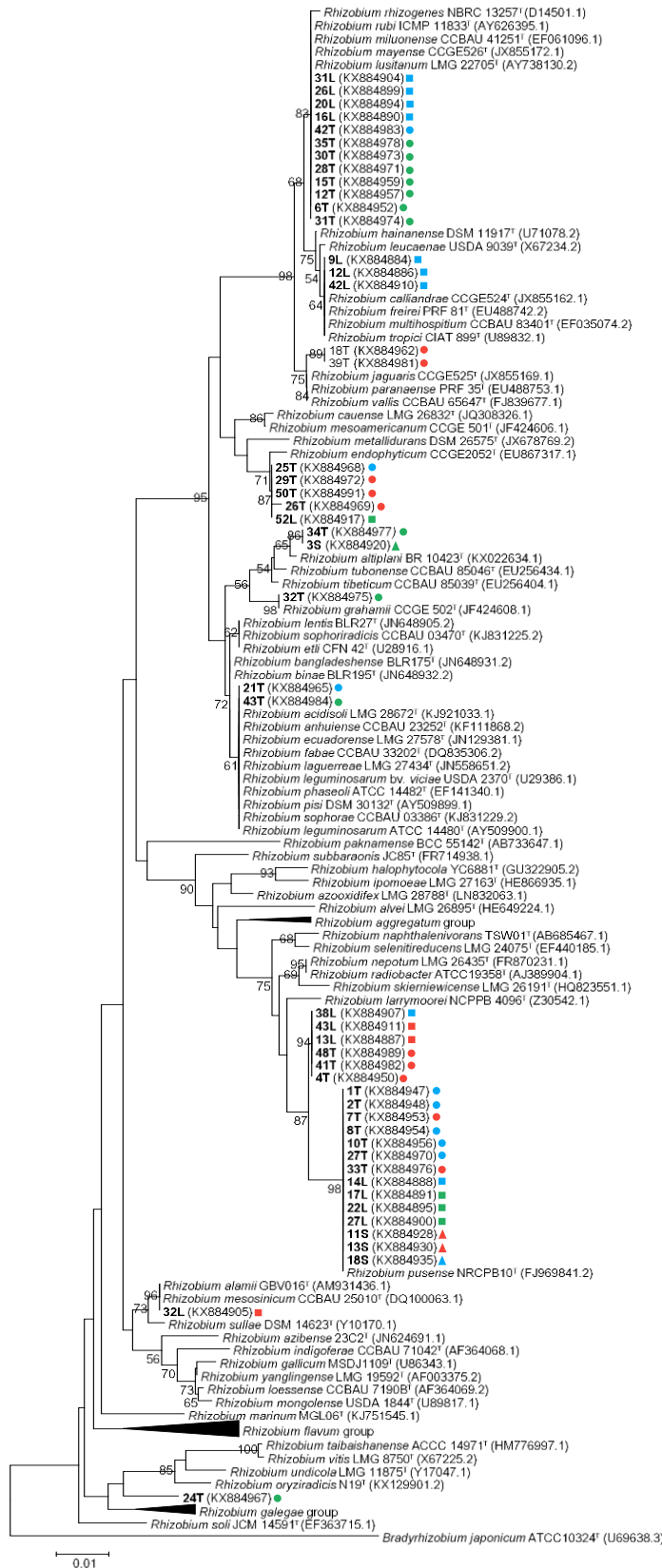


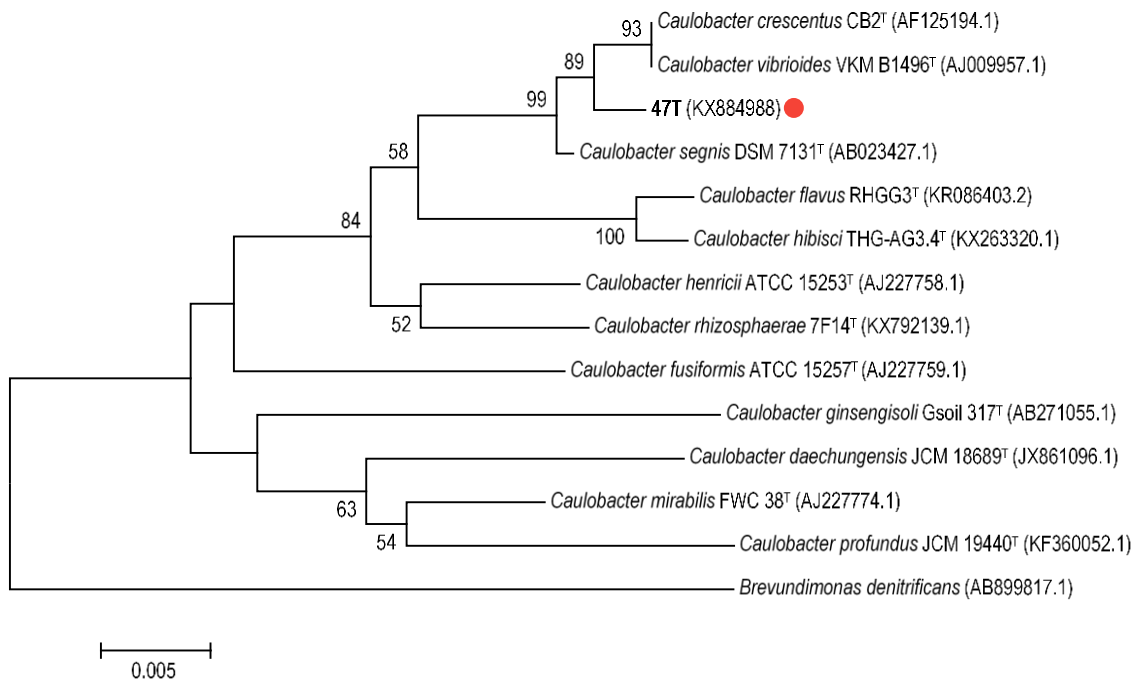
S1 File. Phylogenetic trees based on 16S rRNA gene. Trees from (a) to (k) show the relationship between isolates and the reference species for each genera. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. Specific type strains for each genera were used as outgroup. Isolation sources of the diazotroph/N-scavenger bacterial strains are represented by shapes and colors: BS, soil (triangle); LR, lulo unwashed roots (square); TR, tomato unwashed roots (circle); CH, horticulture soil at conventional management (red); ORG, horticulture soil at organic management (blue); SF, secondary forest soil with no agricultural use (green).



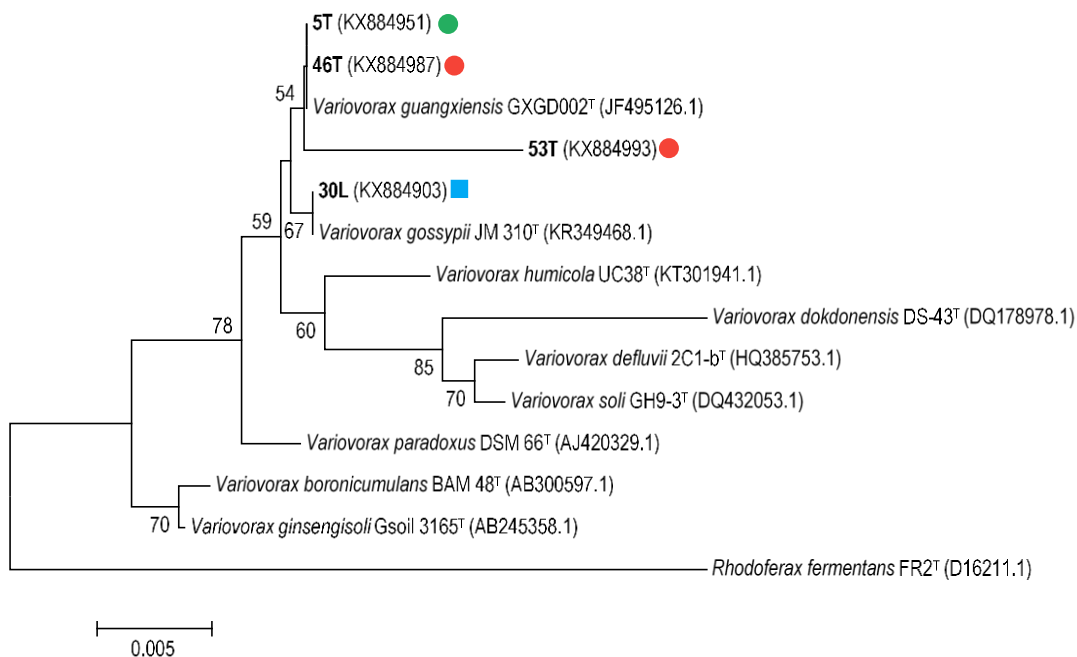
S1a Fig. Phylogenetic tree of 16S rRNA gene of 49 *Rhizobium* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Bradyrhizobium japonicum* ATCC10324^T was used as outgroup.



