

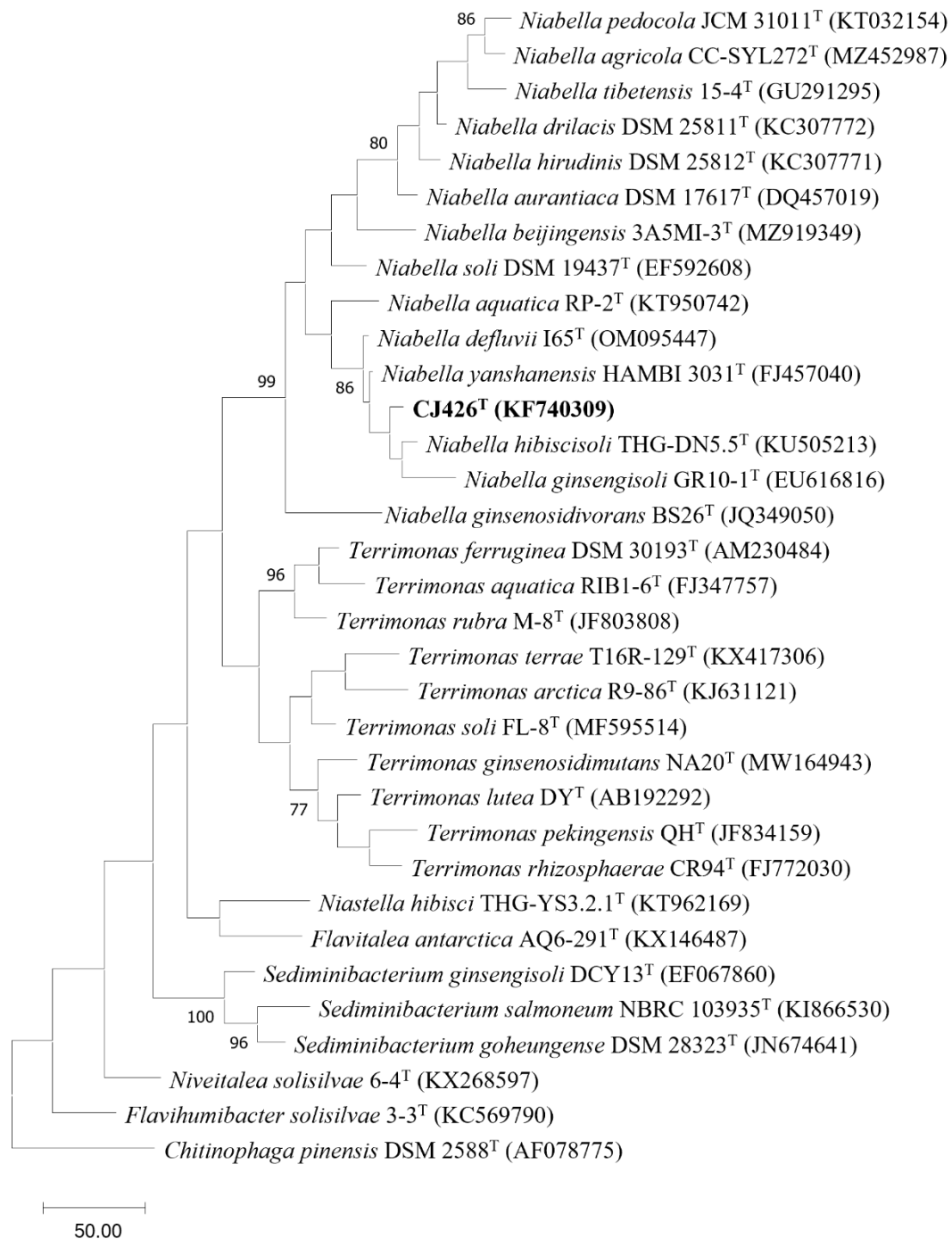


Fig. S2. Maximum-parsimony (MP) tree based on 16S rRNA gene sequences showing the phylogenetic relationships between strain CJ426^T and related type strains of the Genera. Bootstrap values greater than 70% are shown at branch points based on 1,000 replicated datasets. *Chitinophaga pinensis* DSM 2588^T was used as an outgroup.