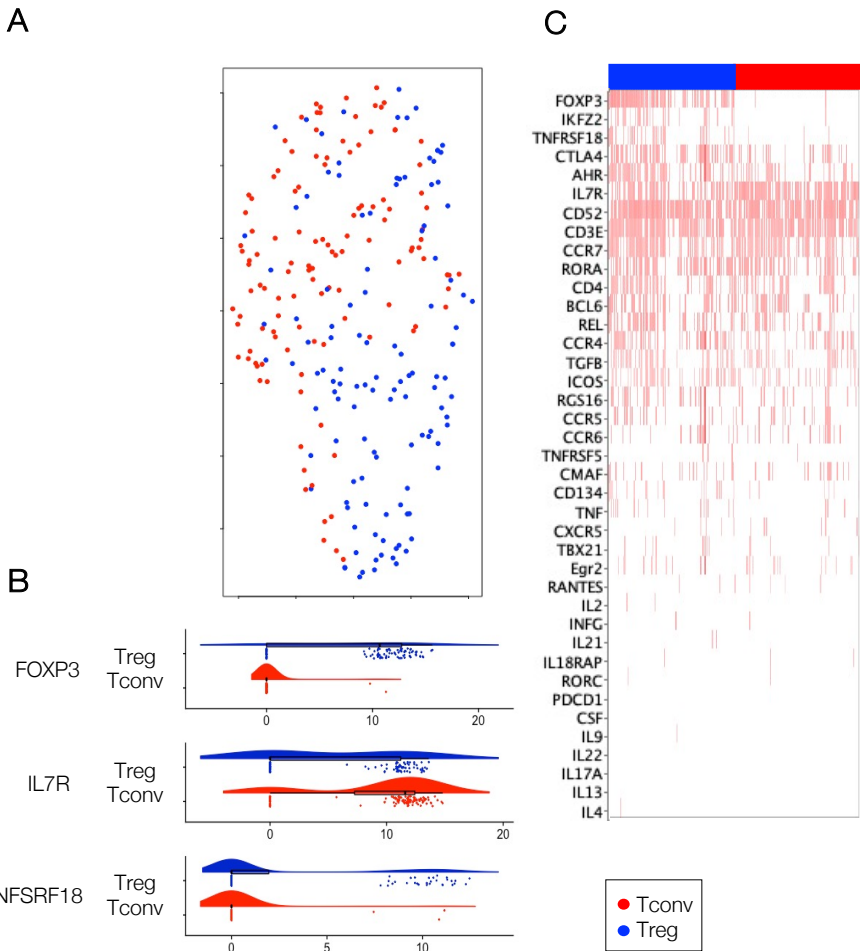
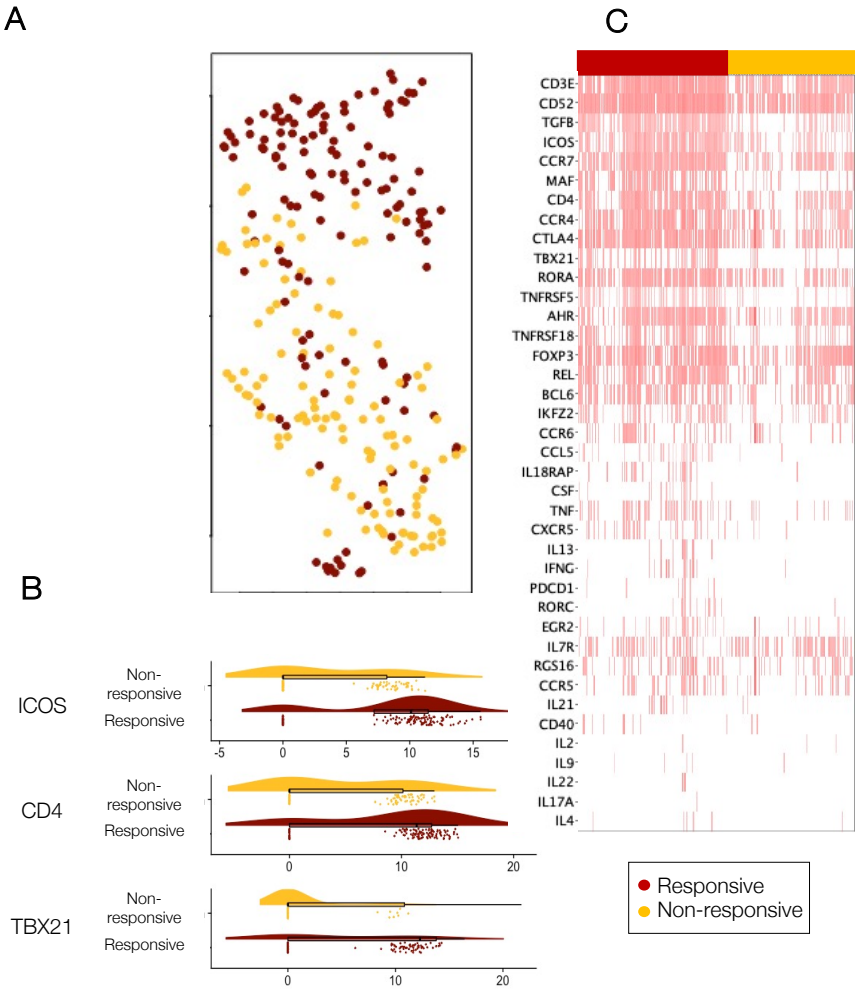