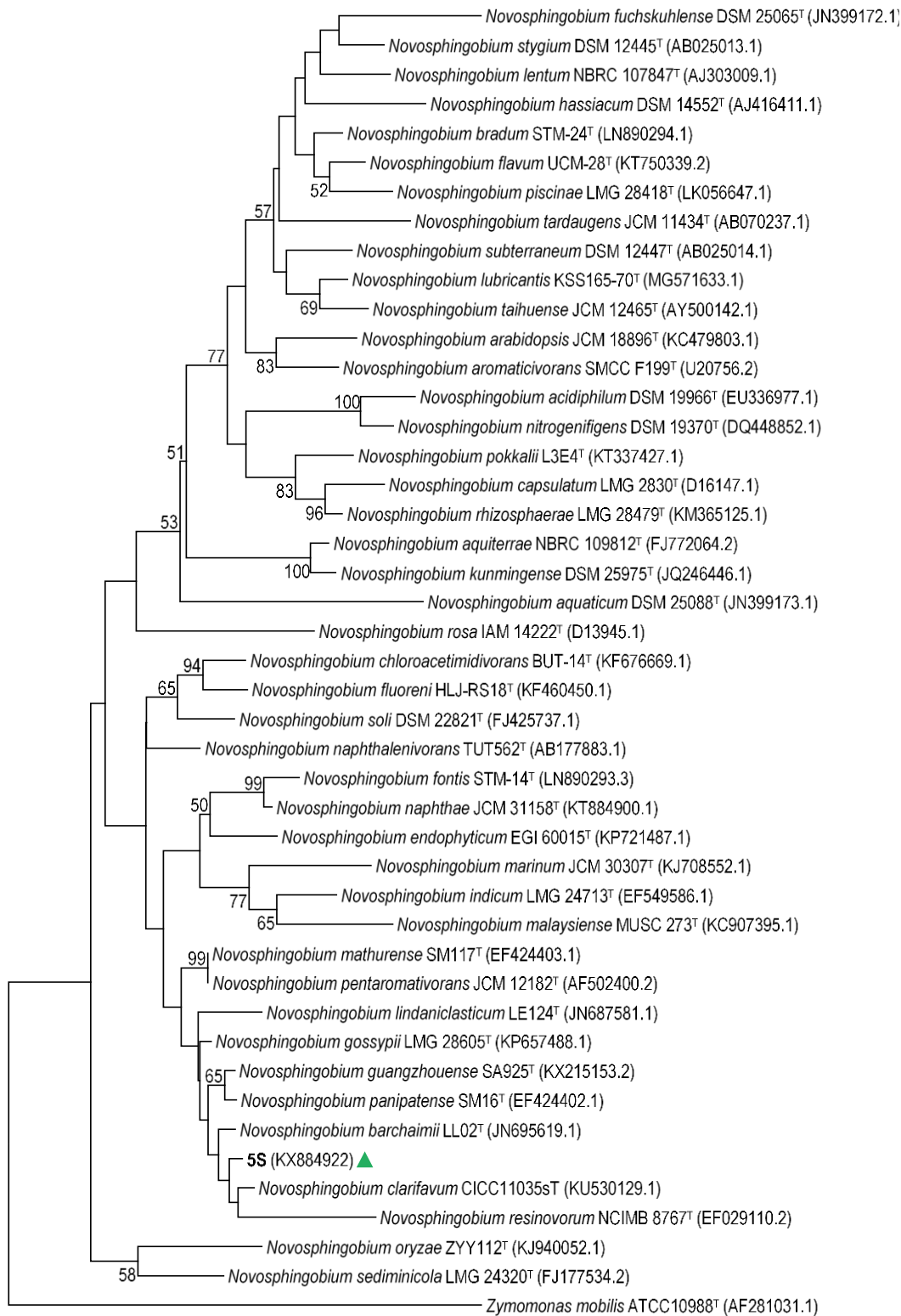
S1b Fig. Phylogenetic tree of 16S rRNA gene of 10 *Rhizobium* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Bradyrhizobium japonicum* ATCC10324^T was used as outgroup.



