The following appendix accompanies the article

Microbial community composition of black band disease on the coral host *Siderastrea siderea* from three regions of the wider Caribbean

Raju Sekar*, Longin T. Kaczmarsky, Laurie L. Richardson

Department of Biological Sciences, Florida International University, Miami, Florida 33199, USA

Email: rajusekar@yahoo.com

Marine Ecology Progress Series 362:85–98 (2008)

Appendix 1. Overview of 16S rRNA gene sequences from clone libraries produced from black band diseased (BBD) *Sidereastrea siderea* at various reef sites. Clone Libraries A, B: Horseshoe Reef, Bahamas; C: Rainbow Garden Reef, Bahamas; D: Watson's Reef, Florida Keys; E, G: Butler Bay, St. Croix; F: Frederiksted, St. Croix. Some of the sequences (48) from Clone Library A and all the sequences (47) from Clone Library B have been previously published as BBD216 and BBD217, respectively (Sekar et al. 2006). Sequences associated with toxin producing bacteria are indicated (see footnotes)

Accession numbers	Libraries (N similar clones)	Sequence length (bp)	Closest relative (accession number) in GenBank database	Similarity (%)	Phylogenetic affiliation
EF123366-76, EF123341, EF123345, EF123347-352	C(11), E(2), G(6)	539–1429	*Roseicyclus mahoneyensis* (AJ315682)	96–97	*Rhodobacterales*, *Alphaproteobacteria*
DQ446094-101, DQ446151, EF123381-382,385, 386-389	A(10), B(1), C(1), E(1), F(1), G(2)	630–1425	*Roseobacter* sp. 8-1 (AJ536670), *Roseobacter* sp. DSS-8 (AF098493)	96–97	*Rhodobacterales*, *Alphaproteobacteria*
DQ446103-108, DQ446154-155 EF123390-396	A(8), B(2), C(1), E(2), G(2)	417–1430	*Roseovarius crassostreae* CV919-312 (AF114484)[a]	94–97	*Rhodobacterales*, *Alphaproteobacteria*
DQ446110, DQ446172, EF123417, 420, 425-431	A(2), B(1), C(1), F(7), G(1)	475–1429	*Thalassobius mediterraneus* (AJ878874)	94–99	*Rhodobacterales*, *Alphaproteobacteria*
DQ644008-15, EF123307-10	A(1), C(1), D(1), F(7), G(2)	556–1432	Alphaproteobacterium C116-18 (AJ294357)[b]	98–99	*Alphaproteobacteria*
EF123443-452, EF123459	D(6), G(5)	729–860	*Rhodobium* sp.(AY588950)	89–90	*Rhizobiales*, *Alphaproteobacteria*
