

## Supplementary Information

### **Coral bacterial community structure responds to environmental change in a host-specific manner**

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Short title: Microbiome flexibility of corals

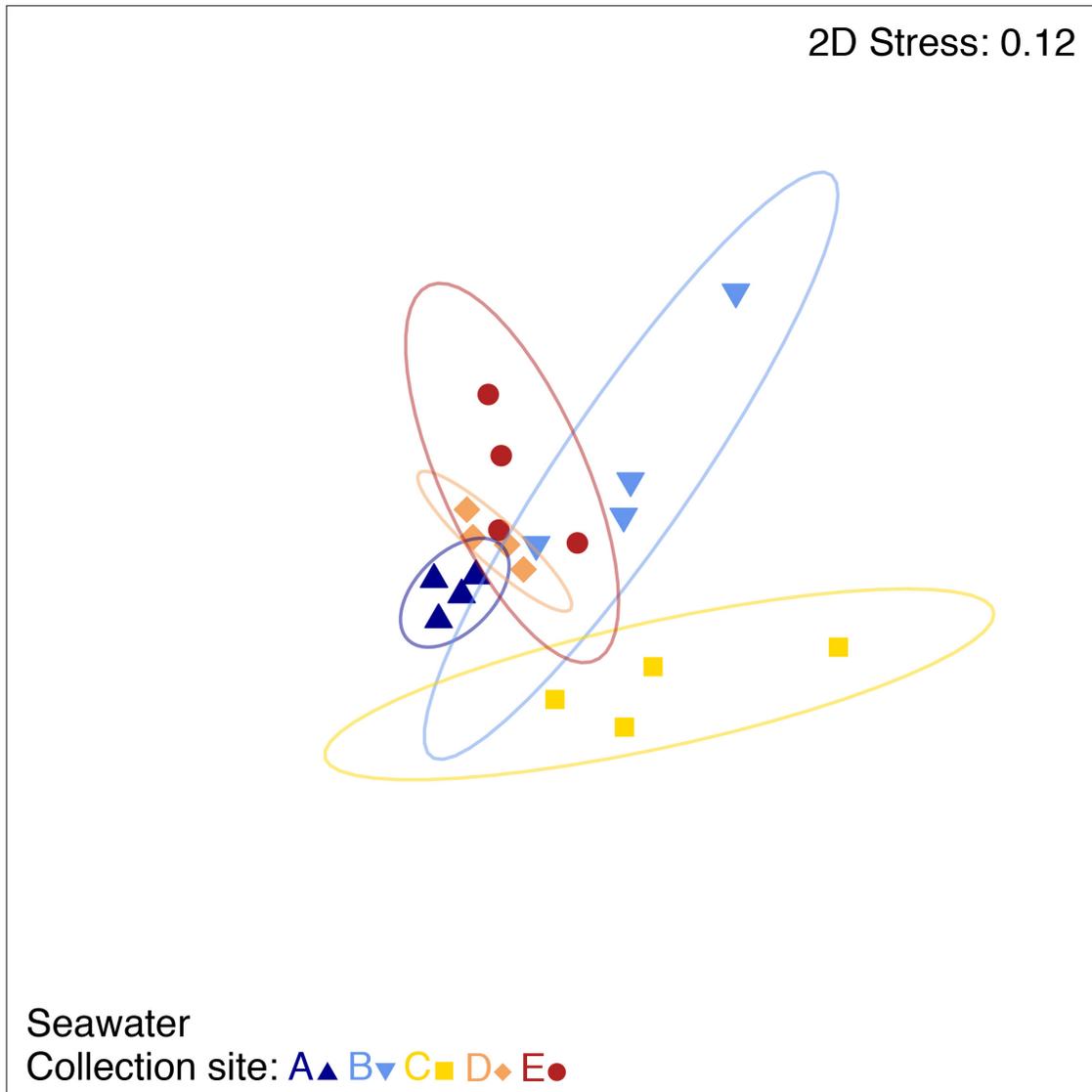
## Supplementary Methods

### *Quantification of anthropogenic impacts*

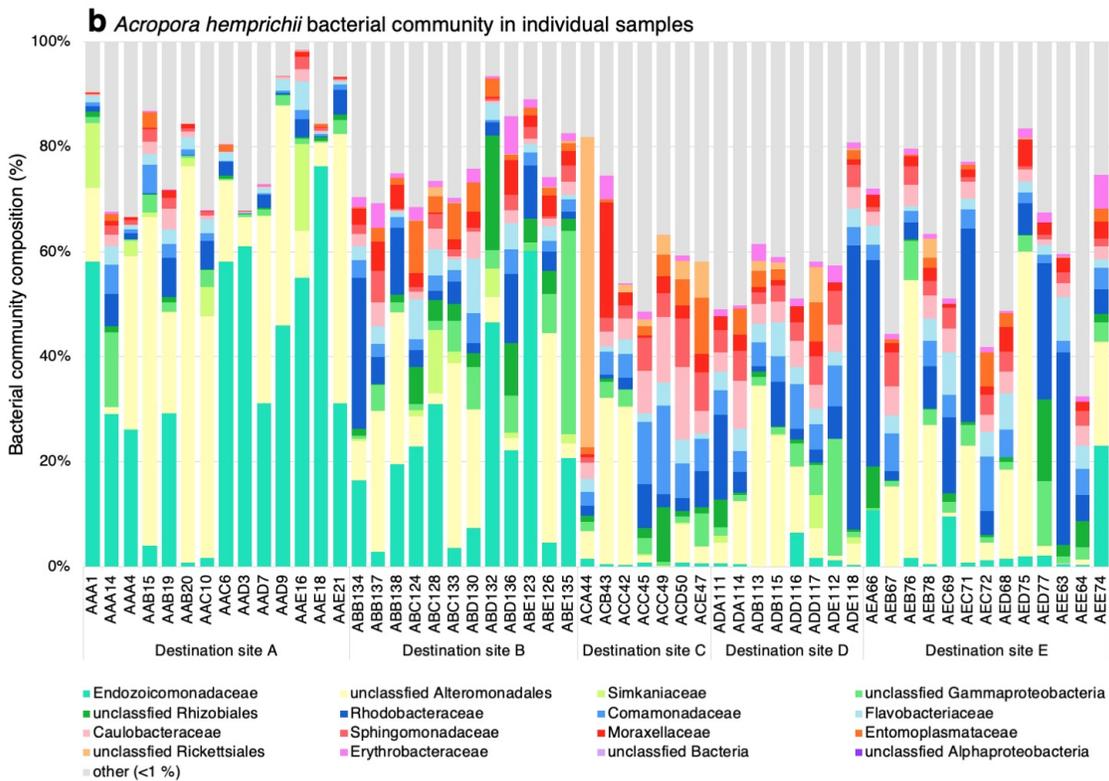
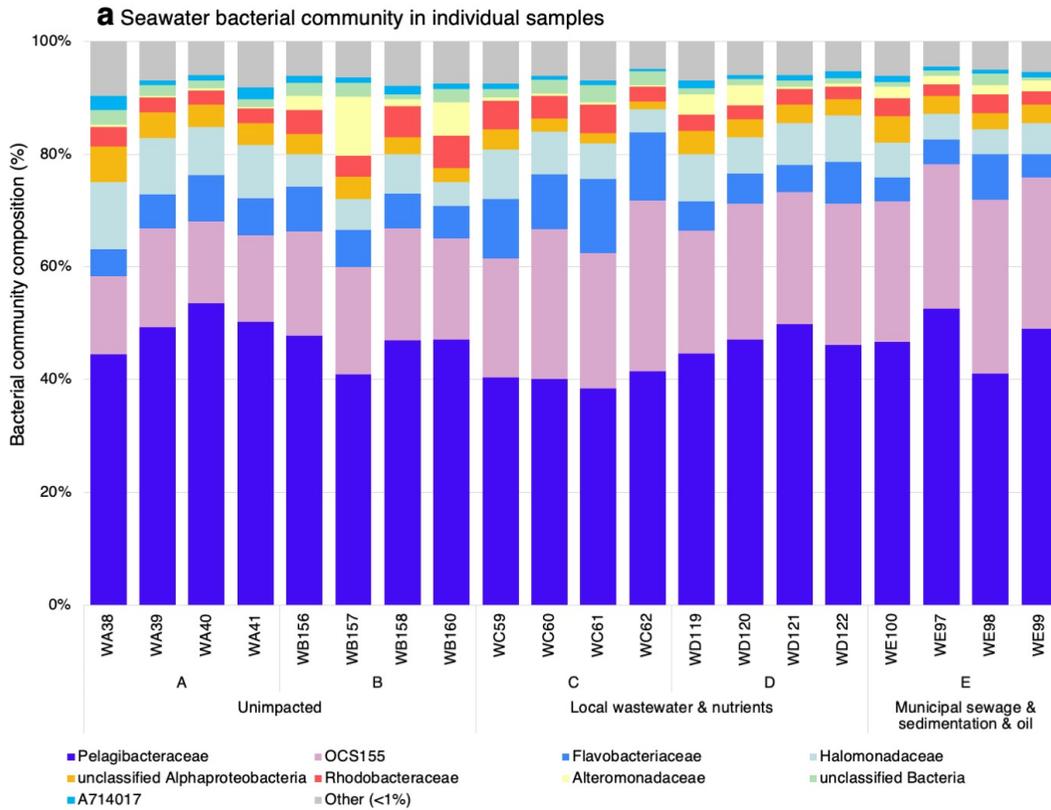
To characterize the anthropogenic impacts at our study sites, we quantified sediment loads, inorganic nitrate and total hydrocarbons over the period of one year. Specifically, sediment loads at the six sites (A-F) were determined using duplicate sediment traps, one attached in mid-water to each end of the coral culture rig. Each trap consisted of a vertically orientated 40 cm long x 10 cm diameter PVC cylinder, with two internal vertical baffles inserted to limit particle resuspension<sup>1,2</sup>. At intervals of 2 - 6 months the traps were first capped (to prevent loss of sediment during transport) and then collected for return to the laboratory, where the sediment from each trap was filtered through 0.45µm GF/C filter paper, dried at 80 °C for 8 h and then weighed. Concentrations of inorganic nitrate were determined according to the method recommended by Parsons *et al.*,<sup>3</sup> using a Pye-Unicam Spectrophotometer (Model PU-8600).

