

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 Materialise Mimics v21; Geomagic Studio 2014; IDAV Landmark Editor.

Data analysis R Statistical software v4.1.3; Morpho v2.9; Geomorph v4.0.3; RRphylo v2.6.0; Arothron v2.0.3. All custom codes and data necessary to replicate the analyses are available in Source codes file.

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 authors declare that the data supporting the findings of this study are available within the paper and its supplementary information files. The available data include a time calibrated phylogeny and the aligned Procrustes coordinates for all the considered specimens. Source codes file include the codes necessary to reproduce all the results generated within the manuscript, the codes to reproduce Figures 1, 2 and 3 and all Extended Data Figures.

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	Sample size was based to cover the extant primates variability. Sample size of fossil hominins was chosen based on availability, conservation status, and to ensure the broadest phylogenetic sampling. Sample size for ontogenetic stages was chosen to represent the morphological variability of each considered growth stage.
Data exclusions	20 species have been removed to generate the CR values matrix because they were represented only by one specimen.
Replication	Semi-automatic landmarking procedure has been assessed using different templates returning consistent results. Four different modular configurations has been tested and the one supported was used in all the analyses. The strategy to measure integration without a priori defined modules has been repeated multiple times to control for consistent results. To account for sampling, phylogenetic uncertainty in tree topology and branch lengths, we used the RRphylo function overfitRR repeated 100 times.
Randomization	Sample was organized into groups based on taxonomic assignment and four growth stages determined by dental eruption timing.
Blinding	Blinding was not possible as all analyses required a priori knowledge of fossil identity in order to accurately reconstruct the endocast morphology.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Palaeontology and Archaeology

Specimen provenance	All specimens used in this study are accessioned into museums with all relevant specimen details. Access to specimen data was granted to the Authors by request to museums and online repositories listed in Supplementary Information. No new specimens were specifically collected as part of this study.
Specimen deposition	All fossils are accessioned. Museums, online repositories and specimen numbers are provided in Supplementary Information.
Dating methods	No new dates are provided. First and last occurrence dates for all species were taken from the literature and provided in Supplementary Information.
☒	Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.
Ethics oversight	No ethical approval or guidance was required for this study.

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

Animals and other organisms

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

Laboratory animals

This study do not involve laboratory animals

Wild animals

No new specimens have been collected for this study.

Field-collected samples

This study do not involve specimens collected in the field.

Ethics oversight

No ethical approval or guidance was required for this study.

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