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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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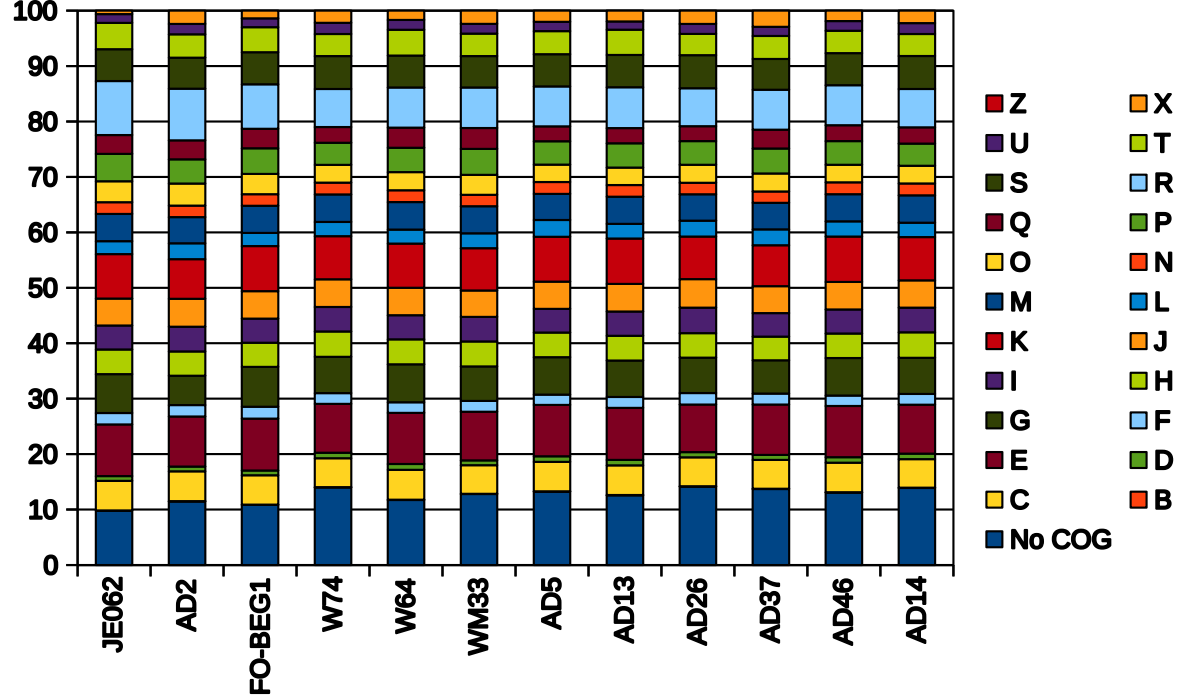


Figure S2 Distribution of the protein-coding genes of the 12 *Pseudovibrio* genomes amongst the COG. J: Translation, ribosomal structure and biogenesis ; K: Transcription; L: Replication, recombination and repair; B: Chromatin structure and dynamics; D: Cell cycle control, cell division, chromosome partitioning; T: Signal transduction mechanisms; M: Cell wall/membrane/envelope biogenesis ; N: Cell motility; Z: Cytoskeleton; U: Intracellular trafficking, secretion, and vesicular transport ; O: Posttranslational modification, protein turnover, chaperones; X: Mobilome: prophages, transposons; C: Energy production and conversion; G: Carbohydrate transport and metabolism; E: Amino acid transport and metabolism; F: Nucleotide transport and metabolism; H: Coenzyme transport and metabolism ; I: Lipid transport and metabolism; P: Inorganic ion transport and metabolism ; Q: Secondary metabolites biosynthesis, transport and catabolism; R: General function prediction only ; S: Function unknown; No COG: proteins not assigned to COG.