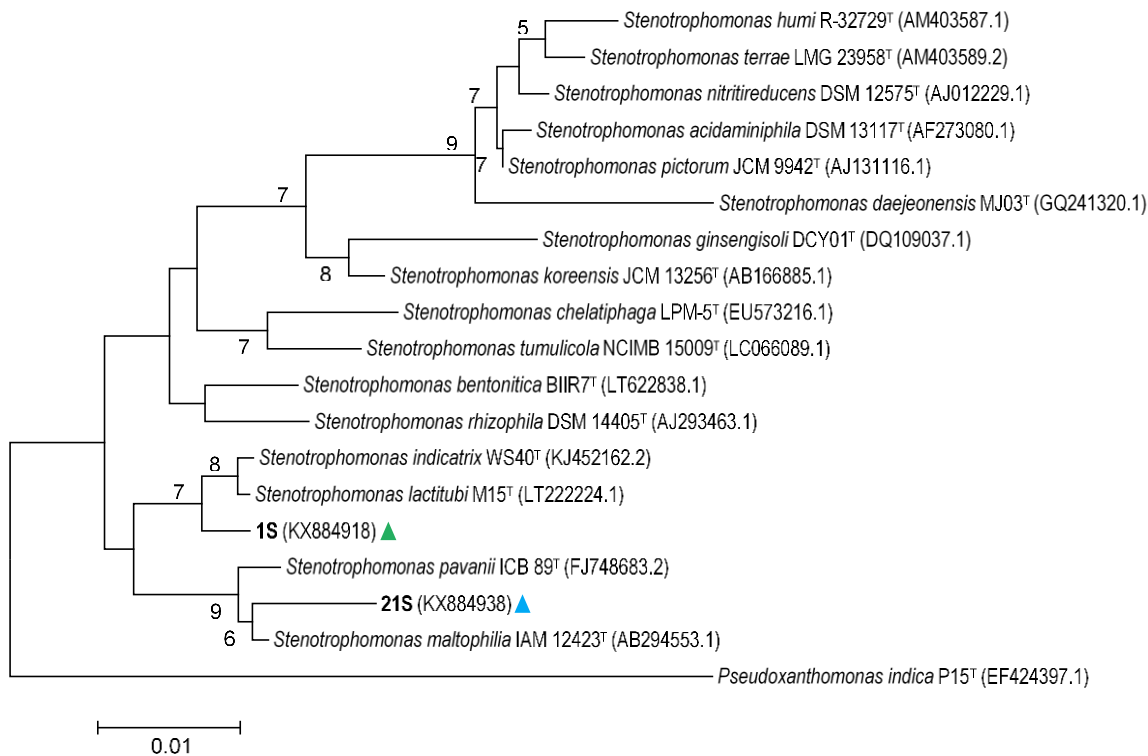
S1c Fig. Phylogenetic tree of 16S rRNA gene of one *Caulobacter* isolate clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Brevundimonas denitrificans* was used as outgroup.



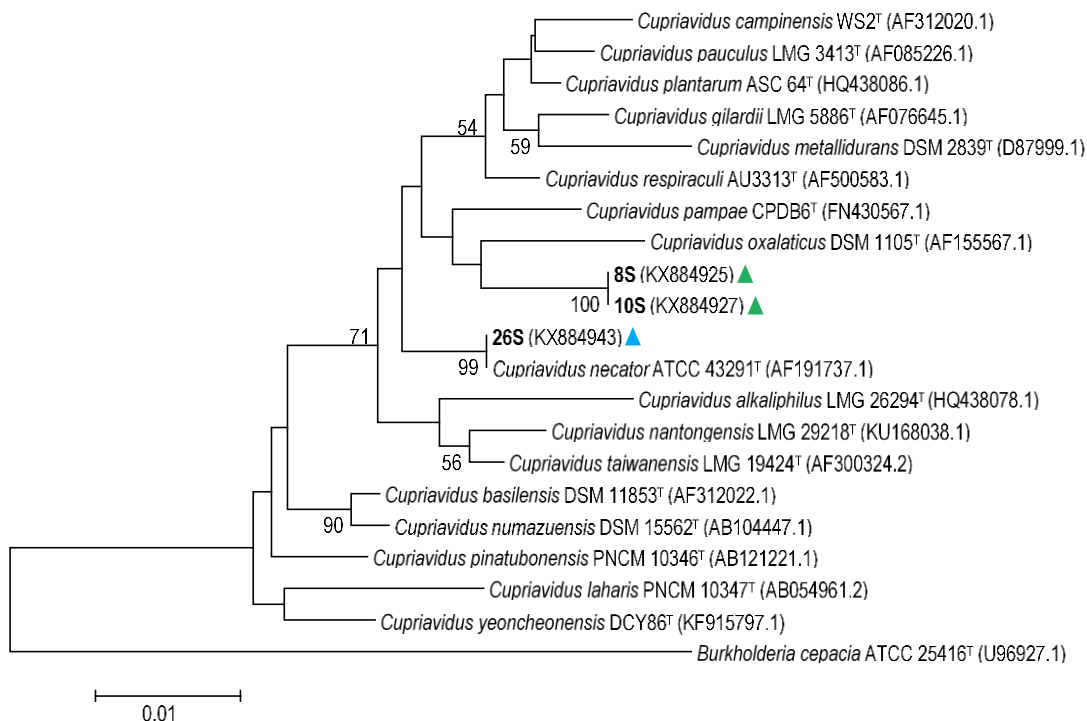
S1d Fig. Phylogenetic tree of 16S rRNA gene of four *Variovorax* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Rhodoferrax fermentans* FR2^T was used as outgroup.



