

Figure S1A. Continued.

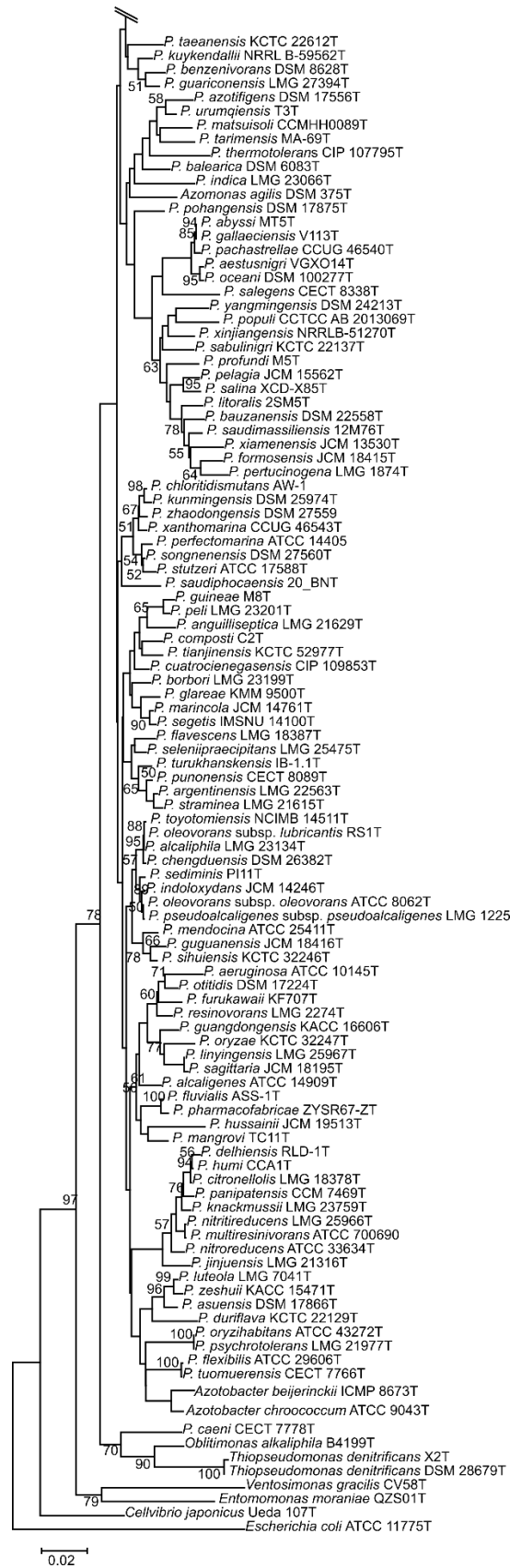


Figure S1. Phylogenetic tree based on the 16S rDNA sequences of the species and subspecies type strains under study. A) *P. fluorescens* lineage, B) *P. aeruginosa* and *P. pertucinogena* lineages. Bootstrap values higher than 50 % are indicated on the nodes.

