

## Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) 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 code was used to collect the data for this study.

Data analysis

Custom code was written using R version 3.4.1 and is available in the Institute for Global Ecology's GitHub repository <https://github.com/InstituteForGlobalEcology/Coral-bleaching-a-global-analysis-of-the-past-two-decades>

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

All the R code, Reef Check data, and diversity data for the data analysis are available in the Institute For Global Ecology's GitHub repository (<https://github.com/InstituteForGlobalEcology>).

All Coral Reef Temperature Anomaly Database (CoRTAD) data used in this analysis are publicly available at NOAA's National Centers for Environmental Information (NCEI) webpage (<https://data.nodc.noaa.gov/cortad/Version6/>)

All sea surface temperature (SST) data used to determine the rate of SST change are publicly available in a downloadable file titled sst.mnmean.nc at NOAA's Earth Systems Research Laboratory (ESRL), Physical Sciences Division (PSD) webpage (<https://www.esrl.noaa.gov/psd/data/gridded/data.noaa.oisst.v2.html>)

## 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     | <i>Describe how sample size was determined, detailing any statistical methods used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.</i> |
| Data exclusions | <i>Describe any data exclusions. If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.</i>                                      |
| Replication     | <i>Describe the measures taken to verify the reproducibility of the experimental findings. If all attempts at replication were successful, confirm this OR if there are any findings that were not replicated or cannot be reproduced, note this and describe why.</i>      |
| Randomization   | <i>Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.</i>  |
| Blinding        | <i>Describe whether the investigators were blinded to group allocation during data collection and/or analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.</i>   |

## Behavioural & social sciences study design

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

|                   |  |
|-------------------|--|
| Study description | <i>Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).</i>   |
| Research sample   | <i>State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.</i>  |
| Sampling strategy | <i>Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.</i> |
| Data collection   | <i>Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.</i>  |
| Timing            | <i>Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.</i>   |
| Data exclusions   | <i>If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.</i>  |
| Non-participation | <i>State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.</i>   |
| Randomization     | <i>If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.</i>   |

## Ecological, evolutionary & environmental sciences study design

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

|                   |   |
|-------------------|---|
| Study description | We synthesized field observations of coral bleaching from nearly 10,000 surveys over the past two decades, and use a suite of environmental covariates and temperature metrics to predict bleaching patterns. |
| Research sample   | Reef Check coral bleaching data is from a global dataset that spans two decades. We used this data because data collection followed   |

|                                   |   |
|-----------------------------------|---|
| Research sample                   | a standardized protocol by trained divers and the data contained information on the percent bleaching of coral populations, rather than the frequently reported severity of coral bleaching in other datasets.  |
| Sampling strategy                 | Sampling was performed by trained divers from 1998 through 2017 on reefs around the globe.  |
| Data collection                   | Reef Check coral bleaching data collection was performed by trained divers who are researchers and citizen scientists. They all followed the same standardized protocol and they filled out the same data tables to describe the percent of coral colony bleaching and percent coral population bleaching. NOAA's publicly available temperature data were also used.   |
| Timing and spatial scale          | Reef Check data used in this study were collected on coral reefs globally from 1998 through 2017.   |
| Data exclusions                   | We describe in the manuscript which data were excluded in particular parts of the study. Coral bleaching surveys which had missing latitude or longitude coordinates were excluded. When building the hierarchical Bayesian Statistical model, we excluded surveys that occurred outside of ecoregion boundaries because we incorporated diversity as a variable in the model, and diversity data were only available inside of ecoregion boundaries. |
| Reproducibility                   | We are making all code and data publicly available so that the study results may be reproduced.   |
| Randomization                     | Covariates from the temperature data used in this study were controlled by running a covariate correlation analysis and removing variables with a correlation coefficient of .65 or greater before we built our Bayesian statistical model.   |
| Blinding                          | Blinding was not relevant to this study because this study focused on collection of spatio-temporal coral bleaching data and statistical modeling.  |
| Did the study involve field work? | <input checked="" type="checkbox"/> Yes <input type="checkbox"/> No   |

