

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

Avizo 7 (VSG), 8 (FEI), and 9 (FEI/Thermo-Fisher Scientific); Amira 6 (FEI/Thermo-Fisher Scientific - measurement tool, spline probe tool); Dragonfly 3.0; Animation Producer in Avizo; Adobe Premiere Pro (Creative Cloud edition); Geomagic Wrap (MeshDoctor and Relax functions); Autodesk 3Ds Max

Data analysis

TNT version 1.1; PAUP* 4.0; JAS version 14 (SAS Institute); Avizo 7 (VSG), 8 (FEI), and 9 (FEI/Thermo-Fisher Scientific); Amira 6 (FEI/Thermo-Fisher Scientific - measurement tool, spline probe tool); Dragonfly 3.0; Animation Producer in Avizo; Adobe Premiere Pro (Creative Cloud edition); Geomagic Wrap (MeshDoctor and Relax functions); Autodesk 3Ds Max

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

The holotypic specimen of *Adalatherium hui* is deposited in the University of Antananarivo (UA), Madagascar. The data matrix for the phylogenetic analysis has been deposited in MorphoBank (<http://morphobank.org/permalink/?P3411>). The Life Science Identifiers (LSID) for the new family, genus, and species are registered with Zoobank (<http://zoobank.org>).

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	Our study entails the description of a new fossil taxon represented by only a single specimen. Comparisons were made with many other taxa from around the world that are documented in detail in the Supplementary Information section. Comparisons with extant mammals were conducted in the large, diverse collections of the Department of Zoology, Denver Museum of Nature & Science and the Section of Mammals, Carnegie Museum of Natural History, Pittsburgh, USA.
Data exclusions	We sampled extinct taxa as broadly as possible, but were limited by the availability to study specimens of some taxa firsthand. In these instances, we used casts, 3D prints, CT scan datasets, and photographs.
Replication	Our taxon-character matrix is a derivative of that employed by Krause et al. (2014 – Nature) with improvements that are explicitly documented so as to allow replication.
Randomization	Our study only reports a single specimen; as such, no randomizations were possible.
Blinding	Character matrices for phylogenetic analysis were developed on the basis of independent observation of each taxon.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Palaeontology

Specimen provenance	The holotypic specimen was collected from the Upper Cretaceous Maevarano Formation, Mahajanga Basin, Madagascar. The specimen was collected under a Collaborative Agreement with the University of Antananarivo and various ministries of the Madagascar government.
Specimen deposition	The University of Antananarivo (UA), Madagascar
Dating methods	No new dates were obtained for this study.
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	