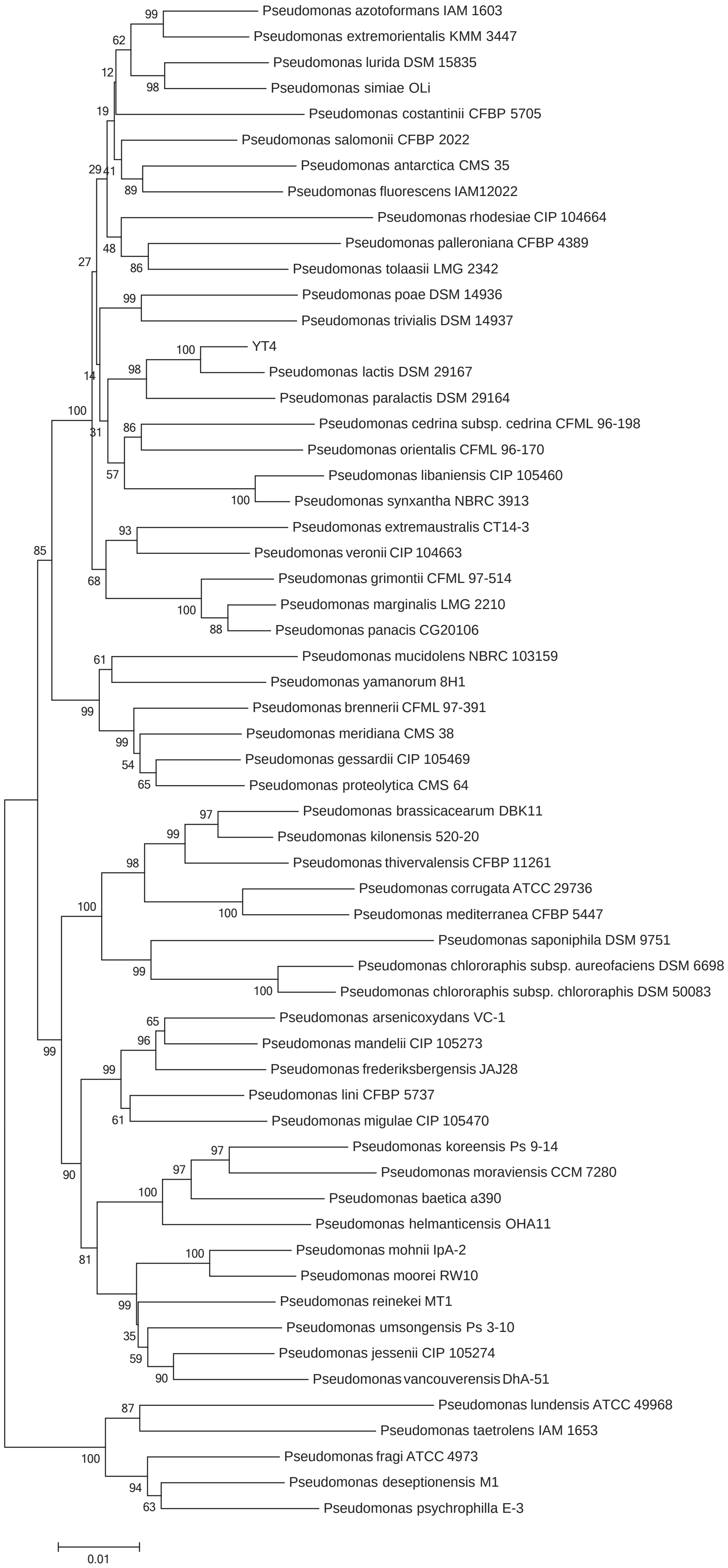

Figure S1. Phylogenetic tree of 58 type strains of *Pseudomonas* and YT4 based on the phylogenetic analysis of four concatenated genes (*16S rRNA*, *gyrB*, *rpoB* and *rpoD*).

The unrooted tree was constructed by neighbor-joining using the MEGA6 (1). The evolutionary distances were computed using the Jukes-Cantor method (2). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches (3). The scale bar represents the substitutions per site.

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