Appendix I-Site selection and coral reef surveys

Sites (Supplemental Figures 2-3, Supplemental Tables 1-2) were chosen based on analysis of satellite images and areal surveys conducted in a seaplane several days before the start of the mission. A total of 578 and 1,703 km^2 of WorldView 2 (8 band) satellite imagery were acquired for the Austral and Cook Islands, respectively. The satellite images had a spatial resolution of 2 x 2 m (i.e., each pixel covered a 4 m^2 area), enabling real-time navigation in the field to locate features of interest and to avoid emergent reefs. In order to navigate, the scenes were used in conjunction with a differential GPS device (dGPS) on a small-craft diving vessel. Drop-cam video footage (http://maps.lof.org/lof/Home/) was used to aid in site selection (*sensu* Goodman et al., 2013). At each point, the drop-cam was held from the survey boat enabling it to glide along the sea floor as it recorded video for 15-60 s. During this time, the laptop operator watched the video in real-time and instructed the drop-cam operator to raise or lower the camera. The video was recorded on a ruggedized laptop, and the geographic position, time, date, boat heading, and boat speed were burned into the video. Drop-cam deployment was limited to depths above 40 m due to the limited length of the tether cable (50 m).

At each site, both temperature (°C) and salinity (psu) were measured with a Castaway® CTD (Sontek). Cover of major functional groups (corals [identified to genus], sponges, and other invertebrates, as well as six groups of algae: macroalgae, crustose coralline algae, erect coralline algae, fine turfs, turf algae with sediment, and cyanobacteria) and substrate type (hard ground, sand, mud, rubble, recently dead coral, bleached coral, and live coral) were assessed *in situ* or via photographic assessments using a point intercept method in which the organism and substrate were identified every 10 cm along a 10 m transect (100 points/transect). At least six transects, typically conducted by three researchers, were examined for each site on SCUBA. When possible, surveys were conducted at 5, 10, 15, 20, 25, and 30 m.

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Appendix II- Nucleic acid extractions, host coral genotyping, phylogenetic analyses, and *Symbiodinium* genotyping

Nucleic acid extractions and host coral genotyping. RNAs and DNAs were extracted from all 123 samples with TRIzol™ (Life Technologies) *sensu* Mayfield et al. (2009) and Putnam et al. (2013), respectively, after having spun down the tissue/skeleton pellet and aspirated the RNALater with a 1-ml pipet tip. RNA and DNA quality control and quantification were conducted as described previously (Mayfield et al., 2011, 2012). A sub-selection of 91 DNAs were randomly chosen for host coral genotyping via PCR amplification and sequence analysis of an ~800-bp portion of the partial mitochondrial ATP synthase subunit 6 (*atp6*) and putative control region (*pmapcr*; Chen et al., 2008). The DNAs were diluted to 10 ng/µl prior to PCRs with the FATP6.1 and RORF primers of Flot et al. (2007, 2008). PCRs (50 µl) were conducted with 1x EZ-TIME™ SYBR® Green real-time PCR mastermix with ROX® (Yeastern Biotech., Ltd.), 500 nM each primer, and 20-100 ng DNA. Although a real-time PCR mastermix was utilized, only standard PCRs were conducted. Thermocycling was executed as described by Schmidt-Roach et al. (2012).

Electrophoresis of 5 µl PCR product was conducted in 1% Tris-borate-EDTA (TBE)-agarose gels at 100 V for 20 min in a Bioer Mini-Run gel electrophoresis tank. Gels were stained in an ethidium bromide bath for 20 min prior to visualization on an ultraviolet (312 nm) transilluminator (MidSci), and images of the gels were taken with an Olympus TG-2 digital camera. PCR products were purified with the AxyPrep™ PCR clean-up kit (Axygen) according to the manufacturer's recommendations, though with a 10 minute, pre-elution incubation in a 65°C oven to remove residual ethanol. Purified PCR products were eluted into 20 µl manufacturer's eluent and sequenced in both directions with the FATP6.1 and RORF primers and BigDye® Terminator (version 3.1) cycle sequencing kit (Life Technologies) on an Applied Biosystems 3730xl DNA analyzer (Life Technologies).

Phylogenetic analyses. DNA sequences were assembled with Geneious (ver. 6.18; created by Biomatters and available from www.geneious.com), compared to published sequences on the NCBI database with

BLASTn to assign a coral species, and submitted to NCBI (see accession numbers in Supplemental Tables 3 and 4.). Sequences were aligned in ClustalW (Thompson et al., 1994) and manually edited with MEGA (ver. 5.22; Tamura et al., 2011). The gap opening and extension values of the aligned parameters were set to 15 and 6.66, respectively. Phylogenetic relationships among sequences were constructed based on neighbor-joining (NJ), maximum likelihood (ML), and maximum parsimony (MP) methods with MEGA (ver. 6.0.6), and Bayesian (BAY) analysis was performed with MrBayes (ver. 3.22; Ronquist et al., 2012). Codon positions included were $1^{st}+2^{nd}+3^{rd}$+non-coding. All positions containing either gaps or missing data were eliminated. The NJ analysis was performed with the Kimura 2-parameter model of nucleotide substitution (Kimura, 1980). In the MP analyses, heuristic searches with tree bisection and reconnection branch swapping and 10 random sequence additions were performed.

For the ML and BAY analyses, the best-fitting model of DNA substitution was the Hasegawa-Kishino-Yano model, which was estimated by the Bayesian information criterion (BIC) feature in MEGA. Five-hundred bootstrap values were used to evaluate support for the NJ, MP, and ML trees. The percentages of replicate trees in which the associated taxa clustered together in the bootstrap tests are shown next to the branches (Fig. 2). In the BAYsian analysis, a Markov Chain Monte Carlo search was run with four chains for 10^6 generations, with trees sampled every 200 generations. The first 10^5 trees were discarded as the ‘‘burn-in,’’ after which the likelihood scores had stabilized. An estimation of evolutionary divergence among lineages was calculated in MEGA using the function for genetic distance computation between groups. The genetic distance was calculated using the maximum composite likelihood model (Tamura et al., 2004), and the variance of the distance was derived from 500 bootstrap replications.

