

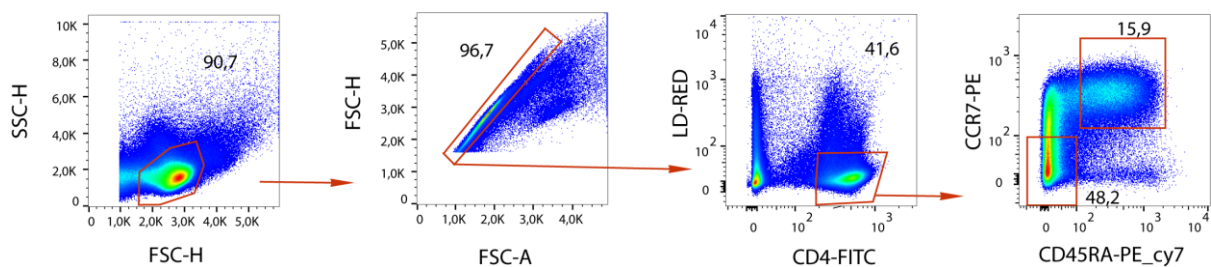
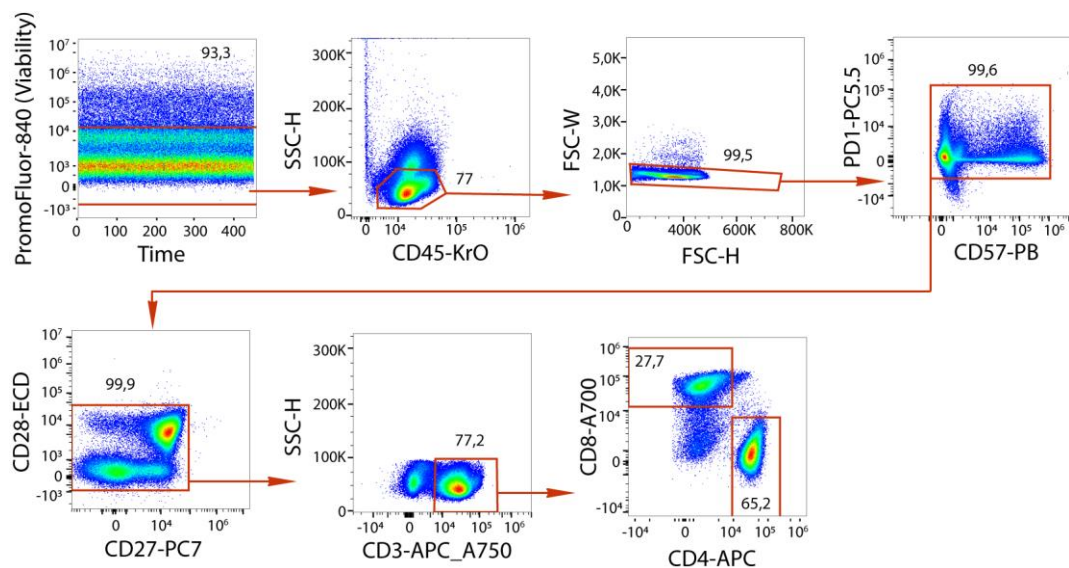
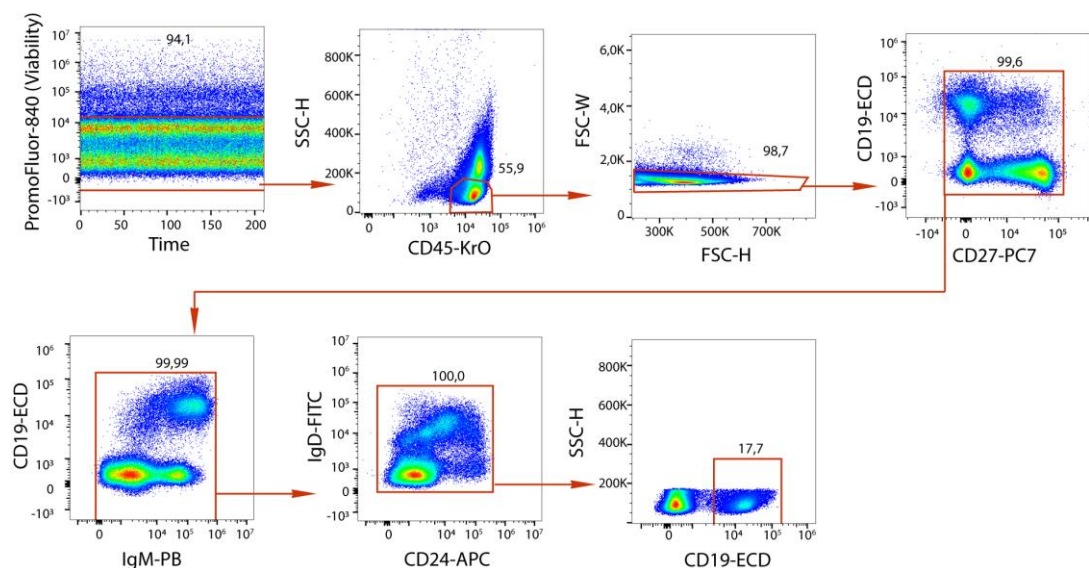
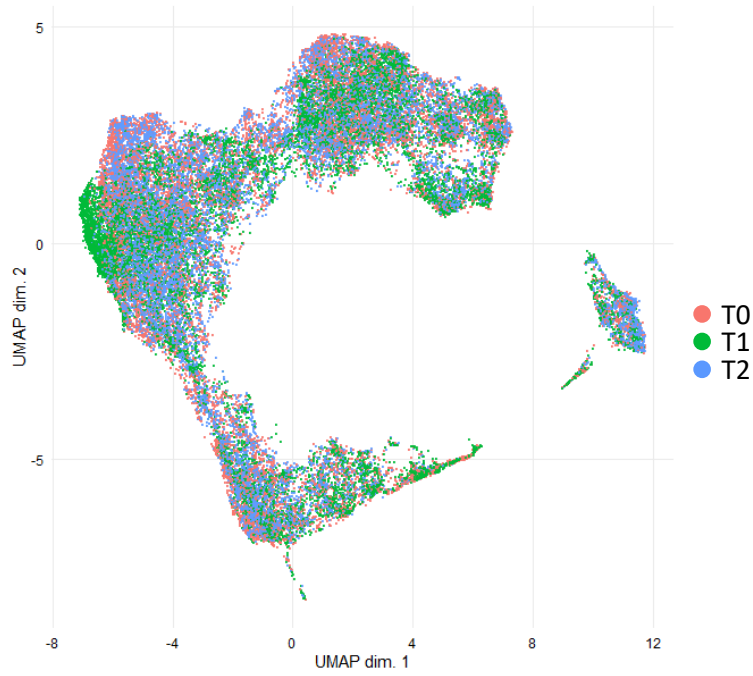
A**B****C**