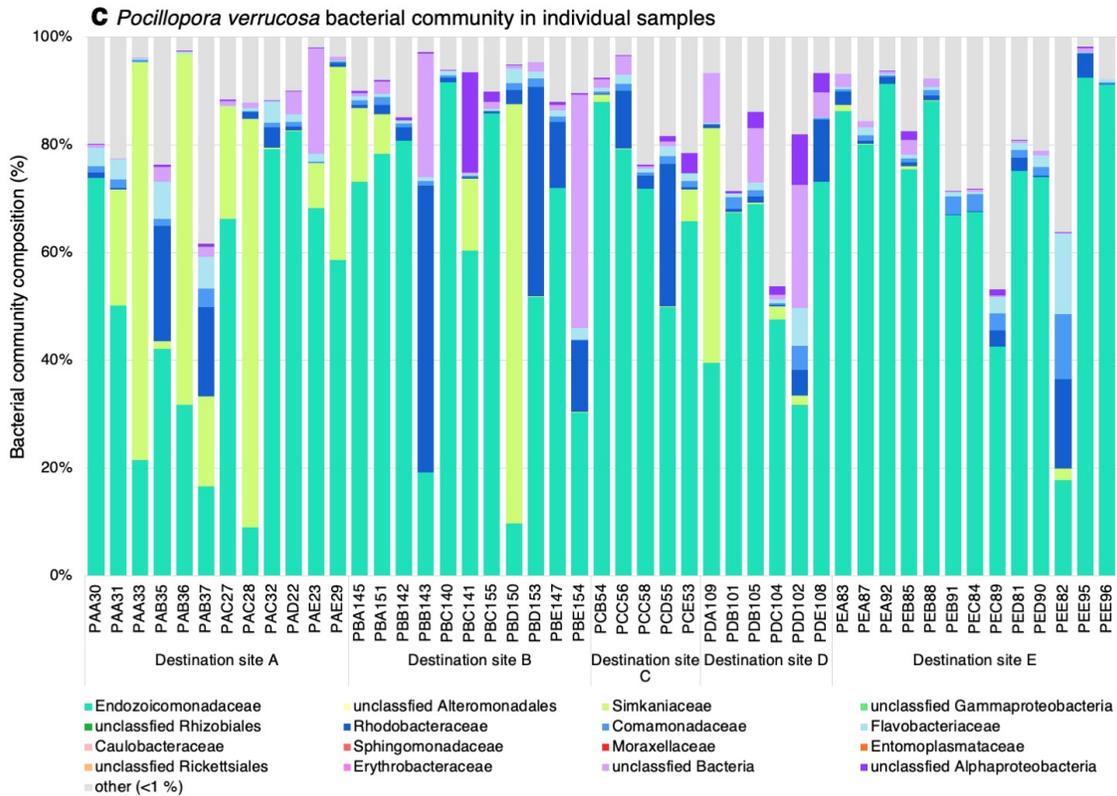
Water samples were analyzed for total hydrocarbons (THCs), based on the method of Law, Fileman, and Portman<sup>4</sup> as adopted by ROMPE<sup>5</sup>. Extraction was carried out with 4 x 25 ml of dichloromethane (CH<sub>2</sub>Cl<sub>2</sub>) after drying over anhydrous sodium sulphate. The solvent was removed by rotary evaporation, and the extracts then taken up in *n*-hexane. Total hydrocarbons, in water extracts, were then measured by fluorescence spectrophotometry on a Shimadzu Dual Beam Difference Spectrofluorophotometer (Model RF-500), with the excitation wavelength at 310 nm and the emission scanned from 320 - 500 nm and quantified at 360 nm. Light Arabian crude oil (LAO) was used for standardization and quantification.

