

1 **Evaluating Predicted Coral Heat Stress Phenotypes and Microbial Associations in**
2 **Nursery-Propagated Corals During a Real-World Bleaching Event**

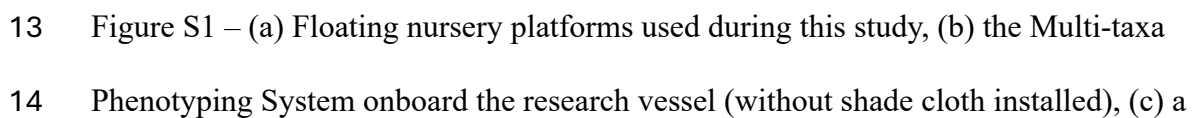
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schematic outlining the workflow for donor colony fragment collection from Blue Lagoon, South North Opal (SNO) and Rayban, the subsequent positioning of fragments into coral nurseries, and fragments retained for preservation or acute heat stress testing, and (d) a timeline showing how many days each timepoint corresponds to

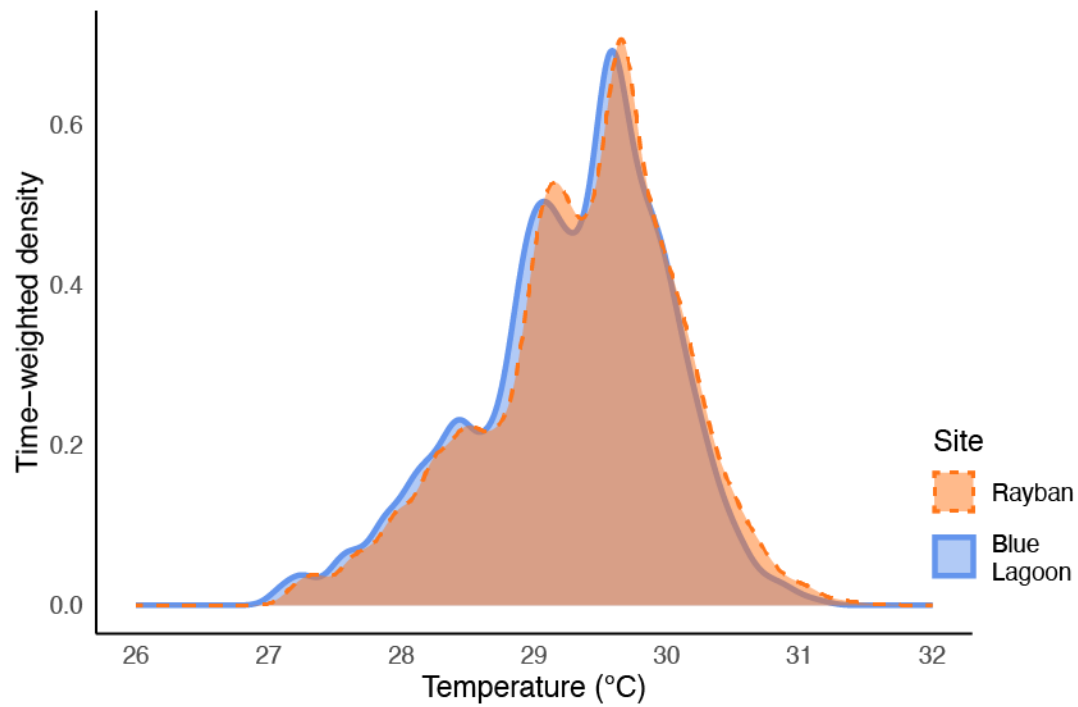
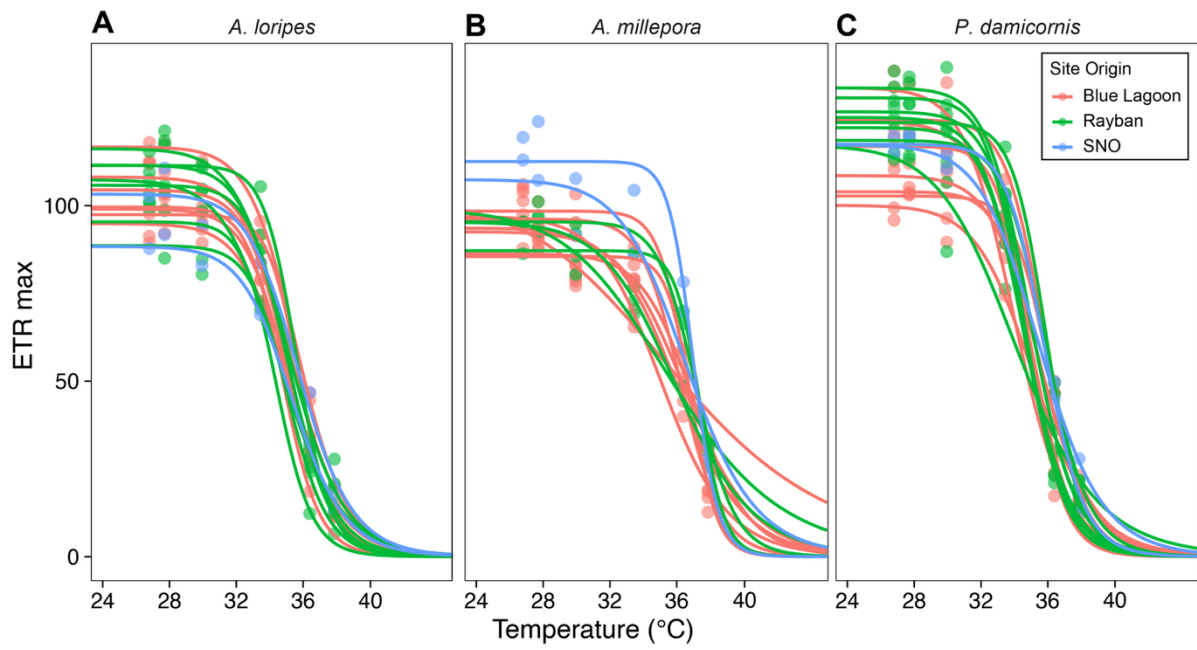
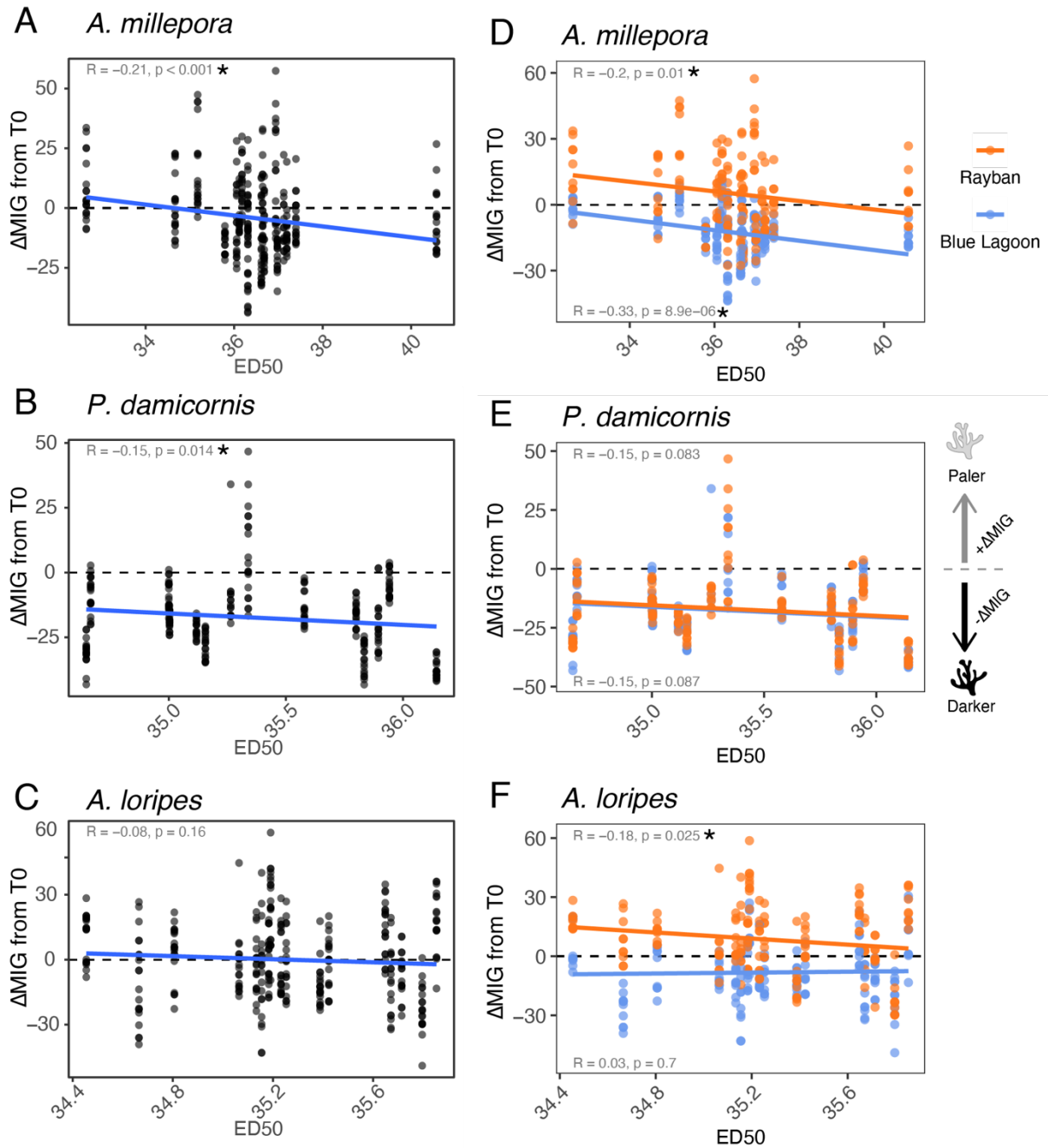


