Fig. S1. Maximum-likelihood (A) and maximum-parsimony (B) trees showing the phylogenetic relationships between strains D3-12^{T} and G2-2^{T} and their closely related taxa, based on 16S rRNA gene sequences. Only bootstrap values exceeding 70% are indicated on the nodes as percentages from 1000 replicates. *Thioclava pacifica* DSM 10166^{T} (KX618934) was used as an outgroup. The scale bars in panels A and B indicate nucleotide changes per nucleotide and throughout the entire sequence, respectively.