## Supplementary Figures

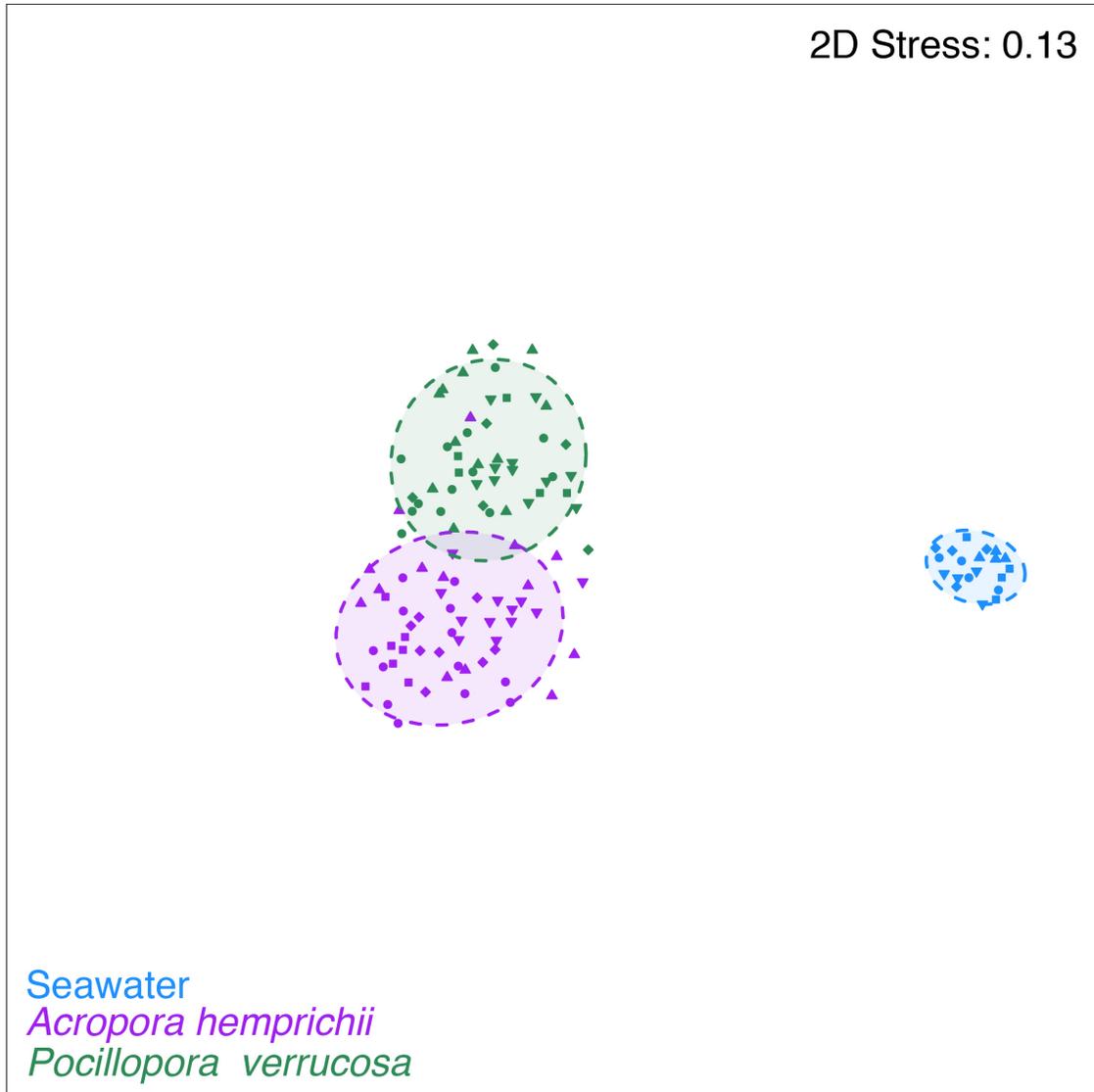


**Supplementary Figure 1. Bacterial community structure and relative dispersion of seawater samples.** Samples were taken from five sites close to the city of Jeddah in the Red Sea and are shown based on non-metric multidimensional scaling (nMDS) of Bray-Curtis distances. Ellipses denote 90 % confidence intervals. Source data are provided as a Source Data file.