Figure S2 – Density distribution plot illustrating the time spent within each temperature between 01-Feb-2024 to 26-Apr-2024 at both nursery sites.



22

23 Figure S3 – ETR max (maximum capacity photosynthetic light reactions) thermal
 24 performance curves modelled using a three parameter log logistic regression model for the
 25 three species (A) *A. loripes*, (B) *A. millepora* and (C) *P. damicornis* parent colonies from
 26 Blue Lagoon, Rayban and SNO reef sites at the start of the study.

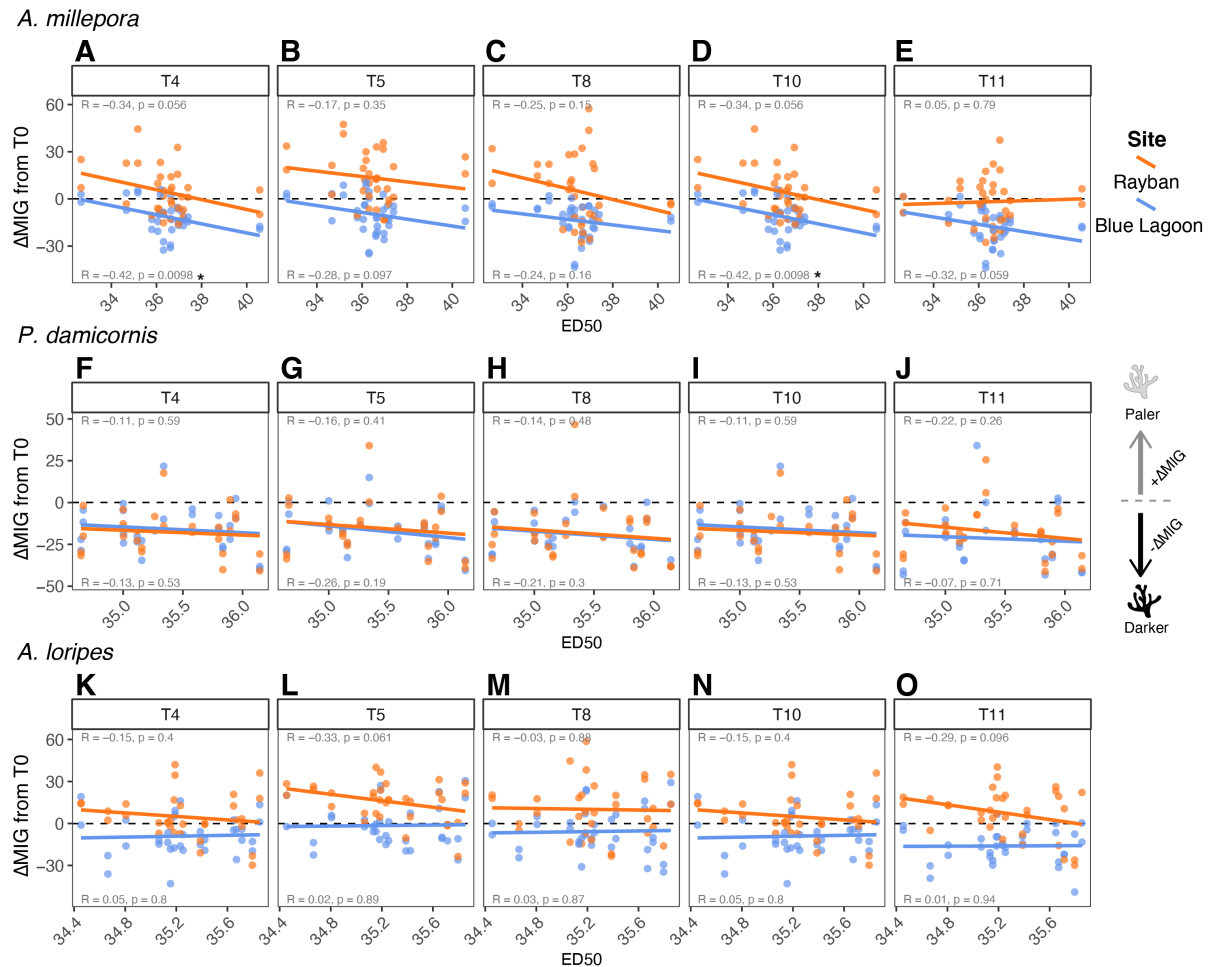


27

28 Figure S4 – Relationship between MTP thermotolerance metric of ED_{50} and change in Mean
 29 Intensity Grey (ΔMIG %) for (pooled time and nursery site) (a) *A. millepora*, (b) *P.*
 30 *damicornis*, and (c) *A. loripes*, and for nursery sites individually for (d) *A. millepora*, (e) *P.*
 31 *damicornis*, and (f) *A. loripes*. r Pearson correlation coefficient and p indicates significance
 32 of the correlation, * indicates significant p value < 0.05 . Points above the dashed line

33 (+ Δ MIG) indicate paling relative to their initial colour at T0 and below the line (- Δ MIG)

34 indicate darkening relative to their individual colour at T0.



35

36 Figure S5 – Correlation plots between ED₅₀ values and change in Mean Intensity Grey

37 (Δ MIG %) for coral fragments of (a) *A. millepora*, (b) *P. damicornis*, and (c) *A. loripes* over