Supplementary Figure 1



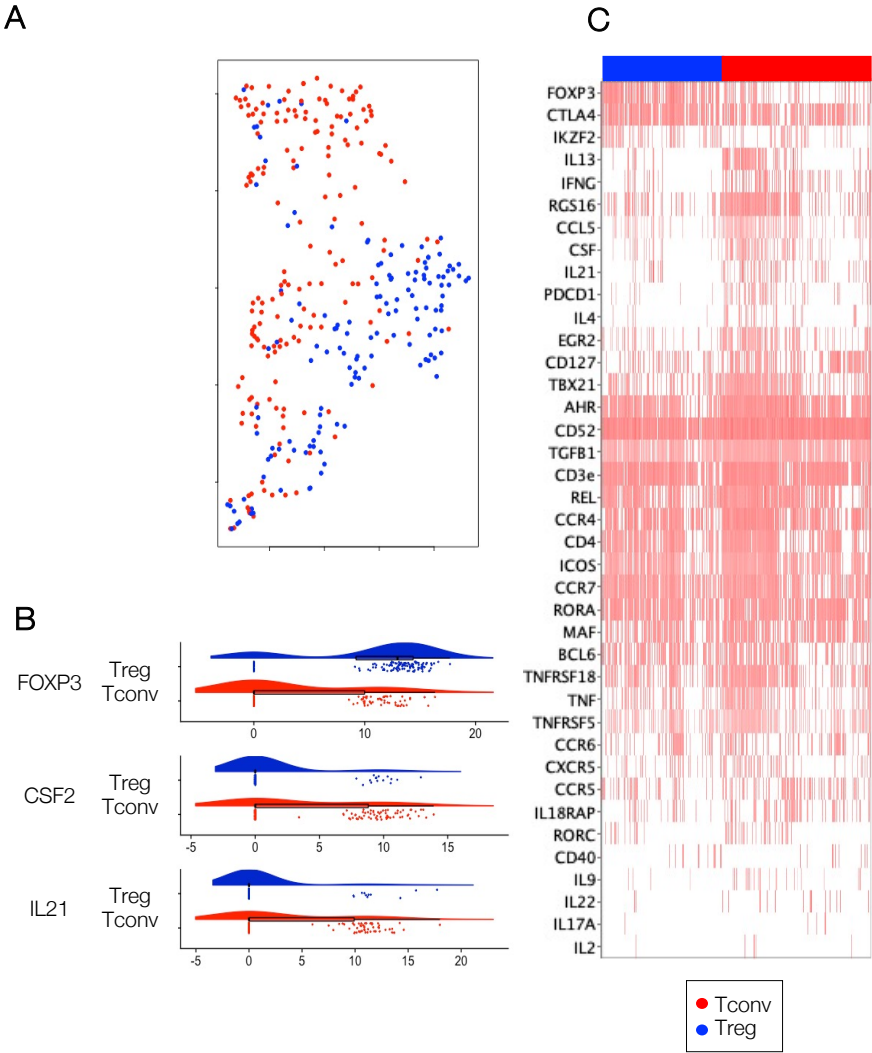
Supplementary Figure 1 Gene expression differences between T conv and T reg non- responding cells as measured on the Biomark. A UMAP visualization of both cell types. T conv are coloured in red, T reg in blue. B Raindot- plots showing the expression of exemplary genes significantly differing between the two cell types. Cell Types are colour- coded as in A. y-axis shows values after processing raw data. C Shown is a heatmap with differentially expressed genes. All genes significantly differing between T reg and T conv in non- responding TT-stimulated cells using the Biomark. From top to bottom are genes with the highest fold change (FC) in T regs and from bottom to top in T conv. T conv are shown in red, T reg in blue.

