

Table S2. Close matches, identification, potential role (identified to closest published relatives on GenBank at the time of comparison), and % contribution to bacterial community structure (based on SIMPER analyses, indicating the average contribution of each bacterial ribotype to the similarity within each grouping factor) of the bacteria occurring in (A) apparently healthy *Stylophora pistillata*, (B) apparently healthy *Acropora hyacinthus*, and (C) diseased *A. hyacinthus* samples collected from the three sites Harry's Bommie, Tenements, and Wistari Reef, Great Barrier Reef.

A) <i>Stylophora pistillata</i>							
band ID	Group affiliation	Family	Close relative (% match)	Potential role (isolation source)	% contribution (to community similarity)		
					Harry's	Wistari	Tenements
11 ^{*3}	γ-proteobacteria	Type-A Associates	EU799933 (96%)	Unknown (marine water)	-	0.86	-
16 ^{*1}	Unknown	-	-	-	-	3.89	-
20	Unknown	-	-	-	-	0.70	-
22	Unknown	-	-	-	-	1.46	-
25	γ-proteobacteria	Type-A Associates	AY700601 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	-	0.77	0.72
30	γ-proteobacteria	Type-A Associates	AY700601 (99%)	Unknown (coral, <i>Pocillopora damicornis</i>)	35.04	29.47	31.61
34 ^{*1}	γ-proteobacteria	<i>Vibrionaceae</i>	DQ110007 (100%)	Potential opportunistic pathogen (marine water)	-	0.77	0.72
35	Unknown	-	-	-	5.55	2.87	13.97
38 ^{*1}	γ-proteobacteria	Type-A Associates	AY700600 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	-	2.94	0.72
41 ^{*1}	γ-proteobacteria	Type-A Associates	FJ015089 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	-	0.25	0.78
42	γ-proteobacteria	Type-A Associates	AY700601 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	29.20	8.40	9.67
44	γ-proteobacteria	Type-A Associates	AY700601 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	25.52	19.68	26.94
48 ^{*2}	γ-proteobacteria	Type-A Associates	AY700600 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	-	0.75	0.72
50	Unknown	-	-	-	-	0.25	-
60	γ-proteobacteria	<i>Moraxellaceae</i>	EF195346 (100%)	Intestinal bacteria (moth)	1.26	0.25	1.57
62	γ-proteobacteria	<i>Moraxellaceae</i>	EF195346 (98%)	Intestinal bacteria (moth)	0.28	6.37	0.90
64	Spirocheates	Undetermined	DQ340184 (84%)	Unknown (intestinal tract mudsucker)	-	0.72	1.17
69	Spirocheates	Undetermined	DQ340184 (84%)	Unknown (intestinal tract mudsucker)	-	6.14	-
74	Unknown	-	-	-	-	0.26	0.67
78	Unknown	-	-	-	-	0.25	-
80	Unknown	-	-	-	-	0.38	-
81	CFB	<i>Bacteroidaceae</i>	EU636524 (89%)	Unknown (coral <i>Fungia</i> sp., near fish farm)	3.15	12.54	4.96
82	CFB	<i>Bacteroidaceae</i>	EU636524 (91%)	Unknown (coral <i>Fungia</i> sp., near fish farm)	-	-	4.86
W8	CFB	<i>Flavobacteraceae</i>	AB294989 (100%)	Unknown (marine water near hot spring)	-	-	0.20

