Figure S1. CT scans of lymph node indicate lymphadenopathy is absent. (A) Red marks left inguinal lymph node (B) Red marks left upper cervical lymph node

Figure S2. UMAP projections of each sequenced sample.

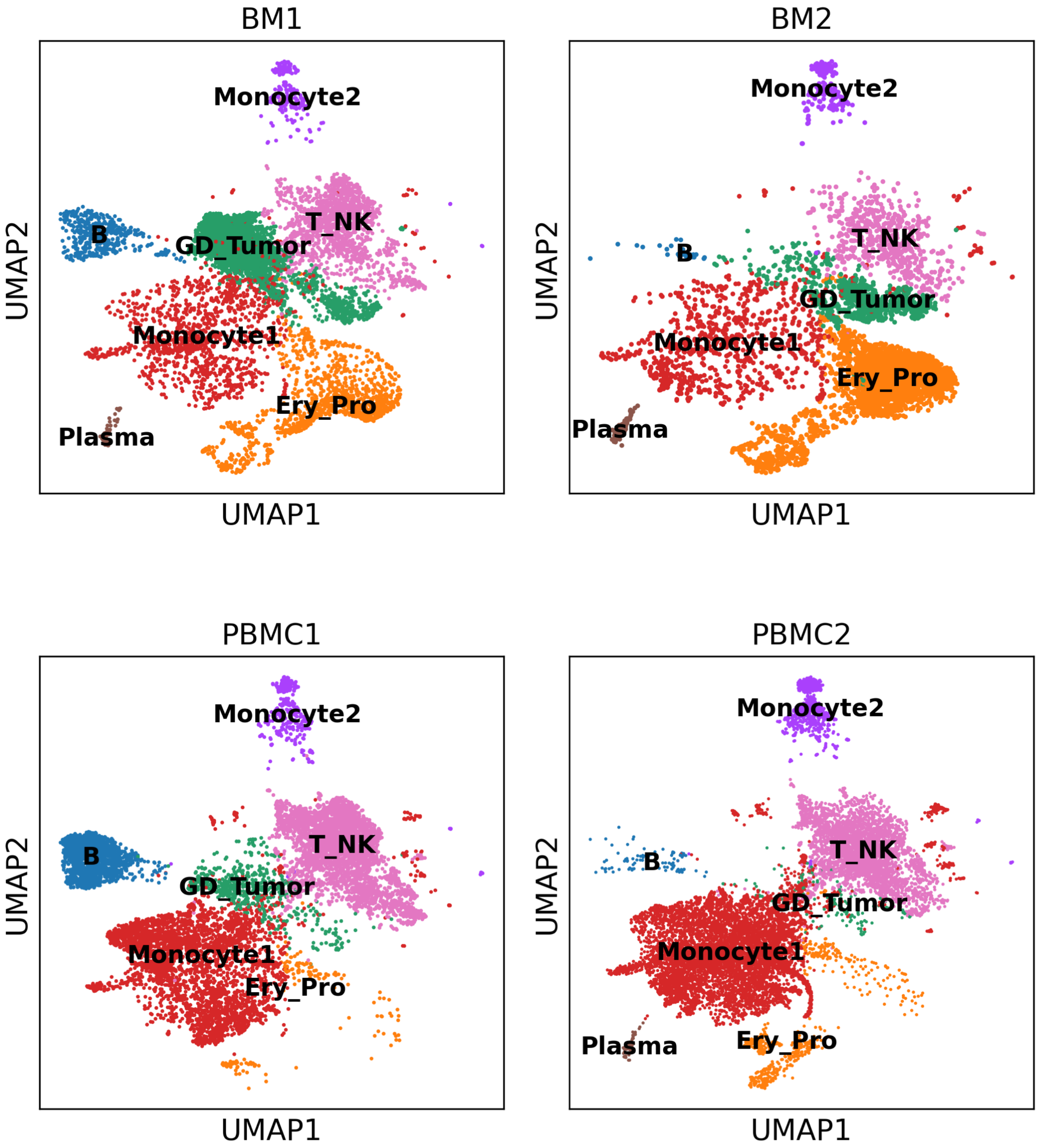

Figure S3. Expression of common markers used for HSTCL diagnosis

