SUPPLEMENTARY FIGURE 1

A  Protein expression (antibody derived tags)

B  Gene expression

C  Goldrath gene signatures
SUPPLEMENTARY FIGURE 1 | Analysis of single-cell CITE-seq dataset used to annotate clusters in Figure 1C, available through the GEO (GSE182664, Lelliott et al, 2021). (A) Protein expression by cluster, as determined by antibody-derived tags. (B) Gene expression by cluster. (C) Goldrath effector and memory signatures taken for Molecular Signatures Database, showing enrichment by cluster.
SUPPLEMENTARY FIGURE 2

A  

Nkg7+/+  Nkg7−/−

![](image1.png)

% Area NKG7/T-cell (average)

% Area NKG7/T-cell (pooled)

SUPPLEMENTARY FIGURE 2
SUPPLEMENTARY FIGURE 2 | NKG7 antibody staining optimization for confocal immunofluorescence microscopy. (Top panel) *Nkg7*+/+ and *Nkg7*−/− T-cells were processed identically for immunofluorescence staining (fix/perm; either PFA/escin, PFA/triton or Bouins’ solution/escin) and NKG7 protein assessed using the NKG7 antibody (Cell Signalling). Figure is representative images of PFA/escin, identical data was obtained using other fix/perm combinations (data not shown). (Bottom panel) The percentage area of NKG7 staining present in images taken from *Nkg7*+/+ and *Nkg7*−/− T cells was determined for each T-cell analysed.