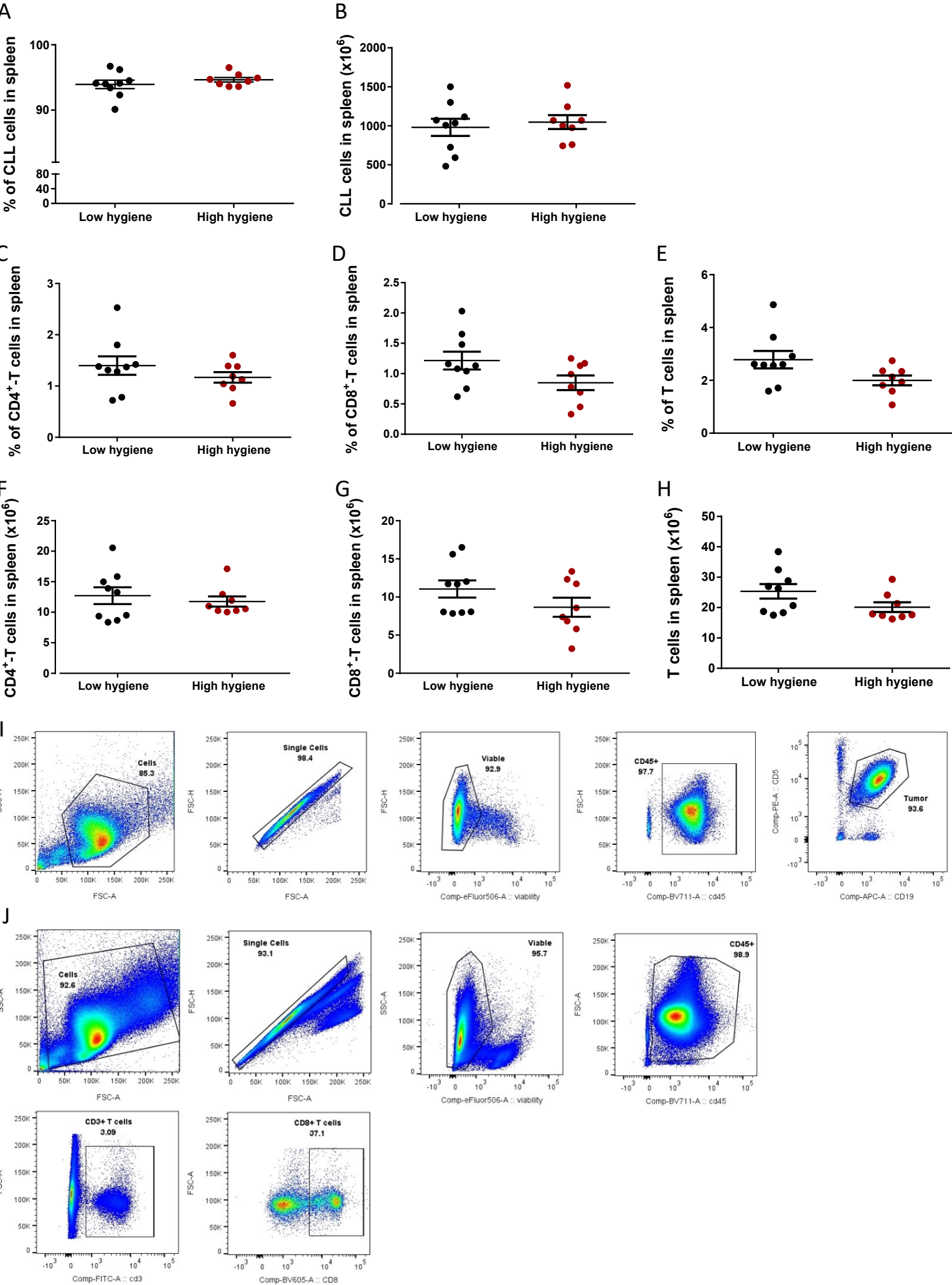