Supplementary Figure 2



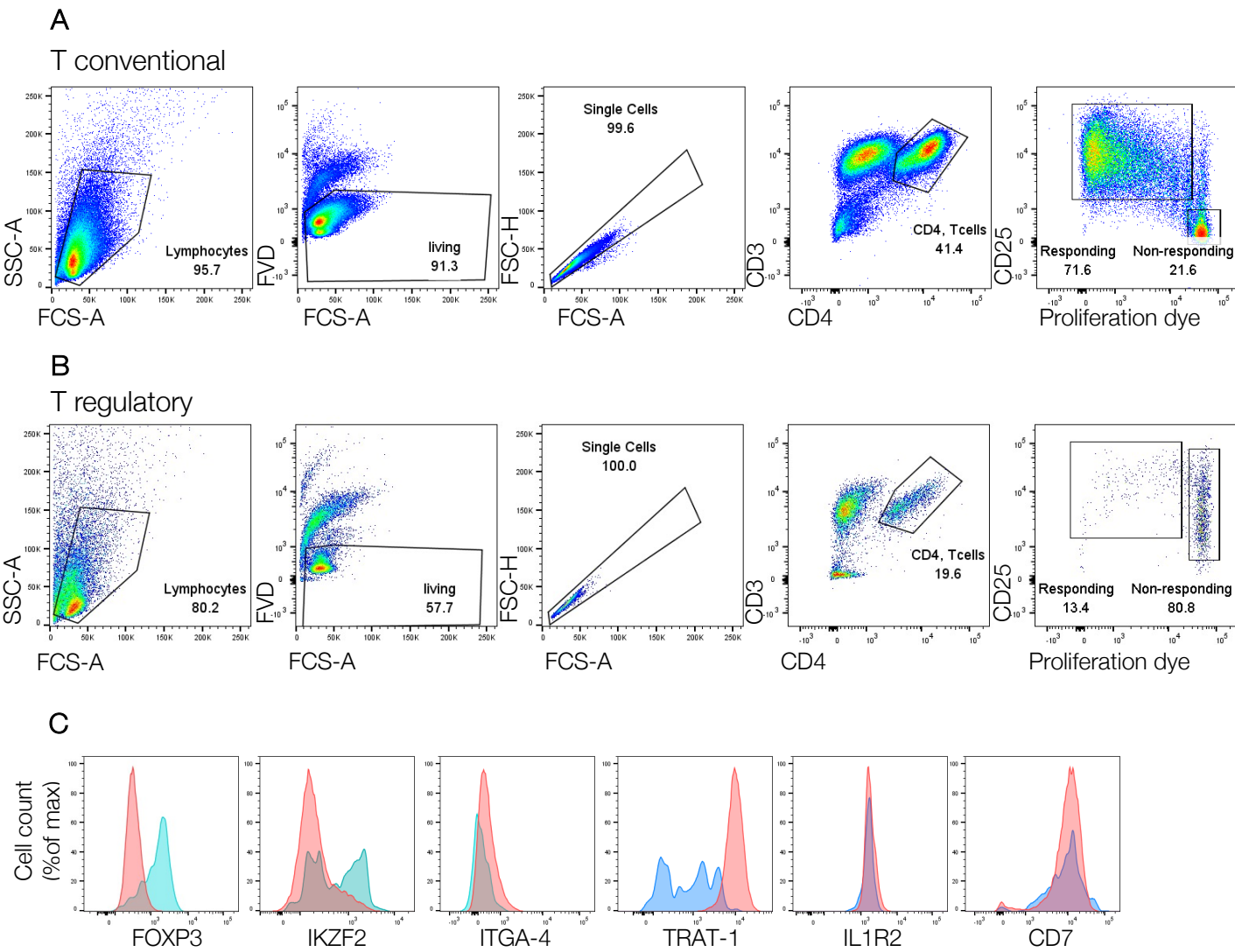
Supplementary Figure 2 Gene expression differences between responding and non- responding T reg cells measured by Biomark. A UMAP visualization of both cell types. Responding are coloured in dark red, non-responding in yellow. B Raindot- plots showing the expression of exemplary genes significantly differing between the two cell types and shared between Biomark and SMARTseq (*CD4*) or Biomark and Rhapsody (*TBX21*) or between all three (ICOS). Cell Types are color- coded as in A. y-axis shows values after processing raw data. C Shown is a heatmap with all genes present in the Biomark Panel; genes significantly differing between responding and non- responding in TT stimulated T regs are shown at the top (*CD3E- EGR2* responding specific; no non- responding specific genes found).

Supplementary Figure 3



Supplementary Figure 3 Gene expression differences between T conv and T reg responding cells obtained by Biomark analysis. A UMAP visualization of both cell types. T conv are coloured in red, T reg in blue. B Raindot- plots show the expression of exemplary genes significantly differing between the two cell types and also found with either SMARTseq or Rhapsody (*FOXP3*, *CSF2*, *IL21*). Cell Types are colour- coded as in A. y-axis shows values after processing raw data. C Shown is a Heatmap with genes differentially expressed between T conv and T reg responding cells. The expression of all genes present in the Biomark Panel are shown; genes significantly differing between T reg and T conv in responding TT-stimulated cells are shown at the top (*FOXP3-IFKZ2*: T reg specific; *IL13-CD127*: T conv specific).

Supplementary Figure 4



Supplementary Figure 4 FACS analysis of Tconv and Treg cell to confirm the signature genes obtained by machine learning. A and B Gating strategy to separate responding from non-responding Tconv (A) and Treg (B). C Histogram showing the expression of the analysed markers in Tregs (blue) and Tconv (red). Shown is the number of events (cells) in each fluorescent channel (marker) scaled as a percentage of the maximum count.