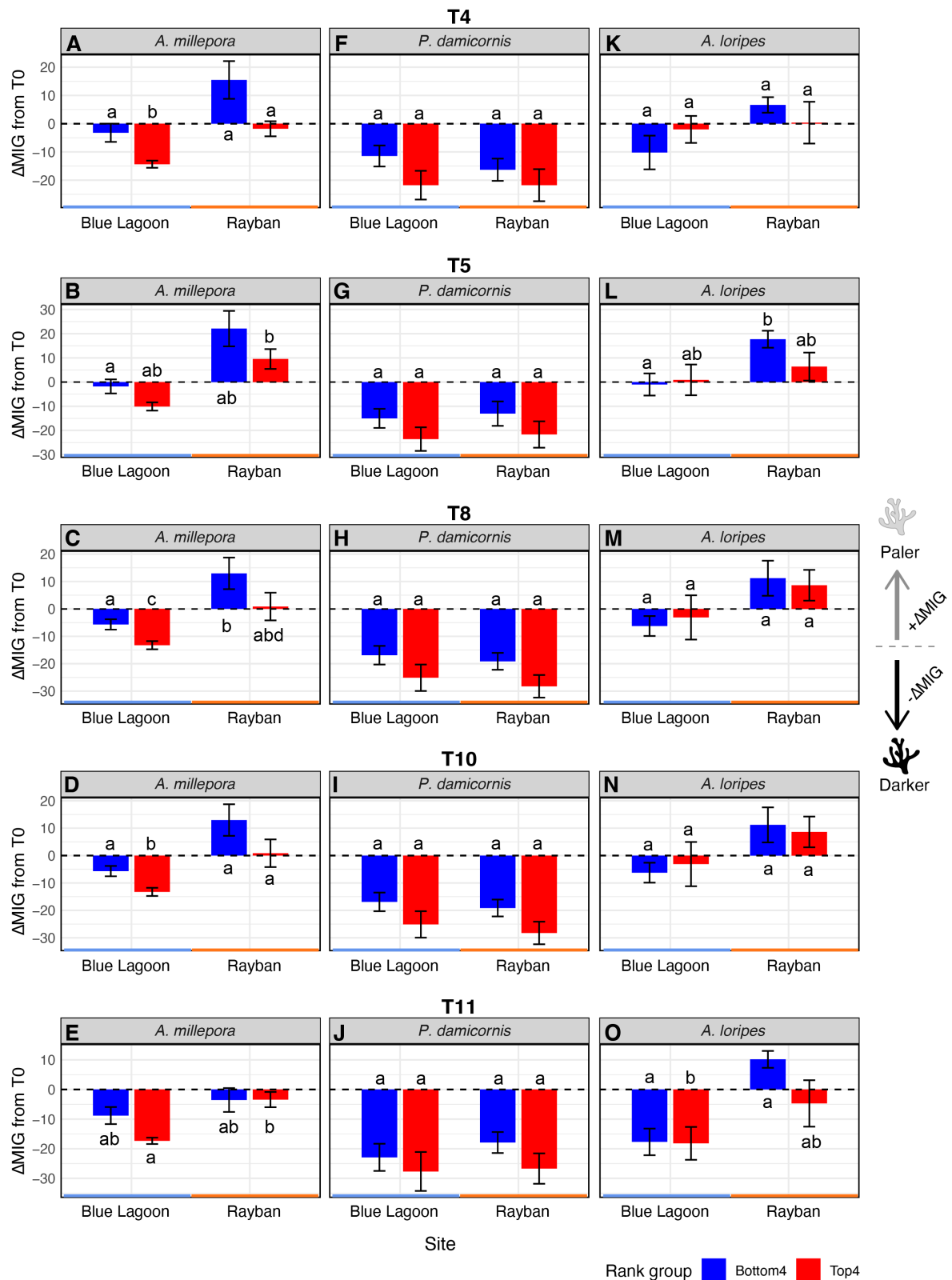
38 the course of the study at T4, T5, T8, T10 and T11. R² values and p values for Rayban are in

39 the top of each graph and for Blue Lagoon are in the bottom of each graph. The dashed line

40 represents (0) no change from Δ MIG at T0, values above the dashed line (+ Δ MIG) indicate

41 paling relative to their individual colour at T0 and below the line (- Δ MIG) indicate darkening

42 relative to their individual colour at T0. * indicates significant correlation where $p < 0.05$.



43

44 Figure S6 – Bar plots displaying change in coral colour ($\pm\Delta$ MIG from T0) for only the top

45 and bottom four ranked corals (ranked from experimental heat stress testing at T0) for (a-e)

A. millepora at timepoint T4, T5, T8, T10 and T11 respectively, (f-j) *P. damicornis* at timepoint T4, T5, T8, T10 and T11 respectively, and (k-o) *A. loripes* at timepoint T4, T5, T8, T10 and T11 respectively. The dashed line represents (0) no change from Δ MIG at T0, values above the dashed line (+ Δ MIG) indicate paling relative to their individual colour at T0 and below the line (- Δ MIG) indicate darkening relative to their individual colour at T0. Different letters above bars are used to indicate significant differences between groups Wilcoxon rank-sum (Mann–Whitney U) test (tested at each timepoint for each species separately).

