Supplementary Information for

Ecosystem transplant from a healthy reef boosts coral health at a degraded reef

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Supplementary Figures

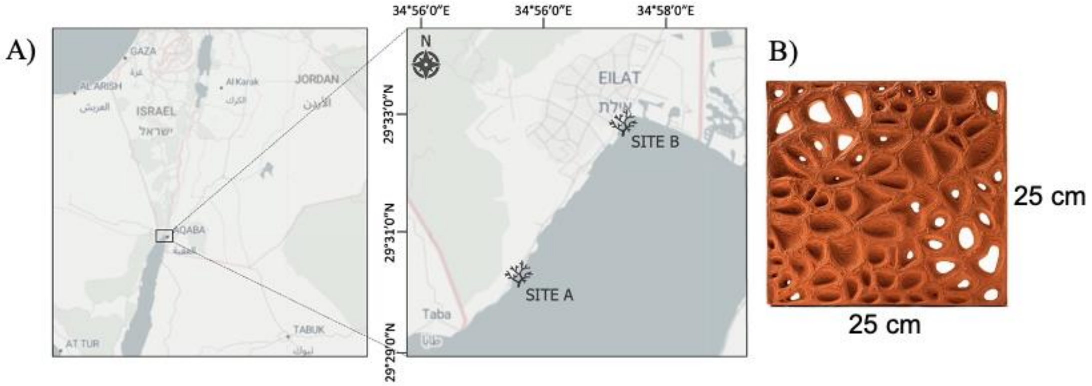

Fig. 1. Location of study and tile design. A) Map of study sites in the Gulf of Eilat/Aqaba, Red Sea (29.5° N) and in its greater geographic location. Map contributors: Leaflet, ©OpenStreetMap, CC-BY-SA, ©Stadia Maps, ©OpenMapTiles, and ©OpenStreetMap (Created in R v4.3.1). **B)** Top view of the biomimetic terracotta tile used in the study.

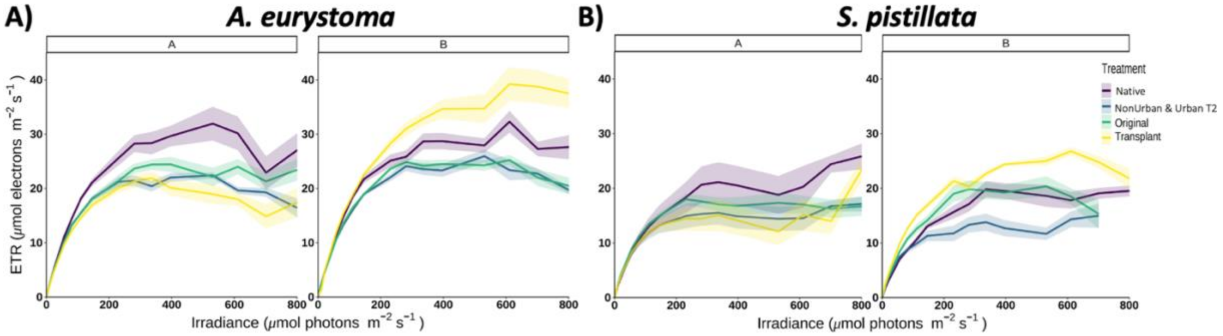

Fig. 2. Regression plot of the raw data for A) *A. eurystoma* and **B)** *S. pistillata* for each site and treatment, showing the relationship between irradiance and ETR. Average ETR + SE for each irradiance level (n= 5).

