Evidence for increased hominid diversity in the Early-Middle Pleistocene of Java, Indonesia

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- Since the first discovery of *Pithecanthropus* (*Homo*) erectus by E. Dubois at Trinil in 1891, over 33
- 34 200 hominid dentognathic remains have been collected from the Early-Middle Pleistocene
- deposits of Java, Indonesia, forming the largest palaeoanthropological collection in Southeast 35
- Asia. Most of these fossils are currently attributed to H. erectus. However, because of the 36
- 37 substantial morphological and metric variation in the Indonesian assemblage, some robust
- specimens, such as the partial mandibles Sangiran 5 and Sangiran 6a, were formerly variably 38
- 39 allocated to other taxa (Meganthropus palaeojavanicus, Pithecanthropus dubius, Pongo sp.). To
- 40 resolve the taxonomic uncertainty surrounding these and other contentious Indonesian hominid
- 41 specimens, we used Occlusal Fingerprint Analysis to reconstruct their chewing kinematics, and
- 42 also used various morphometric approaches based on microtomography to examine internal
- dental structures. Our results confirm the presence of Meganthropus as a Pleistocene 43
- 44 Indonesian hominid distinct from *Pongo*, *Gigantopithecus* and *Homo*, and further reveal that
- Eugene Dubois' Homo erectus paratype molars from 1891 are not hominin (human lineage), but 45

instead are more likely to belong to Meganthropus.

During the Quaternary, eustatic fluctuations episodes of glacial eustasy combined with tectonic uplift and volcanic events volcaniclastic deposition periodically altered the palaeobiogeography of the Sunda region. These physical and resultant environmental changes facilitated or inhibited intermittent faunal exchanges with the Asian mainland¹ and influenced the evolutionary dynamics of the local faunas, including hominids². The presence of hominids (great apes and humans) in Southeast Asia during the Early and Middle Pleistocene is well documented in the fossil record, with at least three firmly established genera: Gigantopithecus, Pongo and Homo³⁻⁶. The existence of a putative "mystery ape" has also been evoked⁷. Due to the implied vicariance and relict survivorship accompanying these geomorphological events, the appraisal of palaeobiodiversity at a regional scale is difficult. The presence of *Homo* in insular Southeast Asia since the Early Pleistocene has been amply documented by cranial, dental and postcranial remains³. Conversely, besides apart from four isolated teeth recently discovered in Peninsular Malaysia⁸, only a few dental specimens representing *Pongo* sp. have been reported from the Early and Middle Pleistocene deposits of Indonesia⁹. Because of the convergence in molar crown size and overall morphology between fossil Homo and Pongo, the taxonomic diagnosis of many Asian Early Pleistocene hominid dentognathic specimens has been debated for over a century, especially concerning isolated teeth and occlusally worn specimens 10,11. The resulting taxonomic confusion has affected the historical debate on the evolution of the genus Homo in Southeast Asia and, more generally, the assessment of Pleistocene hominid palaeobiodiversity⁷.

Using three-dimensional virtual imaging, we reassess the taxonomic assignment *y* of two isolated maxillary molars from Trinil (Trinil 11620 and Trinil 11621)^{10,11}, paratypes of *H. erectus*¹², and of the partial mandibles Sangiran 5, the holotype of *Pithecanthropus dubius*¹³, and Sangiran 6a, the holotype of *Meganthropus paleojavanicus*^{12,14,15}, all currently considered to be *H. erectus*^{165–168}. We also reexamine the mandibular specimen Arjuna 9, regarded as a robust *H. erectus* similar to Sangiran 6a¹⁷6a¹⁹, 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 *Pongo* sp., but whose taxonomic identity remains problematic (Figure 1, Supplementary Figure 1 and Supplementary Material). The analyses and/or examined features include Occlusal Fingerprint Analysis, enamel distribution and relative enamel thickness, crown-root surface area proportions, enamel-dentine junction topography, and pulp chamber morphology. We compare the results from this Indonesian assemblage with similar data from extant and fossil *Homo* and *Pongo*, as well as the fossil hominids *Sivapithecus* (Late Miocene, South Asia), *Lufengpithecus* (Late Miocene, southern China), and *Gigantopithecus* (Pleistocene, China and Southeast Asia) (Supplementary Tables 1-4).