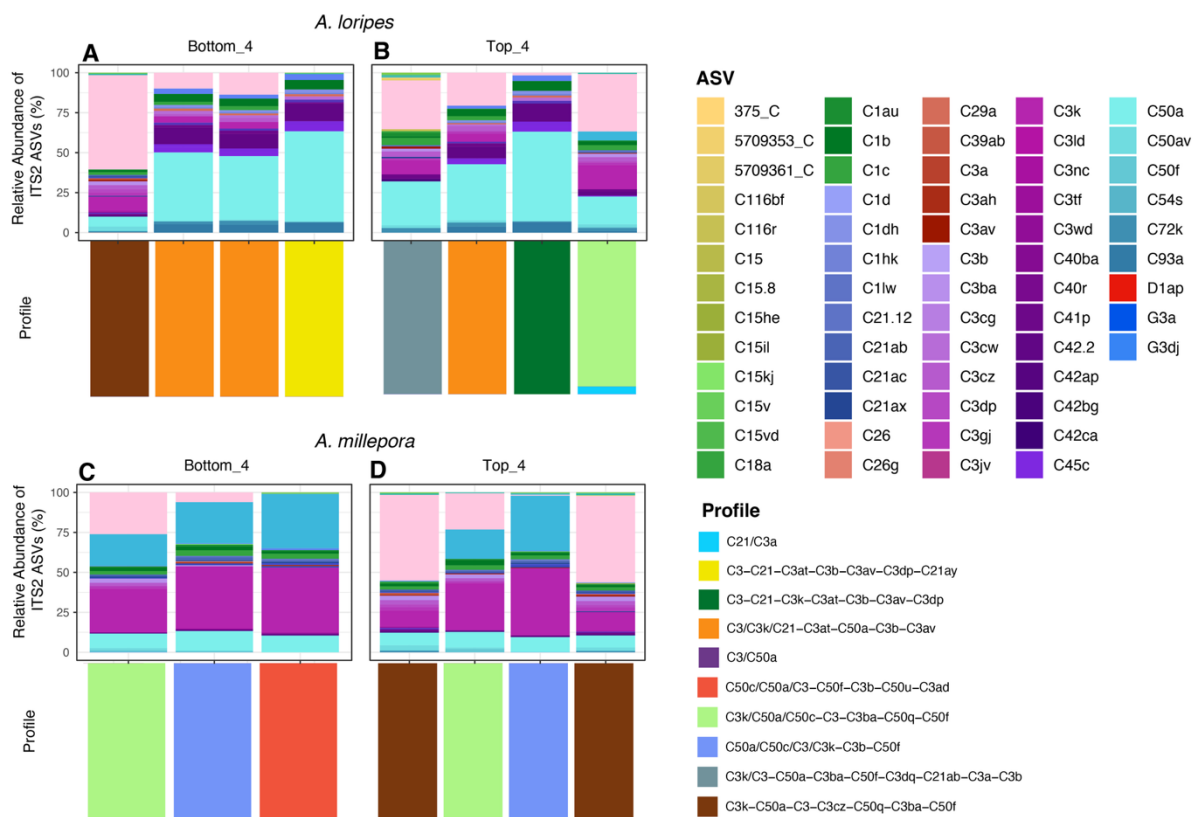


Figure S7 - Symbiodiniaceae community composition (relative abundances) by amplicon sequence variant (ASV) of Bottom_4 and Top_4 (A, B) *A. loripes* and (C, D) *A. millepora* source reef colonies at the start of the study.

Supplementary Tables

Metric	group1	group2	n1	n2	statistic	p	p.adj	p. adj signif
ED ₅₀	<i>A. loripes</i>	<i>A. millepora</i>	18	18	3.27	0.0011	0.002	**
ED ₅₀	<i>A. loripes</i>	<i>P. damicornis</i>	18	18	-0.381	0.7030	0.703	ns
ED ₅₀	<i>A. millepora</i>	<i>P. damicornis</i>	18	18	-3.65	0.0001	0.001	***

Table S1 – Statistical analysis comparing the ED₅₀ values calculated from the Multi-taxa Phenotyping System acute heat-stress assays across species at T0. Data did not meet assumptions of a parametric test and consequently a Kruskal Wallis and Dunn's post-hoc pairwise comparison was conducted, *p* values were corrected for multiple comparisons using a False Discovery Rate correction, differences were considered significant for *p*_{adj} values < 0.05.

Species	n	Mean (°C)	Standard Deviation	Minimum (°C)	Maximum (°C)	Range (°C)
<i>A. loripes</i>	18	35.4	0.517	34.5	36.7	2.29
<i>A. millepora</i>	18	36.4	1.52	32.7	40.6	7.92
<i>P. damicornis</i>	18	35.2	0.607	34	36.1	2.09

Table S2 – Summary of ED₅₀ (°C) values for each species.

	group1	group2	n1	n2	statistic	p	signif
<i>A. loripes</i>	BlueLagoon	Rayban	8	8	-1.37	0.172	ns
<i>A. millepora</i>	BlueLagoon	Rayban	8	8	-0.21	0.834	ns
<i>P. damicornis</i>	BlueLagoon	Rayban	8	8	-1.05	0.294	ns

Table S3 – Statistical analysis comparing the ED₅₀ values calculated from the Multi-taxa Phenotyping System acute heat-stress assays for each species across site of origin (for Blue Lagoon and Rayban colonies) at T0. Data did not meet assumptions of a parametric test and consequently a Kruskal Wallis and Dunn's post-hoc pairwise comparison was conducted, *p* values < 0.05 were considered significant. Colonies from South North Opal were excluded due to only duplicate replication for each coral species.

Species	Timepoint	Site	Estimate	Statistic	P value	Parameter	conf.low	conf.high
	T4	BL	-0.126	-0.634	0.532	25	-0.483	0.267

<i>P. damicornis</i>	T5	RB	-0.107	-0.547	0.589	26	-0.461	0.277
		BL	-0.260	-1.346	0.190	25	-0.582	0.133
		RB	-0.163	-0.841	0.408	26	-0.505	0.224
	T8	BL	-0.205	-1.047	0.305	25	-0.543	0.190
		RB	-0.139	-0.713	0.482	26	-0.486	0.247
	T10	BL	-0.126	-0.634	0.532	25	-0.483	0.267
		RB	-0.107	-0.547	0.589	26	-0.461	0.277
	T11	BL	-0.074	-0.373	0.712	25	-0.442	0.315
		RB	-0.220	-1.148	0.261	26	-0.548	0.167
<i>A. loripes</i>	T4	BL	0.045	0.256	0.800	32	-0.298	0.378
		RB	-0.154	-0.856	0.399	30	-0.477	0.205
	T5	BL	0.024	0.137	0.892	32	-0.317	0.359
		RB	-0.330	-1.947	0.061	31	-0.605	0.015
	T8	BL	0.029	0.164	0.871	32	-0.312	0.364
		RB	-0.026	-0.147	0.884	31	-0.366	0.320
	T10	BL	0.045	0.256	0.800	32	-0.298	0.378
		RB	-0.154	-0.856	0.399	30	-0.477	0.205
	T11	BL	0.013	0.072	0.943	32	-0.327	0.349
		RB	-0.294	-1.716	0.096	31	-0.579	0.054
<i>A. millepora</i>	T4	BL	-0.425	-2.740	0.010	34	-0.661	-0.112
		RB	-0.336	-1.990	0.056	31	-0.609	0.008
	T5	BL	-0.281	-1.710	0.097	34	-0.558	0.052
		RB	-0.167	-0.942	0.353	31	-0.482	0.187
	T8	BL	-0.244	-1.450	0.158	33	-0.534	0.097
		RB	-0.253	-1.460	0.155	31	-0.549	0.099
	T10	BL	-0.425	-2.740	0.010	34	-0.661	-0.112
		RB	-0.336	-1.990	0.056	31	-0.609	0.008
	T11	BL	-0.318	-1.950	0.059	34	-0.585	0.012
		RB	0.048	0.267	0.791	31	-0.300	0.385