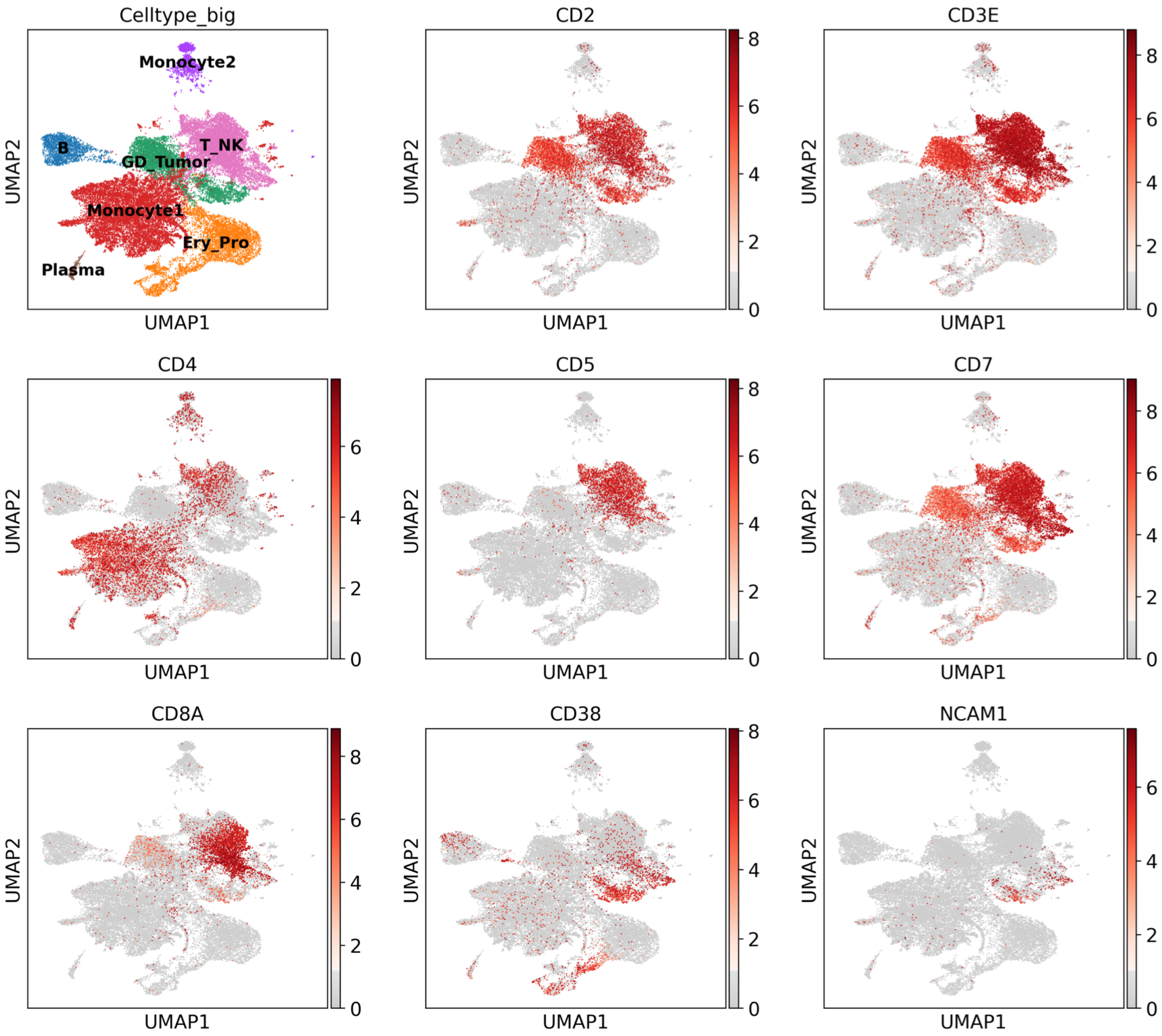

Figure S4. Sub-clusters identified in Ery_Pro. (A) UMAP of sub-clusters in Ery_Pro. Gran: Granulocyte progenitors, Multi_Pro: multipotent progenitors (B) The expression of marker genes for to the sub-clusters annotation