Figure S1. Representative gating strategies

(A) Gating strategy used to identify and isolate viable naïve (CD45RA+CCR7+) and effector memory (CD45RA-CCR7-) within CD4+ T cells. (B) Representative gating strategy used to identify CD4+ and CD8+ T cell among PBMC. (C) Representative gating strategy used to identify B cells among PBMC. Selected CD4+, CD8+, CD19+ main populations were analyzed by unsupervised clustering analyses.

A



B

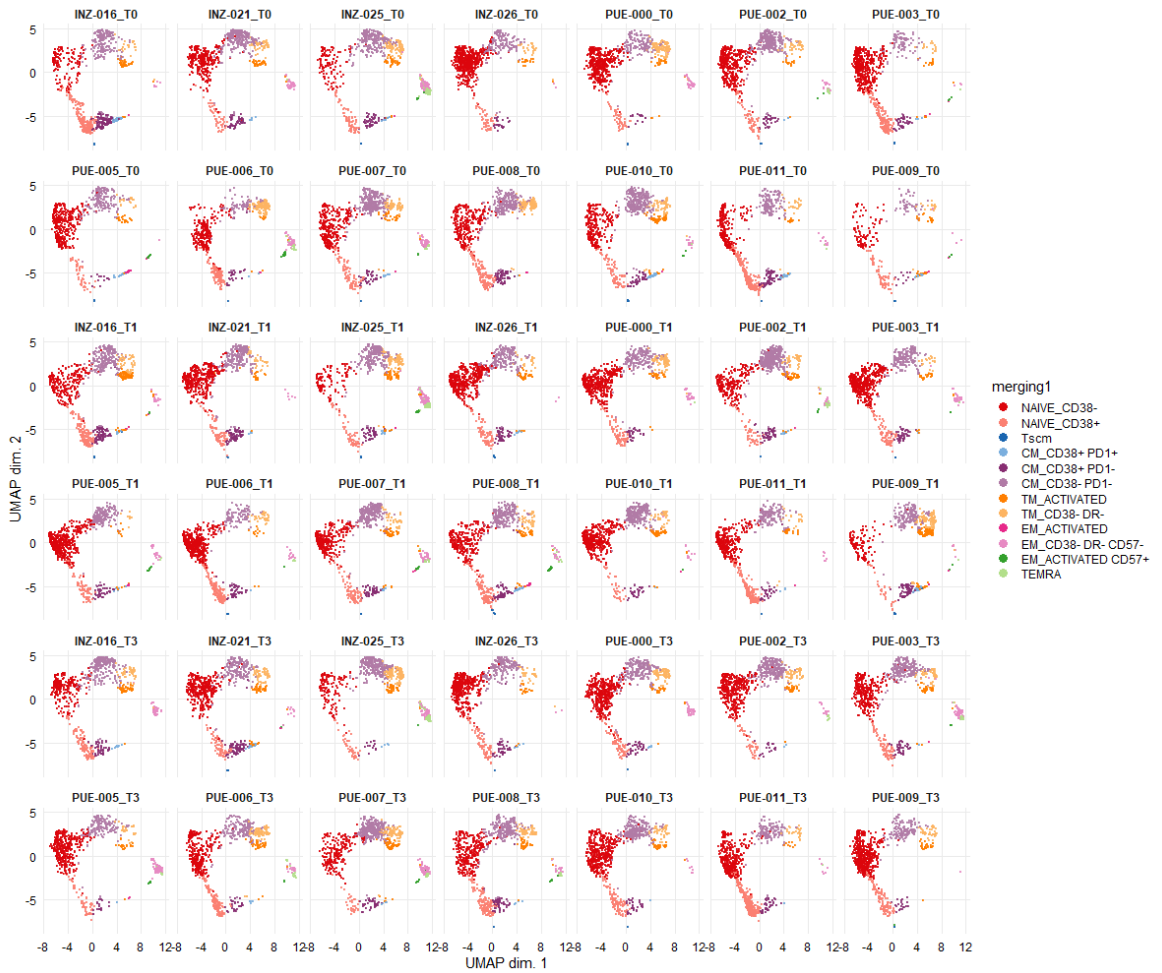
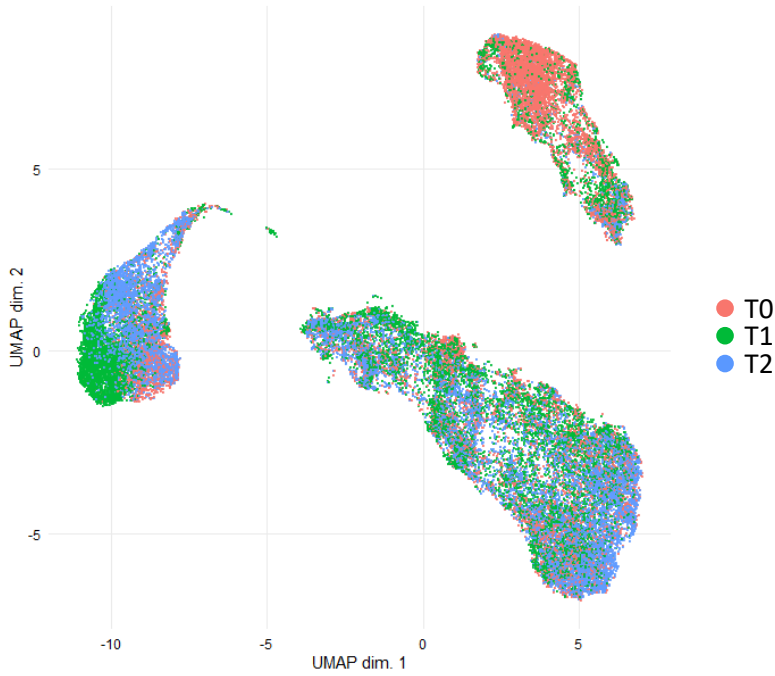


Figure S2. Quality control CD4+ T cells

(A) UMAP graphs of CD4+ T cells overlaid for multiple condition; (B) Projection of UMAP graph stratified by sample.

