



Figure S3. Consensus phylogenetic tree of 16S rRNA gene sequences (>1,100 bp) of *Woeseiaceae/JTB255* and *Gammaproteobacteria* using RAx-maximum likelihood (RAx-ML), Maximum Parsimony (MP), Neighbor-joining (NJ) and MrBayes. Shaded circles indicate $\geq 70\%$ or 90% bootstrap (RAx-ML, MP, NJ) and consensus support (MrBayes). Diverging topologies are displayed as multifurcations. Sequences in blue box belong to the *Woeseiaceae/JTB255*. Sequences given in black originate from deep sea and hydrothermal sites, sequences given in green originate from coastal sediments. Six monophyletic sequence clusters were identified that were supported by all treeing methods. The partial sequence of metagenomic bin WOR_SG8_31 was subsequently added to the consensus tree. The scale bar refers to the evolutionary distance based on RAx-ML.