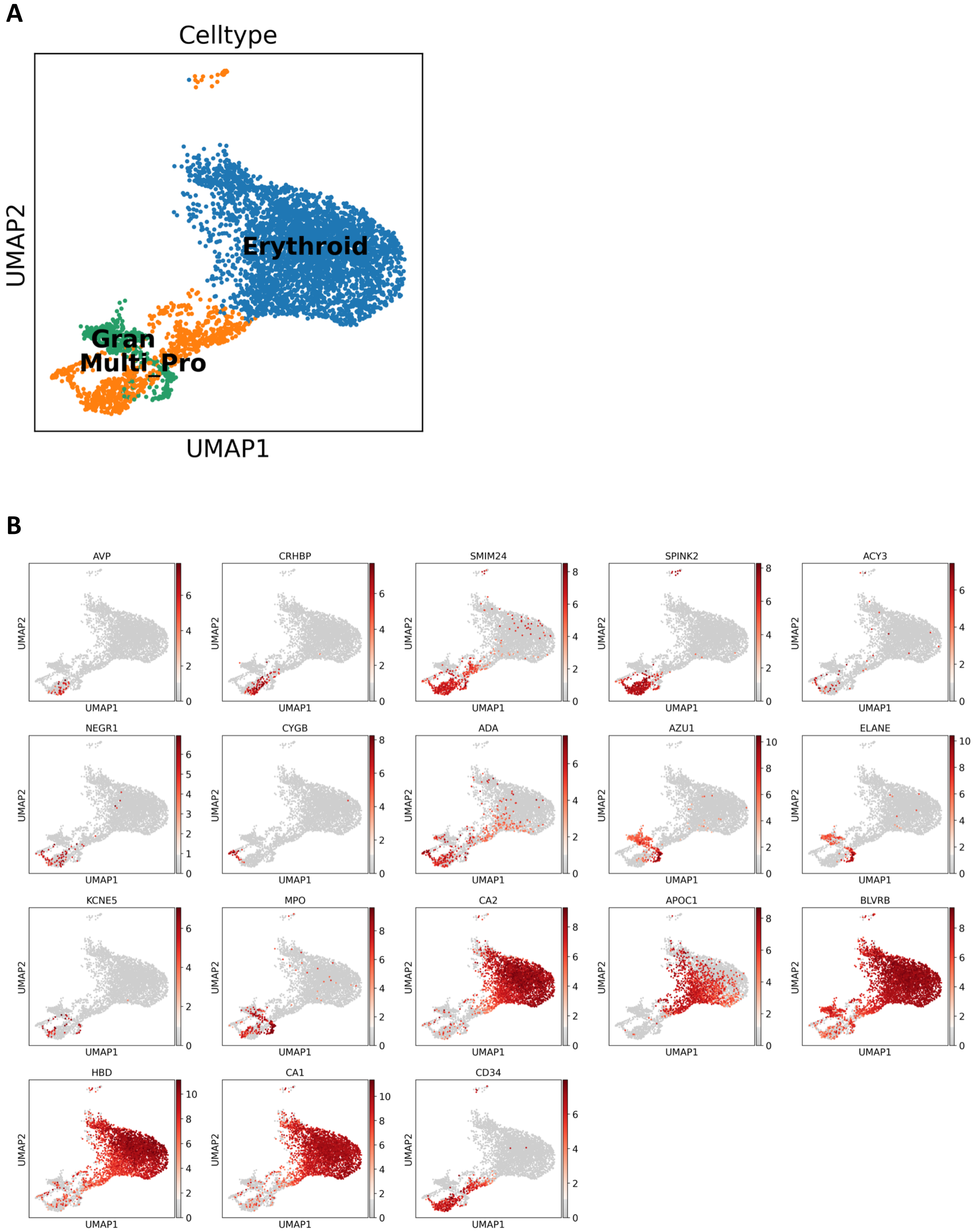

Figure S5. Cytotoxic genes reported to be expressed in normal γδ T cells had no or low expression in malignant γδ T cells

