



Supplementary Fig. 1. Phylogenetic tree constructed by the neighbor-joining method based on 16S rRNA gene analysis displaying relationship of strain YJR13 with the type strains within the genus *Pseudomonas*. Numbers at the branching points represent the bootstrap values (>70%) for 1,000 replications. Circles at the branching points indicate that the corresponding nodes were also recovered in the trees generated with maximum likelihood and maximum parsimony methods. GenBank accession numbers are shown in parentheses. Bar, 1 nucleotide substitution per 100 nt of the 16S rRNA gene sequence. *Cellvibrio japonicus* NCIMB 10462T (AF452103) was used as an outgroup. “T”, the type strain.