Supplementary Tables

Tab S1. Gene enrichment analyses performed for each *Pseudovibrio* genome and for specific subsets of genes.

Strain	**COG ID**	**COG annotation**	**P-value adjusted**	**Q-value**
JCM12308	COG3209	Uncharacterized conserved protein RhaS, contains 28 RHS repeats	5,26E-04	5,26E-04
NCIMB14279	COG1835	Peptidoglycan/LPS O-acetylase OafA/YrhL, contains acyltransferase and SGNH-hydrolase domains	2,87E-02	2,87E-02
P8H04	COG2376	Dihydroxyacetone kinase	1,54E-02	1,54E-02
PHSC04	COG3328	Transposase (or an inactivated derivative)	5,82E-29	5,82E-29
PHSC04	COG3436	Transposase	3,91E-27	3,91E-27
PHSC04	COG4584	Transposase	5,08E-22	5,08E-22
PHSC04	COG2801	Transposase InsO and inactivated derivatives	1,98E-15	1,98E-15
PHSC04	COG3344	Retron-type reverse transcriptase	4,95E-15	4,95E-15
PHSC04	COG1961	Site-specific DNA recombinase related to the DNA invertase Pin	2,17E-06	2,17E-06
PHSC04	COG2826	Transposase and inactivated derivatives, IS30 family	3,37E-04	3,37E-04
PHSC04	COG2963	Transposase and inactivated derivatives	1,76E-03	1,76E-03
PHSC04	COG3316	Transposase (or an inactivated derivative)	2,64E-03	2,64E-03
PHSC04	COG1020	Non-ribosomal peptide synthetase component F	2,05E-02	2,05E-02
Missing in Psty/Phong				

	COG ID	**COG annotation**	**P-value adjusted**	**Q-value**
	COG0477	MFS family permease	1,06E-03	8,08E-04
	COG1028	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family	3,15E-03	2,40E-03
	COG1960	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	4,28E-03	3,27E-03
	COG1309	DNA-binding transcriptional regulator, AcrR family	4,28E-03	3,27E-03
	COG1024	Enoyl-CoA hydratase/carnithine racemase	9,65E-03	7,37E-03
	COG1018	Ferredoxin-NADP reductase	1,11E-02	8,46E-03
	COG3791	Uncharacterized conserved protein	1,53E-02	1,17E-02
	COG1670	Protein N-acetyltransferase, RimJ/RimL family	2,57E-02	1,96E-02

	COG0840	Methyl-accepting chemotaxis protein	3,07E-02	2,34E-02
Unique in *P. stylochi*				
	COG ID	**COG annotation**	**P-value adjusted**	**Q-value**
	COG0840	Methyl-accepting chemotaxis protein	1,88E-04	1,68E-04
	COG0642	Signal transduction histidine kinase	2,29E-02	2,04E-02
	COG1807	4-amino-4-deoxy-L-arabinose transferase or related glycosyltransferase of PMT family	2,29E-02	2,04E-02
	COG2186	DNA-binding transcriptional regulator, FadR family	2,43E-02	2,17E-02
Unique in *P. hongkongensis*				
	COG ID	**COG annotation**	**P-value adjusted**	**Q-value**
	COG0457	Tetratricopeptide (TPR) repeat	2,71E-03	2,48E-03
	COG0840	Methyl-accepting chemotaxis protein	2,71E-03	2,48E-03
Unique in PHSC04				
	COG ID	**COG annotation**	**P-value adjusted**	**Q-value**
	COG3316	Transposase (or an inactivated derivative)	9,14E-03	9,00E-03
	COG2801	Transposase InsO and inactivated derivatives	9,14E-03	9,00E-03
Strain	**KEGG ID**	**KEGG annotation**	**P-value adjusted**	**Q-value**
P3C10	K06871	uncharacterized protein	1,30E-03	1,30E-03
DSM24994	K07498	putative transposase	7,74E-06	7,74E-06
P8H04	K07498	putative transposase	2,11E-04	2,11E-04
PHSC04	K07484	transposase	2,63E-61	2,63E-61
PHSC04	K07483	transposase	8,74E-22	8,74E-22
PHSC04	K07498	putative transposase	1,44E-15	1,44E-15
PHSC04	K00986	RNA-directed DNA polymerase	7,86E-14	7,86E-14
PHSC04	K06223	DNA adenine methylase	1,34E-05	1,34E-05
PHSC04	K07494	putative transposase	3,07E-02	3,07E-02

Phong	K07498	putative transposase	3,34E-02	3,34E-02
Missing in Psty/Phong				
	KEGG ID	**KEGG annotation**	**P-value adjusted**	**Q-value**
	K00249	acyl-CoA dehydrogenase	4,49E-02	4,48E-02
Unique in *P. stylochi*				
	KEGG ID	**KEGG annotation**	**P-value adjusted**	**Q-value**
	K03406	methyl-accepting chemotaxis protein	7,83E-07	7,57E-07
	K05799	GntR family transcriptional regulator, transcriptional repressor for pyruvate dehydrogenase complex	4,34E-02	4,19E-02
Unique in *P. hongkongensis*				
	KEGG ID	**KEGG annotation**	**P-value adjusted**	**Q-value**
	K03406	methyl-accepting chemotaxis protein	7,40E-03	6,98E-03
	K02015	iron complex transport system permease protein	7,40E-03	6,98E-03
Unique in PHSC04				
	KEGG ID	**KEGG annotation**	**P-value adjusted**	**Q-value**
	K07498	putative transposase	4,81E-10	3,99E-10
	K07484	transposase	6,09E-05	5,06E-05
	K07497	putative transposase	6,69E-05	5,56E-05
	K06223	DNA adenine methylase	6,69E-05	5,56E-05
	K07482	transposase, IS30 family	5,01E-03	4,17E-03
	K07483	transposase	1,23E-02	1,02E-02
	K07265	capsular polysaccharide export protein	1,48E-02	1,23E-02

Tab S2. Number of the genes in clade A strains, missing in clade B strains that have been identified as horizontal gene transfer candidates (HGT)* or on mobile genetic elements (MGE). Columns show genes missing from clade B strains but present in all clade A strains and those present in 95% of clade A strains. Percentage of gene counts is shown in brackets.

	clade A-only genes	95% clade A-only genes
Total	136,297	59,486
HGT candidates*	3,095 (2.3%)	887 (1.5%)
Located on MGEs	17,253 (12.7%)	1,662 (2.8%)

* identified by their di-nucleotide signatures

Tab S3. KEGG modules identified in the genes missing in strains belonging to clade B but detected in ≥ 95% of the remaining *Pseudovibrio* strains.

Module Reconstruction Result

Show all objects

Pathway module

Carbohydrate metabolism

Central carbohydrate metabolism

M00307 Pyruvate oxidation, pyruvate => acetyl-CoA [PATH:map00010 map00020 map00620 map01200 map01100] (1) (1 block missing)

M00010 Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate [PATH:map00020 map01200 map01210 map01230 map01100] (2) (1 block missing)

Other carbohydrate metabolism

M00741 Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA [PATH:map00280 map00630 map00640 map01200 map01100] (1) (2 blocks missing)

Energy metabolism

Methane metabolism

M00345 Formaldehyde assimilation, ribulose monophosphate pathway [PATH:map00030 map00680 map01200 map01230 map01120] (1) (2 blocks missing)

M00378 F420 biosynthesis [PATH:map00680 map01120] (5) (complete)

Nitrogen metabolism

M00530 Dissimilatory nitrate reduction, nitrate => ammonia [PATH:map00910 map01120] (3) (1 block missing)

M00529 Denitrification, nitrate => nitrogen [PATH:map00910 map01120] (4) (2 blocks missing)

M00804 Complete nitrification, comammox, ammonia => nitrite => nitrate [PATH:map00910 map01120] (2) (2 blocks missing)

Sulfur metabolism

M00595 Thiosulfate oxidation by SOX complex, thiosulfate => sulfate [PATH:map00920 map01100 map01120] (7) (complete)

Lipid metabolism

Fatty acid biosynthesis and degradation

M00082 Fatty acid biosynthesis, initiation [PATH:map00061 map01212 map01100] (1) (2 blocks missing)

M00083 Fatty acid biosynthesis, elongation [PATH:map00061 map01212 map01100] (3) (1 block missing)

M00086 beta-Oxidation, acyl-CoA synthesis [PATH:map00061 map00071 map01212 map01100] (1) (complete)

M00087 beta-Oxidation [PATH:map00071 map01212 map01100] (7) (1 block missing)

Lipid metabolism

M00093 Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE [PATH:map00564 map01100] (1) (2 blocks missing)

Nucleotide metabolism

Pyrimidine metabolism

M00046 Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate [PATH:map00240 map01100] (2) (1 block missing)

Amino acid metabolism

Serine and threonine metabolism

M00555 Betaine biosynthesis, choline => betaine [PATH:map00260 map01100] (1) (1 block missing)

Arginine and proline metabolism

M00844 Arginine biosynthesis, ornithine => arginine [PATH:map00220 map01230 map01100] (2) (1 block missing)

Polyamine biosynthesis

M00135 GABA biosynthesis, eukaryotes, putrescine => GABA [PATH:map00330 map01100] (1) (2 blocks missing)

Histidine metabolism

M00045 Histidine degradation, histidine => N-formiminoglutamate => glutamate [PATH:map00340 map01100] (5) (complete)

Aromatic amino acid metabolism

M00024 Phenylalanine biosynthesis, chorismate => phenylalanine [PATH:map00400 map01230 map01100 map01110] (1) (2 blocks missing)

Other amino acid metabolism

M00027 GABA (gamma-Aminobutyrate) shunt [PATH:map00250 map00650 map01100] (2) (1 block missing)

Metabolism of cofactors and vitamins

Cofactor and vitamin metabolism

M00123 Biotin biosynthesis, pimeloyl-ACP/CoA => biotin [PATH:map00780 map01100] (4) (complete)

M00573 Biotin biosynthesis, BioI pathway, long-chain-acyl-ACP => pimeloyl-ACP => biotin [PATH:map00780 map01100] (4) (1 block missing)

M00577 Biotin biosynthesis, BioW pathway, pimelate => pimeloyl-CoA => biotin [PATH:map00780 map01100] (4) (1 block missing)

M00842 Tetrahydrobiopterin biosynthesis, GTP => BH4 [PATH:map00790 map01100] (1) (2 blocks missing)

M00843 L-threo-Tetrahydrobiopterin biosynthesis, GTP => L-threo-BH4 [PATH:map00790 map01100] (1) (2 blocks missing)

M00140 C1-unit interconversion, prokaryotes [PATH:map00670 map01100] (1) (2 blocks missing)

Structural complex

Energy metabolism

ATP synthesis

M00144 NADH:quinone oxidoreductase, prokaryotes [PATH:map00190] (1) (1 block missing)

M00417 Cytochrome o ubiquinol oxidase [PATH:map00190] (4) (complete)

Genetic information processing

Ribosome

M00178 Ribosome, bacteria [PATH:map03010] [BR:ko03011] (1) (1 block missing)

Environmental information processing

Mineral and organic ion transport system

M00189 Molybdate transport system [PATH:map02010] [BR:ko02000] (3) (complete)

M00435 Taurine transport system [PATH:map02010] [BR:ko02000] (3) (complete)

M00190 Iron(III) transport system [PATH:map02010] [BR:ko02000] (6) (complete)

M00191 Thiamine transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00299 Spermidine/putrescine transport system [PATH:map02010] [BR:ko02000] (4) (complete)

