

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☐	☒ 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 <i>d</i> , Pearson's <i>r</i>), 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	n/a
Data analysis	tagseq_trim_launch.pl, fastqc 0.11.9, bwa-mem 0.7.17, samtools 1.16, MarkDuplicates 2.18.25 in Picard tools, SplitNCigarReads in GATK 4.2.4.1, FreeBayes 1.1, bamaddrg, VCFtools 0.1.16, BayeScan 2.1, BayPass 2.3, RDA (vegan R package), plink 1.9, plink 2.0, SnpEff, BLASTN, BLASTX, PANNZER2, GOenrich_pannzer2 (PlantNGSTools R package), REVIGO, STRUCTURE 2.3, DAPC (adegenet R package), STRUCTURE HARVESTER, CLUMPAK, divMigrate (diveRsity R package), basic.stats (hierfstat R package), bwa-mem2 2.2.1, popoolation2 R package, poolfstat 2.1.1 R package, pheatmap 1.0.12 R package, AMOVA (pegas R package), Kraken2 2.1.2, Kraken-biom 1.0.1, import_biom (phyloseq R package), simper (vegan R package).

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](#)

Data sharing is not applicable to this article as no new data were created in this study.

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

n/a

Reporting on race, ethnicity, or other socially relevant groupings

n/a

Population characteristics

n/a

Recruitment

n/a

Ethics oversight

n/a

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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

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

Sample size

n/a

Data exclusions

n/a

Replication

n/a

Randomization

n/a

Blinding

n/a

Behavioural & social sciences study design

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

Study description

n/a

Research sample

n/a

Sampling strategy

n/a

Data collection

n/a

Timing

n/a

Data exclusions	n/a
Non-participation	n/a
Randomization	n/a

Ecological, evolutionary & environmental sciences study design

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

Study description	Here we addressed whether corals can adapt to ocean acidification and how, by re-examining transcriptome and genome data of <i>Acropora millepora</i> coral holobionts from volcanic CO ₂ seeps with end-of-century pH levels. We performed different selection scans and genotype-environment association analyses on the coral host and identified 441 candidate adaptive genes involved in calcification, response to acidification and symbiosis. We also report seep-specific genetic clusters and significant differentiation between environments in the dinoflagellate photosymbionts, and shifts towards acidic stress-management functions in microbiome communities.
Research sample	We used existing datasets including transcriptome data for <i>Acropora millepora</i> holobionts and high-quality reference genomes for the coral host and the dinoflagellate photosymbionts. Kenkel and coauthors (2018) sequenced tag-based RNAseq libraries for a total of 59 <i>Acropora millepora</i> colonies originating from two reefs in the shallow-water CO ₂ seep system of Milne Bay Province (Papua New Guinea). For each reef, they sampled coral fragments from both a CO ₂ seep site and an adjacent control site less than 2.5 km apart: 14 colonies from Dobu CO ₂ seep site (pH = 7.72, 998 μ atm pCO ₂), 15 from Dobu control environment (pH = 8.01, 368 μ atm pCO ₂), 15 from Upa-Upasina CO ₂ seep site (pH = 7.81, 624 μ atm pCO ₂), and 15 from Upa-Upasina control environment (pH = 7.98, 346 μ atm pCO ₂) (Kenkel et al., 2018). Control and seep sites had similar seawater temperature, salinity and geomorphology (Fabricius et al., 2011). Raw reads were downloaded from the NCBI SRA project PRJNA362652. Reference genomes were downloaded from NCBI bioproject PRJNA767661 for the coral host <i>Acropora millepora</i> and from http://syms.reefgenomics.org for the <i>Cladocodium goreau</i> dinoflagellate photosymbiont.
Sampling strategy	Not applicable (see research sample)
Data collection	Not applicable (see research sample)
Timing and spatial scale	Not applicable (see research sample)
Data exclusions	Not applicable (see research sample)
Reproducibility	Not applicable (see research sample)
Randomization	Not applicable (see research sample)
Blinding	Not applicable (see research sample)
Did the study involve field work?	☐ Yes ☒ No

Field work, collection and transport

Field conditions	n/a
Location	n/a
Access & import/export	n/a
Disturbance	n/a

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	Involvement 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	Involvement in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	n/a
Validation	n/a

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	n/a
Authentication	n/a
Mycoplasma contamination	n/a
Commonly misidentified lines (See ICLAC register)	n/a

Palaeontology and Archaeology

Specimen provenance	n/a
Specimen deposition	n/a
Dating methods	n/a
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	n/a

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

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	n/a
Wild animals	n/a
Reporting on sex	n/a
Field-collected samples	n/a
Ethics oversight	n/a

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

Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	n/a
Study protocol	n/a
Data collection	n/a
Outcomes	n/a

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes
☒	☐ Public health
☒	☐ National security
☒	☐ Crops and/or livestock
☐	☐ Ecosystems
☒	☐ Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes
☒	☐ Demonstrate how to render a vaccine ineffective
☒	☐ Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐ Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐ Increase transmissibility of a pathogen
☒	☐ Alter the host range of a pathogen
☒	☐ Enable evasion of diagnostic/detection modalities
☒	☐ Enable the weaponization of a biological agent or toxin
☒	☐ Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a

ChIP-seq

Data deposition

- ☐ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- ☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <i>May remain private before publication.</i>	n/a
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Files in database submission

n/a

Genome browser session
(e.g. [UCSC](#))

n/a

Methodology

Replicates

n/a

Sequencing depth

n/a

Antibodies

n/a

Peak calling parameters

n/a

Data quality

n/a

Software

n/a

Flow Cytometry

Plots

Confirm that:

- ☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☐ All plots are contour plots with outliers or pseudocolor plots.
- ☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

n/a

Instrument

n/a

Software

n/a

Cell population abundance

n/a

Gating strategy

n/a

- ☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type

n/a

Design specifications

n/a

Behavioral performance measures

n/a

Acquisition

Imaging type(s)

n/a

Field strength

n/a

Sequence & imaging parameters

n/a

Area of acquisition

n/a

Diffusion MRI

☐

Used

☒

Not used

Preprocessing

Preprocessing software	n/a
Normalization	n/a
Normalization template	n/a
Noise and artifact removal	n/a
Volume censoring	n/a

Statistical modeling & inference

Model type and settings	n/a
Effect(s) tested	n/a
Specify type of analysis:	☐ Whole brain ☐ ROI-based ☐ Both
Statistic type for inference	n/a
(See Eklund et al. 2016)	
Correction	n/a

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☒	☐ Multivariate modeling or predictive analysis