



Figure S4. Analysis of TCR clonotype expansion, diversity along pseudotime, and predicted viral specificity, related to **Figure 4**. **(A)** Most clonotypes in tumor-normal pairs are only expanded in the tumor sample (red) or the normal sample (blue), with few clonotypes dual expanded in both tumor and adjacent normal (shades of purple). **(B)** TCR diversity across pseudotime in the top (purple) and bottom (green) CD8⁺ T cell trajectory branches, compared to the null distribution generated by randomly permuting cells across all samples (left), or only within an individual sample (right). Black lines show 100 random permutations. The predicted percentage of viral-specific T cells within **(C)** each T cell cluster, or **(D)** each sample ($p = 0.266$ for tumor vs normal, paired Wilcoxon rank-sum test; boxplots hinges are 25th to 75th percentiles; central lines are medians, whiskers are highest and lowest values no greater than 1.5x interquartile range, and dots are outliers).