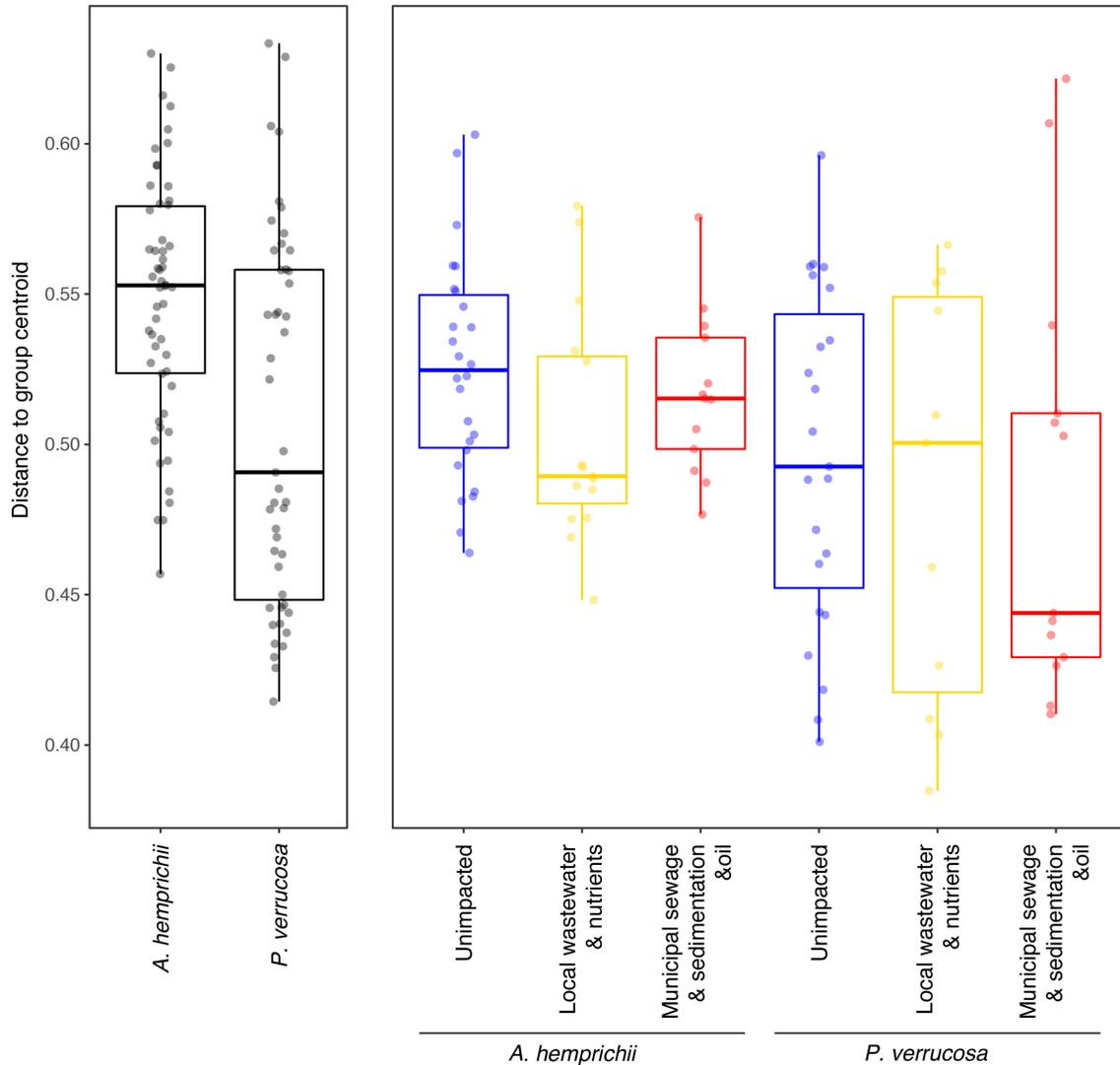




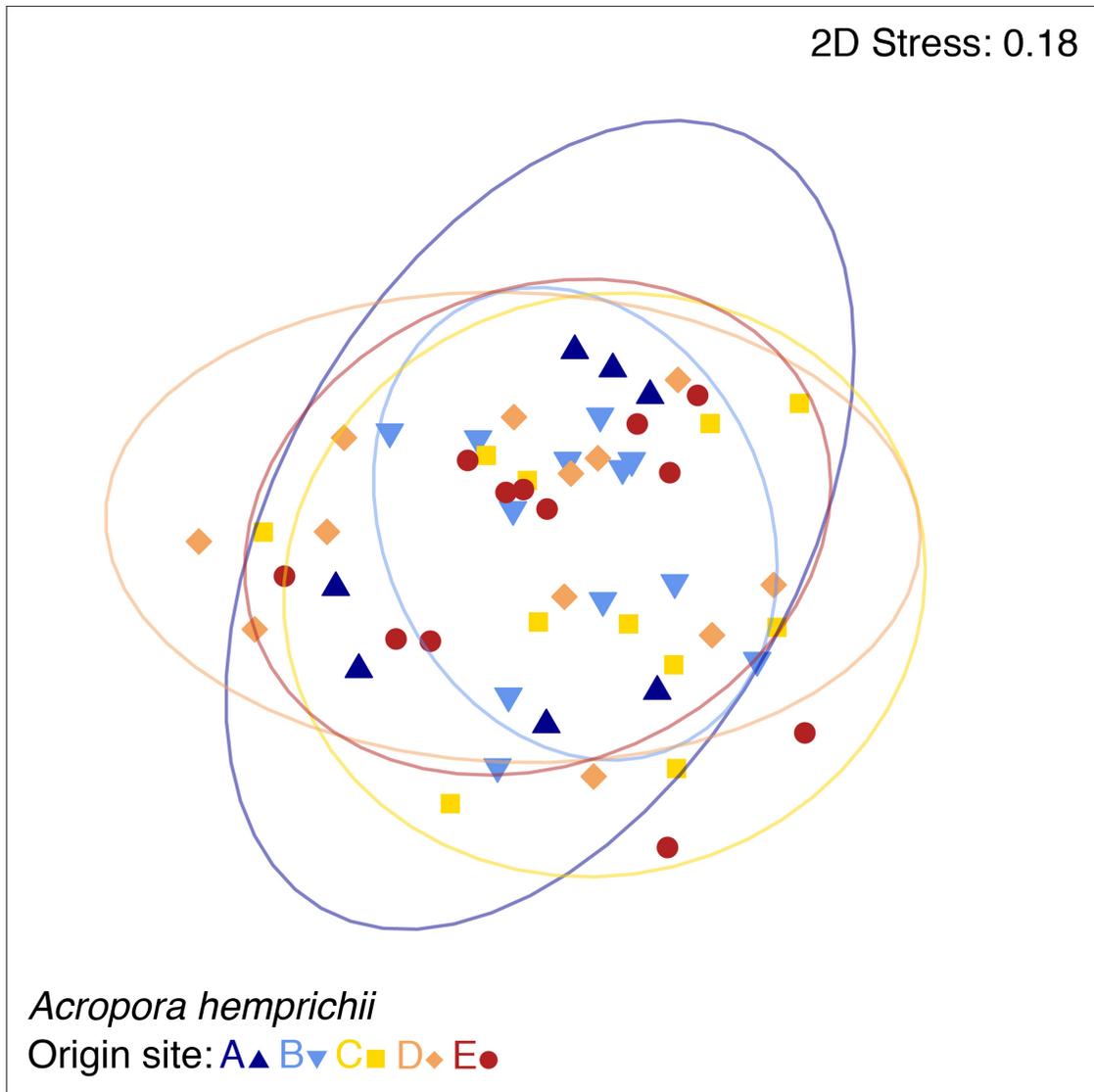
**Supplementary Figure 2. Bacterial community composition in all individual samples.** Bacterial community composition in samples of a) seawater, b) the coral *Acropora hemprichii*, and c) the coral *Pocillopora verrucosa* after a 21-months cross-transplantation experiment close to the city of Jeddah in the Red Sea. Samples denoted by destination site. Source data are provided as a Source Data file.



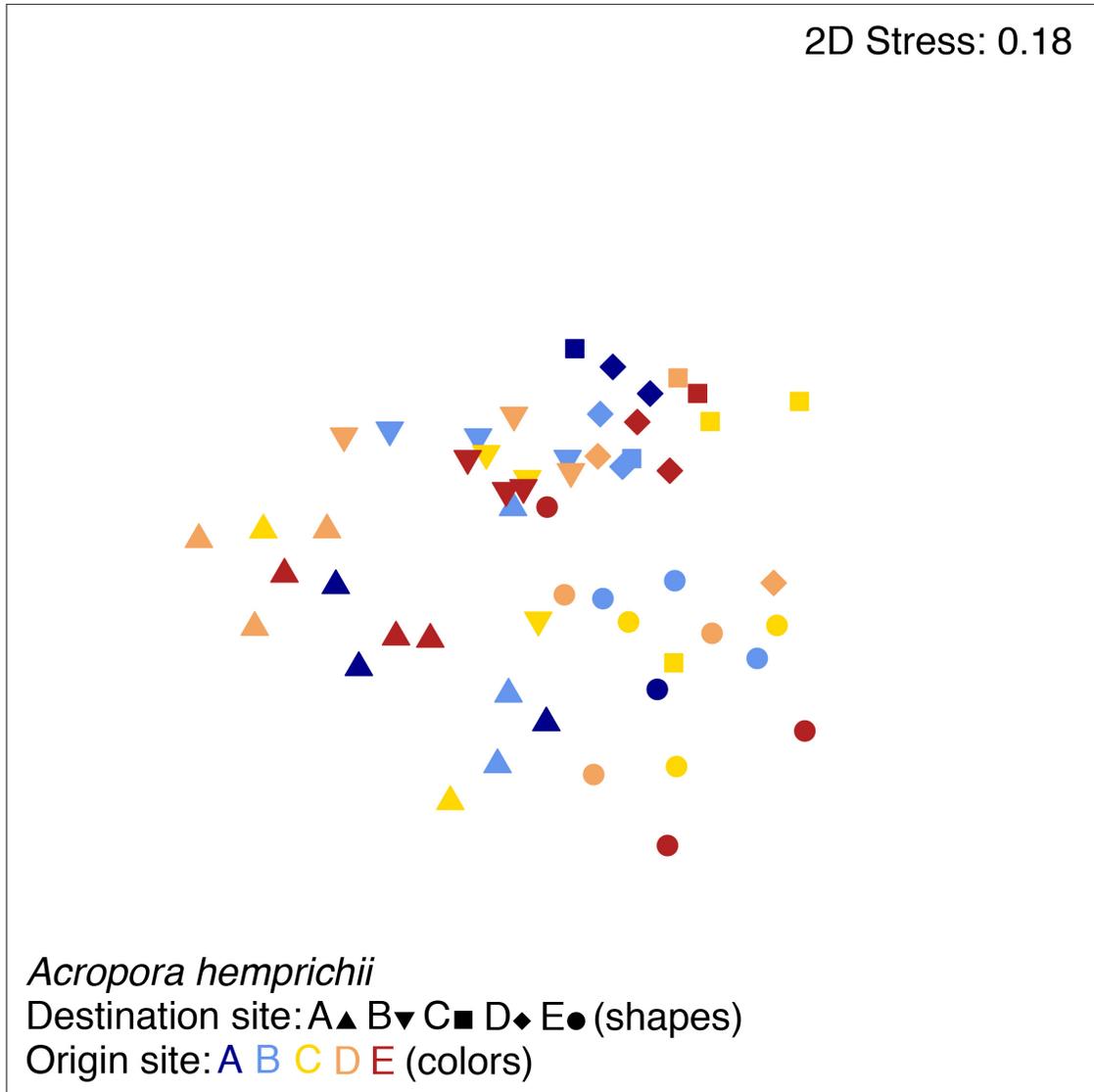
**Supplementary Figure 3. Bacterial community structure and relative dispersion per sample type.** Bacterial communities associated with the coral species *Acropora hemprichii* and *Pocillopora verrucosa* and seawater samples from five sites close to the city of Jeddah in the Red Sea (after 21 months of reciprocal transplantation) based on non-metric multidimensional scaling (nMDS) of Bray-Curtis distances. Ellipses denote 90 % confidence intervals. Source data are provided as a Source Data file.