DQ446092-93, DQ446135-143, EF123441	A(2), B(8), G(1)	651–1450	*Ochrobactrum* sp. (AF028733; AY331580)	91–92	*Rhizobiales*, *Alphaproteobacteria*
DQ446109, DQ446158-62, EF123408-411	A(1), B(5), C(1), E(1), F(2)	586–1428	*Silicibacter* sp. E923 (AY369990), *Silicibacter* sp. JC1077 (AF201086)	97–99	*Rhodobacterales*, *Alphaproteobacteria*
EF123291, EF123294-300, EF123320	D(5), E(1), F(2), G(1)	595–828	Alphaproteobacterium (AJ633975, AJ633977, 968)	96–99	*Alphaproteobacteria*
DQ644016, EF123418, DQ446171, DQ446145-50	A(2), B(7)	671–1427	*Rhodobacteraceae* bacterium (DQ234106; DQ234107)	96–97	*Rhodobacterales*, *Alphaproteobacteria*
EF123359-63, DQ446169, EF123423, EF123364-65	A(5), B(1), C(1), G(2)	619–1436	*Pelagibaca bermudensis* (DQ178660)	95–97	*Rhodobacterales*, *Alphaproteobacteria*
EF123453-457 DQ446134, DQ44664-665	A(4), B(4), E(1)	44–1450	*Sinorhizobium* sp. (AJ012211, AJ012210)	94–96	*Rhizobiales*, *Alphaproteobacteria*
EF123339-40, EF123398-403	C(8)	593–1430	*Roseovarius tolerans* (Y11551)	95–96	*Rhodobacterales*, *Alphaproteobacteria*
DQ446166-168, DQ446170, EF123419, 421, 422, 424	B(4), C(4)	591–1425	*Sulfitobacter pontiacus* (Y13155), *Sulfitobacter* sp. (AY573043)	95–96	*Rhodobacterales*, *Alphaproteobacteria*
EF123321-27	D(6), G(1)	567–1462	*Rhodospirillaceae* bacterium (DQ401091), *Magnetospirillum* sp. CF21 (AJ863154; 51)	89–90	*Rhodospirillales*, *Alphaproteobacteria*
EF123302-306	F(1), G(5)	635–690	Alphaproteobacterium ML42 (AJ315683)	96–97	*Alphaproteobacteria*
EF123333-335, 337, 407, 433	A(3), D(1), G(2)	702–1434	*Rhodobacteraceae* bacterium CL-TA03 (AY962292)	95–96	*Rhodobacterales*, *Alphaproteobacteria*
DQ446087-88, DQ644005-07	A(3), D(1), E(1)	425–1449	Alphaproteobacterium PTB1 (AF260726)[b]	94–97	*Alphaproteobacteria*
EF123507-510, EF123513	D(3), E(1), F(1)	660–1492	*Desulfovibrio profundus* (AF418172)	89–96	*Desulfovibrionales*, *Deltaproteobacteria*
EF123551-555	C(4), D(1)	573–1495	Symbiont cf. *Flavobacterium* of *Tetraponera binghami* (AF459795)	98–99	*Flavobacteriales*, *Bacteroidetes*
EF123329-32	A(2), E(1), F(1)	528–1431	*Rhodobacteraceae* bacterium	95–96	*Rhodobacterales*, *Alphaproteobacteria*