79

80 Table S4 – Pearson correlation coefficients (r) between ED₅₀ and the percentage change in
81 Mean Intensity Grey (MIG%) from T0 at each time point and site for each species.
82 Corresponding *p* values indicate the strength and significance of the relationships over time, *p*
83 values < 0.05 indicate significant correlation. BL is shorthand for Blue Lagoon and RB is
84 shorthand for Rayban.

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)	signif
environment	1096.43	1096.43	1	996.65	14.233	<0.001	***

timepoint	109.67	27.42	4	994.06	0.356	0.840	
species	20.09	10.04	2	53.97	0.130	0.878	
ED50	75.56	75.56	1	53.99	0.981	0.326	
environment:timepoint	24.2	6.05	4	994.07	0.079	0.989	
environment:species	1903.57	951.78	2	994.12	12.355	0.000	***
timepoint:species	435.84	54.48	8	994.05	0.707	0.685	
environment:ED50	896.47	896.47	1	994.13	11.637	0.001	***
timepoint:ED50	87.97	21.99	4	994.06	0.286	0.887	
species:ED50	27.31	13.66	2	53.98	0.177	0.838	
environment:timepoint:species	260.46	32.56	8	994.05	0.423	0.908	
environment:timepoint:ED50	29.97	7.49	4	994.07	0.097	0.983	
environment:species:ED50	1886.17	943.08	2	994.12	12.242	0.000	***
timepoint:species:ED50	420.44	52.55	8	994.05	0.682	0.708	
environment:timepoint:species:ED50	243.94	30.49	8	994.05	0.396	0.923	

85

86 Table S5 - Type III analysis of variance for the linear mixed-effects model fitted by maximum
87 likelihood, testing the significance of fixed effects, including main effects and their
88 interactions, using F-tests with Satterthwaite's approximation for degrees of freedom. Effects
89 were considered significant were p value < 0.05 .

Fixed effects	Estimate	Std. Error	df	t value	p value
(Intercept)	-233.40	200.20	9.24E+01	-1.166	0.247
environmentRB	414.50	146.10	9.94E+02	2.838	0.005
timepointT5	155.60	145.60	9.94E+02	1.069	0.285
timepointT8	37.54	145.60	9.94E+02	0.258	0.797
timepointT10	0.00	145.60	9.94E+02	0.000	1.000
timepointT11	150.20	155.80	9.94E+02	0.965	0.335
speciesA_millepora	327.60	212.00	9.24E+01	1.545	0.126
speciesP_damicornis	400.30	262.50	9.24E+01	1.525	0.131
ED50	6.38	5.66	9.24E+01	1.126	0.263
environmentRB:timepointT5	-65.67	206.50	9.94E+02	-0.318	0.751
environmentRB:timepointT8	-140.70	206.90	9.94E+02	-0.680	0.497
environmentRB:timepointT10	0.00	206.60	9.94E+02	0.000	1.000
environmentRB:timepointT11	-123.30	214.30	9.94E+02	-0.575	0.565
environmentRB:speciesA_millepora	-392.30	154.80	9.94E+02	-2.535	0.011
environmentRB:speciesP_damicornis	-460.00	191.30	9.94E+02	-2.404	0.016
timepointT5:speciesA_millepora	-180.20	154.30	9.94E+02	-1.168	0.243

timepointT8:speciesA_millepora	-82.14	154.30	9.94E+02	-0.532	0.595
timepointT10:speciesA_millepora	0.00	154.30	9.94E+02	0.000	1.000
timepointT11:speciesA_millepora	-176.60	163.90	9.94E+02	-1.078	0.281
timepointT5:speciesP_damicornis	-180.50	191.00	9.94E+02	-0.945	0.345
timepointT8:speciesP_damicornis	-70.24	191.00	9.94E+02	-0.368	0.713
timepointT10:speciesP_damicornis	0.00	191.00	9.94E+02	0.000	1.000
timepointT11:speciesP_damicornis	-246.90	198.80	9.94E+02	-1.242	0.214
environmentRB:ED50	-11.38	4.13	9.94E+02	-2.754	0.006
timepointT5:ED50	-4.21	4.12	9.94E+02	-1.022	0.307
timepointT8:ED50	-0.97	4.12	9.94E+02	-0.237	0.813
timepointT10:ED50	0.00	4.12	9.94E+02	0.000	1.000
timepointT11:ED50	-4.47	4.41	9.94E+02	-1.014	0.311
speciesA_millepora:ED50	-9.27	5.98	9.24E+01	-1.551	0.124
speciesP_damicornis:ED50	-11.55	7.44	9.24E+01	-1.553	0.124
environmentRB:timepointT5:speciesA_millepora	47.01	218.80	9.94E+02	0.215	0.830
environmentRB:timepointT8:speciesA_millepora	197.00	219.10	9.94E+02	0.899	0.369
environmentRB:timepointT10:speciesA_millepora	0.00	218.80	9.94E+02	0.000	1.000
environmentRB:timepointT11:speciesA_millepora	12.59	226.10	9.94E+02	0.056	0.956
environmentRB:timepointT5:speciesP_damicornis	95.25	270.50	9.94E+02	0.352	0.725
environmentRB:timepointT8:speciesP_damicornis	141.30	270.80	9.94E+02	0.522	0.602
environmentRB:timepointT10:speciesP_damicornis	0.00	270.50	9.94E+02	0.000	1.000
environmentRB:timepointT11:speciesP_damicornis	225.40	276.50	9.94E+02	0.815	0.415
environmentRB:timepointT5:ED50	1.97	5.84	9.94E+02	0.338	0.736
environmentRB:timepointT8:ED50	4.04	5.85	9.94E+02	0.690	0.490
environmentRB:timepointT10:ED50	0.00	5.84	9.94E+02	0.000	1.000
environmentRB:timepointT11:ED50	3.81	6.06	9.94E+02	0.629	0.530
environmentRB:speciesA_millepora:ED50	11.20	4.36	9.94E+02	2.567	0.010
environmentRB:speciesP_damicornis:ED50	12.58	5.42	9.94E+02	2.321	0.021
timepointT5:speciesA_millepora:ED50	4.93	4.35	9.94E+02	1.134	0.257
timepointT8:speciesA_millepora:ED50	2.13	4.35	9.94E+02	0.490	0.624
timepointT10:speciesA_millepora:ED50	0.00	4.35	9.94E+02	0.000	1.000
timepointT11:speciesA_millepora:ED50	5.03	4.62	9.94E+02	1.088	0.277
timepointT5:speciesP_damicornis:ED50	4.86	5.41	9.94E+02	0.897	0.370
timepointT8:speciesP_damicornis:ED50	1.78	5.41	9.94E+02	0.328	0.743
timepointT10:speciesP_damicornis:ED50	0.00	5.41	9.94E+02	0.000	1.000
timepointT11:speciesP_damicornis:ED50	7.03	5.63	9.94E+02	1.248	0.213
environmentRB:timepointT5:speciesA_millepora:ED50	-1.26	6.17	9.94E+02	-0.205	0.838
environmentRB:timepointT8:speciesA_millepora:ED50	-5.50	6.18	9.94E+02	-0.890	0.373
environmentRB:timepointT10:speciesA_millepora:ED50	0.00	6.17	9.94E+02	0.000	1.000
environmentRB:timepointT11:speciesA_millepora:ED50	-0.78	6.38	9.94E+02	-0.123	0.902
environmentRB:timepointT5:speciesP_damicornis:ED50	-2.67	7.66	9.94E+02	-0.348	0.728

