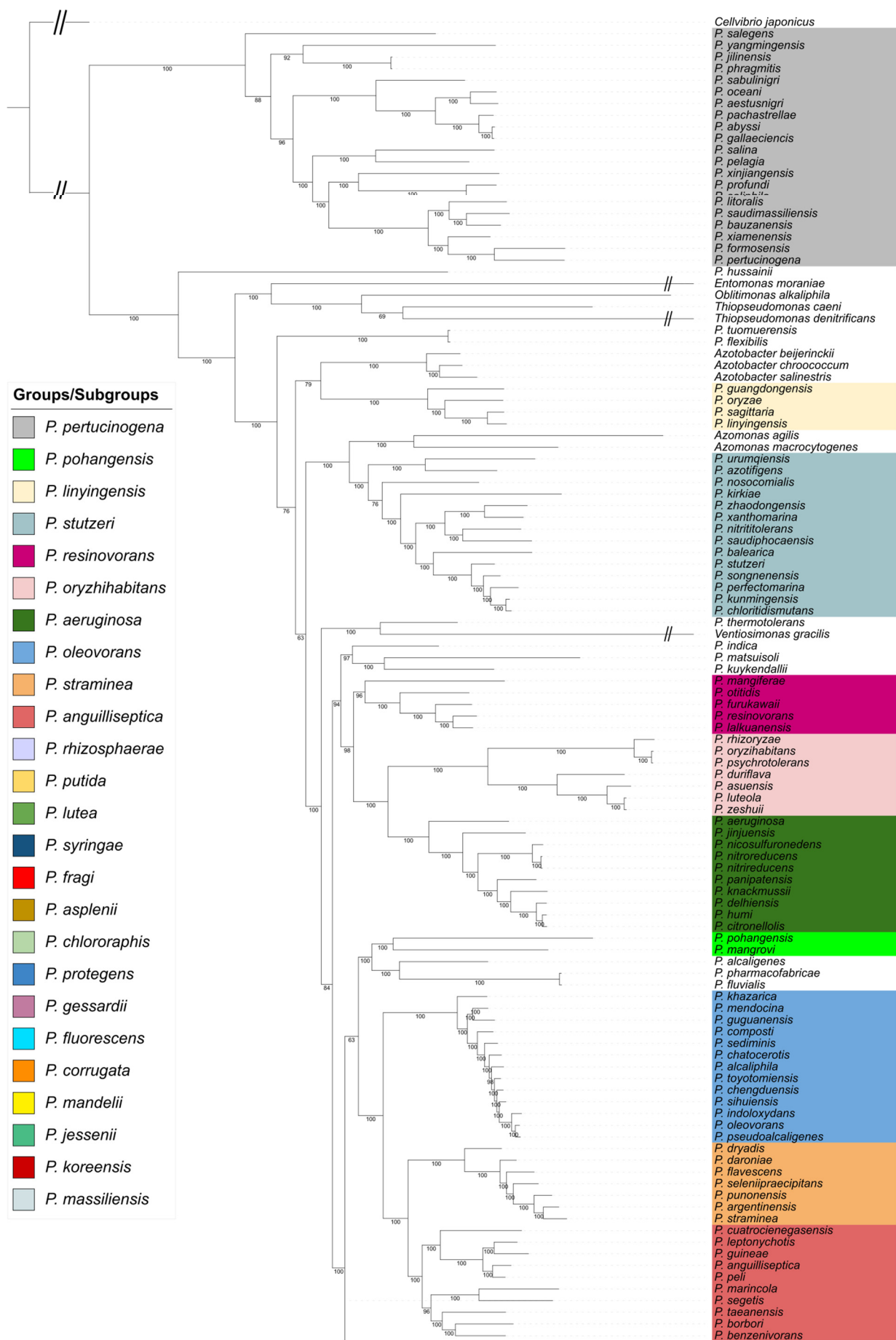
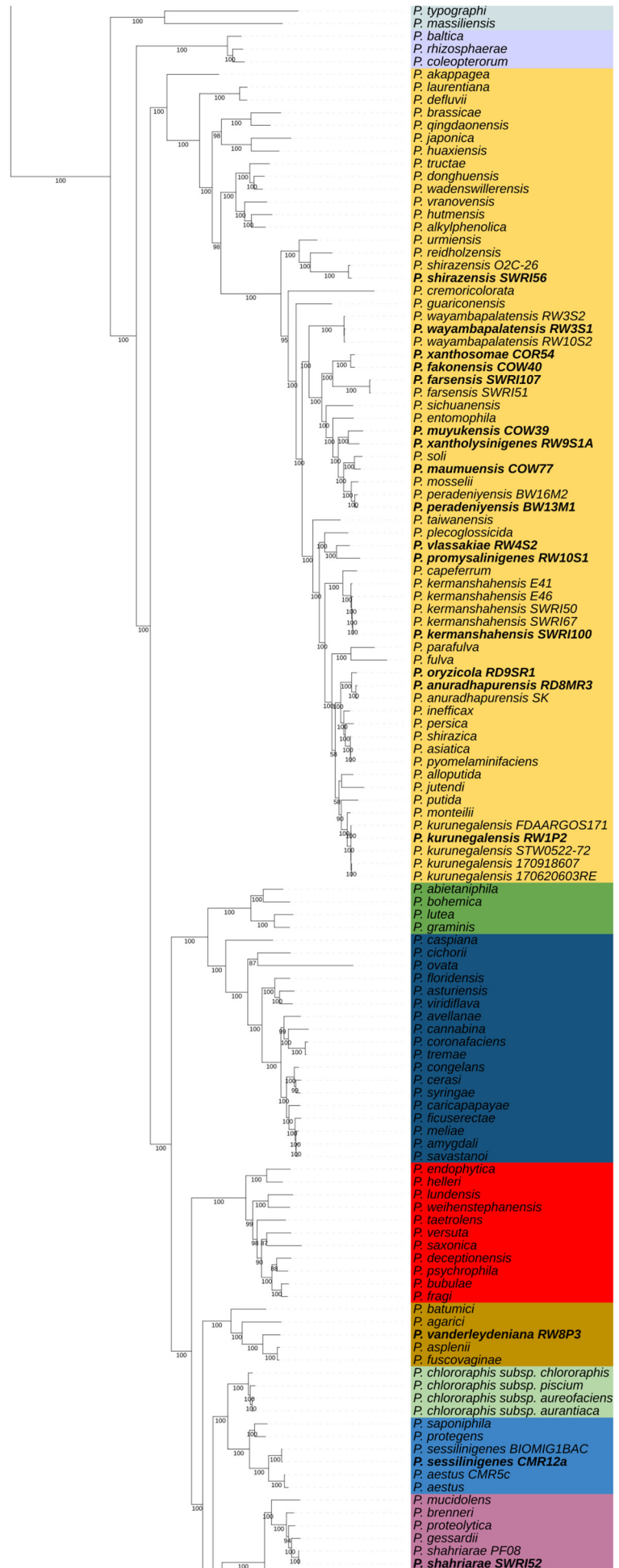