Appendix 1. (continued)

Accession numbers	Libraries (N similar clones)	Sequence length (bp)	Closest relative (accession number) in GenBank database	Similarity (%)	Phylogenetic affiliation
			(AJ810844, 37)		
EF123313-16	G(4)	616–706	Alphaproteobacterium endosymbiont 1a of *Inanidrilus leukodermatus* (AJ890099)	91–92	*Alphaproteobacteria*
EF123342-44, EF123346	E(3), F(1)	431–1429	*Rhodobacteraceae* bacterium (AF513935, 932)	95–96	*Rhodobacterales*, *Alphaproteobacteria*
DQ446090, EF123377-79	A(3), E(1)	504–707	*Roseivivax* sp. NT N51 (AB166989)	93–97	*Rhodobacterales*, *Alphaproteobacteria*
EF123437-440	C(3), F(1)	589–1451	*Ochrobactrum* sp. (AY662685), *Brucella* sp. (DQ305288)	91–92	*Rhizobiales*, *Alphaproteobacteria*
EF123383-384, 397, 404	A(3), D(1)	633–1441	*Roseobacter* sp. (DQ120726)	96–98	*Rhodobacterales*, *Alphaproteobacteria*
DQ446113-115	A(3), D(1)	538–1481	*Desulfobacteraceae* bacterium (AJ582696)	92–93	*Desulfobacterales*, *Deltaproteobacteria*
EF123495-498	C(4)	620–1550	*Desulfovibrio baarsii* (AF418174)	92–94	*Desulfovibrionales*, *Deltaproteobacteria*
EF123499-502, EF123505	D(2), E(2)	764–1515	*Desulfovibrio halophilus* (X99237)	90–91	*Desulfovibrionales*, *Deltaproteobacteria*
DQ446152, DQ644017-18	B(1), C(1), G(1)	667–1426	*Roseobacter* sp. 667-19 (AJ294355)[b]	96	*Rhodobacterales*, *Alphaproteobacteria*
EF123405, EF123412-413	D(3)	572–1426	*Silicibacter pomeroyi* (AF098491)	97	*Rhodobacterales*, *Alphaproteobacteria*
EF123417-419	A(2), G(1)	572–1426	*Stappia alba* (AJ889010)	95–98	*Rhodobacterales*, *Alphaproteobacteria*
EF123477-479	G(3)	1474–1488	*Beggiatoa* sp. 'Bay of Concepcion' (AF035956)	90	*Thiotrichales*, *Gammaproteobacteria*
EF123511, 506, 514	D(1), F(1), G(1)	590–1503	*Desulfovibrio* sp. (AF228128; AF228127)	89–96	*Desulfovibrionales*, *Deltaproteobacteria*
DQ446118, EF123532-533	A(1), E(1), G(1)	708–1495	*Clostridium subatlanticum* (AF458779)	96	*Clostridiales*, *Firmicutes*
DQ446174, EF123560-561	B(1), C(1), F(1)	544–1484	*Flexibacter aggregans* (AB078038)	94–95	*Sphingobacteriales*, *Bacteroidetes*
EF123565-567	D(1), G(2)	615–815	*Denitrovibrio acetiphilus* (AF146526)	93	*Deferribacteres*
EF123502, EF123515-516	E(2), F(1)	604–633	*Desulfovibrio zosterae* (Y18049)	94–97	*Desulfovibrionales*, *Deltaproteobacteria*
EF123520-522	G(3)	606–711	Epsilonproteobacterium (AY038516)	98	*Epsilonproteobacteria*
EF123579-581	A(2), D(1)	1448–1451	*Synechococcus* sp. Dim (AY172803)	99	*Cyanobacteria*
DQ446084 , EF123311	A(1), F(1)	1415, 1425	Alphaproteobacterium (AY701434)[b]	98	*Alphaproteobacteria*
DQ446085-86	A(2)	701, 695	Alphaproteobacterium (AF473915)	96	*Alphaproteobacteria*
DQ446157, DQ446144	B(2)	1451, 668	*Rhodobacteraceae* bacterium (DQ005874)	98	*Rhodobacterales*, *Alphaproteobacteria*
EF123356-57	C(1), G(1)	1417, 1430	*Jannaschia* sp. (AJ534220; AJ534218)[b]	97	*Rhodobacterales*, *Alphaproteobacteria*
DQ446102, DQ446156	A(1), B(1)	680, 1430	*Roseovarius nubinhibens* ISM (AF098495)	97	*Rhodobacterales*, *Alphaproteobacteria*
EF123406, EF123336	D(1), F(1)	1425, 1426	*Ruegeria* sp. AS-36 (AJ391197)	98	*Rhodobacterales*, *Alphaproteobacteria*
DQ446111, EF123462	A(1), E(1),	681, 604	Gammaproteobacterium KTc1119 (AF235120)	94, 97	*Gammaproteobacteria*
EF123465-66	A(1), G(1)	1498, 699	Gammaproteobacterium (U70696)	96	*Gammaproteobacteria*
EF123467-68	E(2)	1502, 565	Gammaproteobacterium (DQ351759)	94, 97	*Gammaproteobacteria*
EF123485-486	A(1), E(1)	1426, 482	*Vibrio* sp. V261 (DQ146982)	98	*Vibrionales*, *Gammaproteobacteria*
EF123487-488	D(2)	1517, 602	*Vibrio* sp. V794 (DQ146993)	99, 98	*Vibrionales*, *Gammaproteobacteria*
EF123504, EF123512	D(1), F(1)	775, 689	*Desulfovibrio* sp. (X95230)	89 -96	*Desulfovibrionales*, *Deltaproteobacteria*
EF123527-528	C(1), G(1)	1493, 703	Uncultured firmicute (AF441880)	97, 98	*Firmicutes*