M00300 Putrescine transport system [PATH:map02010] [BR:ko02000] (4) (complete)

Saccharide, polyol, and lipid transport system

M00194 Maltose/maltodextrin transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00196 Multiple sugar transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00201 alpha-Glucoside transport system [PATH:map02010] [BR:ko02000] (2) (complete)

M00605 Glucose/mannose transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00206 Cellobiose transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00606 N,N'-Diacetylchitobiose transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00212 Ribose transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00197 Putative fructooligosaccharide transport system [BR:ko02000] (2) (1 block missing)

M00607 Glycerol transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00198 Putative sn-glycerol-phosphate transport system [PATH:map02010] [BR:ko02000] (4) (complete)

M00200 Putative sorbitol/mannitol transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00602 Arabinosaccharide transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00669 gamma-Hexachlorocyclohexane transport system [BR:ko02000] (1) (1 block missing)

M00210 Phospholipid transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00670 Mce transport system [BR:ko02000] (1) (1 block missing)

M00491 arabinogalactan oligomer/maltooligosaccharide transport system [PATH:map02010] [BR:ko02000] (2) (1 block missing)

M00207 Putative multiple sugar transport system [BR:ko02000] (8) (complete)

M00221 Putative simple sugar transport system [BR:ko02000] (5) (complete)

M00211 Putative ABC transport system [BR:ko02000] (1) (1 block missing)

Phosphate and amino acid transport system

M00222 Phosphate transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00237 Branched-chain amino acid transport system [PATH:map02010] [BR:ko02000] (13) (complete)

M00236 Putative polar amino acid transport system [BR:ko02000] (1) (1 block missing)

Peptide and nickel transport system

M00239 Peptides/nickel transport system [PATH:map02010] [BR:ko02000] (15) (complete)

Metallic cation, iron-siderophore and vitamin B12 transport system

M00240 Iron complex transport system [PATH:map02010] [BR:ko02000] (5) (complete)

M00242 Zinc transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00581 Biotin transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00582 Energy-coupling factor transport system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

ABC-2 type and other transport systems

M00762 Copper-processing system [PATH:map02010] [BR:ko02000] (1) (1 block missing)

M00258 Putative ABC transport system [BR:ko02000] (2) (complete)

M00254 ABC-2 type transport system [BR:ko02000] (1) (1 block missing)

Bacterial secretion system

M00330 Adhesin protein transport system [BR:ko02044] (5) (complete)

M00429 Competence-related DNA transformation transporter [BR:ko02044] (1) (1 block missing)

Functional set

Environmental information processing

Two-component regulatory system

M00445 EnvZ-OmpR (osmotic stress response) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

M00453 QseC-QseB (quorum sensing) two-component regulatory system [PATH:map02020] [BR:ko02022] (2) (complete)

M00504 DctB-DctD (C4-dicarboxylate transport) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

M00517 RpfC-RpfG (cell-to-cell signaling) two-component regulatory system [PATH:map02020] [BR:ko02022] (1) (1 block missing)

Drug efflux transporter/pump

M00647 Multidrug resistance, efflux pump AcrAB-TolC/SmeDEF (2) (2 blocks missing)

M00699 Multidrug resistance, efflux pump AmeABC (2) (2 blocks missing)

Drug resistance

M00742 Aminoglycoside resistance, protease FtsH (1) (2 blocks missing)

M00743 Aminoglycoside resistance, protease HtpX (1) (2 blocks missing)

M00729 Fluoroquinolone resistance, gyrase-protecting protein Qnr (1) (2 blocks missing)

Cell signaling

M00695 cAMP signaling [PATH:map04024] (4) (2 blocks missing)

Signature module

Gene set

Drug resistance

M00718 Multidrug resistance, efflux pump MexAB-OprM (2) (2 blocks missing)

Module set

Metabolic capacity

M00615 Nitrate assimilation (2) (1 block missing)

Tab S4. Environmental distribution of the *Pseudovibrio* genus based on 16S rRNA gene amplicon datasets. 16S rRNA sequences of 8 strains were queried against raw 16S rRNA gene amplicon data from 422,880 metagenomic samples as accessed by the IMNGS platform[1]. Samples with zero relative abundances for all strains as well as samples with only 1 sequence count over all strains were excluded from the table. Colors correspond to isolation source.

Run	**BioProject**	**BioSample**	**Isolation Source**	**Description**	**P4B07**	***P.denitri-ficans***	***P.axinellae***	***P.ascidia-ceicola***	***P.japon-icus***	***P.hongkong-ensis***	***P.stylochi***
SRR2040958	PRJNA284506	SAMN03731496	aquarium water		0	0	0	0	0	0.19	0.095
SRR2040959	PRJNA284506	SAMN03731497	aquarium water		0	0	0	0	0	0.218	0.109
SRR2041111	PRJNA284506	SAMN03731628	aquarium water		0	0	0	0	0	0.167	0.083
SRR2041124	PRJNA284506	SAMN03731640	aquarium water		0	1.485	0	0	0	0	0
SRR2041127	PRJNA284506	SAMN03731643	aquarium water		0	0	0	0	0	0	0.084
SRR2041129	PRJNA284506	SAMN03731644	aquarium water		0	0.544	0	0	0	0	0
SRR2041157	PRJNA284506	SAMN03731652	aquarium water		0	0.245	0	0	0	0	0
SRR2041159	PRJNA284506	SAMN03731653	aquarium water		0	0.183	0	0	0	0.11	0.055
SRR2041161	PRJNA284506	SAMN03731654	aquarium water		0	0.302	0	0	0	0	0
SRR584302		SAMN01760520	aquarium water		0	0.053	0	0	0	0	0
SRR584313		SAMN01760531	aquarium water		0	0.051	0	0	0	0	0
SRR584321		SAMN01760539	aquarium water		0	0.047	0	0	0	0	0
ERR951498	PRJEB9766	SAMEA3753223	coral	*Lophelia pertusa* mucus	0.416	0	0	0.416	0	0	0
SRR1791581	PRJNA274309	SAMN03329635	coral		0	0.164	0	0	0	0	0

SRR1791583	PRJNA274309	SAMN03329637	coral		0	0.205	0	0	0	0	0
SRR1791586	PRJNA274309	SAMN03329639	coral		0	1.442	0	0.801	0	0	0
SRR1812952	PRJNA275249	SAMN03344620	coral		0	0.048	0	0	0	0	0
SRR1812962	PRJNA275249	SAMN03344621	coral		0	0.032	0	0	0	0	0
SRR1813077	PRJNA275249	SAMN03344648	coral		0	0.004	0	0	0	0	0
SRR1813114	PRJNA275249	SAMN03344670	coral		0	0.007	0	0	0	0	0
SRR1813679	PRJNA275249	SAMN03344687	coral		0	0.013	0	0	0	0	0
SRR1818601	PRJNA275249	SAMN03353475	coral		0	0.266	0	0	0	0	0
SRR1819186	PRJNA275249	SAMN03353547	coral		0	0	0	0	0	0	0.075
SRR1819637	PRJNA275249	SAMN03353555	coral		0	0.041	0	0	0	0	0
SRR1819653	PRJNA275249	SAMN03353572	coral		0	0.085	0	0	0	0	0
SRR1992897	PRJNA280923	SAMN03480770	coral		0	1.922	0	0	0	0	0
SRR1992903	PRJNA280923	SAMN03480776	coral		0	0.013	0	0	0	0	0
SRR1992926	PRJNA280923	SAMN03480799	coral		0	26.248	0	0	0	0	0
SRR1992927	PRJNA280923	SAMN03480800	coral		0	25.592	0	0	0	0	0
SRR1992939	PRJNA280923	SAMN03480812	coral		0	0.004	0	0	0	0	0
SRR1992963	PRJNA280923	SAMN03480836	coral		0	0.114	0	0	0	0	0
SRR1992967	PRJNA280923	SAMN03480840	coral		0	0.055	0	0	0	0	0
SRR1993007	PRJNA280923	SAMN03480880	coral		0	0.004	0	0	0	0	0
SRR1993013	PRJNA280923	SAMN03480886	coral		0	0.018	0	0	0	0	0
SRR1993015	PRJNA280923	SAMN03480888	coral		0	0.008	0	0	0	0	0
SRR1993021	PRJNA280923	SAMN03480894	coral		0	0.033	0	0	0	0	0
SRR3145836	PRJNA310360	SAMN04451934	coral		0	0.073	0	0	0	0	0
SRR3145913	PRJNA310360	SAMN04451994	coral		0	0.134	0	0	0	0	0
SRR3145932	PRJNA310360	SAMN04452012	coral		0	0	0.013	0	0.013	0	0
SRR3184449	PRJNA312300	SAMN04497664	coral		0	0	0	0	0	0	0.009
SRR3184451	PRJNA312300	SAMN04497666	coral		0	0.018	0	0	0	0	0
SRR3184475	PRJNA312300	SAMN04497690	coral		0	0	0	0	0	0.082	0.041

SRR3204409	PRJNA313192	SAMN04531901	coral		0	0	0	0	0	0.168	0.084
SRR3204411	PRJNA313192	SAMN04531911	coral		0	1.056	0	0	0	0	0
SRR3204412	PRJNA313192	SAMN04531912	coral		0	0.068	0	0	0	0	0
SRR3204414	PRJNA313192	SAMN04531914	coral		0	0.125	0	0	0	0	0
SRR3204415	PRJNA313192	SAMN04531915	coral		0	0.009	0	0	0	0	0
SRR3204416	PRJNA313192	SAMN04531916	coral		0	0.449	0	0	0	0	0
SRR3204419	PRJNA313192	SAMN04531919	coral		0	0	0	0	0	0.144	0.072
SRR3204432	PRJNA313192	SAMN04531930	coral		0	0.109	0	0	0	0	0
SRR3204434	PRJNA313192	SAMN04531932	coral		0	1.264	0	0	0	0	0
SRR3204454	PRJNA313192	SAMN04531950	coral		0	0.486	0	0	0	0	0
SRR3204455	PRJNA313192	SAMN04531951	coral		0	0.579	0	0	0	0	0
SRR3204456	PRJNA313192	SAMN04531952	coral		0	0.014	0	0	0	0	0
SRR3204473	PRJNA313192	SAMN04531968	coral		0	0.162	0	0	0	0	0
SRR3204476	PRJNA313192	SAMN04531970	coral		0	0.163	0	0	0	0	0
SRR3204477	PRJNA313192	SAMN04531971	coral		0	0.907	0	0	0	0	0
SRR3204478	PRJNA313192	SAMN04531972	coral		0	0.681	0	0	0	0	0
SRR4471363	PRJNA350361	SAMN05938545	coral	seawater	0	0.049	0	0	0	0	0
SRR4471383	PRJNA350361	SAMN05938552	coral	seawater	0	9.292	0	0	0	0	0
SRR4471384	PRJNA350361	SAMN05938559	coral	seawater	0	0.032	0	0	0	0	0
SRR4471385	PRJNA350361	SAMN05938555	coral	seawater	0	0.023	0	0	0	0	0
SRR5437923	PRJNA382610	SAMN06711101	coral	*Agaricia undata*	0	0.013	0	0	0	0	0
SRR5437929	PRJNA382610	SAMN06711095	coral	*Agaricia undata*	0	0.022	0	0	0	0	0
SRR5447849	PRJNA382809	SAMN06733055	coral	seawater	0	0.018	0	0	0	0	0
SRR5970173	PRJNA393088	SAMN07315126	coral		0	0.428	0	0	0	0	0
SRR7541461	PRJNA481946	SAMN09692599	coral		0.028	0	0	0.028	0.028	0	0
SRR7541462	PRJNA481946	SAMN09692600	coral		0.024	0	0	0.024	0.024	0	0
SRR7541483	PRJNA481946	SAMN09692584	coral		0.068	0	0	0.068	0.068	0	0