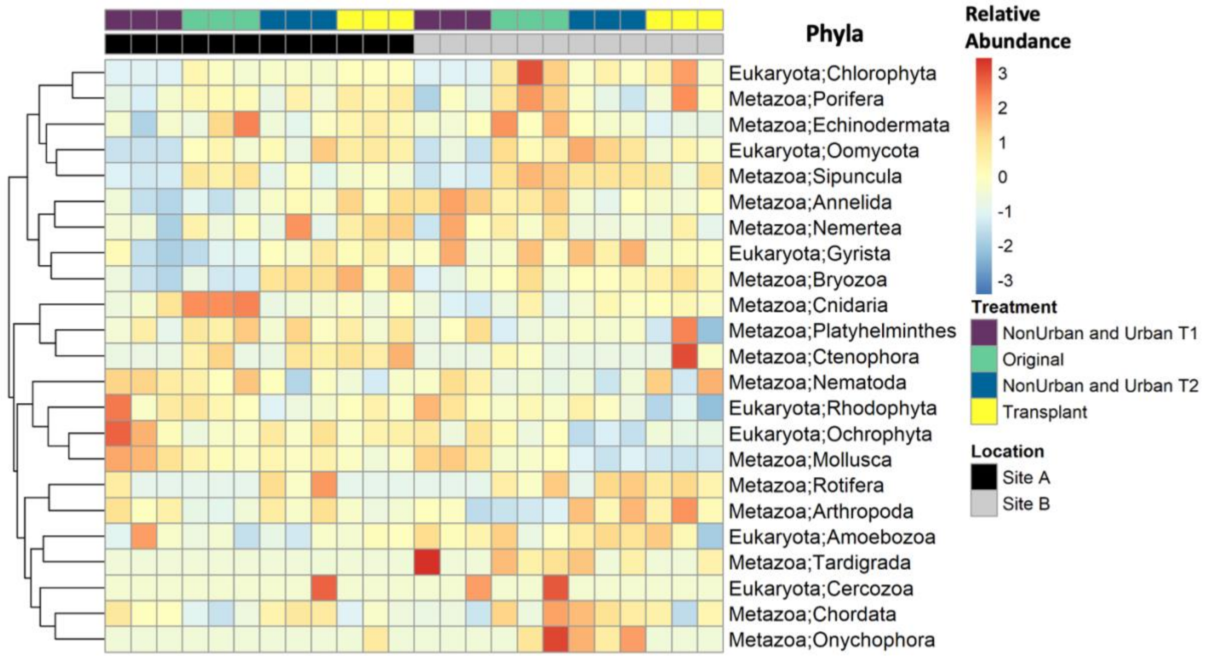

Fig. 3. Relative read abundance of main invertebrate phyla from two different timepoints T1 and T2. Scale bars and cell colors show count values after variance stabilizing transformations and the taxa list is clustered by similarity and ordered phylogenetically (n= 24).

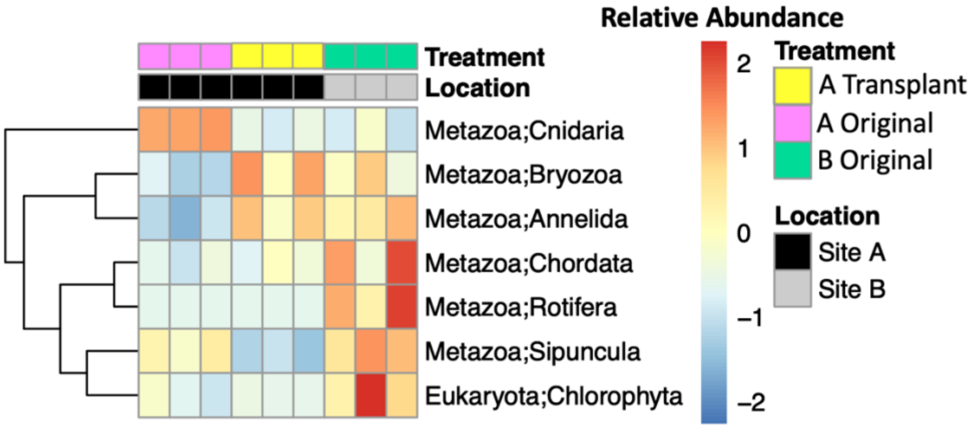

Fig. 4. Relative abundance of the significantly different invertebrate phyla between the Original tiles from both sites and the tiles Transplanted from Site A to B. Scale bars and cell colors show count values after variance stabilizing transformations and the taxa list is clustered by similarity and ordered phylogenetically. Significance was determined by p-adj<0.001 (n= 9).