environmentRB:timepointT8:speciesP_damicornis:ED50	-3.96	7.67	9.94E+02	-0.517	0.605
environmentRB:timepointT10:speciesP_damicornis:ED50	0.00	7.66	9.94E+02	0.000	1.000
environmentRB:timepointT11:speciesP_damicornis:ED50	-6.52	7.83	9.94E+02	-0.833	0.405

90

91 Table S6 - Results of the linear mixed-effects model fitted using maximum likelihood
92 estimation. Fixed effects are presented with associated estimates, standard errors, degrees of
93 freedom, *t* values, and *p* values. Statistical significance of fixed effects was assessed using t-
94 tests with Satterthwaite's approximation for degrees of freedom. Effects and interactions were
95 considered significant were *p* value < 0.05. BL is shorthand for Blue Lagoon and RB is
96 shorthand for Rayban.

	npar	logLik	AIC	LRT	Df	Pr(>Chisq)	signif
<none>	63	-3866.7	7859.3				
(1 environment:treatment)	62	-3870.5	7865.1	7.75	1	0.005363	**
(1 sampleid)	62	-4236.9	8597.8	740.41	1	< 2.2e-16	***

97

98 Table S7 – Random effects ANOVA table showing the results of single-term deletion from
99 the linear mixed-effects model. Each term was sequentially removed to assess its contribution
100 to model fit, with changes in variance explained and associated test statistics reported.

group1	group2	n1	n2	Statistic	p value	Signif	Species	Site	Comparison Type	Time point
Bottom4	Top4	8	8	54	0.021	*	<i>A. millepora</i>	Blue Lagoon	within treatment	T4
Bottom4	Top4	7	7	38	0.097	ns	<i>A. millepora</i>	Rayban	within treatment	T4
Bottom4	Top4	8	8	22	0.328	ns	<i>A. loripes</i>	Blue Lagoon	within treatment	T4
Bottom4	Top4	8	8	40	0.442	ns	<i>A. loripes</i>	Rayban	within treatment	T4
Bottom4	Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	Blue Lagoon	within treatment	T4
Bottom4	Top4	8	8	39	0.505	ns	<i>P. damicornis</i>	Rayban	within treatment	T4
Bottom4	Top4	8	8	51	0.050	*	<i>A. millepora</i>	Blue Lagoon	within treatment	T5
Bottom4	Top4	7	7	35	0.209	ns	<i>A. millepora</i>	Rayban	within treatment	T5
Bottom4	Top4	8	8	30	0.878	ns	<i>A. loripes</i>	Blue Lagoon	within treatment	T5
Bottom4	Top4	8	8	46	0.161	ns	<i>A. loripes</i>	Rayban	within treatment	T5
Bottom4	Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	Blue Lagoon	within treatment	T5
Bottom4	Top4	8	8	44	0.234	ns	<i>P. damicornis</i>	Rayban	within treatment	T5
Bottom4	Top4	8	7	50	0.009	**	<i>A. millepora</i>	Blue Lagoon	within treatment	T8
Bottom4	Top4	7	7	34	0.259	ns	<i>A. millepora</i>	Rayban	within treatment	T8
Bottom4	Top4	8	8	29	0.798	ns	<i>A. loripes</i>	Blue Lagoon	within treatment	T8
Bottom4	Top4	8	7	32	0.694	ns	<i>A. loripes</i>	Rayban	within treatment	T8
Bottom4	Top4	8	8	44	0.234	ns	<i>P. damicornis</i>	Blue Lagoon	within treatment	T8
Bottom4	Top4	8	8	48	0.105	ns	<i>P. damicornis</i>	Rayban	within treatment	T8
Bottom4	Top4	8	8	54	0.021	*	<i>A. millepora</i>	Blue Lagoon	within treatment	T10
Bottom4	Top4	7	7	38	0.097	ns	<i>A. millepora</i>	Rayban	within treatment	T10
Bottom4	Top4	8	8	22	0.328	ns	<i>A. loripes</i>	Blue Lagoon	within treatment	T10
Bottom4	Top4	8	8	40	0.442	ns	<i>A. loripes</i>	Rayban	within treatment	T10
Bottom4	Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	Blue Lagoon	within treatment	T10
Bottom4	Top4	8	8	39	0.505	ns	<i>P. damicornis</i>	Rayban	within treatment	T10
Bottom4	Top4	8	8	53	0.028	*	<i>A. millepora</i>	Blue Lagoon	within treatment	T11
Bottom4	Top4	7	7	26	0.902	ns	<i>A. millepora</i>	Rayban	within treatment	T11
Bottom4	Top4	8	7	26	0.867	ns	<i>A. loripes</i>	Blue Lagoon	within treatment	T11
Bottom4	Top4	8	7	38	0.281	ns	<i>A. loripes</i>	Rayban	within treatment	T11
Bottom4	Top4	8	8	40	0.442	ns	<i>P. damicornis</i>	Blue Lagoon	within treatment	T11
Bottom4	Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	Rayban	within treatment	T11
Blue Lagoon Bottom4	Rayban Bottom4	8	7	11	0.054	ns	<i>A. millepora</i>	NA	across treatment	T4

Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	54	0.021	*	<i>A. millepora</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Rayban Top4	8	7	25	0.779	ns	<i>A. millepora</i>	NA	across treatment	T4
Rayban Bottom4	Blue Lagoon Top4	7	8	55	0.001	**	<i>A. millepora</i>	NA	across treatment	T4
Rayban Bottom4	Rayban Top4	7	7	38	0.097	ns	<i>A. millepora</i>	NA	across treatment	T4
Blue Lagoon Top4	Rayban Top4	8	7	2	0.001	**	<i>A. millepora</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Rayban Bottom4	8	8	12	0.038	ns	<i>A. loripes</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	22	0.328	ns	<i>A. loripes</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Rayban Top4	8	8	23	0.382	ns	<i>A. loripes</i>	NA	across treatment	T4
Rayban Bottom4	Blue Lagoon Top4	8	8	47	0.130	ns	<i>A. loripes</i>	NA	across treatment	T4
Rayban Bottom4	Rayban Top4	8	8	40	0.442	ns	<i>A. loripes</i>	NA	across treatment	T4
Blue Lagoon Top4	Rayban Top4	8	8	28	0.721	ns	<i>A. loripes</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Rayban Bottom4	8	8	41	0.382	ns	<i>P. damicornis</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Rayban Top4	8	8	44	0.234	ns	<i>P. damicornis</i>	NA	across treatment	T4
Rayban Bottom4	Blue Lagoon Top4	8	8	40	0.442	ns	<i>P. damicornis</i>	NA	across treatment	T4
Rayban Bottom4	Rayban Top4	8	8	39	0.505	ns	<i>P. damicornis</i>	NA	across treatment	T4
Blue Lagoon Top4	Rayban Top4	8	8	35	0.798	ns	<i>P. damicornis</i>	NA	across treatment	T4
Blue Lagoon Bottom4	Rayban Bottom4	8	7	9	0.029	ns	<i>A. millepora</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	51	0.050	ns	<i>A. millepora</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Rayban Top4	8	7	15	0.152	ns	<i>A. millepora</i>	NA	across treatment	T5

Rayban Bottom4	Blue Lagoon Top4	7	8	52	0.004	*	<i>A. millepora</i>	NA	across treatment	T5
Rayban Bottom4	Rayban Top4	7	7	35	0.209	ns	<i>A. millepora</i>	NA	across treatment	T5
Blue Lagoon Top4	Rayban Top4	8	7	0	0.000	**	<i>A. millepora</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Rayban Bottom4	8	8	7	0.007	*	<i>A. loripes</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	30	0.878	ns	<i>A. loripes</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Rayban Top4	8	8	22	0.328	ns	<i>A. loripes</i>	NA	across treatment	T5
Rayban Bottom4	Blue Lagoon Top4	8	8	51	0.050	ns	<i>A. loripes</i>	NA	across treatment	T5
Rayban Bottom4	Rayban Top4	8	8	46	0.161	ns	<i>A. loripes</i>	NA	across treatment	T5
Blue Lagoon Top4	Rayban Top4	8	8	27	0.645	ns	<i>A. loripes</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Rayban Bottom4	8	8	29	0.798	ns	<i>P. damicornis</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Rayban Top4	8	8	42	0.328	ns	<i>P. damicornis</i>	NA	across treatment	T5
Rayban Bottom4	Blue Lagoon Top4	8	8	48	0.105	ns	<i>P. damicornis</i>	NA	across treatment	T5
Rayban Bottom4	Rayban Top4	8	8	44	0.234	ns	<i>P. damicornis</i>	NA	across treatment	T5
Blue Lagoon Top4	Rayban Top4	8	8	32	1.000	ns	<i>P. damicornis</i>	NA	across treatment	T5
Blue Lagoon Bottom4	Rayban Bottom4	8	7	8	0.020	*	<i>A. millepora</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Blue Lagoon Top4	8	7	50	0.009	*	<i>A. millepora</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Rayban Top4	8	7	22	0.536	ns	<i>A. millepora</i>	NA	across treatment	T8
Rayban Bottom4	Blue Lagoon Top4	7	7	42	0.026	*	<i>A. millepora</i>	NA	across treatment	T8
Rayban Bottom4	Rayban Top4	7	7	34	0.259	ns	<i>A. millepora</i>	NA	across treatment	T8
Blue Lagoon Top4	Rayban Top4	7	7	7	0.026	*	<i>A. millepora</i>	NA	across treatment	T8

Blue Lagoon Bottom4	Rayban Bottom4	8	8	14	0.065	ns	<i>A. loripes</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	29	0.798	ns	<i>A. loripes</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Rayban Top4	8	7	10	0.040	ns	<i>A. loripes</i>	NA	across treatment	T8
Rayban Bottom4	Blue Lagoon Top4	8	8	43	0.279	ns	<i>A. loripes</i>	NA	across treatment	T8
Rayban Bottom4	Rayban Top4	8	7	32	0.694	ns	<i>A. loripes</i>	NA	across treatment	T8
Blue Lagoon Top4	Rayban Top4	8	7	21	0.463	ns	<i>A. loripes</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Rayban Bottom4	8	8	38	0.574	ns	<i>P. damicornis</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	44	0.234	ns	<i>P. damicornis</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Rayban Top4	8	8	48	0.105	ns	<i>P. damicornis</i>	NA	across treatment	T8
Rayban Bottom4	Blue Lagoon Top4	8	8	46	0.161	ns	<i>P. damicornis</i>	NA	across treatment	T8
Rayban Bottom4	Rayban Top4	8	8	48	0.105	ns	<i>P. damicornis</i>	NA	across treatment	T8
Blue Lagoon Top4	Rayban Top4	8	8	40	0.442	ns	<i>P. damicornis</i>	NA	across treatment	T8
Blue Lagoon Bottom4	Rayban Bottom4	8	7	11	0.054	ns	<i>A. millepora</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	54	0.021	*	<i>A. millepora</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Rayban Top4	8	7	25	0.779	ns	<i>A. millepora</i>	NA	across treatment	T10
Rayban Bottom4	Blue Lagoon Top4	7	8	55	0.001	**	<i>A. millepora</i>	NA	across treatment	T10
Rayban Bottom4	Rayban Top4	7	7	38	0.097	ns	<i>A. millepora</i>	NA	across treatment	T10
Blue Lagoon Top4	Rayban Top4	8	7	2	0.001	**	<i>A. millepora</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Rayban Bottom4	8	8	12	0.038	ns	<i>A. loripes</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	22	0.328	ns	<i>A. loripes</i>	NA	across treatment	T10

