

Figure S1: Cell population and antigen-specificity quantification

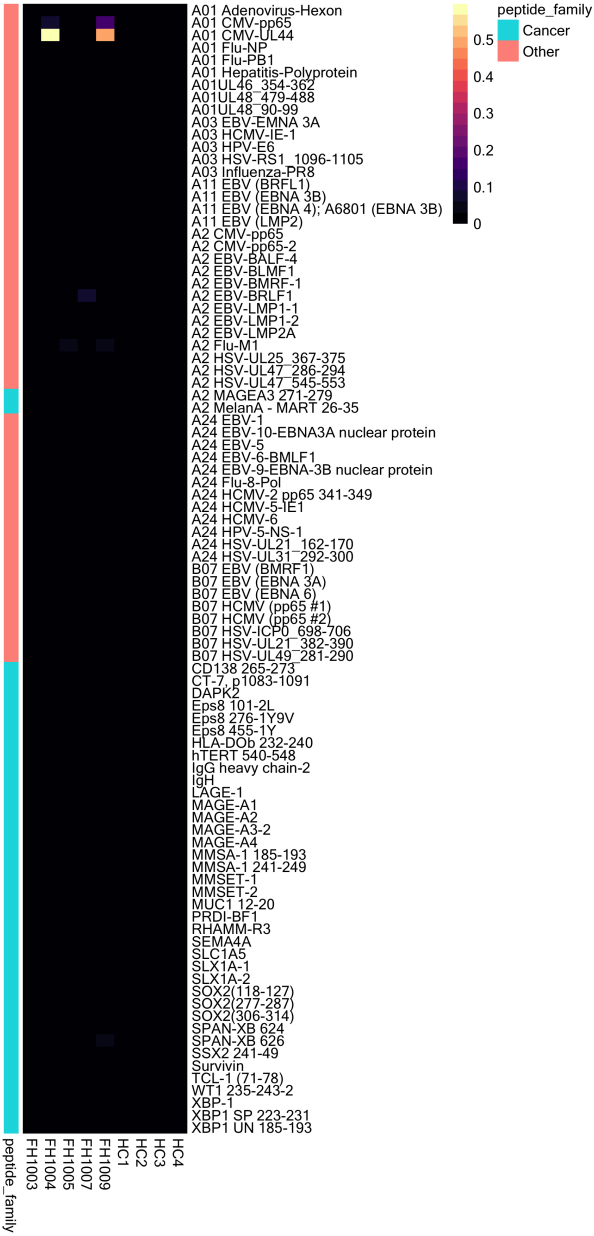
S1A: TotalVI-UMAP separated by tissue and colored by density

S1B: Frequency of cell populations by tissue, separated into newly-diagnosed multiple myeloma (NDMM) patients (top) and HCs (bottom); p calculated by Wilcoxon rank sum test.

S1C: Representative gating of PD-1⁺⁺CD39⁺ CD8⁺ T cells from NDMM, lung cancer (LC), and colorectal cancer (CRC) patients.

S1D: Frequency of cell populations by disease status (MM or HC), separated by tissue; p calculated by Wilcoxon rank sum test.

