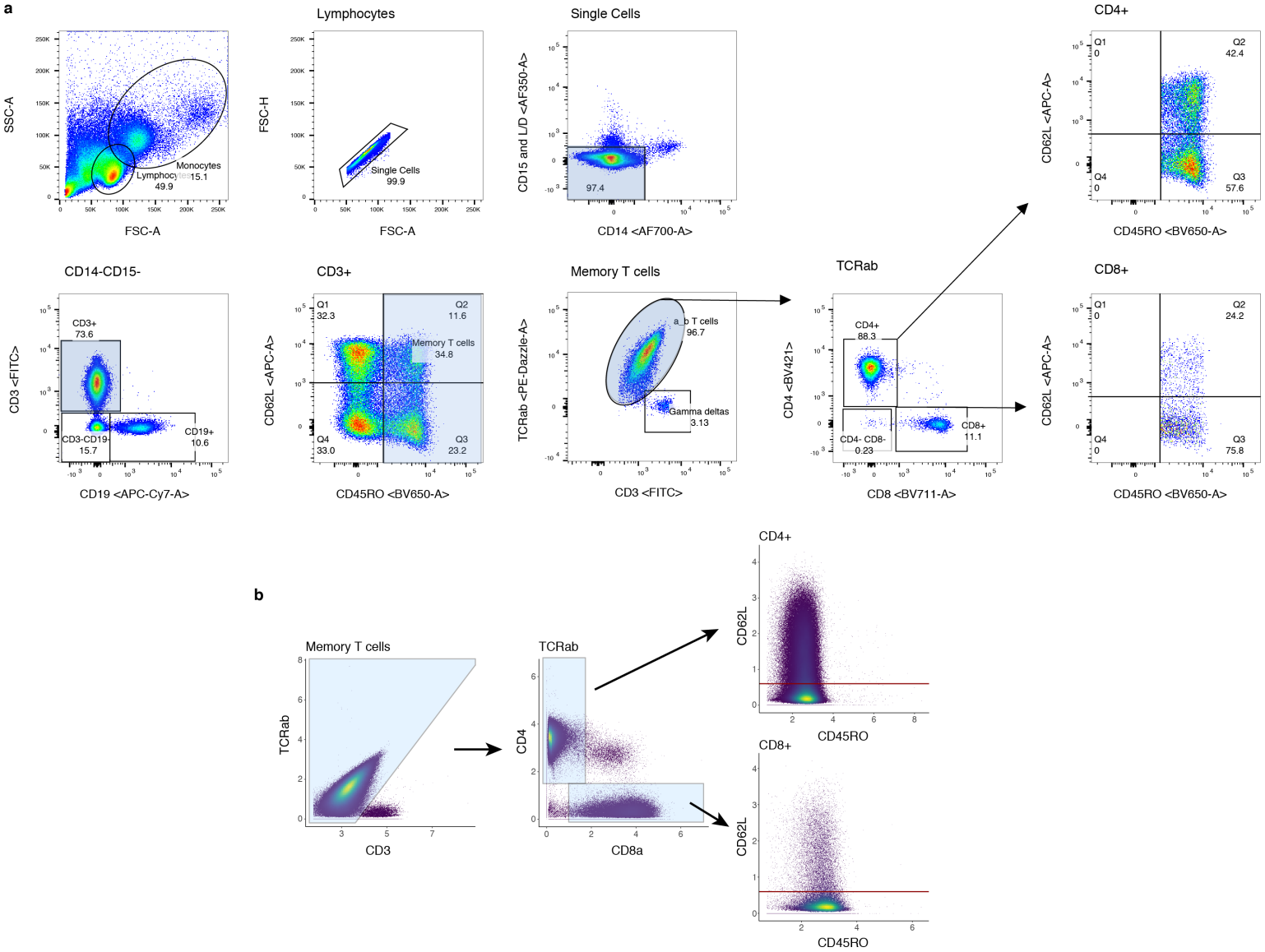
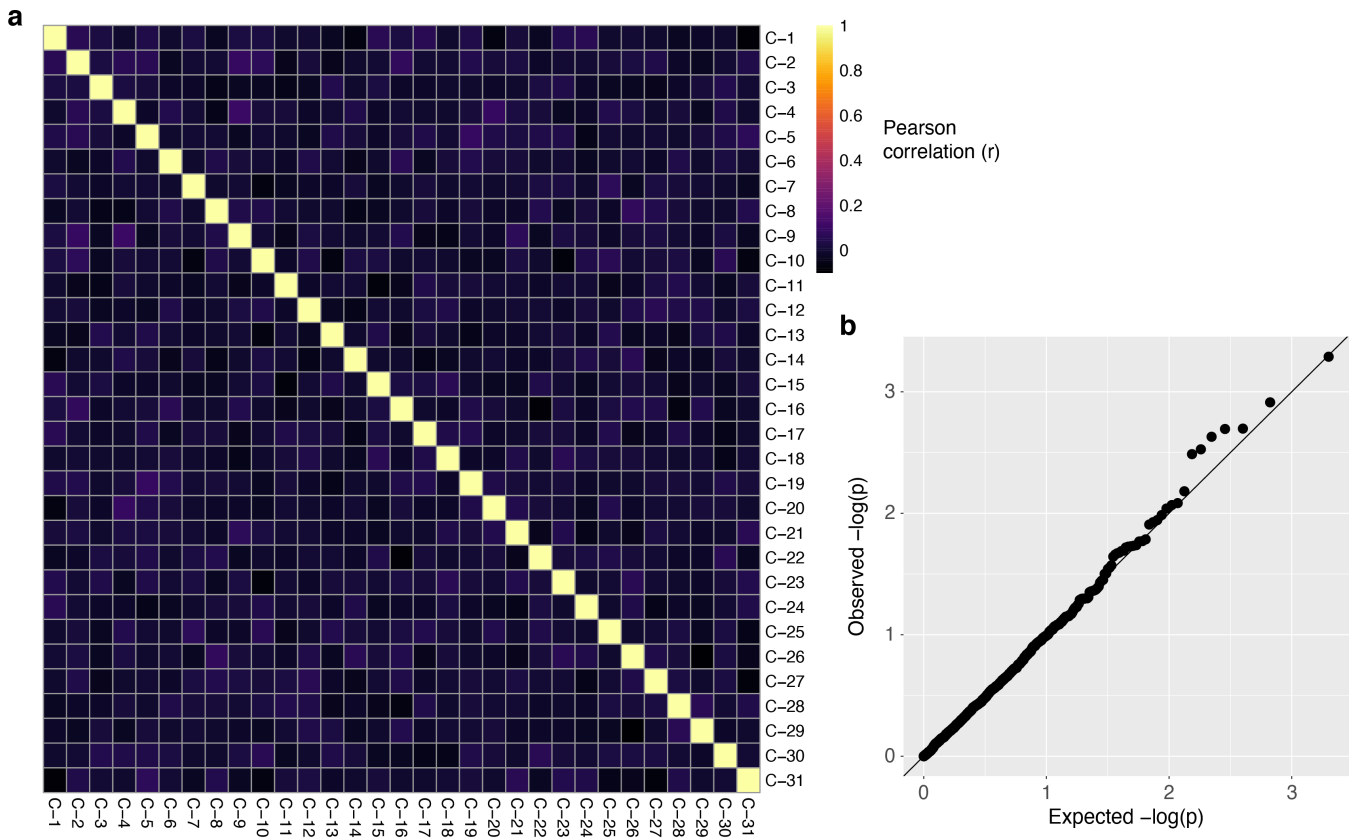
Supplementary Figures

