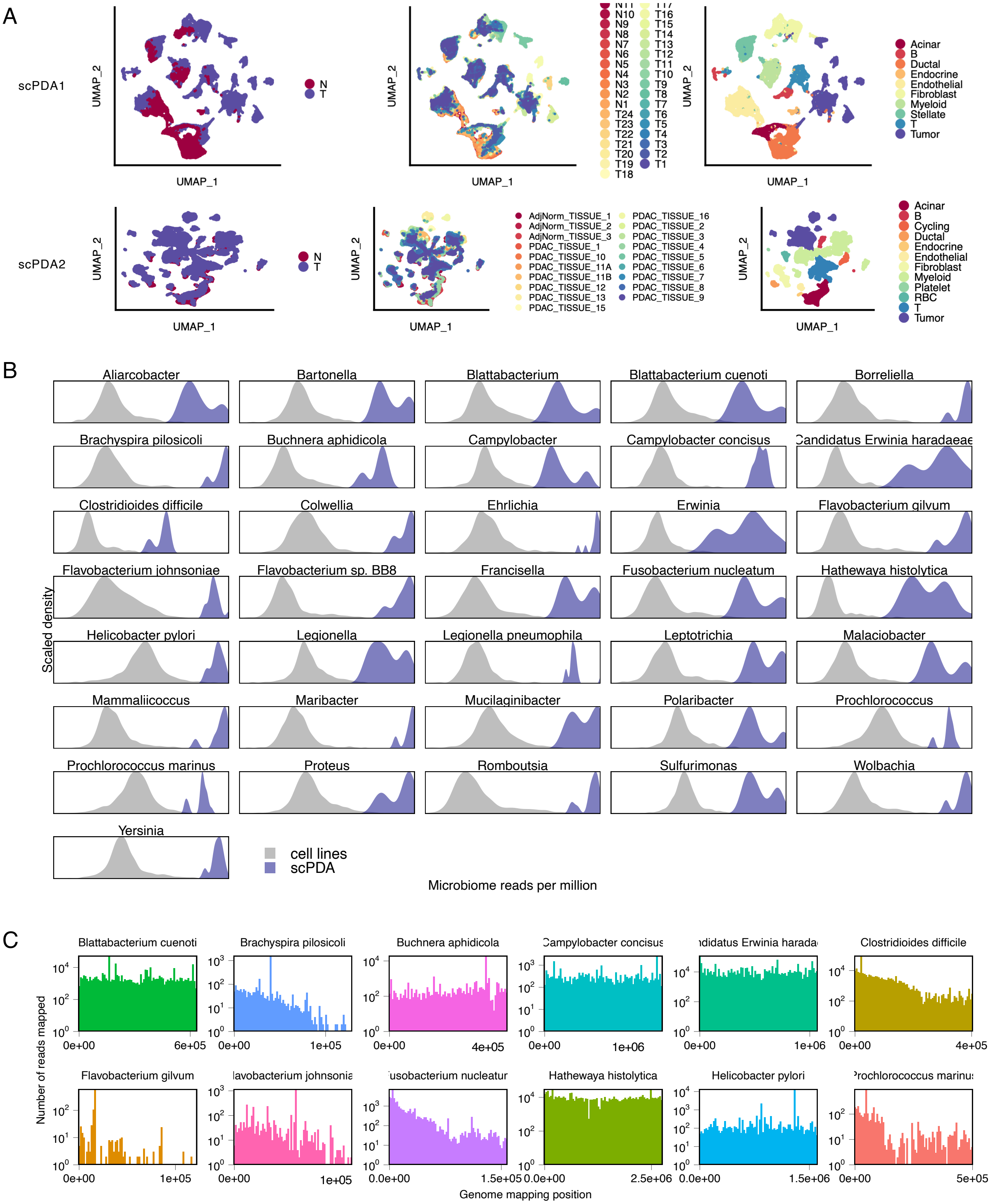

Figure S1. Cell-type clustering and bacterial detection, Related to Figure 1 (**A**) Uniform manifold projection and approximation (UMAP) plots for somatic cell data from scPDA1 (top, n=57,530 cells) and scPDA2 (bottom, n=59,473 cells). Cells are colored by: left: tumor or normal sample; middle: sample ID; right: cell type. (**B**) Density plots comparing bacterial reads per million in scPDA1-2 and the cell-line negative control reference. (**C**) Histograms of the genome mapping positions for the taxa resolved to the species level in scPDA1-2.