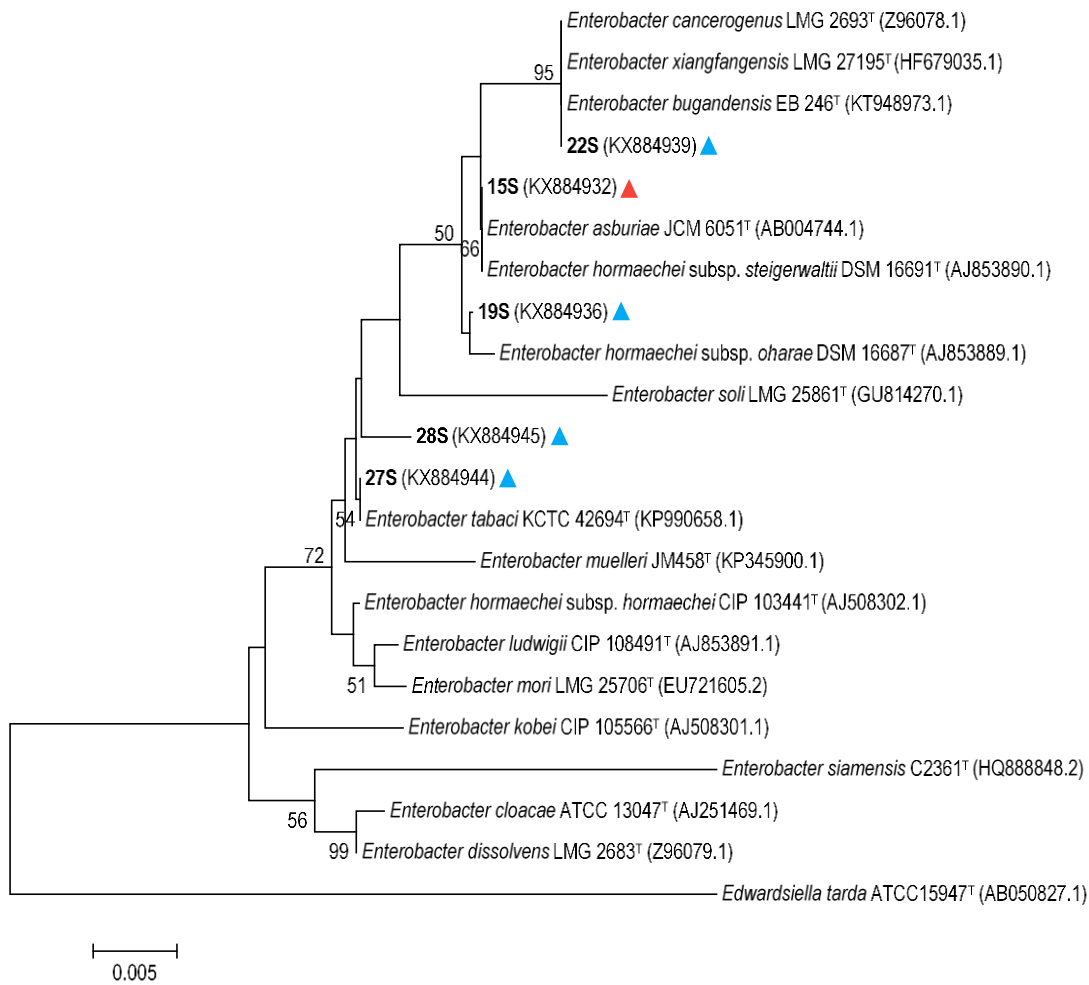
S1e Fig. Phylogenetic tree of 16S rRNA gene of one *Novosphingobium* isolate clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Zymomonas mobilis* ATCC10988^T was used as outgroup.



