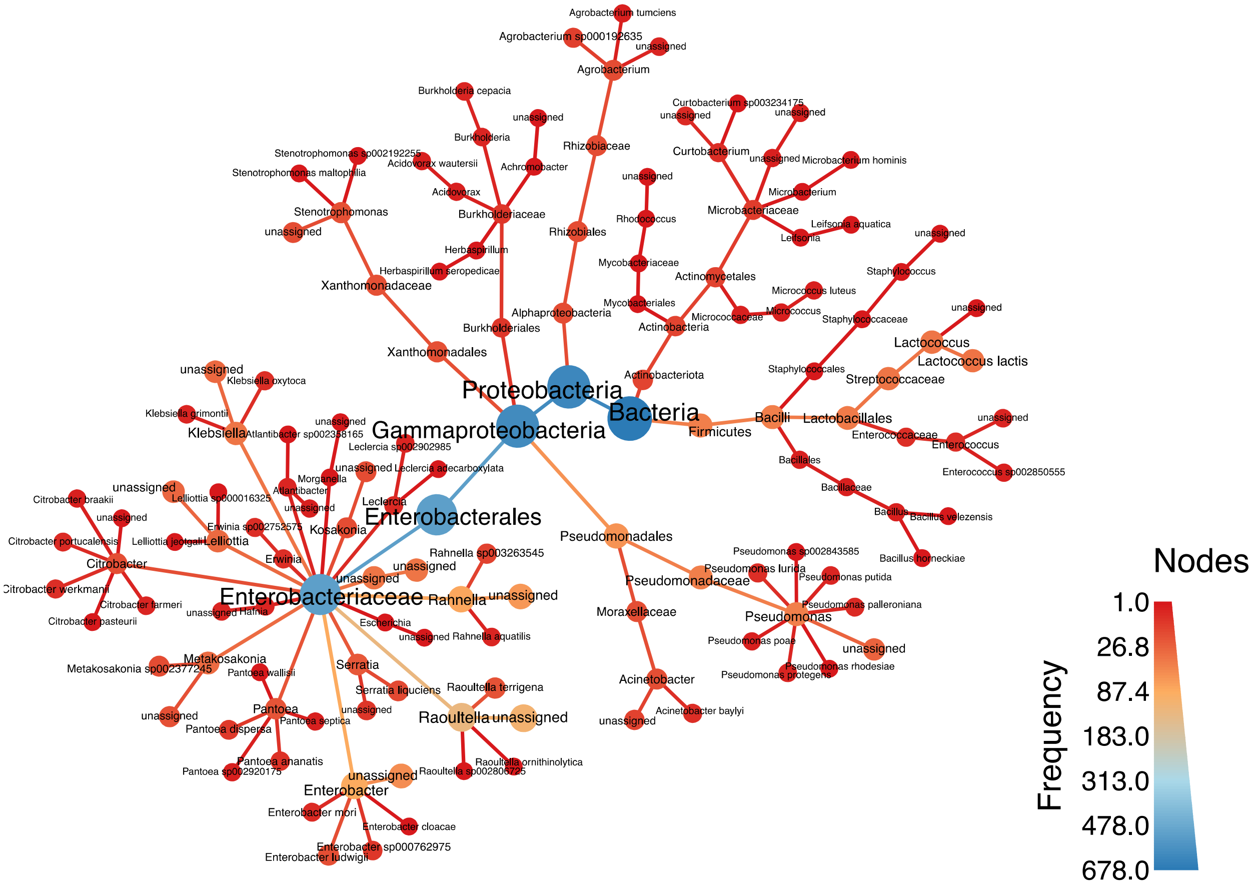
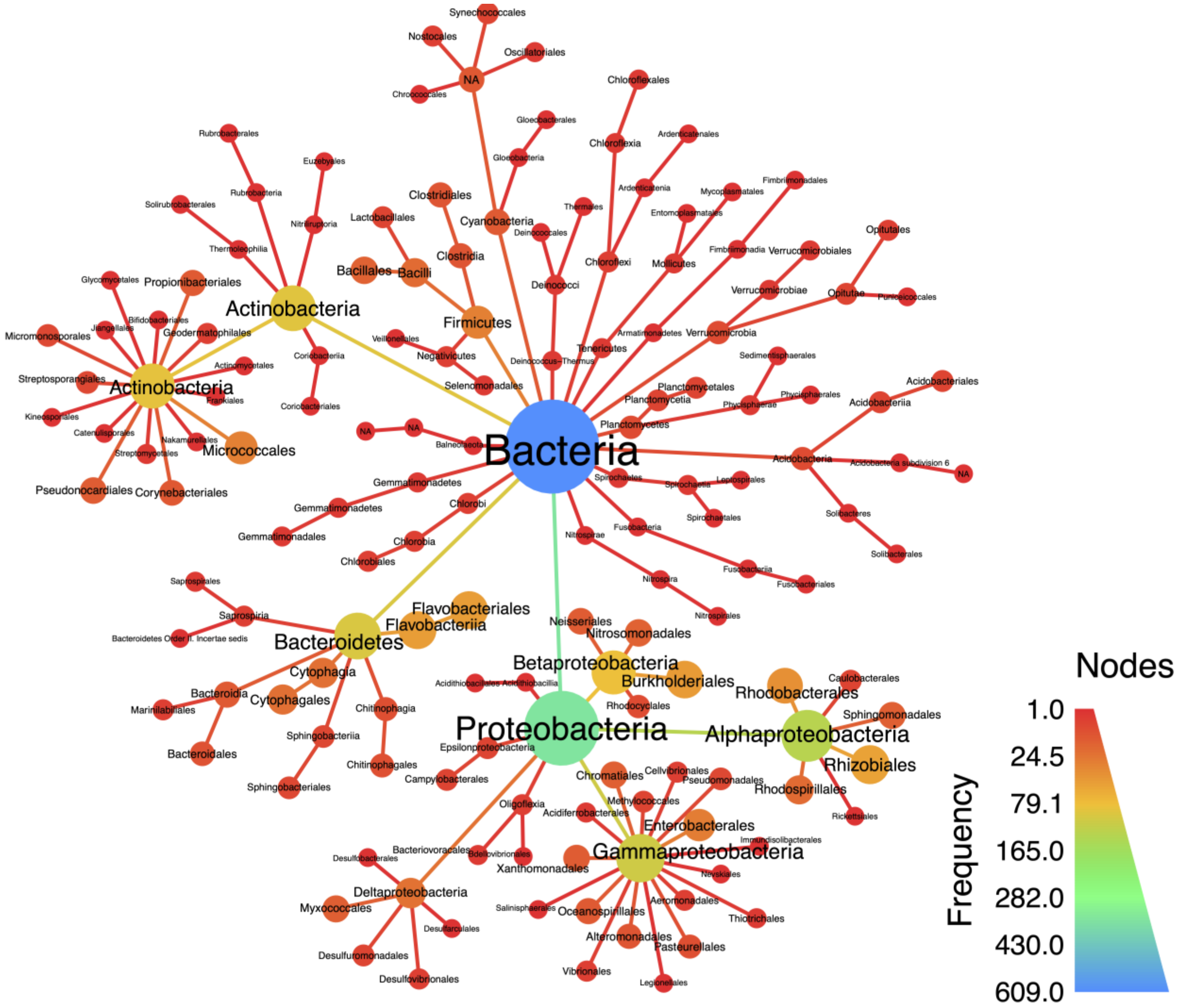
