

SUPPORTING INFORMATION

Production of endotoxin-free microbial biomass for food applications by gas fermentation of Gram-positive H₂-oxidizing bacteria

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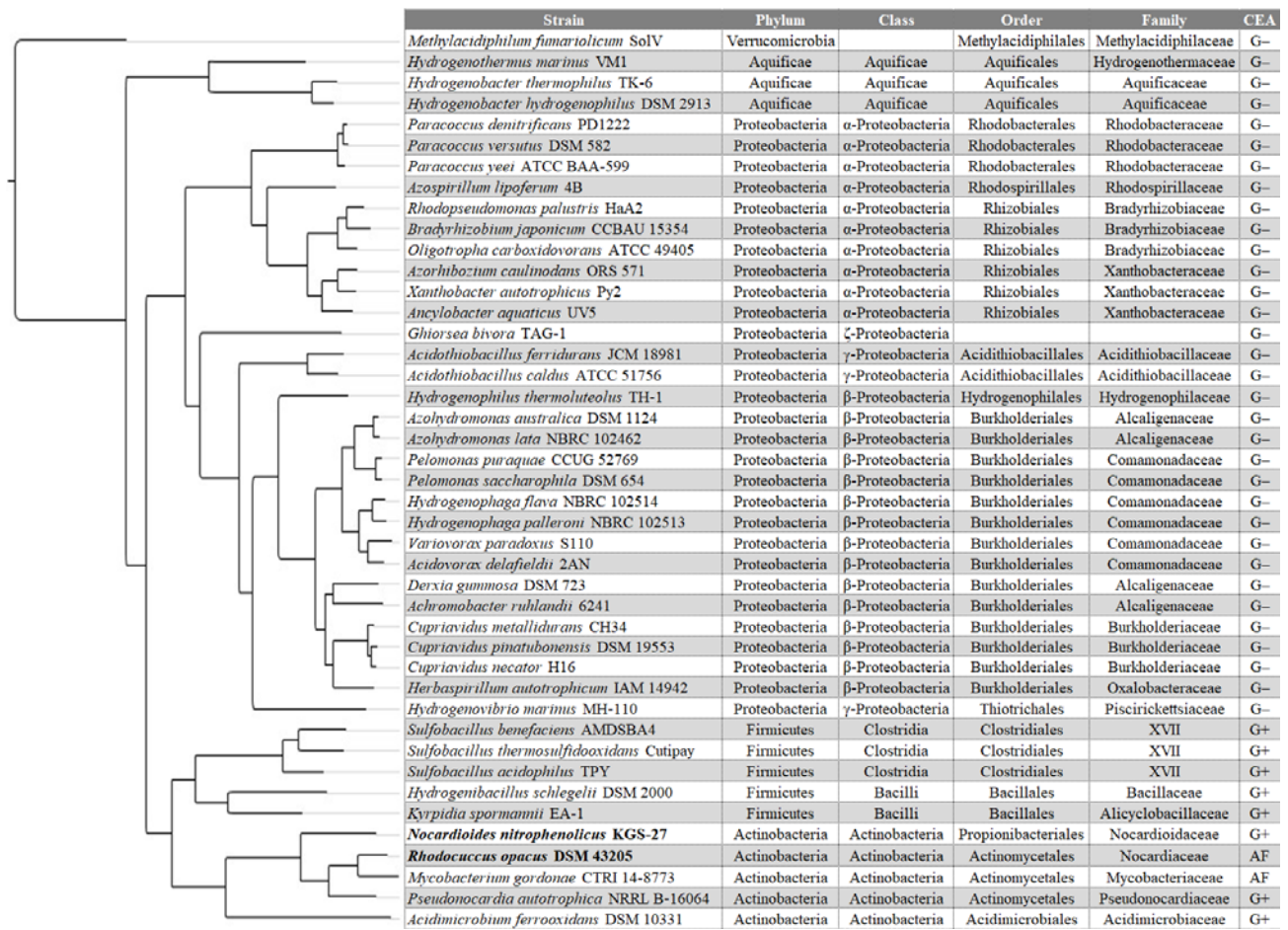


Figure S1. Phylogenomic clustering of HOB strains based on whole genome sequences of 59 Benchmarking Universal Single-Copy Orthologs (BUSCO) from orthoDB v9. The analysed set of HOAB genome assemblies includes those of *N. nitrophenolicus* KGS-27 and *R. opacus* DSM 43205 (Salusjärvi *et al.*, unpublished) as well as assemblies of other currently known HOB species classified as HOB based on the presence of both autotrophy and hydrogenotrophy marker genes (EC: 4.1.1.39, EC: 1.12.1.2, EC: 1.12.1.3, and EC:1.12.5.1) or by empirical literature evidence. The amino acid sequences of the BUSCO genes were aligned and trimmed using MAFFT v7 and TrimAL v1.4, respectively. The alignments were concatenated into a super-alignment matrix, clustered using RAxML v8 and rooted on the longest branch (i.e., *Methylacidiphilum fumariolicum* SolV). The respective taxonomic classification and cell envelope architecture (CEA) is indicated next to each HOAB strain name with the latter identifying them either as Gram-negative (G-), Gram-positive (G+) or acid-fast bacteria (AF).