

Reporting Summary

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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

Phylogenetic analyses were performed in PAUP* (version 4.0a), CVAs were performed in R (R Studio Team, 2016), μ CT data was processed in Avizo (ThermoFisher Scientific, Version 9.2).

Data analysis

The code used to run the CVAs follows Chen and Wilson (2015) in Paleobiology.

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

Data is available through the Supplementary Information.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	New multituberculate mammal fossils from the Late Campanian (ca. 75.5 Ma) of western Montana are described. This material constitutes a new genus. The taphonomy, geology, ichnology of the site, and the functional morphology and phylogeny of these specimens are investigated in order to understand the behavior of these extinct animals.
Research sample	MOR 11747; MOR 11755; MOR 11748; MOR 11749; MOR 11750; MOR 11751; MOR 11756; MOR 10908; MOR 11752; MOR 11754; MOR 11753
Sampling strategy	All of the multituberculate specimens that have been discovered at Egg Mountain.
Data collection	All <i>Filikomys primaevus</i> specimens described herein were collected during the 2010–2016 field seasons at Egg Mountain (Teton County, Montana, U.S.A.). MOR 10908, 11750, and 11753 were manually prepared by Robert Masek. MOR 10908 was μ CT scanned at the University of Washington on a North Star Imaging X5000 CT scanner with a Feinfocus FXE [11164478] Xray source and Perkin Elmer [XRD 1620/1621 AM/AN] detector, 85 kV voltage and 500 μ A current. Post-processing and virtual reconstructions of μ CT data were performed using Avizo Software (ThermoFisher Scientific, Version 9.2). Measurements were taken on virtually reconstructed elements in Avizo using the 'Measure' tool. Multivariate analyses follow methodologies in Chen and Wilson (2015, Paleobiology). Phylogenetic parsimony analyses were performed in PAUP* (version 4.0a) based on a previously compiled multituberculate character-taxon matrix (Wang et al., 2019; Nature), and node support was calculated using bootstrapping and Bremer support.
Timing and spatial scale	Late Campanian of Montana (ca. 75.5 Ma), 7 x 8 x 1 m quarry
Data exclusions	n/a
Reproducibility	Methodologies are clearly outlined in the main text and Supplementary Information, such that all analyses are clearly defined and replicable.
Randomization	n/a
Blinding	n/a
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Summer (June–August) of northwestern Montana. Mostly hot and dry, but some severe thunderstorms in the evenings.
Location	Northwestern Montana, just outside of Choteau, MT USA.
Access and import/export	Private land owned by the Museum of the Rockies.
Disturbance	Quarrying results in the removal of rock, this was mitigated by limiting work to just to fossiliferous regions of the quarry.

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	n/a	Involved in the study
☒	☐ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☐	☒ Palaeontology	☒	☐ MRI-based neuroimaging
☒	☐ Animals and other organisms		
☒	☐ Human research participants		
☒	☐ Clinical data		

Palaeontology

Specimen provenance	The specimens come from the Egg Mountain locality (MOR Locality TM-006), Two Medicine Formation, just west of Choteau, MT, USA. The locality is owned by the Museum of the Rockies, and permissions to work there were given to David J. Varricchio, a co-author on this paper, and Jack Horner.
Specimen deposition	The ultimate repository for all specimens described here is the Museum of the Rockies, Bozeman, MT, USA. Specimens are currently on loan at the University of Washington, Seattle, WA, USA.
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.