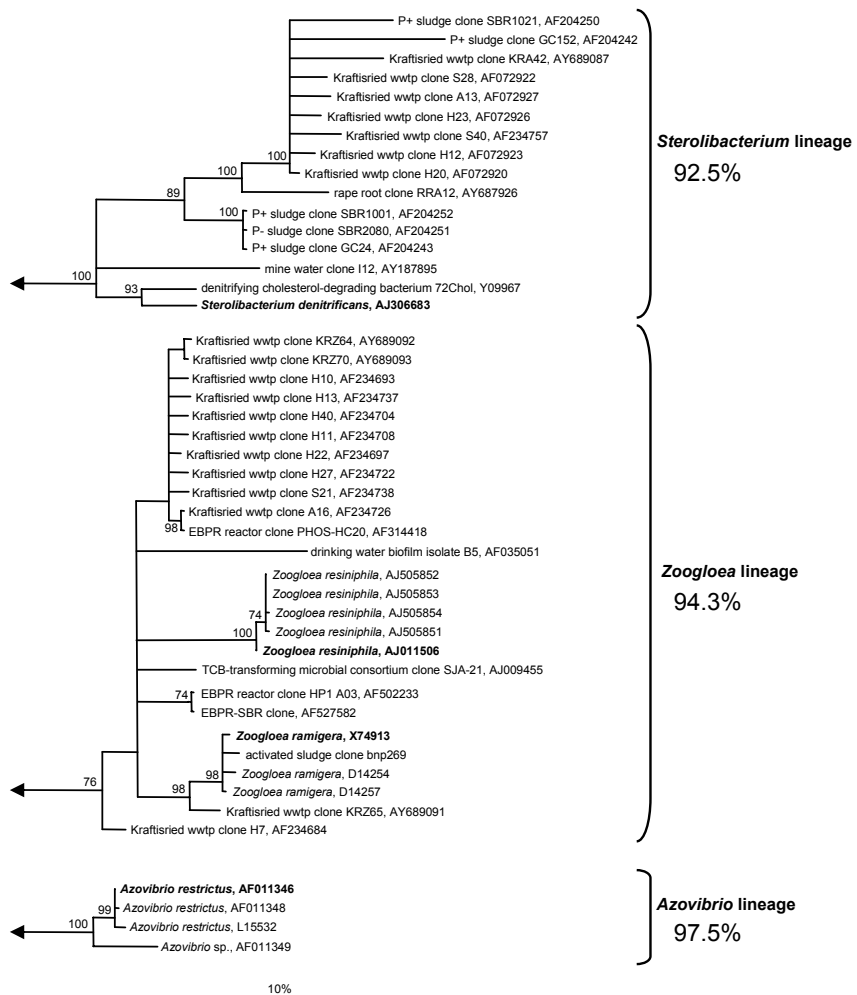


**Supplementary web Figure 1.** 16S rRNA-based phylogenetic trees showing the affiliation of all cultured and uncultured members of the nine “*Rhodocyclales*” lineages. The consensus tree is based on maximum-likelihood analysis (AxML) of full-length sequences (>1,300 nucleotides) performed with a 50% conservation filter for the “*Betaproteobacteria*”. Named type species are indicated by boldface type. Bar indicates 10% estimated sequence divergence. Polytomic nodes connect branches for which a relative order could not be determined unambiguously by applying neighbor-joining, maximum-parsimony, and maximum-likelihood treeing methods. Numbers at branches indicate parsimony bootstrap values in percent. Branches without numbers had bootstrap values of less than 75%. The minimum 16S rRNA sequence similarity for each “*Rhodocyclales*” lineage is shown.





10%

