



**Figure S4.** Extended Data for Matched scRNAseq and scTCRseq Analysis of Tumor Samples. (A) Gene expression of the indicated individual genes in tumor CD8<sup>+</sup> T cells overlaid onto the UMAP. Individual cells are colored on a scale of gray (0) to red (1) according to the quantile of their expression. (B) Expression of indicated genes associated with a naive/stem-like phenotype (y-axis) plotted according to the size of a given clonotype (rank ordered on the x-axis). (C) TCR clone composition and phenotype sharing across clusters. Clonotypes are grouped by their primary cluster assignment on the x-axis, as indicated by dot color (Green: 8.2-T<sub>EM</sub>, Blue: 8.3a-T<sub>RM</sub>, Purple: 8.3b-T<sub>RM</sub>, Red: 8.3c-T<sub>RM</sub>). Heatmap demonstrates the fraction of each clonotype that falls into each cluster phenotype, depicted as a gradient from 0% (white) to 100% (black). Within each primary cluster, clones are rank ordered according to gradation of cell fraction. The sum clone size of each clonotype is indicated at the top.