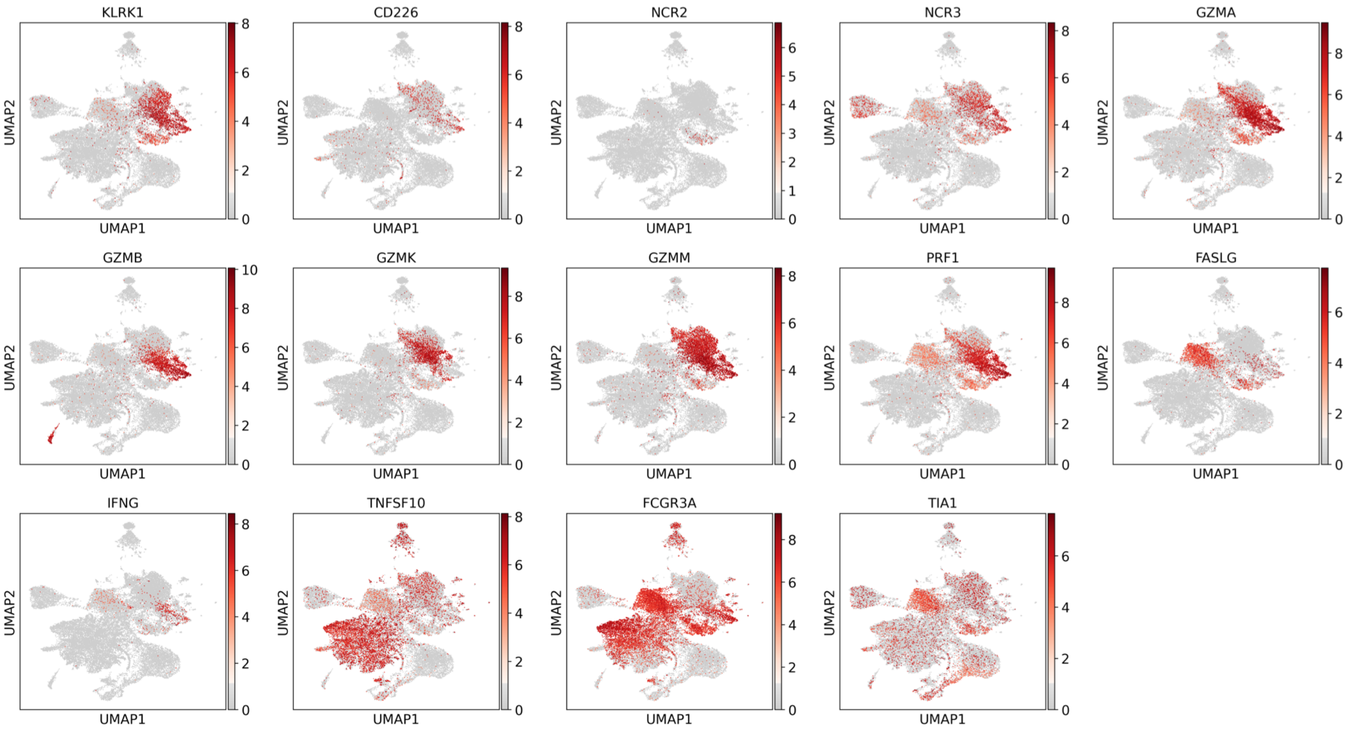

Figure S6. Cell Cycle phase distribution in Tumor sub-clusters

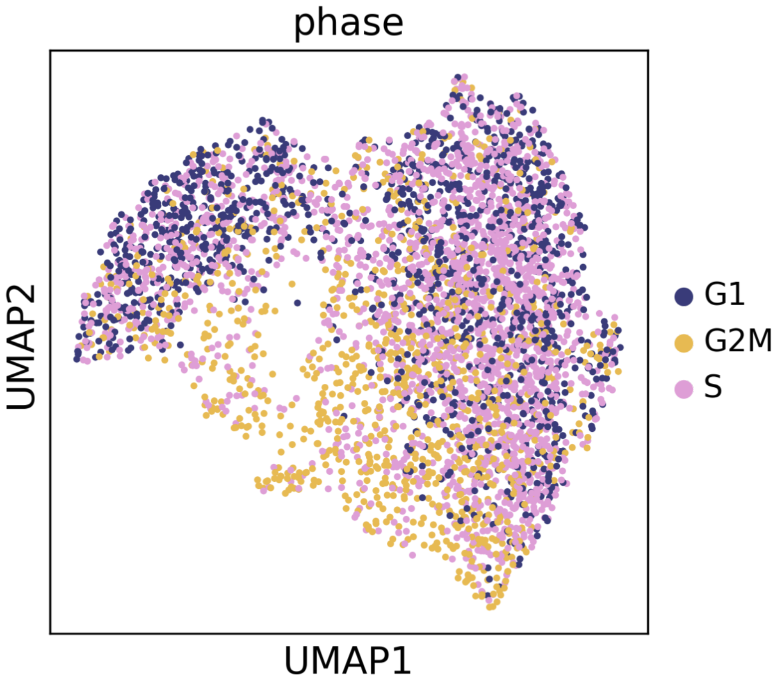

Figure S7. CD19 was highly expressed in Tumor_1 but not Tumor_2. Other B cell marker were