Supplementary Figures

Saponin treatment for eukaryotic DNA depletion alters the microbial DNA profiles by reducing the abundance of Gram-negative bacteria in metagenomics analyses

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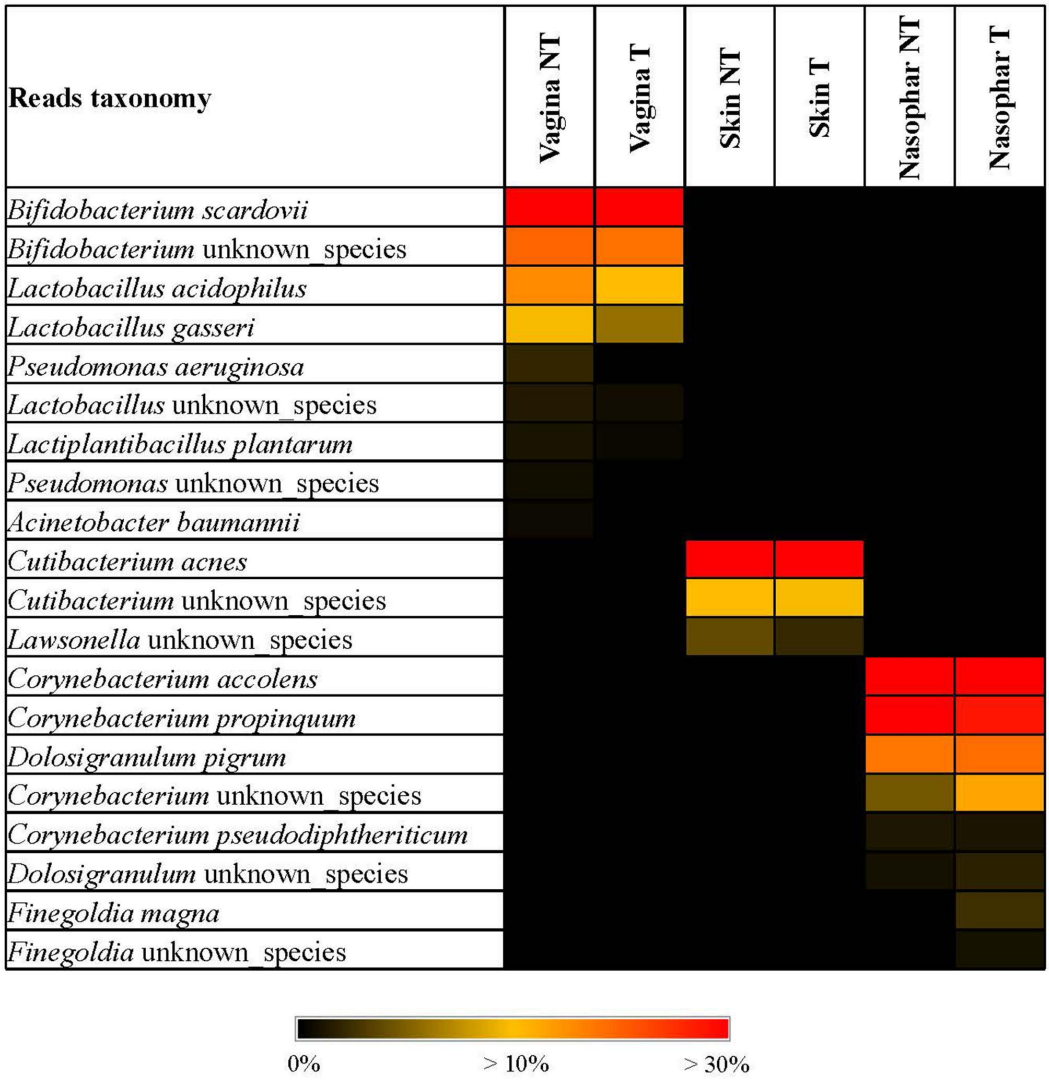
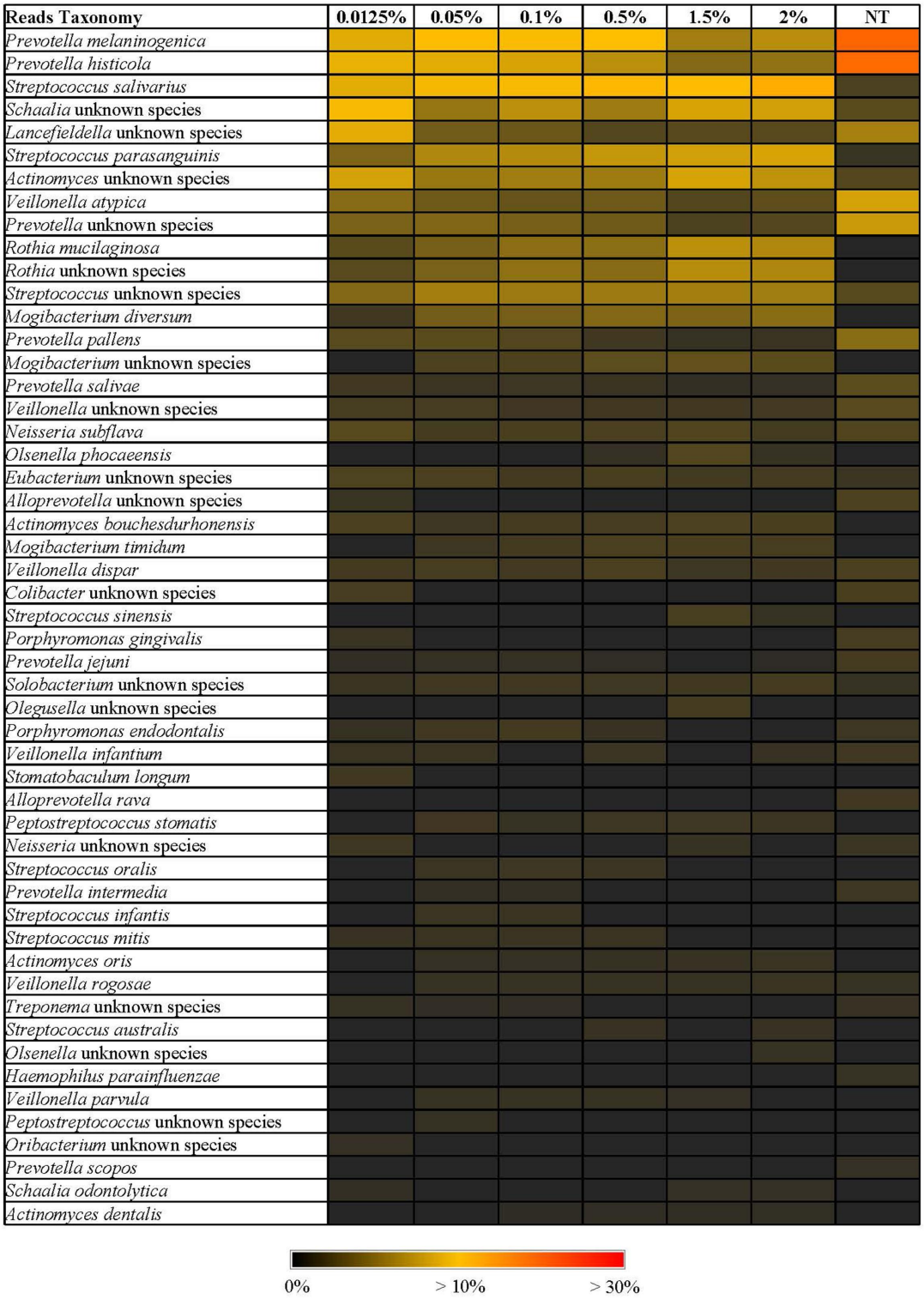


Supplementary Figure 1. Taxonomic microbial profiling of biological samples showing limited biases in microbial taxonomy after 2.5% wt/vol saponin treatment. The histogram displays the relative abundance of each microbial species identified in the vagina, skin, and nasopharynx samples. Both saponin-treated (T) and saponin-untreated samples (NT) are reported for each matrix. From left to right, the color-coding order of the legend reflects average abundances from largest to smallest.

Supplementary Figure 2. Taxonomic microbial profiling of biological samples showing marked biases in microbial taxonomy after 2.5% wt/vol saponin treatment. The histogram displays the relative abundance of each microbial species identified in the biopsies, gastric antrum and body, saliva, and sputum. Both saponin-treated (T) and saponin-untreated samples (NT) are reported for each matrix. From left to right, the color-coding order of the legend reflects average abundances from largest to smallest. Most representative bacterial species are indicated with different colors.



Supplementary Figure 3. Taxonomic microbial profiling of the same sputum sample treated with different saponin amounts. From left to right, the color-coding order of the legend reflects average abundances from largest to smallest. Most representative bacterial species are highlighted with different colors. The untreated sample is reported as NT.