Blue Lagoon Bottom4	Rayban Top4	8	8	23	0.382	ns	<i>A. loripes</i>	NA	across treatment	T10
Rayban Bottom4	Blue Lagoon Top4	8	8	47	0.130	ns	<i>A. loripes</i>	NA	across treatment	T10
Rayban Bottom4	Rayban Top4	8	8	40	0.442	ns	<i>A. loripes</i>	NA	across treatment	T10
Blue Lagoon Top4	Rayban Top4	8	8	28	0.721	ns	<i>A. loripes</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Rayban Bottom4	8	8	41	0.382	ns	<i>P. damicornis</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Rayban Top4	8	8	44	0.234	ns	<i>P. damicornis</i>	NA	across treatment	T10
Rayban Bottom4	Blue Lagoon Top4	8	8	40	0.442	ns	<i>P. damicornis</i>	NA	across treatment	T10
Rayban Bottom4	Rayban Top4	8	8	39	0.505	ns	<i>P. damicornis</i>	NA	across treatment	T10
Blue Lagoon Top4	Rayban Top4	8	8	35	0.798	ns	<i>P. damicornis</i>	NA	across treatment	T10
Blue Lagoon Bottom4	Rayban Bottom4	8	7	19	0.336	ns	<i>A. millepora</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	53	0.028	ns	<i>A. millepora</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Rayban Top4	8	7	17	0.232	ns	<i>A. millepora</i>	NA	across treatment	T11
Rayban Bottom4	Blue Lagoon Top4	7	8	47	0.029	ns	<i>A. millepora</i>	NA	across treatment	T11
Rayban Bottom4	Rayban Top4	7	7	26	0.902	ns	<i>A. millepora</i>	NA	across treatment	T11
Blue Lagoon Top4	Rayban Top4	8	7	0	0.000	**	<i>A. millepora</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Rayban Bottom4	8	8	2	0.001	**	<i>A. loripes</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Blue Lagoon Top4	8	7	26	0.867	ns	<i>A. loripes</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Rayban Top4	8	7	18	0.281	ns	<i>A. loripes</i>	NA	across treatment	T11
Rayban Bottom4	Blue Lagoon Top4	8	7	55	0.001	**	<i>A. loripes</i>	NA	across treatment	T11
Rayban Bottom4	Rayban Top4	8	7	38	0.281	ns	<i>A. loripes</i>	NA	across treatment	T11

Blue Lagoon Top4	Rayban Top4	7	7	19	0.535	ns	<i>A. loripes</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Rayban Bottom4	8	8	24	0.442	ns	<i>P. damicornis</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Blue Lagoon Top4	8	8	40	0.442	ns	<i>P. damicornis</i>	NA	across treatment	T11
Blue Lagoon Bottom4	Rayban Top4	8	8	36	0.721	ns	<i>P. damicornis</i>	NA	across treatment	T11
Rayban Bottom4	Blue Lagoon Top4	8	8	46	0.161	ns	<i>P. damicornis</i>	NA	across treatment	T11
Rayban Bottom4	Rayban Top4	8	8	45	0.195	ns	<i>P. damicornis</i>	NA	across treatment	T11
Blue Lagoon Top4	Rayban Top4	8	8	27	0.645	ns	<i>P. damicornis</i>	NA	across treatment	T11

Table S8 – Summary table of Wilcox test results for comparisons in change in Mean Intensity Grey (MIG %) between Top and Bottom ranked corals for each species at each site and across sites. All comparisons were conducted separately and summarised in this table.

Emergent Phenotype Ranking Location	Community	species	group1	group2	F	R2	p value
Blue Lagoon	Bacterial	<i>A.millepora</i>	Other	Top4	1.320769	0.107199	0.077
Blue Lagoon	Bacterial	<i>A.millepora</i>	Other	Bottom4	1.336389	0.100206	0.0855
Blue Lagoon	Bacterial	<i>A.millepora</i>	Top4	Bottom4	1.098375	0.135629	0.1098
Blue Lagoon	Bacterial	<i>A.loripes</i>	Bottom4	Other	0.796639	0.126518	0.9753
Blue Lagoon	Bacterial	<i>A.loripes</i>	Bottom4	Top4	0.84428	0.21962	0.8467
Blue Lagoon	Bacterial	<i>A.loripes</i>	Other	Top4	1.019874	0.169418	0.4068
Blue Lagoon	Bacterial	<i>P.damicornis</i>	Other	Top4	1.161816	0.188551	0.1735
Blue Lagoon	Bacterial	<i>P.damicornis</i>	Other	Bottom4	0.974335	0.150492	0.5048
Blue Lagoon	Bacterial	<i>P.damicornis</i>	Top4	Bottom4	0.938579	0.238304	0.5867
Rayban	Bacterial	<i>A.millepora</i>	Other	Bottom4	0.936391	0.072384	0.6738
Rayban	Bacterial	<i>A.millepora</i>	Other	Top4	1.000298	0.083356	0.3378
Rayban	Bacterial	<i>A.millepora</i>	Bottom4	Top4	0.971756	0.1219	0.4681
Rayban	Bacterial	<i>A.loripes</i>	Bottom4	Other	0.804787	0.127647	0.9497
Rayban	Bacterial	<i>A.loripes</i>	Bottom4	Top4	0.817347	0.214114	0.9323
Rayban	Bacterial	<i>A.loripes</i>	Other	Top4	0.958605	0.160877	0.5966
Rayban	Bacterial	<i>P.damicornis</i>	Other	Bottom4	1.101088	0.166804	0.2056
Rayban	Bacterial	<i>P.damicornis</i>	Other	Top4	1.094358	0.179569	0.2747
Rayban	Bacterial	<i>P.damicornis</i>	Bottom4	Top4	0.777127	0.205746	0.998
Emergent Phenotype	Species		Df	SumOfSqs	R²	F	Pr(>F)

Ranking Location							
Blue Lagoon	A.loripes	Model	1	0.02216	0.01959	0.1398	0.8746
Blue Lagoon	A.loripes	Residual	7	1.10903	0.98041		
Blue Lagoon	A.loripes	Total	8	1.13118	1		
Blue Lagoon	A.millepora	Model	1	0.03323	0.0358	0.2228	0.6543
Blue Lagoon	A.millepora	Residual	6	0.89505	0.9642		
Blue Lagoon	A.millepora	Total	7	0.92828	1		
Rayban	A.loripes	Model	1	0.13844	0.13831	1.1236	0.3012
Rayban	A.loripes	Residual	7	0.86247	0.86169		
Rayban	A.loripes	Total	8	1.00091	1		
Rayban	A.millepora	Model	1	0.05164	0.08786	0.5779	0.4716
Rayban	A.millepora	Residual	6	0.53612	0.91214		
Rayban	A.millepora	Total	7	0.58776	1		

Table S9 – Summary table of PERMANOVA test results for comparisons in Symbiodiniaceae and coral-associated bacterial community beta diversity (community structure) between emergent phenotype (least paling: Top4 and most paling: Bottom4) alternative ranking groups. All comparisons were conducted separately and summarised in this table. P value < 0.05 is considered significant.