BM % antigen-specific



PB % antigen-specific

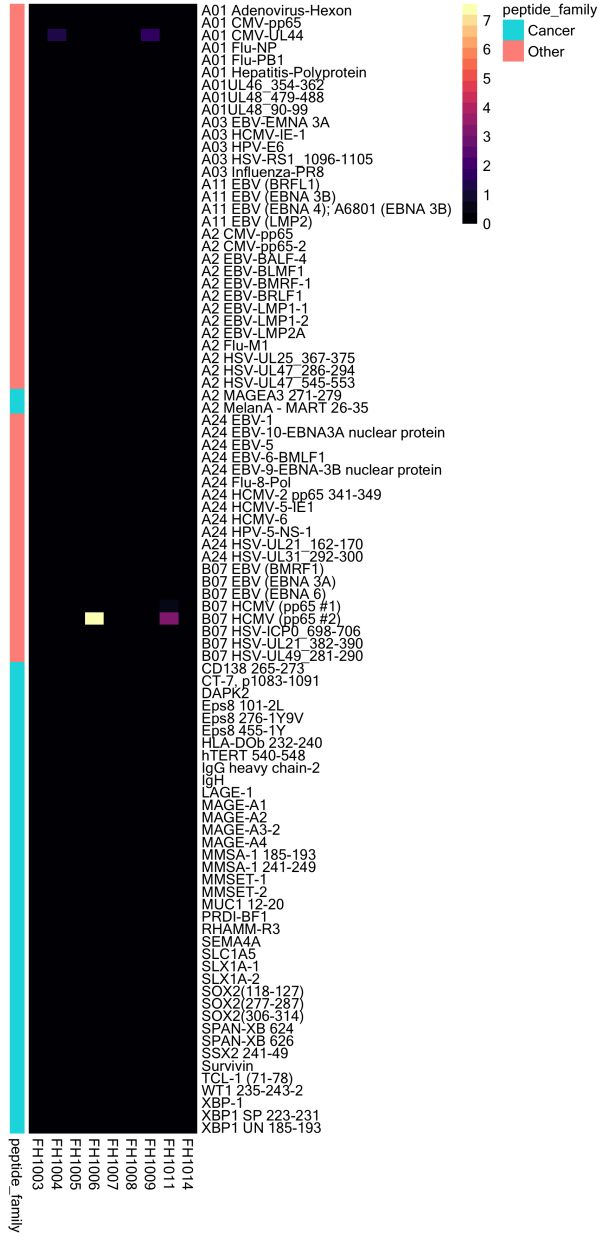


Figure S2: PRETX Frequency of peptide-MHC tetramer⁺CD8⁺ T cells by peptide, tissue, and individual.

