Supplements

Thiomicrorhabdus psychrophila SVAL-D^T (AJ404732)

Thiomicrorhabdus arctica DSM 13458^T(ARLF01000004)

Thiomicrorhabdus chilensis DSM 12352^T(KI519609)

Thiomicrorhabdus lithotrophica XGS-01^T(CP102381)

Thiomicrorhabdus hydrogeniphila MAS2^T(LC010781)

Thiomicrorhabdus frisia JB-A2^T(AF013974)

Thiomicrorhabdus xiamenensis G2^T(MT514495)

Thiomicrorhabdus sediminis G1^T(MK938301)

Thiomicrorhabdus indica 13-15A^T(MH590687)

Hydrogenovibrio marinus DSM 11271^T(JOML01000002)

Hydrogenovibrio kuenenii DSM 12350^T(JAGP01000001)

Hydrogenovibrio halophilus DSM 15072^T(KB913033)

Hydrogenovibrio thermophilus I78^T(AB166731)

Hydrogenovibrio crunogenus ATCC 35932^T(L40810)
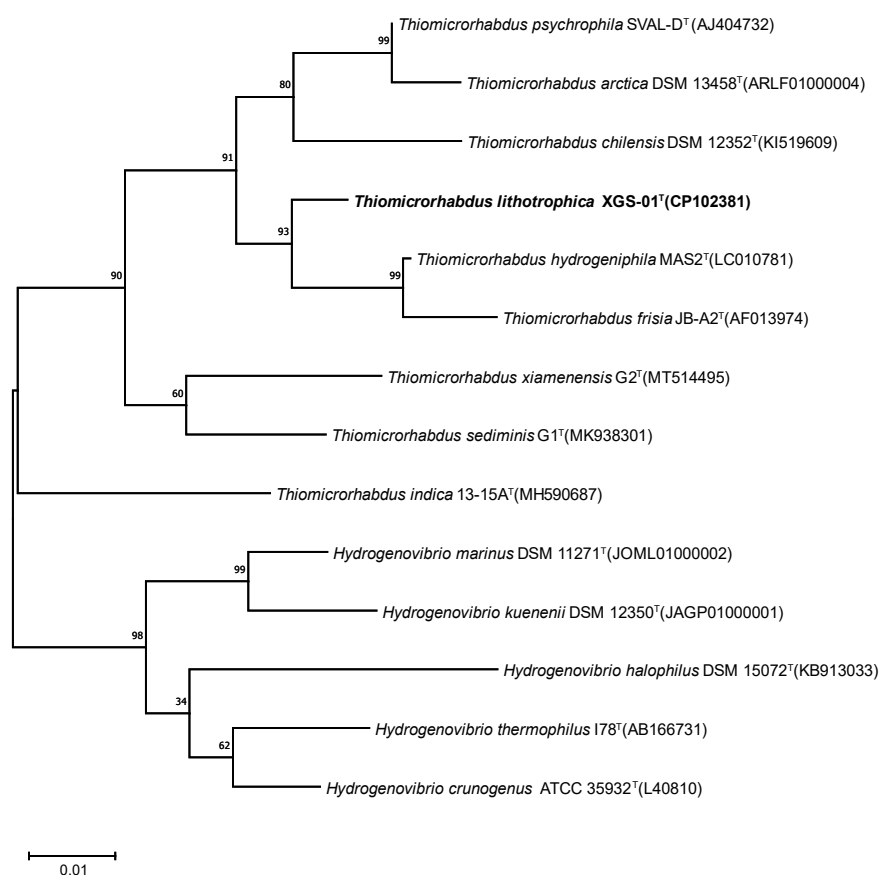
0.01