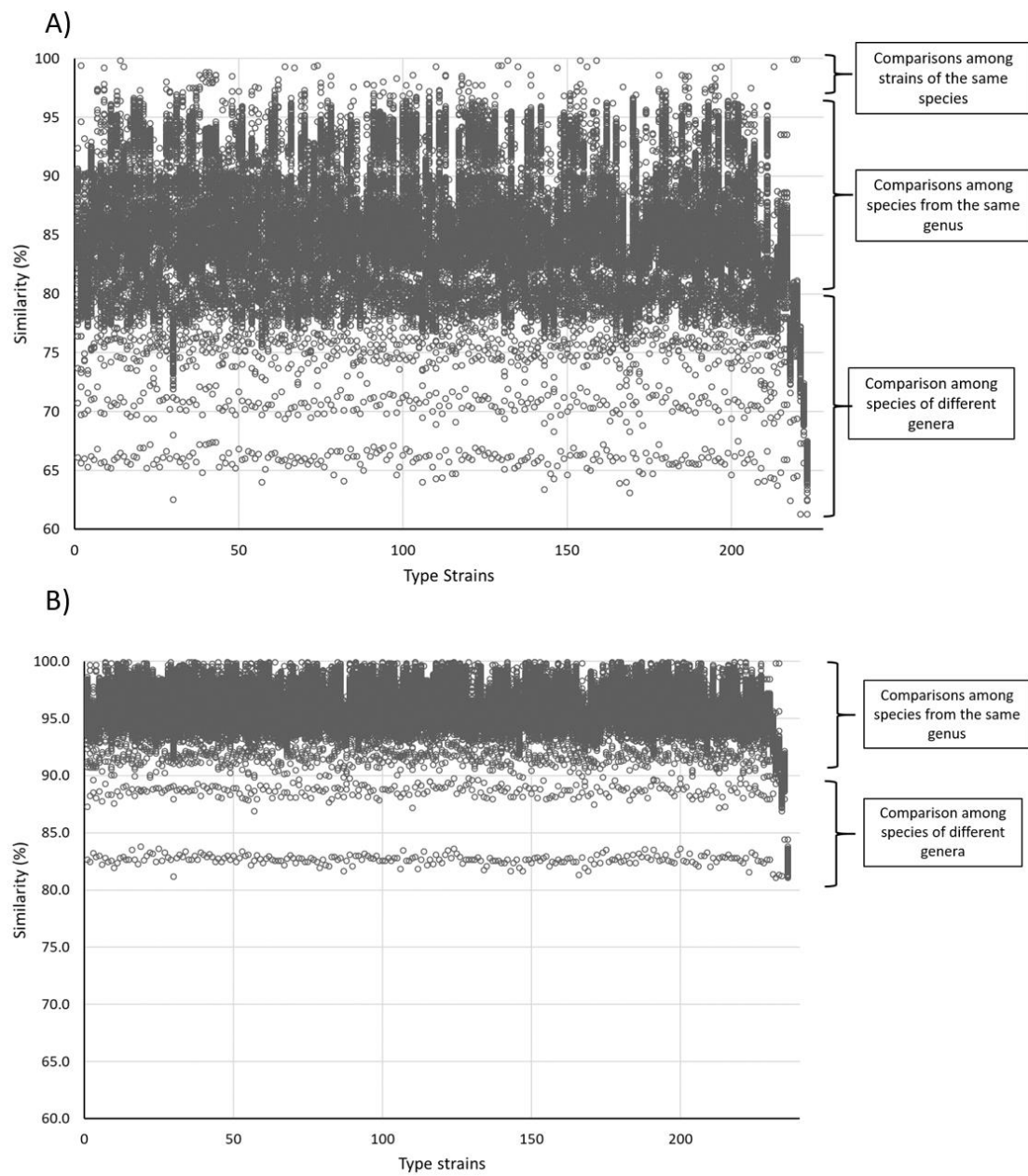


Figure S2. Pairwise similarities of the concatenated 4-genes partial sequences (A) and the 16S rDNA sequences (B) among the studied type strains.

