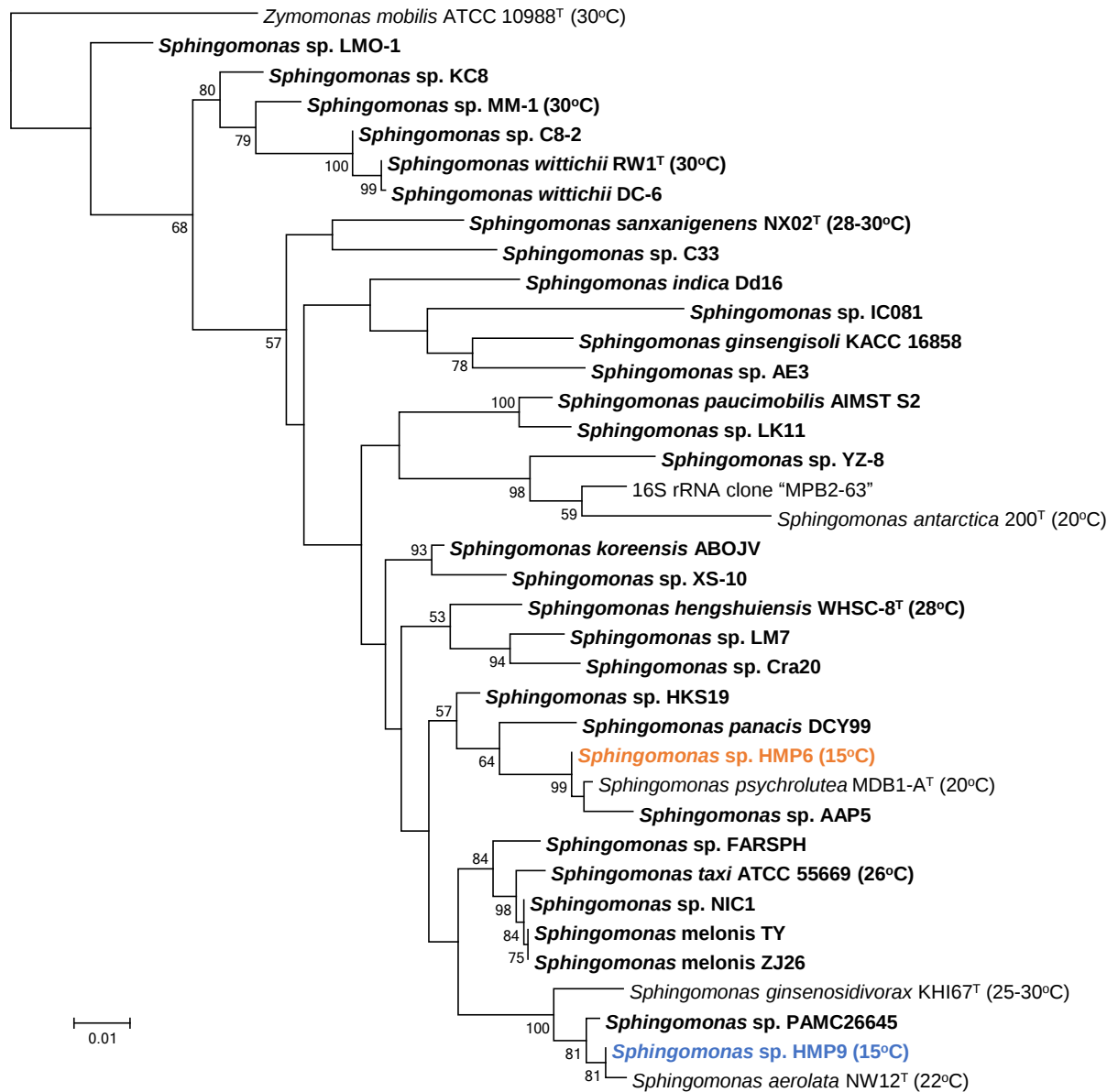




Supplementary Figure 1. Phylogenetic tree based on 16S rRNA sequence data of 36 *Sphingomonas* strains, constructed using the maximum-likelihood method under the Tamura-Nei model. *Zymomonas mobilis* ATCC 10988 was used as an outgroup. Species names in bold lettering: genome-sequenced strains; values in parentheses: growth temperatures; species names with superscript "T": type strains; numbers next to branches: bootstrap percentage values for 1000 replicates. Values inside parentheses are temperatures of optimum growth. Orange and blue text represents the Antarctic HMP6 and HMP9 strains, respectively.