SRR7541488	PRJNA481946	SAMN09692587	coral		0.064	0	0	0.064	0.064	0	0
SRR7541512	PRJNA481946	SAMN09692641	coral		0.038	0	0	0	0.038	0	0
SRR7541529	PRJNA481946	SAMN09692624	coral		0.011	0	0	0	0	0	0
SRR7541531	PRJNA481946	SAMN09692622	coral		0.011	0	0	0	0.011	0	0
SRR7541534	PRJNA481946	SAMN09692629	coral		0.099	0	0	0.099	0.099	0	0
SRR7541538	PRJNA481946	SAMN09692614	coral		0.034	0	0	0.034	0.034	0	0
SRR7541542	PRJNA481946	SAMN09692618	coral		0.012	0	0	0.012	0.012	0	0
SRR7541545	PRJNA481946	SAMN09692610	coral		0.005	0	0	0.005	0.005	0	0
SRR7541548	PRJNA481946	SAMN09692605	coral		0	0.021	0	0	0	0	0
SRR7541551	PRJNA481946	SAMN09692602	coral		0.028	0	0	0.028	0.028	0	0
SRR7541553	PRJNA481946	SAMN09692604	coral		3.423	0	0	3.423	3.423	0	0
SRR7598225	PRJNA482722	SAMN09711476	coral		0	2.288	0	0	0	0	0
SRR7598226	PRJNA482722	SAMN09711432	coral		0	20.039	0	0	0	0	0
SRR7598233	PRJNA482722	SAMN09711426	coral		0	10.31	0	0	0	0	0
SRR7598235	PRJNA482722	SAMN09711424	coral		0	12.408	0	0	0	0	0
SRR7598237	PRJNA482722	SAMN09711430	coral		0	13.875	0	0	0	0	0
SRR7598239	PRJNA482722	SAMN09711428	coral		0	22.796	0	0	0	0	0
SRR7598241	PRJNA482722	SAMN09711475	coral		0	1.156	0	0	0	0	0
SRR7598247	PRJNA482722	SAMN09711444	coral		0	0.499	0	0	0	0	0
SRR7598267	PRJNA482722	SAMN09711472	coral		0	6.865	0	0	0	0	0
SRR7598268	PRJNA482722	SAMN09711474	coral		0	3.062	0	0	0	0	0
SRR7598269	PRJNA482722	SAMN09711473	coral		0	12.404	0	0	0	0	0
SRR7598270	PRJNA482722	SAMN09711478	coral		0	5.75	0	0	0	0	0
SRR7598274	PRJNA482722	SAMN09711481	coral		0	3.807	0	0	0	0	0
SRR7598276	PRJNA482722	SAMN09711477	coral		0	3.192	0	0	0	0	0
SRR7598277	PRJNA482722	SAMN09711466	coral		0	0.079	0	0	0	0	0
SRR7598279	PRJNA482722	SAMN09711434	coral		0	11.953	0	0	0	0	0

SRR8243359	PRJNA506563	SAMN10462717	coral		0	0.145	0	0	0	0	0
SRR3708167	PRJNA326427	SAMN05277842	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.294	0.147
SRR3708170	PRJNA326427	SAMN05277843	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.17	0.085
SRR3708179	PRJNA326427	SAMN05277844	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.295	0.148
SRR3708282	PRJNA326427	SAMN05277845	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.162	0.081
SRR3708283	PRJNA326427	SAMN05277846	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.012	0.006
SRR3708284	PRJNA326427	SAMN05277847	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.172	0.086
SRR3708342	PRJNA326427	SAMN05277851	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0	0.005
SRR5280714	PRJNA376395	SAMN06435126	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0	0.015
SRR5280717	PRJNA376395	SAMN06435123	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	0.369	0.185
SRR5280718	PRJNA376395	SAMN06435122	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	1.65	0.825
SRR5280719	PRJNA376395	SAMN06435121	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	0.916	0.458
SRR5280720	PRJNA376395	SAMN06435120	echino-derm	sea urchin, *Lytechinus*	0	0	0	0	0	0.696	0.348

				variegatus feces							
SRR5280721	PRJNA376395	SAMN06435119	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	0.314	0.157
SRR5280722	PRJNA376395	SAMN06435118	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	0.077	0.039
SRR5280723	PRJNA376395	SAMN06435117	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	1.341	0.67
SRR5280724	PRJNA376395	SAMN06435116	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	0.457	0.229
SRR5280725	PRJNA376395	SAMN06435115	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	2.62	1.31
SRR5280726	PRJNA376395	SAMN06435114	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	3.29	1.645
SRR5280727	PRJNA376395	SAMN06435113	echino-derm	sea urchin, *Lytechinus variegatus* feces	0	0	0	0	0	2.892	1.446
SRR5280728	PRJNA376395	SAMN06435112	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.198	0.099
SRR5280734	PRJNA376395	SAMN06435106	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.062	0.031
SRR5280735	PRJNA376395	SAMN06435105	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.636	0.318

SRR5280736	PRJNA376395	SAMN06435104	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.031	0.016
SRR5280737	PRJNA376395	SAMN06435103	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0	0.003
SRR5280738	PRJNA376395	SAMN06435102	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.693	0.347
SRR5280739	PRJNA376395	SAMN06435101	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.208	0.104
SRR5280740	PRJNA376395	SAMN06435100	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.166	0.083
SRR5280741	PRJNA376395	SAMN06435099	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.204	0.102
SRR5280742	PRJNA376395	SAMN06435098	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	1.495	0.748
SRR5280749	PRJNA376395	SAMN06435091	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.004	0.002
SRR5280751	PRJNA376395	SAMN06435089	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.005	0.003
SRR5280753	PRJNA376395	SAMN06435087	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.535	0.267
SRR5280755	PRJNA376395	SAMN06435085	echino-derm	sea urchin, *Lytechinus variegatus*	0	0	0	0	0	0.002	0.001
SRR5468278	PRJNA383901	SAMN06819339	echino-derm	sea star	0	0	0	0	0	0.044	0.022
ERR2209755	PRJEB23513	SAMEA104410679	marine lichen		0.011	0	0	0.011	0	0	0
ERR2209764	PRJEB23513	SAMEA104410688	marine lichen		0.185	0	0.185	0.185	0	0	0
ERR2209765	PRJEB23513	SAMEA104410689	marine lichen		0.285	0	0	0.285	0.214	0	0

ERR2209766	PRJEB23513	SAMEA104410690	marine lichen		0.239	0	0	0.239	0.193	0	0
ERR2209768	PRJEB23513	SAMEA104410706	marine lichen		0.08	0	0	0.08	0	0	0
ERR2209769	PRJEB23513	SAMEA104410691	marine lichen		0	0	0	0	0.025	0	0
ERR2209770	PRJEB23513	SAMEA104410692	marine lichen		0.06	0	0	0.06	0	0	0
ERR2209771	PRJEB23513	SAMEA104410693	marine lichen		0	0	0	0	0.04	0	0
ERR2209772	PRJEB23513	SAMEA104410694	marine lichen		0	0	0	0	0.131	0	0
ERR2209773	PRJEB23513	SAMEA104410695	marine lichen		0.055	0	0	0.055	0.049	0	0
ERR2209774	PRJEB23513	SAMEA104410696	marine lichen		0.071	0	0	0.071	0	0	0
ERR2209775	PRJEB23513	SAMEA104410697	marine lichen		0.065	0	0	0.065	0	0	0
ERR2209776	PRJEB23513	SAMEA104410698	marine lichen		0.858	0	0	0.858	0.757	0	0
ERR2209779	PRJEB23513	SAMEA104410701	marine lichen		0.28	0	0.234	0.28	0.234	0	0
ERR2209781	PRJEB23513	SAMEA104410703	marine lichen		0.04	0	0	0.04	0	0	0
ERR2209782	PRJEB23513	SAMEA104410704	marine lichen		0.249	0	0	0.143	0.107	0	0
ERR2098464	PRJEB87662	SAMEA104212366	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098470	PRJEB87662	SAMEA104212374	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098471	PRJEB87662	SAMEA104212375	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098474	PRJEB87662	SAMEA104212378	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098476	PRJEB87662	SAMEA104212380	marine plankton	*in silico* sample	0.001	0	0	0.001	0.001	0	0
ERR2098481	PRJEB87662	SAMEA104212387	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098483	PRJEB87662	SAMEA104212389	marine plankton	*in silico* sample	0	0	0	0	0	0	0

ERR2098484	PRJEB87662	SAMEA104212390	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098525	PRJEB87662	SAMEA104212372	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098529	PRJEB87662	SAMEA104212376	marine plankton	*in silico* sample	0.001	0	0	0.001	0.001	0	0
ERR2098530	PRJEB87662	SAMEA104212377	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098531	PRJEB87662	SAMEA104212378	marine plankton	*in silico* sample	0	0	0.001	0	0	0	0
ERR2098535	PRJEB87662	SAMEA104212384	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR2098543	PRJEB87662	SAMEA104212392	marine plankton	*in silico* sample	0	0	0.001	0	0	0	0
ERR2098576	PRJEB87662	SAMEA104212366	marine plankton	*in silico* sample	0	0	0	0	0	0	0
ERR1679675	PRJEB15713	SAMEA4501368	mollusc	abalone	0.017	0	0	0.017	0	0	0
ERR1679689	PRJEB15713	SAMEA4501382	mollusc	abalone	0	0	0.007	0	0	0	0
ERR1679704	PRJEB15713	SAMEA4501397	mollusc	abalone	0.005	0	0	0.005	0	0	0
ERR1679721	PRJEB15713	SAMEA4501414	mollusc	abalone	0.006	0	0	0.006	0	0	0
SRR5620594	PRJNA386685	SAMN07169047	mollusc		0.009	0	0	0.009	0.009	0	0
SRR5620595	PRJNA386685	SAMN07169046	mollusc		0.005	0	0	0.005	0.005	0	0
SRR5620596	PRJNA386685	SAMN07169045	mollusc		0.022	0	0	0.022	0.022	0	0
SRR5620597	PRJNA386685	SAMN07169044	mollusc		0.02	0	0	0.02	0.02	0	0
SRR5620602	PRJNA386685	SAMN07169053	mollusc		0.004	0	0	0.004	0	0	0
SRR5620617	PRJNA386685	SAMN07169054	mollusc		0.005	0	0	0.005	0.005	0	0
SRR5620621	PRJNA386685	SAMN07169058	mollusc		0.026	0	0	0.026	0.026	0	0
SRR6434179	PRJNA428215	SAMN07205150	mollusc		0.006	0	0	0	0	0	0
SRR6434191	PRJNA428215	SAMN07204621	mollusc		0.031	0	0.031	0.031	0	0	0
SRR7244762	PRJNA474068	SAMN09291245	mollusc	abalone	0.002	0	0	0.002	0.002	0	0
SRR7244765	PRJNA474068	SAMN09291242	mollusc	abalone	0	0.004	0	0	0	0	0
SRR7244774	PRJNA474068	SAMN09291231	mollusc	abalone	0.002	0	0	0.002	0	0	0