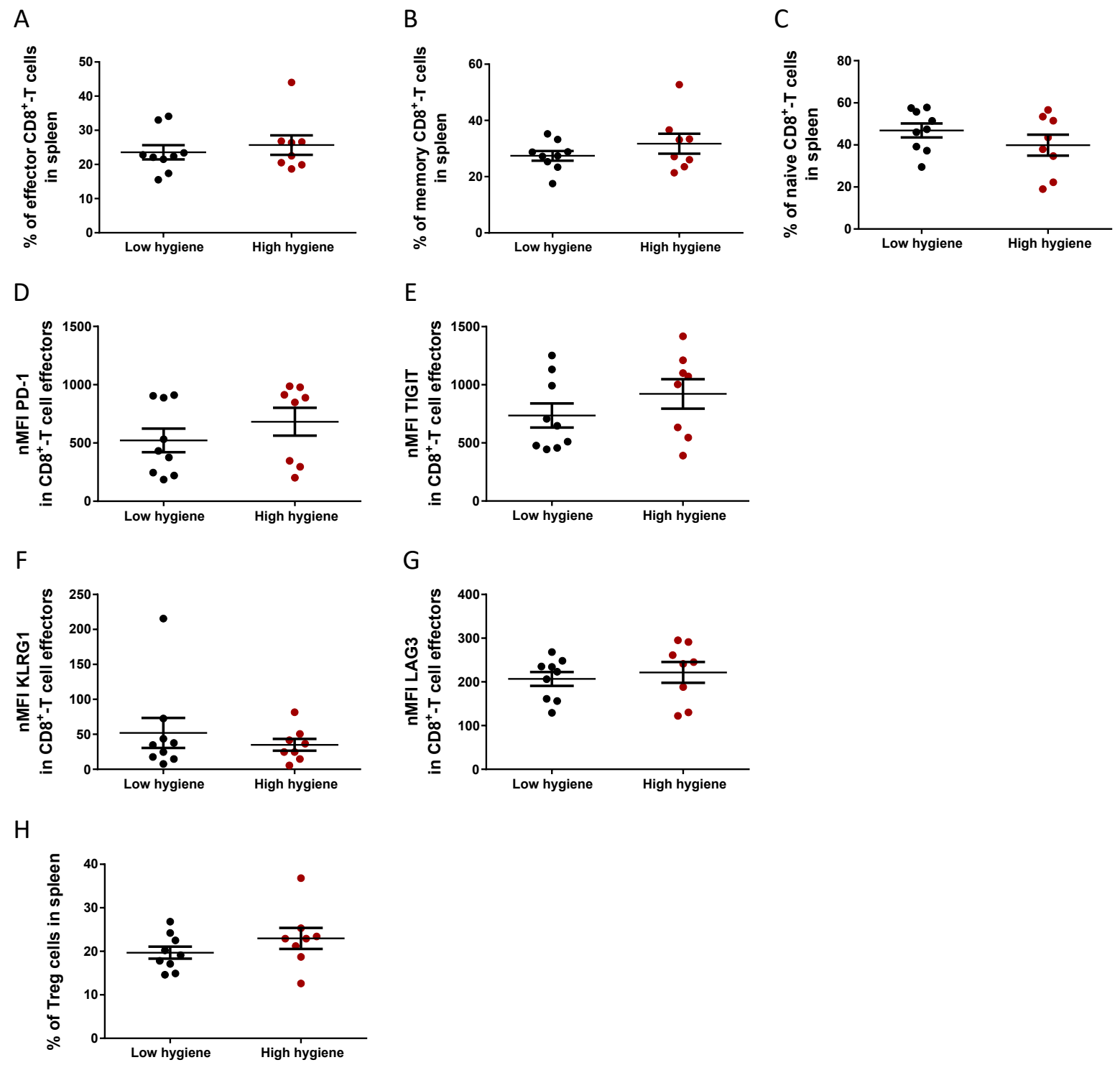