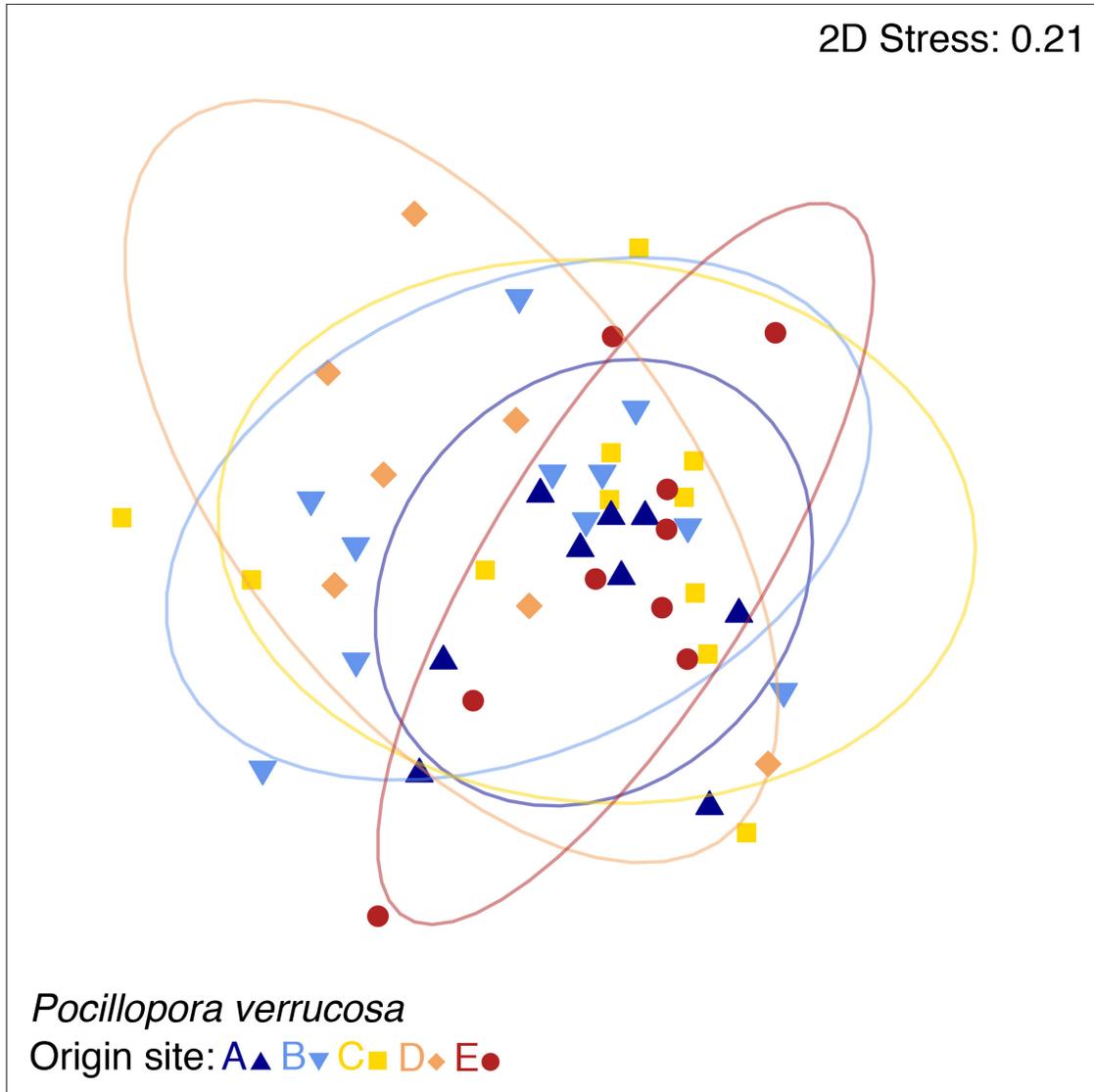
**Supplementary Figure 4. Multivariate dispersion of microbial community samples.** Bacterial community dispersion from the coral species *Acropora hemprichii* and *Pocillopora verrucosa* after 21 months of reciprocal transplantation between 3 levels of anthropogenic impact (colors: blue = unimpacted, yellow = local wastewater & nutrients, red = municipal wastewater & sedimentation & oil) close to the city of Jeddah in the Red Sea. Microbial communities of *A. hemprichii* are significantly more variable than those of *P. verrucosa* (left graph, ANOVA,  $F = 16.01$ ,  $p < 0.001$ ), while differences between destination impacts within species were not significantly different (right graph, ANOVA, all  $p > 0.05$ ). Boxes represent the 25<sup>th</sup> to 75<sup>th</sup> percentile, lines show medians, error bars represent smallest/largest values to a maximum of  $1.5 * IQR$ . Source data are provided as a Source Data file.