Symbiodinium *genotyping*. Genotyping assays of *Symbiodinium* populations are well established (e.g., Mieog et al., 2007), and the real-time PCR-based clade-level genotyping assays for clades A, B, C, and D from Correa et al. (2009) were utilized with 83 of the same 91 DNA samples in which the host genotype was determined. The real-time PCR mastermix described above was used with the primers and primer concentrations of Correa et al. (2009) and 20 ng DNA in 20 µl reactions. Real-time PCRs were conducted

76in triplicate as in Correa et al. (2009) in an Applied Biosystems 7500 real-time PCR machine under the
77SYBR Green setting, and melt curves were conducted after each run to verify absence of non-specific
78amplification products or primer-dimers. “Presence” of a particular clade was defined *a priori* to occur
79when threshold cycles (C_t) less than 35 were measured.
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Appendix III- Environmental data and site descriptions

***Raivavae, Austral Islands, French Polynesia*.** A wide shelf extended around Raivavae (Supplemental Fig. 2A), sloping gradually from the reef crest to the edge of the slope at 20 to 25 m (average live coral cover [ALCC] at depths >20 m=40±16%; standard error for this and all ALCC values henceforth). Depths of 10-20 m extended hundreds of meters out, before plunging more steeply. The shallows transitioned from a high-energy reef crest dominated by branching acroporids and pocilloporids, to a spur and groove structure with narrow, scoured, hard-bottom channels and wide, flattened spurs. The spurs were constructed mostly of low-relief massive corals in the genus *Astreopora*, with some larger outcrops containing other massive species such as *Favia* and *Leptoria*, as well as short, stout-branched, and digitate acroporids and pocilloporids. ALCC across all eight sites was 34%±4.9, and it did not vary significantly across the surveys depths of 5 (23±8.0%), 10 (25±9.2%), 15 (36±7.1%), and 20 m (31±11%; 1-way ANOVA effect of depth nested within island, F=1.1, p=0.41). The average temperature of the survey sites was 25.5°C (±0.059°C; standard deviation for this and all temperature and salinity values henceforth), and the average salinity was 35.7±0.025 psu.

P. damicornis-like colonies were only found at and sampled from six of the eight sites (Supplemental Table 1), and 13 of these were genotyped (Supplemental Table 3); twelve and one were found to be *P. damicornis* genotype α (*sensu* Supplemental Fig. 1) and *P. acuta*, respectively (Fig. 1). Clade-specific real-time PCR assays were conducted with 12 of these samples (Supplemental Table 3), all of which were found to contain *Symbiodinium* of clade C only (C_t>35 for clade A, B, and D assays).

Tubuai, Austral Islands, French Polynesia. The reef structure of Tubuai (Supplemental Fig. 2B) consisted largely of shallow, low-relief spur and groove framework with wide spurs and narrow channels that extended gradually from 3-5 to 10 m. The slopes were dominated by *Astreopora*, with a mix of smaller branching, digitate, and table *Acropora*, some *Pocillopora*, *Leptoria, Hydnophora, Montastraea*, and *Favia stelligera*, and some rarer corals like *Turbinaria*. Shallow areas often had large patches of soft corals and *Millepora*. Deeper areas were typically dominated by large stands of very thick, stout, and short branching acroporids that sometimes formed thickets tens of meters in diameter. These thickets were often

intermixed with low-relief, massive *Pavona, Favia*, and *Lobophyllia* colonies, as well as plates of *Leptastrea* and *Echinopora* and scattered massive *Porites*. ALCC was 41% and did not vary significantly between survey depths (10 [55±14%], 10-15 [37±5.0%], 15 [30±6.3%], 15-20 [37±5.8%], 20 [53±8.2%], and >20 m [52±14%]; F=1.5, p=0.25). The average salinity and temperature of the surveyed reefs were 35.6±0.023 psu and 25.8±0.06°C, respectively.

Nine sites were visited over three days (Supplemental Table 1), and *P. damicornis*-like pocilloporid colonies were found at seven of these sites. Of the 18 colonies genotyped (Supplemental Table 3), 17 (94%) were the α genotype of *P. damicornis* (Fig. 1). The remaining colony was found to be *P. meandrina* and was likely sampled inadvertently due to its small (<10 cm) size. *P. acuta* was not present at this island. Regarding the *Symbiodinium* assemblages, all with the exception of one *P. damicornis* sample from site AUTB11 were found to host only clade C *Symbiodinium* (Supplemental Table 3); the sample "*P. damicornis* Tubuai 26" possessed *Symbiodinium* populations of clades A and C.

Rurutu, Austral Islands, French Polynesia. Only eight corals were collected from Rurutu (Supplemental Fig. 2C), as severe crown of thorns starfish (COTS) outbreaks were reported by local scientists to have occurred in 2006 and 2007. All corals were consumed nearly in their entirety from very shallow water (<5 m) to 40 m or deeper. Colonies remained in growth position, although rubble was present in sand channels and in grooves between coral heads and spurs. There were few tissue remnants left on colonies, and only low numbers of recruits were present. The only survivors were some larger colonies of *P. eydouxi* and *P. verrucosa*, as well as some digitate *A. humilis* and very small pocilloporids. It appeared that recovery has been negligible; coral cover was less than 0.1% in certain areas, averaged ~3.6±0.5% across the three sites (Supplemental Table 1), and only reached values over 5% at depths >20 m (6.0±2.2%). The average temperature and salinity of the three sites were 25.6±0.053°C and 35.7±0.044 psu, respectively.

Two corals were genotyped, and one from site AURR18 was determined to be the α genotype of *P. damicornis*. This sample only hosted *Symbiodinium* of clade C (Supplemental Table 3). The other sample, which was from site AURR20 (Supplemental Table 3), was found to be haplotype 8a (*sensu* Pinzon et al., 2013). This represents the only specimen of this haplotype from the Austral Islands, and only

three additional samples out of the 87 analyzed were found to be of this genotype (described below).

