



Supplementary Fig. S10: Diversity of endogenous T-cell responses within the glioma TIME post CAR T-cell treatment. Seurat clusters 2, 8, and 16 were reclustered to further analyze lymphoid responses post CAR T-cell treatment. **(A)** UMAP plots of the T-cell subclusters visualized by treatment group. **(B)** Summary plot of T-cell subcluster distribution per treatment. **(C)** Dot plot depicting T-cell lineage and differentiation markers, T-cell immune inhibitory genes, T-cell cytolysis and immune activation genes, and chemotaxis genes per T-cell subcluster. Dot size represents the percentage of cells expressing each gene and dot color represents mean expression level with a gradient of lowest expression in blue to highest expression in red. **(D)** Table showing top upregulated genes corresponding with the functional phenotype for each of the 10 T-cell subclusters.

Tex – Exhausted T-cells, *Treg* – Regulatory T-cells, *Teff* – Effector memory T-cells, *Tquin* – Quiescent T-cells, *Trm* – Tissue resident memory T-cells, *Prol.* – Proliferating.