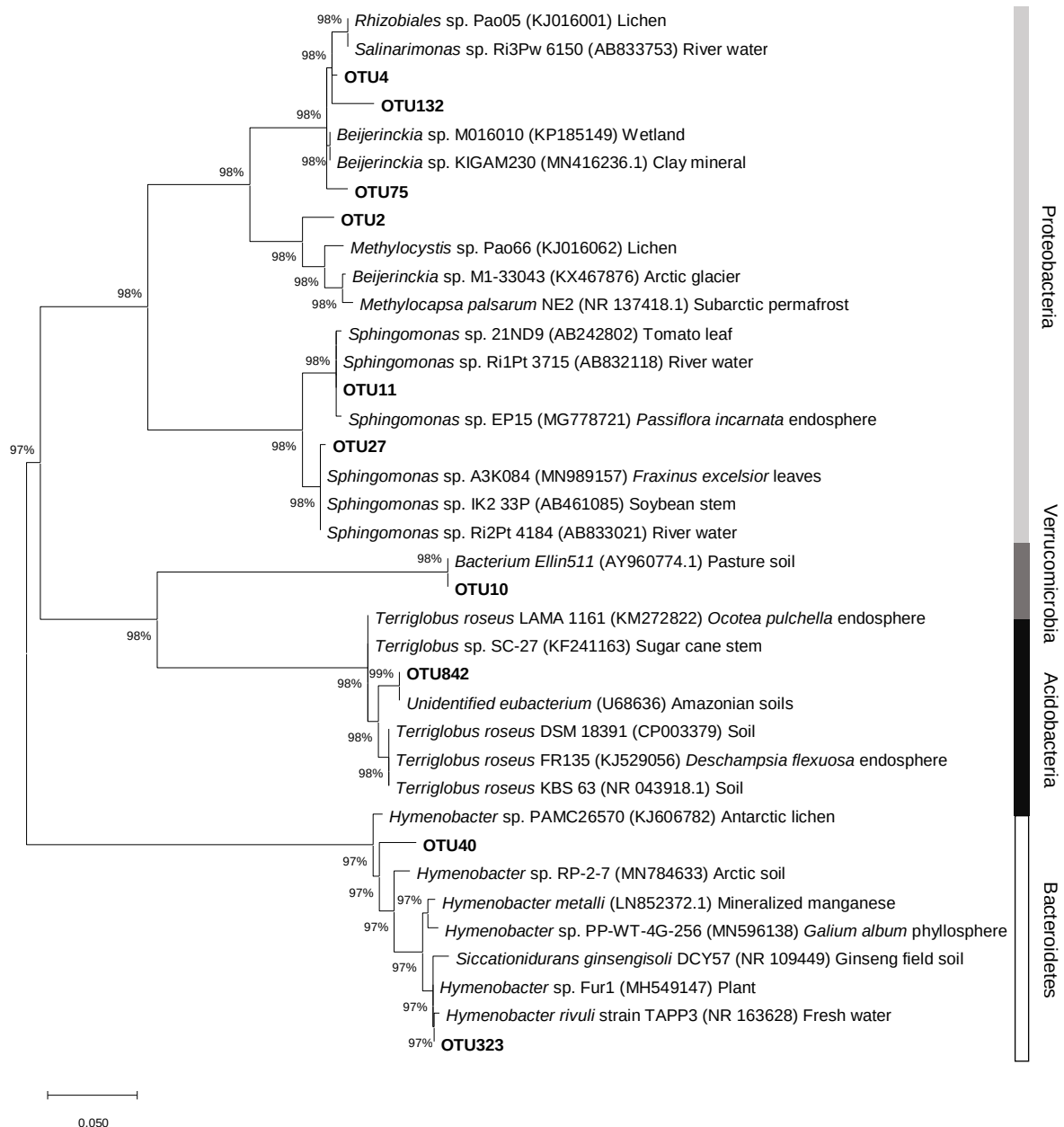




S10 Fig: Phylogenetic maximum-likelihood analysis based on 16S rRNA gene PCR amplicon sequences of core phyllosphere OTUs and bacterial isolates with the closest sequence identity. Isolates were identified using BLASTn; the accession number and isolation source of each isolate is provided. Sequences were aligned with ClustalW. Bootstrap probabilities based on 1000 replications are shown. Bar: 0.05 nucleotide substitutions rate (Knuc) units.