Supplementary Materials
Figure S1

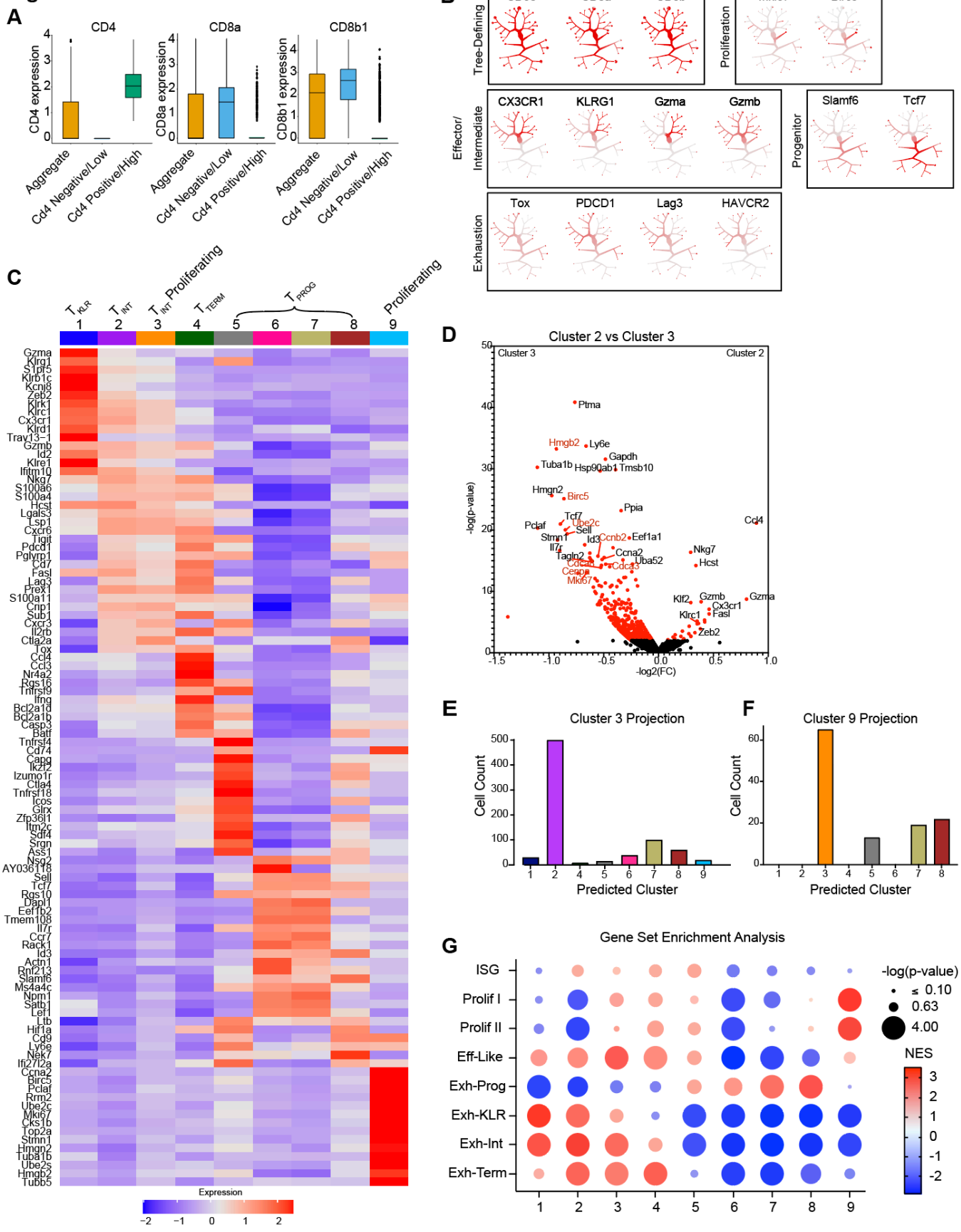

Figure S1: A complete pathway of CD8$^+$ T_{EX} differentiation can be identified in both Trib1 WT and Trib1 KO mice. (A) Relative expression of *CD4*, *CD8a*, and *CD8b* mRNA in all aggregate cells sorted for scRNA-seq as referenced in Rome et al[16] (yellow), in the *CD4*-low tree in Figure 1b (blue), or in the *CD4*-postive/high cells which were excluded from the tree in Figure 1b (green). (B) Normalized reference gene expression on the CD8$^+$ tree, where red = higher expression and gray/white = lower expression. (C) Heatmap demonstrating top DEGs within each of 9 clusters, where red = higher expression within that cluster and blue = lower expression. (D) Volcano plot of differentially expressed genes between Cluster 2 and Cluster 3. Proliferation genes are highlighted in red font. (E) Predicted identity of cluster 3 cells when proliferating genes were regressed out of analysis using the SCTransform function in Seurat. (F) Predicted identify of cluster 9 cells when proliferating genes were regressed out of analysis using the SCTransform function in Seurat. (F) GSEA analysis comparing the 9 clusters identified in this paper (x-axis) to the 8 populations identified at day 15 of LCMV clone 13 infection by Giles et al [4] (y axis). Trib1 WT: CD4-cre$^+$ Trib1$^{+/+}$, Trib1 KO: CD4-cre$^+$ Trib1$^{F/F}$