Appendix 1. (continued)

Accession numbers	Libraries (N similar clones)	Sequence length (bp)	Closest relative (accession number) in GenBank database	Similarity (%)	Phylogenetic affiliation
EF123530-531	A(1), F(1)	527, 669	*Clostridium straminisolvens* (AB125279)	92	*Clostridiales*
DQ446120, EF123534	A(1), D(1)	1447,1483	*Fusibacter* sp. (AB189368)	91	*Clostridiales*
EF123542-543	F(2)	563, 587	*Bacteroidetes* bacterium (AY822216)	95, 96	*Bacteroidetes*
EF123545-546	F(2)	712, 659	*Bacteroidetes* bacterium (AY348722)	99	*Bacteroidetes*
EF123563-564	C(2)	1482, 589	Candidate division SR1 bacterium (AY193173)	89	Candidate division SR1
DQ446126-127	A(2)	1465, 1469	*Lyngbya hieronymusii var hieronymusii* (AB045906)	91	*Cyanobacteria*
EF123282	A(1)	1442	Marine bacterium SCRIPPS_423 (AF359547)	96	*Bacteria*
EF123283	E(1)	592	Uncultured bacterium (AB120831)	92	*Bacteria*
DQ446131	B(1)	1429	Uncultured bacterium (AY354160)	93	*Bacteria*
EF123284	E(1)	594	Uncultured bacterium (AY654387)	89	*Bacteria*
EF123285	F(1)	689	Uncultured bacterium (AF424322)	96	*Bacteria*
EF123286	F(1)	687	Uncultured bacterium (DQ228575)	95	*Bacteria*
EF123287	F(1)	608	Alphaproteobacterium (AY712297)	95	*Alphaproteobacteria*
DQ446132	B(1)	679	Alphaproteobacterium (AY701455)[b]	97	*Alphaproteobacteria*
EF123288	C(1)	620	Alphaproteobacterium (AB089097)	89	*Alphaproteobacteria*
EF123290	C(1)	614	Alphaproteobacterium (AB026194)	99	*Alphaproteobacteria*
EF123289	C(1)	614	Alphaproteobacterium (AY822189)	91	*Alphaproteobacteria*
EF123292	D(1)	557	Alphaproteobacterium (AY499668)	96	*Alphaproteobacteria*
EF123293	D(1)	825	Alphaproteobacterium (AY711168)	91	*Alphaproteobacteria*
DQ446089	A(1)	685	Alphaproteobacterium (DQ200416)	92	*Alphaproteobacteria*
EF123319	F(1)	568	Alphaproteobacterium J487 (AY369982)	95	*Alphaproteobacteria*
EF123317	F(1)	593	Alphaproteobacterium (DQ200432)	96	*Alphaproteobacteria*
EF123318	F(1)	653	Alphaproteobacterium (AF473929)	97	*Alphaproteobacteria*
EF123312	F(1)	1455	Alphaproteobacterium endosymbiont 2 of *Inanidrilus leukodermatus* (AJ890097)	96	*Alphaproteobacteria*
EF123328	G(1)	681	*Rhodovibrio* sp. 2Mb1 (AY987846)	94	*Rhodospirillales*, *Alphaproteobacteria*
EF123338	F(1)	583	*Rhodobacteraceae* bacterium (AB180391)	98	*Rhodobacterales*, *Alphaproteobacteria*
EF123354	F(1)	701	*Ahrensia kielensis* (AY771772)	97	*Rhodobacterales*, *Alphaproteobacteria*
EF123353	F(1)	697	*Amaricoccus macauensis* (U88042)	94	*Rhodobacterales*, *Alphaproteobacteria*
EF123355	A(1)	1415	*Hyphomonas oceanitis* (AF082797)	96	*Rhodobacterales*, *Alphaproteobacteria*
DQ446133	B(1)	1433	*Oceanicaulis alexandrii* (AJ309862)	98	*Rhodobacterales*, *Alphaproteobacteria*
EF123358	F(1)	1427	*Parvularcula bermudensis* (AF544016)	94	*Rhodobacterales*, *Alphaproteobacteria*
EF123380	A(1)	695	*Roseobacter* sp. (AY663966)	97	*Rhodobacterales*, *Alphaproteobacteria*
DQ446153	B(1)	1425	*Roseobacter* NAC1-19 (AF245628)	95	*Rhodobacterales*, *Alphaproteobacteria*

