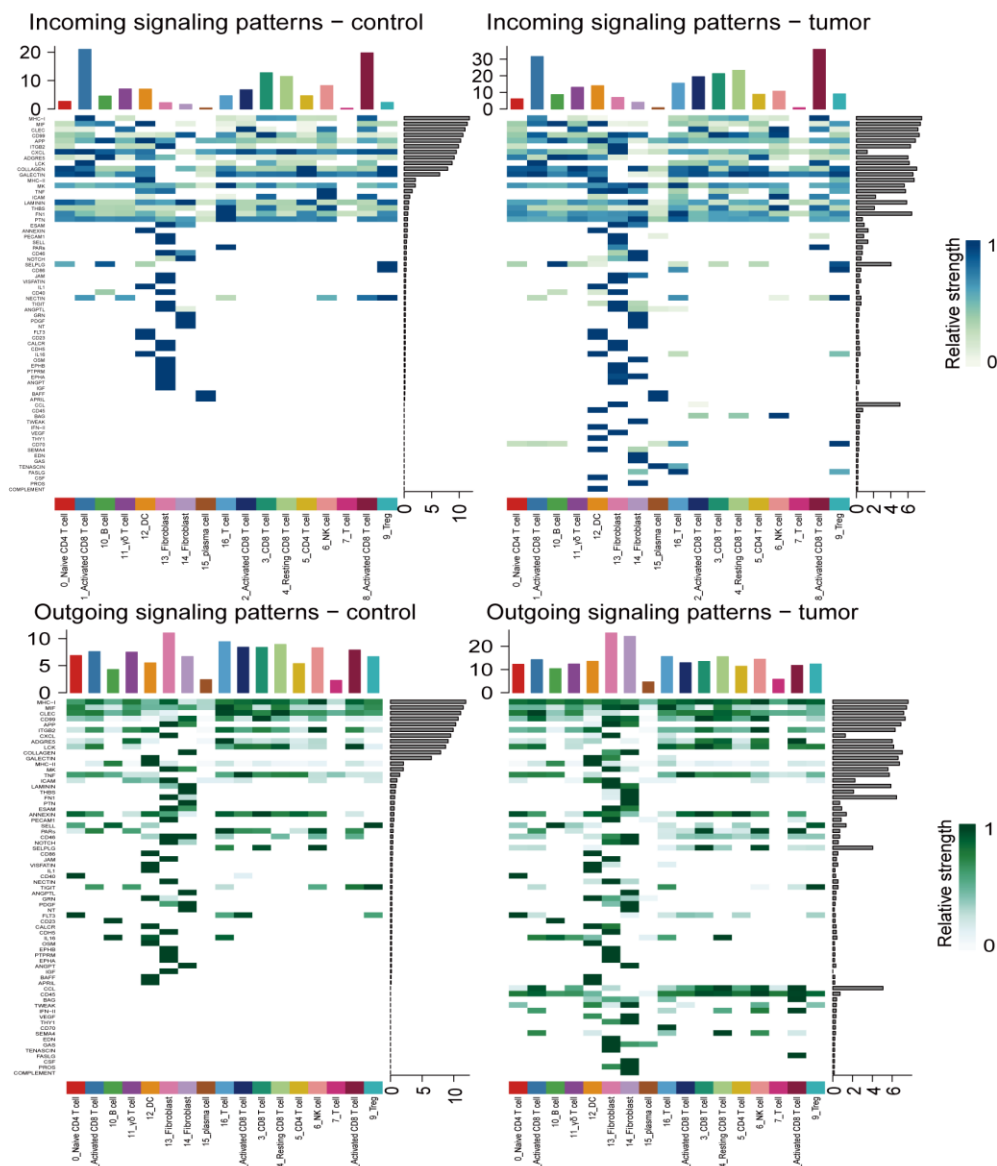
A



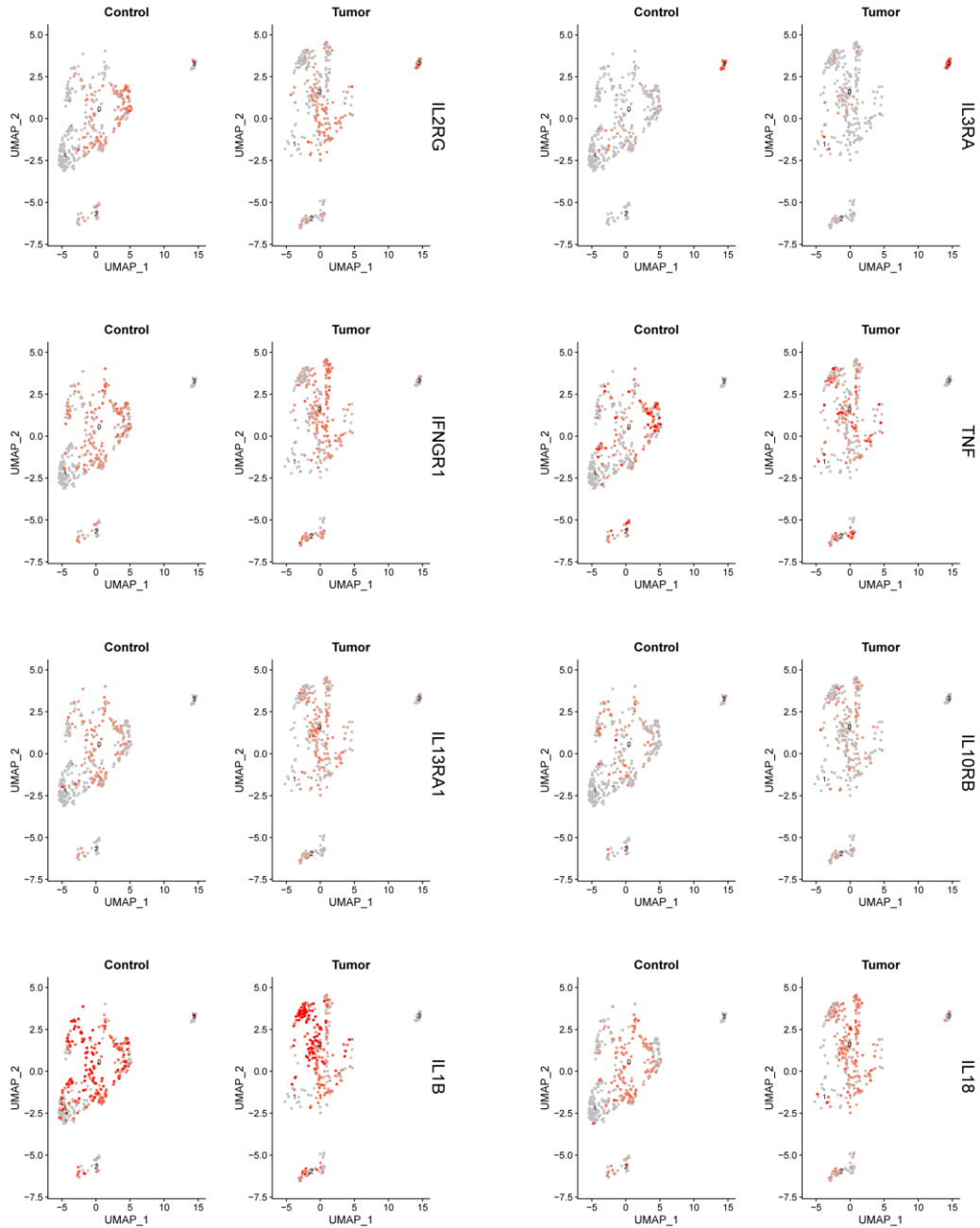
B



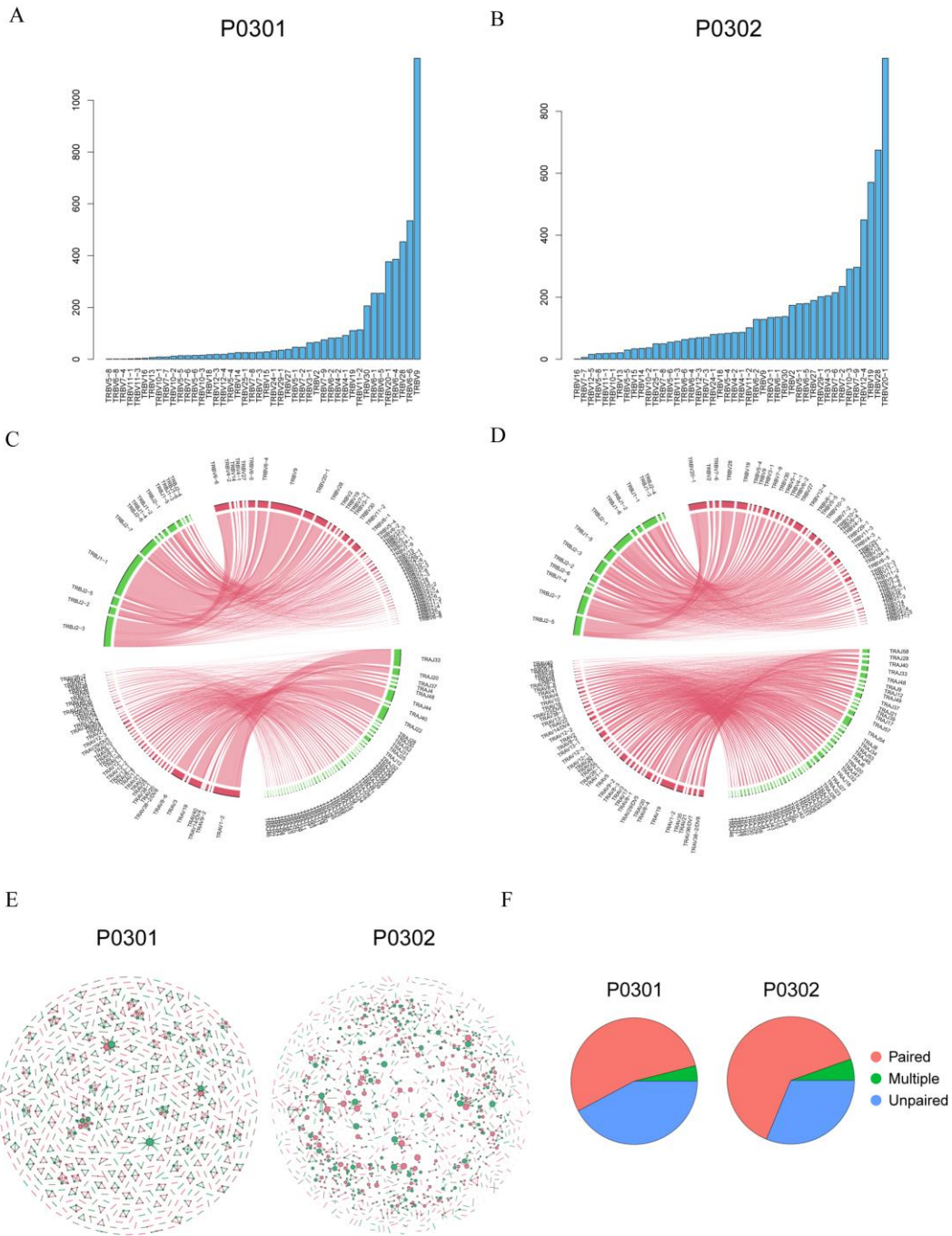
C



Supplementary Figure 2 Analysis of cell subset signaling activity. A: Scatterplots of the intensity of incoming and outgoing signals from different cell subsets. Different colors represent different cell subsets, with larger dots indicating higher intensity; B: Incoming and outgoing signaling patterns for P0301 and Supplementary Figure 2C P0302. The horizontal axis is a different subpopulation, each row of the vertical axis is a different gene, and the darker the color, the stronger the signal.