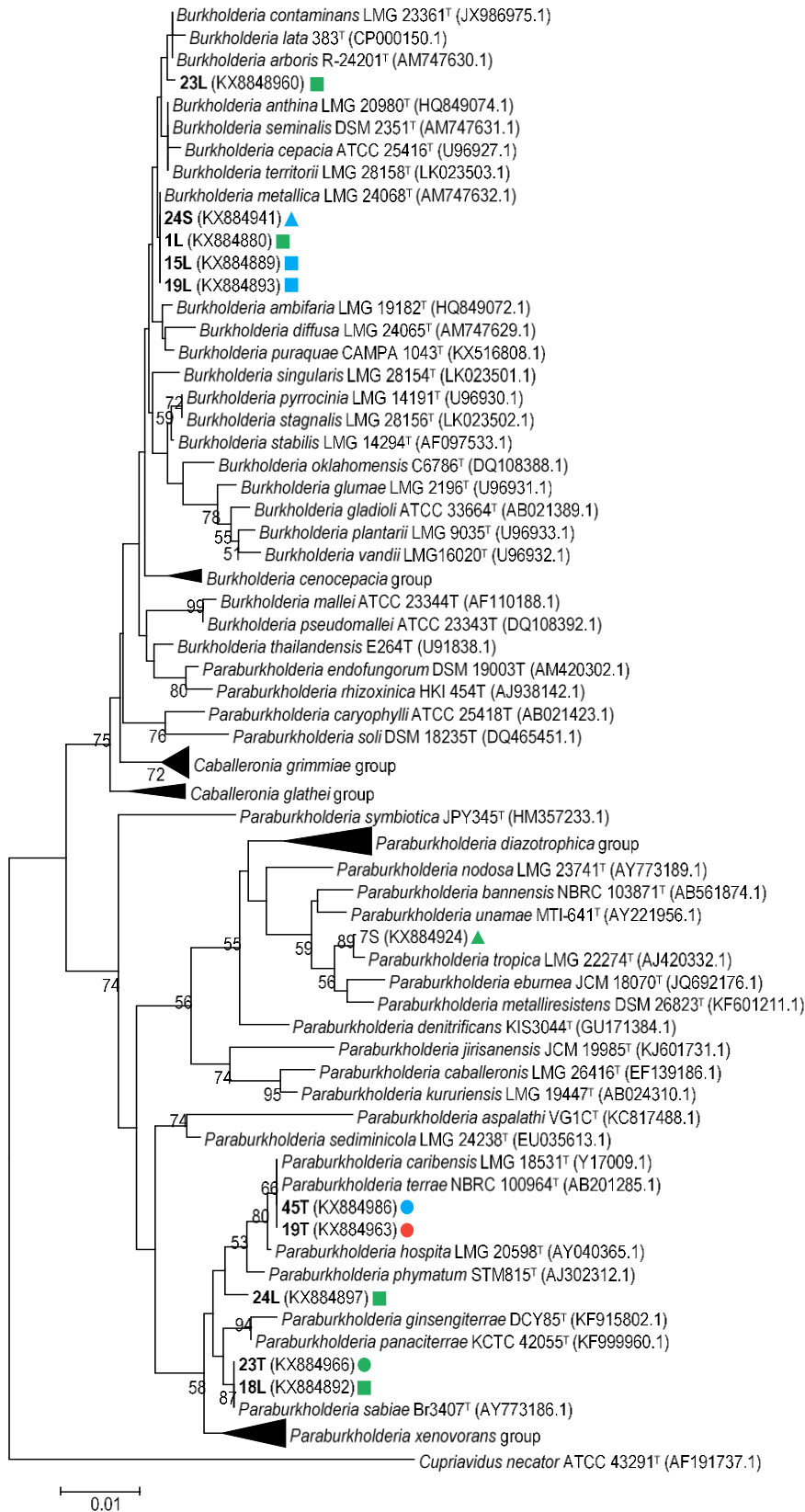
S1f Fig. Phylogenetic tree of 16S rRNA gene of two *Stenotrophomonas* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Pseudoxanthomonas indica* P15^T was used as outgroup.



