

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](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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 statistics 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
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection VGStudio Max version 2.1

Data analysis VGStudio Max version 2.1, R version 3.4.3, R package "smatr" version 3.4-8

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 upon request. 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

Computed tomography (CT) data are archived at The University of Texas High-Resolution Computed-Tomography Facility (UTCT), and are available from the authors upon reasonable request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

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

Study description	Description of new fossil clutch of the tritylodontid <i>Kayentatherium wellsi</i> , with statistical analysis of shape change across three ontogenetic stages.
Research sample	Remains of new fossil clutch of at least 38 perinates, and remains of the associated adult. Two more individuals of <i>Kayentatherium wellsi</i> (MCZ 8811, MCZ 8812) were chosen for the allometric analysis on the basis of their intermediate size and large size, respectively.
Sampling strategy	Sample sizes were determined by the availability of fossil specimens that preserve the relevant features.
Data collection	Individual elements were segmented in VGStudio Max 2.1. Measurements were performed on 3D isosurfaces in VGStudio Max 2.1. Segmentation and measurements were performed by Eva Hoffman.
Timing and spatial scale	N/A
Data exclusions	We considered all identifiable fossil material that was visible in CT scans or on the surface of the collected matrix.
Reproducibility	N/A
Randomization	No groups were used.
Blinding	Segmentation of individual elements was performed before elements were identified.
Did the study involve field work?	☐ Yes ☒ No

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☐	☒ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Palaeontology

Specimen provenance	Fossils were collected from the Kayenta Formation of northeastern Arizona, at the southern end of the Gold Spring drainage, under a permit issued by the Navajo Nation Minerals Division to Timothy Rowe on March 27, 2000.
Specimen deposition	Specimens were deposited at the Vertebrate Paleontology Laboratory at The University of Texas at Austin. CT data are archived at UTCT.
Dating methods	No new dates are provided.
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	