

Supplementary Table 3A Best BLAST hits for the 16S rRNA genes of the PacBio-Illumina hybrid assembly bins.

Genome	Query coverage	Identity	BLAST hit accession	description	Sponge-derived	Sponge species
bin131	94%	94%	JX206636.1	Uncultured bacterium clone TO10-919_C31	yes	<i>Ircinia oros</i>
bin56	95%	99%	JX206526.1	Uncultured bacterium clone AF10-915_C9	yes	<i>Ircinia fasciculata</i>
bin52	no 16S rRNA gene available					
bin65	95%	99%	JX206637.1	Uncultured bacterium clone TO10-919_C32	yes	<i>Ircinia oros</i>
bin36	94%	97%	EF076136.1	Uncultured alpha proteobacterium clone AD015	yes	<i>Agelas dilatata</i>
bin98	86%	92%	EU350888.1	Uncultured alpha proteobacterium clone HAL-T-35	yes	<i>Haliclona simulans</i>
bin129	98%	99%	HE817825.1	Uncultured bacterium partial 16S rRNA gene, clone B293/GW947	yes	<i>Vaceletia crypta</i>
bin95	no 16S rRNA gene available					
bin107	94%	99%	JX206591.1	Uncultured bacterium clone TO10-97_C15	yes	<i>Ircinia oros</i>
bin63	97%	99%	JN002375.1	Uncultured microorganism clone WGA_alt_1-4E-16S(clone3-3)	yes	<i>Aplysina aerophoba</i>
bin18	97%	99%	JX206694.1	Uncultured bacterium clone TV10-97_C2	yes	<i>Ircinia variabilis</i>
bin40	99%	92%	CP013251.1	<i>Endozoicomonas montiporae</i> CL-33	no (coral)	-
	97%	92%	KC669143.1	Uncultured bacterium clone 15E04	no (coral)	-
	97%	92%	AB205011.1	<i>Spongiobacter nickelotolerans</i> gene for 16S rRNA	yes	-
bin55	90%	93%	KF286003.1	Uncultured gamma proteobacterium clone CtgComparison_34	yes	<i>Aplysina cauliformis</i>
bin106	83%	98%	AM259914.1	Uncultured proteobacterium partial 16S rRNA gene, clone CN28	yes	<i>Chondrilla nucula</i>
bin75	98%	99%	JQ359623.1	Uncultured bacterium clone bac37	yes	<i>Xestospongia testudinaria</i>
bin110	95%	99%	JX206593.1	Uncultured bacterium clone TO10-97_C17	yes	<i>Ircinia oros</i>
bin61	97%	99%	FJ269286.1	Uncultured Acidobacteria bacterium clone XA2H05F	yes	<i>Xestospongia testudinaria</i>
bin70 (NODE_864)	100%	96%	AY713479.1	Uncultured Poribacteria bacterium 64K2	yes	-
bin70 (NODE_1427)	97%	96%	AY713479.1	Uncultured Poribacteria bacterium 64K2	yes	-
bin44 (NODE_5671)	97%	99%	AY713479.1	Uncultured Poribacteria bacterium 64K2	yes	-
bin44 (NODE_8211)	99%	97%	AY713479.1	Uncultured Poribacteria bacterium 64K2	yes	-
bin80	97%	99%	JX206706.1	Uncultured bacterium clone TV10-97_C25	yes	<i>Ircinia variabilis</i>
bin25	96%	98%	JN655253.1	Uncultured bacterium clone AF10-3-9_C14	yes	<i>Ircinia fasciculata</i>
bin43	95%	98%	HQ270243.1	Uncultured bacterium clone XA2F08F	yes	<i>Xestospongia testudinaria</i>
bin94	94%	98%	JX280155.1	Uncultured bacterium clone BA01-C14-seq	yes	<i>Ircinia felix</i> tan morph
bin103	95%	98%	JQ612254.1	Uncultured bacterium clone GBc085	yes	<i>Geodia barretti</i>
bin76	98%	99%	KC669080.1	Uncultured bacterium clone 14H01	no (coral)	-
	98%	98%	FJ229928.1	Uncultured actinobacterium clone XA3F02F	yes	<i>Xestospongia testudinaria</i>
bin134	95%	99%	JX206600.1	Uncultured bacterium clone TO10-97_C25	yes	<i>Ircinia oros</i>
bin119	88%	99%	HQ270284.1	Uncultured <i>Truepera</i> sp. Clone XE1D04	yes	<i>Xestospongia muta</i>
bin9	99%	99%	KJ174471.1	<i>Candidatus</i> <i>Synechococcus</i> spongiarum SH4	yes	<i>Carteriospongia foliascens</i>
bin5	99%	99%	FJ560485.1	Uncultured Chloroflexi bacterium li19	yes	<i>Aplysina aerophoba</i>
bin34	97%	99%	JX206705.1	Uncultured bacterium clone TV10-97_C23	yes	<i>Ircinia variabilis</i>
bin22	95%	98%	EF076083.1	Uncultured Chloroflexi bacterium clone PK016	yes	<i>Plakortis</i> sp.
bin127	95%	98%	JQ612181.1	Uncultured bacterium clone GBc144	yes	<i>Geodia barretti</i>
bin90	97%	98%	HE985083.1	Uncultured bacterium partial 16S rRNA gene, clone A48/GW950	yes	<i>Astrosclera willeyana</i>
bin16	95%	99%	JX206718.1	Uncultured bacterium clone TV10-912_C6	yes	<i>Ircinia variabilis</i>
bin125	95%	98%	FJ481340.1	Uncultured <i>Chloroflexus</i> sp. Clone XB3G04F	yes	<i>Xestospongia muta</i>
bin20	87%	99%	AJ347043.1	Uncultured bacterium 16S rRNA gene, clone TK35	yes	<i>Aplysina aerophoba</i>
bin87	no 16S rRNA gene available					

