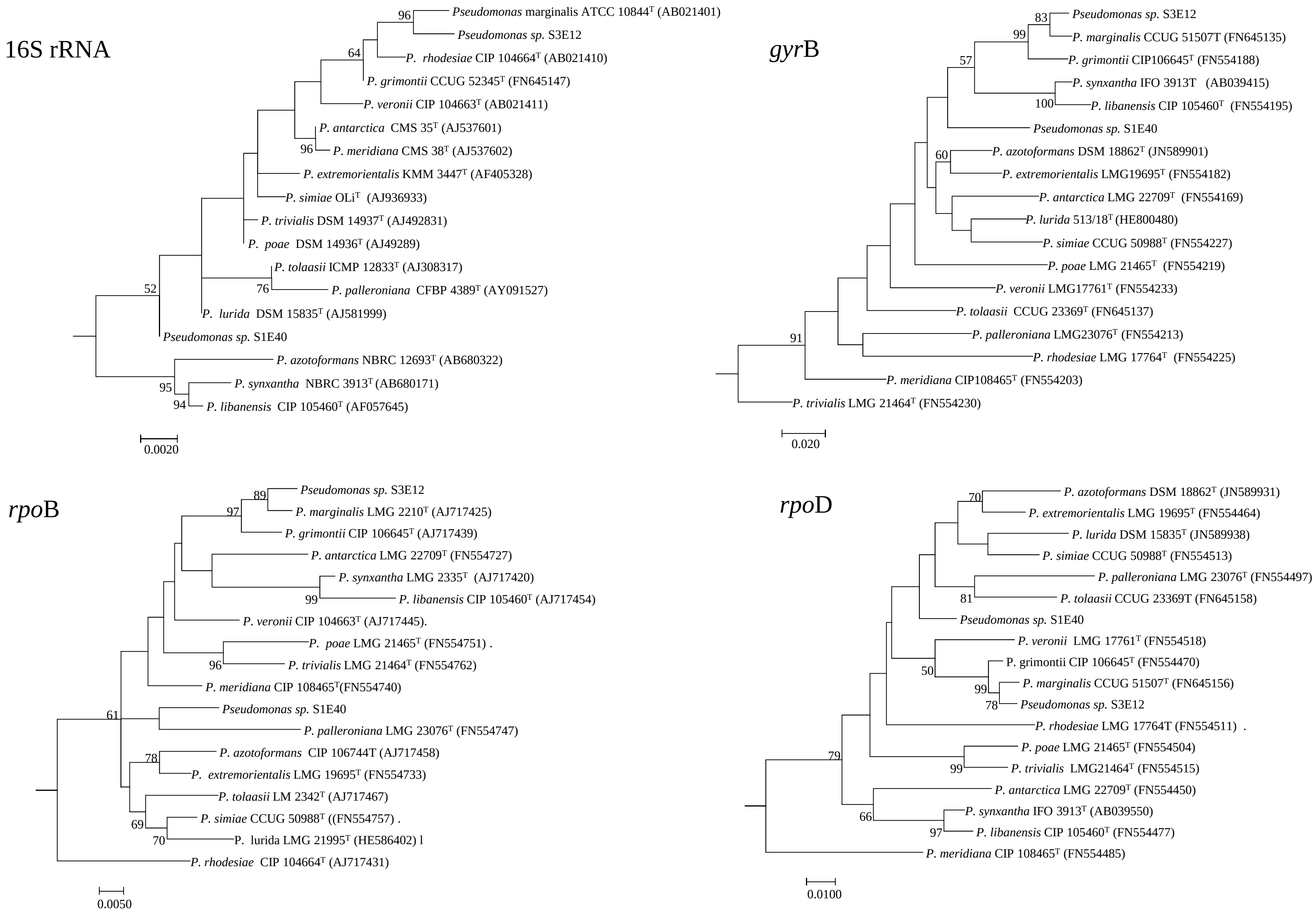

Figure S1. Single gene phylogenetic trees inferred by maximum-likelihood (ML) of *Pseudomonas sp.* strains S1E40 and S3E12 with type strains of close lineages using the general time reversible substitution model. A, 16S rRNA; B, *gyr*B; C, *rpo*B; and D, *rpo*D; ML trees were reconstructed for each gene sequences with 1000 bootstrap replicates. Bootstrap values higher than 50 are shown on nodes. *Pseudomonas aeruginosa* LMG1242^{T} was used as outgroup.