not expressed in both Tumor sub-clusters

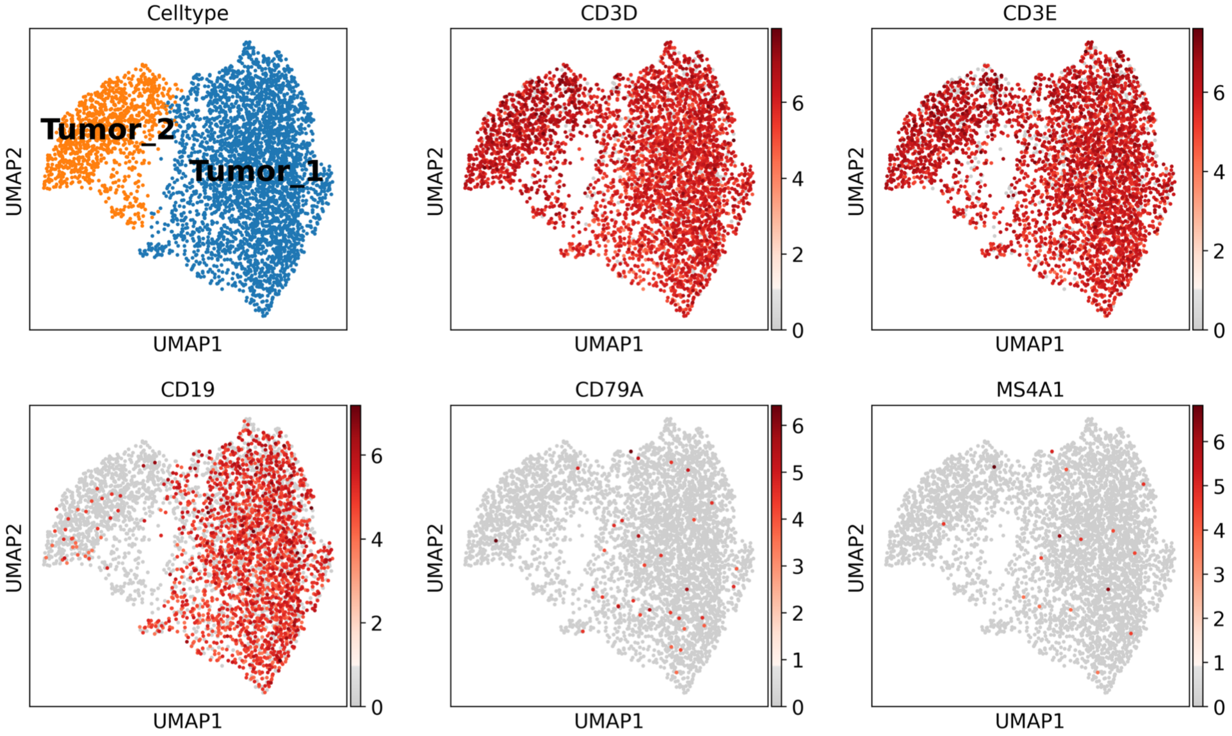

Figure S8. T cell sub-clusters identified from the tumor microenvironment. (A and B) The expression of marker genes for the T cell sub-clusters annotation

