

Table S1. Barcoded primers for obtaining bacterial 16S rDNA amplicons from the coral samples. Refer to Table 1 for sample ID.

Sample ID	Primer ID	Barcode	Universal primer
S1-Pv	S11F, S11R	CTATAT	U341F, R685
S1-Am	S12F, S12R	CTATCA	U341F, R685
S2-Pv	S13F, S13R	CTACTG	U341F, R685
S2-Sa-I	S14F, S14R	CTACAC	U341F, R685
S2-Sa-II	BP1F, BP1R	ACCATG	U341F, R685
S3-Pv	S32F, S32R	TGATCA	U341F, R685
S3-Sp	BP2F, BP2R	ACTGCA	U341F, R685
S3-Sa-I	S33F, S33R	TGACTG	U341F, R685
S3-Am	S34F, S34R	TGACAC	U341F, R685

Table S2 Similarity-based OTUs and species diversity and richness estimates of the coral-associated microbial communities at a dissimilarity level of 3%. Data presented are based on non-normalized data. Refer to Table 1 for sample ID.

Sample ID	Qualified Reads	OTU	Shannon	Simpson	Chao1
S1-Pv	8057	631	5.06	0.91	920.5
S1-Am	5708	219	3.19	0.76	394.5
S2-Pv	2165	194	4.31	0.88	603.9
S2-Sa-I	4596	361	5.10	0.92	634.5
S2-Sa-II	4030	501	6.50	0.97	1055.9
S3-Pv	3869	179	4.26	0.89	320.4
S3-Sa-I	8121	395	4.84	0.91	513.4
S3-Am	4086	195	4.23	0.89	350.2
S3-Sp	2947	230	5.23	0.95	373.5

Table S3 The best BLAST matches of representative sequences of the 10 most abundant OTUs associated with the coral species. Refer to Table 1 for sample ID.

Coral species	ID of representative read	Percentage in the library (%)	Best BLAST match			
			Species	Accession number	Similarity (%)	Source
S1-Pv	J1Y01E2Z6G	41.4	<i>Serratia marcescens</i> B4	GQ981178	98	Tropical fruit trees, Mexico
	J1Y01DTIYM	14.8	<i>Endozoicomonas</i> sp. PDTNROCT018	GU185622	97	Coral associated bacterial on Ningaloo Reef, Western Australia
	J1Y01AK3GX	10.8	<i>Endozoicomonas</i> sp. PDTNROCT018	GU185622	99	Coral associated bacterial on Ningaloo Reef, Western Australia
	J1Y01E354G	9.4	<i>Serratia</i> sp. F7may2.21	GQ416460	98	Biological degreasing systems, France
	J1Y01BZIM1	6.6	<i>Pseudomonas</i> sp. OTU1-2	HM156661	99	Symbiont of <i>Sitobion miscanthi</i> , China
	J1Y01DIMDM	2.2	Uncultured <i>Ralstonia</i> sp. clone BF65B_B95	HM141378	99	Supraglacial spring outflow, Canada
	J1Y01CLSZO	2.0	<i>Endozoicomonas</i> sp. PDTNROCT049	GU185625	98	Coral associated bacterial on Ningaloo Reef, Western Australia
	J1Y01EBU15	2.0	<i>Rhodococcus</i> sp. NSA5-1	AB177889	99	Soils polluted with polychlorinated dioxins, Japan
	J1Y01ERH14	1.9	<i>Achromobacter xylosoxidans</i> CL-10.6a	HQ113220	98	Swine waste biotreatment, Canada
	J1Y01EQBN7	1.2	<i>Endozoicomonas</i> sp. OFU2-3	FJ015068	98	<i>Pocillopora damicornis</i> , American
S1-Am	J1Y01CVSQP	34.7	<i>Serratia</i> sp. PT1	GU458279	98	Gut of <i>Reticulitermes speratus</i> , South Korea
	J1Y01C1PXD	26.3	<i>Serratia marcescens</i> B2	GQ981176	99	Tropical fruit trees, Mexico