B) *Acropora hyacinthus* – Healthy samples

band ID	Group affiliation	Family	Close relative (% match)	Potential role (isolation source)	% contribution (to community similarity)		
					Harry's	Wistari	Tenements
1	Actinobacteria	Undetermined	EU515763 (100%)	Phosphate accumulation (freshwater lake)	5.51	-	-
3	Firmicutes	<i>Bacillales</i>	AF142576 (89%)	Potential probiotic (commercial probiotic)	0.76	-	-
4	Unknown	-	-	-	-	-	0.37
8	γ-proteobacteria	<i>Enterobacteraceae</i>	AY528815 (97%)	Alkane degradation (activated sludge)	4.96	0.64	-
9 ^{*3}	Unknown	-	-	-	-	-	1.33
10	Unknown	-	-	-	2.36	-	-
11 ^{*3}	γ-proteobacteria	Type-A Associates	FJ489773 (99%)	Unknown (coral, <i>Acropora</i> sp.)	0.88	5.74	-
13 ^{*1}	α-proteobacteria	<i>Rhizobiaceae</i>	EU286550 (100%)	Nitrogen-fixation (Agava plant)	15.12	-	-
14	Unknown	-	-	-	-	-	4.34
15 ^{*2}	α-proteobacteria	<i>Rhodobacteraceae</i>	FJ203405 (100%)	Sulphur cycling (coral, <i>Montastraea annularis</i>)	-	5.65	-
21	γ-proteobacteria	Type-A Associates	FJ489741 (98%)	Unknown (coral, <i>Acropora</i> sp.)	4.87	-	-
23	Unknown	-	-	-	-	0.52	-
24 ^{*2}	γ-proteobacteria	Type-A Associates	FJ489741 (99%)	Unknown (coral, <i>Acropora</i> sp.)	8.14	8.68	6.29
26 ^{*2}	γ-proteobacteria	Type-A Associates	FJ489775 (99%)	Unknown (coral, <i>Acropora</i> sp.)	12.54	8.85	2.39
27	γ-proteobacteria	-	EU537177 (98%)	Unknown (human skin)	1.35	-	-
29 ^{*2}	γ-proteobacteria	Type-A Associates	FJ489775 (98%)	Unknown (coral, <i>Acropora</i> sp.)	0.00	0.74	-
31 ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (99%)	Unknown (coral, <i>Pocillopora damicornis</i>)	4.87	12.69	12.78
32 ^{*1}	Unknown	-	-	-	0.82	-	-
33	Unknown	-	-	-	-	0.52	0.41
34 ^{*1}	γ-proteobacteria	<i>Vibrionaceae</i>	DQ110007 (100%)	Potential opportunistic pathogen (marine water)	0.92	-	-
36	Unknown	-	-	-	-	0.64	-
37 ^{*2}	γ-proteobacteria	<i>Enterobacteraceae</i>	DQ818938 (99%)	Gut microbiota (zebrafish intestinal tract)	20.57	0.52	4.57
38 ^{*1}	γ-proteobacteria	Type-A Associates	AY700600 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	0.88	-	-
39 ^{*1}	Unknown	-	-	-	0.85	-	-
40 ^{*1}	Unknown	-	-	-	-	6.28	-
41 ^{*1}	γ-proteobacteria	Type-A Associates	FJ015089 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	0.85	-	-
42b ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (99%)	Unknown (coral, <i>Pocillopora damicornis</i>)	-	9.46	12.78
43 ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	0.72	12.69	16.59
45 ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	0.72	12.66	9.18
49	β-proteobacteria	<i>Comamonadaceae</i>	EU151530 (92%)	Diaphorobacter; nitrogen-cycler (waste water)	-	2.07	-
51 ^{*2}	Firmicutes	Undetermined	EF188440 (97%)	Unknown (terrestrial cave)	0.92	2.50	-
52 ^{*1}	Unknown	-	-	-	0.88	-	-
53 ^{*2}	Unknown	-	-	-	0.72	0.52	-
55 ^{*2}	Unknown	-	-	-	-	3.32	6.57
56 ^{*2}	Unknown	-	-	-	-	0.49	9.53

58 ^{*1}	Unknown	-	-	-	-	0.70	-
61 ^{*2}	γ-proteobacteria	<i>Pseudomonadaceae</i>	EU434636 (100%)	Unknown (<i>Solanum</i> sp. roots)	-	0.74	9.95
63 ^{*2}	γ-proteobacteria	<i>Pseudomonadaceae</i>	AM886099 (98%)	Proteolytic activity (milk)	0.74	5.86	0.41
65 ^{*1}	CFB	<i>Bacteroidaceae</i>	EU636524 (92%)	Unknown (coral <i>Fungia</i> sp., near fish farm)	6.70	-	-
76 ^{*2}	Unknown	-	-	-	2.36	-	-