Supplemental Figure 1



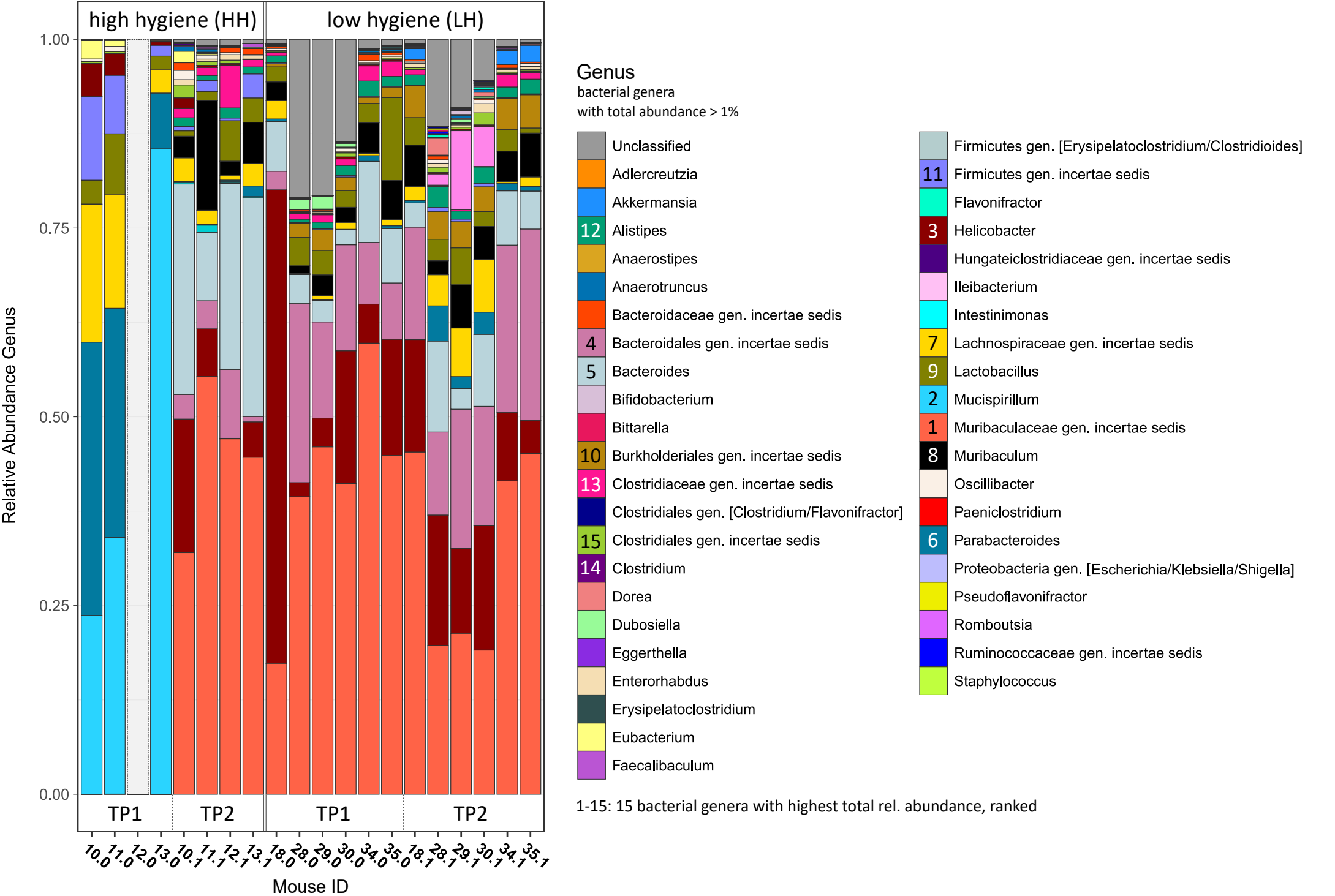
Supplemental Figure 1. A) Percentage of CLL cells (CD19+CD5+) out of CD45+ compartment in spleen. B) Absolute number of CLL cells in spleen ($\times 10^6$). C-E) Percentage of CD4+, CD8+ and CD3+ T cells in spleen out of viable compartment. F-H) Absolute number of CD4+, CD8+ and CD3+ T cells in spleen ($\times 10^6$). I) Exemplary gating strategy for CD19+CD5+ CLL cells ("Tumor"). J) Exemplary gating strategy for CD8+ T cells.