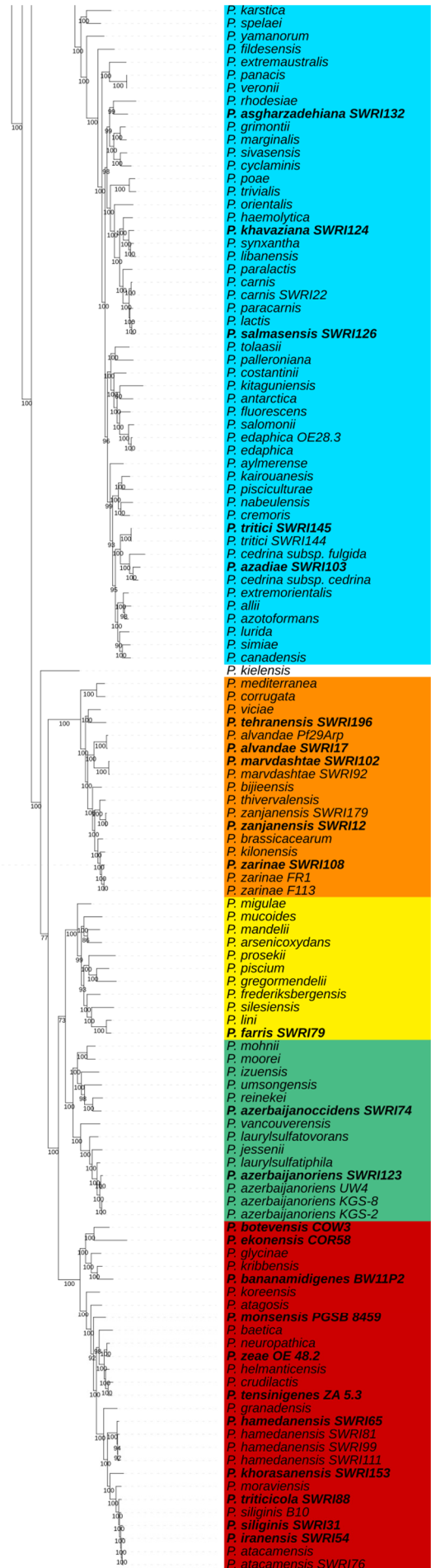


