

Supplemental FIGURES

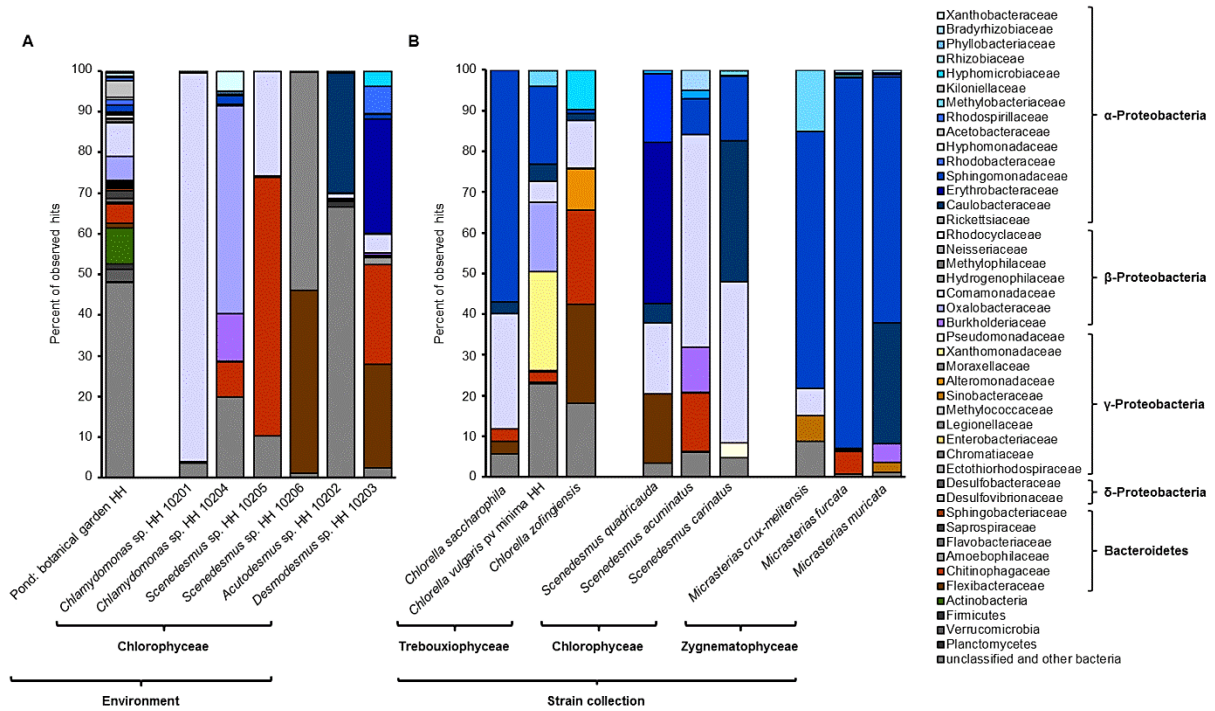


FIGURE S1: Identification and bacterial distribution of dominant bacterial families via 16S rRNA amplicon based phylogenetic analysis attached to various microalgae from (A) fresh water environment (pond “Botanical Garden” of the University of Hamburg, Germany), and (B) samples of the microalgae strain collection of Hamburg.