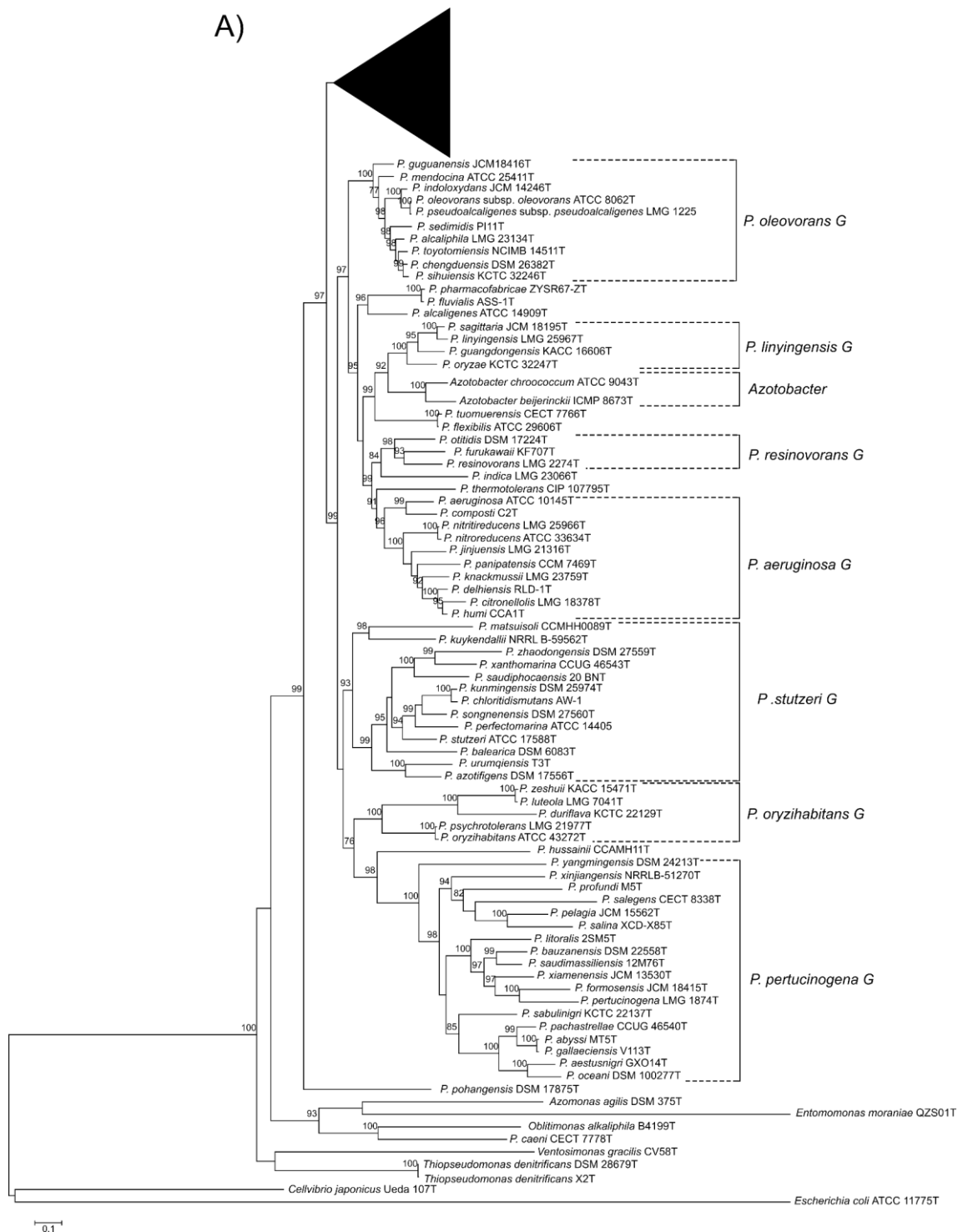


Figure S3A. Continued.

