Supplemental Information for:

Increased diversity and concordant shifts in community structure of coral-associated Symbiodiniaceae and bacteria subjected to chronic human disturbance

Danielle C. Claar, Jamie M. McDevitt-Irwin, Melissa Garren, Rebecca Vega Thurber, Ruth D. Gates, Julia K. Baum

Table of Contents:

Figure S1. Study sites (n = 11) across five levels of human disturbance on Kiritimati. Villages are denoted with red circles, scaled by population size.
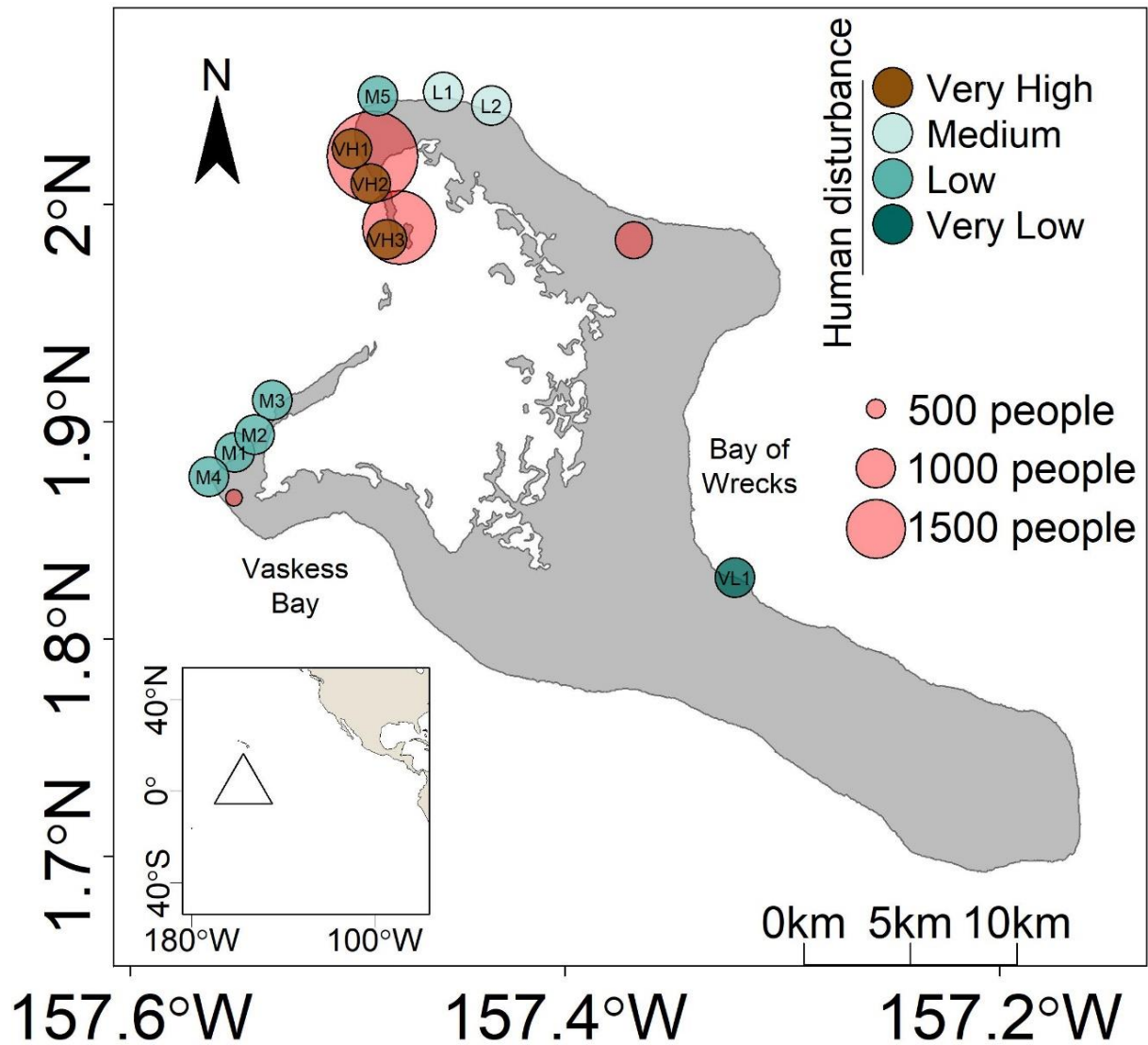
Figure S2. Beta diversity variation (i.e., distance to centroid) of Symbiodiniaceae communities in individual