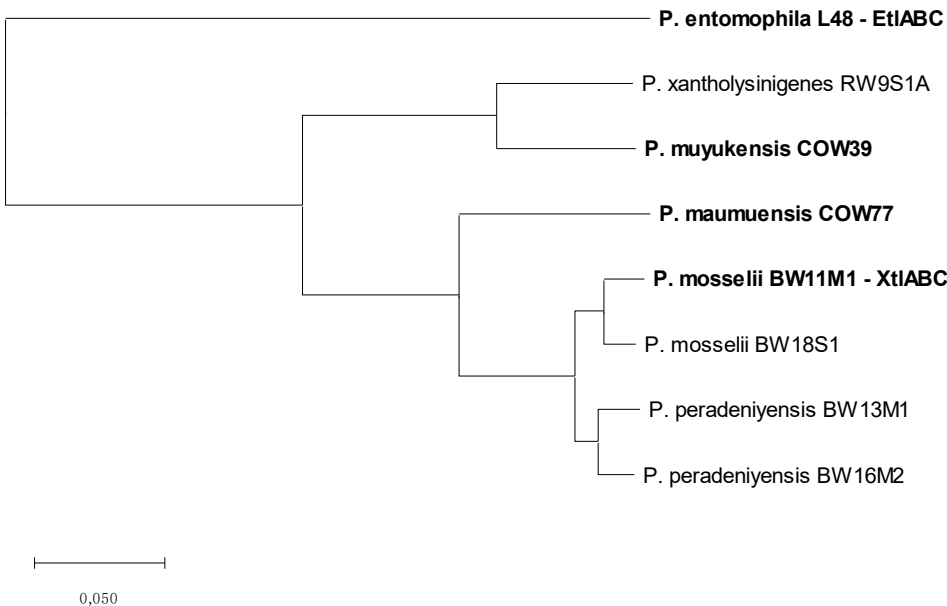
Tree scale: 0.1



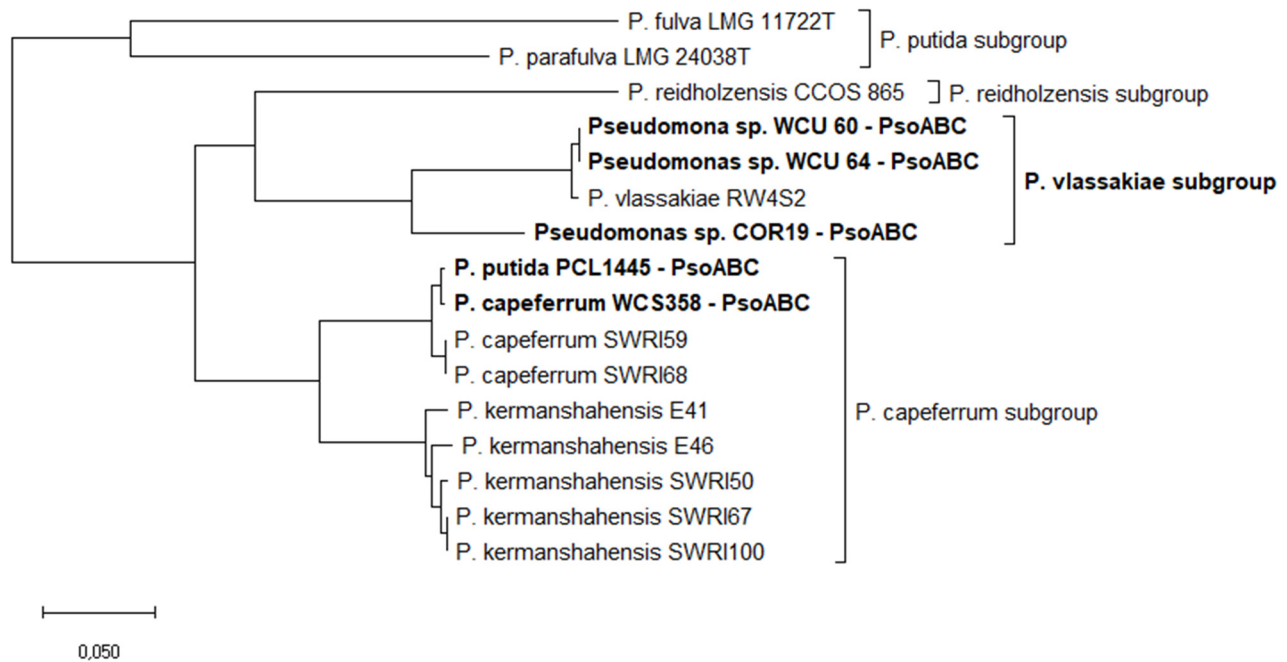




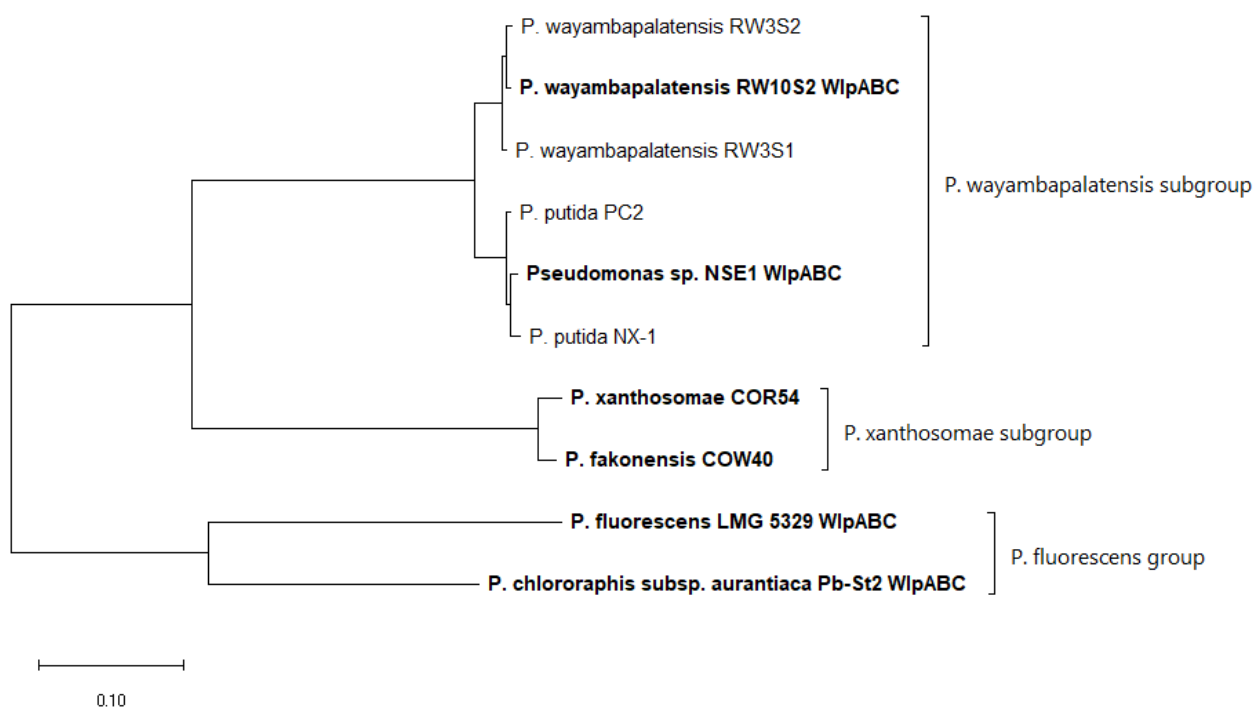
**Figure S1.** Genome-based phylogeny of the *Pseudomonadaceae*. The phylogenetic tree was inferred using IQ-TREE with automatic model selection and 1,000 ultrafast bootstrap based on an alignment of 1,063 core orthogroup from the 272 *Pseudomonas* species (270 + *P. hussainii* and *P. caeni*/*Thiopseudomonas caeni*), the type strains of the newly described species and affiliated strains (n=76; Table S5) and type strains of other genera within the *Pseudomonadaceae* (n=9; Table S1). Newly described species are highlighted in bold. *Cellvibrio japonicus* is used as outgroup.



**Figure S2.** Phylogenetic tree based on concatenated NRPS proteins from the Xantholysin and Entolysin families. The maximum likelihood tree was constructed using the JTT+F+I+G model (MEGA-X). Characterized producers are highlighted in bold (Table S6). All Xantholysin and Entolysin producers belongs to the *P. mosselii* subgroup.

