



Figure S4. Consensus phylogenetic trees of 16 concatenated ribosomal proteins and of the corresponding 16S rRNA sequences from 120 bacterial species. On the left, ribosomal protein tree; on the right, 16S rRNA tree. Sequences given in red are affiliated with the *Woeseiaceae*/JTB255. 16S rRNA sequences given in blue diverge from the corresponding Rpo phylogeny. Shaded circles indicate $\geq 70\%$ or 90% bootstrap (Rax-ML, MP, NJ) and consensus support (MrBayes). Partial sequences of Rpo from metagenomic bin JSS_woes1 and of 16S rRNA sequences from bin WOR_SG8_31 were subsequently added to the consensus trees. The scale bar refers to the evolutionary distance based on Rax-ML.