

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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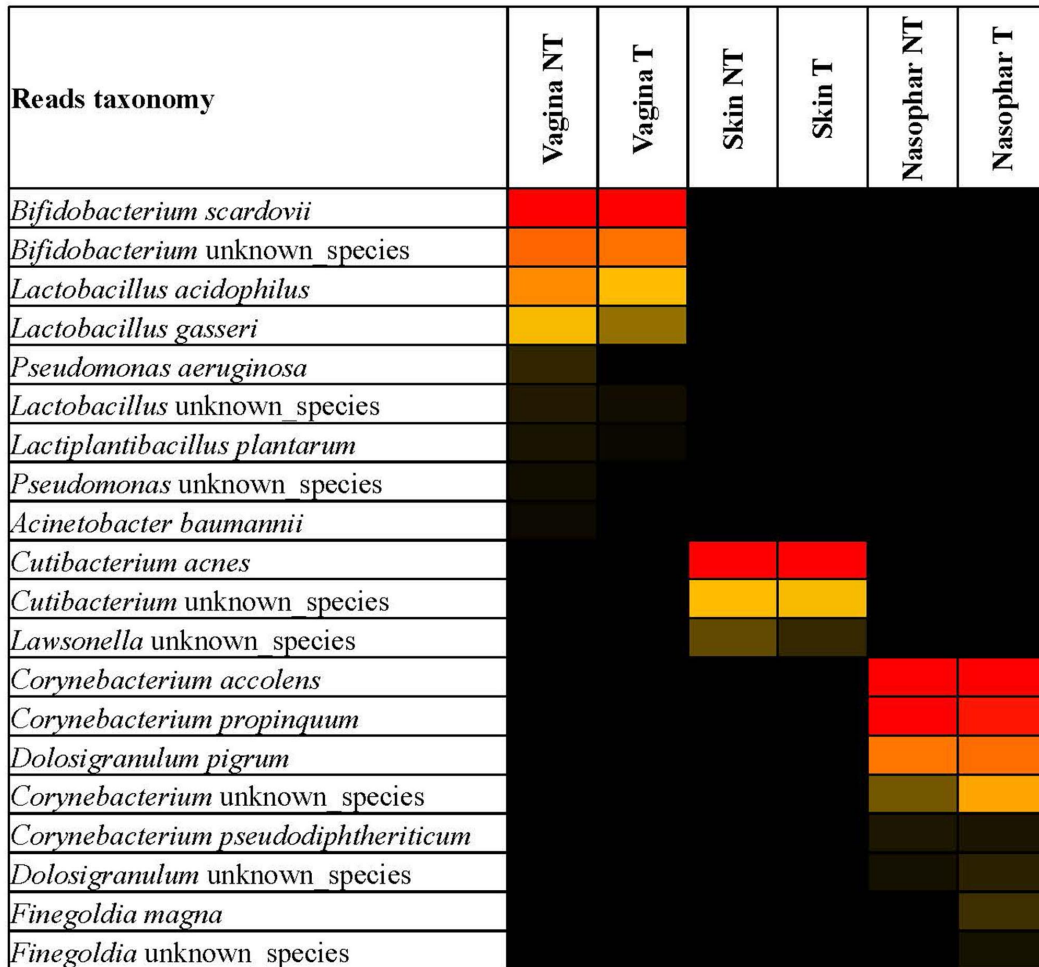
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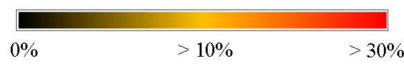
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Supplementary Figure 1. Taxonomic microbial profiling of biological samples showing limited biases in microbial taxonomy after 2.5% wt/vol saponin treatment. The histogram displays the relative abundance of each microbial species identified in the 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.

Reads Taxonomy	0.0125%	0.05%	0.1%	0.5%	1.5%	2%	NT
<i>Prevotella melaninogenica</i>							NT
<i>Prevotella histicola</i>							
<i>Streptococcus salivarius</i>							
<i>Schaalia</i> unknown species							
<i>Lancefieldella</i> unknown species							
<i>Streptococcus parasanguinis</i>							
<i>Actinomyces</i> unknown species							
<i>Veillonella atypica</i>							
<i>Prevotella</i> unknown species							
<i>Rothia mucilaginoso</i>							
<i>Rothia</i> unknown species							
<i>Streptococcus</i> unknown species							
<i>Mogibacterium diversum</i>							
<i>Prevotella pallens</i>							
<i>Mogibacterium</i> unknown species							
<i>Prevotella salivae</i>							
<i>Veillonella</i> unknown species							
<i>Neisseria subflava</i>							
<i>Olsenella phocaeensis</i>							
<i>Eubacterium</i> unknown species							
<i>Alloprevotella</i> unknown species							
<i>Actinomyces bouchedurhonensis</i>							
<i>Mogibacterium timidum</i>							
<i>Veillonella dispar</i>							
<i>Colibacter</i> unknown species							
<i>Streptococcus sinensis</i>							
<i>Porphyromonas gingivalis</i>							
<i>Prevotella jejuni</i>							
<i>Solobacterium</i> unknown species							
<i>Olegusella</i> unknown species							
<i>Porphyromonas endodontalis</i>							
<i>Veillonella infantium</i>							
<i>Stomatobaculum longum</i>							
<i>Alloprevotella rava</i>							
<i>Peptostreptococcus stomatis</i>							
<i>Neisseria</i> unknown species							
<i>Streptococcus oralis</i>							
<i>Prevotella intermedia</i>							
<i>Streptococcus infantis</i>							
<i>Streptococcus mitis</i>							
<i>Actinomyces oris</i>							
<i>Veillonella rogosae</i>							
<i>Treponema</i> unknown species							
<i>Streptococcus australis</i>							
<i>Olsenella</i> unknown species							
<i>Haemophilus parainfluenzae</i>							
<i>Veillonella parvula</i>							
<i>Peptostreptococcus</i> unknown species							
<i>Oribacterium</i> unknown species							
<i>Prevotella scopos</i>							
<i>Schaalia odontolytica</i>							
<i>Actinomyces dentalis</i>							



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.