Results

One important distinction between humans and non-human apes concerns their dietary ecology and feeding behaviours, reflected in their masticatory apparatus by different morphological adaptations and structural characteristics 19,2021,22. Occlusal Fingerprint Analysis 243 of crown wear patterns reveals that all robust Indonesian hominid molars suitable for this investigation (9 of 13) exhibit an ape-like functional macrowear pattern that differs significantly (p<0.05) from that of extant and extinct hominin samples, including Javanese H. erectus (Figure 2 and Supplementary Table 5). This pattern is characterised by a high dominance of power stroke Phase II over Phase I, evidenced by enlarged Phase II wear facets (Supplementary Table 6). In contrast, humans and extinct hominins, including Chinese and Indonesian H. erectus, display proportionately larger buccal Phase I wear facets, indicative of distinct masticatory behaviour (Figure 2).

Patterns of enamel distribution are sensitive indicators of dietary adaptations and taxonomic affinities in anthropoids²⁶². Morphometric cartographies distinguish between hominin and ape patterns: in the former, the thickest enamel is deposited on the "functional cusps" rather than on the "guiding" cusps²²⁶, while in apes, and notably in *Pongo*, it lies at the periphery of the occlusal basin²⁴²⁻²⁶⁴. Our analyses reveal that all but one of the modestly worn hominid molars from Java (n=8) show an ape pattern. The maxillary molar Trinil 11620 displays even relatively thicker peripheral enamel at the periphery of the occlusal basin than is typically found in *Pongo*, more closely approximating the Miocene apes *Sivapithecus* and *Lufengpithecus* (Figure 3). Conversely, the specimen SMF-8865 closely resembles the condition characterising African and Indonesian *H. erectus*, showing the thickest enamel localized on the buccal cusps, while Arjuna 9, FS-77, SMF8855, SMF-8864 and SMF-8879 have the thickest enamel distributed along the marginal ridges around the occlusal basin. Crown tissue proportions, including the commonly used Relative Enamel Thickness index^{22,24,26,27}, overlap across all extinct and extant samples and do not discriminate the Javanese robust specimens (Supplementary Figure 2 and Supplementary Tables 7-8).

Crown-root surface area proportions have also been demonstrated to show a strong phylogenetic signal, independent of feeding adaptions in tooth morphology²⁸⁶. Both upper molars from Trinil and the lower post-canine teeth of Sangiran 6a and Arjuna 9 exhibit proportionally large root surfaces compared to the lateral (non-occlusal) crown area, resembling pongines and *Lufengpithecus* and differing substantially from *Homo* (Figure 4, Supplementary Figure 3 and Supplementary Table 119).

The topography of the enamel-dentine junction (EDJ), which reliably distinguishes fossil and extant hominid taxa²²⁴,²⁴²⁶,²⁷²⁹, approximates the inner enamel epithelium of the developing tooth and provides useful information about taxon-specific processes underlying crown growth²⁹⁷. Six of the Javanese lower molars show a cingulum-like, mesiodistally extended buccal protostylid at the EDJ,

which is distinct from the morphology commonly found in *Homo* and *Pongo* but similar to the condition expressed by the Miocene Chinese ape *Lufengpithecus* (Supplementary Figure 4; see also Supplementary Figure 5 for the lower P4P4 EDJ morphology). The specimen SMF-8865 does not show the same coarse wrinkling pattern at the EDJ as the other robust Indonesian hominids, or the dense crenulation pattern typical of *Pongo*, but rather resembles the *H. erectus* condition (Supplementary Figure 4).