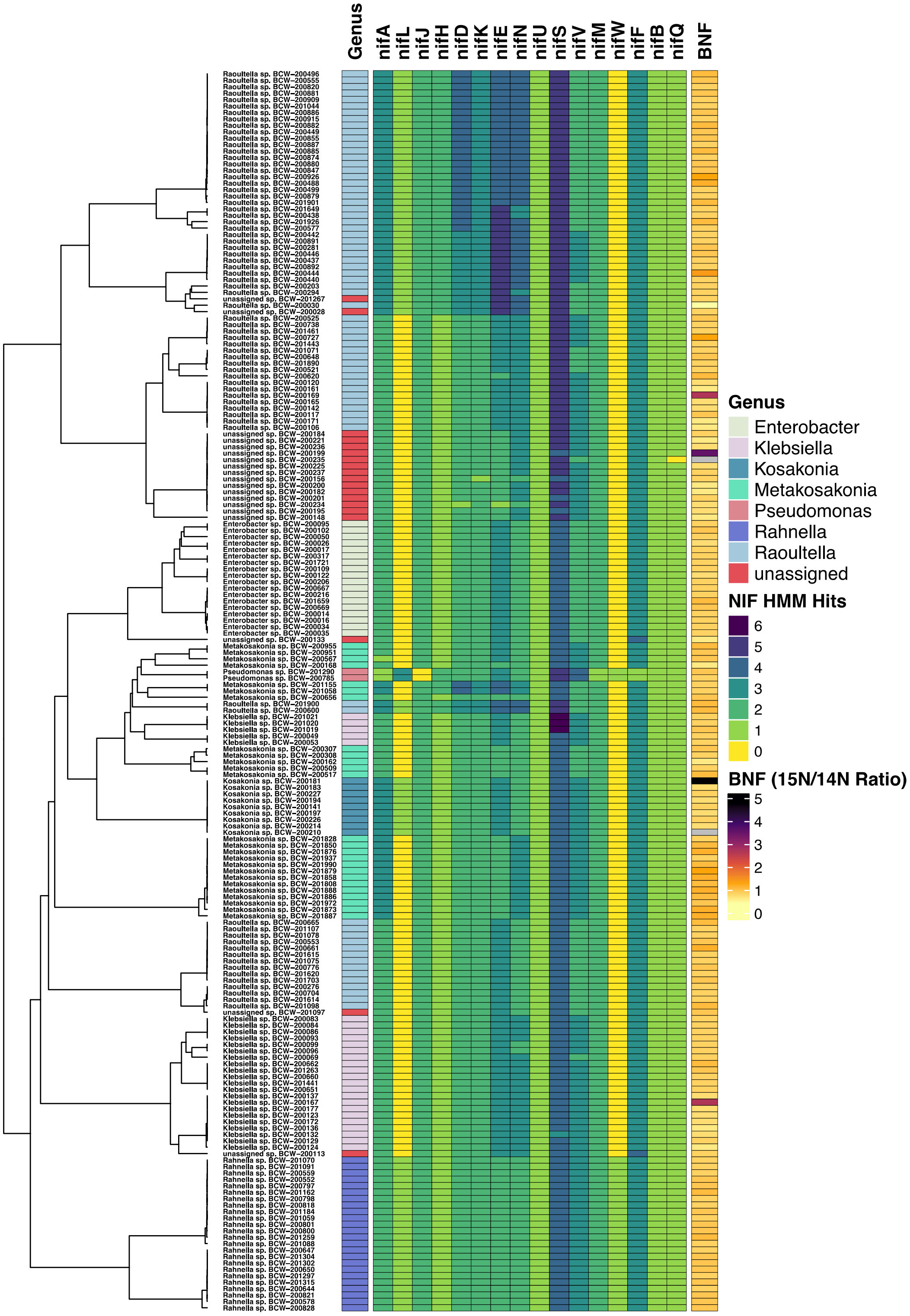
Supporting Information – Figures