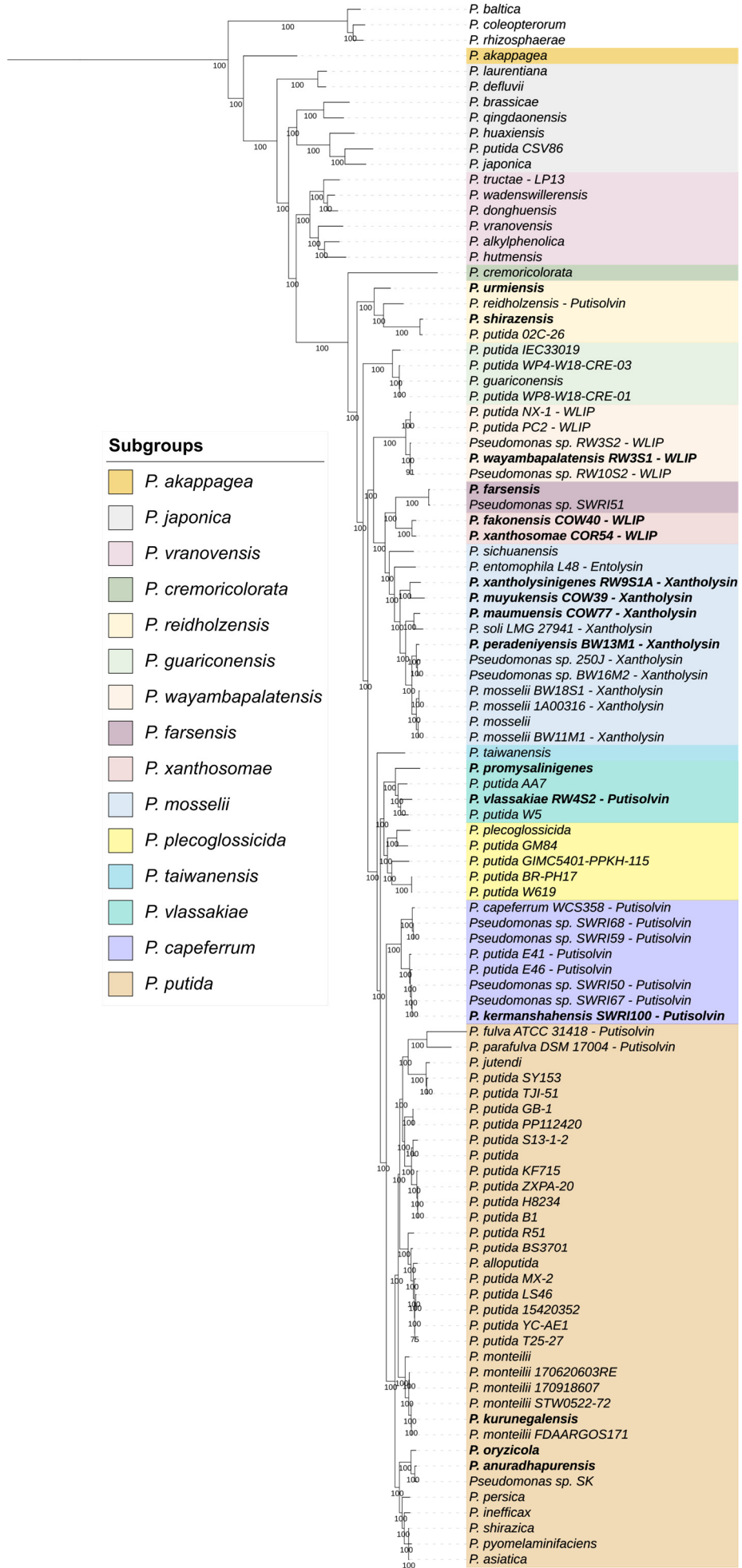


**Figure S3.** Phylogenetic tree based on concatenated NRPS proteins from the Putisolvin family. Maximum likelihood tree constructed using the JTT+F+I+G model (MEGA-X). Characterized producers are highlighted in bold (Table S6).



**Figure S4.** Phylogenetic tree based on concatenated NRPS proteins of WLIP producers from the Viscosin family. Maximum likelihood tree constructed using the JTT+F+I+G model (MEGA-X). Characterized producers are highlighted in bold (Table S6). NRPSs accession number for producers belonging to the *P. fluorescens* group: *P. fluorescens* LMG 5329 (WlpA AFZ61501; WlpB AFZ61525; WlpC AFZ61526) and *P. chlororaphis* subsp. *aurantiaca* Pb-St2 (WlpA AZD30270; WlpB AZD30268; WlpC AZD30267).

Tree scale: 0.1



**Figure S5.** Genome-based phylogeny of the *P. putida* group. The phylogenetic tree was inferred using IQ-TREE with automatic model selection (LG+F+R10) and 1,000 ultrafast bootstraps, based on an alignment of 2,570 orthogroups from 97 *Pseudomonas* strains (accession numbers Table S6). All strains included in this analysis, together with their accession numbers and the output of the prospection for CLP BGC are detailed in Table S6. Newly described species are highlighted in bold. The *P. rhizosphaerae* group are used as outgroup.