We also performed geometric morphometric (GM) analyses of the molar EDJ to compare the Indonesian fossil specimens to an assemblage of fossil and extant hominids (Figure 5). The results show statistical discrimination between *Pongo* and *Homo* and unambiguously classify the robust Javanese specimens as non-human apes, again with the exception of SMF-8865 (Supplementary Table 910). Indeed, except for the latter specimen, the EDJ shape of this Javanese sample of robust teeth is distinguished from *Homo* and overlaps those of *Pongo* and *Lufengpithecus*, even if some specimens like the holotype of $Meganthropus^{\frac{13}{14},\frac{14}{14},\frac{15}{15}}$, Sangiran 6a, are outside the variation of Pongo(Figure 5, Supplementary Figures \$6). As in fossil $Pongo^{242}$, $Gigantopithecus^{224}$, Sivapithecus and Lufengpithecus, the EDJ of these teeth consistently exhibits a low topography with higher mesial than distal dentine horns. Interestingly, comparable results are obtained when the same analysis is performed on the lower P4P4 of Sangiran 6a (Supplementary Figures 97-108 and Supplementary Table 101). Conversely, in *Homo*^{264,27}_29 and in SMF-8865 as well, the EDJ typically shows higher relief, with dentine horns of sub-equal height and more distally-set buccal cusps (Figure 5). In light of this, it is noteworthy that a pongine-like endostructural signature (but different from that typical of *Pongo*) was recently identified in an isolated deciduous mandibular molar from the Early Pleistocene of Sangiran that was originally labelled as Meganthropus¹³Meganthropus¹⁴, but later allocated to early Homo (rev. in ref. 2426).

While the taxonomic significance of the EDJ is supported by previous studies²⁷⁹, that of pulp chamber shape has not been systematically evaluated. However, marked morphological differences are notable in the height, thickness and shape of the pulp chamber between fossil and extant hominid taxa (Supplementary Figures 96-107). Accordingly, we performed a preliminarily GM analysis limited to the four extant hominid genera. Our results demonstrate that *Homo* and *Pongo* are statistically distinguished by pulp chamber morphology (Supplementary Material and Supplementary Figure 11). Based on these results, three-dimensional landmark-based analyses of the shape of the pulp chamber (not possible for SMF-8865) were thus extended to the fossil specimens. Similar to the analyses of the EDJ, they clearly discriminate the robust Javanese specimens from *Homo* (Supplementary Table 910). However, in contrast to the results of EDJ shape, the shape of the pulp chamber also distinguishes most of the fossil specimens forming the Javanese assemblage from *Pongo* (except for SMF-8879) and shows overlap with approximates *Lufengpithecus* (Figure 5 and

151 Supplementary Figure 12).

> When only non-hominin taxa are considered in the GM analyses of the EDJ and pulp chamber, the robust Indonesian molars are generally distinguished from *Pongo* (except for SMF-8879, which falls close to or within the *Pongo* range of variation) and approximate the Miocene representatives, especially *Lufengpithecus* (Figure 6 and Supplementary Figures 13-14).