A



B

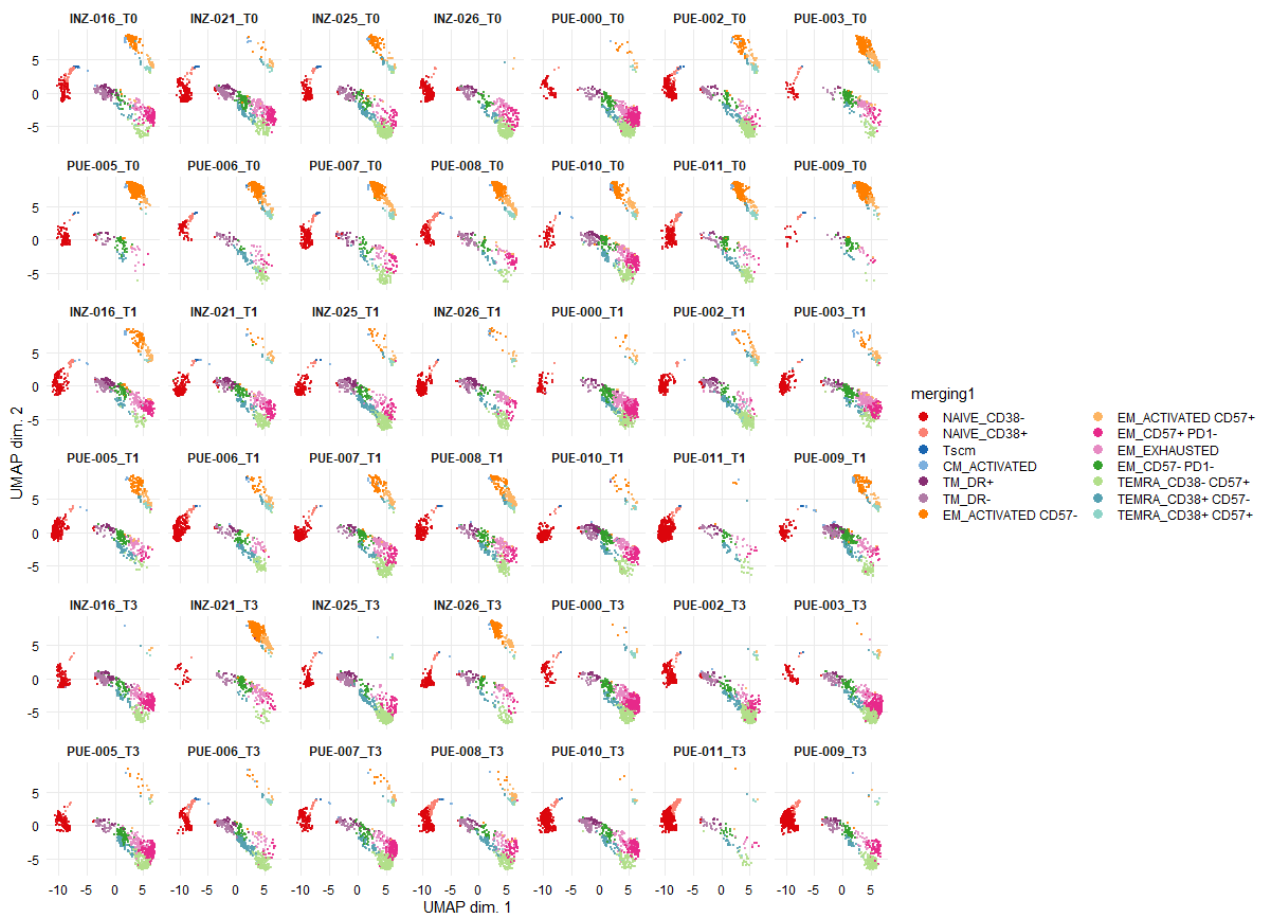
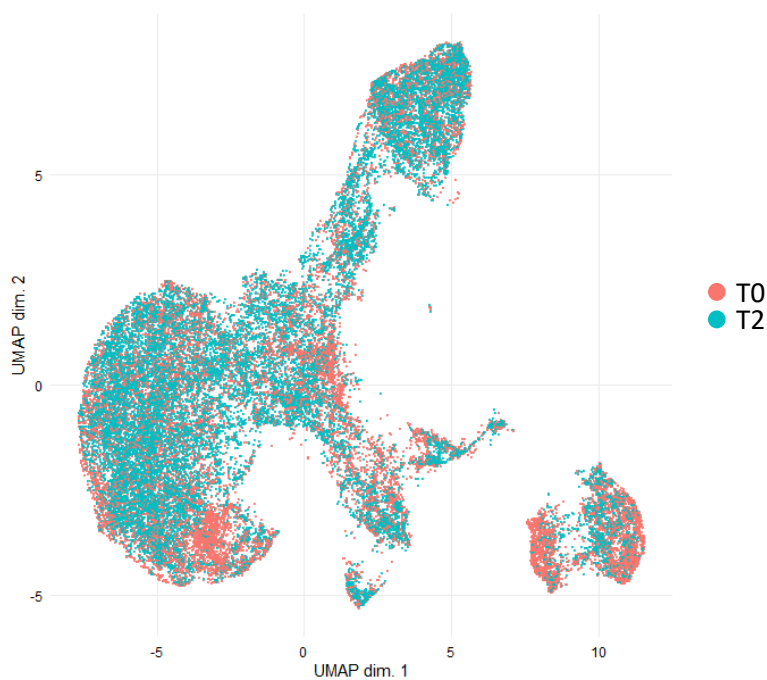


Figure S3. Quality control CD8+ T cells

(A) UMAP graphs of CD8+ T cells overlaid for multiple condition; (B) Projection of UMAP graph stratified by sample.