***Maria, Austral Islands, French Polynesia*.** The fore reef communities of uninhabited Maria Atoll (Supplemental Fig. 2D) were typical of French Polynesian atolls, with a shallow reef flat that was partially emergent at low tide. There were prominent spur and groove habitats in the shallows consisting of coralline algae-dominated spurs with isolated, low-lying acroporids, pocilloporids, and various encrusting corals and deep, narrow, scoured hard-bottom channels with some rubble. The spurs extended out most prominently to 3-5 m depth, becoming low-relief, wider spurs with shallow channels, sand, and rubble, with 30-50 cm relief. The shallow fore reef from 5 to 10 m had dense coral communities (ALCC=57±7.5%) dominated by pocilloporids, digitate and table acroporids, some heavy branched acroporids, encrusting *Leptastrea,* plates of *Montipora*, and low-lying *Favia* colonies. At 10-15 m depth (ALCC=75±13%), coral cover varied; some spurs and mounds were composed of dense coral assemblages, though some low-lying areas were comprised of a mix of coral and open substrate. The reefs sloped gradually to about 18-20 m (ALCC=32±7.5%) before dropping steeply to 30+ m. ALCC across all sites was 51%, which was significantly higher than that of all other islands within the Austral Islands with the exception of Tubuai (see Tukey's HSD groups in Supplemental Table 1.) and did not vary across the surveys depths (F=2.0, p=0.13). Temperature averaged 26.7±0.083°C, and the salinity was 35.7 psu at every site.

Although pocilloporids were common at depths <20 m, none resembled the classic morphotypes of *P. damicornis*. Of the 14 pocilloporids genotyped (Supplemental Table 1), 1 from site AUMA28 was found to be *P. meandrina* (Supplemental Table 3), and it hosted *Symbiodinium* of clade C only. The remaining 13 colonies were of an undescribed genotype of *P. verrucosa*. *P. damicornis* and *P. acuta* were absent from Maria. The *Symbiodinium* genotype was determined in 12 of these 13 *P. verrucosa* samples, and numerous colonies were found to host multiple *Symbiodinium* types; four of the twelve colonies (33%) hosted more than one clade of *Symbiodinium* at Maria; two hosted both clade A and C, and the other two housed both clades C and D. Mixed clade *Symbiodinium* assemblages were relatively more common at Maria, as well as in *P. verrucosa* (which was only collected from Maria), compared to all other

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sites from both the Austral and Cook Island archipelagos (X^2 tests, $p<0.05$ for both spatial and species comparisons).

Rarotonga, Cook Islands. Twelve sites were surveyed over the course of five days at Rarotonga (Supplemental Fig. 3A and Supplemental Table 2). The reefs of Rarotonga have a history of disturbance including: 1) a severe COTS outbreak in the middle of the 1970s and a second outbreak from 1995-2001; 2) several major cyclones in the early 2000s; and 3) minor bleaching during recent El Niño years. Sites on the north coast still showed evidence of storm damage, as large accumulations of rubble were observed from 10-12 m depth (ALCC=37±9.6%) to the base of the reef at 25 m, and continuing down the slope. The fore reef lacked a prominent spur and groove structure. Generally, the shallows (5-10 m; ALCC=28±3.9%) were a sloping hard ground with some micro relief. Below this was a highly eroded framework with large, scattered boulders constructed primarily of large *Porites* skeletons. Many very large overturned boulders were apparent, and some still had living remnants of *Porites*. Some reefs had a framework of large *Porites* skeletons intermixed with living colonies to about 25 m (ALCC=31±7.8%), followed by a deeper, gently sloping rubble field. The overall ALCC of 29% was significantly higher than that of Aitutaki (15%), but lower than that of Palmerston (51%; Supplemental Table 2). ALCC was also significantly different across survey depths ($F=2.8$, $p<0.05$); this was mainly driven by a significantly higher coral cover at 15-20 m (44±4.5%) versus 10 m (24±3.9%; Tukey's HSD, $p<0.05$). Finally, the average salinity across these sites was 35.7±0.026 psu, and the average temperature was 25.5±0.059°C.

Thirty-four pocilloporid colonies were collected across the 12 sites. Fifteen of these samples were genotyped (Supplemental Table 4), and only two (13%) were of the α genotype of *P. damicornis* (Fig. 1). Both of these *P. damicornis* colonies hosted clade C *Symbiodinium* C only. Four (26%) colonies were found to be *P. meandrina* (Supplemental Table 4), and one of these hosted *Symbiodinium* of clades A and C. This was the only colony sampled in Rarotonga that hosted multiple *Symbiodinium* clades and is one of only three samples in the entire Cook Islands collection (Supplemental Table 4) to be comprised of a mixed-clade *Symbiodinium* population. The remaining nine colonies were all found to be *P. damicornis* genotype β (i.e., *P. acuta*).

Aitutaki, Cook Islands. Ten sites were visited over the course of four days at Aitutaki (Supplemental Fig. 3B and Supplemental Table 2). The average temperature was 28.4±0.25°C, and the average salinity was 35.5±0.08 psu. Outer, fore reef communities had been impacted by a severe COTS outbreak that was reported to have begun in 2012 and was still going at the time of surveying. Additional damage was caused by Cyclone Pat, which passed directly over the island in February 2010. Coral cover had declined substantially throughout the fore reef as a result of COTS predation, with some additional damage possibly attributed to Cyclone Pat. Coral cover had declined by 80-99.9% throughout deep (15-30 m) fore reef sites surrounding the atoll, with <0.05% live cover remaining in most locations. Similar declines were noted at shallower depths (3-15 m) off the west, north, northeast, and south sides. In these areas, a very low number of undamaged, intact corals remained. Survivors were predominantly coral taxa that are not preferred COTS food sources. The ALCC of 15±1.6% did not differ significantly across survey depths (F=0.59, p=0.73). Notably, the standard deviation between sites was high (13%) and the range was 0-62% across all sites and depths due to the COTS not having reached certain regions of the atoll at the time of sampling.

Thirteen corals were collected at eight of the ten sites, and twelve of these were genotyped (Supplemental Table 4). All but one were *P. acuta* (Fig. 1); the lone remaining colony was *P. meandrina*. *P. damicornis* was not present at Aitutaki. The *Symbiodinium* populations were genotyped in 10 of the 12 samples, and all with the exception of two were found to house *Symbiodinium* of clade C only; both sample "*P. acuta* Aitutaki 97" from site CIAT13 and sample "*P. acuta* Aitutaki 105" from site CIAT19 hosted *Symbiodinium* of both clades C and D (Supplemental Table 4).