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- **Discussion** 157 158 Based on multiple independent aspects of dental morphology, our re-analysis of this long-159 controversial sample of robust Pleistocene dentognathic specimens from Java demonstrates that, with 160 the exception of the isolated crown SMF-8865, which we attribute to *H. erectus*, all the specimens 161 investigated here most likely represent non-hominin species. Moreover, Trinil 11620, Trinil 11621, 162 Sangiran 5, Sangiran 6a, Arjuna 9, FS-77 and SMF-8864 are dentally distinct from *Pongo* and 163 represent a third ape lineage in addition to Pongo and Gigantopithecus that survived beyond the Miocene in South-eastern Asia. We propose to allocate this material to the resurrected species 164 Meganthropus palaeojavanicus von Koenigswald, 1950^{14,153,14}, but as a non-hominin. The holotype 165 is Sangiran 6a and the other specimens are paratypes. Consequently, Pithecanthropus dubius 153 166 167 becomes a junior synonym of Meganthropus palaeojavanicus. Unlike most apes, Sangiran 6a and Sangiran 9¹⁴⁻¹⁷ lack the canine/P3 honing complex and the P3 168 169 is non-sectorial, being more similar to the P4 with reduced crown height, a relatively prominent 170 metaconid (thus being clearly bicuspid) and a more buccolingually oriented crown major axis. In all 171 these features, Meganthropus is similar to Plio-Pleistocene hominins, which might argue for Meganthropus being a hominin rather than a non-hominin hominid as we conclude from our analysis 172 173 of internal dental structure. However, there are other fossil apes in which the P3 is non-sectorial and converges on a hominin-like morphology, most strikingly among megadont species that have 174 undergone marked canine reduction such the Late Miocene Indopithecus³⁰, and especially the 175 Pleistocene Gigantopithecus^{6,31}, in which the P3 is typically bicuspid. A relatively low-crowned and 176 177 more transversely oriented P3 associated with some degree of canine reduction (at least with respect to its cervical dimensions) also characterizes the Late Miocene megadont *Ouranopithecus*³². While 178 179 having a sectorial P3, *Lufengpithecus* also shows strong expression of the metaconid, in some cases bordering on a bicuspid morphology³³.
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- 181 Concerning Trinil 11620, this tooth was among those in another recent attempt to sort out the
- identities of Pleistocene dental remains, mostly from China but including several teeth from Southeast 182
- 183 Asia as well¹¹. Other than 2D enamel thickness and EDJ topography, that study examined different
- 184 aspects of dental morphology than those examined here, and, with the exception of Trinil 11620, on
- an entirely different sample. While Trinil 11620 is identified a priori as a hominin in a previous 185

study¹¹, it is based on a prior analysis³⁴ to decide only whether it should be assigned to *Homo* or 186 187 *Pongo* without considering the possible presence of an additional Pleistocene ape lineage in Southeast 188 Asia in addition to *Pongo* and *Gigantopithecus*, no results or conclusions are reported for it other than 189 a long-period developmental line periodicity of either 6 or 7. These values are well below the reported 190 range of periodicities for fossil or extant *Pongo* and a value of 6 would be an unusually low value for fossil or extant *Homo*^{11,34,35}. Although we did not examine long-period line periodicity and there is 191 substantial variation in long-period line periodicities in hominid taxa^{34,35}, the low value for Trinil 192 11620 could perhaps be considered as additional support for the assignment of this tooth to 193 194 Meganthropus.

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In keeping with its prior definition, Meganthropus is distinguished from Homo by having absolutely large teeth 143,1415, a mandibular corpus with a thick and rounded inferior border, a large extramolar sulcus and strong lateral prominence 14-1615-17, molarised premolars, and low molar crowns with coarse wrinkling converging toward the centre of the occlusal surface ¹³ surface ^{14,14}. Our results demonstrate that Meganthropus is further distinguished from Homo by an ape-like molar occlusal macrowear pattern, peripherally-distributed thicker molar enamel, low crowned EDJ with relatively short dentine horns, a particularly slender pulp shape with high horns, and lower crown/root surface area proportions. It further differs from penecontemporaneous H. erectus by the presence of a cingulum-like protostylid in both the enamel and the underlying EDJ. This feature is commonly found in Australopithecus and Paranthropus, but Meganthropus differs from these two hominins by its apelike occlusal wear pattern (Supplementary Figure 15), thicker peripheral enamel (whereas thicker enamel is found at the cusp tip in australopiths 3628), the lower EDJ topography, and more slender pulp chamber with vertically elongated pulp horns (Supplementary Figure 4516). As a further consequence of recognizing Meganthropus as non-hominin, certain features commonly regarded as characteristic of hominins, such as the loss of the canine/P3 honing complex, lack of a marked mandibular simian shelf, moderately mesiodistally elongated premolars with a double root and premolar/molar size proportions 124,1314-1617, more likely represent homoplastic traits in *Meganthropus*. From our results, it is also evident that, aside from marked differences in mandibular morphology and proportions, Meganthropus differs from Pongo by having laterally-positioned molar dentine horns, a slender pulp chamber, and a cingulum-like expression of the protostylid (Figure 6 and Supplementary Figures 4 and 69). Meganthropus is also clearly distinct from Gigantopithecus, the latter displaying highercrowned and narrower molars with low bulbous cusps and rounded crests, a large cuspule formed by a lobe between the protoconid and metaconid giving the lower molars a distinctive cusp pattern comprised of two pairs of main cusps arranged peripherally, a line of smaller midline cusps that includes the talonid cuspule and the hypoconulid, the lack or faint expression of the protostylid, strong buccolingual mid-crown waisting⁶, thicker occlusal enamel, and higher EDJ topography²²⁴ (for a

detailed differential diagnosis of *Meganthropus*, see Supplementary Material section 3 and Table 12).

