

Supplementary Table 1. List of the 42 genome-pairs analyzed.

GPIDs	Genome-pair	Host association	Size (Mb)	Coding density	No. of genes	Ks	(Ka/Ks)
184_19643	<i>Clavibacter michiganensis</i> (str. ATCC 33113_NCPPB 382)	Facultative	3.28	89%	225	0.74	0.017
16342_17109	<i>Salinispora (tropica_arenicola)</i>	Free-living	5.48	88%	233	0.76	0.037
15604_214	<i>Dehalococcoides ethenogenes</i> (str. CBDBI_195)	Free-living	1.43	91%	226	0.53	0.075
10642_244	<i>Anabaena variabilis_Nostoc</i> sp. PCC 7120	Free-living	6.39	83%	468	0.19	0.085
13548_13910	<i>Prochlorococcus marinus</i> (str. AS9601_MIT 9312)	Free-living	1.69	91%	225	0.59	0.052
309_384	<i>Bacillus (anthracis_cereus)</i>	Facultative	5.32	85%	525	0.39	0.045
276_85	<i>Listeria monocytogenes</i> (str. EGD-e_4b F2365)	Facultative	2.92	90%	378	0.26	0.030
28855_28857	<i>Clostridium botulinum</i> (str. Alaska E43_Eklund 17B)	Facultative	3.73	84%	352	0.36	0.039
196_44	<i>Bartonella (henselae_quintana)</i>	Obligate	1.76	73%	240	0.49	0.095
12514_19485	<i>Brucella ovis_Ochrobactrum anthropi</i>	Facultative	4.03	84%	318	0.89	0.042
18637_19559	<i>Methylobacterium (extorquens_populi)</i>	Free-living	5.64	85%	339	0.83	0.026
13932_28021	<i>Rhizobium etli</i> (str. CFN 42_CIAT 652)	Facultative	4.45	87%	499	0.54	0.035
15747_15749	<i>Rhodopseudomonas palustris</i> (str. HaA2_BisB5)	Free-living	5.11	87%	389	0.80	0.039
16304_19	<i>Sinorhizobium (medicae_meliloti)</i>	Facultative	3.72	87%	444	0.68	0.033
15754_15755	<i>Rhodobacter sphaeroides</i> (str. ATCC 17029_17025)	Free-living	3.79	90%	271	1.02	0.026
12952_12953	<i>Rickettsia (canadensis_akari)</i>	Obligate	1.20	76%	158	0.53	0.093
272_30313	<i>Wolbachia pipientis</i> (str. wMel_wPip)	Obligate	1.38	82%	165	0.52	0.113
17411_178	<i>Burkholderia (ambifaria_pseudomallei)</i>	Facultative	7.29	85%	256	0.92	0.045
13467_16549	<i>Herminiimonas arsenicoxydans_Janthinobacterium</i> sp.	Free-living	3.77	89%	248	0.95	0.045
13603_15733	<i>Ralstonia eutropha_Cupriavidus taiwanensis</i>	Free-living	6.44	89%	471	0.68	0.030
23_252	<i>Neisseria (gonorrhoeae_meningitidis)</i>	Obligate	2.17	81%	230	0.21	0.080
12634_19743	<i>Anaeromyxobacter (dehalogenans_sp. K)</i>	Free-living	5.04	91%	330	0.53	0.024
17163_303	<i>Campylobacter jejuni</i> (str. 269.97_RM1221)	Facultative	1.81	88%	231	0.19	0.055
17251_233	<i>Helicobacter (acinonychis_pylori)</i>	Obligate	1.61	91%	213	0.27	0.116
16697_16723	<i>Aeromonas (hydrophila_salmonicida)</i>	Facultative	4.72	86%	425	0.75	0.034