A



B

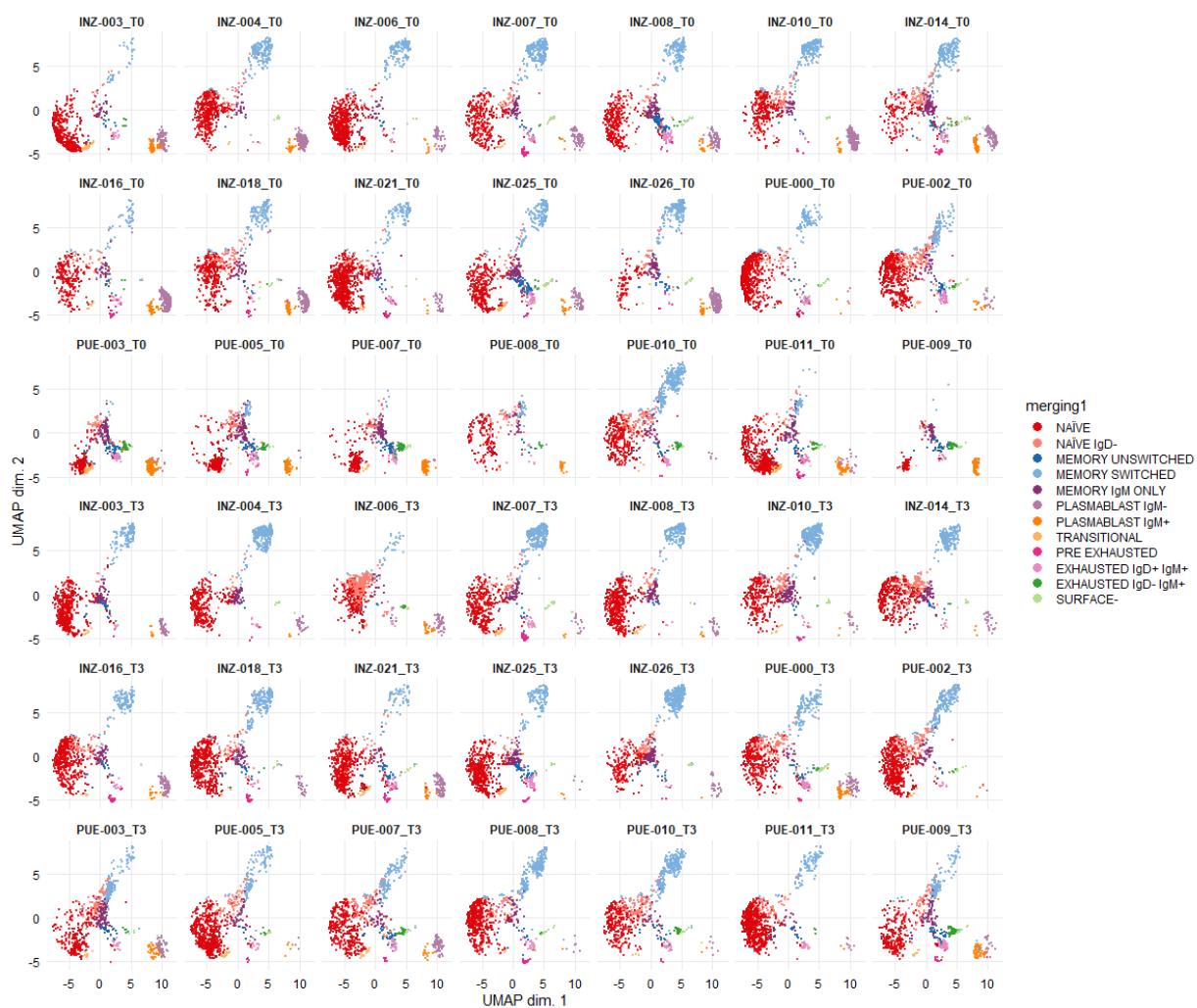


Figure S4. Quality control CD19+ B cells

(A) UMAP graphs of CD19+ B cells overlaid for multiple condition; (B) Projection of UMAP graph stratified by sample.