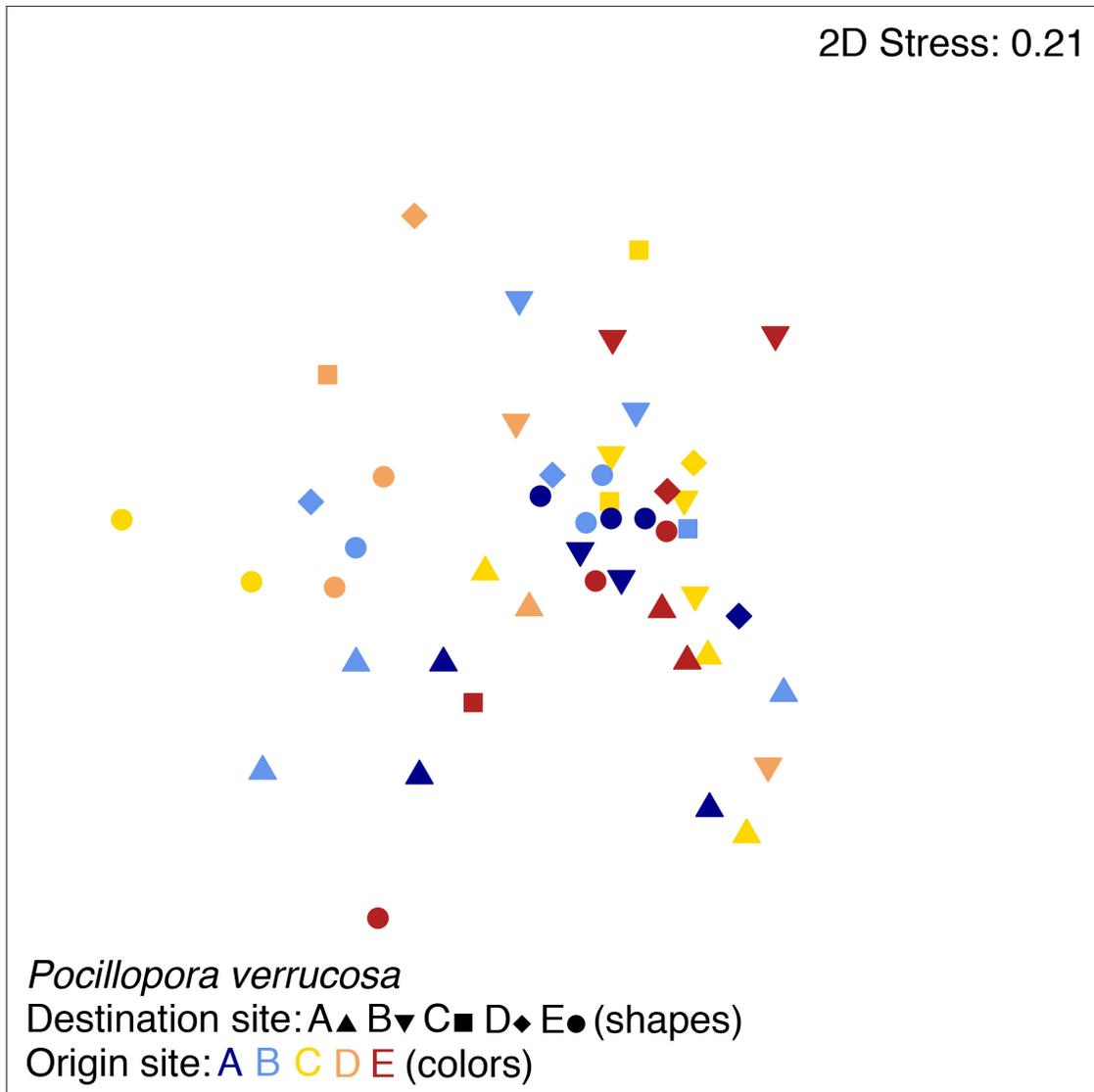
**Supplementary Figure 5. Bacterial community structure and relative dispersion in *A. hemprichii*.** Data shown based on non-metric multidimensional scaling (nMDS) of Bray-Curtis distances. Data shown as site of origin after 21 months of reciprocal transplantation. A/B unimpacted sites; C/D local wastewater & nutrients; E municipal sewage & sedimentation & oil. Ellipses denote 90 % confidence intervals. Source data are provided as a Source Data file.



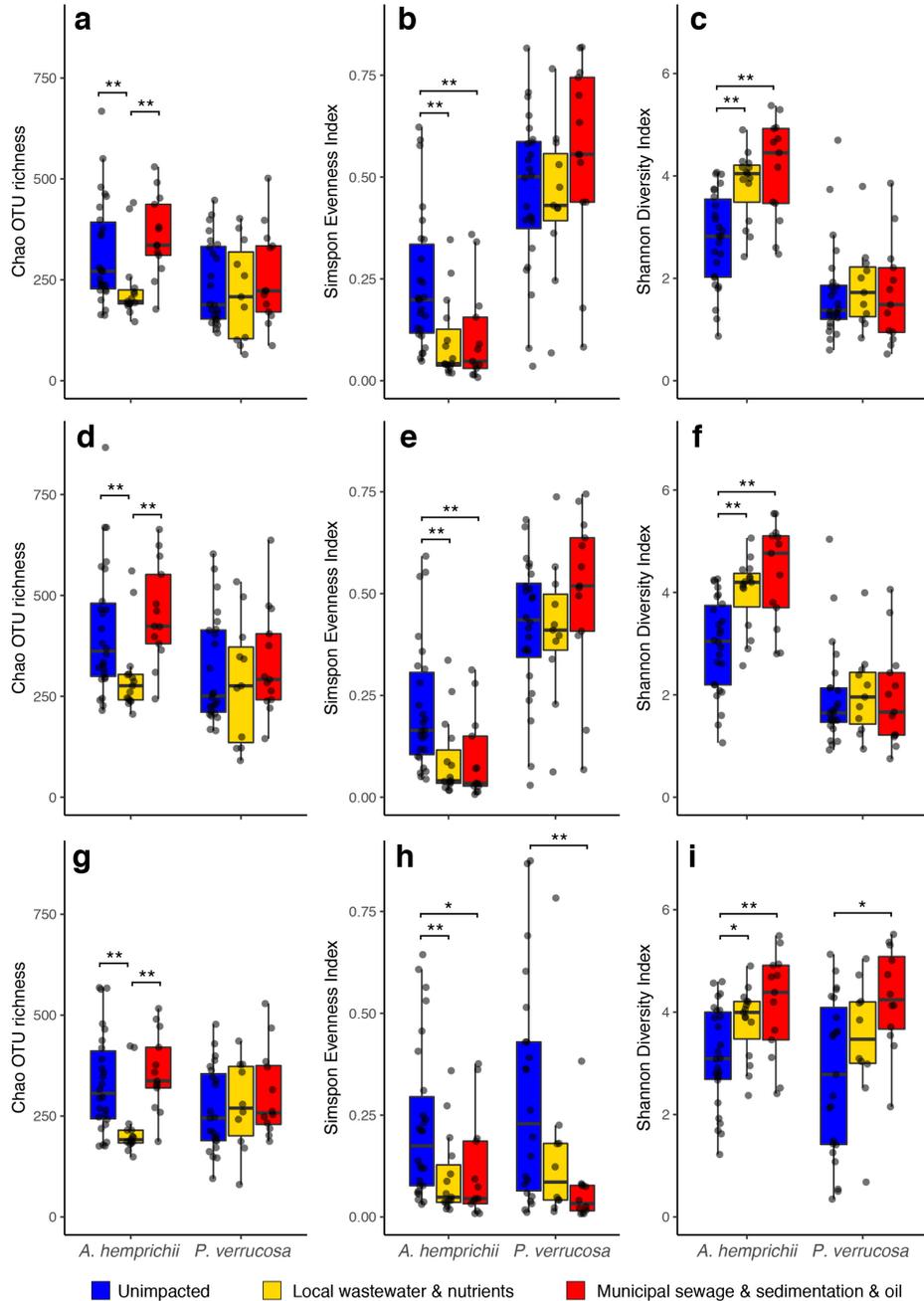
**Supplementary Figure 6. Bacterial community structure in *A. hemprichii*.** Data shown based on non-metric multidimensional scaling (nMDS) of Bray-Curtis distances. Data shown as site of destination (shapes) and site of origin (colors) after 21 months of reciprocal transplantation. A/B unimpacted sites; C/D local wastewater & nutrients; E municipal sewage & sedimentation & oil. Source data are provided as a Source Data file.



**Supplementary Figure 7. Bacterial community structure and relative dispersion in *P. verrucosa*.** Data shown based on non-metric multidimensional scaling (nMDS) of Bray-Curtis distances. Data shown as site of origin after 21 months of reciprocal transplantation. A/B unimpacted sites; C/D local wastewater & nutrients; E municipal sewage & sedimentation & oil. Ellipses denote 90 % confidence intervals. Source data are provided as a Source Data file.