We provisionally assign SMF-8879 to *Pongo* sp. Future analyses should clarify the taxonomic status of the specimens SMF-8855, SMF-8898 and SMF-10055, currently regarded as pongines, but which also share some features with the Asian Miocene apes, as well as other specimens from Early Pleistocene Java whose status continues to be debated (e.g., Sangiran 8, Sangiran 9, Sangiran 27)^{165,1617}.

Evidence concerning palaeoenvironments is compatible with the above conclusions regarding hominid palaeobiodiversity. During the Quaternary, episodes of glacial custasy, tectonic uplift, and volcaniclastic deposition structured the dispersal routes of hominids and other fauna, and exerted a strong influence on the habitats of Southeast Asia². The Early Pleistocene palaeoenvironments of Sangiran and Trinil in which the hominids lived likely included a variety of mixed and temporally shifting habitats. These included large areas of open woodland, indicated by the presence of *Stegodon trigonocephalus*, an abundance of large bovids (e.g., *Bubalus palaeokerabau*, *Bibos palaeosondaicus*), and various cervids and carnivores (e.g., *Panthera*)^{2,29}, and by a pollen record revealing the dominance of sedges, grasses, and ferns, with scattered trees such as *Acacia*, leaf-flower and Indian albizia²⁰. Freshwater marsh and lake-edge habitats, as well as wet grasslands with scattered shrubs, were also found in lower elevations of the landscape, indicated by a variety of aquatic and semi-aquatic vertebrate (*Hexaprotodon*, tortoise, crocodiles, turtles, fish) and invertebrate species^{2,20}. The occurrence of two monkey species, *Macaca fascicularis* and *Trachypithecus cristatus*, is a strong indicator for the presence of forested areas in the ecosystem as well².

The mosaic nature of habitats at Sangiran and Trinil has recently been corroborated by stable isotope analysis³¹. Tooth enamel δ¹³C and δ¹⁸O values indicate that some bovids (*Bubalus palaeokerabau*, *Duboisia santeng*) and cervids (*Axis lydekkeri*) were preferentially grazers, with a strongly C₄-dominated diet in an open woodland, while suids (*Sus brachygnathus*) express either a C₃-or C₄ signal, indicating that closed canopy C₃ vegetation was also present in the area³¹. The tiger *Panthera tigris* consumed prey with a C₃-C₄-mixed diet³¹. In such a dynamic and complex mosaic environment, it is therefore not surprising that multiple hominid lineages would have inhabited Southeast Asia at this time.

Across most of Eurasia, apes became extinct prior to the end of the Miocene. They survived into the Plio-Pleistocene only in South-eastern Asia, represented by *Gigantopithecus* and *Pongo*, both known from southern-most China into Southeast Asia^{5,3237}. To these can now be added *Meganthropus* from Java, formerly suggested to be an ape by some 142,4314,44_15 but only confidently demonstrated to be so by the comparative analyses presented here. As demonstrated by paleobotanical, paleontological and geochemical proxies^{2,38-40}, the Early to Middle Pleistocene palaeoenvironments of Sangiran and Trinil included a variety of mixed and temporally shifting habitats, ranging from open woodland areas

to dense forests capable of supporting the presence of multiple large-bodied hominid species in addition to at least two arboreal monkeys, *Macaca fascicularis* and *Trachypithecus cristatus*². Of the Miocene—apes present during the late Miocene in South and Southeast Asia, *Sivapithecus*, *Khoratpithecus*, and *Lufengpithecus*, *Meganthropus* appears to be dentally most closely related to the last, evidenced by the presence in both of low-cusped and wrinkled molar crowns^{21+9,3341,42} with a squat EDJ, an extended protostylid and a slender pulp chamber (Figure 5, Supplementary Figures 4 and 69). In contrast, *Sivapithecus* and *Khoratpithecus* have higher, more bunodont molars with marked mid-crown buccolingual constriction^{19,2021,22} and proportionally higher dentine horns in *Sivapithecus* has proportionally higher dentine horns (Figure 5).

