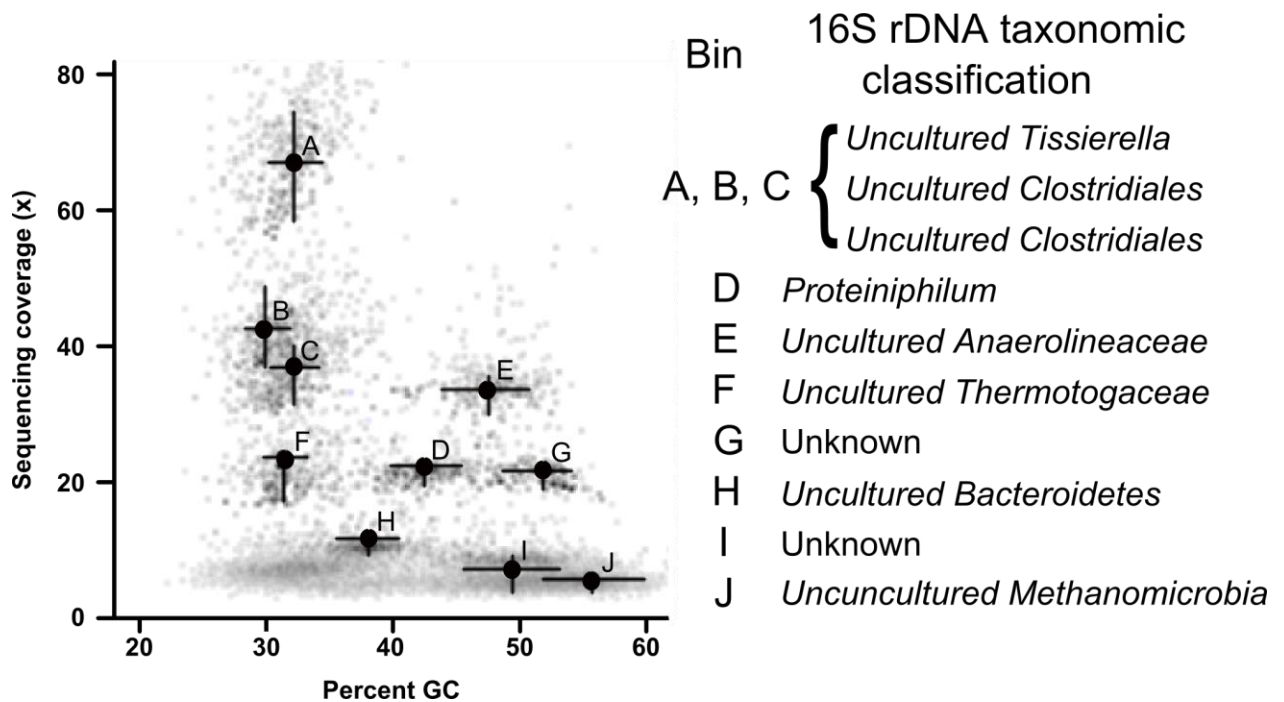


Metagenome analysis and biogas production from the anaerobic digestion of the protein rich microalga *Spirulina*

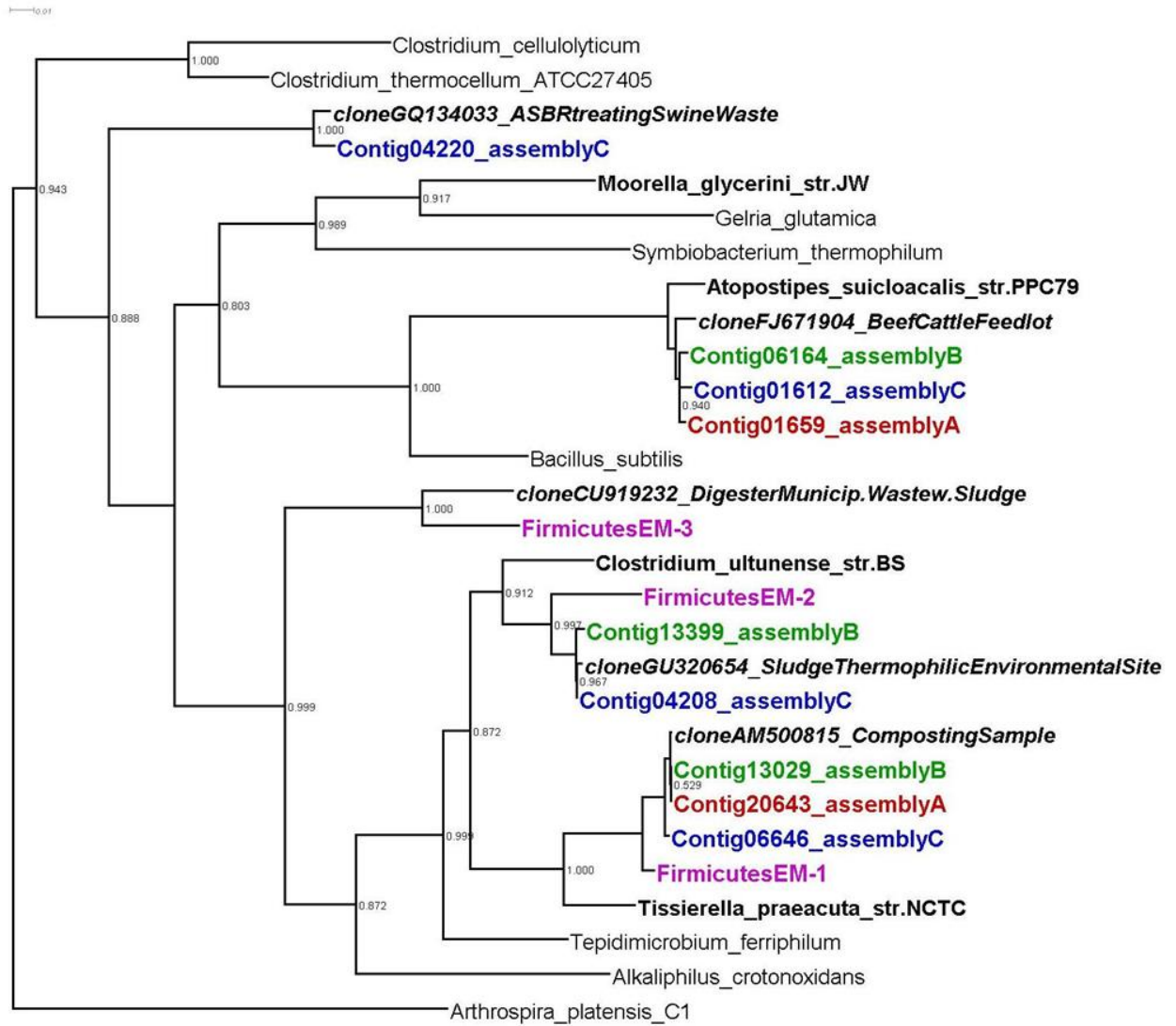
V. Nolla-Ardèvol, M. Peces, M. Strous, H.E. Tegetmeyer

