

Life Sciences Reporting Summary

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► Experimental design

1. Sample size

Describe how sample size was determined.

Our study reports on finding of original fossils. All fossil specimens available for this study has been have been reported. Their skeletal and dental measurements of the single holotype specimens and comparative measurements of skeletons of extant mammals are reported in supplementary information. Skeletal and dental measurement of the single holotype specimen and the body mass estimates of the new fossil species are reported in SI Tables S1, S2 and S3.

2. Data exclusions

Describe any data exclusions.

No data on fossils available for this study have been excluded. All extant specimens for morphological comparison are also figured in the study. To the best of our ability, we exhausted sampling of all characters of the three main fossils used in this study. For ecomorphological morphometrical analyses, data from all extant comparative taxa that were measured are included in the quantitative analyses. Skeletal data from other early mammal taxa are compiled from existing literatures are all used in the analyses (SI Tables S3-S13)

3. Replication

Describe whether the experimental findings were reliably reproduced.

For ecomorphological morphometrical analyses, data from all extant comparative taxa that were measured are included in the quantitative analyses. Skeletal data from other early mammal taxa are compiled from existing literatures are all used in the analyses (SI Tables S3-S13), to the best of our ability.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Not applicable

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Not applicable

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☒ ☐ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ A statement indicating how many times each experiment was replicated
- ☒ ☐ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☒ ☐ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☒ ☐ The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
- ☒ ☐ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☒ ☐ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

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

7. Software

Describe the software used to analyze the data in this study.

Not applicable

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

The morphometrical data are already included in the online Supplementary Information at Nature.Com. The STL files on the shoulder Girdle of BMNH3258 from the CT scanning will be deposited in MorphoSource.Org, a public repository of CT-derived data. Because we are still working on a separate functional analysis with the shoulder girdle and forelimb from the master CT dataset, we cannot yet release the raw CT dataset that is under active study for other structures, which cannot be covered by short Nature paper.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Not applicable

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

Not applicable

b. Describe the method of cell line authentication used.

Not applicable

c. Report whether the cell lines were tested for mycoplasma contamination.

Not applicable

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

Not applicable

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

Not applicable

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

Not applicable