Figure S1. Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showing the relationship between strain XGS-01T and members of the genus *Thiomicrorhabdus*. Bootstrap values (>50%) based on 1000 replicates are shown at branch nodes. Bar, 0.01 substitutions per nucleotide position.
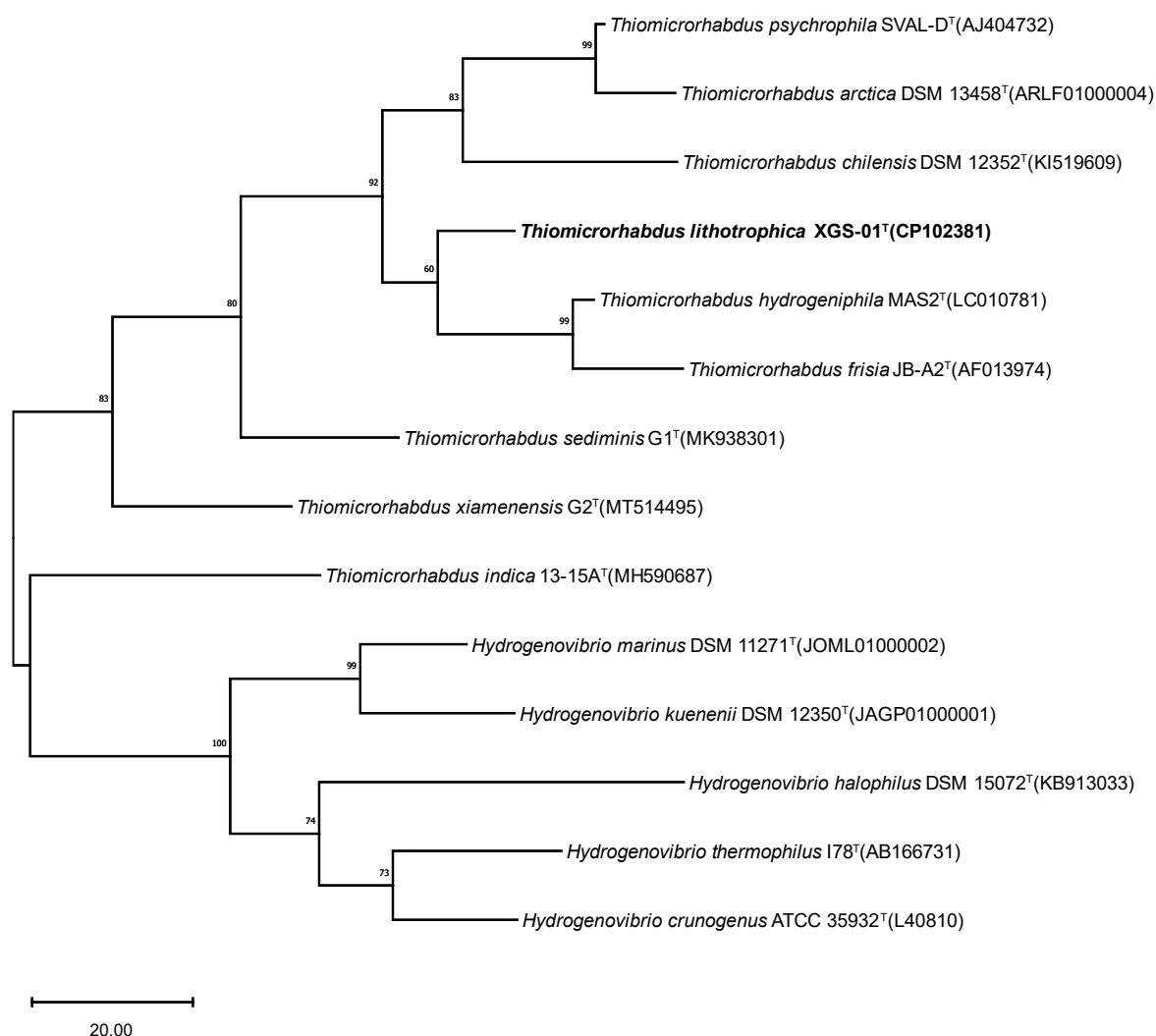
Figure S2. Maximum-Parsimony phylogenetic tree based on 16S rRNA gene sequences showing the relationship between strain XGS-01T and members of the genus *Thiomicrorhabdus*. Bootstrap values (>50%) based on 1000 replicates are shown at branch nodes. Bar, 0.01 substitutions per nucleotide position.

> *Thiomicrorhabdus lithotrophica* XGS-01ᵀ 16S ribosomal RNA gene, complete sequence

ATTAAACTGAAGAGTTTGATCCTGGCTCAGAATGAACGCTGGCGGTAGGCTTAACACATG
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CGAATATGCTCTACGGAGTAAAGGAGCCCTCTTCTTGAAAGGTTTCGCTATAGGATGAGC
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