	J1Y01BI52N	11.2	<i>Pseudomonas</i> sp. OTU1-2	HM156661	99	Symbiont of <i>Sitobion miscanthi</i>
	J1Y01ECJ64	3.9	<i>Achromobacter</i> sp. FBHYA-B2	HQ166063	98	Activated sludge from the aeration tank of oil refinery complex, Iran
	J1Y01A5V80	2.8	<i>Rhodococcus erythropolis</i> BAC2162	HM355749	98	Endophytic bacteria in the leaves of <i>Phaseolus vulgaris</i>
	J1Y01BRBVI	2.5	<i>Dyella marensis</i> CS5-B2	AM939778	96	Cliff soil, South Korea
	J1Y01BVAS1	1.8	<i>Ralstonia pickettii</i> AR1	HM004352	98	Activated sludge, Isfahan, Iran
	J1Y01A3MZZ	1.5	<i>Serratia marcescens</i> FZ-4	FJ588870	98	Activated sludge from an oil field wastewater-treating system, China
	J1Y01B5HM3	1.5	<i>Stenotrophomonas maltophilia</i> 13635L	EU741084	98	Marine sediment, Costa Rica, Caribbean
	J1Y01C47KE	1.0	<i>Serratia</i> sp. N1	GU944773	98	Isolated from <i>Galleria mellonella</i> , USA
S2-Pv	J1Y01CCYG0	44.8	<i>Serratia</i> sp. N1	GU944773	98	<i>Oscheius carolinensis</i> , isolated from <i>Galleria mellonella</i>
	J1Y01EYPD3	10.3	<i>Endozoicomonas</i> sp. OFU2-3	FJ015068	97	<i>Pocillopora damicornis</i> , American Samoa: Ofu.
	J1Y01DUFII	8.5	<i>Pseudomonas</i> sp. OTU1-2	HM156661	98	<i>Pseudomonas</i> sp. symbiont of <i>Sitobion miscanthi</i> , China
	J1Y01CYAEX	6.5	<i>Endozoicomonas elysicola</i> NQ27	EU919205	97	Sea anemones, Weihai, China
	J1Y01DKW8U	5.9	<i>Ralstonia pickettii</i> AR1	HM004352	98	Activated sludge, Iran
	J1Y01C3JFQ	5.0	<i>Achromobacter xylosoxidans</i> CL-10.6a	HQ113220	98	Swine waste biotreatment, Canada
	J1Y01D0I7Y	4.2	<i>Simkania negevensis</i> Z	U68460	95	Type strain of <i>Simkania negevensis</i>
	J1Y01BW4B7	2.3	<i>Stenotrophomonas maltophilia</i> strain 13635L	EU741084	98	Costa Rica: Gandoca-Manzanillo Wildlife Reserve, Caribbean

	J1Y01ELWGE	1.6	<i>Serratia</i> sp. PT3	GU458285	98	Microorganisms isolated from termite guts, Korea
	J1Y01CWQXV	1.2	<i>Rhodococcus erythropolis</i> AC6	FN825785	98	Pyrite cinder-contaminated soil, Italy
S2-Sa-I	J1Y01APS1L	24.6	<i>Serratia marcescens</i> B2	GQ981176	99	Tropical fruit trees, Mexico.
	J1Y01EG7MU	12.1	<i>Serratia</i> sp. PT1B	GU458280	98	Gut of <i>Reticulitermes speratus</i> , Korea
	J1Y01ASTU3	9.1	<i>Ralstonia pickettii</i> AR1	HM004352	98	Activated sludge, Iran
	J1Y01EDQEU	8.8	<i>Pseudomonas</i> sp. clone OTU1-2	HM156661	99	Symbiont of <i>Sitobion miscanthi</i> , China
	J1Y01APPPZ	7.1	<i>Rhodococcus erythropolis</i> BAC2162	HM355749	98	Leaves of <i>Phaseolus vulgaris</i>
	J1Y01D877N	4.7	Uncultured gamma proteobacterium clone ME42	DQ917904	95	Wild-type <i>Muricea elongata</i> , USA
	J1Y01DZK21	3.1	<i>Achromobacter</i> sp. FBHYA-B2	HQ166063	98	Activated sludge from the aeration tank, Iran
	J1Y01C47Y5	2.9	<i>GpIIa</i> sp.	FM160911	99	Uncultured bacterium from the sponge <i>Aplysina fulva</i> , Brazilian
	J1Y01ECJ7J	1.6	<i>Candidatus Synechococcus</i> clone PA0599C6	EU307491	99	Sponge <i>Aplysina cauliformis</i> voucher PA0599, Panama
	J1Y01AJSIR	1.1	<i>Serratia marcescens</i> DHU-35	HM047514	99	Activated sludge from Plant, China
S2-Sa-II	J1Y01CC0KA	12.1	<i>Rhodococcus erythropolis</i> GT4	FN796872	98	Bacteria associated with <i>Cytisus striatus</i> , Spain
	J1Y01D8DNZ	11.3	<i>Serratia</i> sp. HSL22	HM461146	98	Bacteria that grow on N-acyl homoserine lactones, Colombia
	J1Y01BRUPN	11.5	Uncultured <i>Ralstonia</i> sp. clone BF64A_B33	HM141130	99	Supraglacial spring outflow, Canada
	J1Y01AZ4CF	3.8	Uncultured bacterium i167	FM160914	99	Sponge <i>Aplysina fulva</i> , Brazil
	J1Y01AGKOL	3.4	<i>Pseudoalteromonas</i> sp. N137	HQ188648	98	Marine aerosols above the East Sea, South

