



Figure S2. Heterogeneous T cell populations identified through additional sub-clustering of only T cells, related to **Figure 2**. **(A)** tSNE representation of scRNA-seq data, with labeling of individual T cell populations after sub-clustering. **(B)** Representation of each sample within each T cell cluster, colored by tissue of origin. **(C)** Expression of individual lineage and functional marker genes in each cluster, scaled from minimum to maximum for the expression of each gene ($\log[\text{count} + 1]$).