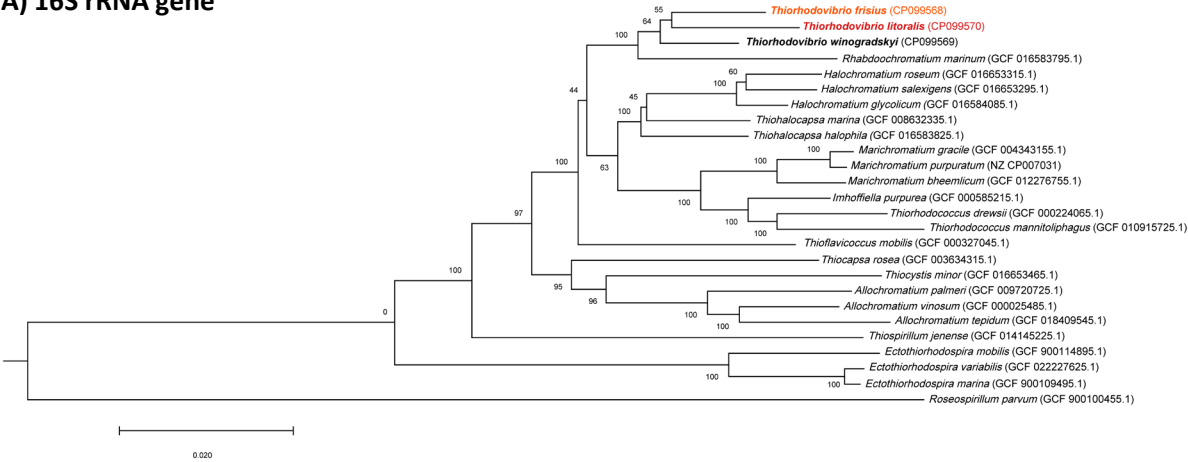
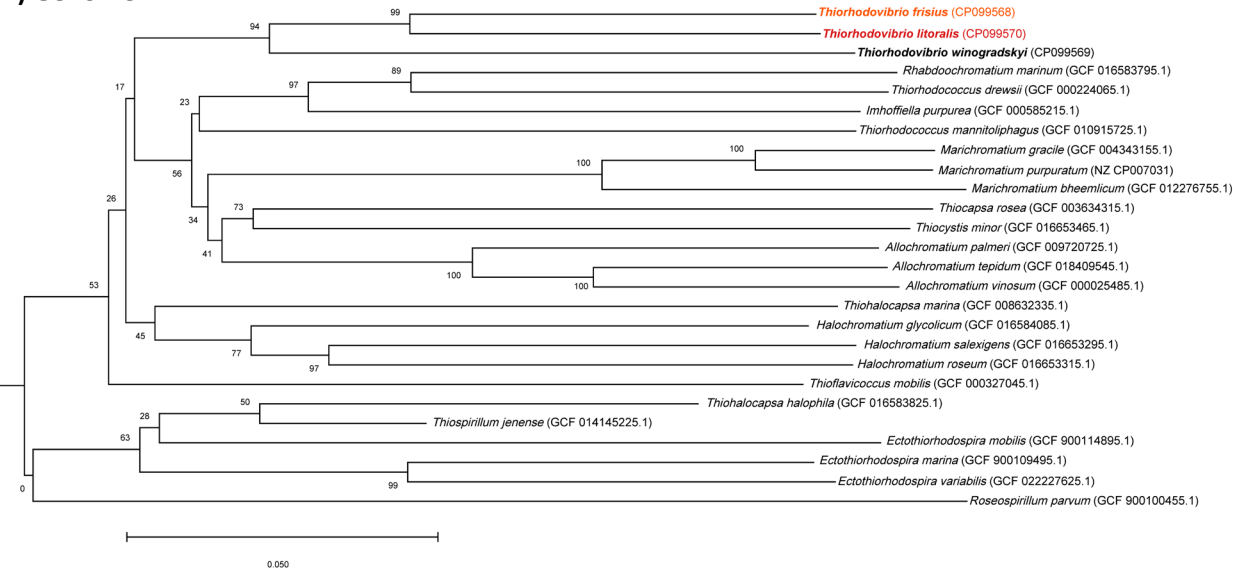


A) 16S rRNA gene



B) Genome



C) Proteome

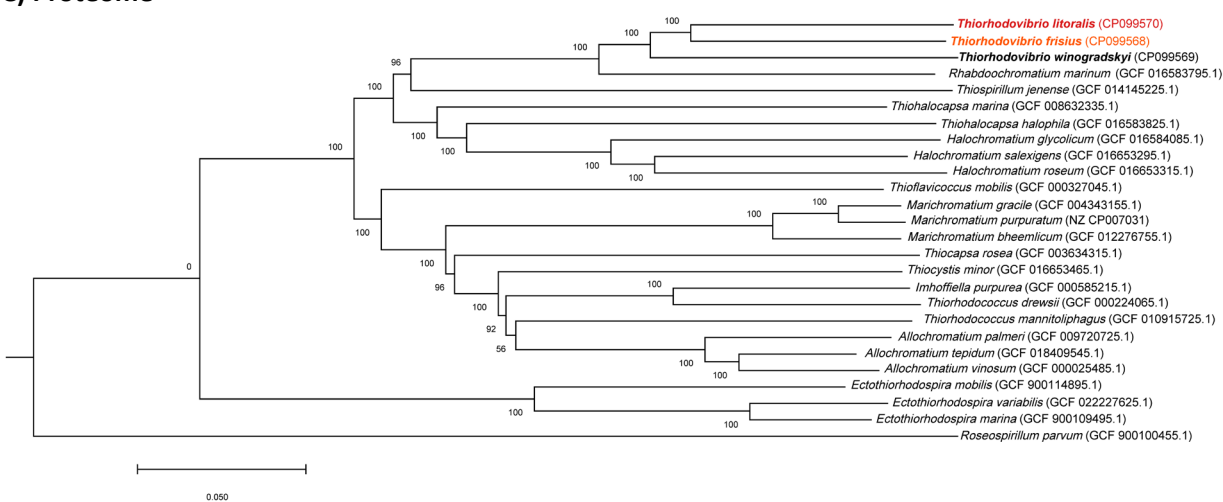


Figure S3. TYGS based phylogenetic trees. Trees rooted at midpoint were inferred with FastME 2.1.6.1 from GBDP distances calculated with formula d_s using **(A)** 16S rRNA gene, **(B)** genome, or **(C)** whole-proteome amino acid sequences. Pseudo-bootstrap support values >60% from 100 replications are depicted, with an average branch support of 87.8, 67.9, and 97.4% respectively.