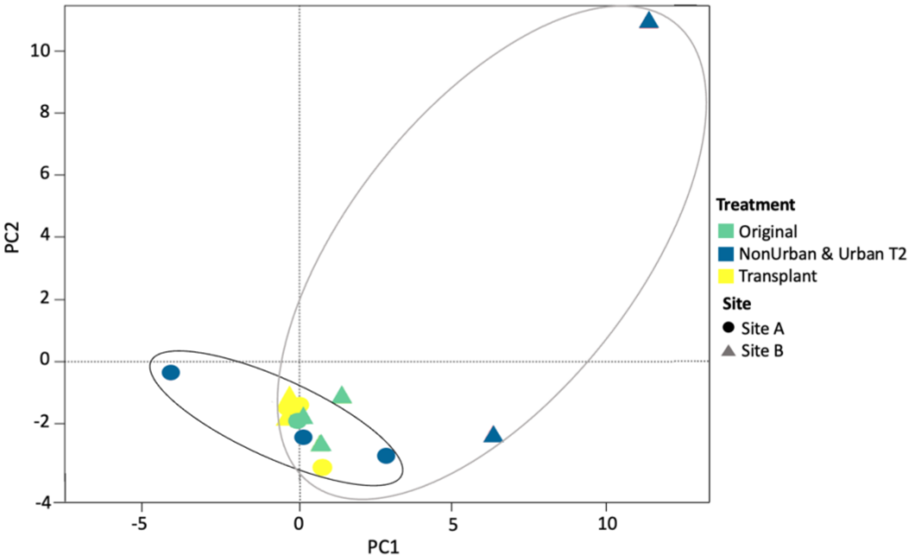

Fig. 5. Community composition of bacteria on tiles. Ellipses show distinct clustering using Bray-Curtis dissimilarities to test PERMANOVA differences between site and treatment (n= 18).