Conclusions •

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During the Early-Middle Pleistocene, at least three and perhaps four hominid genera inhabited what is now Indonesia: *Homo*, *Pongo* and *Meganthropus*, with the possible presence of *Gigantopithecus*³² *Gigantopithecus*³⁷. This is a higher level of diversity than previously recognised and is particularly noteworthy for the late survival of two to three large ape lineages. Whether related to the expansion of *H. erectus*, palaeoenvironmental changes, competition with *Pongo* or *Gigantopithecus*, or some combination of these factors, *Meganthropus* did not persist beyond the Middle Pleistocene, leaving only three species of the genus *Pongo* (*P. pygmaeus*, *P. abelii* and *P. tapanuliensis*) subsisting today in remote and protected Indonesian localities³⁴ localities⁴³.

Methods

- 277 **X-ray and neutron microtomography.** Except for the Trinil molars and Sangiran 5 (see below), all Javanese hominid specimens studied here (Sangiran 6a, Arjuna 9, FS-77, SMF-8855, SMF-8864,
- SMF-8865, SMF-8879, SMF-8898 and SMF-10055) were scanned using the X-ray microfocus
- sources (X-μCT) at: the Helmholtz-Zentrum Berlin (equipment CONRAD II instrument), the
- Department of Human Evolution of the Max Plank Institute of Leipzig (equipment BIR ACTIS
- 282 225/300), the University of Poitiers (equipment X8050-16 Viscom AG), and the Seckenberg
- 283 Research Institute (Phoenix Nanotom s 180). Acquisitions were performed according to the
- following parameters: 100-160 kV, 0.11-90 μA , $0.14\text{-}0.36^{\circ}$ of angular step. The final volumes were
- reconstructed with voxel sizes ranging from 20.8 to 40.7 μm . The two Trinil molars (11620 and
- 286 11621) were scanned by SR-μCT at theon beamline ID 19 of the European Synchrotron Radiation
- Facility <u>atof</u> Grenoble using absorption mode with an isotropic voxel size of 31.12 μm³ at an energy
- of 60 keV¹⁰. The dataset of 632 images is available in 8 bits .tif format at the ESRF Paleontological
- Database (http://paleo.esrf.eu). The X-μCT acquisitions of the comparative fossil and extant

hominid specimens were performed using various equipments with the following parameters: 95 145 kV, 0.04-0.40 μA, 0.17-0.36° of angular step. The final volumes were reconstructed with voxel
 sizes ranging from 8.3 to 60.0 μm.

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sizes ranging from 8.3 to 60.0 μ m. The specimens Sangiran 5 and Sangiran 6a were scanned by neutron microtomography (n- μ CT)³⁵⁻³⁹⁴⁴⁻⁴⁸ at the ANTARES Imaging facility (SR4a beamline) of the Heinz Maier-Leibnitz Center (FRM II) of Technische Universität München. The neutron beam originated from the cold source of the FRM II reactor, with an energy range mostly from 3 to 20 meV, a collimation ratio of L/D=500 (ratio between sample-detector distance and collimator aperture) and an intensity of 6.4 x 10^7 n/cm²s. A 20 μ m Gadox screen was used to detect neutrons. Both a cooled scientific CCD camera (Andor ikon-L) and cooled scientific CMOS camera (Andor NEO) were used as detectors. The final virtual volume of these specimens was reconstructed with an isotropic voxel size of 20.45 μ m.

