Table S3. Representative genes and functional description listed for each cluster of HCC.

Cluster No.	Tag	Representative genes	Functional description
0	C0-CD8-GZMA	GZMA,IFNG,TIGIT,NKG7,PDCD1	Cytotoxic and partially exhausted T cells
1	C1-CD4-CD44	IL7R,CD69, LTB,CD44	Activated T cells
2	C2-CD4-CD40LG	IL7R,CD69,CD40LG,KLRG1	T helper cells
3	C3-CD4-FOXP3	TIGIT,FOXP3,CTLA4,IL2RA	Treg
4	C4-CD8-CXCL13	CXCL13,PDCD1,CD27,CTLA4	Exhausted cells
5	C5-CD8-GNLY	GNLY,GZMA, NKG7,PRF1	Effector T cells
6	C6-PCNA	PCNA,MKI67,STMN1	Proliferating T cells
7	C7-CD68	CD68,C1QA,SERPINA1	Natural killer T cells

To generate a comprehensive view of the infiltrated T cells ecosystem of HCC, we applied single cell RNA sequencing on 8047 sorted CD3^{+}CD45RO^{+} cells from the HCC adjacent non-cancerous tissue (ANT) and tumor core (TM). *CD8A* and *IL-7R* were used as markers to classify CD8^{+} or CD4^{+} T cells. To reveal the intrinsic structure and potential functional subtypes of the overall T cell populations, we performed unsupervised clustering of all T cells using spectral clustering. A total of 8 stable clusters emerged from the integrated data. We named each cluster and compared genes expression.