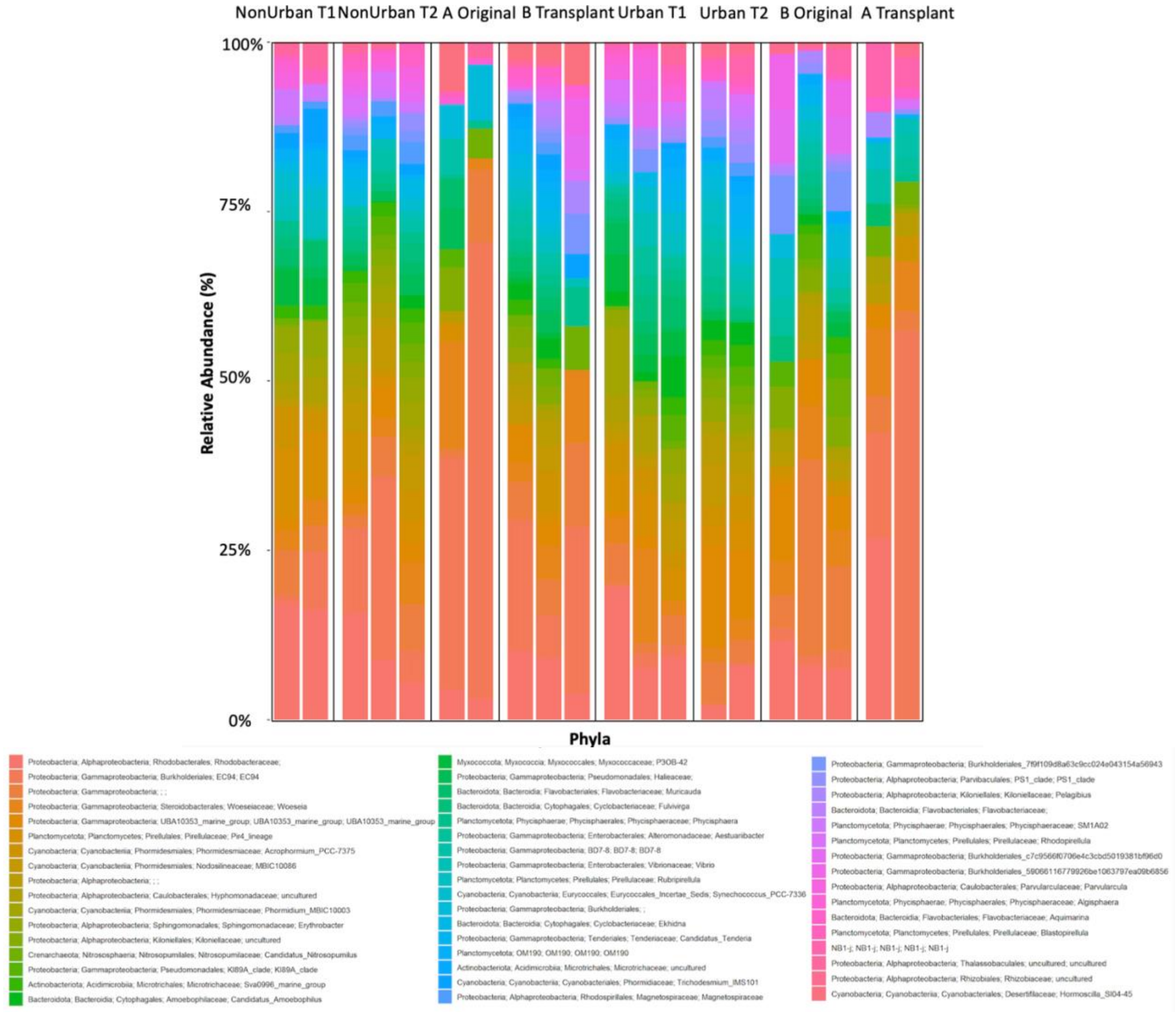

Fig. 6. Percent relative abundance of the 50 most abundant bacteria phyla. Samples are categorized by treatment type and site to the family level (n= 20). Missing samples are due to QIIME’s quality filtering or a low read abundance.

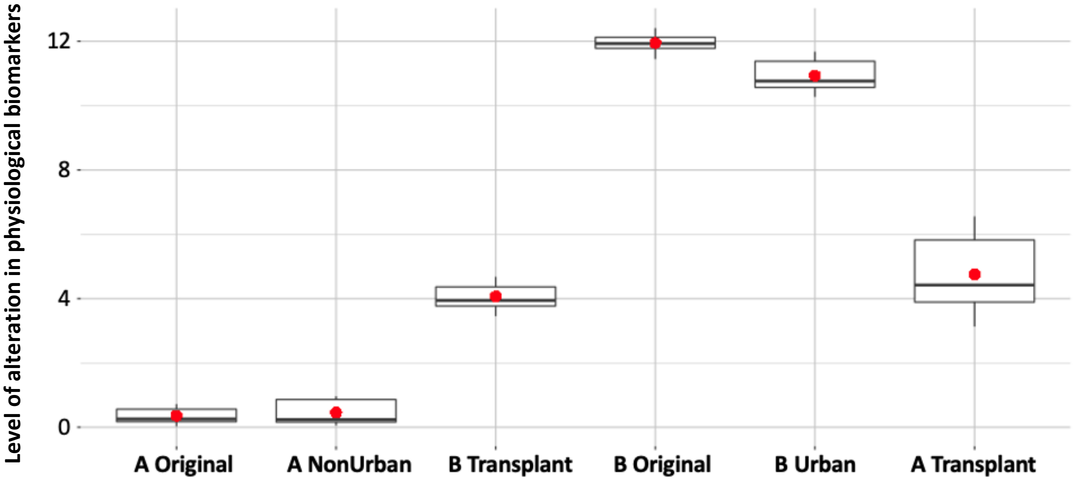

Fig. 7. Box plot of the IBR approach for *A. eurystoma* correlated to the star plots showing the difference in alteration in the physiological biomarkers. The higher numerical values associated with each plot indicate increased physiological stress (n= 5).

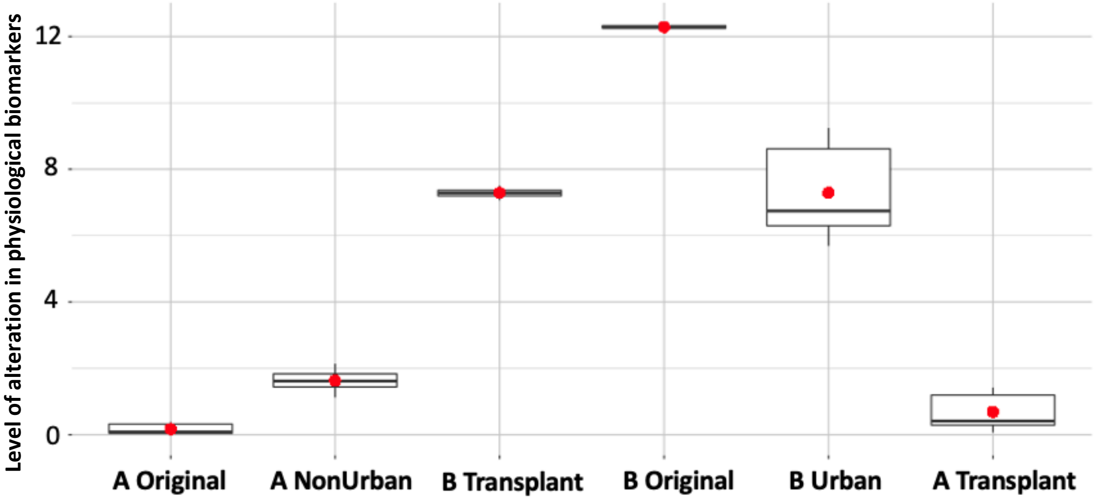

Fig. 8. Boxplot of the IBR approach for *S. pistillata* correlated to the star plots showing the difference in alteration in the physiological biomarkers. The higher numerical values associated with each plot indicate increased physiological stress (n= 5).