Appendix 1. (continued)

Accession numbers	Libraries (N similar clones)	Sequence length (bp)	Closest relative (accession number) in GenBank database	Similarity (%)	Phylogenetic affiliation
EF123434	D(1)	730	*Brucella melitensis* (AY594216)	90	*Rhizobiales*, *Alphaproteobacteria*
EF123435	F(1)	641	*Erythrobacter aquimaris* (AY461443)	99	*Rhizobiales*, *Alphaproteobacteria*
EF123436	A(1)	665	Hyphomicrobiaceae bacterium (AY711104)	97	*Rhizobiales* , *Alphaproteobacteria*
DQ446091	A(1)	670	*Hyphomicrobium* sp. (AY499905)	95	*Rhizobiales*, *Alphaproteobacteria*
DQ446138	B(1)	1451	*Ochrobactrum* sp. (DQ989292;AY623625)	95	*Rhizobiales*, *Alphaproteobacteria*
EF123442	A(1)	660	*Phyllobacteriaceae* bacterium (AY711355)	96	*Rhizobiales*, *Alphaproteobacteria*
EF123458	F(1)	460	*Sinorhizobium* sp. (AY505141; AY505138)	96	*Rhizobiales*, *Alphaproteobacteria*
EF123460	G(1)	713	*Delftia acidovorans* (AB074256)	99	*Betaproteobacteria*
EF123463	E(1)	630	Gammaproteobacterium (AF369720)	97	*Deltaproteobacteria*
EF123464	F(1)	701	Gammaproteobacterium (AY580744)	94	*Gammaproteobacteria*
EF123469	E(1)	455	Gammaproteobacterium (AF424066)	97	*Gammaproteobacteria*
EF123470	G(1)	689	Gammaproteobacterium (AY499942);	97	*Gammaproteobacteria*
EF123471	F(1)	612	Gammaproteobacterium (DQ351796)	97	*Gammaproteobacteria*
EF123472	F(1)	670	Gammaproteobacterium (AY348861)	97	*Gammaproteobacteria*
EF123473	F(1)	620	Gammaproteobacterium (DQ200552)	93	*Gammaproteobacteria*
EF123474	F(1)	603	Gammaproteobacterium (AY499948)	99	*Gammaproteobacteria*
EF123461	D(1)	1466	*Congregibacter litoralis* (AY007676)	96	*Gammaproteobacteria*
EF123475	E(1)	580	*Chromatiales bacterium* (AY711463)	99	*Chromatiales*, *Gammaproteobacteria*
EF123476	G(1)	639	*Stenotrophomonas* sp. AHL 1 (AY379973)	99	*Xanthomonadales*, *Gammaproteobacteria*
EF123480	E(1)	619	*Oceanospirillaceae* bacterium (DQ421584)	90	*Oceanospirillales*, *Gammaproteobacteria*
EF123481	F(1)	616	*Oceanospirillum* sp. MED92 (AY136116)	96	*Oceanospirillales*, *Gammaproteobacteria*
EF123482	G(1)	670	*Halomonas meridiana* (AJ306891; AJ306888)	99	*Oceanospirillales*, *Gammaproteobacteria*
EF123483	G(1)	593	*Pseudomonas* sp. (DQ219372; DQ200851)	99	*Pseudomonadales*, *Gammaproteobacteria*
EF123484	A(1)	712	*Alteromonas hispanica* (AY926460)	96	Alteromonadales, *Gammaproteobacteria*
DQ446112	A(1)	1428	*Ferrimonas marina* (AB193751)	97	Alteromonadales, *Gammaproteobacteria*
EF123489	D(1)	1524	Deltaproteobacterium (AB121098)	94	*Deltaproteobacteria*
EF123490	E(1)	561	Deltaproteobacterium (DQ200599)	97	*Deltaproteobacteria*
EF123491	E(1)	640	Deltaproteobacterium (DQ394898)	97	*Deltaproteobacteria*
EF123492	F(1)	1484	Deltaproteobacterium (AY678523)	92	*Deltaproteobacteria*
EF123493	F(1)	709	Deltaproteobacterium (AY499989)	96	*Deltaproteobacteria*
EF123494	F(1)	685	Deltaproteobacterium (AJ704676)	94	*Deltaproteobacteria*, *Deltaproteobacteria*
EF123503	D(1)	562	*Desulfovibrio profundus* (U90726)	89	*Desulfovibrionales*,
EF123518	D(1)	581	Epsilonproteobacterium (AY038436)	98	*Epsilonproteobacteria*
EF123519	E(1)	580	Epsilonproteobacterium (AF468737)	95	*Epsilonproteobacteria*