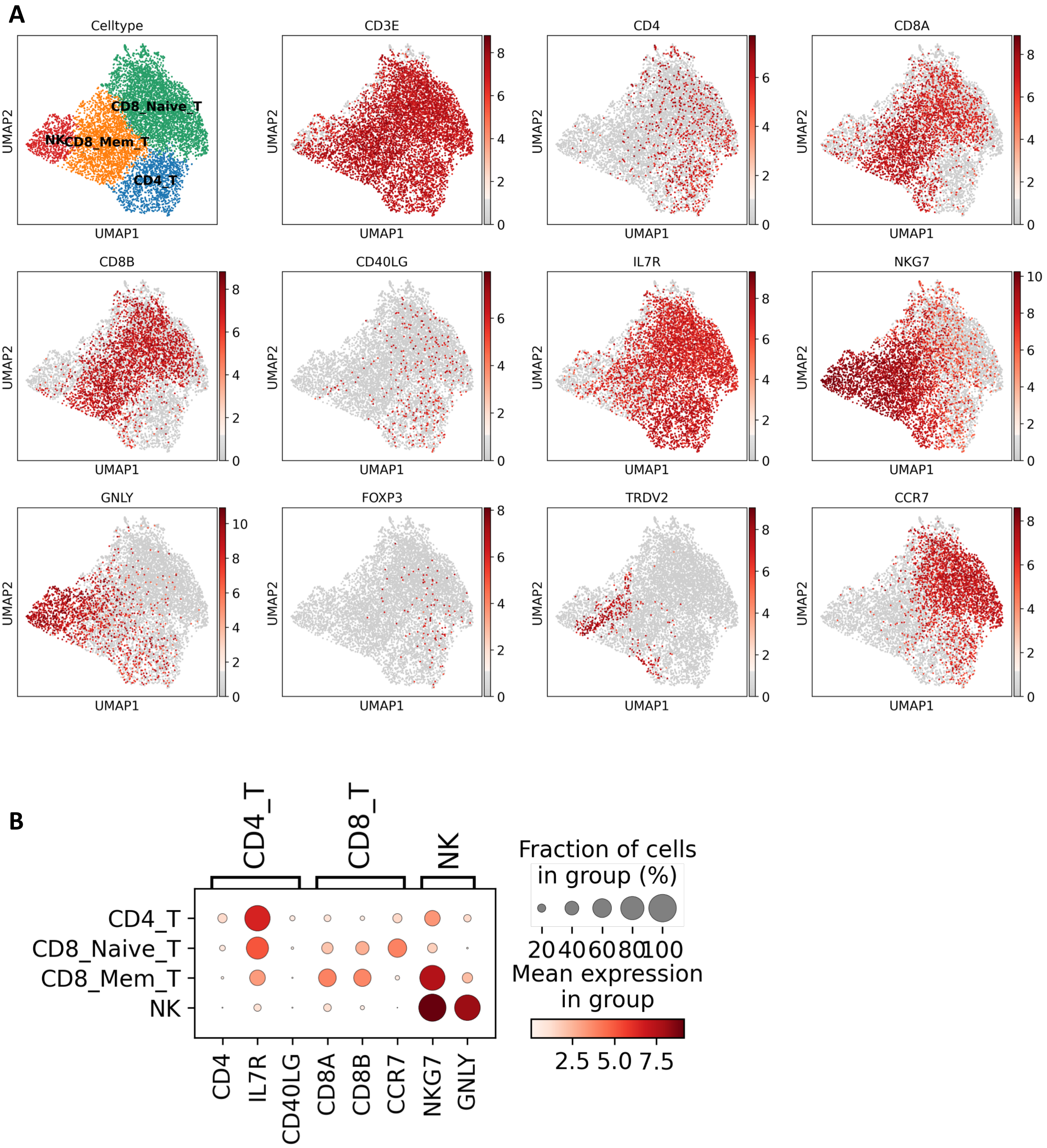

Figure S9. Total interaction counts and interaction strength inferred from each sample