SRR7244775	PRJNA474068	SAMN09291230	mollusc	abalone	0.002	0	0	0.002	0.002	0	0
DRR090716	PRJDB5638	SAMD00078073	seawater	planktonic	0.011	0	0	0.011	0	0	0
ERR1145293	PRJEB11870	SAMEA3673350	seawater	surface	0	0	0	0	0.003	0	0
ERR1145314	PRJEB11870	SAMEA3673371	seawater	surface	0.003	0	0	0.003	0.003	0	0
ERR1145327	PRJEB11870	SAMEA3673384	seawater	surface	0.004	0	0	0.004	0.004	0	0
ERR1145330	PRJEB11870	SAMEA3673387	seawater	surface	0	0	0	0	0.008	0	0
ERR1145335	PRJEB11870	SAMEA3673392	seawater	surface	0.004	0	0	0.004	0.004	0	0
ERR1145337	PRJEB11870	SAMEA3673394	seawater	surface	0.004	0	0	0.004	0.004	0	0
ERR1145351	PRJEB11870	SAMEA3673408	seawater	surface	0.005	0	0	0.005	0.005	0	0
ERR1145352	PRJEB11870	SAMEA3673409	seawater	surface	0	0	0	0	0.004	0	0
ERR1145353	PRJEB11870	SAMEA3673410	seawater	surface	0.005	0	0	0.005	0.005	0	0
ERR1145354	PRJEB11870	SAMEA3673411	seawater	surface	0.004	0	0	0.004	0	0	0
ERR1145360	PRJEB11870	SAMEA3673417	seawater	surface	0.002	0	0	0.002	0.002	0	0
ERR1145367	PRJEB11870	SAMEA3673424	seawater	surface	0.004	0	0	0.004	0.004	0	0
ERR1145371	PRJEB11870	SAMEA3673428	seawater	surface	0.002	0	0	0.002	0	0	0
ERR1145387	PRJEB11870	SAMEA3673444	seawater	surface	0.006	0	0	0.006	0.006	0	0
ERR1145392	PRJEB11870	SAMEA3673449	seawater	surface	0.002	0	0	0.002	0	0	0
ERR1145394	PRJEB11870	SAMEA3673451	seawater	surface	0.001	0	0	0.001	0.001	0	0
ERR1145395	PRJEB11870	SAMEA3673452	seawater	surface	0.002	0	0	0.002	0.002	0	0
ERR1433668	PRJEB12234	SAMEA4020579	seawater		0	0.009	0	0	0	0	0
ERR1433681	PRJEB12234	SAMEA4020592	seawater		0	0	0	0	0	0	0
ERR1578841	PRJEB14899	SAMEA4353568	seawater	oil accomodated	0	0	0.001	0	0	0	0
ERR867783	PRJEB8682	SAMEA3275466	seawater		0.002	0	0	0.002	0.002	0	0
ERR867837	PRJEB8682	SAMEA3275491	seawater		0	0	0	0	0.05	0	0
SRR1662190	PRJNA268133	SAMN03217544	seawater		0.002	0	0	0.002	0.002	0	0
SRR1734277	PRJNA268533	SAMN03223628	seawater		0	0.026	0	0	0	0	0
SRR1819671	PRJNA275249	SAMN03353589	seawater	coral associated	0	0.01	0	0	0	0	0

SRR1819674	PRJNA275249	SAMN03353592	seawater	coral associated	0	0.003	0	0	0	0	0
SRR1819721	PRJNA275249	SAMN03353595	seawater	coral associated	0	0.024	0	0	0	0	0
SRR1819723	PRJNA275249	SAMN03353598	seawater		0	0	0	0	0	0	0.039
SRR1819727	PRJNA275249	SAMN03353603	seawater	coral associated	0	0.02	0	0	0	0	0
SRR1819729	PRJNA275249	SAMN03353605	seawater	coral associated	0	0.009	0	0	0	0	0
SRR1819740	PRJNA275249	SAMN03353614	seawater	coral associated	0	0.004	0	0	0	0	0
SRR1927857	PRJNA279146	SAMN03436114	seawater		0	0.009	0	0	0	0	0
SRR1927891	PRJNA279146	SAMN03436127	seawater		0	0	0	0	0	0	0.013
SRR2097599	PRJNA283545	SAMN03847006	seawater		0.096	0	0	0.096	0.096	0	0
SRR2808381	PRJNA299536	SAMN04209913	seawater	algae associated	0.01	0	0	0.01	0.01	0	0
SRR2808383	PRJNA299536	SAMN04209913	seawater	algae associated	0.006	0	0	0.006	0.006	0	0
SRR2808779	PRJNA299536	SAMN04209914	seawater	algae associated	0.104	0	0	0.104	0.104	0	0
SRR2808988	PRJNA299536	SAMN04209914	seawater	algae associated	0.011	0	0	0.011	0.011	0	0
SRR2819368	PRJNA299536	SAMN04209914	seawater	algae associated	0.019	0	0	0.019	0.019	0	0
SRR2975942	PRJNA304389	SAMN04299799	seawater		0.001	0	0.001	0.001	0	0	0
SRR2993394	PRJNA305512	SAMN04328997	seawater		0.02	0	0.02	0.02	0.02	0	0
SRR2993396	PRJNA305512	SAMN04328999	seawater		0.015	0	0	0.015	0.015	0	0
SRR2993399	PRJNA305512	SAMN04329002	seawater		0.047	0	0	0.047	0.047	0	0
SRR2993401	PRJNA305512	SAMN04329004	seawater		0.024	0	0	0.024	0	0	0
SRR2993402	PRJNA305512	SAMN04329005	seawater		0.015	0	0	0.015	0.015	0	0
SRR3146264	PRJNA309390	SAMN04433038	seawater		0	0.014	0	0	0	0	0
SRR3184418	PRJNA312300	SAMN04497633	seawater		0	0.055	0	0	0	0	0
SRR3184419	PRJNA312300	SAMN04497634	seawater		0	0	0	0	0	0	0.015
SRR3184431	PRJNA312300	SAMN04497646	seawater		0	0	0	0	0	0	0.015

SRR3647521	PRJNA324417	SAMN05203189	seawater		0	0.01	0	0	0	0	0.006
SRR3669451	PRJNA325151	SAMN05209046	seawater		0.007	0	0	0	0	0	0
SRR5640746	PRJNA388809	SAMN07185828	seawater	surface	0	0.001	0	0	0	0	0
SRR5640747	PRJNA388809	SAMN07185871	seawater		0	0.004	0	0	0	0	0
SRR5640756	PRJNA388809	SAMN07185868	seawater		0	0.003	0	0	0	0	0
SRR5640856	PRJNA388812	SAMN07187154	seawater		0	0.048	0	0	0	0	0
SRR5640862	PRJNA388812	SAMN07187152	seawater		0	0	0	0	0	0.149	0.075
SRR5640883	PRJNA388812	SAMN07187158	seawater		0	0.013	0	0	0	0	0
SRR5640906	PRJNA388812	SAMN07187137	seawater		0	0.065	0	0	0	0	0
SRR5640908	PRJNA388812	SAMN07187135	seawater		0	0.039	0	0	0	0	0
SRR5640913	PRJNA388812	SAMN07187140	seawater		0	0.018	0	0	0	0	0
SRR5640916	PRJNA388812	SAMN07187091	seawater		0	0.005	0	0	0	0	0
SRR5640928	PRJNA388812	SAMN07187110	seawater		0	0.005	0	0	0	0	0
SRR5640929	PRJNA388812	SAMN07187109	seawater		0.003	0	0	0.003	0.003	0	0
SRR5640932	PRJNA388812	SAMN07187106	seawater		0	0.005	0	0	0	0	0
SRR5640936	PRJNA388812	SAMN07187115	seawater		0	0.027	0	0	0	0	0
SRR5640958	PRJNA388812	SAMN07187101	seawater		0	0.003	0	0	0	0	0
SRR5877064	PRJNA358589	SAMN07374776	seawater	coastal	0.003	0	0	0.003	0.003	0	0
SRR5918861	PRJNA385736	SAMN07483521	seawater	pelagic	0	0	0.006	0	0	0	0
SRR6401393	PRJNA385736	SAMN08219415	seawater	coastal	0	0	0	0.018	0	0	0
SRR6401795	PRJNA385736	SAMN08219576	seawater	coastal	0	0	0	0.035	0	0	0
SRR6457099	PRJNA429259	SAMN08327522	seawater		0	0.009	0	0	0	0	0
SRR6457207	PRJNA429259	SAMN08327467	seawater		0	0.046	0	0	0	0	0
SRR7035597	PRJNA385736	SAMN08954024	seawater	coastal	0	0	0	0.009	0	0	0
SRR7598258	PRJNA482722	SAMN09711465	seawater		0	0.053	0	0	0	0	0
SRR7633224	PRJNA483963	SAMN09754533	seawater	coastal	0.003	0	0	0.003	0.003	0	0
DRR027450	PRJDB3347	SAMD00023376	sponge		0.008	0	0	0.008	0.008	0	0

DRR027451	PRJDB3347	SAMD00023376	sponge		0.007	0	0	0.007	0.007	0.011	0
DRR027453	PRJDB3347	SAMD00023377	sponge		0.001	0	0	0.001	0.001	0	0
ERR2073734	PRJEB22033	SAMEA104190825	sponge	*Dysidea avara*	0.045	0	0	0.045	0	0	0
SRR1039445	PRJNA229984	SAMN02420362	sponge		0.208	0	0	0.208	0.208	0	0
SRR2154157	PRJNA292036	SAMN03960302	sponge		0.608	0	0	0.608	0.608	0	0
SRR2154172	PRJNA292036	SAMN03960309	sponge		0.075	0	0	0.075	0.075	0	0
SRR2154175	PRJNA292036	SAMN03960338	sponge		0.116	0	0	0.116	0.116	0	0
SRR2154188	PRJNA292036	SAMN03960303	sponge		41.394	0	0	41.394	41.394	0	0
SRR2154190	PRJNA292036	SAMN03960336	sponge		0.322	0	0	0.322	0.322	0	0
SRR2154191	PRJNA292036	SAMN03960339	sponge		16.552	0	0	16.552	16.552	0	0
SRR2154192	PRJNA292036	SAMN03960307	sponge		2.042	0	0	2.042	2.042	0	0
SRR2154193	PRJNA292036	SAMN03960337	sponge		38.444	0	0	38.444	38.444	0	0
SRR2154195	PRJNA292036	SAMN03960340	sponge		33.034	0	0	33.034	33.034	0	0
SRR2972724	PRJNA301178	SAMN04308135	sponge		0	0.167	0	0	0	0	0
SRR2972730	PRJNA301178	SAMN04308135	sponge		0	0.43	0	0	0	0	0
SRR2976095	PRJNA301178	SAMN04308129	sponge	*Cinachyrella sp.*	0	0.386	0	0	0	0	0
SRR2976096	PRJNA301178	SAMN04308130	sponge	*Cinachyrella sp.*	0	0.223	0	0	0	0	0
SRR2976097	PRJNA301178	SAMN04308131	sponge	*Cinachyrella sp.*	0	0.303	0	0	0	0	0
SRR2976098	PRJNA301178	SAMN04308132	sponge	seawater	0	0.086	0	0	0	0	0
SRR2976099	PRJNA301178	SAMN04308133	sponge	seawater	0	0.175	0	0	0	0	0
SRR2976100	PRJNA301178	SAMN04308134	sponge	seawater	0	0.181	0	0	0	0	0
SRR2976103	PRJNA301178	SAMN04308137	sponge		0	0.224	0	0	0	0	0
SRR2976104	PRJNA301178	SAMN04308138	sponge		0	1.579	0	0	0	0	0
SRR2976105	PRJNA301178	SAMN04308139	sponge		0	0.04	0	0	0	0	0
SRR2976106	PRJNA301178	SAMN04308140	sponge		0	0.266	0	0	0	0	0
SRR2976107	PRJNA301178	SAMN04308141	sponge		0	1.38	0	0	0	0	0