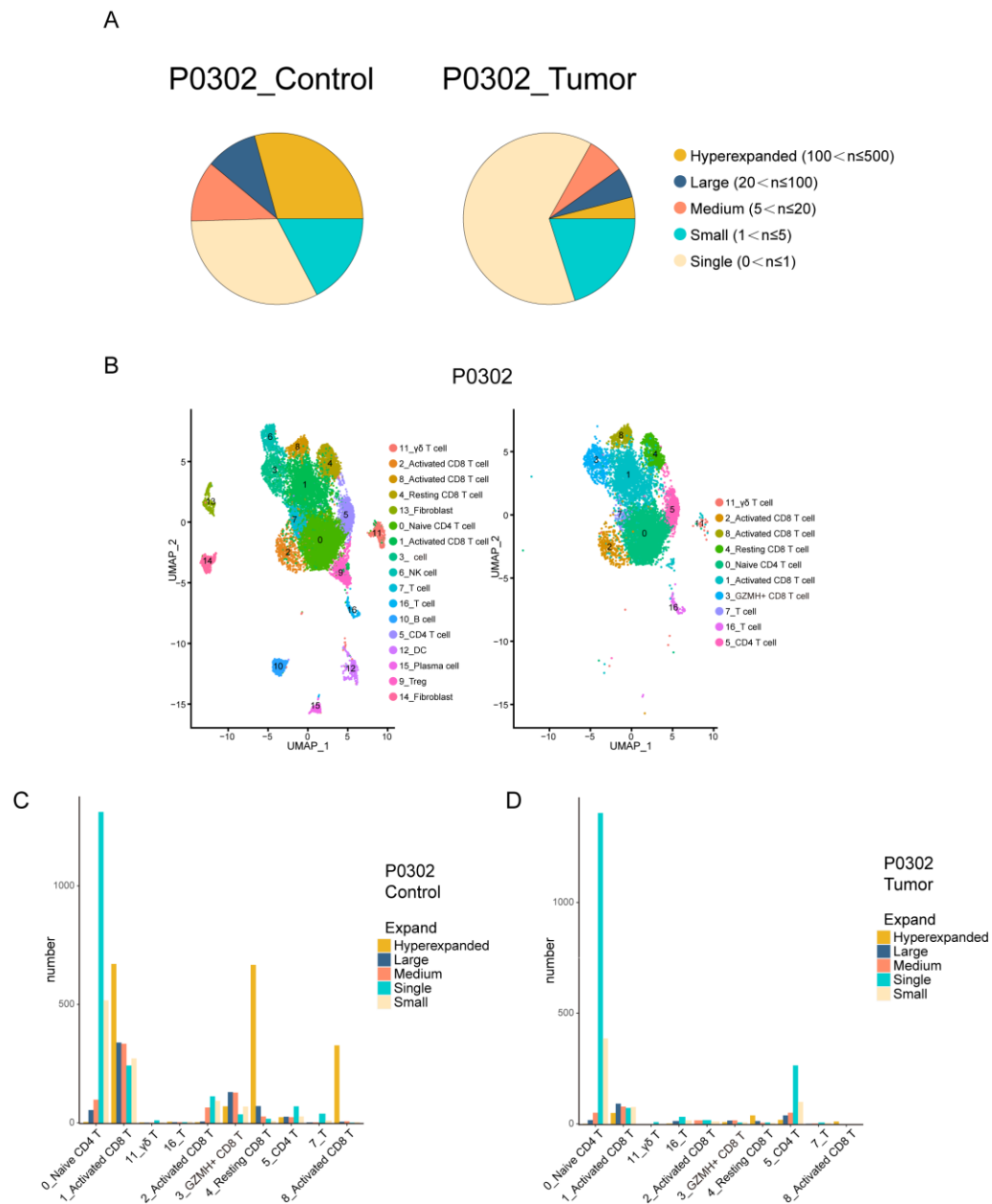
Supplementary Figure 3 Expression levels of cytokines and cytokine receptors in DCs cell subsets of different tissues (IL2RG, IL3RA, IFNGR1, TNF, IL13RA, IL10RB, IL1B, and IL18).



Supplementary Figure 4 Diversity of TCRs and pairing frequencies of V(D)J genes.

The major V genes of TRB are shown in P0301 (Supplementary Figure 4A) and P0302 (Supplementary Figure 4B). The combination of different V-J pairs is similar in P0301(Supplementary Figure 4C) and P0302 (Supplementary Figure 4D); E: TCR lineage maps show T cells with similar nucleotide sequences. The red and green dots are derived

from tumor tissue and paracancerous tissue, respectively. Two dots with nucleotide differences ≤ 2 are connected by line segments; F. Sector plots show the proportion of paired α and β chains detected in the cells.



Supplementary Figure 5 Distribution analysis of TCR cloning frequency in P0302A: Sectoral graph showing the extent of TCR clone amplification in P0302; B: The UMAP clustering map of T cells drawn by combining TCR expression data in P0302. The expansion levels of five different types of TCR amplification groups in each cell subtype of P0302 control (Supplementary Figure 5C) and tumor (Supplementary Figure 5D).