

## 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 | We used code in the phyluce package (v 1.6.8), which is available freely on line to obtain ultraconserved and exon loci from our samples.                                                                                                                                                                                                                                                                                                                                                                                            |
| Data analysis   | List of used softwares in the analyses: Trimmomatic v 0.39; SPAdes v 3.1; Phyluce v 1.6.8 ; PhyloMad v 1.2; IQTree v 2.1; ASTRAL III (which include the programs LogCombiner and TreeAnnotator); TreeShrink v1.3.9; BEAST2 v2.5; Tracer v.1.7; RevBayes version 1.0.12; RevBayes version 1.2.2; newick utility (nw_ed). We used freely available software programs and/or code to analyze data. All programs and R packages (phytools, RevGadget) are provided in the text with relevant citations or with links to access the code. |

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](#)

Nuclear UCEs and exon loci sequences were deposited as a Targeted Locus Study [TLS] at DDBJ/ENA/GenBank under the BioProject PRJNA1294964,

BioSamples #SAMN50172845-SAMN50173024, accession numbers KJBF00000000-KJIC00000000 (See also Supplementary Table 1). Scleractinia bait set and tree files: figshare <https://doi.org/10.6084/m9.figshare.29242487>

## 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://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        | This is a time-calibrated molecular phylogenetic analysis, which includes hundreds of newly sequenced coral taxa, to shed new light on the deep-time evolution of scleractinian corals.                                                                            |
| Research sample          | This work is focused on the order Scleractinia (stony corals) in the phylum Cnidaria. We used 291 specimens from museum collections or using previously published data. Information about each sample included in the study are included in Supplementary Table 1. |
| Sampling strategy        | Our strategy was to use species from most families of scleractinians to ensure complete representation across the phylogeny.                                                                                                                                       |
| Data collection          | We used museum preserved specimens and already published data.                                                                                                                                                                                                     |
| Timing and spatial scale | n/a                                                                                                                                                                                                                                                                |
| Data exclusions          | n/a                                                                                                                                                                                                                                                                |
| Reproducibility          | n/a                                                                                                                                                                                                                                                                |
| Randomization            | n/a                                                                                                                                                                                                                                                                |
| Blinding                 | n/a                                                                                                                                                                                                                                                                |

Did the study involve field work? ☐ Yes ☒ No

## 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                                        |
| <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 and archaeology          |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data                          |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern           |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Plants                                 |

## Methods

|                                     |                                                 |
|-------------------------------------|-------------------------------------------------|
| n/a                                 | Involvement 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 |

## 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 | No field work was conducted for this present study. All specimens were deposited in collections. |
| Ethics oversight        | n/a                                                                                              |

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

## Plants

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