Palmerston, Cook Islands. The final island visited during the Australs-Cook Islands mission was Palmerston (Supplemental Fig. 3C), a remote atoll with only 60-70 inhabitants. Eight reefs were visited over the course of three days, and pocilloporids were sampled from seven of them (Supplemental Table 2). The average temperature was 28.0±0.096°C, and the salinity was 35.5 psu at every site. The fore reef communities of Palmerston appear to have been spared damage from cyclones, COTS, bleaching events, or other disturbances, and most areas had very high cover of living corals (ALCC=51±3.1%, statistically

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similar to that of Maria [$p>0.05$]). Reefs tended to have a fairly wide, gently sloping fore reef terrace extending from 5 to 10 m depth (ALCC=29±3.6%), followed by a gradual slope to 20 m (ALCC=53±4.7%), and then a steeper slope. Two very narrow channels allowed access to the lagoonal areas, in which small coral bommies occurred in shallow waters near the margins of the reef crest. Within the lagoon there were a few isolated patch reefs. These tended to have a high cover of small branching and table acroporids on the upper surfaces (1-2 m depth) and steeply sloping sides with little coral. On the fore reef, shallow reef communities were dominated by large, massive colonies of *Astreopora*, while middle depths (15-20 m; ALCC =53±5.1%) had a band of *Favia stelligera* and large *Lobophyllia.* ALCC was significantly different across depths ($F=6.3$, $p<0.0001$) due to the average cover at 5-10 m being significantly less than that of all other surveyed depths (Tukey's HSD, $p<0.05$).

Fifteen pocilloporid coral biopsies were collected, of which thirteen were genotyped. Three different pocilloporid genotypes were found (Supplemental Table 4): *P. acuta* ($n=7$), *Pocillopora* sp. haplotype 8a ($n=3$), and *P. meandrina* ($n=3$). All thirteen of the genotyped colonies hosted *Symbiodinium* of clade C only. Palmerston was only one of two island groups visited during the 3.5-week mission in which haplotype 8a specimens were collected. These corals appear morphologically similar to *P. verrucosa* and *P. meandrina* (Supplemental Figure 4), and not *P. damicornis*. The α genotype of *P. damicornis* was not present at Palmerston, and in total only 2 of the 39 colonies (~5%) genotyped from the Cooks Islands were found to be *P. damicornis* (Fig. 1).

Supplemental tables

Supplemental Table 1. Austral Islands, French Polynesia sampling site characteristics. The fraction below the island name represents the number of sites (all of which were on the fore reef) at which corals were collected over the total number of sites surveyed, and pocilloporid corals were sampled from 21 out of the 30 sites surveyed. Although five sites at Rimatara were surveyed between April 18 and 19, 2013, no pocilloporids other than *P. eydouxi* were found due to a crown of thorns starfish outbreak. The live coral cover presented for each site represents the average across all survey depths, and the average live coral cover (ALCC) presented for each island (±standard error of the mean) reflects the average across all sites within an island, not just those from which specimens were taken. A significant island effect on ALCC was detected within the Austral Islands dataset (F=30, p<0.0001), and letters adjacent to ALCC values for each island represent Tukey's honestly significant difference (p<0.05) groups. All statistical analyses were conducted with JMP® (ver. 11), and error terms represent standard error of the mean.

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Island	Site	Exposure	Latitude	Longitude	Date	Temp. (°C)	Salinity (psu)	ALCC (%)	# corals genotyped/ # collected
Raivavae	AURV01	leeward	-23.8605	-147.7151	2013-Apr-11	25.7	35.7	23	0/1
(6/8 sites)	AURV03	windward	-23.8318	-147.6574	2013-Apr-11	25.7	35.7	12	1/2
	AURV04	windward	-23.8282	-147.5901	2013-Apr-12	25.5	35.6	55	1/1
	AURV06	leeward	-23.8962	-147.7123	2013-Apr-12	25.6	35.7	46	4/5
	AURV07	leeward	-23.9123	-147.6609	2013-Apr-13	25.5	35.7	34	3/3
	AURV08	leeward	-23.9108	-147.6843	2013-Apr-13	25.5	35.7	41	4/6
					Raivavae ALCC and total genotyped/total collected			**34±4.9(b)**	**13/18**
Tubuai	AUTB09	leeward	-23.4213	-149.4402	2013-Apr-14	25.8	35.6	42	3/4
(7/9 sites)	AUTB10	leeward	-23.3827	-149.5493	2013-Apr-14	25.9	35.6	40	3/3
	AUTB11	leeward	-23.4253	-149.5184	2013-Apr-14	25.9	35.6	33	5/5
	AUTB12	windward	-23.4251	-149.4057	2013-Apr-15	25.8	35.6	32	2/2
	AUTB13	windward	-23.3786	-149.3853	2013-Apr-15	25.8	35.6	43	3/3
	AUTB15	leeward	-23.3485	-149.5313	2013-Apr-16	25.7	35.7	51	1/1
	AUTB16	leeward	-23.3561	-149.5518	2013-Apr-16	25.8	35.6	52	1/1
					Tubuai ALCC and total genotyped/total collected			**41±4.1(ab)**	**18/19**
Rurutu	AURR18	windward	-22.4522	-151.3235	2013-Apr-17	26.5	35.7	4.4	1/3
(3/3 sites)	AURR19	leeward	-22.4323	-151.3760	2013-Apr-17	26.6	35.6	2.6	0/2
	AURR20	windward	-22.5204	-151.3327	2013-Apr-17	26.6	35.7	3.8	1/3
					Rurutu ALCC and total genotyped/total collected			**3.6±0.5(c)**	**2/8**
Maria	AUMA26	windward	-21.8130	-154.6891	2013-Apr-20	26.7	35.7	53	3/4
(5/5 sites)	AUMA27	windward	-21.7901	-154.7037	2013-Apr-20	26.8	35.7	41	3/3
	AUMA28	leeward	-21.8200	-154.7239	2013-Apr-20	26.8	35.7	42	2/3
	AUMA29	windward	-21.7972	-154.6917	2013-Apr-21	26.8	35.7	47	3/3
	AUMA30	leeward	-21.8008	-154.7180	2013-Apr-21	26.6	35.7	71	3/3
					Maria ALCC and total genotyped/total collected			**51±5.4(a)**	**14/16**
					Austral Islands ALCC and total genotyped/total collected			**32±3.5**	**47/61**
					ALCC minus Rurutu and Rimatara			**40±2.8**	

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Supplemental Table 2. **Cook Islands sampling site characteristics**. The fraction below the island name represents the number of sites at which corals were collected over the total number of sites; all sites except CIAT22 were on the fore reef, and pocilloporid corals were sampled from 27 of the 30 sites visited. The average live coral cover (ALCC) presented for each site represents the average across all survey depths, and the ALCC presented for each island (±standard error of the mean) reflects the average across all sites within an island, not just those from which specimens were taken. Letters adjacent to ALCC values represent Tukey's honestly significant difference ($p<0.05$) groups, as a significant effect of island was detected within the Cook Islands dataset ($F=37$, $p<0.0001$). ALCC was similar between the Austral (32%) and Cook (31%) Islands ($F=0.23$, $p=0.64$), though differed significantly across all eight islands surveyed during the 3.5-week research cruise ($F=46$, $p<0.0001$). All statistical analyses were conducted with JMP® (ver. 11), and error terms represent standard error of the mean. "ND"=no data.

