

Reporting Summary

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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

Data was collected on the original specimen using a phoenix v|tome|x s CT scanner at GeoZentrum Nordbayern (Friedrich-Alexander Universität Erlangen-Nürnberg, Germany) and a YXLON FF35 CT scanner at YXLON Inspection Service facility (Heidelberg / Germany). Comparative data of extant species were collected by using an Artec Space Spider surface scanner and Artec Studio software (versions 11-14).

Data analysis

For the micro CT-scan data analysis, we used Avizo 9.0 (ThermoFisher Scientific) and Geomagic Wrap 2017 (3D Systems Software) for the virtual reconstruction of longbones. 3D-prints were generated with Z-Suite 2.11 and printed on a Zortrax M200 FDM printer. Lateral tibia ellipse estimates we obtained using the Matlab function "EllipseDirectFit" of Nikolai Chernov available from mathworks.com

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

All data generated or analysed during this study are included in the published article (and its supplementary information files). The CT-scans analysed during the current study are available from the corresponding author on 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	Morphologic description and functional interpretation of fossil hominid specimens.
Research sample	The research sample consists of 36 original fossil hominid bones/teeth from Hammerschmiede. The extant primates samples for skeletal comparison consists of about 350 adult and non-captive individuals of cercopithecids and hominids of both sexes.
Sampling strategy	No sample size calculation was performed. The sample size of fossils is limited by availability. The size of extant comparative samples (primates) varies between 10 and 60 individuals, which is a normal size in primatological anatomic comparisons.
Data collection	Data from the original fossil specimens were collected by M.B, D.R.B., N.S. and J.F. Micro-CT and surface scan data processing and collection was conducted by J.F. and A.T., in collaboration with A.S.D., U.K., T.L. and J.P.
Timing and spatial scale	Data collection started in spring 2018, followed by comparative data collection from summer 2018 to summer 2019.
Data exclusions	No data was excluded from the analysis.
Reproducibility	not applicable
Randomization	not applicable
Blinding	not applicable
Did the study involve field work?	☐ Yes ☐ No

Field work, collection and transport

Field conditions	not applicable for palaeontological excavations
Location	Hammerschmiede, Allgäu, Bavaria, southern Germany;), coordinates N 47° 55' 38.5", E 10° 35.5'; fluvial channel of level HAM 5 at stratigraphic meter 12 in the local section, 685 m above sea level
Access and import/export	According to German (Bavarian) law no permissions needed for palaeontological excavations. Permission from the land owner have been obtained.
Disturbance	No disturbance (active mining pit)

Reporting for specific materials, systems and methods

Materials & experimental systems

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

Methods

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

Palaeontology

Specimen provenance	See above: According to German (Bavarian) law no permissions needed for palaeontological excavations. Non-formal permission from the land owner have been obtained.
Specimen deposition	All Hammerschmiede fossils are stored in the paleontological collection of the University of Tübingen (acronym GPIT), a research infrastructure of the Senckenberg Institute for Human Evolution and Palaeoenvironment (SHEP) Tübingen.
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.	