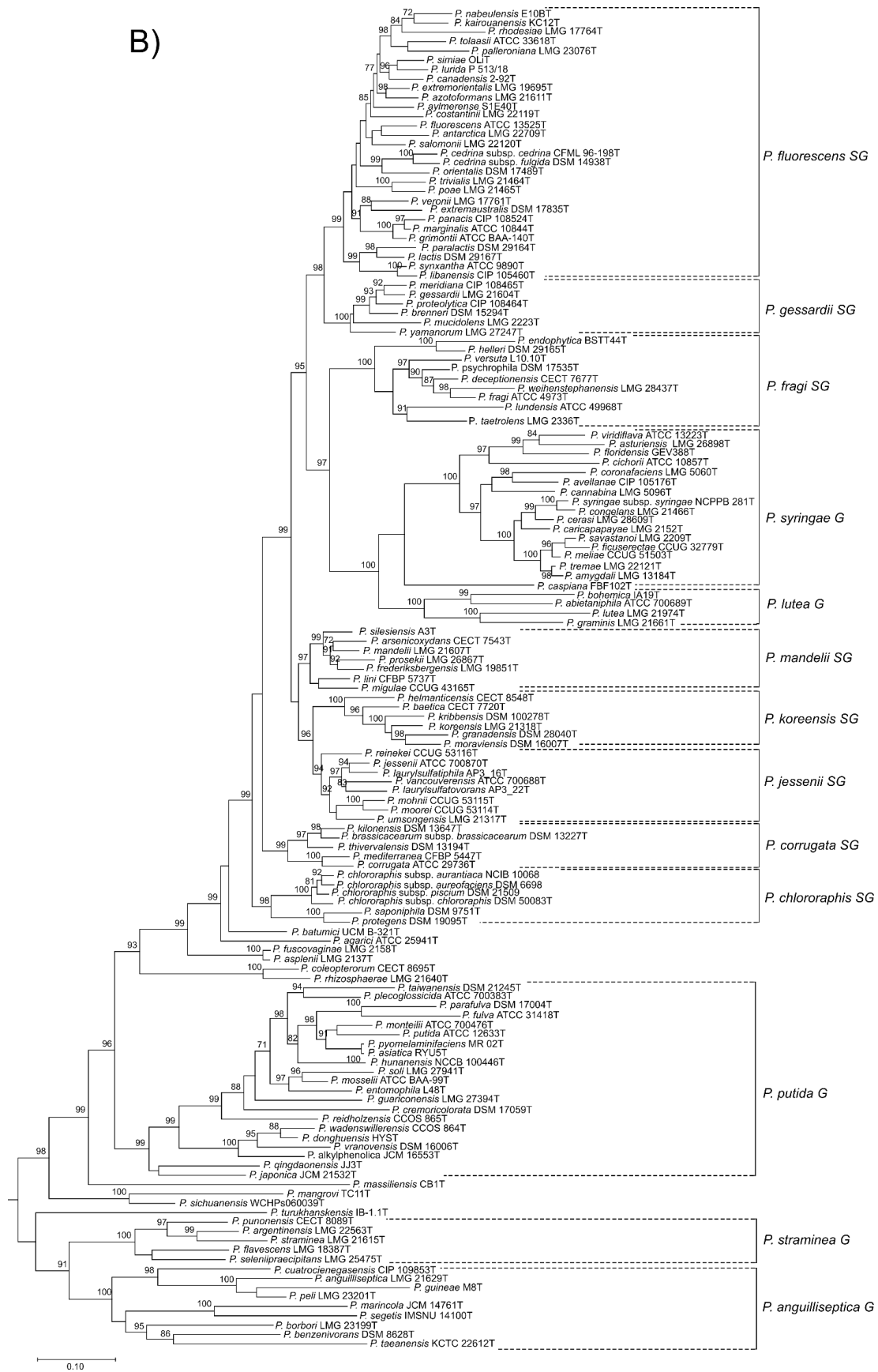


Figure S3. Maximum likelihood phylogenetic tree based on the 4-genes MLSA for the 241 species and subspecies type strains under study. A) *P. aeruginosa* and *P. pertucinogena* lineages. B) *P. fluorescens* lineage. Bootstrap values higher than 70% are indicated on the nodes. Bars indicate sequence divergence.

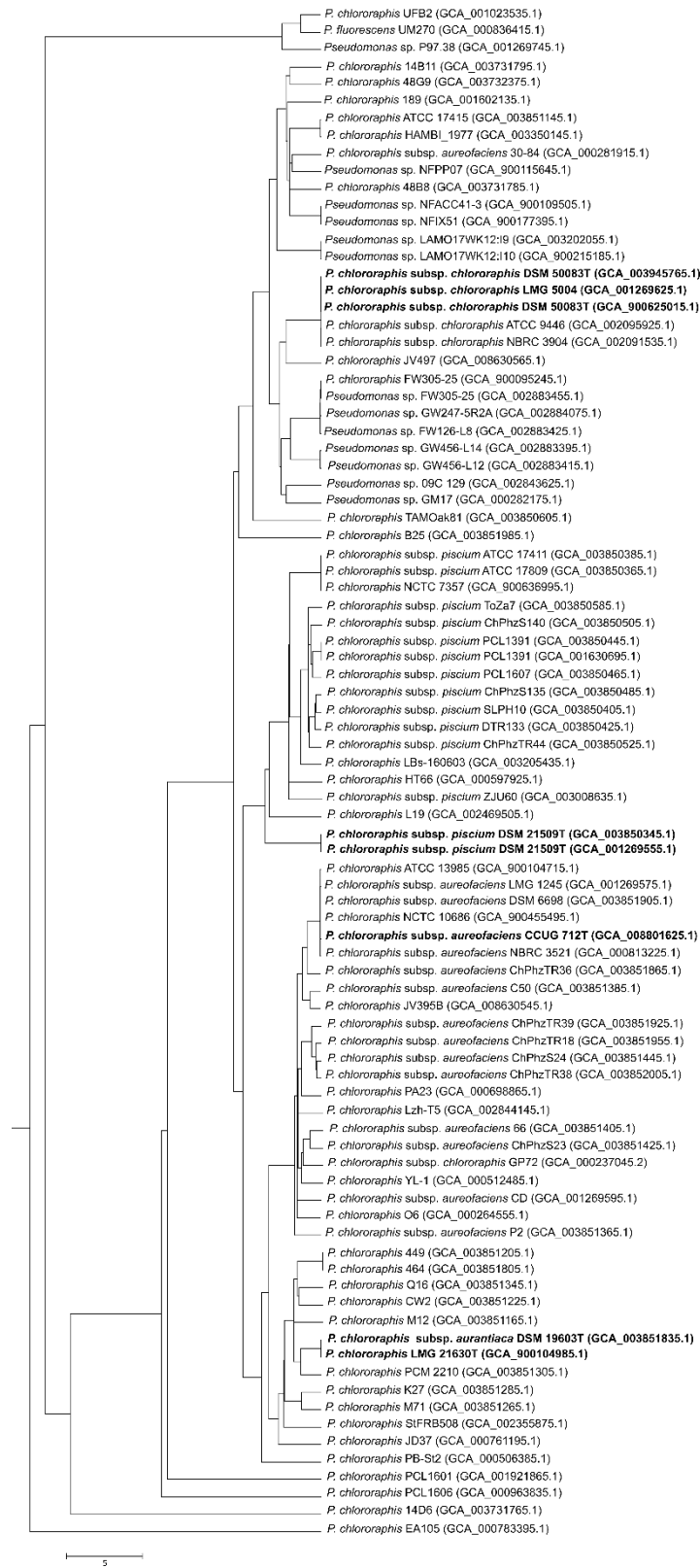


Figure S4. UPGMA dendrogram of the ANiB similarities among the *P. chlororaphis* strains studied.