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Island	Site	Exposure	Latitude	Longitude	Date	Temp. (°C)	Salinity (psu)	ALCC (%)	# corals genotyped/ # collected
Rarotonga	CIRR01[a]	leeward	-21.1941	-159.8091	2013-Apr-22	27.4	35.7	38	4/5
(12/12 sites)	CIRR02[a]	windward	-21.2513	-159.8290	2013-Apr-23	ND	ND	28	2/2
	CIRR03[a]	windward	-21.2136	-159.8331	2013-Apr-23	ND	ND	30	0/4
	CIRR04[a]	leeward	-21.2417	-159.7225	2013-Apr-24	27.4	35.5	19	1/3
	CIRR05[a]	leeward	-21.2136	-159.7330	2013-Apr-24	27.4	35.7	29	2/3
	CIRR06[a]	leeward	-21.1993	-159.7569	2013-Apr-24	ND	ND	45	1/3
	CIRR07[b]	windward	-21.2642	-159.8165	2013-Apr-26	27.3	35.7	16	3/3
	CIRR08[b]	windward	-21.2745	-159.7725	2013-Apr-26	27.3	35.7	21	2/4
	CIRR09[a]	windward	-21.2719	-159.7299	2013-Apr-26	27.4	35.7	21	0/1
	CIRR10[a]	windward	-21.2007	-159.7714	2013-Apr-27	27.4	35.7	39	0/2
	CIRR11[b]	windward	-21.2300	-159.8335	2013-Apr-27	27.3	35.7	29	0/3
	CIRR12[a]	leeward	-21.1935	-159.7965	2013-Apr-27	27.4	35.7	33	0/1
				Rarotonga ALCC and total genotyped/total collected				**29±2.6(b)**	**15/34**
Aitutaki	CIAT13[a]	windward	-18.9043	-159.7236	2013-Apr-28	28.6	35.5	26	3/3
(8/10 sites)	CIAT15[a]	leeward	-18.8897	-159.8272	2013-Apr-29	28.4	35.5	7.7	1/1
	CIAT16[a]	leeward	-18.8672	-159.8188	2013-Apr-29	28.4	35.5	13	2/2
	CIAT17[a]	leeward	-18.8331	-159.7941	2013-Apr-30	28.4	35.3	8.5	2/2
	CIAT18[a]	windward	-18.9173	-159.8452	2013-Apr-30	28.3	35.4	17	1/1
	CIAT19[a]	leeward	-18.8517	-159.8054	2013-Apr-30	27.7	35.4	24	1/1
	CIAT20[a]	windward	-18.9283	-159.7943	2013-May-1	28.2	35.5	12	2/2
	CIAT22[b]	windward	-18.9271	-159.7250	2013-May-1	28.3	35.1	7.1	0/1
				Aitutaki ALCC and total genotyped/total collected				**15±2.8(c)**	**12/13**
Palmerston	CIPA23[a]	windward	-17.9926	-163.1535	2013-May-3	27.9	35.5	56	2/2
(7/8 sites)	CIPA24[a]	windward	-18.0291	-163.1178	2013-May-3	28.0	35.5	31	1/1
	CIPA25[a]	windward	-18.0489	-163.1128	2013-May-3	28.2	35.5	47	2/2
	CIPA26[a]	windward	-18.0885	-163.1521	2013-May-4	28.0	35.5	60	2/3
	CIPA27[a]	windward	-18.0697	-163.1293	2013-May-4	28.0	35.5	57	1/2
	CIPA28[a]	leeward	-18.0412	-163.1876	2013-May-5	27.9	35.5	41	3/3
	CIPA29[a]	leeward	-18.0057	-163.1757	2013-May-5	28.0	35.5	64	2/2
				Palmerston ALCC and total genotyped/total collected				**51±3.1(a)**	**13/15**
				Cook Islands ALCC and total genotyped/total collected				**30±3.2**	**40/62**
				ALCC and total genotyped/total collected from both archipelagos				**31±2.3**	**87/123**

258[a]fringing reef. [b]reef flat.

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Supplemental Table 3. **Austral Islands, French Polynesia pocilloporid samples (*n*=47).** Additional site characteristics can be found in Supplemental Table 1. "ND" = no data.