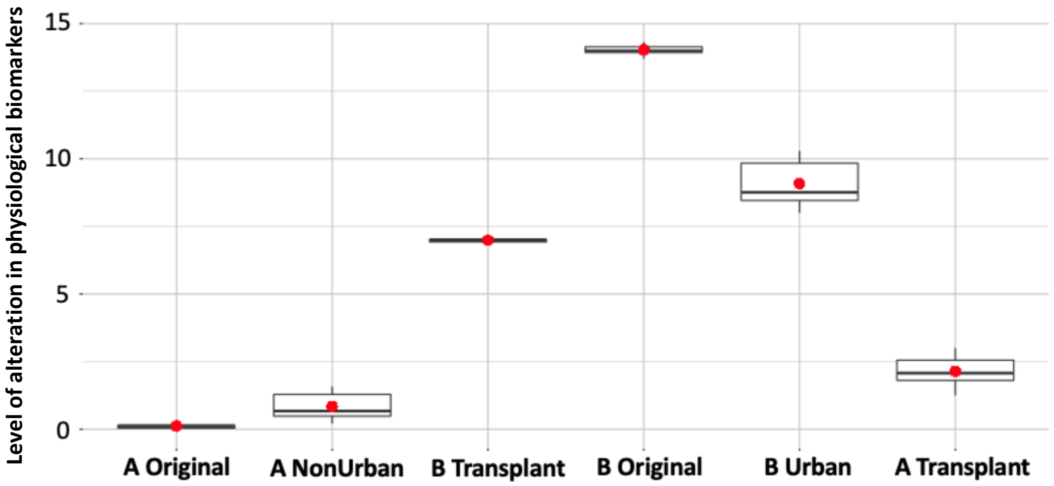

Fig. 9. Boxplot of the IBR approach for both coral species correlated to the star plots showing the difference in alteration in the physiological biomarkers. The higher numerical values associated with each plot indicate increased physiological stress (n= 5).

Supplementary Tables

Table 1. PERMANOVA was established using a Bray-Curtis dissimilarity metric for all tile samples (eDNA) across sites, treatment, sites and treatment, and treatments within Site A and B. Levels of significance are indicated by p-values using the 9999-permutation test: $p<0.0001$ (***).

	Terms	**Df**	**SS**	**MS**	**F model**	**R^2**	**P-value**	**Sign.**
All Samples	Site:Treatment	3	0.71557	0.23852	4.5749	0.22697	1e-04	***
	Residuals	12	0.62564	0.05214		0.19845		
	Total	19	3.15268			1.00000		
Site A	Treatment	3	0.89798	0.299326	7.6537	0.79282	4e-04	***
	Residuals	6	0.23465	0.039109		0.20718		
	Total	9	1.13263			1.00000		
Site B	Treatment	3	1.00759	0.33586	5.1541	0.72044	5e-04	***
	Residuals	6	0.39099	0.06517		0.27956		

Table 2. Significant interactions of light curves obtained for *A. eurystoma*. Pairwise analysis of ETR_{max} and PAR_{50} values for sites and treatment within each site, using a 2-way ANOVA, post-hoc tests, and the Benjamini-Hochberg (FDR) correction to adjust p-values. Data is expressed as averages ± SE, $p<0.05$ (*), $p<0.001$ (**), and $p<0.0001$ (***).

Metric	**Location**	**Treatments**	**SE**	**Df**	**T-ratio**	**P-value**	
ETR_{max}	Across A←→B	Transplant	3.5287	30	-7.4224	0.0001	***
PAR_{50}	Across A←→B	Transplant	16.1812	30	-6.8086	0.0001	***

Table 3. Significant interactions of light curves obtained for *S. pistillata*. Pairwise analysis of ETR_{max} and PAR_{50} values for sites and treatment within each site, using a 2-way ANOVA, post-hoc tests, and the Benjamini-Hochberg (FDR) correction to adjust p-values. Data is expressed as averages ± SE, $p<0.05$ (*), and $p<0.001$ (**).