SRR2976115	PRJNA301178	SAMN04308149	sponge		0	1.644	0	0	0	0	0
SRR2976117	PRJNA301178	SAMN04308151	sponge		0	3.174	0	0	0	0	0
SRR2976126	PRJNA301178	SAMN04308160	sponge		0	0.054	0	0	0	0	0
SRR4244547	PRJNA342549	SAMN05762057	sponge	*Ircinia felix*	0	0.004	0	0	0	0	0
SRR6428887	PRJNA427280	SAMN08226088	sponge		0	0	0	0.001	0	0	0
SRR7177965	PRJNA453898	SAMN09220636	sponge		0	0.443	0	0	0	0	0
SRR7177972	PRJNA453898	SAMN09220633	sponge		0	0.011	0	0	0	0	0
SRR7178012	PRJNA453898	SAMN09220629	sponge		0	0.009	0	0	0	0	0
SRR7178014	PRJNA453898	SAMN09220625	sponge		0	0.249	0	0	0	0	0
SRR7178015	PRJNA453898	SAMN09220626	sponge		0	0.119	0	0	0	0	0
SRR7178016	PRJNA453898	SAMN09220627	sponge		0	0.02	0	0	0	0	0
SRR7178017	PRJNA453898	SAMN09220628	sponge		0	0.072	0	0	0	0	0
SRR7178020	PRJNA453898	SAMN09220623	sponge		0.004	0	0	0.004	0.004	0	0
SRR7178026	PRJNA453898	SAMN09220676	sponge		0	0.013	0	0	0	0	0
SRR7178027	PRJNA453898	SAMN09220675	sponge		0	0.005	0	0	0	0	0
SRR7513539	PRJNA479568	SAMN09605380	sponge		0	0.022	0	0	0	0	0
SRR7513549	PRJNA479568	SAMN09605374	sponge		0	0.026	0	0	0	0	0
SRR7513601	PRJNA479655	SAMN09604650	sponge		0	0.064	0	0	0	0	0
SRR7513603	PRJNA479655	SAMN09604634	sponge		0	0.107	0	0	0	0	0
SRR7513605	PRJNA479655	SAMN09604632	sponge		0	0.09	0	0	0	0.039	0.019
SRR7513607	PRJNA479655	SAMN09604638	sponge		0	0	0	0	0	0.015	0.007
SRR7513608	PRJNA479655	SAMN09604635	sponge		0	0	0	0	0	0.004	0.002
SRR7513609	PRJNA479655	SAMN09604636	sponge		0	0	0	0	0	0.026	0.013
SRR768455		SAMN00780655	sponge		0	6.667	0	0	0	0	0
SRR768472		SAMN00780660	sponge		0	0.341	0	0	0	0	0
DRR090690	PRJDB5638	SAMD00078047	tunicate	sea squirt	0.041	0	0	0.041	0	0	0
DRR090694	PRJDB5638	SAMD00078051	tunicate	sea squirt	0.078	0	0	0.078	0	0	0

DRR090696	PRJDB5638	SAMD00078053	tunicate	sea squirt	0.366	0	0	0.366	0	0	0
DRR090702	PRJDB5638	SAMD00078059	tunicate	sea squirt	0.035	0	0	0.035	0	0	0
DRR090705	PRJDB5638	SAMD00078062	tunicate	sea squirt	0.04	0	0	0.04	0	0	0
DRR090706	PRJDB5638	SAMD00078063	tunicate	sea squirt	0	0	0	0	0	0	0
DRR090711	PRJDB5638	SAMD00078068	tunicate	sea squirt	0.08	0	0	0.08	0	0	0
DRR090714	PRJDB5638	SAMD00078071	tunicate	sea squirt	0.19	0	0	0.19	0	0	0.066
SRR2994101	PRJNA305909	SAMN04334514	tunicate	sea squirt	0.159	0	0	0.159	0	0	0
SRR2994143	PRJNA305909	SAMN04334552	tunicate	sea squirt	0.052	0	0	0.052	0	0	0
SRR2994155	PRJNA305909	SAMN04334563	tunicate	sea squirt	0.102	0	0	0.102	0	0	0
ERR2608107	PRJEB26735	SAMEA4701556	algae	*Ascophyllum nodosum*	0.002	0	0.002	0.002	0	0	0
ERR2612167	PRJEB25256	SAMEA4707959	algae		0.002	0	0.002	0	0	0	0
SRR7598245	PRJNA482722	SAMN09711450	algae		0	0.519	0	0	0	0	0
SRR7598259	PRJNA482722	SAMN09711484	blank	coral negative control	0	2.376	0	0	0	0	0
SRR6187169	PRJNA414515	SAMN07806884	canine feces		0	0	0	0	0	0.006	0.003
SRR1528894	PRJNA255238	SAMN02923789	contin-uous culture biomass		0.05	0	0	0.05	0.05	0	0
SRR1563085	PRJNA260027	SAMN03016022	crusta-cean		0	0	0	0	0	0	0.007
SRR2072205	PRJNA287619	SAMN03784717	crusta-cean	*Penaeus monodon*	0	0.001	0	0	0	0	0
SRR2072206	PRJNA287619	SAMN03784718	crusta-cean	*Penaeus monodon*	0	0	0	0	0	0	0
ERR1638126	PRJEB15432	SAMEA4443155	dairy fermentation		0	0	0.096	0	0	0	0
SRR3536885	PRJNA320639	SAMN04957371	estuarine water		0	0	0	0	0	0	0.002
ERR688133	PRJEB7828	SAMEA3140714	landplant	*Metrosideros polymorpha*	0.002	0	0	0.002	0	0	0
SRR3536878	PRJNA320639	SAMN04957364	marine NA		0.008	0	0	0.008	0	0	0
SRR3171429	PRJNA311983	SAMN04491975	marine biofilm on		0	0.301	0	0	0	0	0

			corroded steel								
SRR3171430	PRJNA311983	SAMN04491976	marine biofilm on corroded steel		0	0.107	0	0	0	0	0
SRR3171431	PRJNA311983	SAMN04491977	marine biofilm on corroded steel		0	1.451	0	0	0	0	0
SRR3171432	PRJNA311983	SAMN04491978	marine biofilm on corroded steel		0	1.749	0	0	0	0	0
SRR3170225	PRJNA310850	SAMN04457233	oil field		0	0	0	0	0	0.039	0.02
SRR6435254	PRJNA428129	SAMN08281134	oil field		0	0	0	0	0	1.253	0.627
SRR6435261	PRJNA428129	SAMN08281127	oil field		0	0	0	0	0	2.782	1.391
ERR867764	PRJEB8682	SAMEA3275621	reef environment		0	0.015	0	0	0	0	0
SRR1293925		SAMN02796399	skin		0	0	0	0	0	0.005	0.003
ERR1777360	PRJEB14655	SAMEA43942168	squid	*Euprymna scolopes*	0	0.077	0	0	0	0	0
ERR2210048	PRJEB23513	SAMEA104410709	syntheic		0.006	0	0	0.012	0	0	0
SRR1735276	PRJNA271063	SAMN03272672	*Thalassia hemprichii*		0	0	0	0	0	0	0.105

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[1] Lagkouvardos I, Joseph D, Kapfhammer M, Giritli S, Horn M, Haller D, et al. IMNGS: A comprehensive open resource of processed 16S rRNA microbial profiles for ecology and diversity studies. Sci Rep . 2016;6(April):1–9. Available from: http://dx.doi.org/10.1038/srep33721

Tab S5. PFAM domains used to identify restriction-modification systems in *Pseudovibrio* genomes.

Accession	**ID**	**Description**
PF01420	Methylase_S	Type I restriction modification DNA specificity domain
PF04313	HSDR_N	Type I restriction enzyme R protein N terminus (HSDR_N)
PF06616	BsuBI_PstI_RE	BsuBI/PstI restriction endonuclease domain
PF07669	Eco57I	Eco57I restriction-modification methylase
PF12008	EcoR124_C	Type I restriction and modification enzyme - subunit R C terminal
PF12564	TypeIII_RM_meth	Type III restriction/modification enzyme methylation subunit
PF13588	HSDR_N_2	Type I restriction enzyme R protein N terminus (HSDR_N)
PF05066	HARE-HTH	HB1, ASXL, restriction endonuclease HTH domain
PF07275	ArdA	Antirestriction protein (ArdA)
PF08819	DUF1802	Domain of unknown function (DUF1802)
PF10592	AIPR	AIPR protein
PF11058	Ral	Antirestriction protein Ral
PF13707	RloB	RloB-like protein
PF14354	Lar_restr_allev	Restriction alleviation protein Lar
PF17728	BsuBI_PstI_RE_N	BsuBI/PstI restriction endonuclease HTH domain
PF18135	Type_ISP_C	Type ISP C-terminal specificity domain
PF18273	T3RM_EcoP15I_C	Type III R-M EcoP15I C-terminal domain
PF18062	RE_AspBHI_N	Restriction endonuclease AspBHI N-terminal
PF02384	N6_Mtase	N-6 DNA Methylase
PF02963	EcoRI	Restriction endonuclease EcoRI
PF04471	Mrr_cat	Restriction endonuclease
PF09015	NgoMIV_restric	NgoMIV restriction enzyme
PF09019	EcoRII-C	EcoRII C terminal
PF02980	FokI_C	Restriction endonuclease FokI, catalytic domain
PF02981	FokI_N	Restriction endonuclease FokI, recognition domain
PF04555	XhoI	Restriction endonuclease XhoI
PF04556	DpnII	DpnII restriction endonuclease

PF09126	NaeI	Restriction endonuclease NaeI
PF09194	Endonuc-BsobI	Restriction endonuclease BsobI
PF09195	Endonuc-BglII	Restriction endonuclease BglII
PF09208	Endonuc-MspI	Restriction endonuclease MspI
PF09226	Endonuc-HincII	Restriction endonuclease HincII
PF09254	Endonuc-FokI_C	Restriction endonuclease FokI, C terminal
PF09519	RE_HindVP	HindVP restriction endonuclease
PF09520	RE_TdeIII	Type II restriction endonuclease, TdeIII
PF09521	RE_NgoPII	NgoPII restriction endonuclease
PF09553	RE_Eco47II	Eco47II restriction endonuclease
PF09567	RE_MamI	MamI restriction endonuclease
PF09568	RE_MjaI	MjaI restriction endonuclease
PF09570	RE_SinI	SinI restriction endonuclease
PF09571	RE_XcyI	XcyI restriction endonuclease
PF09572	RE_XamI	XamI restriction endonuclease
PF09573	RE_TaqI	TaqI restriction endonuclease
PF00145	DNA_methylase	C-5 cytosine-specific DNA methylase
PF01555	N6_N4_Mtase	DNA methylase
PF02086	MethyltransfD12	D12 class N6 adenine-specific DNA methyltransferase
PF08463	EcoEI_R_C	EcoEI R protein C-terminal
PF09491	RE_AlwI	AlwI restriction endonuclease
PF09504	RE_Bsp6I	Bsp6I restriction endonuclease
PF09561	RE_HpaII	HpaII restriction endonuclease
PF11463	R-HINP1I	R.HinP1I restriction endonuclease
PF02923	BamHI	Restriction endonuclease BamHI
PF06300	Tsp45I	Tsp45I type II restriction enzyme
PF07832	Bse634I	Cfr10I/Bse634I restriction endonuclease
PF09217	EcoRII-N	Restriction endonuclease EcoRII, N-terminal
PF09225	Endonuc-PvuII	Restriction endonuclease PvuII
PF09233	Endonuc-EcoRV	Restriction endonuclease EcoRV