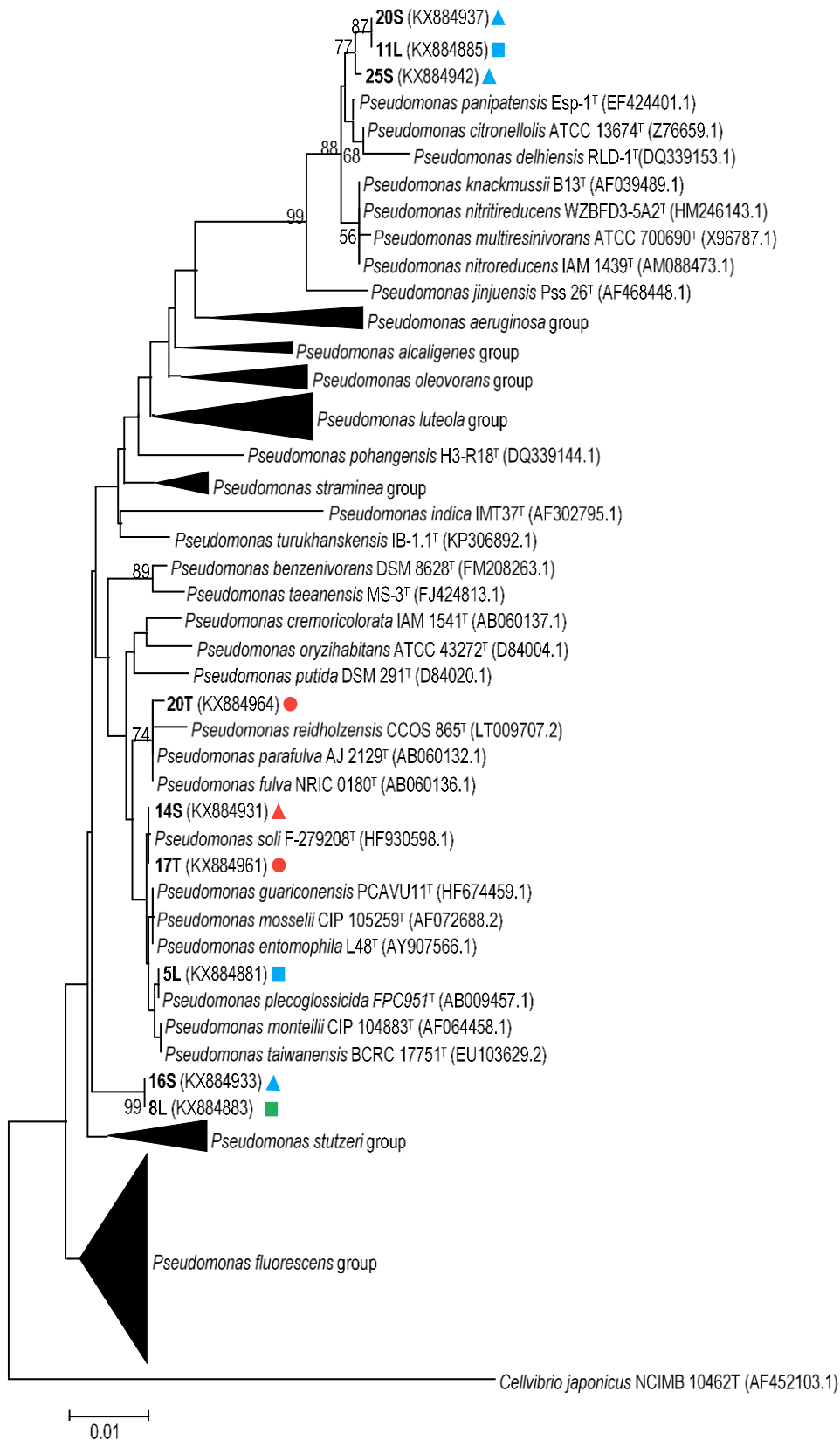
S1g Fig. Phylogenetic tree of 16S rRNA gene of three *Cupriavidus* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Burkholderia cepacia* ATCC25416^T was used as outgroup.



