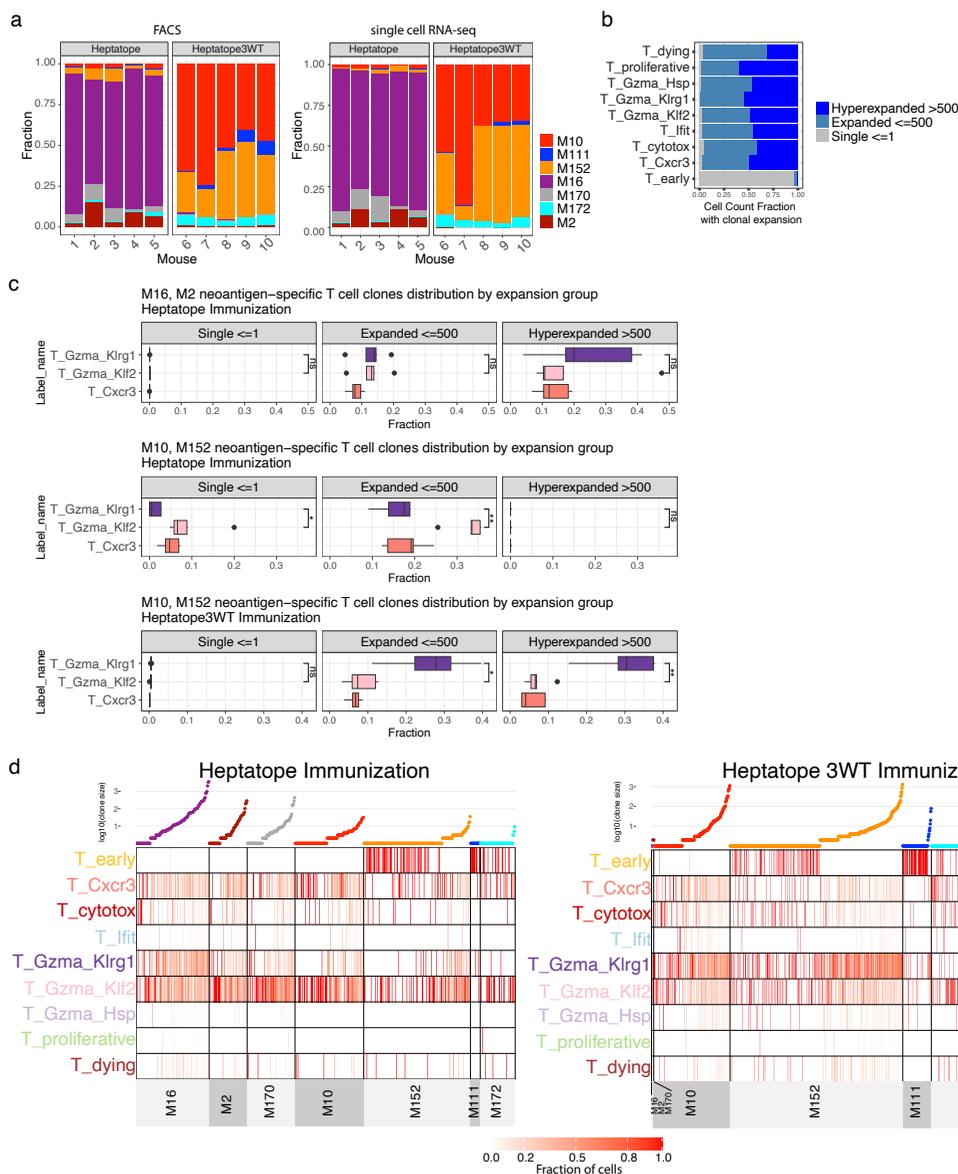


Extended Data Figure 5



Extended Data Fig. 5. Clonal expansion tracks with preferential differentiation of subdominant CD8⁺ T cells into a memory-precursor and progenitor-like phenotype

a, Cell count fraction of neoantigen-specific tetramer-positive T cells after heptatope and heptatope3WT immunization, as quantified by FACS and analyzed through single-cell RNA/ADT/TCR sequencing. **b**, Distribution of clonal expansion across T cell phenotypes, shown as the fraction of cells with an assigned clonotype expansion: single (≤ 1 cell with clonotype), expanded (≤ 500 cells with a clonotype), hyperexpanded (> 500 cells with a clonotype). **c**, Clonal expansion of cells with a specific T cell phenotype and neoantigen-specificity represented as the fraction of cells in each clonotype expansion group, T cell phenotype, and neoantigen-specificity relative to the total number of cells with a given neoantigen-specificity and T cell phenotype in a mouse. **d**, Distribution of neoantigen-specific clonotypes across T cell phenotypes as heatmap with columns representing each specific clonotype of a neoantigen-specificity and rows representing the T cell phenotypes. Colors indicate the fraction of cells of a specific clonotype in a T cell phenotype relative to all cells of that clonotype and neoantigen-specificity. Clonotypes are ordered by increasing clone size, with a scatterplot above the heatmap illustrating the \log_{10} clone size of each clonotype.