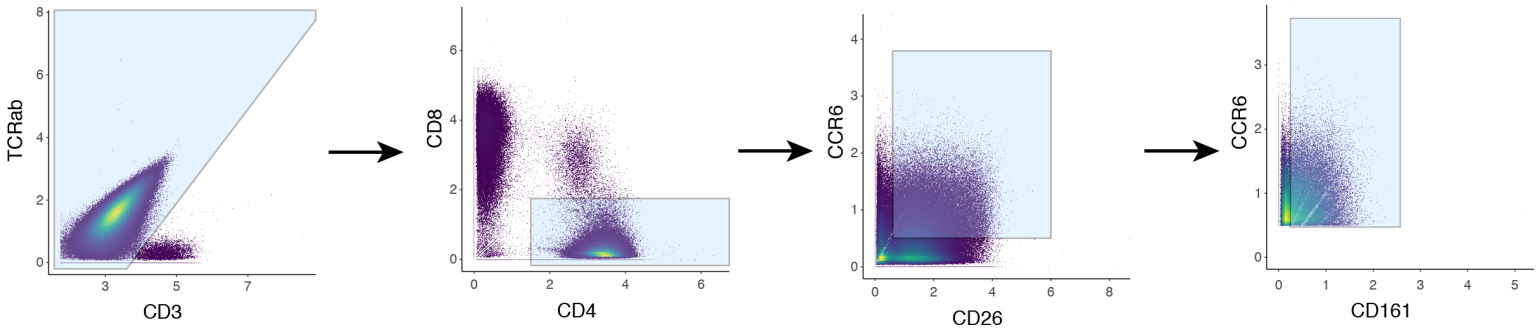


Supplementary Fig. 1. Representative gating of memory T cell subpopulations. a, Cells gated on flow cytometry protein expression. **b,** Cells passing QC gated on CITE-seq protein expression. Biaxial plots show cells passing QC plotted on centered-log-ratio-normalized protein measurements.