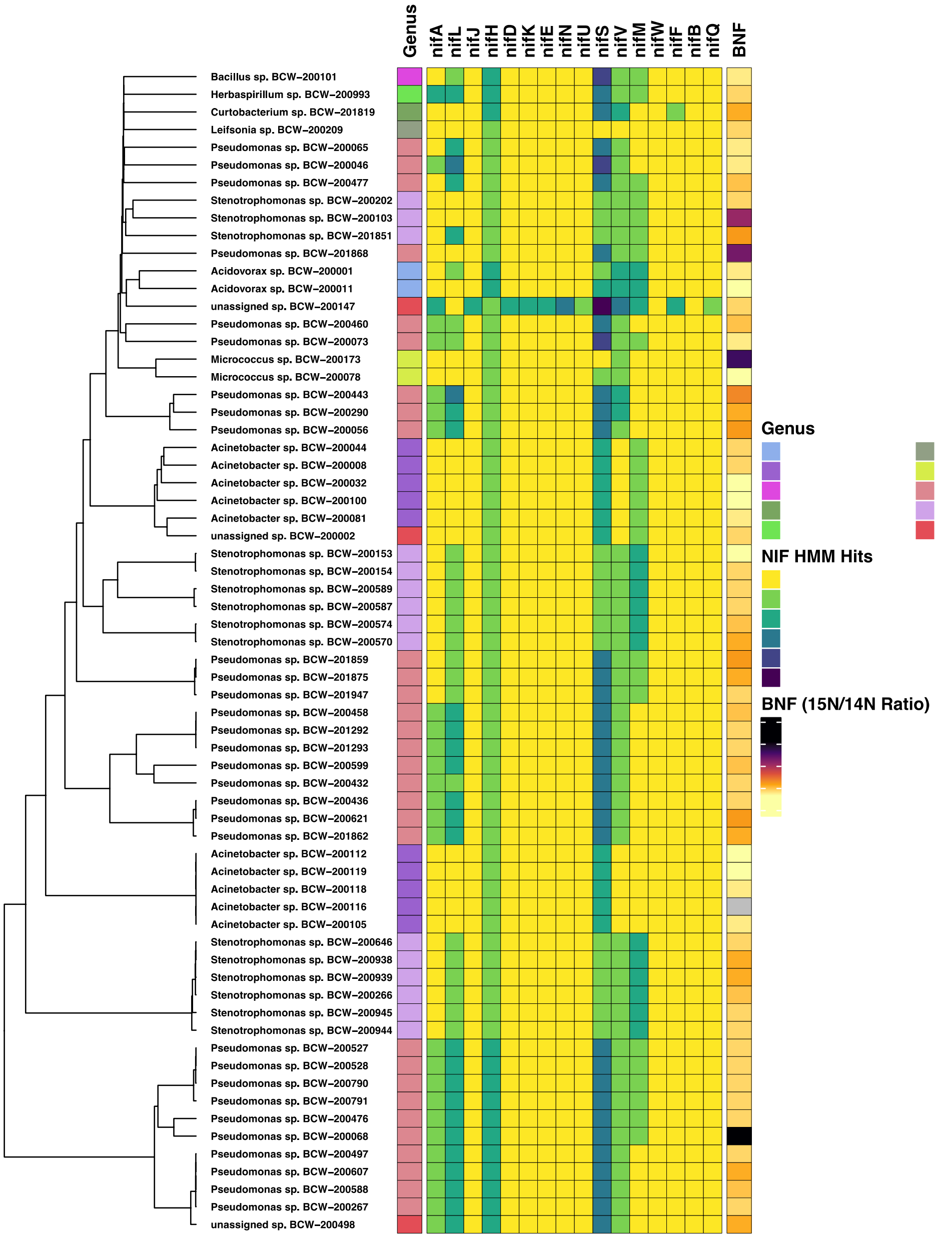
S1 Fig. Taxonomic classification of genome bins from mucilage isolates. Heat Tree showcasing the phylogenetic diversity of all Metabat [1] genome bins derived from isolate draft genome assemblies. Node size corresponds to the frequency of occurrence at each level of taxonomic classification. Dark blue corresponds to the highest observation count of a taxonomic assignment and dark red indicates low observation frequency.