	J1Y01EVMNO	3.3	<i>Meiothermus</i> sp. B-R2A5-50-3	AM229107	99	Korea Colored deposit-forming in paper industry, Finland
	J1Y01ALQMC	3.0	Uncultured bacterium clone Gven_G10,	GU118518	95	From <i>Gorgonia ventalina</i> , USA
	J1Y01CM8FD	2.7	<i>Vibrio</i> sp. LL004.15	HM012783	99	Marine hatchery, USA
	J1Y01BZ0Z0	2.6	<i>Pseudomonas</i> sp. clone OTU1-2	HM156661	99	Symbiont of <i>Sitobion miscanthi</i> , China
	J1Y01AHB4G	0.9	<i>Vibrio</i> sp. PaD2.05	GQ406613	98	Mucopolysaccharide layer, <i>Pseudopterogorgia americana</i>
S3-Pv	J1Y01AJINV	34.8	<i>Pseudoalteromonas</i> sp. B296	FN295786	98	Bacteria isolated from <i>Carbasa papyrea</i> , Croatia
	J1Y01AMX2C	11.6	<i>Vibrio</i> sp. PaH1.25	GQ406712	99	Mucopolysaccharide layer, <i>Pseudopterogorgia Americana</i> , USA
	J1Y01E5PU5	11.6	<i>Vibrio</i> sp. PaH1.29	GQ406714	97	Mucopolysaccharide layer, <i>Pseudopterogorgia Americana</i> , USA
	J1Y01AWTE3	4.7	<i>Vibrio</i> sp. IMTB-15	GQ907038	98	Fecal sample from cloacal swab, Ecuador
	J1Y01E2XRX	4.2	<i>Vibrio</i> sp. JF45	FJ952671	99	<i>Mytilus edulis</i> , Germany
	J1Y01AWPCT	3.5	<i>Vibrio</i> sp. S2394	FJ457441	98	Jelly fish, Denmark
	J1Y01CB90W	2.7	<i>Alteromonas macleodii</i> CAIM 1335	HM584088	99	<i>Lutjanus guttatus</i> , Mexico
	J1Y01BGTQI	2.1	<i>Vibrio</i> sp. PMS8	EU372934	98	<i>Pachyseris speciosa</i> , Australia
	J1Y01CAZQO	1.4	Uncultured Proteobacteria clone PDTNROCT049	GU185625	97	Coral associated bacteria on Ningaloo Reef, Western Australia
	J1Y01DELL9	1.3	<i>Shewanella</i> sp. N04IS9	EF629566	97	Sponge <i>Ircinia strobilina</i> , USA
S3-Sa-I	J1Y01C4GBX	16.8	<i>Vibrio</i> sp. PaH3.33c	GQ406794	98	Mucopolysaccharide layer of

						<i>Pseudopterogorgia americana</i> , USA
	J1Y01BHV2O	11.4	<i>Serratia marcescens</i> , FZ-4	FJ588870	99	Activated sludge from an oil field wastewater-treating system, China
	J1Y01DDDBT	11.0	<i>Vibrio harveyi</i> Mj284	GQ455007	98	Hemolymph of spider crab, Spain
	J1Y01DSF2E	6.1	<i>Endozoicomonas</i> sp. clone Gven_G10	GU118518	95	<i>Gorgonia ventalina</i> , USA
	J1Y01AP6NU	5.6	<i>Vibrio</i> sp. PaD2.05	GQ406613	97	Mucopolysaccharide layer of <i>Pseudopterogorgia americana</i> , USA
	J1Y01E7QMO	4.3	<i>Pseudoalteromonas</i> sp. B296	FN295786	97	<i>Carbasa papyrea</i> , Croatia: Adriatic Sea: Rovinj
	J1Y01AS0YW	4.1	<i>Vibrio harveyi</i> strain Mj284	GQ455007	98	Hemolymph of spider crab, Spain
	J1Y01ANUTW	3.1	<i>Pseudomonas</i> sp. VS05_112	FJ662898	99	Normal basalt, American Samoa
	J1Y01C974W	2.4	<i>Rhodococcus erythropolis</i> strain BAC2162	HM355749	98	Leaves of <i>Phaseolus vulgaris</i> , Brazil
	J1Y01C0KE5	0.7	Uncultured <i>Stenotrophomonas</i> sp. clone GI2-SSB-cs-D11	FJ193670	98	Clean room, USA
S3-Am	J1Y01DL2PO	29.4	Uncultured <i>Ralstonia</i> sp. clone F3Bjun.58	GQ417776	98	Bacterial community composition in degreasing systems, France
	J1Y01AP940	22.3	Uncultured <i>Ralstonia</i> sp. clone BF64A_B29	HM141126	99	Supraglacial spring outflow
	J1Y01DAD04	14.1	<i>Serratia marcescens</i> C3	GU212864	99	Pupa used to rear <i>Chouioia cunea</i> on beef extract peptone medium, China
	J1Y01EW987	3.6	<i>Rhodococcus erythropolis</i> AC6	FN825785	99	Pyrite cinder-contaminated soil, Italy
	J1Y01D3DD2	3.1	<i>Vibrio parahaemolyticus</i> CT12	EU660364	99	Coral <i>Acropora digitifera</i> , Gulf of Mannar
	J1Y01DKH36	2.5	<i>Pseudomonas</i> sp. VS05_112	FJ662898	99	Normal basalt, American Samoa: Vailulu