Metric	**Location**	**Treatments**	**SE**	**Df**	**T-ratio**	**P-value**	
ETR_{max}	Across A←→B	Transplant	3.8148	29	-3.1387	0.05	*
PAR_{50}	Across A←→B	Transplant	16.7578	29	-3.0399	0.05	*

Table 4. Chlorophyll-*a* measurements per µg/cm^2 and algae per cell (pg/cell) for *A. eurystoma* for sites and treatment within each site. 2-way ANOVAs, post-hoc tests, and the Benjamini-Hochberg (FDR) correction were used to adjust p-values. Data is expressed as averages ± SE, ns (no significance), $p<0.05$ (*), $p<0.001$ (**), and $p<0.0001$ (***).

Metric	Location	Treatments	SE	Df	T-ratio	P-value	
µg/cm^2	Across A←→B	Native	0.5242	23	-1.2173	0.4193	ns
	Across A←→B	Original	0.5242	23	-5.8105	0.0001	***
	Across A←→B	NonUrban - Urban	0.4604	23	-1.7582	0.2454	ns
	Across A←→B	Transplant	0.4853	23	1.3331	0.3911	ns
pg/cell	Across A←→B	Native	1.1603	23	-3.5519	0.0068	**
	Across A←→B	Original	1.1603	23	-2.8851	0.0223	*
	Across A←→B	NonUrban - Urban	1.0191	23	-5.2508	0.0004	***
	Across A←→B	Transplant	1.0742	23	1.1493	0.4196	ns

Table 5. Density of algae (symbionts) for *A. eurystoma* for sites and treatment within each site. 2-way ANOVAs, post-hoc tests, and the Benjamini-Hochberg (FDR) correction were used to adjust p-values. Data is expressed as averages ± SE, ns (no significance), $p<0.05$ (*), $p<0.001$ (**), and $p<0.0001$ (***).

Location	Treatments	SE	Df	T-ratio	P-value	
Across A←→B	Native	276483.9	22	-0.3872	0.8488	ns
Across A←→B	Original	298636.8	22	1.9505	0.1662	ns
Across A←→B	NonUrban - Urban	285551.4	22	5.6511	0.0002	***
Across A←→B	Transplant	298636.8	22	0.1673	0.8687	ns

Table 6. Chlorophyll-*a* measurements per $\mu g/cm^2$ and algae per cell (pg/cell) for *S. pistillata* for sites and treatment within each site. 2-way ANOVAs, post-hoc tests, and the Benjamini-Hochberg (FDR) correction were used to adjust p-values. Data is expressed as averages ± SE, ns (no significance), $p<0.05$ (*), $p<0.001$ (**), and $p<0.0001$ (***).

Metric	Location	Treatments	SE	Df	T-ratio	P-value	
$\mu g/cm^2$	Across A←→B	Native	0.8459	22	-2.2553	0.0612	ns
	Across A←→B	Original	0.8459	22	-3.7064	0.0039	**
	Across A←→B	NonUrban - Urban	0.8088	22	0.4871	0.7766	ns
	Across A←→B	Transplant	0.8088	22	3.4592	0.006	**
pg/cell	Across A←→B	Native	0.9464	22	-9.514	0	***
	Across A←→B	Original	0.9464	22	-3.6256	0.003	**
	Across A←→B	NonUrban - Urban	0.905	22	-4.4214	0.0006	***
	Across A←→B	Transplant	0.905	22	3.3914	0.0047	**

Table 7. Density of algae (symbionts) for *S. pistillata* for sites and treatment within each site. 2-way ANOVAs, post-hoc tests, and the Benjamini-Hochberg (FDR) correction were used to adjust p-values. Data is expressed as averages ± SE, ns (no significance), $p<0.05$ (*), $p<0.001$ (**), and $p<0.0001$ (***).

Location	Treatments	SE	Df	T-ratio	P-value	
Across A←→B	Native	870206.4	17	2.0528	0.1786	ns
Across A←→B	Original	930289.8	17	1.8013	0.2044	ns
Across A←→B	NonUrban - Urban	930289.8	17	1.8916	0.2019	ns
Across A←→B	Transplant	930289.8	17	-2.4973	0.0923	ns

Table 8. All interactions of total antioxidant capacity (TAC) for *A. eurystoma* and S. *pistillata*. Pairwise analysis of TAC values across Sites and Treatments and Treatments within each site was conducted using a 2-way ANOVA, post-hoc tests, and the Benjamini-Hochberg (FDR) correction to adjust p-values. Ns (no significance), p<0.05 (*), p<0.001 (**), and p<0.0001 (***).