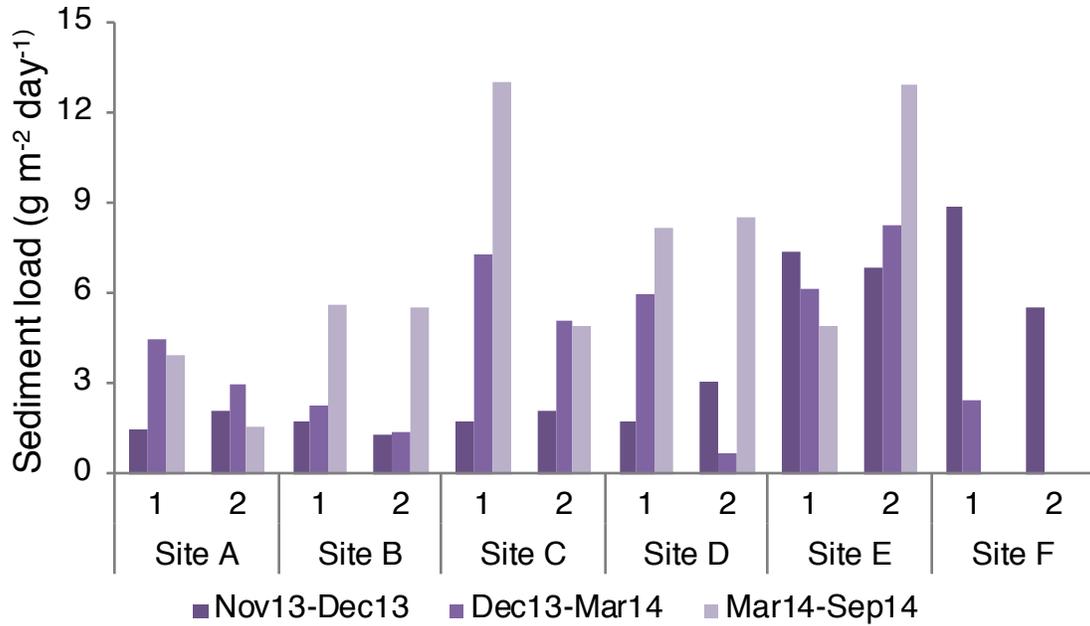


**Supplementary Figure 8. Bacterial community structure in *P. verrucosa*.** Data shown based on non-metric multidimensional scaling (nMDS) of Bray-Curtis distances. Data shown as site of destination (shapes) and site of origin (colors) after 21 months of reciprocal transplantation. A/B unimpacted sites; C/D local wastewater & nutrients; E municipal sewage & sedimentation & oil. Source data are provided as a Source Data file.

