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Corresponding author(s): 2018-03-04291C
Katerina Harvati, Vassilis Gorgoulis

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 collected from the reconstructed Apidima specimens were collected in FEI Avizo 9.2.0 Lite (FEI Visualization Sciences Group)
Data analysis	The comparative data were processed with the DVLR (dorsal-ventral-left-right fitting) program (http://www.nycep.org/nmg/programs.html). The curve semilandmarks were calculated by resampling each curve as a predetermined number of equally spaced points, using Resample.exe (http://www.nycep.org/nmg/programs.html). Missing data in the comparative sample were reconstructed either 1. through reflected relabeling in Excel and Morpheus or by using a function in R based on Claude (2008) or 2. by using Generalized Procrustes Analysis (GPA) mean substitution in Morpheus. Semilandmarks were slid along their respective closed curves using the Morpho package in R. Specimen configurations were superimposed using Morphologika, and Principal Components Analysis and shape change visualization were performed also in Morphologika. The resulting PCs were exported to PAST 3.04, where Linear Discriminant Analysis and Classification was performed and plots were constructed. Posterior probabilities for classification results were calculated in SPSS (IBM Inc., version 24 for Windows). Manual superimposition was conducted in FEI Avizo 9.2.0 Lite. Figures were produced using Illustrator and Photoshop.

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

The data that support the findings of this study will be made available from the corresponding 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

Life sciences study design

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

Sample size	The main samples of this study were the two fossil human crania from the Apidima site. Each comparative sample of fossil specimens was designed in order to maximize the number of available specimens for each analysis, according the the anatomical elements preserved in the Apidima fossils. Detailed information on the samples are given Methods.
Data exclusions	Distorted specimens (due to pathology, taphonomy or possible artificial deformation) were a priori excluded from the analyses, as they could affect the analyses and results.
Replication	This work does not involve experiments, but we tested the results by conducting multiple analyses with different sets of measurements and/or different compositions of the comparative samples. All analyses gave similar results.
Randomization	Comparative samples were allocated to groups on the basis of previous taxonomic assessments. Randomization was not relevant to our study.
Blinding	Our analytical framework did not require blinding.

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	All specimens included in this study were studied with permission from the curating institutions. For the Apidima specimens, this is the Museum of Anthropology, Medical School, National and Kapodistrian University of Athens, Greece, directed by one of the authors, Prof. M. Kouloukoussa. Samples for dating were analyzed with permit from the Greek Ministry of Culture and Sports, issued on August 2nd, 2018, to Prof. M. Kouloukoussa, one of the authors (ΥΠΠΟΑ/ΓΔΑΠΚ/ΔΣΑΝΜ/ΤΕΕ/Φ77/299995/215105/2663/281).
Specimen deposition	The Apidima specimens are housed at the Museum of Anthropology, Medical School of the National and Kapodistrian University of Athens, Greece
Dating methods	New U-series dates reported were obtained on bone fragments produced during cleaning of the Apidima specimens, with permit

Dating methods	from the Greek Ministry of Culture and Sports (ΥΠΠΟΑ/ΓΔΑΠΚ/ΔΣΑΝΜ/ΤΕΕ/Φ77/299995/215105/2663/281). Dating was performed by Prof. Rainer Grün, one of the authors, at the Australian Research Centre for Human Evolution, Griffith University, Australia.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.