Supplemental Figure 2

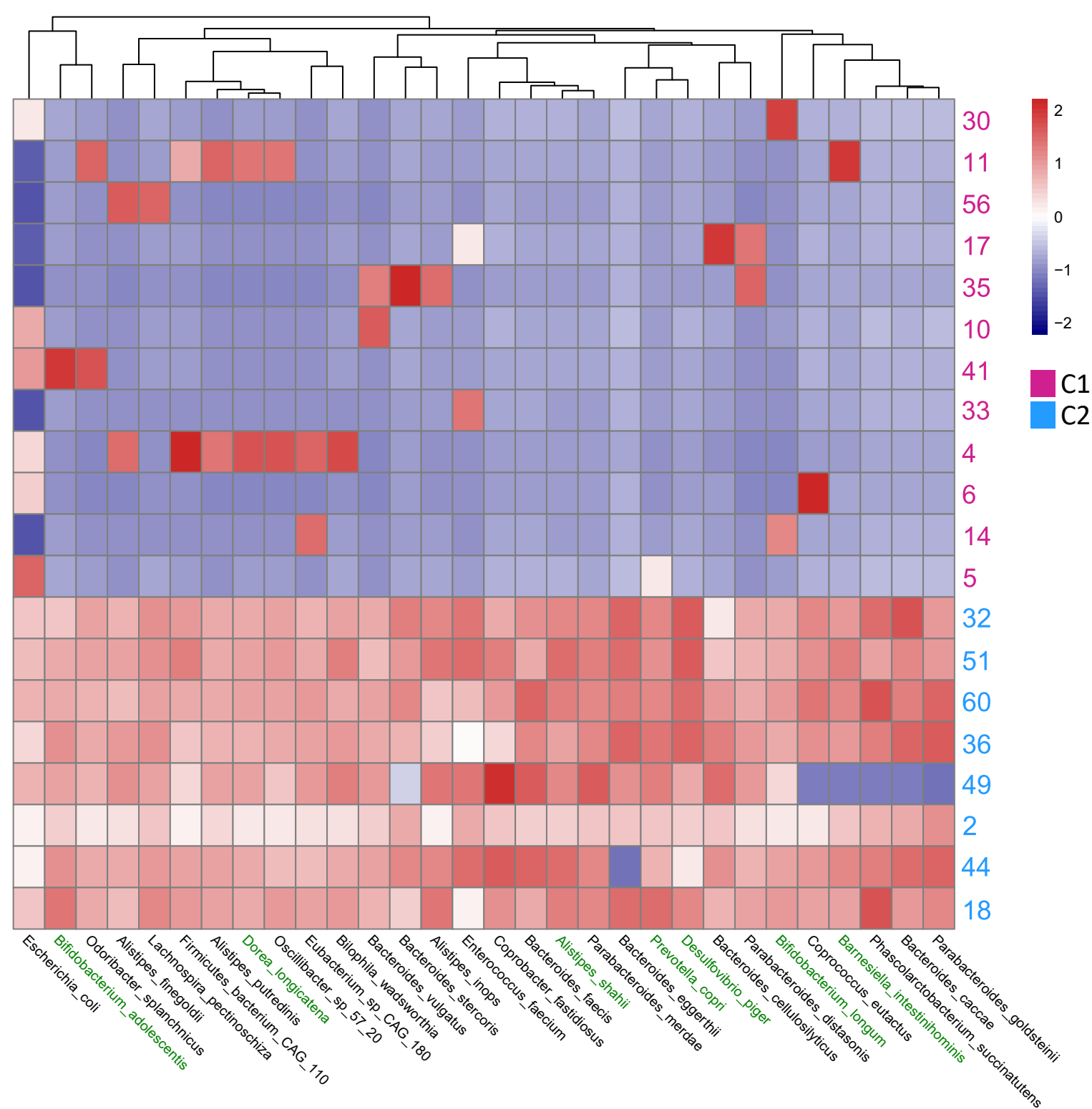


Supplemental Figure 2. A-C) Percentage of effector, memory and naive CD8+ T cells out of T cell splenic compartment. D-G) Normalized median fluorescence intensity (nMFI) of PD-1, TIGIT, KLRG1 and LAG3 in CD8+ T effector cells in the splenic compartment. H) Percentage of FoxP3+CD25+ Treg cells out of CD4+ cells in the splenic compartment.

Supplemental Figure 3



Supplemental Figure 4



Supplemental Figure 4. Heatmap visualization of differentially abundant bacterial species between C1 and C2. Thirty bacterial species (x-axis) with highest fold change (analysis by SIAMCAT; Supplemental Table 4) were selected for visualization. Patient samples (y-axis) were labeled according to the cluster membership from Figure 3. Bacterial species enriched in patients from C2 corresponding to healthy signature identified by Gacesa et al. (31) are marked in green. Data used for visualization were clr-transformed relative abundances of bacterial species. Clustered heatmap was built and visualized using kmeans clustering method from *pheatmap* function in R.