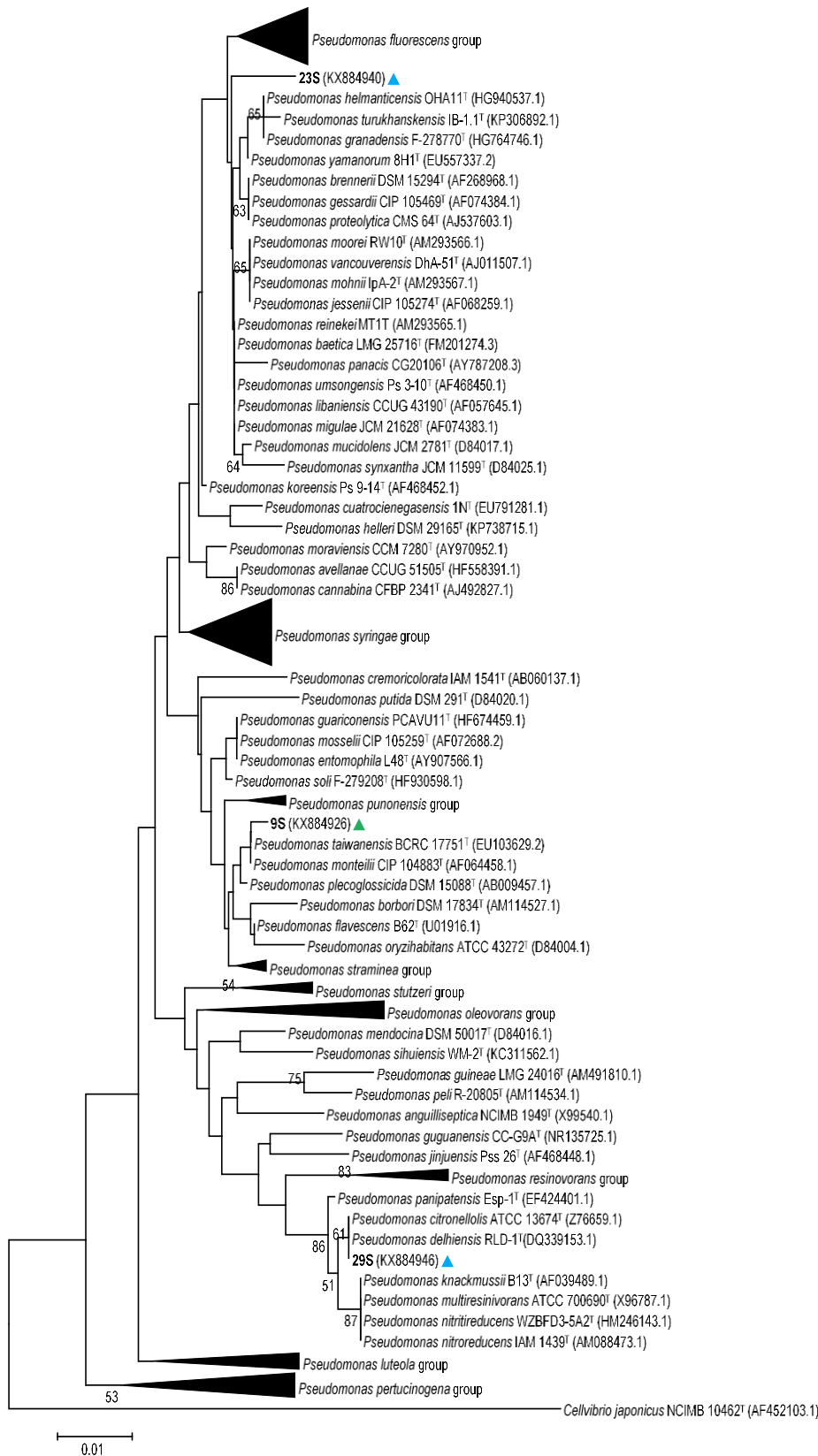
S1h Fig. Phylogenetic tree of 16S rRNA gene of five *Enterobacter* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Edwardsiella tarda* ATCC15947^T was used as outgroup.



S1i Fig. Phylogenetic tree of 16S rRNA gene of 11 *Burkholderia* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Cupriavidus necator* ATCC43291^T was used as outgroup.



S1j Fig. Phylogenetic tree of 16S rRNA gene of nine *Pseudomonas* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Cellvibrio japonicus* NCIMB 10462^T was used as outgroup.



S1k Fig. Phylogenetic tree of 16S rRNA gene of three *Pseudomonas* isolates clustered with the type strains. Phylogeny was built with MEGA v.7 using the Neighbor-Joining method based on the Kimura 2-parameter model. Support values are shown next to the branches when $\geq 50\%$, based on 1000 bootstrap replications. Bar indicates the percentage of nucleotide substitutions. *Cellvibrio japonicus* NCIMB 10462^T was used as outgroup.