Appendix 1. (continued)

Accession numbers	Libraries (N similar clones)	Sequence length (bp)	Closest relative (accession number) in GenBank database	Similarity (%)	Phylogenetic affiliation
EF123523	A(1)	688	Low G+C Gram-positive bacterium (AJ241007)	92	*Firmicutes*
EF123526	F(1)	580	Low G+C Gram-positive bacterium (AJ969455)	91	*Firmicutes*
EF123525	D(1)	799	*Anaerovorax odorimutans* (AJ251215)	92	*Clostridiales*, *Firmicutes*
EF123524	A(1)	710	*Clostridium* sp.(AY548783)	90	*Clostridiales*, *Firmicutes*
EF123529	A(1)	661	*Clostridium disporicum* (CDI18176)	97	*Clostridiales*, *Firmicutes*
DQ446119	A(1)	659	*Desulfitobacter alkalitolerans* (AY538171)	90	*Clostridiales*, *Firmicutes*
EF123535	C(1)	1514	*Ruminococcus* sp. 5 (AJ315982)	89	*Clostridiales*
EF123536	A(1)	662	Uncultured spirochete (AY711111)	92	*Spirochaetes*
DQ446116	A(1)	1442	*Leptonema illini* (AY714984)	89	*Spirochaetes*
DQ446117	A(1)	1471	*Leptonema illini* (M88719)	85	*Spirochaetes*
EF123537	C(1)	1488	*Bacteroidetes* bacterium JS5 (AY372916)	94	*Bacteroidetes*
EF123538	D(1)	1456	*Bacteroidetes* bacterium (DQ351801)	87	*Bacteroidetes*
EF123539	E(1)	1494	*Bacteroidetes* bacterium (AJ441221)	92	*Bacteroidetes*
EF123540	E(1)	1488	*Bacteroidetes* bacterium (AF449260)	89	*Bacteroidetes*
EF123541	E(1)	558	*Bacteroidetes* bacterium (DQ395008)	97	*Bacteroidetes*
DQ644019	F(1)	655	*Bacteroidetes* bacterium (AY701462)[b]	98	*Bacteroidetes*
EF123544	F(1)	696	*Bacteroidetes* bacterium (DQ330315)	96	*Bacteroidetes*
EF123547	F(1)	642	*Bacteroidetes* bacterium (AY711066)	96	*Bacteroidetes*
EF123548	D(1)	813	*Candidatus Cardinium hertigii* (AY599768)	89	*Bacteroidetes*
EF123549	E(1)	564	*Croceibacter atlanticus* (AY163576)	93	*Flavobacteriales*, *Bacteroidetes*
EF123550	A(1)	1490	*Nonlabens tegetincola* (AY987349)	99	*Flavobacteriales*, *Bacteroidetes*
DQ446173	B(1)	1465	*Adhaeribacter aquaticus* (AJ626894)	88	*Sphingobacteriales*, *Bacteroidetes*
EF123556	G(1)	667	*Cytophagales* bacterium (AY038396)	97	*Sphingobacteriales*, *Bacteroidetes*
EF123557	A(1)	1489	*Cytophaga* sp. (AB015260)	94	*Sphingobacteriales*, *Bacteroidetes*
EF123558	D(1)	1480	*Cytophaga* sp. (AB017048)	96	*Sphingobacteriales*, *Bacteroidetes*
EF123559	E(1)	538	*Cytophaga* sp. (AB189358)	91	*Sphingobacteriales*, *Bacteroidetes*
DQ446175	B(1)	665	*Flexibacter tractuosus* (AB078076)	91	*Sphingobacteriales*, *Bacteroidetes*
EF123562	A(1)	671	*Hongiella* sp. (AY576756)	87	*Sphingobacteriales*, *Bacteroidetes*
EF123568	F(1)	690	Uncultured actinomycete (AB015539)	96	*Actinobacteria*
DQ446122	A(1)	707	*Verrucomicrobia* bacterium (AY499794)	93	*Verrucomicrobia*
DQ446123	A(1)	1479	*Verrucomicrobia* bacterium (AY028220)	96	*Verrucomicrobia*
DQ446124	A(1)	674	*Verrucomicrobia* bacterium (AY500056)	92	*Verrucomicrobia*
DQ446125	A(1)	664	*Verrucomicrobiales* Sva0821 (AJ297461)	87	*Verrucomicrobia*
DQ446176	B(1)	665	*Verrucomicrobia* bacterium (AF424507)	89	*Verrucomicrobia*

