nature portfolio

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Last updated by author(s): 30/10/24

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☐	☒	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	no software used for data collection.
Data analysis	DADA2 package version 1.26.0 and R software v.4.1.0. QIIME (v. 1.9). QIIME 2 v2022.2. R packages car, ggplot2, factoextra, corrplot, vegan, treemapify, CALculate IBR Interface, ampvis, DESeq2, and apeglm.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The sequencing data generated from this study has been deposited in the NCBI public database under accession code PRJNA1114437 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1114437/]. The supporting figures and tables of sequencing and coral physiology data generated in this study are provided in the Supplementary Information file. Water quality information to inform this study can be found in the Supplementary Data 1 file. The coral physiology data generated in this study is publicly available at SEANOE (sea scientific open data publication) [https://doi.org/10.17882/102809]. All data accession codes can be

found in the Supplementary Data 2 file.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	Permits to collect samples were issued by The Israel Nature and Parks Authority (Permit #2020/42549) and Permit #2021/42831).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We deployed 18 biomimetic tiles (25 cm x 25 cm) fabricated with 3D design, printing, and molding to replicate the rugosity of natural reef surfaces. Three biomimetic tiles were held together in a stainless-steel frame (one complete structure; n= 3, per site) and were spaced apart by 45 cm to allow light access and water flow29. Biomimetic tiles within each frame were attached to the coral reef at roughly 8 m at Site A (n= 9) and Site B (n= 9) from February 2021 – February 2022 (Permit #2020/42549). The tile treatments at either site were described by the time and status of the organismal community accumulated on each tile. Site A and B each contained a set of 'Original' tiles (Original A and Original B) that never left the site and stayed for the total 12-month duration of the study. The next tile treatment was sampled twice during the study for eDNA (i.e., marine invertebrates and bacteria); the first time was after the first 6 months of community development to mark timepoint 1, before corals were attached (Phase I). Site A tiles were referred to as 'NonUrban T1' and Site B tiles were referred to as 'Urban T1' tiles (Phase I). After sampling, these tiles were scrapped clean, washed, and dried visibly of any organisms or biofilms, and redeployed as clean tiles for an additional 6 months at Site A as 'NonUrban T2', and at Site B as 'Urban T2' tiles (Phase II), where they remained at either site until they were sampled for the second time at the end of the study (Phase III). The last tile treatment were the 'Transplant' tiles that were reciprocally transferred from either site, Transplant A tiles (conditioned at Site A) went to Site B and Transplant B tiles (conditioned at Site B) went to Site A (6 months of growth at both sites) (Phase II). Tiles were monitored visually every 2 months using photogrammetry. After the reciprocal transplant of biomimetic tiles between sites, fragments were collected from mature, native colonies of two common branching corals at each site to attach to tiles. This study utilized two prevalent scleractinian coral species in the GoE/A: Acropora eurystoma, a broadcast spawner from the Complexa clade, and Stylophora pistillata, a brooder from the Robusta clade. Corals were collected (n= 5, per species) per site at a depth of 8 m (Permit #2021/42831), fragmented into smaller colonies and secured to each tile treatment for an additional 6 months. Coral treatments were based on the specific tile treatment that they were attached to during the study. 'Native' corals were directly collected from colonies at either site and were never attached to tiles, serving as the site baseline. 'Original' corals remained on the original Site A or Site B tiles that stayed at one site for all 12-months. 'NonUrban T2' and 'Urban T2' corals were attached to clean tiles that stayed at either site until the end of the study. 'Transplant' corals were on the tiles that came from the opposite site (Transplant A - conditioned at A went to Site B and Transplant B –

conditioned at B went to Site A) (Fig. 1). All remaining corals not used in the experiment were replanted back on their original reef. Tiles and corals were monitored every 2 months using photogrammetry. After the second 6-month period (Phase III; 12 months), the organisms on all tiles were assessed using eDNA (COI and 16S rRNA) to determine species diversity, richness, and relative abundance. Coral health was evaluated based on photochemical efficiency (i.e., ETR curves and Fv/Fm), protein content of coral tissues, endosymbiont algae density and chlorophyll concentration, and total antioxidant capacity (TAC) and lipid peroxidation (LPO) as a measure of oxidative stress and cellular damage.

Research sample	This study utilized two prevalent scleractinian coral species in the GoE/A: Acropora eurystoma, a broadcast spawner from the Complexa clade, and Stylophora pistillata, a brooder from the Robusta clade. Corals were collected (n= 5, per species) per site at a depth of 8 m (Permit #2021/42831), fragmented into smaller colonies and secured to each tile treatment for an additional 6 months. Coral treatments were based on the specific tile treatment that they were attached to during the study.
Sampling strategy	Sample sizes were determined based on previous literature on coral physiology that used 5 fragments per species per treatment as a robust sample size. We also used a number of corals that was consistent with our permitting organization and according to our permits as to not disturb the coral reef.
Data collection	Data was collected by the authors and volunteers. Visual documentation was conducted via in situ and ex situ photographs, as well as recorded via notebooks and computers to track data.
Timing and spatial scale	Sampling took place between Feb 2021 - Feb 2022. The first 6-month sampling period was between Feb 2021-July 2021. July 2021 marked the end of the first 6 months and tiles were sampled for eDNA. The second six months July 2021 to Feb 2022 marked the second 6 months of the 12 month study, where all tiles were collected for eDNA sampling to understand the invertebrate and bacteria communities growing on the tiles as well as both species of corals that were attached to tiles were sampled for coral physiology. Native corals from each site were collected at the beginning of the second 6 months in July 2021 as the baseline.
Data exclusions	We did not include the native coral baseline for TAC and LPO measurements as they were unfortunately compromised during the preservation process.
Reproducibility	We made comprehensive efforts to make sure that this study would be able to be reproduced in the same location as well as different locations by using accessible methods. This is included in the sampling size as well as the different methods used in this study to comprehensively evaluate coral health and physiology as well as common eDNA metrics to evaluate the invertebrate and bacteria communities. The methods we used are all heavily described in common literature and we also made extensive efforts to write a detailed methods section that would allow the study to be reproduced.
Randomization	Samples were collected and divided by treatments in the field in sterile plastic bags, however, there were more than 5 corals of each species per treatment and the corals that were used in this study were randomly chosen for health and physiology.
Blinding	Blinding was conducted by using only numbers to identify each species per treatment. The authors worked together to ensure that blinding was consistent throughout each of the measurements.