coral species across the disturbance gradient. A) *M. aequituberculata*, B) *P. grandis,* C) *P. lobata*, D) *H. microconos,* E) *P. ryukyuensis*, F) *F. pentagona*, and G) *D. matthaii*.
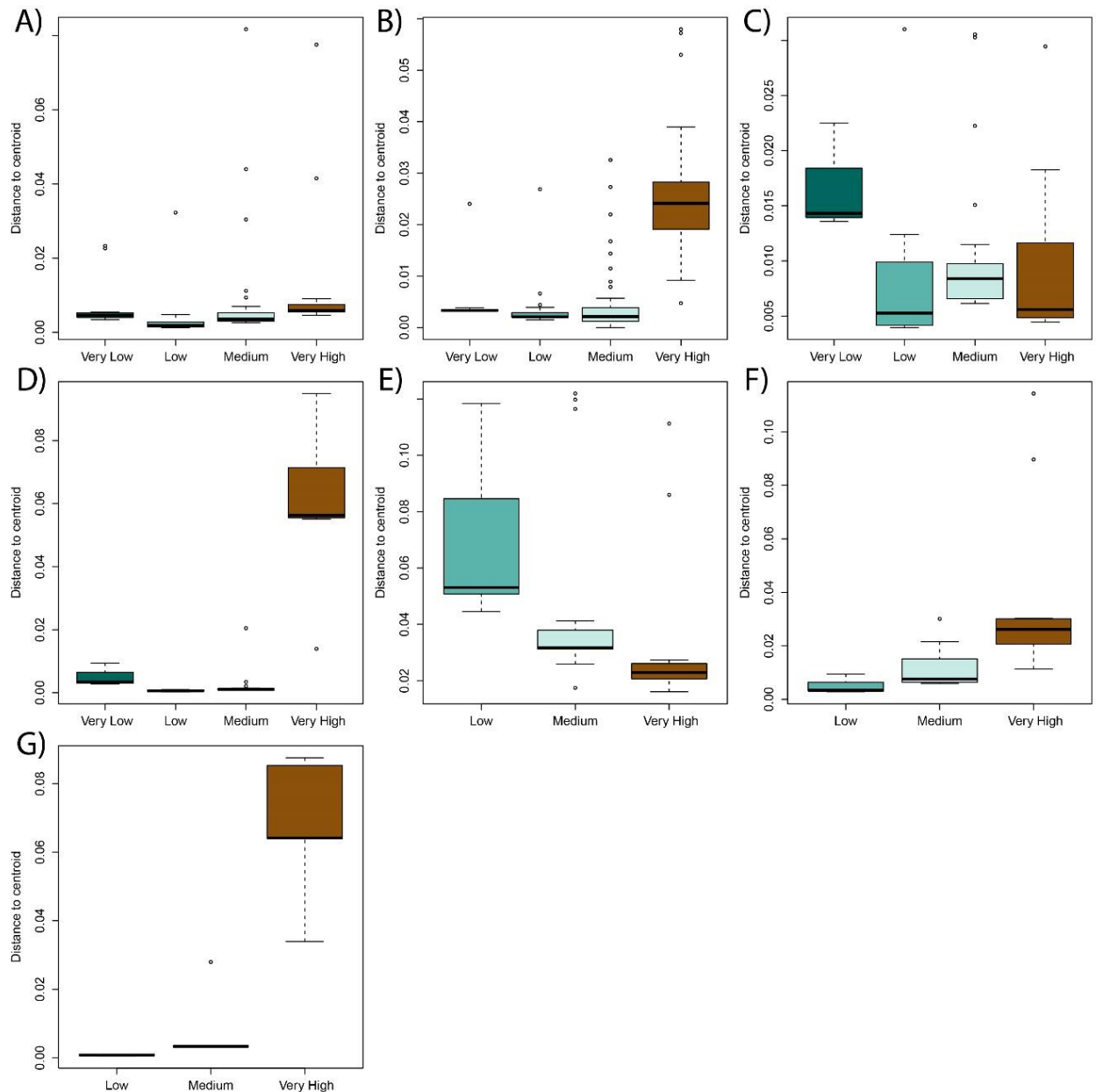
Figure S3. Multivariate ordination (PCoA) of Symbiodiniaceae communities associated with each coral species, showing community structure (multivariate location) and variation (multivariate dispersion). Points indicate individual samples (connected to the centroid point in the center), color indicates sampling time point, and shaded areas indicate boundaries of observed community structure.