Supplementary Table 3B Closest reference genomes to bins based on 16S rRNA genes.

Genome	Closest reference genome	Identity	Alignment length
bin103	<i>Sphaerochaeta coccoides</i> DSM17374	84.23	1547
bin106	<i>Alcanivorax borkumensis</i> SK2	81.77	1563
bin107	<i>Nitrospina gracilis</i> NZ_HG422173.1.2	85.31	1572
bin110	<i>Acidobacterium capsulatum</i> ATCC51196	84.99	1079
bin119	<i>Truepera radiovictrix</i> DSM17093	88.71	1523
bin125	<i>Caldilinea aerophila</i> NC_017079.1	82.99	1523
bin127	SAR202 cluster SCGC-AAA240-N13	82.79	1528
bin129	<i>Azospirillum brasilense</i> Sp245	87.94	1236
bin131	<i>Sulfitobacter geojensis</i>	87.55	1494
bin134	<i>Acidimicrobium ferrooxidans</i> DSM10331	89.5	1515
bin16	SAR202 cluster SCGC-AAA240-N13	83.57	1534
bin18	<i>Desulfovibrio desulfuricans</i> ND132	80.47	901
bin20	<i>Anaerolinea thermophila</i> UNI-1	81.45	1531
bin22	SAR202 cluster SCGC-AAA240-N13	91.69	1517
bin25	Flavobacteria bacterium MS024-2A	91.17	1529
bin34	<i>Caldilinea aerophila</i> NC_017079.1	87.6	1508
bin36	<i>Sulfitobacter geojensis</i>	89.64	1486
bin40	<i>Marinobacter hydrocarbonoclasticus</i> VT8	88.76	1539
bin43	Gemmatimonadetes bact. SCGC-AAA240-J22	92.2	1565
bin44 NODE 5671	Ca. Poribacteria sp. WGA3G KC713965.1	98.49	199
bin44 NODE 8211	Dehalococcoidia bact. SCGC-AB-539-J10	84.39	173
bin5	<i>Caldilinea aerophila</i> NC_017079.1	87.39	1522
bin55	<i>Marinobacter hydrocarbonoclasticus</i> VT8	85.35	1386
bin56	<i>Azospirillum brasilense</i> Sp245	87.08	1501
bin61	<i>Nitrospina gracilis</i> NZ_HG422173.1.2	82.24	1571
bin63	SBR1093 genome 210566.2	88.39	1567
bin65	<i>Azospirillum brasilense</i> Sp245	88.84	1496
bin70 NODE 1427	Dehalococcoidia bact. SCGC-AB-539-J10	86.54	156
bin70 NODE 864	Ca. Poribacteria sp. WGA3G KC713965.1	95.48	199
bin75	Ca. Nitrospira defluvii	89.21	1548
bin76	<i>Acidimicrobium ferrooxidans</i> DSM10331	86.29	1087
bin80	<i>Rhodothermus marinus</i> DSM4252	86.96	1541
bin9	Ca. Synechococcus spongiarum 15L	100	1491
bin9	<i>Synechococcus</i> sp. RS9917	95.23	1489
bin90	SAR202 cluster SCGC-AAA240-N13	84.06	1524
bin94	Gemmatimonadetes bact. SCGC-AAA240-J22	92.02	1566
bin98	<i>Azospirillum brasilense</i> Sp245	83.48	1029