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<b>Title</b>	Comparative genomic analysis reveals a diverse repertoire of genes involved in prokaryote-eukaryote interactions within the Pseudovibrio Genus
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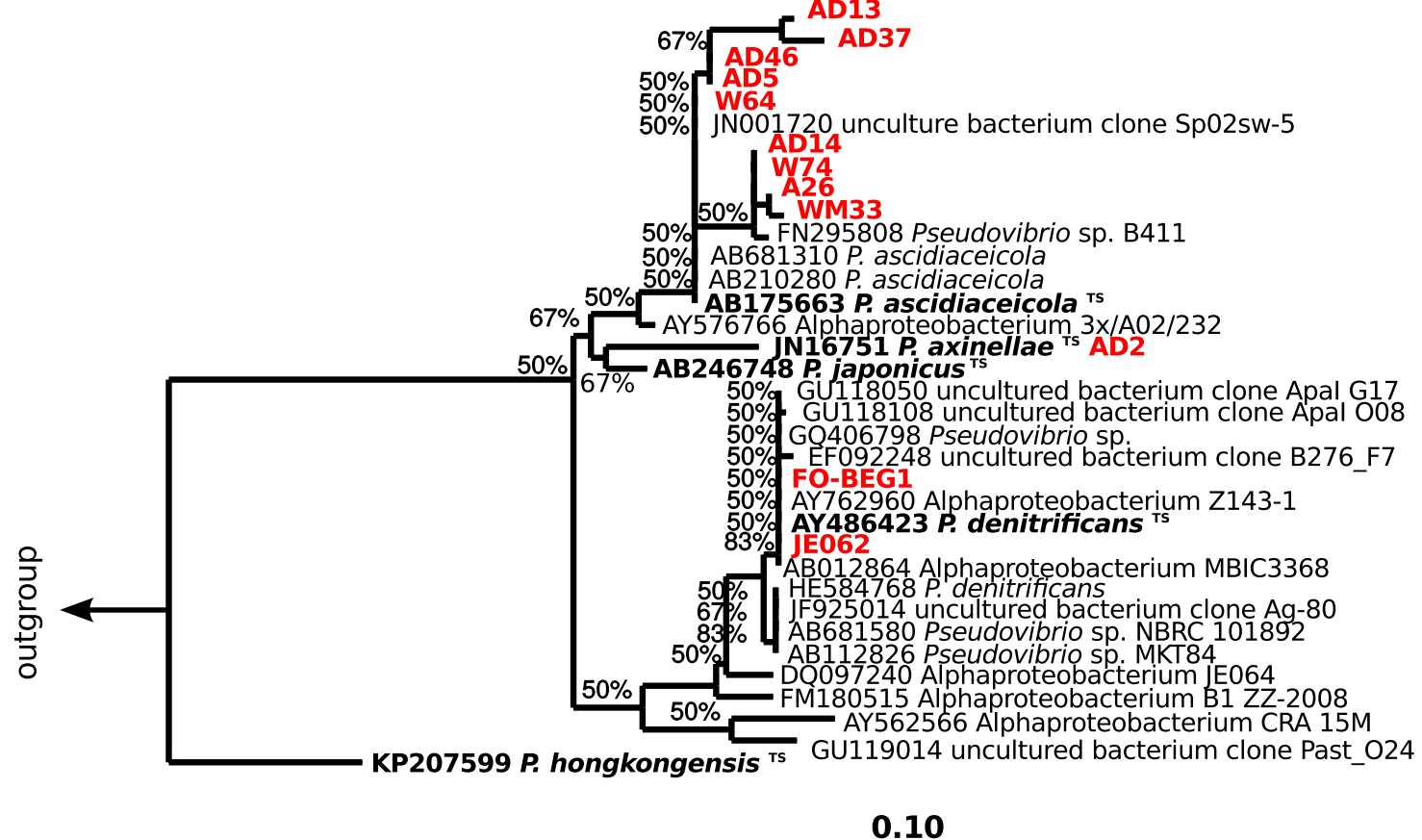
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**Figure S1** 16S rRNA genes phylogenetic analysis. Consensus phylogenetic tree constructed using the 16S rRNA genes of *Pseudovibrio* related bacteria. The values at the nodes indicate the bootstrap obtained during the reconstruction of the consensus tree performed with the build-in function in the ARB program. Strains investigated in the present work are indicated in bold red. Type stains are reported in bold black with the superscript "TS"