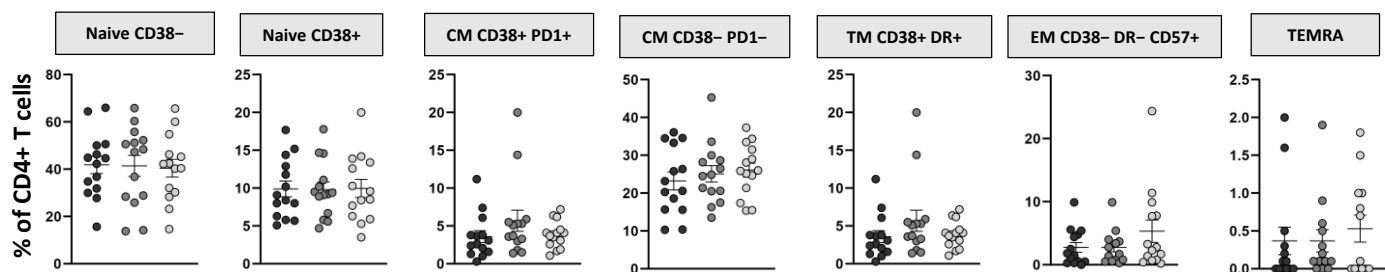
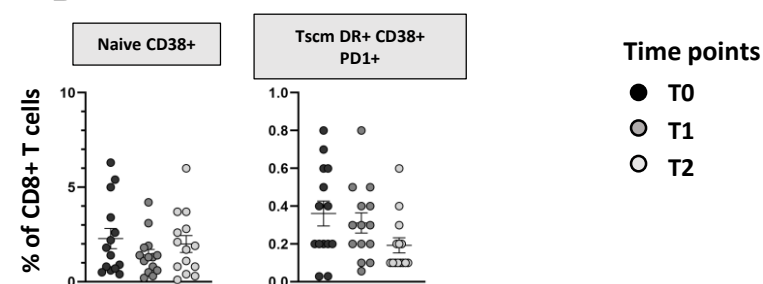
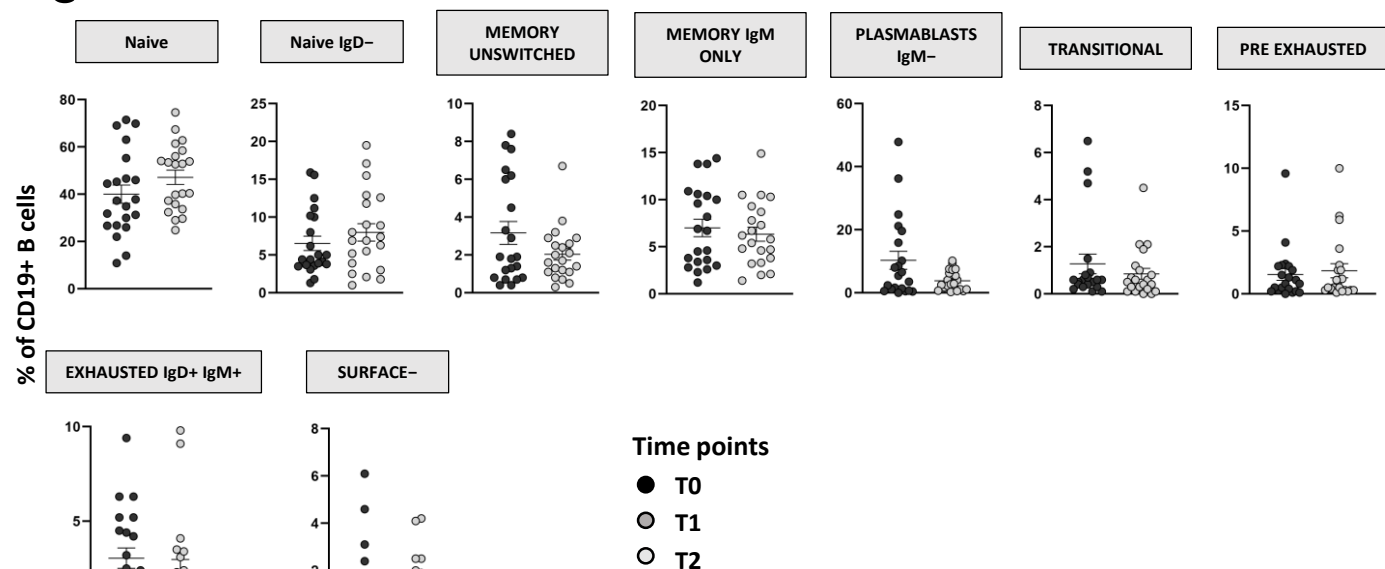
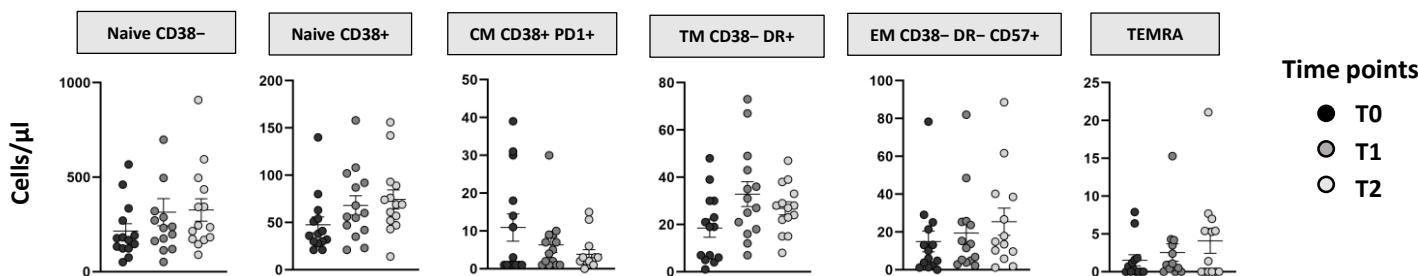
A**B****C**

Figure S5. Dotplots showing the percentage of cells whose percentage remains unchanged after therapy initiation. (A) CD4+ T cells; (B) CD8+ T cells and (C) CD19+ B cells. T0 (black circles; n=14), T1 (grey circles; n=14) and T2 (lightgrey circles; n=14) timepoints. The central bar represents the mean \pm SEM. The adjusted p-values were obtained by patient pairing generalized linear mixed model (GLMM) that compares cluster percentages at T0, T1 and T2 (threshold: FDR \leq 0.05).

