

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

Data analysis

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](#)

Sponge barcoding data for 18S and COI markers are accessioned at GenBank under MZ416255-MZ416736 and MZ486496-MZ487633 respectively. Microbial 16S miniseq reads and metagenomic libraries are available through NCBI Short Read Archive under BioProject PRJNA555077. Complete bioinformatic pipeline including scripts for figure reproduction available through the GitHub repository <https://github.com/scriptomika/SpongeDOB>

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)

Ecological, evolutionary & environmental sciences study design

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

Study description	Replicate (n=3-10) samples of 93 sponge species were collected at 4 Caribbean sites (total N=1756). Samples were genetically barcoded and placed within a phylogenetic tree along with 445 reference taxa. Of these samples, 1361 were successfully amplified and sequenced for microbial 16S microbiomes.
Research sample	93 sponge species common to shallow Caribbean reefs and spanning sponge biodiversity.
Sampling strategy	Sampling replicates between 3 and 10 are commonly used in microbial ecology. Species vary in abundance, ease of collection on SCUBA and recalcitrance to molecular biology, so when possible, higher replicates were collected.
Data collection	Data was collected by Pankey, Macartney and Gastaldi by processing sponge samples in the lab to isolate and amplify genetic material.
Timing and spatial scale	Sponges were collected in March 2017 (Curacao), May 2017 (Belize), January 2018 (Grand Cayman) and August 2018 (St Croix) based on availability of SCUBA facilities at each locale.
Data exclusions	Data were excluded from microbial taxa only observed in a single sample or accounting for fewer than 10 reads. Samples were excluded from analyses if fewer than 4000 reads, which acted as a cut-off for outlier samples poorly sequenced.
Reproducibility	The complete analytical pipeline, available on GitHub, was repeated four times, including phylogenomic analyses and 16S microbiome variant prediction.
Randomization	Samples were allocated based on phylogenetic placement. Accepted taxonomic orders were used when monophyletic. In the case of paraphyly and polyphyly, monophyletic orders were created as placeholders.
Blinding	Samples were given sequential field codes with no indication of species of origin (field notes were recorded). Genetic barcoding was used to identify samples definitively.
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Sponges were sampled at 15m depth at each of 4 localities.
Location	A table of latitudes and longitudes is presented in the Supplementary information.
Access & import/export	Samples were collected under the following permits: Belize Marine Scientific Research Permit Number 000034-17, Virgin Islands Division of Fish and Wildlife Research/Export Permit DFW18078X, Curaçao Scientific Collection Permit 2012/48584, and a Cayman Islands Government Department of Environment Research Permit.
Disturbance	Samples were harvested carefully on SCUBA to minimized damage to reef, taking less than 5-10% of any specimen's biomass.

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

Methods

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

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

Animals and other organisms

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

Laboratory animals	No laboratory animals were used.
Wild animals	Sponges were not aged or sexed. Samples collected from wild specimens were approximately 5ml or smaller.
Field-collected samples	Sponges were collected in sterile Whirl-paks on SCUBA, brought back to field station in cooler submerged in ambient seawater, and processed directly into sterile microcentrifuge tubes
Ethics oversight	No ethical approval was required.

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