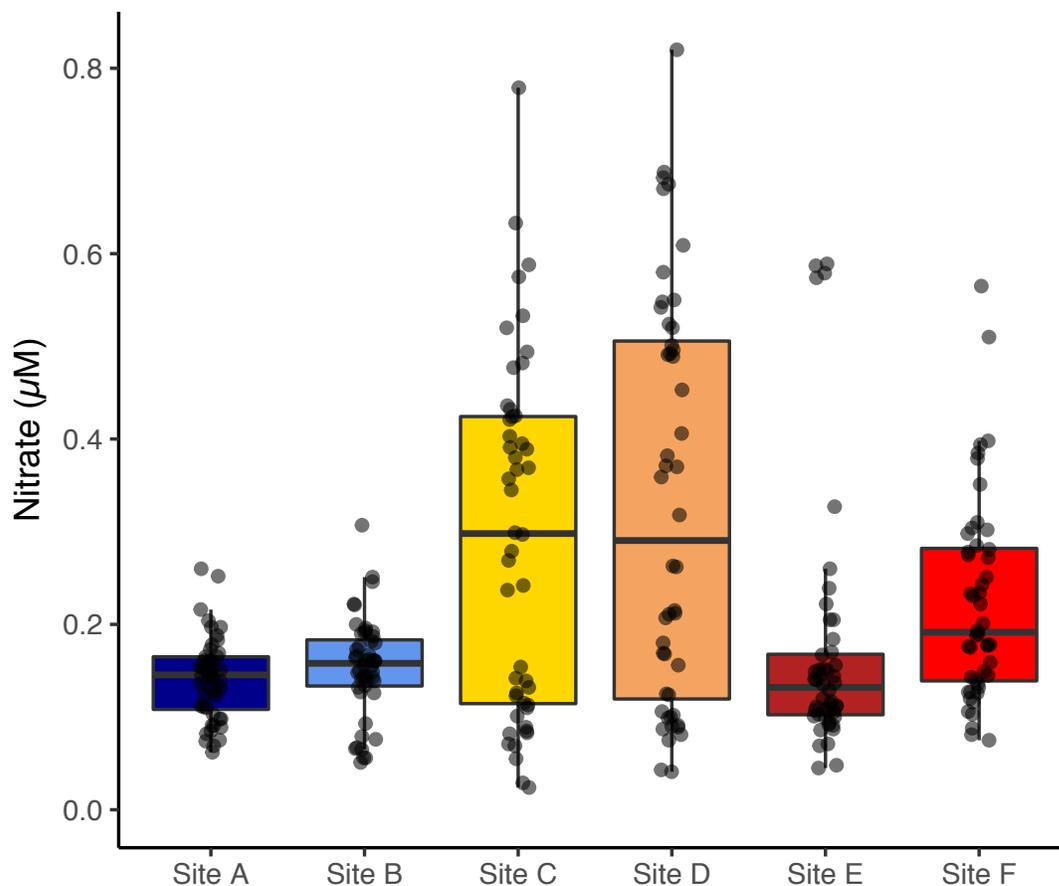


**Supplementary Figure 9. Bacterial richness and diversity of Red Sea corals.**

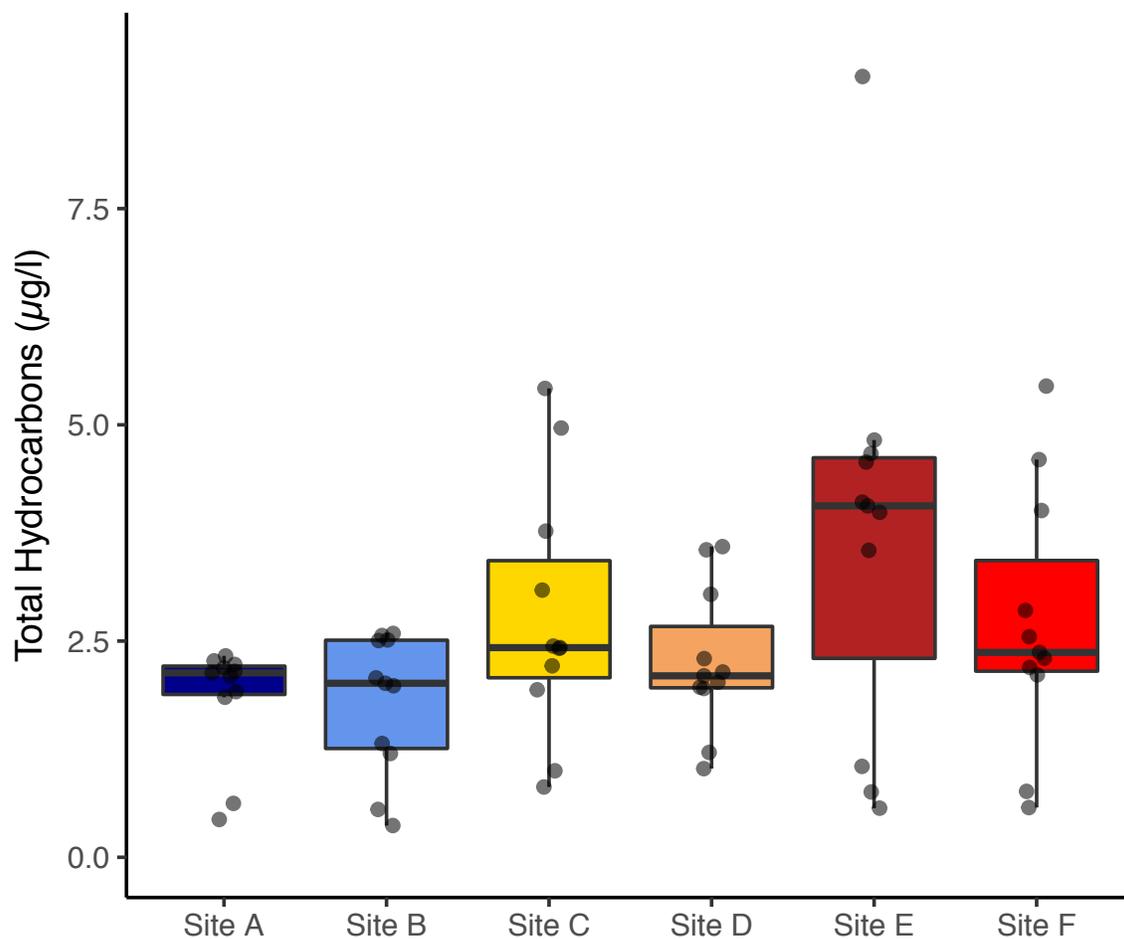
Fragments of the corals *Acropora hemprichii* and *Pocillopora verrucosa* were exposed to different levels of anthropogenic impact near Jeddah, Red Sea. Samples were collected after 21 months of reciprocal transplantation across different impacts and are displayed by destination impact. Different rows represent separate data analyses: **(a – c)** 97 % OTU data, **(d – f)** 99 % OTU data, **(g – i)** 97 % OTU data without Endozoicomonadaceae lineage. Boxes represent the 25<sup>th</sup> to 75<sup>th</sup> percentile, lines show medians, error bars represent smallest/largest values to a maximum of 1.5 \* IQR, Kruskal\_Wallis test significance levels: \*  $p < 0.05$ , \*\*  $p < 0.005$ . Source data are provided as a Source Data file.



**Supplementary Figure 10. Sediment load at six reef sites at Jeddah.** Measurements were taken during three deployment periods (colors) and determined from duplicate sediment traps (shown separately) at six reef sites close to the city of Jeddah in the Red Sea. Site F including all corals and sediment traps was lost prior to the last collection in September 2014, and replicate 2 at site F was lost during the second deployment (missing data). Source data are provided as a Source Data file.



**Supplementary Figure 11. Dissolved inorganic nitrate at six reef sites at Jeddah.** Measurements were taken in the Red Sea between October 2013 – September 2014. Four measurements were taken each month, one each per depth (1, 5, 10, 20 m). Boxes represent the 25<sup>th</sup> to 75<sup>th</sup> percentile, lines show medians, error bars represent smallest/largest values to a maximum of 1.5 \* IQR. Source data are provided as a Source Data file.



**Supplementary Figure 12. Concentration of total hydrocarbons ( $\mu\text{g L}^{-1}$ ) at six reef sites at Jeddah.** Samples were collected monthly from 1 m below the surface between October 2013 – September 2014 and measurements were standardized against Light Arabian Oil. Boxes represent the 25<sup>th</sup> to 75<sup>th</sup> percentile, lines show medians, error bars represent smallest/largest values to a maximum of 1.5 \* IQR. Source data are provided as a Source Data file.

## Supplementary Table

**Supplementary Table 1. Core microbiome of two Red Sea coral species.** List of members of the bacterial core microbiome for the corals *Acropora hemprichii* and *Pocillopora verrucosa* after a 21-months cross-transplantation experiment at reef sites close to the city of Jeddah in the Red Sea. OTUs were considered part of the core microbiome if they were identified in at least 75 % of samples at every site. The highest level of annotation is provided for each OTU, followed by the level of that classification.

Core microbiome of <i>Acropora hemprichii</i>		Fraction of corals with OTU at each destination site (A - E)					Number of sequences per sample at each destination site as means (SD)				
OTU	Greengenes annot. (taxonomic level)	A	B	C	D	E	A	B	C	D	E
Otu0002	<i>Melitea</i> sp. (g)	1.00	1.00	0.86	1.00	0.77	991 (704)	558 (521)	348 (430)	502 (428)	567 (633)
Otu0007	<i>Caulobacter</i> sp. (g)	1.00	1.00	1.00	1.00	1.00	30 (34)	64 (49)	187 (111)	155 (67)	100 (37)
Otu0014	<i>Sphingomonas</i> sp. (g)	0.93	1.00	0.86	1.00	1.00	16 (20)	36 (44)	90 (80)	79 (47)	42 (33)
Otu0017	<i>Flavobacterium</i> sp. (g)	1.00	1.00	1.00	1.00	1.00	16 (16)	20 (11)	30 (25)	57 (28)	47 (24)
Otu0021	Unclassified Comamonadaceae (f)	0.86	1.00	0.86	1.00	0.92	8 (11)	22 (10)	33 (22)	48 (32)	26 (16)
Otu0026	<i>Pelomonas</i> sp. (g)	1.00	0.92	1.00	0.88	1.00	7 (7)	11 (7)	32 (26)	32 (18)	29 (15)
Otu0031	<i>Staphylococcus</i> sp. (g)	0.86	0.83	0.86	0.88	1.00	5 (6)	15 (18)	34 (45)	22 (21)	20 (22)

Core microbiome of <i>Pocillopora verrucosa</i>		Fraction of corals with OTU at a site (A - E)					Number of sequences per sample at a site as means (SD)				
OTU	Greengenes annot. (taxonomic level)	A	B	C	D	E	A	B	C	D	E
Otu0001	Unclassified Endozoicomonadaceae (f)	1.00	1.00	1.00	1.00	1.00	1,427 (809)	1,756 (842)	2,045 (526)	2,225 (665)	2,220 (647)
Otu0003	Unclassified Endozoicomonadaceae (f)	0.92	1.00	1.00	0.83	1.00	52 (67)	53 (53)	20 (23)	28 (21)	42 (32)
Otu0007	<i>Caulobacter</i> sp. (g)	1.00	0.91	1.00	1.00	1.00	17 (22)	18 (14)	22 (11)	41 (45)	30 (27)
Otu0011	<i>Erythrobacter</i> sp. (g)	0.92	1.00	1.00	1.00	1.00	8 (13)	32 (20)	13 (12)	79 (84)	24 (19)
Otu0014	<i>Sphingomonas</i> sp. (g)	0.85	0.91	0.80	0.83	1.00	9 (11)	7 (8)	6 (3)	8 (6)	12 (12)
Otu0017	<i>Flavobacterium</i> sp. (g)	0.85	1.00	1.00	1.00	0.92	13 (15)	60 (2)	13 (3)	10 (9)	27 (55)

## Supplementary References

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