A



B

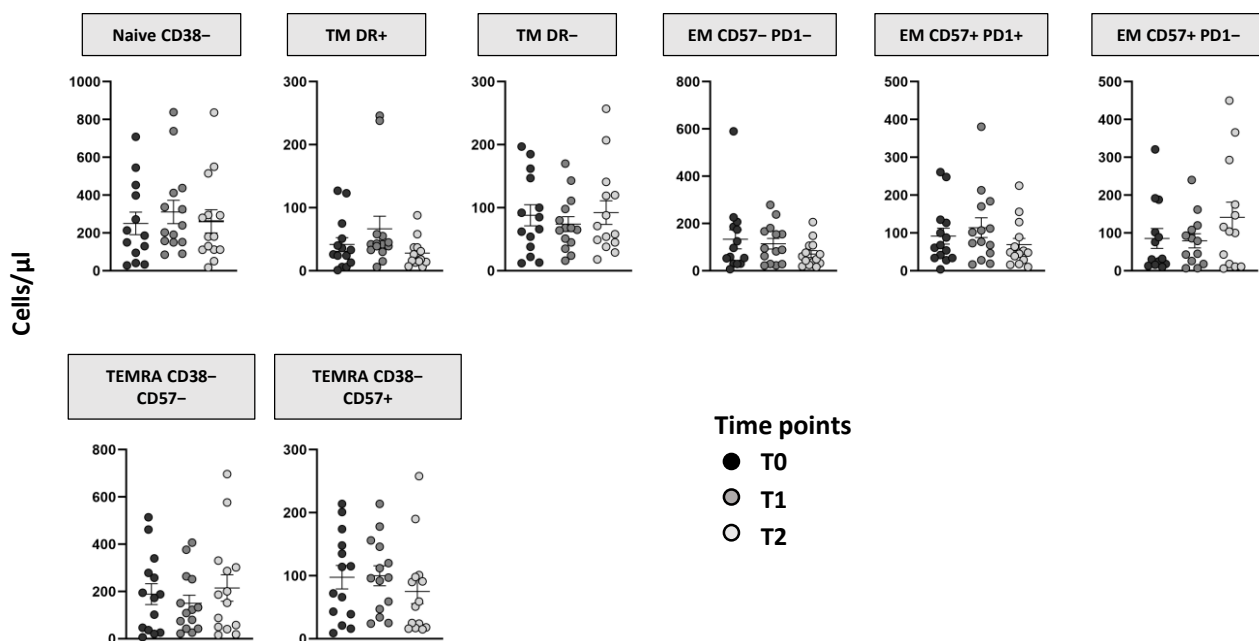