PF09499	RE_ApaLI	ApaLI-like restriction endonuclease
PF09516	RE_CfrBI	CfrBI restriction endonuclease
PF09517	RE_Eco29kI	Eco29kI restriction endonuclease
PF09518	RE_HindIII	HindIII restriction endonuclease
PF09545	RE_AccI	AccI restriction endonuclease
PF09554	RE_HaeII	HaeII restriction endonuclease
PF09556	RE_HaeIII	HaeIII restriction endonuclease
PF09562	RE_LlaMI	LlaMI restriction endonuclease
PF09564	RE_NgoBV	NgoBV restriction endonuclease
PF09565	RE_NgoFVII	NgoFVII restriction endonuclease
PF09566	RE_SacI	SacI restriction endonuclease
PF09569	RE_ScaI	ScaI restriction endonuclease
PF09665	RE_Alw26IDE	Type II restriction endonuclease (RE_Alw26IDE)
PF11564	BpuJI_N	Restriction endonuclease BpuJI - N terminal
PF04851	ResIII	Type III restriction enzyme, res subunit
PF09509	Hypoth_Ymh	Protein of unknown function (Hypoth_ymh)
PF09563	RE_LlaJI	LlaJI restriction endonuclease
PF12161	HsdM_N	HsdM N-terminal domain
PF13156	Mrr_cat_2	Restriction endonuclease
PF13643	DUF4145	Domain of unknown function (DUF4145)
PF14511	RE_EcoO109I	Type II restriction endonuclease EcoO109I
PF15514	ThaI	Restriction endonuclease ThaI
PF15516	BpuSI_N	BpuSI N-terminal domain
PF18643	RE_BsaWI	BsaWI restriction endonuclease type 2
PF18755	RAMA	Restriction Enzyme Adenine Methylase Associated
PF08684	ocr	DNA mimic ocr
PF11407	RestrictionMunI	Type II restriction enzyme MunI
PF12957	DUF3846	Domain of unknown function (DUF3846)

Tab S6. PFAM domains used to identify transposases in *Pseudovibrio* genomes

Accession	**ID**	**Description**
PF01498	HTH_Tnp_Tc3_2	Transposase
PF01609	DDE_Tnp_1	Transposase DDE domain
PF01797	Y1_Tnp	Transposase IS200 like
PF02914	DDE_2	Bacteriophage Mu transposase
PF11427	HTH_Tnp_Tc3_1	Tc3 transposase
PF01359	Transposase_1	Transposase (partial DDE domain)
PF02281	Dimer_Tnp_Tn5	Transposase Tn5 dimerisation domain
PF02316	HTH_Tnp_Mu_1	Mu DNA-binding domain
PF05699	Dimer_Tnp_hAT	hAT family C-terminal dimerisation region
PF09299	Mu-transpos_C	Mu transposase, C-terminal
PF14706	Tnp_DNA_bind	Transposase DNA-binding
PF17906	HTH_48	HTH domain in Mos1 transposase
PF00872	Transposase_mut	Transposase, Mutator family
PF01526	DDE_Tnp_Tn3	Tn3 transposase DDE domain
PF01527	HTH_Tnp_1	Transposase
PF01548	DEDD_Tnp_IS110	Transposase
PF02371	Transposase_20	Transposase IS116/IS110/IS902 family
PF03400	DDE_Tnp_IS1	IS1 transposase
PF04986	Y2_Tnp	Putative transposase
PF12017	Tnp_P_element	Transposase protein
PF01385	OrfB_IS605	Probable transposase
PF01610	DDE_Tnp_ISL3	Transposase
PF01710	HTH_Tnp_IS630	Transposase
PF03004	Transposase_24	Plant transposase (Ptta/En/Spm family)
PF03050	DDE_Tnp_IS66	Transposase IS66 family
PF03108	DBD_Tnp_Mut	MuDR family transposase
PF03221	HTH_Tnp_Tc5	Tc5 transposase DNA-binding domain
PF04693	DDE_Tnp_2	Archaeal putative transposase ISC1217

PF04754	Transposase_31	Putative transposase, YhgA-like
PF04827	Plant_tran	Plant transposon protein
PF04937	DUF659	Protein of unknown function (DUF 659)
PF05598	DUF772	Transposase domain (DUF772)
PF07282	OrfB_Zn_ribbon	Putative transposase DNA-binding domain
PF07592	DDE_Tnp_ISAZ013	Rhodopirellula transposase DDE domain
PF08483	IstB_IS21_ATP	IstB-like ATP binding N-terminal
PF08721	Tn7_Tnp_TnsA_C	TnsA endonuclease C terminal
PF08722	Tn7_Tnp_TnsA_N	TnsA endonuclease N terminal
PF10551	MULE	MULE transposase domain
PF12323	HTH_OrfB_IS605	Helix-turn-helix domain
PF12596	Tnp_P_element_C	87kDa Transposase
PF12760	Zn_Tnp_IS1595	Transposase zinc-ribbon domain
PF12762	DDE_Tnp_IS1595	ISXO2-like transposase domain
PF13005	zf-IS66	zinc-finger binding domain of transposase IS66
PF13006	Nterm_IS4	Insertion element 4 transposase N-terminal
PF13007	LZ_Tnp_IS66	Transposase C of IS166 homeodomain
PF13011	LZ_Tnp_IS481	leucine-zipper of insertion element IS481
PF13340	DUF4096	Putative transposase of IS4/5 family (DUF4096)
PF13358	DDE_3	DDE superfamily endonuclease
PF13359	DDE_Tnp_4	DDE superfamily endonuclease
PF13542	HTH_Tnp_ISL3	Helix-turn-helix domain of transposase family ISL3
PF13546	DDE_5	DDE superfamily endonuclease
PF13586	DDE_Tnp_1_2	Transposase DDE domain
PF13610	DDE_Tnp_IS240	DDE domain
PF13612	DDE_Tnp_1_3	Transposase DDE domain
PF13613	HTH_Tnp_4	Helix-turn-helix of DDE superfamily endonuclease
PF13700	DUF4158	Domain of unknown function (DUF4158)
PF13701	DDE_Tnp_1_4	Transposase DDE domain group 1
PF13737	DDE_Tnp_1_5	Transposase DDE domain

PF13751	DDE_Tnp_1_6	Transposase DDE domain
PF13808	DDE_Tnp_1_assoc	DDE_Tnp_1-associated
PF13952	DUF4216	Domain of unknown function (DUF4216)
PF13963	Transpos_assoc	Transposase-associated domain
PF14319	Zn_Tnp_IS91	Transposase zinc-binding domain
PF14372	DUF4413	Domain of unknown function (DUF4413)
PF14690	zf-ISL3	zinc-finger of transposase IS204/IS1001/IS1096/IS1165
PF01695	IstB_IS21	IstB-like ATP binding protein
PF02992	Transposase_21	Transposase family tnp2
PF02994	Transposase_22	L1 transposable element RBD-like domain
PF03017	Transposase_23	TNP1/EN/SPM transposase
PF03184	DDE_1	DDE superfamily endonuclease
PF04195	Transposase_28	Putative gypsy type transposon
PF05717	TnpB_IS66	IS66 Orf2 like protein
PF06782	UPF0236	Uncharacterised protein family (UPF0236)
PF12784	PDDEXK_2	PD-(D/E)XK nuclease family transposase
PF13022	HTH_Tnp_1_2	Helix-turn-helix of insertion element transposase
PF13518	HTH_28	Helix-turn-helix domain
PF13843	DDE_Tnp_1_7	Transposase IS4
PF18758	KDZ	Kyakuja-Dileera-Zisupton transposase
PF10683	DBD_Tnp_Hermes	Hermes transposase DNA-binding domain
PF09322	DUF1979	Domain of unknown function (DUF1979)
PF10536	PMD	Plant mobile domain
PF11426	Tn7_TnsC_Int	Tn7 transposition regulator TnsC
PF12851	Tet_JBP	Oxygenase domain of the 2OGFeDO superfamily
PF04236	Transp_Tc5_C	Tc5 transposase C-terminal domain
PF06465	DUF1087	Domain of Unknown Function (DUF1087)
PF06869	DUF1258	Protein of unknown function (DUF1258)
PF13017	Maelstrom	piRNA pathway germ-plasm component
PF18717	CxC4	CxC4 like cysteine cluster associated with KDZ transposases

PF18718	CxC5	CxC5 like cysteine cluster associated with KDZ transposases
PF18721	CxC6	CxC6 like cysteine cluster associated with KDZ transposases
PF18759	Plavaka	Plavaka transposase
PF18802	CxC1	CxC1 like cysteine cluster associated with KDZ transposases
PF18803	CxC2	CxC2 like cysteine cluster associated with KDZ transposases
PF18804	CxC3	CxC3 like cysteine cluster associated with KDZ transposases
PF18866	CxC7	CxC7 like cysteine cluster associated with KDZ transposases