Sample (locus) name	NCBI accession	Site	Depth (m)	*Symbiodinium* clade(s)
Pocillopora damicornis (genotype α[a])				
P. damicornis Raivavae 3	KJ720218	AURV03	11.5	C only
P. damicornis Raivavae 4	KM975289	AURV04	16.0	C only
P. damicornis Raivavae 5	KM975290	AURV06	14.0	C only
P. damicornis Raivavae 6	KM975291	AURV06	13.0	C only
P. damicornis Raivavae 7	KJ790160	AURV06	13.0	C only
P. damicornis Raivavae 9	KJ720219	AURV07	16.5	C only
P. damicornis Raivavae 10	KM975292	AURV07	15.6	C only
P. damicornis Raivavae 11	KJ720220	AURV07	17.0	C only
P. damicornis Raivavae 13	KJ720221	AURV08	14.5	C only
P. damicornis Raivavae 14	KJ790161	AURV08	14.5	ND
P. damicornis Raivavae 17	KJ720222	AURV08	14.0	C only
P. damicornis Raivavae 18	KJ720223	AURV08	14.0	C only
P. damicornis Tubuai 19	KJ790162	AUTB09	15.0	C only
P. damicornis Tubuai 20	KJ720224	AUTB09	14.5	C only
P. damicornis Tubuai 21	KJ720225	AUTB09	15.0	C only
P. damicornis Tubuai 23	KJ720226	AUTB10	15.5	C only
P. damicornis Tubuai 24	KJ790163	AUTB10	15.0	C only
P. damicornis Tubuai 25	KJ720227	AUTB10	15.5	C only
P. damicornis Tubuai 26	KJ720228	AUTB11	14.5	A + C
P. damicornis Tubuai 27	KJ720229	AUTB11	14.5	C only
P. damicornis Tubuai 28	KJ720230	AUTB11	14.5	C only
P. damicornis Tubuai 29	KJ720231	AUTB11	14.5	C only
P. damicornis Tubuai 30	KJ720232	AUTB11	14.0	C only
P. damicornis Tubuai 31	KJ720233	AUTB12	15.0	C only
P. damicornis Tubuai 33	KJ720234	AUTB13	14.5	C only
P. damicornis Tubuai 34	KJ720235	AUTB13	15.0	C only
P. damicornis Tubuai 35	KJ720236	AUTB13	14.5	C only
P. damicornis Tubuai 36	KJ790164	AUTB15	18.0	C only
P. damicornis Tubuai 37	KJ720237	AUTB16	18.0	C only
P. damicornis Rurutu 40	KJ720238	AURR18	11.0	C only
Pocillopora acuta (genotype β[a])				
P. acuta Raivavae 12	KJ720240	AURV06	13.0	ND
Pocillopora meandrina (genotype m[a])				
P. meandrina Tubuai 32	KJ720263	AUTB12	14.5	C only
P. meandrina Maria 54	KJ720264	AUMA28	14.5	C only
Pocillopora verrucosa (undescribed genotype)				
P. verrucosa Maria 46	KJ720271	AUMA26	15.0	C + D
P. verrucosa Maria 47	KJ720272	AUMA26	16.0	C only
P. verrucosa Maria 49	KJ720273	AUMA26	13.5	C only
P. verrucosa Maria 50	KJ720275	AUMA27	16.5	C only
P. verrucosa Maria 51	KJ720274	AUMA27	15.0	C only
P. verrucosa Maria 52	KJ790173	AUMA27	16.5	ND
P. verrucosa Maria 53	KJ720276	AUMA29	13.5	C only
P. verrucosa Maria 55	KJ720277	AUMA28	14.0	C only

P. verrucosa Maria 57	KJ720278	AUMA29	13.0	A + C
P. verrucosa Maria 58	KJ790174	AUMA29	13.5	C only
P. verrucosa Maria 59	KJ720279	AUMA30	14.0	C only
P. verrucosa Maria 60	KJ720280	AUMA30	9.0	C + D
P. verrucosa Maria 61	KJ720281	AUMA30	6.5	A + C
***Pocillopora* sp.** (haplotype 8a[b])				
Pocillopora sp. haplotype 8A Rurutu 45	KJ790172	AURR20	9.0	ND

262[a]Nomenclature of Schmidt-Roach et al. (2014). [b]Nomenclature of Pinzon et al. (2013).
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Supplemental Table 4. **Cook Islands pocilloporid samples (*n*=41).** Additional site characteristics can be found in Supplemental Table 2. "ND"=no data.

Sample (locus) name	NCBI accession	Site	Depth (m)	*Symbiodinium* clade(s)
Pocillopora damicornis (genotype α[a])				
P. damicornis Rarotonga 81	KJ720239	CIRR06	16.0	C only
P. damicornis Rarotonga 86	KJ790165	CIRR08	16.0	C only
Pocillopora acuta (genotype β[a])				
P. acuta Rarotonga 62	KJ790168	CIRR01	15.0	C only
P. acuta Rarotonga 64	KJ790169	CIRR01	16.0	ND
P. acuta Rarotonga 73	KJ720241	CIRR04	14.0	C only
P. acuta Rarotonga 76	KJ720242	CIRR05	14.5	C only
P. acuta Rarotonga 78	KJ720243	CIRR05	15.5	C only
P. acuta Rarotonga 82	KJ720244	CIRR07	16.0	C only
P. acuta Rarotonga 83	KJ720245	CIRR07	17.0	C only
P. acuta Rarotonga 84	KJ720246	CIRR07	14.5	C only
P. acuta Rarotonga 88	KJ720247	CIRR08	9.0	C only
P. acuta Aitutaki 96	KJ720248	CIAT13	11.5	C only
P. acuta Aitutaki 97	KJ720249	CIAT13	10.0	C + D
P. acuta Aitutaki 98	KJ720250	CIAT13	10.5	C only
P. acuta Aitutaki 99	KJ720251	CIAT15	5.0	C only
P. acuta Aitutaki 100	KJ720252	CIAT16	10.0	C only
P. acuta Aitutaki 101	KJ880801	CIAT16	6.5	C only
P. acuta Aitutaki 102	KJ720253	CIAT17	15.0	C only
P. acuta Aitutaki 103	KJ720254	CIAT17	15.0	C only
P. acuta Aitutaki 104	KJ790170	CIAT18	14.5	ND
P. acuta Aitutaki 105	KJ720255	CIAT19	12.0	C + D
P. acuta Aitutaki 107	KJ720256	CIAT20	8.0	C only
P. acuta Palmerston 109	KJ720257	CIPA23	8.0	C only
P. acuta Palmerston 110	KJ790171	CIPA23	6.5	C only
P. acuta Palmerston 112	KJ720258	CIPA25	11.0	C only
P. acuta Palmerston 119	KJ880803	CIPA28	10.0	C only
P. acuta Palmerston 120	KJ720259	CIPA28	9.0	C only
P. acuta Palmerston 121	KM975293	CIPA28	9.0	C only
P. acuta Palmerston 123	KJ880804	CIPA29	7.0	C only
Pocillopora meandrina (genotype m[a])				
P. meandrina Rarotonga 65	KJ720265	CIRR02	18.5	C only
P. meandrina Rarotonga 66	KJ720266	CIRR02	18.5	C only
P. meandrina Rarotonga 71	KJ720267	CIRR01	16.0	C only
P. meandrina Rarotonga 72	KJ720268	CIRR01	16.0	A + C
P. meandrina Aitutaki 106	KJ720269	CIAT20	11.0	C only
P. meandrina Palmerston 113	KJ720270	CIPA25	12.0	C only
P. meandrina Palmerston 117	KJ880802	CIPA27	13.5	ND
P. meandrina Palmerston 118	KJ790166	CIPA27	6.5	C only
P. meandrina Palmerston 122	KJ790167	CIPA29	7.0	C only
***Pocillopora* sp.** (haplotype 8a[b])				
Pocillopora sp. haplotype 8A Palmerston 111	KJ720260	CIPA24	14.0	C only
Pocillopora sp. haplotype 8A Palmerston 114	KJ720261	CIPA26	12.0	C only

Pocillopora sp. haplotype 8A Palmerston 115	KJ720262	CIPA26	10.0	C only

[a]Nomenclature of Schmidt-Roach et al. (2014). [b]Nomenclature of Pinzon et al. (2013).