.

Figure S4. Beta diversity variation (i.e., distance to centroid) of bacterial communities. A) *M. aequituberculata*, B) *P. lobata*, C) *H. microconos,* D) *P. ryukyuensis*, E) *F. pentagona*, and F) *D. matthaii*.

Figure S5. Multivariate ordination (PCoA) of bacterial communities associated with each coral species, showing community structure and variation (multivariate dispersion). Points indicate individual samples (connected to the centroid point in the center), color indicates sampling time point, and shaded areas indicate boundaries of observed community structure.
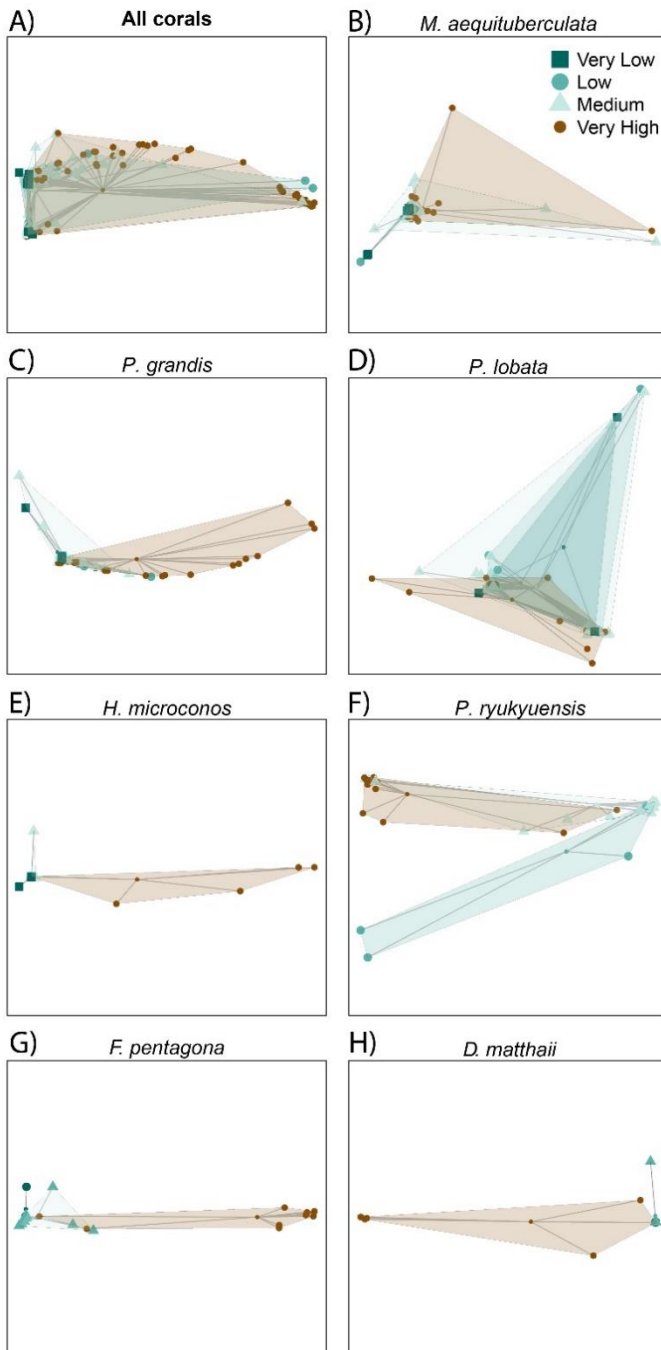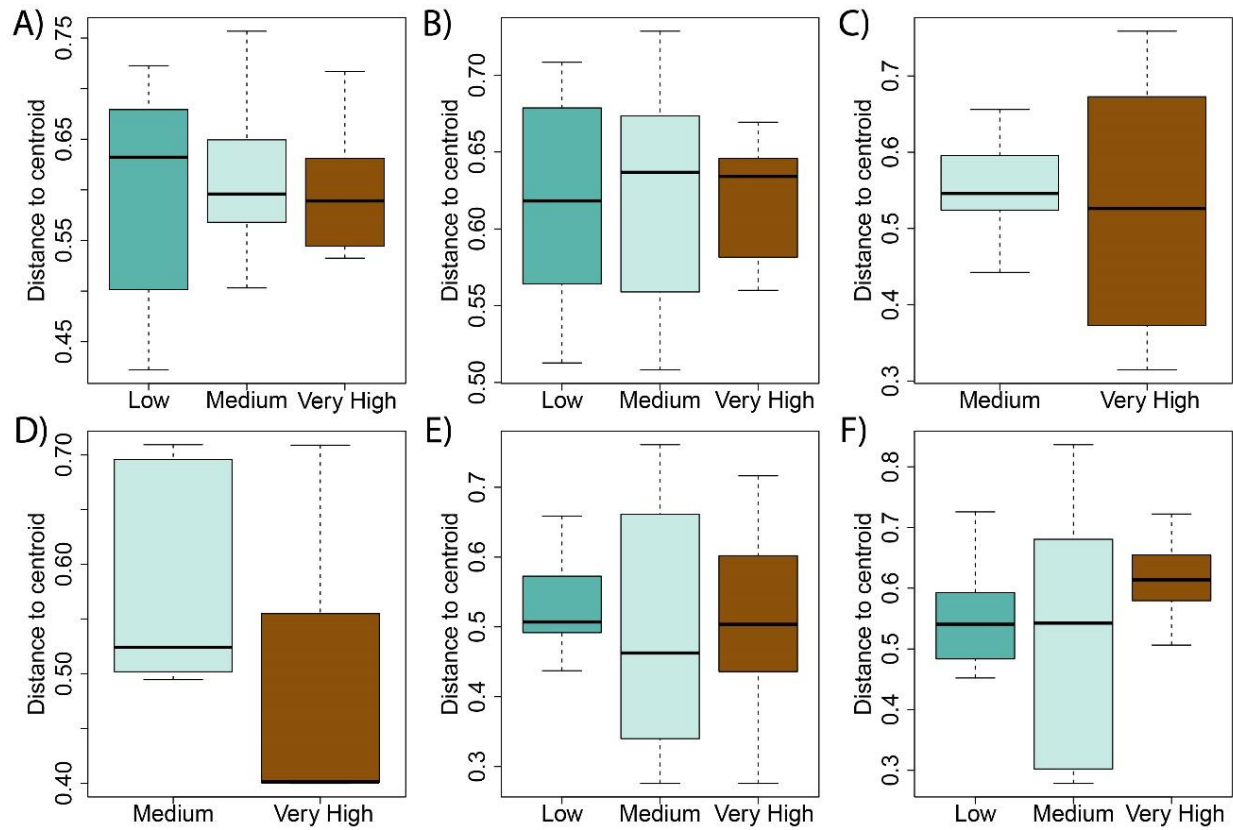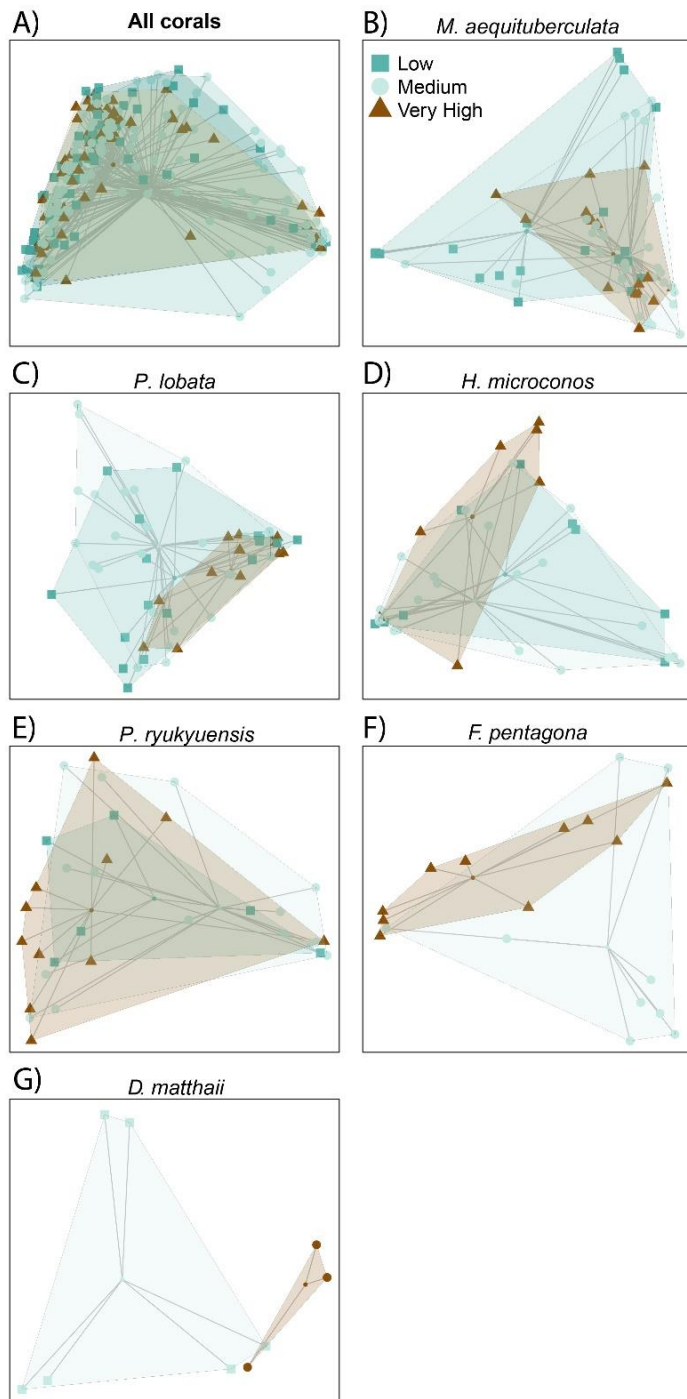
Table S1. **Calculation of human disturbance categories on Kiritimati.** Intersect_Pop_2km includes the number of people residing within 2 km of each site. Calculated based on Kiribati Population Census report. Fishing Buffer is a kernel density function of fishing intensity with ten discrete levels (from Watson et al. 2016). Intersect_Pop+Fishing is the sum of the previous two columns. Based on these calculations, sites are categorized into four distinct human disturbance categories (there is a fifth disturbance category, *high*, which was not sampled for this study). Site Name is included for cross-comparisons with other related Kiritimati publications.