## Field work, collection and transport

|                          |  |
|--------------------------|--|
| Field conditions         | Field conditions differ for the nearly 10,000 surveys in the Reef Check dataset.   |
| Location                 | Reef Check field observations were conducted on reefs globally. All latitude/longitude coordinates, reef names, country names, water depth, and other information were recorded by divers, and are made available in our data published to the Institute for Global Ecology's GitHub repository. |
| Access and import/export | No import/export was required.   |
| Disturbance              | No disturbances were caused because data collection only required observation.   |

## 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                                 | Involves in the study   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                             |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines                  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology                          |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data                          |

### Methods

|                                     |   |
|-------------------------------------|---|
| n/a                                 | Involves in the study                           |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |

## Antibodies

|                 |   |
|-----------------|---|
| Antibodies used | <i>Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.</i>   |
| Validation      | <i>Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.</i> |

## Eukaryotic cell lines

Policy information about [cell lines](#)

|                     |   |
|---------------------|---|
| Cell line source(s) | <i>State the source of each cell line used.</i> |
|---------------------|---|

|  |  |
|--|--|
| Authentication   | <i>Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.</i>  |
| Mycoplasma contamination   | <i>Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.</i> |
| Commonly misidentified lines<br>(See <a href="#">ICLAC</a> register) | <i>Name any commonly misidentified cell lines used in the study and provide a rationale for their use.</i>   |

## Palaeontology

|                     |  |
|---------------------|--|
| Specimen provenance | <i>Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information).</i>  |
| Specimen deposition | <i>Indicate where the specimens have been deposited to permit free access by other researchers.</i>  |
| Dating methods      | <i>If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.</i> |

Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

|                         |   |
|-------------------------|---|
| Laboratory animals      | No laboratory animals were used in this study.  |
| Wild animals            | Corals were observed by divers and bleaching metrics were recorded. No corals were collected. |
| Field-collected samples | No samples were collected.  |
| Ethics oversight        | Reef Check surveys required no ethics oversight.  |

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

## Human research participants

Policy information about [studies involving human research participants](#)

|                            |  |
|----------------------------|--|
| Population characteristics | <i>Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural &amp; social sciences study design questions and have nothing to add here, write "See above."</i> |
| Recruitment                | <i>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.</i>   |
| Ethics oversight           | <i>Identify the organization(s) that approved the study protocol.</i>  |

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 | <i>Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.</i>                            |
| Study protocol              | <i>Note where the full trial protocol can be accessed OR if not available, explain why.</i>                              |
| Data collection             | <i>Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.</i> |
| Outcomes                    | <i>Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.</i>          |

## 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  
May remain private before publication.

For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.

Files in database submission

Provide a list of all files available in the database submission.

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

Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.

## Methodology

Replicates

Describe the experimental replicates, specifying number, type and replicate agreement.

Sequencing depth

Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.

Antibodies

Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.

Peak calling parameters

Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.

Data quality

Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.

Software

Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

## 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

Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.

Instrument

Identify the instrument used for data collection, specifying make and model number.

Software

Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.

Cell population abundance

Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.

Gating strategy

Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.

- 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

Indicate task or resting state; event-related or block design.

Design specifications

Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures

State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

## Acquisition

Imaging type(s)

Field strength

Sequence & imaging parameters

Area of acquisition

Diffusion MRI  Used  Not used

## Preprocessing

Preprocessing software

Normalization

Normalization template

Noise and artifact removal

Volume censoring

## Statistical modeling & inference

Model type and settings

Effect(s) tested

Specify type of analysis:  Whole brain  ROI-based  Both

Statistic type for inference (See [Eklund et al. 2016](#))

Correction

## Models & analysis

n/a | Involved in the study

Functional and/or effective connectivity

Graph analysis

Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Graph analysis

Multivariate modeling and predictive analysis