Supplemental Table 5. **Estimation of evolutionary divergence over sequence pairs among different pocilloporid lineages/species using the maximum composite likelihood model.** The number of base substitutions per site (averaged over all sequence pairs between groups) between lineages is shown below the diagonal. The associated standard error for the respective comparison is shown above the diagonal.

	P. acuta	*P. damicornis*	*P. meandrina*	*P. verrucosa*	*Pocillopora* sp. haplotype 8a
P. acuta		0.0029	0.0036	0.0048	0.0036
P. damicornis	0.0079		0.0048	0.0054	0.0044
P. meandrina	0.0119	0.0196		0.0052	0.0031
P. verrucosa	0.0196	0.0248	0.0209		0.0047
Pocillopora sp. haplotype 8a	0.0117	0.0168	0.0078	0.0181	

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Supplemental Table 6. **Pocilloporids sampled in the Austral (Raivavae, Tubuai, Rurutu, and Maria) and Cook Islands (Rarotonga, Aitutaki, and Palmerston).** The corresponding percent abundance value for each genotype at each island data are summarized in pie graphs in Fig. 1.

Island	*P. damicornis* (genotype α)	*P. acuta* (genotype β)	*P. verrucosa* (undescribed genotype)	*Pocillopora* sp. (haplotype 8a)	*P. meandrina* (genotype m)	Total	%
Raivavae	12	1	0	0	0	13	14.9
Tubuai	17	0	0	0	1	18	20.7
Rurutu	1	0	0	1	0	2	2.3
Maria	0	0	13	0	1	14	16.1
Rarotonga	2	9	0	0	4	15	17.2
Aitutaki	0	11	0	0	1	12	13.8
Palmerston	0	7	0	3	3	13	14.9
Total	32	28	13	4	10	87	100
%	36.8	32.2	14.9	4.6	11.5	100	

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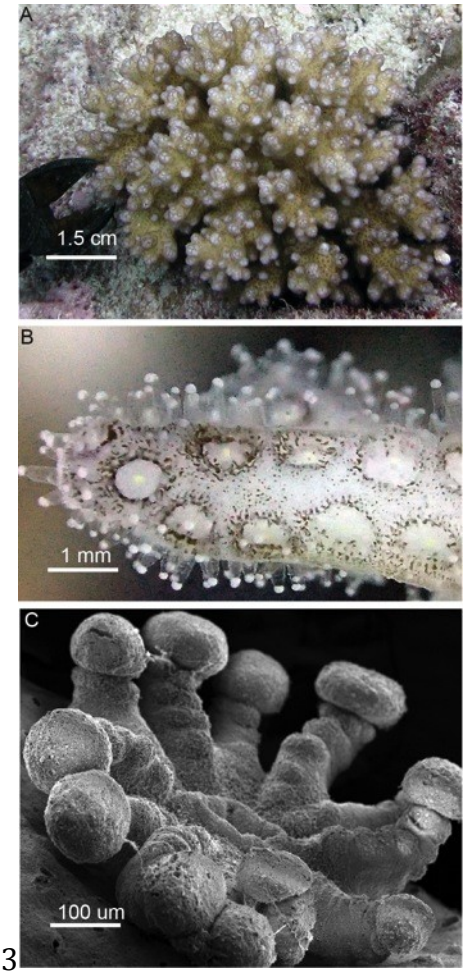
Supplemental Figures

Supplemental Fig. 1. ***Pocillopora damicornis*** **(genotype α) across two orders of magnitude**. (A) The specimen "*P. damicornis* Rarotonga 81" of Supplemental Table 4. (B) Using the "microscope" (i.e., macro) mode of an Olympus Tough TG-2 camera in underwater housing (also from Olympus), the ~1-mm diameter polyps are evident. The brown coloration in (A) and (B) represents the endosymbiotic dinoflagellate (genus *Symbiodinium*) populations residing within the coral gastroderm. (C) The mouth and tentacles of an individual *P. damicornis* polyp are more clearly seen with scanning electron microscopy (SEM). The sample was prepared for SEM and imaged as in Mayfield et al. (2013). Although *P. damicornis* polyps should have 12 tentacles, only 10-11 can be seen due to 2-3 having been fused together during the sample preparation process.



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Supplemental Fig. 2. **Sampling sites of the Austral Islands of French Polynesia**. In total 8, 9, 3, 5, and 5 reef sites were surveyed around (A) Raivavae, (B) Tubuai, (C) Rurutu, Rimatara, and (D) Maria, respectively. The map of Rimatara was not presented for reasons described in the text.