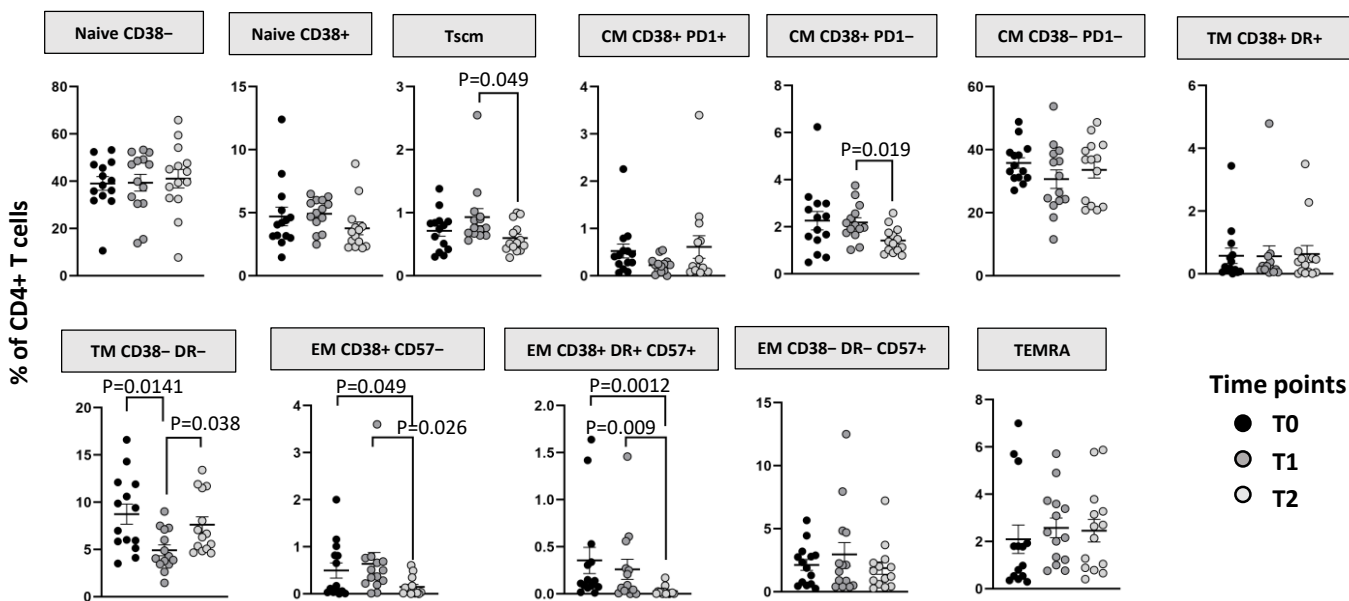
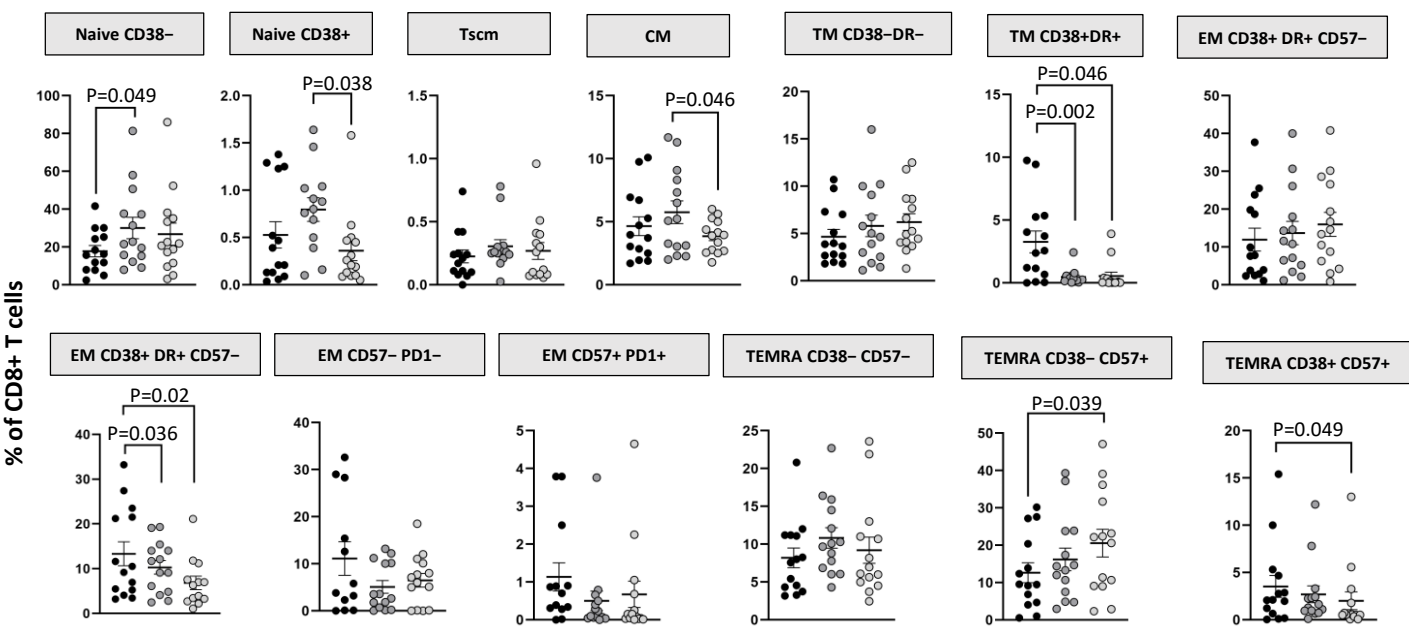