A. eurystoma

Location	Treatments	SE	Df	T-ratio	P-value	
Across A←→B	Original	906.0947	21	5.1129	0.0001	***
Across A←→B	NonUrban - Urban	961.0586	21	2.2589	0.039	*
Across A←→B	Transplant	1046.268	21	-4.4715	0.0001	***
S. pistillata						
Across A←→B	Original	2023.119	13	5.9801	0.0001	***
Across A←→B	NonUrban - Urban	1892.454	13	1.4521	0.2188	ns
Across A←→B	Transplant	2023.119	13	-5.8459	0.0001	***

Table 9. Differential abundance analysis identified 10 bacteria families with significant differences between Original A and Transplant A tiles. Significance was determined using general linear model coefficients with a log2 fold change to achieve adjusted p-values, where p-adj<0.05 (*), p<0.001 (**), and p<0.0001 (***).

Phyla	**adjusted p-value**
Cyanobacteria; Cyanobacteriia; Phormidesmiales; Phormidesmiaceae; Acrophormium PCC-7375	2.27E-15
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Halieaceae	1.19E-09
Planctomycetota; Planctomycetes; Pirellulales; Pirellulaceae; Pir4 lineage	1.49E-08
Proteobacteria; Gammaproteobacteria; Pseudomonadales; KI89A clade	2.53E-05
Planctomycetota; Planctomycetes; Pirellulales; Pirellulaceae; Rubripirellula	0.00080038
NB1-j; NB1-j; NB1-j; NB1-j; NB1-j	0.00541498
Proteobacteria; Alphaproteobacteria; Caulobacterales; Hyphomonadaceae; uncultured	0.00633812
Proteobacteria; Gammaproteobacteria; Enterobacterales; Vibrionaceae; Vibrio	0.02391366
Proteobacteria; Gammaproteobacteria; Burkholderiales	0.03842134
Proteobacteria; Gammaproteobacteria; UBA10353_marine group; UBA10353	0.04575013

Table 10. Differential abundance analysis identified 21 bacteria families with significant differences between Original B and Transplant A tiles. Significance was determined using general linear model coefficients with a log2 fold change to achieve adjusted p-values, where p-adj<0.05 (*), p<0.001 (**), and p<0.0001 (***).

Phyla	**adjusted p-value**
Cyanobacteria; Cyanobacteriia; Phormidesmiales; Nodosilineaceae; MBIC10086	7.26E-11
Proteobacteria; Gammaproteobacteria; Pseudomonadales; Halieaceae	6.99E-10
Planctomycetota; Planctomycetes; Pirellulales; Pirellulaceae; Pir4 lineage	9.22E-08
Proteobacteria; Gammaproteobacteria; Pseudomonadales; KI89A clade	1.82E-07
Bacteroidota; Bacteroidia; Cytophagales; Cyclobacteriaceae; Ekhidna	1.32E-07
Bacteroidota; Bacteroidia; Flavobacteriales; Flavobacteriaceae	5.59E-06
Bacteroidota; Bacteroidia; Chitinophagales; Saprospiraceae; uncultured	4.49E-05
Bacteroidota; Bacteroidia; Cytophagales; Amoebophilaceae; Candidatus Amoebophilus	8.18E-05
Proteobacteria; Gammaproteobacteria; Burkholderiales; c7c9566f0706e4c3cbd5019381bf96d0	9.75E-05
Proteobacteria; Gammaproteobacteria; Burkholderiales; 59066116779926be1063797ea09b6856	9.93E-05
Proteobacteria; Gammaproteobacteria; Burkholderiales; 7f9f109d8a63c9cc024e043154a56943	9.93E-05
Myxococcota; Myxococcia; Myxococcales; Myxococcaceae; P3OB-42	0.00012701
Chloroflexi; Anaerolineae; SBR1031; A4b; A4b	0.00039664
Bacteroidota; Bacteroidia; Cytophagales; Cyclobacteriaceae; Fulvivirga	0.00325593
Proteobacteria; Gammaproteobacteria; Tenderiales; Tenderiaceae; Candidatus Tenderia	0.01572549
Gemmatimonadota; BD2-11_terrestrial_group; BD2-11	0.02120412
Proteobacteria; Alphaproteobacteria; Rhizobiales; Stappiaceae; Labrenzia	0.02120412
Proteobacteria; Gammaproteobacteria; Burkholderiales;	0.02120412
Proteobacteria; Gammaproteobacteria; Burkholderiales; EC94	0.02120412
Proteobacteria; Alphaproteobacteria; Rhizobiales; Stappiaceae	0.0246093
Actinobacteriota; Acidimicrobiia; Microtrichales; Microtrichaceae; Sva0996_marine group	0.02675962