Site Name	Intersect_Pop_2km	Fishing_Buffer	Intersect_Pop+Fishing	Disturbance Category
VH1	4042	3234	7276	Very High
VH2	1223	3638	4861	Very High
VH3	3065	2021	5086	Very High
M1	0	1213	1213	Medium
M2	0	1213	1213	Medium
M3	0	1213	1213	Medium
M4	351	809	1160	Medium
M5	0	1617	1617	Medium
L1	0	809	809	Low
L2	0	809	809	Low
VL1	0	0	0	Very Low

Table S2. Symbiodiniaceae sample size by coral species (ordered from most to least available samples). Coral life history strategies (Stress tolerant - *Porites lobata, Hydnophora microconos, Platygyra ryukyuensis, Favites pentagona*; Competitive - *Pocillopora eydouxi*; Generalist - *Montipora aequituberculata*) (Darling et al. 2012).

	SITE											
Coral Species	VH1	VH2	VH3	M1	M2	M3	M4	M5	L1	L2	VL1	All
M. aequituberculata	13	5	10	11	12	12	13	12	12	12	12	124
P. grandis	10	5	12	12	11	12	12	10	12	12	9	117
P. lobata	11	4	10	10	11	9	10	8	9	11	3	96
H. microconos	3	1	4	5	4	7	4	5	5	4	4	46
P. ryukyuensis	7	2	3	5	1	5	5	4	6	1	0	39
F. pentagona	4	4	3	2	1	3	3	3	1	3	0	27
D. matthaii	3	2	5	2	2	3	2	1	1	2	0	23
Total	51	23	47	47	42	51	49	43	46	45	28	472

Table S3. Bacterial microbiome sample size by coral species (ordered from most to least available samples).

	SITE									
Coral Species	**VH1**	**VH2**	**M1**	**M2**	**M3**	**M4**	**M5**	**L1**	**L2**	**All**
M. aequituberculata	5	10	7	6	5	8	5	12	9	67
P. lobata	4	8	5	6	5	6	5	10	7	56
H. microconos	4	3	4	4	5	4	5	5	4	38
P. ryukyuensis	3	8	3	1	3	4	4	5	1	32
F. pentagona	3	7	1	1	2	2	3	1	3	23
P. grandis	0	0	7	3	0	0	0	1	4	15
D. matthaii	1	2	2	1	1	1	1	1	0	10
Total	20	38	29	22	21	25	23	35	28	241

Table S4. Sample size by coral species for coral colonies where sequence data is available for both the bacterial microbiome and Symbiodiniaceae (ordered from most to least available samples). This is a subset of samples from Tables S1 and S2.

	SITE									
Coral Species	VH1	VH3	M1	M2	M3	M4	M5	L1	L2	All
M. aequituberculata	10	5	6	6	5	8	5	12	9	66
P. lobata	7	4	3	6	3	4	3	7	7	44
H. microconos	3	4	4	4	5	4	5	5	4	38
P. ryukyuensis	8	3	3	1	3	4	4	5	1	32
F. pentagona	7	3	1	1	2	2	3	1	3	23
P. grandis	0	0	7	3	0	0	0	1	4	15
D. matthaii	2	1	1	1	1	1	0	1	0	8
Total	37	20	25	22	19	23	20	32	28	226

Table S5. Symbiodiniaceae lineage for each dominant ASV, based on NCBI Blast results. All lineages that begin with "C" are in genus *Cladocopium*, and the lineage that begins with "D" is in genus *Durusdinium*.

ASV	Max score	Total score	Query cover	E value	Percent ID	Accession	Lineage
ASV1	525	525	95%	4.00E-145	100.00%	AY258496.1	C31
ASV2	555	555	100%	5.00E-154	100.00%	EU074966.1	C1
ASV3	549	549	100%	2.00E-152	99.67%	MN394935.1	C3
ASV4	555	555	100%	5.00E-154	100.00%	JN558044.1	C15
ASV5	555	555	100%	5.00E-154	100.00%	MN394940.1	C42
ASV6	551	551	100%	7.00E-153	100.00%	MN394923.1	D1
ASV9	529	529	100%	3.00E-146	98.35%	JN558044.1	C15
ASV10	544	544	100%	1.00E-150	99.33%	AB778606.1	C3
ASV25	553	553	100%	2.00E-153	100.00%	MN394975.1	C1
ASV29	549	549	99%	2.00E-152	99.67%	JN558044.1	C15
ASV34	555	555	99%	5.00E-154	100.00%	JN558044.1	C15
ASV58	549	549	100%	2.00E-152	99.67%	AB778606.1	C3
ASV153	544	544	100%	1.00E-150	99.33%	JN558044.1	C15
ASV155	527	527	100%	1.00E-145	98.33%	JN558044.1	C15
ASV162	538	538	100%	5.00E-149	99.00%	AB778606.1	C3