Figure S2

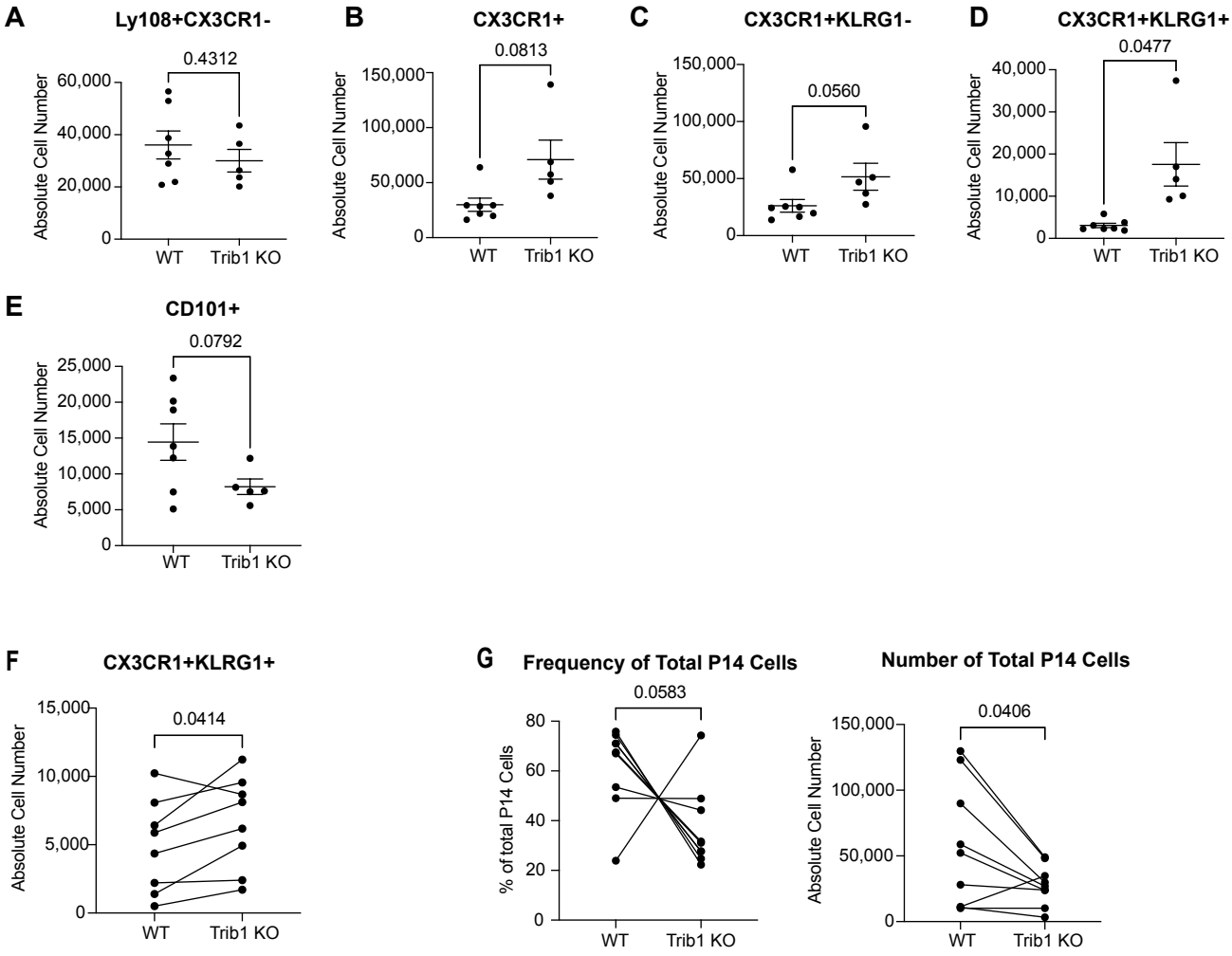

Figure S2: Trib1 restrains the absolute number of T_{KLR} that persist during chronic infection. (A-E) Absolute numbers of the indicated population from the same experiment shown in Figure 2C-E. For this analysis, cells were gated on $CD8^+CD44^+D^BGp33^+$ events as shown in Figures 2C-E. (F) Absolute number of $CX3CR1^+KLRG1^+$ P14 cells in the adoptive transfer experiments described in Figure 2G-H. Events are gated on $CD8^+D^BGp33^+$ cells and the appropriate congenic marker for WT (CD4.1/2) or KO (CD45.1) cells to identify genotype-specific P14 cells. (G) Frequency of total P14 cells by genotype as a percentage of total P14 cells or as absolute number. For A-G, absolute cell numbers were calculated by multiplying the frequency of each gated population as a percentage of live cells and by total live splenocytes for each mouse. For A-E, Error bars are mean ± SEM. P values calculated using either Student's t test or unpaired t test with Welch's correction based on variance between genotypes. For F-G, P values were calculated using a paired T test given that WT and KO cells were co-transferred into the same individual recipients. Trib1 WT: CD4-cre^+ $Trib1^{+/+}$, Trib1 KO: CD4-cre^+ $Trib1^{F/F}$