C) *Acropora hyacinthus* – Disease samples

Species (band ID)	Species ID (Group affiliation)	Species ID (Family)	Close relative (% match)	Potential role (isolation source)	% contribution (to community similarity)		
					Harrys	Wistari	Tenements
9 ^{*3}	Unknown	-	-	-	N/A	4.07	-
11 ^{*3}	γ-proteobacteria	Type-A Associates	FJ489773 (99%)	Unknown (coral, <i>Acropora</i> sp.)	N/A	2.87	-
24 ^{*2}	γ-proteobacteria	Type-A Associates	FJ489741 (99%)	Unknown (coral, <i>Acropora</i> sp.)	N/A	-	10.69
31 ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (99%)	Unknown (coral, <i>Pocillopora damicornis</i>)	N/A	58.49	25.69
43 ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	N/A	3.68	10.69
45 ^{*2}	γ-proteobacteria	Type-A Associates	FJ015090 (98%)	Unknown (coral, <i>Pocillopora damicornis</i>)	N/A	3.68	-
53 ^{*2}	Unknown	-	-	-	N/A	4.30	-
55 ^{*2}	Unknown	-	-	-	N/A	-	16.81
61 ^{*2}	γ-proteobacteria	<i>Pseudomonadaceae</i>	EU434636 (100%)	Unknown (Solanum roots)	N/A	-	10.69
84	α-proteobacteria	<i>Rhizobiaceae</i>	EU083440 (98%)	Unknown (glacier soil)	N/A	11.24	-
86	Unknown	-	-	-	N/A	4.30	-
92	Unknown	-	-	-	N/A	3.68	-
93	Unknown	-	-	-	N/A	3.68	-
94	Unknown	-	-	-	N/A	-	2.42
109	Unknown	-	-	-	N/A	-	13.88
108	γ-proteobacteria	Type-A Associates	EF576992 (96%)	Unknown (Coral mucus)	N/A	-	4.47
106	Unknown	-	-	-	N/A	-	3.47
110	CFB	<i>Bacteroidaceae</i>	EU636519 (100%)	Unknown (coral <i>Fungia</i> sp., near fish farm)	N/A	-	1.21

Bands occurring only once in diseased samples but with high intensity (see Figure 6), not contributing significantly to the similarity within diseased samples (#)

100	Unknown	-	-	-	#
101	γ-proteobacteria	<i>Vibrionaceae</i>	EF466026 (100%)	Potential opportunistic pathogen (coral mucus)	#
102	γ-proteobacteria	<i>Vibrionaceae</i>	EU372929 (100%)	Potential opportunistic pathogen (WS affected)	#
103	CFB	<i>Bacteroidaceae</i>	DQ289934 (86%)	Unknown	#
107	α-proteobacteria	Undetermined	EU133428 (86%)	Unknown	#
111	α-proteobacteria	Undetermined	DQ446152 (94%)	Unknown (BBB affected <i>Siderastrea sidereal</i>)	#
112	γ-proteobacteria	<i>Vibrionaceae</i>	DQ978262 (98%)	<i>Photobacterium</i> (oyster digestive tract)	#
113	γ-proteobacteria	<i>Vibrionaceae</i>	AY368537 (100%)	<i>Photobacterium</i> (marine sponge)	#
114	α-proteobacteria	Undetermined	AM911486 (98%)	Unknown (seawater)	#

115	α -proteobacteria	Undetermined	EU636519 (98%)	Unknown (coral <i>Fungia</i> sp., near fish farm)	#
116	α -proteobacteria	-	EU917612 (92%)	Unknown (biofilm)	#
117	CFB	<i>Flavobacteraceae</i>	DQ482737 (93%)	Unknown (dinoflagellate associated bacterium)	#

The bacteria are host species specific unless otherwise indicated: *1 occurring in apparently healthy *Stylophora* and *Acropora*; *2 occurring in apparently healthy *Stylophora* and diseased *Acropora*, or in apparently healthy *Acropora* and diseased *Acropora*; *3 occurring in apparently healthy *Stylophora* and *Acropora*, as well as diseased *Acropora*. # = bands in diseased *Acropora* samples that were only present in a single sample. CFB = *Cytophaga-Flavobacterium-Bacteroides*; band ID = DGGE band. Sequenced bands 59, 60, 62, 67 and 97 were very rare and are not included in the table as they did not contribute to the SIMPER analyses. Their phylogenetic affiliations are instead shown in Figure 4.