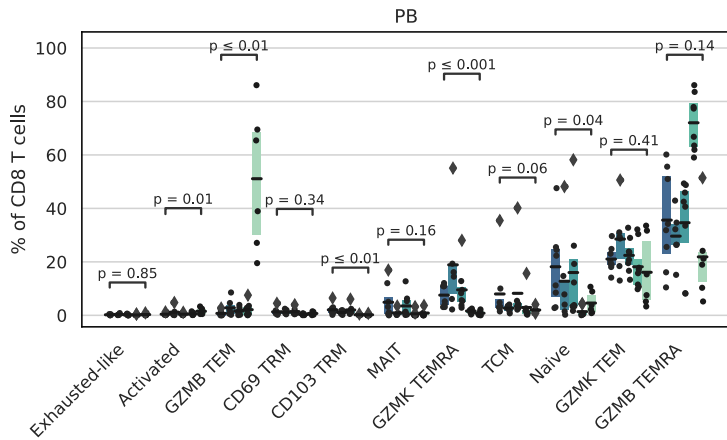
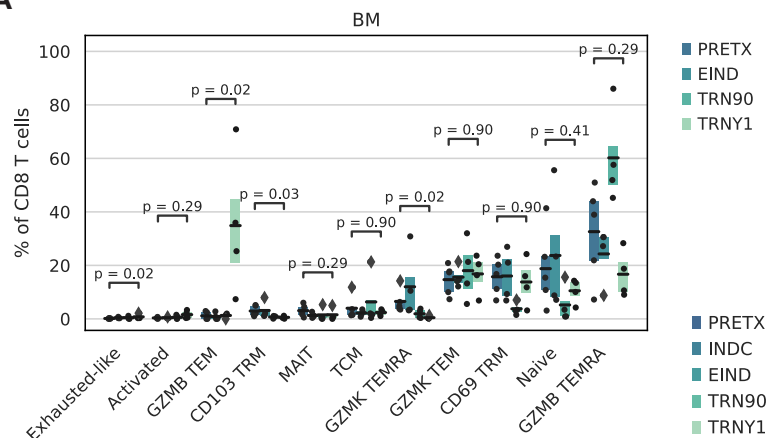
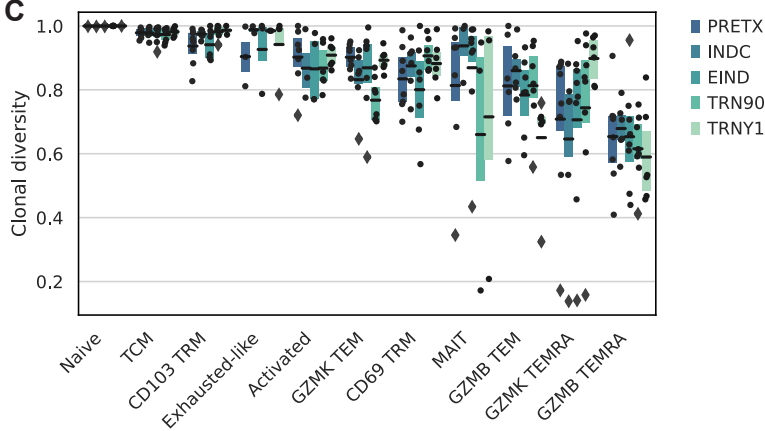
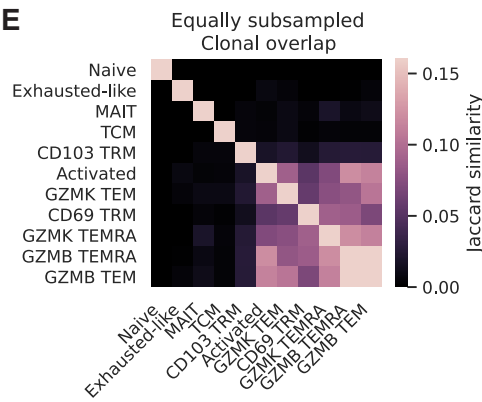
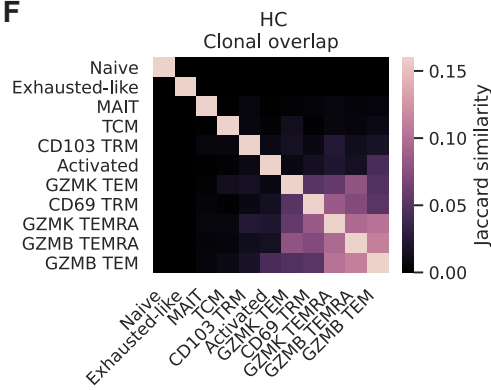
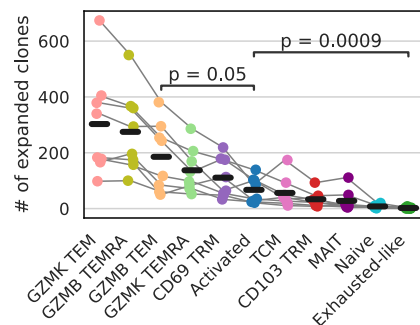
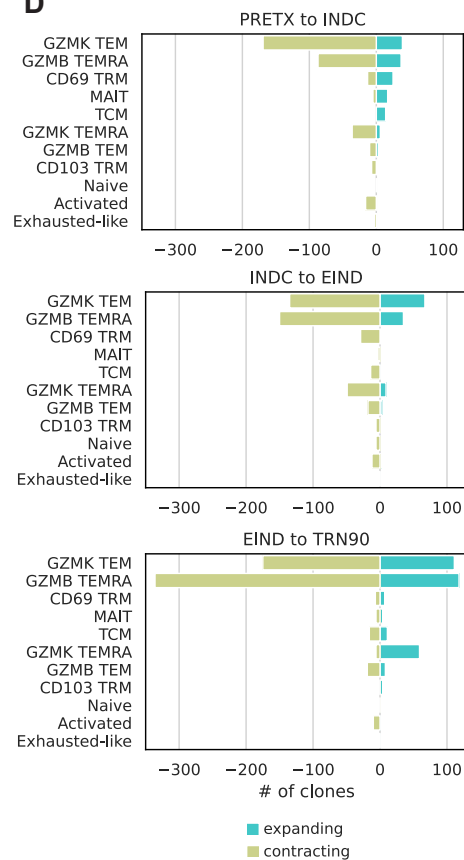
A**C****E****F****B****D**