Supplementary Figures

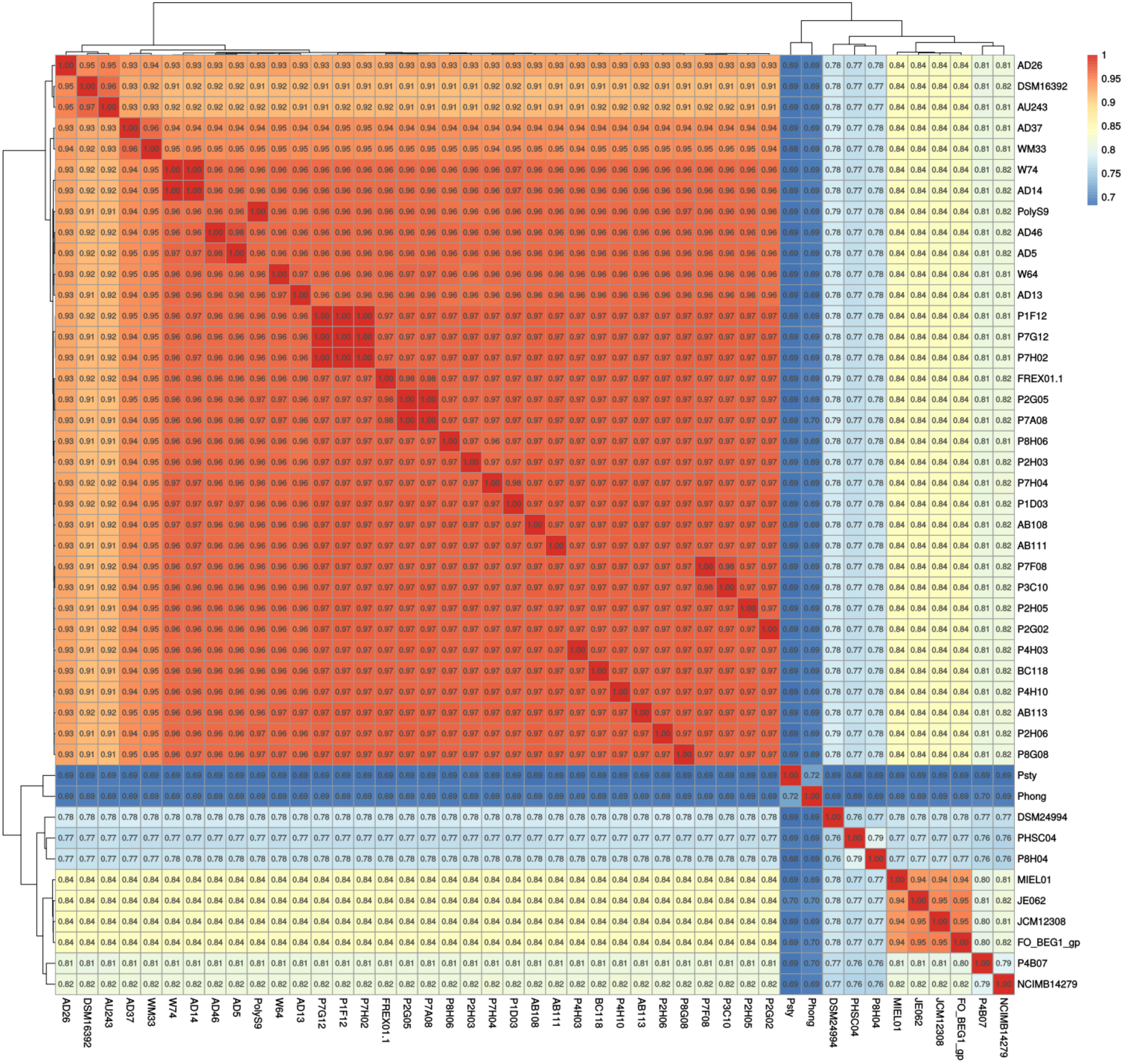

Fig S1. Heat map of average nucleotide identity (ANI) values among 45 *Pseudovibrio* strains. Percentages are given inside of squares. Type strains: DSM16392 = *Pseudovibrio ascidiaceicola*, DSM24994 = *Pseudovibrio axinellae*, JCM12308 = *Pseudovibrio denitrificans*, NCIMB14279 = *Pseudovibrio japonicus*, Psty = *Pseudovibrio stylochi*, Phong = *Pseudovibrio hongkongensis*.

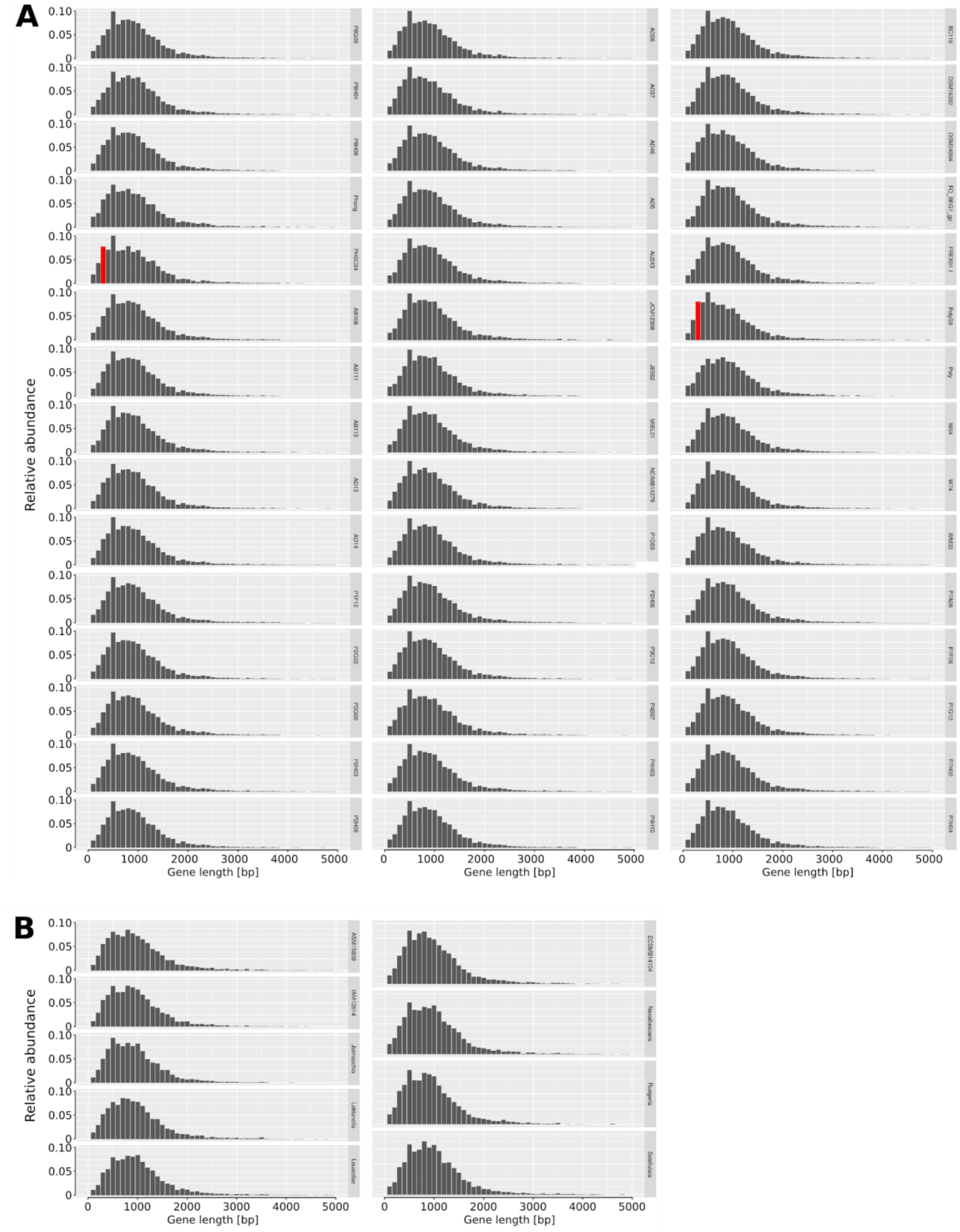

Fig S2. Length distributions and relative abundances of protein coding genes in all *Pseudovibrio* (A) and selected outgroups (B) included in this study. Gene length interval is 100 and the bar is indicating the maximum gene length. For example, all genes with a length between 0 and 100 bp are depicted in the first bar. Strains PolyS9 and PHSC04 had a proportionally higher amount, > 7.5%, of short genes with lengths 200 – 300 bp (shown in red).

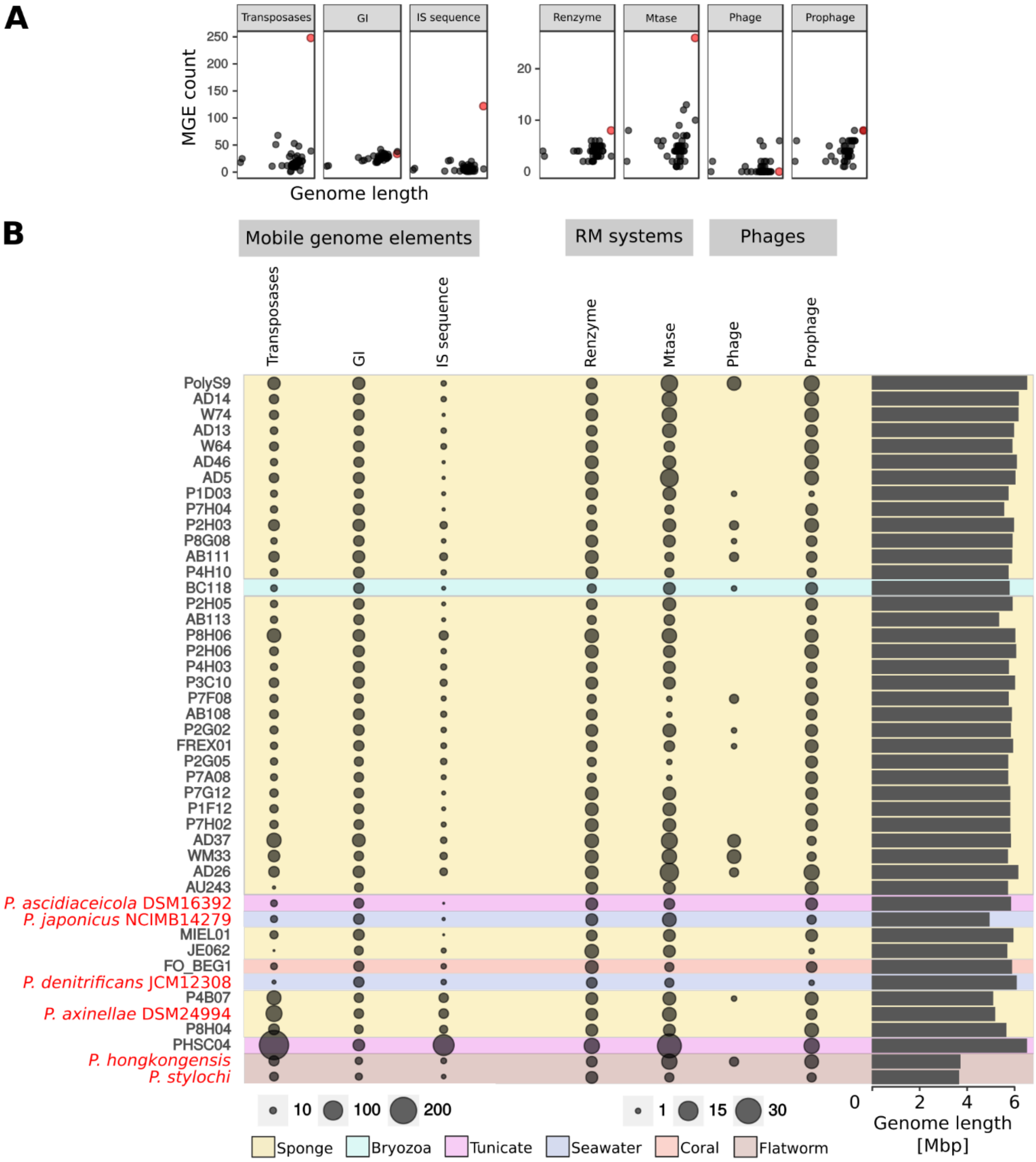

Fig S3. Mobile genetic elements (MGE) of the *Pseudovibrio* genus. Genomes were screened for transposases, genomic islands (GI), insertion sequences (IS), restriction enzyme (Renzyme) and methylase (Mtase) of restriction-modification systems, and phage contigs or prophages. The number of MGEs per genome were plotted against genome lengths (**A**). MGE counts for strain PHCS04 are colored in red. In **B** MGE counts are shown for all *Pseudovibrio* strains of this study (**B**). Colors correspond to isolation source.

