

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	Segmentation and surface generation of the microtomographic data were performed using the software Avizo 8.0 (FEI Visualization Sciences Group). Further surface models derived from surface scanning data (smartSCAN 3D + OPTOCAT software, Breuckmann GmbH)
Data analysis	The occlusal Fingerprint Analyses were done with PolyWorks 2016 (InnovMetric Inc.). Other analyses were performed In Avizo 8.0 (FEI Visualization Sciences Group) and in R v.3.4. The R packages ggtern package v.2.2.2, RVAideMemoire 0.9-66, and ade4 v.1.7-6 were used to perform the analyses.

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

The authors declare that all data supporting the findings of this study are available within the paper [and its supplementary information files].

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

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

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

Study description	The manuscript highlights the underestimated Indonesian hominid diversity in the Early and Middle Pleistocene and reassesses the taxonomic identity of some key specimens generally considered to belong to <i>Homo erectus</i> . This work represents the first and the most comprehensive study of Indonesian hominid dental structural organization using noninvasive X-ray and neutron microtomographic analyses and integrates unique unpublished data of a vast number of comparative fossil and extant hominid specimens. Besides ascribing to <i>Meganthropus paleojavanicus</i> , a non-hominin hominid taxon, the specimens Arjuna 9, Sangiran 5, Sangiran 6a, Trinil 11620, and Trinil 11621 previously attributed to the Indonesian <i>H. erectus</i> hypodigm (the Trinil specimens even being described by E. Dubois in 1891 as paratypes of <i>Pithecanthropus erectus</i>) and seven unpublished isolated molars considered by the late G.H.R. von Koenigswald as belonging in fossil Pongo. We also demonstrate here that at least three and perhaps four hominid taxa - <i>H. erectus</i> , Pongo, <i>Meganthropus</i> and maybe <i>Gigantopithecus</i> - coexisted in Java during the Early-Middle Pleistocene. These results have consequences for our understanding of hominid and human diversity and evolution in Indonesia and Southeast Asia.
Research sample	Using three-dimensional virtual imaging, we reassess the taxonomy of two isolated maxillary molars from Trinil (Trinil 11620 and Trinil 11621), paratypes of <i>H. erectus</i> , and of the partial mandibles Sangiran 5, the holotype of <i>Pithecanthropus dubius</i> , and Sangiran 6a, the holotype of <i>Meganthropus paleojavanicus</i> , all currently considered to be <i>H. erectus</i> . We also re-examine the mandibular specimen Arjuna 9, regarded as a robust <i>H. erectus</i> similar to Sangiran 6a, and seven isolated upper and lower permanent molar crowns from the Early-Middle Pleistocene Sangiran Dome formations (FS-77, SMF-8855, SMF-8864, SMF-8865, SMF-8879, SMF-8898 and SMF-10055), provisionally labelled as <i>Pongo</i> sp., but whose taxonomic identity remains problematic.
Sampling strategy	These specimens were selected for their relevance in the field of paleoanthropology as many of them represent holotypes of previously described species or are the paratypes of <i>H. erectus</i> (in the case of the Trinil molars).
Data collection	The specimens were scanned by X-ray and neutron microtomography
Timing and spatial scale	The scans were performed between 2009 and 2017.
Data exclusions	No available data was excluded from this study.
Reproducibility	The methods included in this study have been previously tested and published on numerous occasions and fully demonstrated to be reliable and replicable. All variables are provided in the SI document which allows full reproducibility.
Randomization	Not relevant here as the study is based on a limited fossil sample. Allocation to the groups was based on taxonomic identity of the fossil and extant hominid specimens/samples included in the study.
Blinding	No blinding was necessary in this study. Not applicable to palaeontology/palaeoanthropology
Did the study involve field work?	☐ Yes ☒ No

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

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

Methods

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

Palaeontology

Specimen provenance

The fossil specimens analyzed here come from Java, Indonesia. Permits to export to France for scanning the specimen Arjuna 9 were obtained from the Indonesian authorities. The other specimens are permanently stored in European museums and the authorizations for scanning were obtained from the curators.

Specimen deposition

The specimens are stored at the Senckenberg Research Institute of Frankfurt (Germany) and at the Balai Pelestarian Situs Manusia Purba Sangiran (Indonesia)

Dating methods

No new dates are proposed

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