Figure S3: Clonal and temporal dynamics

S3A: Frequency of cell populations by time and tissue; p calculated by Wilcoxon rank sum test.

S3B: Number of expanded clones by population; p calculated by Wilcoxon rank sum test.

S3C: Alpha diversity (Shannon entropy) of clones by time and population.

S3D: Number of significantly ($p < 0.05$) expanding and contracting clones by population and timepoint; p calculated by Fisher's exact test.

S3E: Jaccard similarity of clonal composition by population, equally sampled by population.

S3F: Jaccard similarity of clonal composition by population, for HCs only

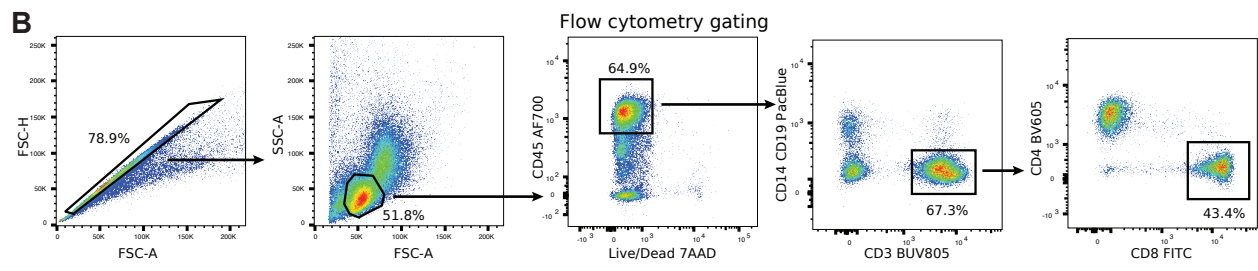
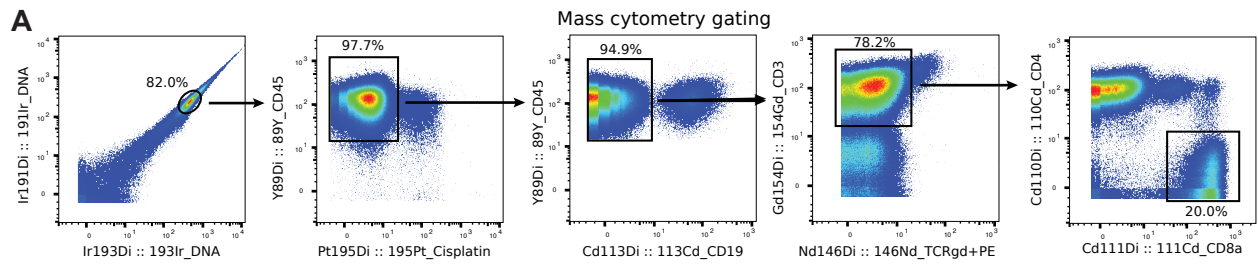


Figure S4: Cytometry gating of CD8⁺ T cells

S4A: Representative gating of CD8⁺ T cells in mass cytometry data

S4B: Representative gating of CD8⁺ T cells in flow cytometry sorting data

Table S1: Cohort demographics and clinical information

Table S2: Mass cytometry panel

Table S3: Mass cytometry peptide list

Table S4: Flow cytometry panel

Table S5: Antibody-derived tag (ADT) panel