

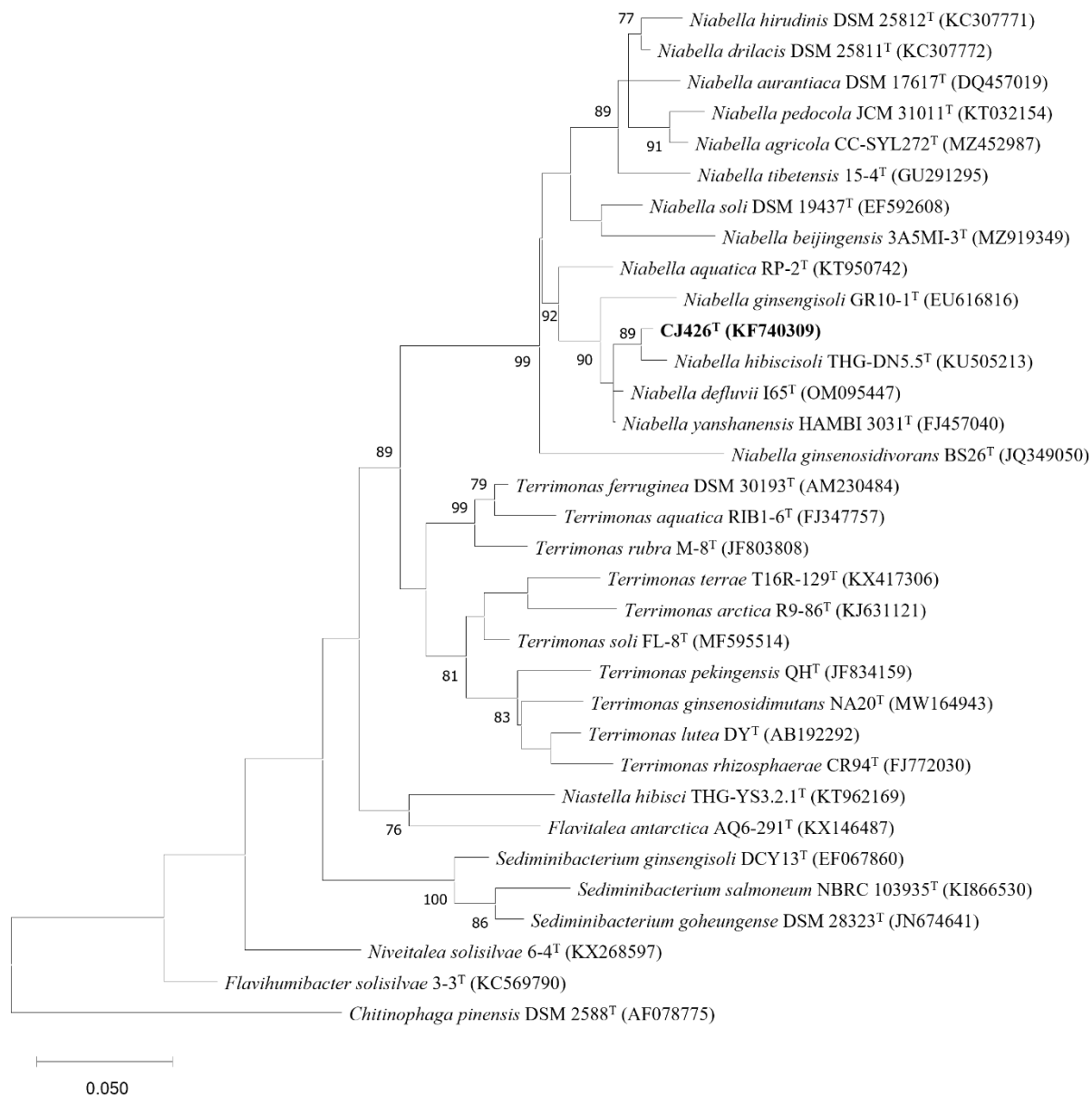


Fig. S1. Maximum-likelihood phylogenetic tree of strain CJ426^T and related type strains based on 16S rRNA gene sequences. Bootstrap values greater than 70% are shown at branch points based on maximum-likelihood analysis of 1,000 replicated datasets. *Chitinophaga pinensis* DSM 2588^T was used as an outgroup. Bars, 0.050 substitutions per nucleotide position.