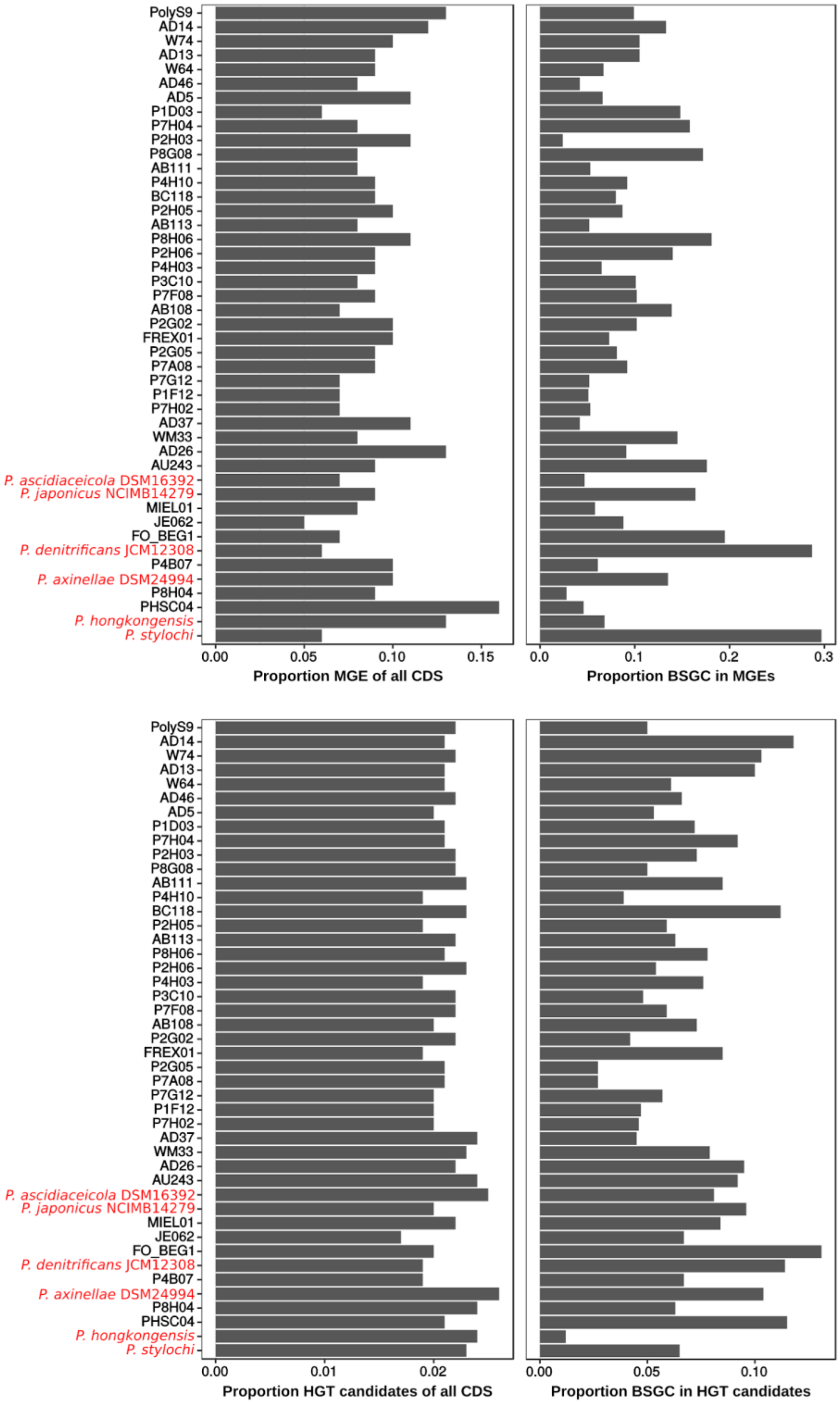

Fig S4. Proportion of genes on mobile genetic elements (MGE) and horizontally acquired (HGT) gene candidates of all CDS and proportion of biosynthetic genes on MGEs or HGT candidates.

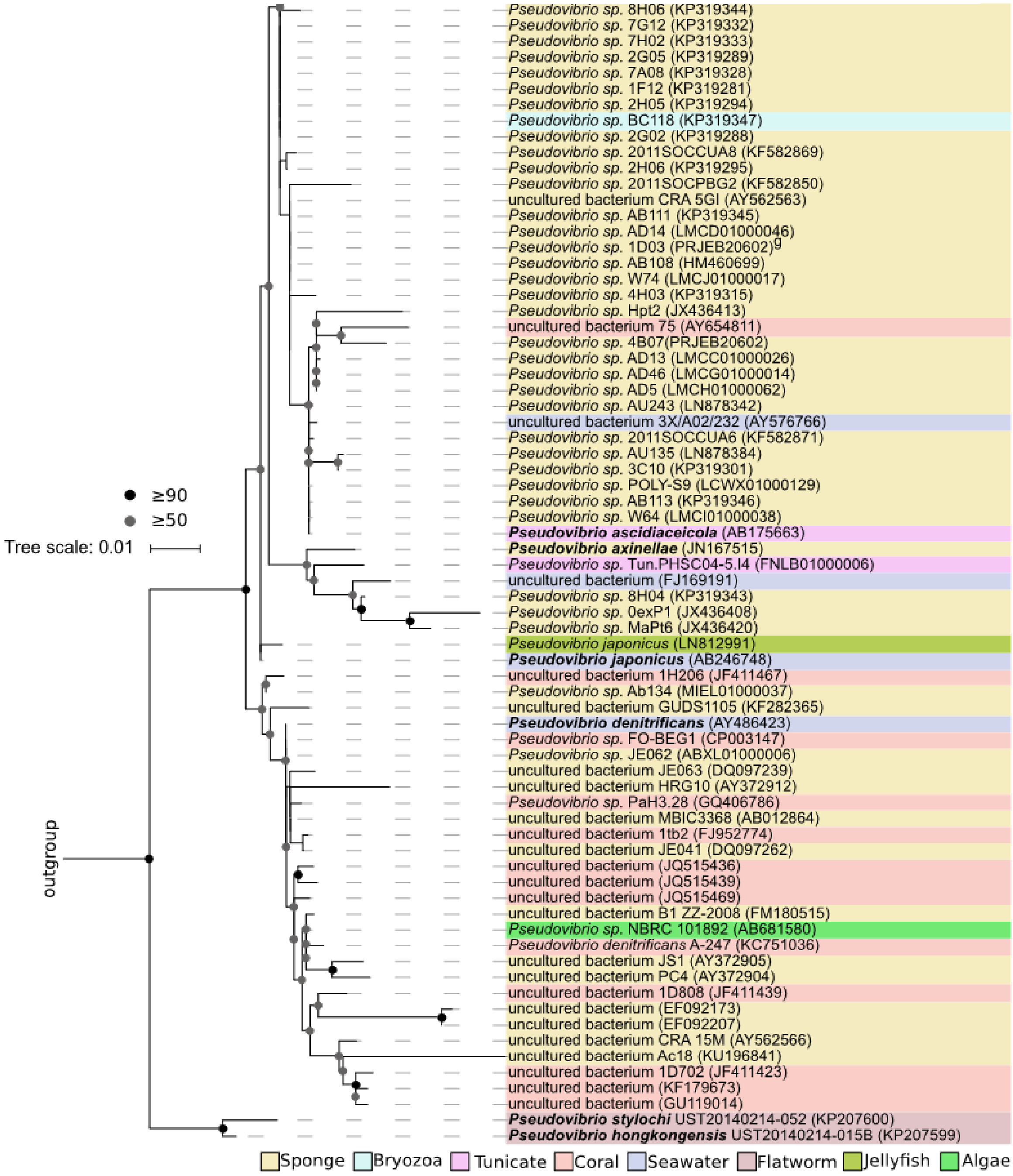

Fig S5. 16S rRNA Maximum Likelihood tree of the genus *Pseudovibrio*. Branch support values are derived using ultrafast bootstrap (UFBoot)[1] with 1000 replicates. Colors indicate isolation source.

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[1] Hoang DT, Chernomor O, Von Haesler A, Minh BQ, Vinh LS. 2017. UFBoot2: improving the ultrafast bootstrap approximation. Mol Biol Evol 35(2):518–522

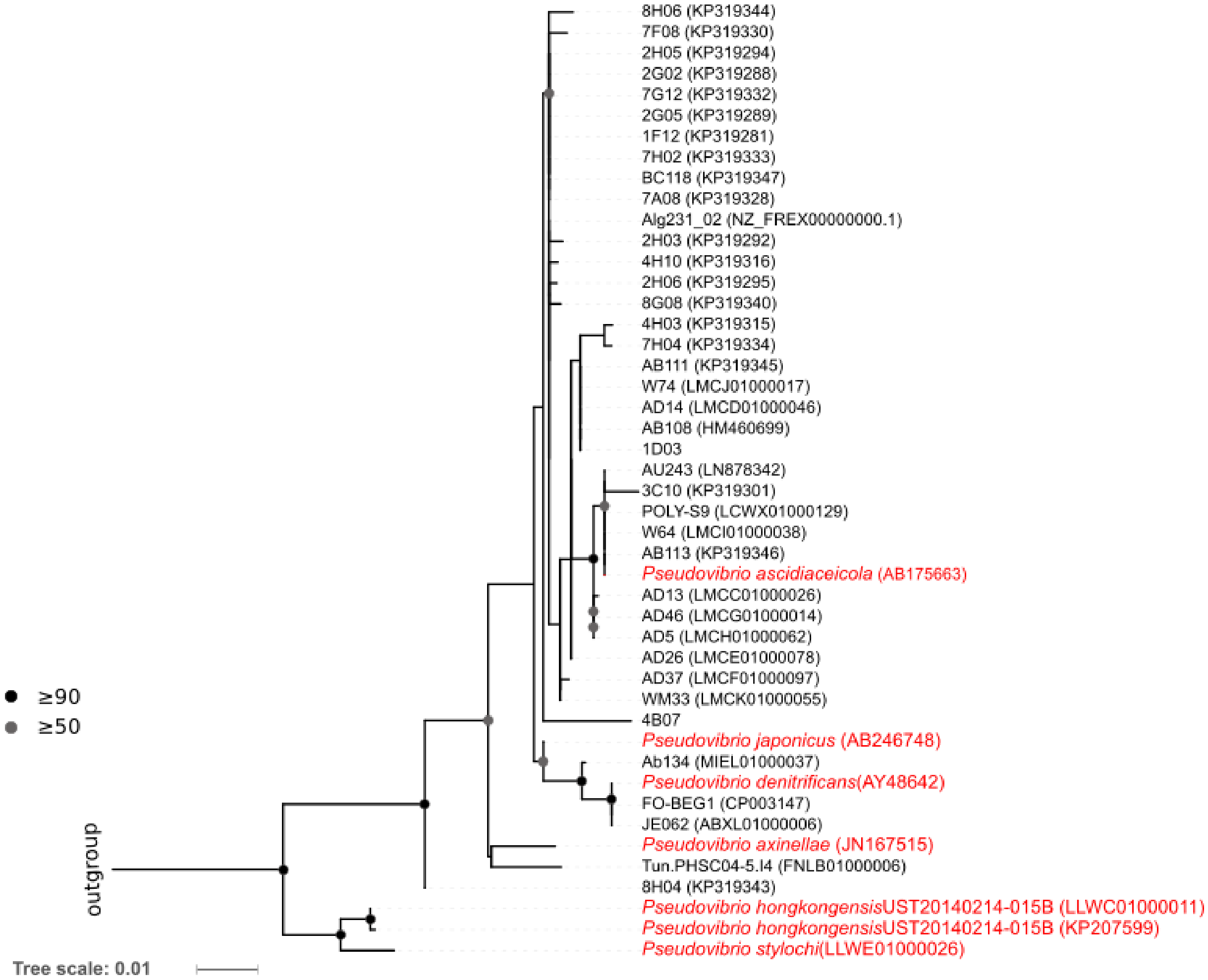

Fig S6. 16S rRNA Maximum Likelihood tree of the *Pseudovibrio* strains included in the comparative genomic analyses (Fig 1). Branch support values are derived using ultrafast bootstrap (UFBoot)[1] with 1000 replicates. Type strains are indicated in red.

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[1] Hoang DT, Chernomor O, Von Haesler A, Minh BQ, Vinh LS. 2017. UFBoot2: improving the ultrafast bootstrap approximation. Mol Biol Evol 35(2):518–522