Table 11. Level of significance (adjusted for multiple comparisons) for the pairwise comparisons of IBR values between categories in *A. Eurystoma*. The IBR value is an average of all permutations, with the highest values indicating the highest biological alteration. Ns (no significance), p<0.05 (*), p<0.001 (**), and p<0.0001 (***).

Condition	**adjusted p-value**
A NonUrban vs. A Original	0.803
A Transplant from Site B vs. A Original	**5.67e-05**
A Transplant from Site B vs. A NonUrban	**0.000383**
B Original vs. A Original	**6.38e-07**
B Original vs. A NonUrban	**1.29e-06**
B Original vs. A Transplant from Site B	**1.77e-05**
B Urban vs. A Original	**1.5e-06**
B Urban vs. A NonUrban	**6.34e-06**
B Urban vs. A Transplant from Site B	**2.25e-05**
B Urban vs. B Original	**0.00948**
B Transplant from Site A vs. A Original	**0.00226**
B Transplant from Site A vs. A NonUrban	**0.00218**
B Transplant from Site A vs. A Transplant from Site B	0.422
B Transplant from Site A vs. B Original	**0.000374**
B Transplant from Site A vs. B Urban	**0.000683**

Table 12. Level of significance for the IBR approach (adjusted for multiple comparisons) for the pairwise comparisons of IBR values between categories in *S. pistillata*. The IBR value is an average of all permutations, with the highest values indicating the highest biological alteration. Ns (no significance), p<0.05 (*), p<0.001 (**), and p<0.0001 (***).

Condition	**adjusted p-value**
A NonUrban vs. A Original	**0.000228**
A Transplant from Site B vs. A Original	**1.73e-07**
A Transplant from Site B vs. A NonUrban	**2.3e-06**
B Original vs. A Original	**2.53e-08**
B Original vs. A NonUrban	**3.27e-07**
B Original vs. A Transplant from Site B	**2.77e-07**
B Urban vs. A Original	**0.000432**
B Urban vs. A NonUrban	**0.000927**
B Urban vs. A Transplant from Site B	0.929
B Urban vs. B Original	**0.00115**
B Transplant from Site A vs. A Original	0.313
B Transplant from Site A vs. A NonUrban	0.0596
B Transplant from Site A vs. A Transplant from Site B	**1.79e-05**
B Transplant from Site A vs. B Original	**9.31e-07**
B Transplant from Site A vs. B Urban	**0.00129**

Table 13. Level of significance for the IBR approach (adjusted for multiple comparisons) for the pairwise comparisons of IBR values between categories for both corals together. The IBR value is an average of all permutations, with the highest values indicating the highest biological alteration. Ns (no significance), p<0.05 (*), p<0.001 (**), and p<0.0001 (***).

Condition	**adjusted p-value**
A NonUrban vs. A Original	**0.000897**
A Transplant from Site B vs. A Original	**<2e-16**
A Transplant from Site B vs. A NonUrban	**7.66e-12**
B Original vs. A Original	**<2e-16**
B Original vs. A NonUrban	**1.39e-13**
B Original vs. A Transplant from Site B	**4.24e-15**
B Urban vs. A Original	**1.16e-10**
B Urban vs. A NonUrban	**2.16e-09**
B Urban vs. A Transplant from Site B	**2.45e-05**
B Urban vs. B Original	**1.26e-08**
B Transplant from Site A vs. Original	**1.28e-06**
B Transplant from Site A vs. A NonUrban	**6e-04**
B Transplant from Site A vs. A Transplant from Site B	**8.42e-10**
B Transplant from Site A vs. Original	**3.44e-13**
B Transplant from Site A vs. B Urban	**9.63e-09**