S2 Fig. Observation counts of classified taxa in the mucilage metagenome. Quality trimmed short reads of the OLMM00 mucilage metagenome were input to Kraken2 [2] and classified using the RefSeq complete database for microbial genomes installed with built-in commands of Kraken2. Bracken2 [3] was used to re-estimate classified read counts and the data was imported to R in biom-format. Taxa with readcounts less than 500 were filtered using Phyloseq [4] and the data were visualized using MetacodeR [5]. Terminal nodes represent taxa classified at the order level and node size corresponds to frequency of observation for each taxonomic level.



S3 Fig. *Nif* gene profile and BNF assay performance of Dos Santos Positive isolates. *Nif* gene profiles for isolate genomes of the DSP group were extracted and visualized independently using the ComplexHeatmaps [6] package in R. Isolate genomes were clustered using the dendrogram output from Sourmash [7] and each genome row is presented along with annotations to indicate lowest common ancestor (LCA) classification data at the genus level.



S4 Fig. *Nif* gene profile and BNF assay performance of Semi-Dos Santos isolates. *Nif* gene profiles for isolate genomes of the SDS group were extracted and visualized independently using the ComplexHeatmaps [6] package in R. Isolate genomes were clustered using the dendrogram output from Sourmash [7] and each genome row is presented along with annotations to indicate LCA classification data at the genus level.

S5 Fig. *Nif* gene profile and BNF assay performance of Dos Santos Negative isolates. *Nif* gene profiles for isolate genomes of the DSN group were extracted and visualized independently using the ComplexHeatmaps [6] package in R. Isolate genomes were clustered using the dendrogram output from Sourmash [7] and each genome row is presented along with annotations to indicate LCA classification data at the genus level.

References

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