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Title	Comparative genomic analysis reveals a diverse repertoire of genes involved in prokaryote-eukaryote interactions within the Pseudovibrio Genus
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Publication date	2016-03-30
Original Citation	Romano, S., Fernàndez-Guerra, A., Reen, F. J., Glöckner, F. O., Crowley, S. P., O'Sullivan, O., Cotter, P. D., Adams, C., Dobson, A. D. W. and O'Gara, F. (2016) 'Comparative genomic analysis reveals a diverse repertoire of genes involved in prokaryote-eukaryote interactions within the Pseudovibrio Genus', Frontiers in Microbiology, 7, 387 (20pp.). doi: 10.3389/fmicb.2016.00387
Type of publication	Article (peer-reviewed)
Link to publisher's version	http://journal.frontiersin.org/article/10.3389/fmicb.2016.00387/full - 10.3389/fmicb.2016.00387
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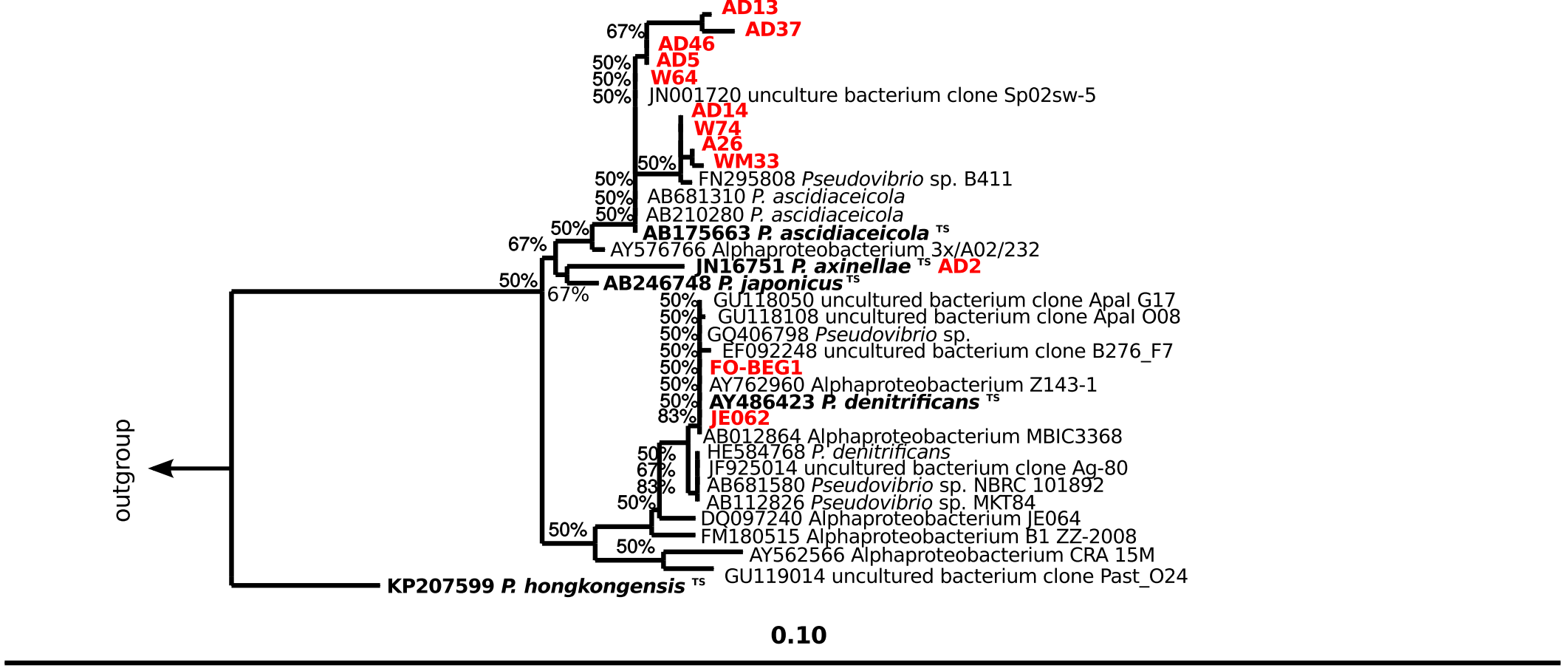


Figure S1 16S rRNA genes phylogenetic analysis. Consensus phylogenetic tree constructed using the 16S rRNA genes of *Pseudovibrio* related bacteria. The values at the nodes indicate the bootstrap obtained during the reconstruction of the consensus tree performed with the build-in function in the ARB program. Strains investigated in the present work are indicated in bold red. Type stains are reported in bold black with the superscript "TS"