Appendix 1. (continued)

Accession numbers	Libraries (N similar clones)	Sequence length (bp)	Closest relative (accession number) in GenBank database	Similarity (%)	Phylogenetic affiliation
EF123569	D(1)	584	*Verrucomicrobia* bacterium (DQ302113)	96	*Verrucomicrobia*
EF123570	G(1)	664	*Verrucomicrobia* bacterium (DQ351768)	96	*Verrucomicrobia*
EF123571	E(1)	595	*Verrucomicrobia* bacterium (AY222315)	94	*Verrucomicrobia*
EF123572	F(1)	609	*Verrucomicrobia* bacterium (DQ302114)	91	*Verrucomicrobia*
DQ446121	A(1)	1506	*Fucophilus fucoidanolyticus* (AB073978)	90	*Verrucomicrobia*
EF123573	E(1)	699	Planctomycete (AB231079)	94	*Planctomycetes*
EF123574	E(1)	1492	Planctomycete (AY225652)	92	*Planctomycetes*
EF123575	G(1)	712	Planctomycete (AY921761)	84	*Planctomycetes*
EF123576	G(1)	656	Planctomycete (AB116406)	93	*Planctomycetes*
EF123577	F(1)	655	Planctomycete (AY534068)	98	*Planctomycetes*
DQ446128	A(1)	718	Uncultured cyanobacterium (AF473911)	93	*Cyanobacteria*
EF123578	E(1)	540	Uncultured cyanobacterium (DQ200596)	99	*Cyanobacteria*
DQ644020	D(1)	1456	Uncultured cyanobacterium LR-3L (AF474001)[c] *Geitlerinema* sp. PCC 7105 (AB039010)	98 97	*Cyanobacteria*
EF123582	G(1)	605	*Synechococcus* sp. PCC 7001 (AB015058)	97	*Cyanobacteria*
DQ446129-130	A(2)	704, 658	Uncultured Coscinodiscophyceae (AY038449)	97	Eukaryota
DQ446177	B(1)	677	Uncultured prasinophyte (AY038432)	89	Eukaryota

[a]Bacterium associated with juvenile oyster disease (JOD)
[b]Bacterium associated with toxic dinoflagellates
[c]Cyanobacterium associated with toxin