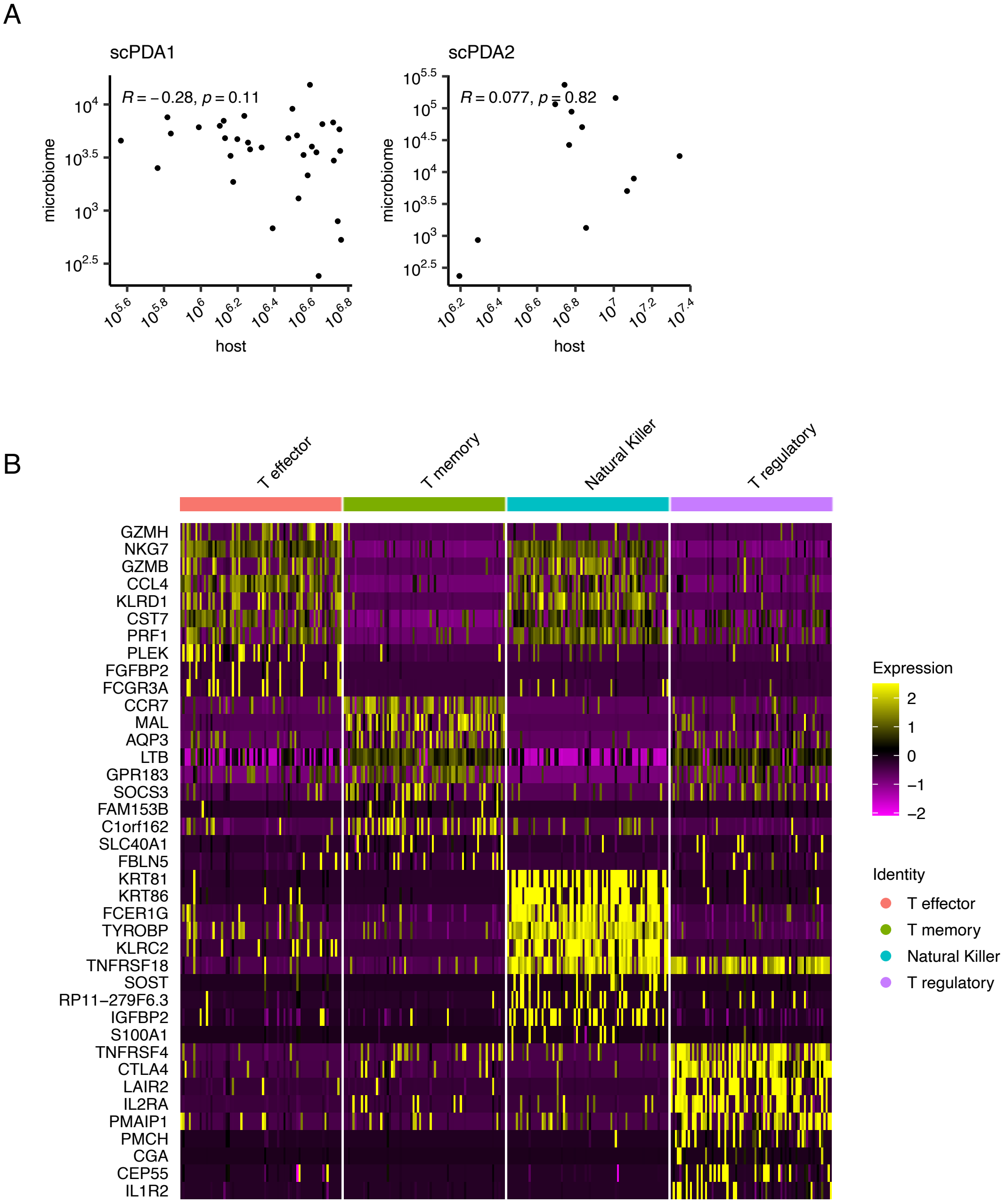

Figure S2.Microbiome and somatic counts and T-cell subtype markers, Related to Figure 2 and Figure 4 (**A**) Scatter plot showing the number of somatic vs. microbial gene counts per sample in scPDA1 (left, n=35 samples) and scPDA2 (right, n=20 samples). Spearman correlation tests. (**B**) Heatmap of scaled normalized expression highlighting differentially expressed genes as defined by two-sided Wilcoxon rank-sum test with Bonferroni FDR correction in scPDA1-2 T-cell subtypes.