	J1Y01EGVJZ	2.4	Uncultured <i>Ralstonia</i> sp. clone S-175	HQ132457	98	Seamount Heavy metal contaminated estuarine sediment, China
	J1Y01E6FNZ	2.2	<i>Pseudoalteromonas</i> sp. N137	HQ188648	99	Aerosol sample, South Korea: the East Sea
	J1Y01BAE8K	1.6	<i>Meiothermus</i> sp. B-R2A5-50-3	AM229107	98	Paper industry processes and end products, Finland
	J1Y01CSEGJ	1.4	<i>Vibrio</i> sp. PaH1.29	GQ406714	99	<i>Pseudopterogorgia Americana</i> , USA
S3-Sp	J1Y01EYC4W	18.2	<i>Serratia</i> sp. N1	GU944773	99	<i>Oscheius carolinensis</i> , isolated from <i>Galleria mellonella</i> , USA
	J1Y01A51LS	13.0	<i>Pseudoalteromonas</i> sp. N137	HQ188648	99	Marine aerosols above the East Sea, South Korea: the East Sea
	J1Y01COWCF	11.1	<i>Vibrio</i> sp. PaH1.29	GQ406714	98	<i>Pseudopterogorgia Americana</i> , USA
	J1Y01E61DU	8.0	<i>Vibrio</i> sp. SW004.15	HM012797	99	Lobster hatchery, USA
	J1Y01COV7N	5.2	<i>Rhodococcus erythropolis</i> GT4	FN796872	98	Bacteria associated with <i>Cytisus striatus</i> , Spain
	J1Y01A73XH	4.4	<i>Pseudomonas</i> sp. OTU1-2	HM156661	99	Symbiont of <i>Sitobion miscanthi</i> , China
	J1Y01CLACE	1.3	<i>Vibrio</i> sp. JF45	FJ952671	98	German Bight, <i>Mytilus edulis</i> , Germany
	J1Y01ETO19	1.2	<i>Vibrio fortis</i> strain Mj242	GQ454986	98	Hemolymph of spider crab, <i>Maja brachydactyla</i> , Spain
	J1Y01BF9PW	1.1	<i>Vibrio</i> sp. PaD1.28	GQ406596	99	Mucopolysaccharide, <i>Pseudopterogorgia Americana</i> , USA

Table S4. Summary of RDA. Three separated RDA runs were performed to examine how much variance is explained by 1) coral species only, 2) environmental parameters only and 3) a combination of both. Automatic forward selection was performed with Monte Carlo permutation tests.

Axes	Coral species only				Environmental parameters only				Coral species + Environmental parameters			
	1	2	3	4	1	2	3	4	1	2	3	4
Eigenvalues	0.153	0.088	0.066	0.050	0.350	0.083	0.233	0.117	0.452	0.139	0.096	0.066
Species environment correlations	0.757	0.880	0.889	0.517	0.874	0.895	0.000	0.000	0.967	0.969	0.945	0.914
Cumulative percentage variance												
of species data	15.3	24.0	30.6	35.6	35.0	43.3	66.6	78.3	45.2	59.1	68.7	75.3
of species-environment relations	42.8	67.4	85.8	100.0	80.9	100.0	0.0	0.0	55.2	72.2	84.0	92.0
Sum of all canonical eigenvalues	0.356				0.433				0.819			

Table S5. Correlation (r value) between other environmental parameters measured in this study with salinity and depth.

	Depth	Salinity
Depth	1.0000	0.7810
Salinity	0.7810	1.0000
Temp.	-0.9887	-0.6783
DO	-0.8772	-0.9849
pH	0.3201	0.8417
Turbidity	0.3961	0.8828
Chl a	-0.3627	-0.8653
TOC	-0.2378	-0.7924
TC	-0.6108	-0.9715
TN	-0.1430	-0.7298
NO ₃	0.1792	-0.4745
NH ₄	-0.7695	-0.9998
TP	-0.9902	-0.8535