13905_335	<i>Shewanella (sp. ANA-3_oneidensis)</i>	Free-living	4.97	86%	422	0.63	0.034
12716_17461	<i>Citrobacter koseri_Enterobacter sp.</i>	Facultative	4.62	91%	290	0.97	0.042
225_371	<i>Escherichia coli_Salmonella enterica</i>	Facultative	4.72	85%	336	0.89	0.036
28471_31	<i>Klebsiella pneumoniae (str. 342_MGH 78578)</i>	Facultative	5.48	88%	554	0.23	0.034
190_34	<i>Yersinia (enterocolitica_pestis)</i>	Facultative	4.63	83%	346	0.86	0.035
18797_72	<i>Lactococcus lactis (str. MG1363_IL1403)</i>	Facultative	2.45	86%	202	0.79	0.027
16720_331	<i>Pseudomonas aeruginosa (str. PA7_PA01)</i>	Facultative	6.43	90%	566	0.41	0.023
13909_17629	<i>Pseudomonas putida (str. FI_GB-1)</i>	Free-living	6.02	90%	575	0.48	0.025
12416_323	<i>Pseudomonas syringae (str. I448A_B728a)</i>	Facultative	6.01	86%	603	0.50	0.029
13920_9633	<i>Psychrobacter (cryohalolentis_arcticus)</i>	Free-living	2.86	83%	313	0.45	0.045
19857_360	<i>Vibrio (harveyi_paraahaemolyticus)</i>	Facultative	5.57	87%	342	0.81	0.038
17107_30351	<i>Stenotrophomonas maltophilia (str. R551-3_K279a)</i>	Facultative	4.71	90%	371	0.48	0.025
297_29801	<i>Xanthomonas (axonopodis_campestris)</i>	Facultative	5.13	87%	287	0.84	0.029
13597_29637	<i>Borrelia (turicatae_hermsii)</i>	Obligate	0.92	95%	134	0.43	0.084
13478_9615	<i>Candidatus Phytoplasma asteris (str. AY_OY)</i>	Obligate	0.78	75%	80	0.22	0.115
10616_16208	<i>Mycoplasma (mycoides_capricolum)</i>	Obligate	1.11	86%	105	0.59	0.042
111_17089	<i>Thermotoga (maritima_petrophila)</i>	Free-living	1.84	96%	172	0.21	0.086
GPIDs	Genome-pair	Host association	Size (Mb)	Coding density	No. of genes	Ks	(Ka/Ks)

Phylum	Class	Order	GPIDs
Actinobacteria	Actinobacteria	Actinomycetales	184_19643
Actinobacteria	Actinobacteria	Actinomycetales	16342_17109
Chloroflexi	Dehalococcoidetes	unclassified	15604_214
Cyanobacteria	unclassified	Nostocales	10642_244
Cyanobacteria	unclassified	Prochlorales	13548_13910
Firmicutes	Bacilli	Bacillales	309_384
Firmicutes	Bacilli	Bacillales	276_85
Firmicutes	Clostridia	Clostridiales	28855_28857
Proteobacteria	Alphaproteobacteria	Rhizobiales	196_44
Proteobacteria	Alphaproteobacteria	Rhizobiales	12514_19485
Proteobacteria	Alphaproteobacteria	Rhizobiales	18637_19559
Proteobacteria	Alphaproteobacteria	Rhizobiales	13932_28021
Proteobacteria	Alphaproteobacteria	Rhizobiales	15747_15749
Proteobacteria	Alphaproteobacteria	Rhizobiales	16304_19
Proteobacteria	Alphaproteobacteria	Rhodobacterales	15754_15755
Proteobacteria	Alphaproteobacteria	Rickettsiales	12952_12953
Proteobacteria	Alphaproteobacteria	Rickettsiales	272_30313
Proteobacteria	Betaproteobacteria	Burkholderiales	17411_178
Proteobacteria	Betaproteobacteria	Burkholderiales	13467_16549
Proteobacteria	Betaproteobacteria	Burkholderiales	13603_15733
Proteobacteria	Betaproteobacteria	Neisseriales	23_252
Proteobacteria	Deltaproteobacteria	Myxococcales	12634_19743
Proteobacteria	Epsilonproteobacteria	Campylobacterales	17163_303
Proteobacteria	Epsilonproteobacteria	Campylobacterales	17251_233
Proteobacteria	Gammaproteobacteria	Aeromonadales	16697_16723

Proteobacteria	Gammaproteobacteria	Alteromonadales	13905_335
Proteobacteria	Gammaproteobacteria	Enterobacteriales	12716_17461
Proteobacteria	Gammaproteobacteria	Enterobacteriales	225_371
Proteobacteria	Gammaproteobacteria	Enterobacteriales	28471_31
Proteobacteria	Gammaproteobacteria	Enterobacteriales	190_34
Proteobacteria	Gammaproteobacteria	Lactobacillales	18797_72
Proteobacteria	Gammaproteobacteria	Pseudomonadales	16720_331
Proteobacteria	Gammaproteobacteria	Pseudomonadales	13909_17629
Proteobacteria	Gammaproteobacteria	Pseudomonadales	12416_323
Proteobacteria	Gammaproteobacteria	Pseudomonadales	13920_9633
Proteobacteria	Gammaproteobacteria	Vibrionales	19857_360
Proteobacteria	Gammaproteobacteria	Xanthomonadales	17107_30351
Proteobacteria	Gammaproteobacteria	Xanthomonadales	297_29801
Spirochaetes	Spirochaetes	Spirochaetales	13597_29637
Tenericutes	Mollicutes	Acholeplasmatales	13478_9615
Tenericutes	Mollicutes	Mycoplasmatales	10616_16208
Thermotogae	Thermotogae	Thermotogales	111_17089
Phylum	Class	Order	GPIDs

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