Supplementary Figures



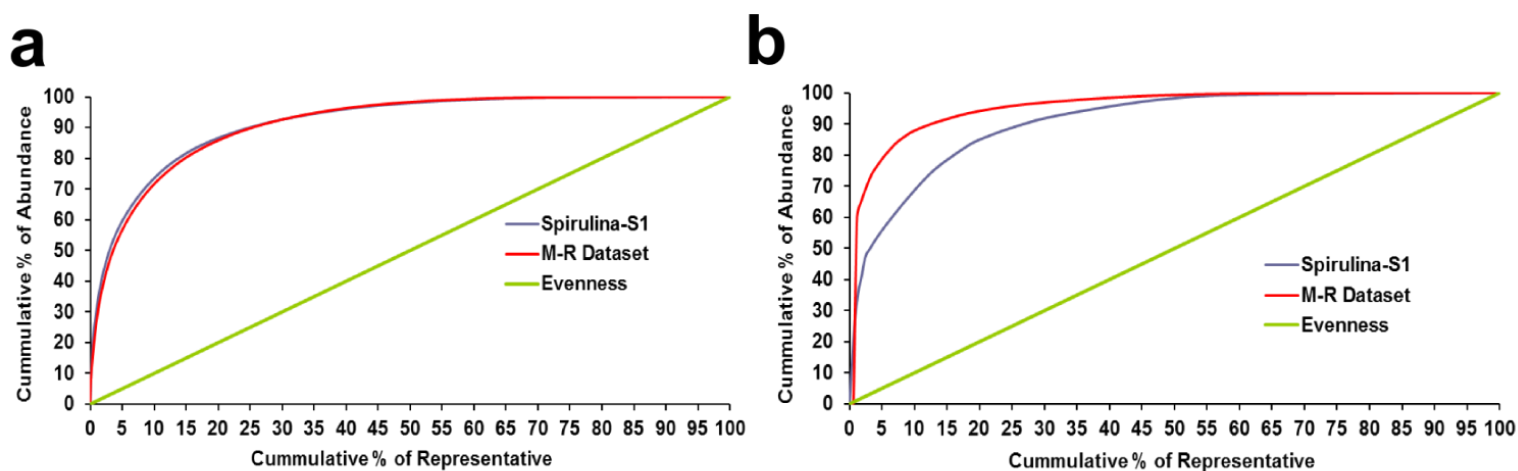
Suppl. Figure 1 Contig coverage, GC content and taxonomic classification of selected bins

Dot plot graph generated with the Metawatt v1.7 pipeline representing all the assembled contigs (grey) and the 10 selected bins (represented by black dots in the center of the bins, including bars showing contig distribution in each bin.)



Suppl. Figure 2 16S rDNA Firmicutes phylogenetic tree

Includes the sequences of the Firmicutes branch in Figure 2a and additionally the unbinned contigs listed in Suppl. Table 2 that are not included in Figure 2a. Values at nodes are from the FastTree default Shimodaira-Hasegawa test.



Suppl. Figure 3 Microbial population evenness

Lorenz curves for the estimation of population evenness at species level from the *Spirulina*-S1 and the Maize-Rye datasets. **a)** Bacterial evenness curves. **b)** Archaeal evenness curves.