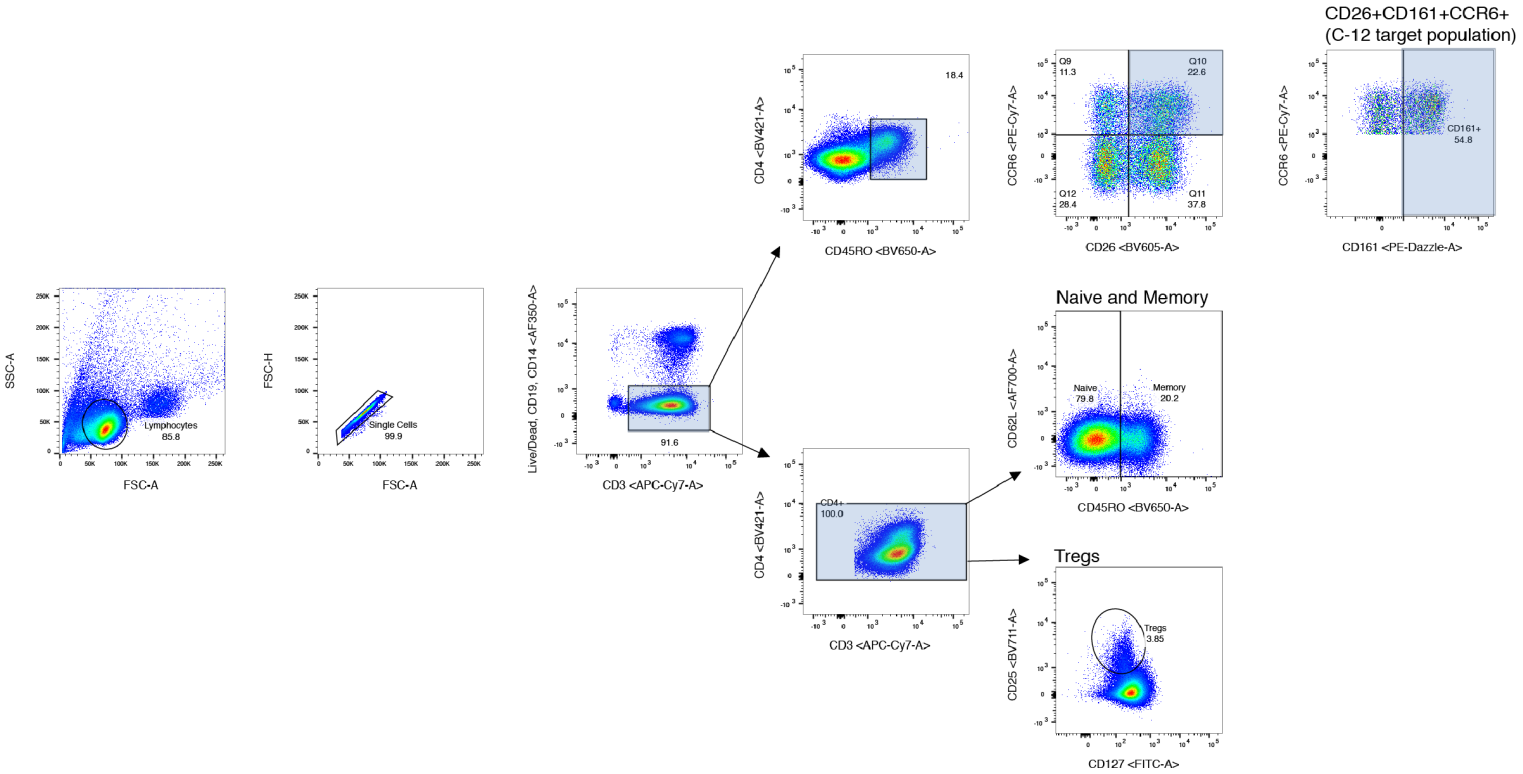


Supplementary Fig. 2. Gamma distribution of aggregated MASC p-values under the null. a, Heatmap showing Pearson correlations (r) of -ln(MASC LRT p value) between pairs of clusters under the null hypothesis. MASC LRT p values were obtained from 1,000 iterations of MASC to associate cluster membership with TB progression status permuted across donors. Average r between clusters' -ln(p values)=0.003. **b**, Quantile-quantile plot comparing observed gamma p values under the null hypothesis with expected quantiles. Gamma p values were computed from the simulated p values described in **(a).**

a


TCRab
CD3
CD8
CD4
CCR6
CD26
CCR6
CD161

b


SSC-A
FSC-A
Lymphocytes
85.8
FSC-H
FSC-A
Single Cells
99.9
Live/Dead, CD19, CD14 <AF350-A>
CD3 <APC-Cy7-A>
91.6
CD4 <BV421-A>
CD45RO <BV650-A>
18.4
CCR6 <PE-Cy7-A>
CD26 <BV605-A>
Q9
11.3
Q10
22.6
Q12
28.4
Q11
37.8
CD26+CD161+CCR6+
(C-12 target population)
CCR6 <PE-Cy7-A>
CD161 <PE-Dazzle-A>
CD161+
54.8
Naive and Memory
CD62L <AF700-A>
CD45RO <BV650-A>
Naive
79.8
Memory
20.2
CD4 <BV421-A>
CD3 <APC-Cy7-A>
CD4+
100.0
Tregs
CD25 <BV711-A>
CD127 <FITC-A>
Tregs
3.85

Supplementary Fig. 3. Representative gating of C-12. a, Biaxial plots showing gating of TCRαβ+CD4+CD8-CD26+CD161+CCR6+ cells in CITE-seq data. **b,** Biaxial plots showing gating of target (CD3+CD4+CD26+CD161+CCR6+) and control populations from a Boston donor.