Figure S6. Dotplots showing the absolute number of cells whose remains unchanged after therapy initiation. (A) CD4⁺ T cells; (B) CD8⁺ T cells. T0 (black circles; n=14), T1 (grey circles; n=14) and T2 (lightgrey circles; n=14) timepoints. The central bar represents the mean \pm SEM. The adjusted p-values were obtained by patient pairing generalized linear mixed model (GLMM) that compares cluster percentages or absolute count at T0, T1 and T2 (threshold: FDR \leq 0.05).

A



B



C

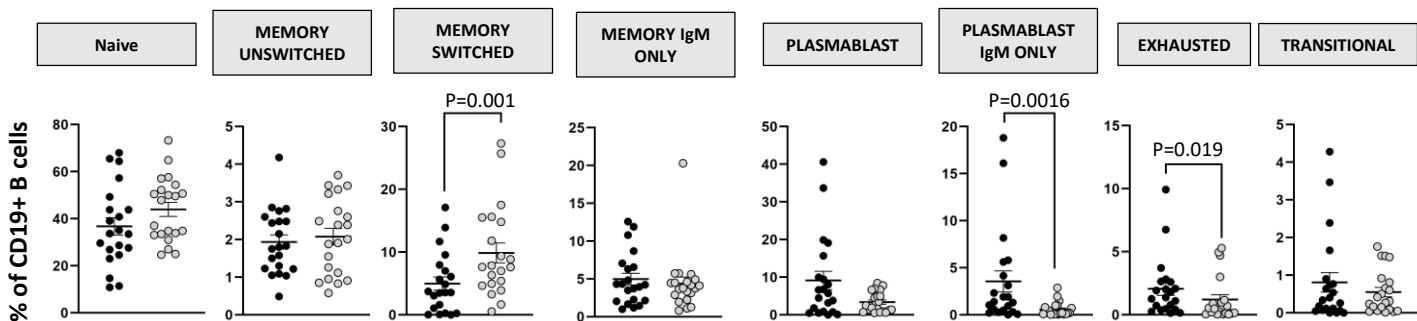


Figure S7.

Dotplots showing the relative cells percentage obtained by regular manual-gating analysis from T0 (black circles; n=14), T1 (grey circles; n=14) and T2 (lightgrey circles; n=14) conditions in (A) CD4+ T cells, (B) CD8+ T cells and (C) CD19+ B cells. The central bar represents the mean \pm SEM. One-way Kruskal-Wallis test with Benjamini-Hochberg correction for multiple comparisons was used to test the differences (for CD4+ and CD8+ T cells) among the three groups; q-values are indicated in the figure. For CD19+ B cells was used Mann-Whitney nonparametric test to test the differences among the two groups. Exact p-values are indicated in the figure.