Did the study involve field work? [x] Yes [ ] No

Field work, collection and transport

Field conditions	Field conditions all year round were generally pleasant and the seawater maintained decent conditions.
Location	Two coral reefs were chosen as study sites based on their location, health, and biodiversity status in the GoE/A. The 'healthy' reef (Site A) is characterized by accreting patch reefs and a coral reef biorock structure in the southernmost, non-urbanized portion of the Gulf, away from human disturbances, it is right next to the Eilat Marine Observatory in a site called the "Igloo". This site was chosen based on its high diversity, abundance, and richness of coral reef species and its stable environmental condition (i.e., temperature, water quality, nutrient levels). The 'degraded' reef (Site B) is in the northernmost area of the Gulf, roughly 6 km from Site A, in a heavily urbanized region due to human impacts and characterized by fringing reefs interspersed with sand and seagrass33. Site B is known to experience poor water quality, exposure to salinity fluctuations, pollution, human impacts, and enriched nutrients (e.g., nitrates and phosphates). Both sites contained small and large patch reefs in addition to long-standing artificial structures such as a biorock reef and nursery tables sitting at roughly 8-12 m. Site B was located near the Naval base in the northern part of the Gulf at Kisosky beach.
Access & import/export	We received two permits to conduct this research from the Israel Nature Parks Authority. We received one permit for deploying and retrieving our tiles Permit #2020/42549 and another permit for the collection and sampling of corals Permit #2021/42831. We used SCUBA equipment to get to both sites. Site A was very close to our open water seawater tables, which is where corals and tiles were kept before preserving and sampling, and were immediately taken there from the water. Site B was a bit farther and therefore, we put samples in plastic bags with seawater in cold coolers and immediately drove for 15 min by car back to the institute for processing.
Disturbance	The main disturbance was with the preservation of some of the samples for TAC and LPO measurements of the native corals from each site, but it truly did not have any affect on our study overall.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	This study utilized two prevalent scleractinian coral species in the GoE/A: Acropora eurystoma, a broadcast spawner from the Complexa clade, and Stylophora pistillata, a brooder from the Robusta clade.
Wild animals	Corals were collected (n= 5, per species) per site at a depth of 8 m (Permit #2021/42831), fragmented into smaller colonies and secured to each tile treatment for an additional 6 months. Coral treatments were based on the specific tile treatment that they were attached to during the study. All remaining corals not used in the experiment were replanted back on their original reef. Tiles and corals were monitored every 2 months using photogrammetry.
Reporting on sex	N/A.
Field-collected samples	Organismal community samples were collected from biomimetic tiles at each site at time point 1 (end of Phase I) after first 6 months (n= 8, 2 controls) and again at 12 months (Phase III) (n= 18, 2 controls) via SCUBA diving. Biomimetic tiles were photographed inside and outside of the water before sampling. A clean control tile was brought into the water at each site during each tile retrieval timepoint. All tiles were secured in a sterile bag in the field, before arriving to a wet lab at the Interuniversity Institute for Marine Sciences in Eilat (IUI). The seawater that was collected in the bag with the tile was not included in the processing. Sessile reef organisms from both sides of the tile were scraped into a sterile tray, collected, and homogenized as a whole community. Samples were preserved and frozen at -20°C for DNA extractions. To avoid potential contamination between samples all tools and equipment were sterilized with three disinfectant baths of 10% bleach, 90% ethanol, and fresh water, which were replaced regularly. Corals that were never attached to tiles and served as the 'Native' (baseline) treatment for each site were snap-frozen in liquid nitrogen at the time of fragmentation at the end of the first 6 months (Phase II). At the end of the 12-month study, coral fragments that were attached to tiles for 6 months (Phase III) were collected. Corals were carefully removed from each tile, labeled, and sealed in sterile bags in the field at both sites. Corals were separated by treatment and site (n= 5) in outdoor, open system water tables at IUI, before measuring quantum yield with pulse amplitude modulation (Imaging PAM) fluorometry. Water tables were maintained with a consistent pH, salinity, and temperature with a direct flow from the GoE/A. Subsequently, all corals were wrapped in aluminum foil, tagged, and snap-frozen in liquid nitrogen before being stored at -80°C until future processing.
Ethics oversight	The approving authority was the Israel Nature and Parks Authority

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Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*