Table S6. Sample size of dominant Symbiodiniaceae ancestral lineage by coral species. All lineages that begin with "C" are in genus *Cladocopium*, and the lineage that begins with "D" is in genus *Durusdinium*.

	C1	C3	C15	C31	C42	D1
D. matthaii	0	18	1	0	0	4
F. pentagona	0	18	0	0	0	9
H. microconos	42	1	0	0	0	3
M. aequituberculata	0	1	1	120	2	0
P. ryukyuensis	0	23	0	0	0	16
P. grandis	3	0	2	2	107	3
P. lobata	0	1	91	3	1	0
TOTAL	45	62	95	125	110	35

Table S7. Symbiodiniaceae beta diversity variation (i.e., distance to centroid). Individual coral species by disturbance level that are not included in this table were not significant.

Model	Model Test	Significant Post-hoc Groups
Disturbance (pooled across coral species)	F = 86, df = 3, p < 0.001	Very High - Medium; p < 0.001 Very High - Low; p < 0.001 Very High - Very Low; p < 0.001
Species (pooled across disturbance levels)	F = 106, df = 6, p < 0.001	*M. aequituberculata - H. microconos;* p < 0.001 *M. aequituberculata - P. ryukyuensis;* p < 0.001 *M. aequituberculata - F. pentagona;* p < 0.001 *M. aequituberculata - D. matthaii;* p < 0.001 *P. grandis - P. ryukyuensis;* p < 0.001 *P. grandis - F. pentagona;* p < 0.001 *P. grandis - D. matthaii;* p < 0.001 *P. lobata - P. ryukyuensis;* p < 0.001 *P. lobata - F. pentagona;* p <0.001 *P. lobata - D. matthaii;* p < 0.001 *H. microconos - P. ryukyuensis;* p < 0.001 *H. microconos - F. pentagona;* p < 0.001 *H. microconos - D. matthaii;* p < 0.001 *P. ryukyuensis - D. matthaii;* p < 0.001 *D. matthaii - F. pentagona;* p = 0.010
Individual coral species, by disturbance level (only significant models shown)		
P. grandis	F = 39, df = 3, p < 0.001	Very High - Medium; p < 0.001 Very High - Low; p < 0.001 Very High - Very Low; p < 0.001
D. matthaii	F = 76, df = 2, p < 0.001	Very High - Medium; p < 0.001 Very High - Low; p < 0.001
H. microconos	F = 68, df = 3, p < 0.001	Very High - Medium; p < 0.001 Very High - Low; p < 0.001 Very High - Very Low; p < 0.001
F. pentagona	F = 5, df = 2, p = 0.012	Very High - Medium; p = 0.044 Very High - Low; p = 0.024

Table S8. Bacterial beta diversity variation (i.e., distance to centroid). When coral species were evaluated individually, no species showed a significant difference in variation by disturbance category.

Model	Model Test	Significant Post-hoc Groups
Pooled models		
Disturbance (pooled across coral species)	Not significant	Not significant
Species (pooled across disturbance levels)	F = 7.9, df = 6, p < 0.001	*M. aequituberculata - H. microconos;* p < 0.001 *P. lobata - H. microconos;* p < 0.001 *H. microconos - P. ryukyuensis;* p = 0.01 *H. microconos - F. pentagona;* p = 0.02 *H. microconos - D. matthaii*; p = 0.03