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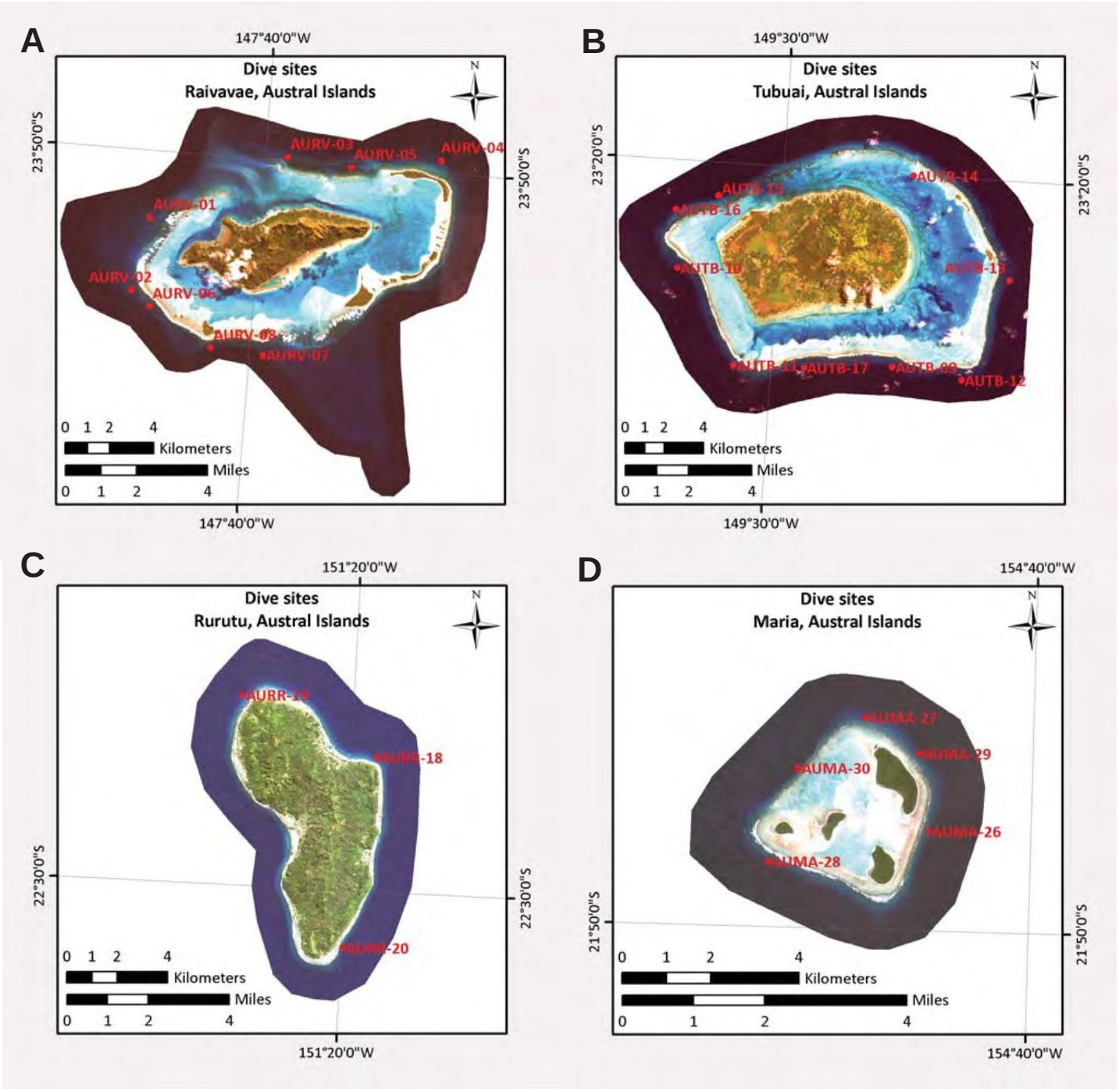

Supplemental Fig. 3. **Sampling sites of the Cook Islands**. In total 12, 10, and 8 reef sites were surveyed on SCUBA around (A) Rarotonga, (B) Aitutaki (atoll), and (C) Palmerston (atoll), respectively. Two

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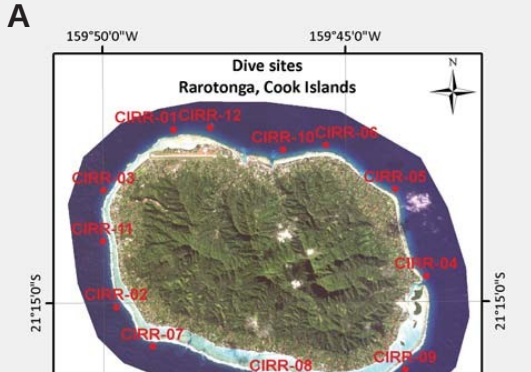
302snorkel survey sites (CIATS-1 and CIATS-2) have also been marked on the map of Aitutaki.



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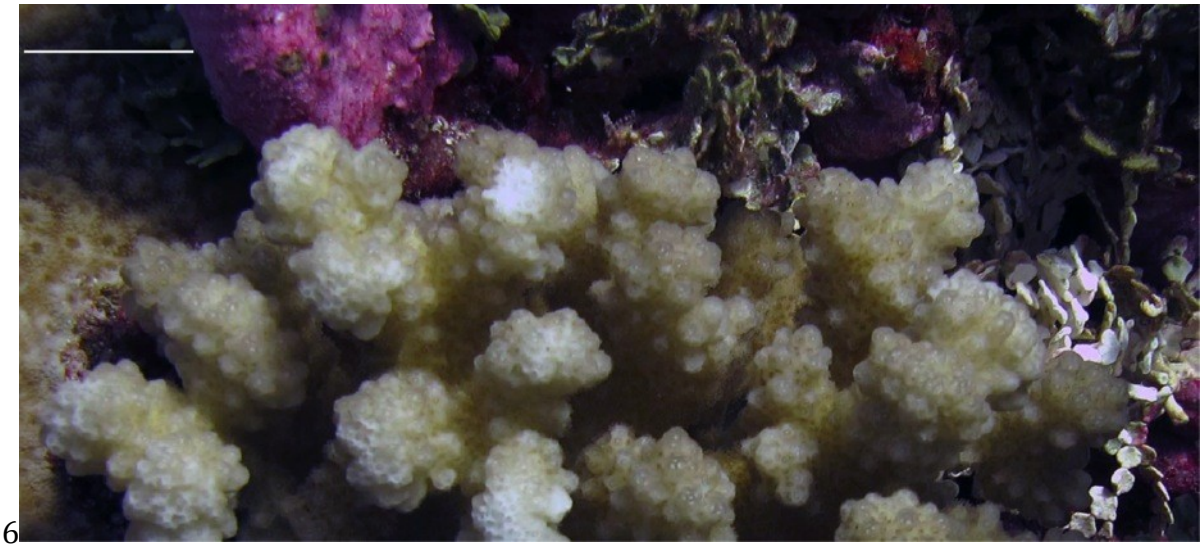
Supplemental Fig. 4. A *Pocillopora* sp. haplotype 8a colony from Palmerston Atoll in the Cook Islands. The scale bar represents 1.5 cm.



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