a

- CD4_C1_LEF1
- CD4_C2_PRF1
- CD4_C3_GZMK
- CD4_C4_CCL4
- CD4_C5_LMNA
- CD4_C6_NKG7
- CD4_C7_CD5
- CD4_C8_FOXP3
- CD4_C9_CXCL13
- CD4_C10_MKI67

b

- CD8_C1_LTB
- CD8_C2_CX3CR1
- CD8_C3_GZMK
- CD8_C4_ANXA1
- CD8_C5_NR4A2
- CD8_C6_TYROBP
- CD8_C7_FGFBP2
- CD8_C8_CXCL13
- CD8_C9_MKI67

c

d

e

Supplementary information, Fig. S2: Clustering and evolutionary analysis of all T cells. a, t-SNE projection of all CD4$^+$ T cells from tumors of the ten patients using specific marker genes of the nine clusters identified in expanded CD4$^+$ T cells. **b,** t-SNE projection of all CD8$^+$ T cells from tumors of the ten patients using specific marker genes of the ten clusters identified in expanded CD8$^+$ T cells. **c,** Dot plot showing the expression of marker genes of the expanded CD4 clusters in the clusters of all tumor T cells from the 10 patients. **d,** The expression of marker genes of the expanded CD8 clusters in the clusters of all tumor T cells from the 10 patients. **e,** The frequencies of the four types of TCRs (1α1β, 1α2β, 2α1β, and 2α2β) in CD4$^+$CXCL13$^+$, CD4$^+$CXCL13$^-$, CD8$^+$CXCL13$^+$, and CD8$^+$CXCL13$^+$ T cells of the 10 patients.