Data processing. Some specimens showed low contrasts between the enamel and dentine in some parts of the dataset, precluding automatic segmentation. In such cases, enamel and dentine were segmented using the magic wand tool in Avizo 8.0 (FEI Visualization Sciences Group) and manual corrections were locally applied. The Use of the interpolation tool was limitedly used in the to areas where the distinction between enamel and dentine could not be precisely demarcated was not accurately distinguishable. A volumetric reconstruction was then generated for each specimen. In most cases, the contrast resolution enabled carrying out a semi-automatic threshold-based segmentation following the half-maximum height method (HMH 409) and the region of interest thresholding protocol (ROI-Tb⁵⁰⁴⁴) taking repeated measurements on different slices of the virtual $stack^{5142}$. Because the detection of the tissue interfaces is based on attenuation at the boundary of a structure in both X-ray and neutron-based microtomography, we performed a threshold-based segmentation with manual corrections, as usually applied for X-ray acquisitions 52,5343,44. We quantified the degree of morphological and dimensional coherence between the X-ray microtomography (X-μCT) and n-μCT datasets of Sangiran 6a. The superimposed EDJ based on the X-µCT and n-µCT records show maximum 240 µm differences and an average of 65.7 µm variation (Supplementary Figure 1617). Considering the difference in voxel size of the two original datasets (39.33 µm and 20.45 µm for the X-ray and neutron data, respectively), the differences in LM1 enamel volume (349.26 µm³ and 346.61 µm³), dentine-pulp volume (529.1 µm³ and 526.7µm³) and crown volume (878.4 µm³ and 873.3 µm³) are inferior toless than 1% and can be regarded as negligible.

Occlusal Fingerprint Analyses. The analysis of dental wear facets enables the reconstruction of

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occlusal behaviour<sup>21</sup>behaviour<sup>23</sup>. Qualitative wear facet analysis perfored by Mills<sup>45</sup>-Mills<sup>54</sup>
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        already led to the conclusion that in primates and insectivores the occlusal power stroke of the
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        chewing cycle consists of two phases (buccal Phase and lingual Phase), which are were later
        determined as Phase I and Phase II<sup>46,4755,56</sup>. The chewing cycle starts with the preparatory (closing)
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        stroke where three-body contact (tooth-food-tooth) leads to puncture-crushing activity with rare
        contacts of antagonistic crowns. Real chewing starts with the Phase I<sup>47</sup>I<sup>56</sup>, whereas in which during
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       stereotypic cycles tooth-tooth contacts may occur more commonly, producing guiding buccal and
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        lingual Phase I facets through shearing activity along the buccal slopes of the buccal and lingual
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        cusps of the lowers and complementary facets on the lingual cusp slopes of the upper molars. Phase
       I ends in maximum intecuspation (centric occlusion) leading into Phase II with a more or less
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        lateral shift of the lower jaw leading to grinding activity until the last antagonistic contacts. During
       the recovery stroke the jaws open with no dental contacts<sup>243,2325,4756</sup>. The Phase I and Phase II
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       pathway of the power stroke is recorded in the wear facet pattern on the occlusal occlusing
        molars<sup>231,48-51</sup> 57-60. To assess the occlusal motion pattern(s) characteristic of the Early Pleistocene
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       robust Javanese hominid dental assemblage teeth considered in this here, we applied Occlusal
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        Fingerprint Analysis (OFA) to attribute proportions of wear facet areas to power stroke phases in
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        order to compare occlusal motion patterns in a sample of extant and fossil Asian great apes and
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        Homo. Occlusal macrowear areas, including wear facets after-following Maier and
        Schneck<sup>48</sup>Schneck<sup>57</sup>, were identified on virtual surface models of upper and lower molar crowns
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        following the OFA method described in Kullmer et al. ^{234} and Fiorenza et al. ^{6152}. The 3D surface data
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        acquisition derived either from µCT datasets or from 3D surface scanning such as with a
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       smartSCAN-HE (Breuckmann GmbH). Scans have been were taken either from originals or from
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       high resolution casts providing that provide reasonable resolution of macrowear for mapping wear
        facet areas<sup>49</sup> areas<sup>58</sup>. We used the modular software package PolyWorks® 2016 (InnovMetric Inc.)
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        to edit the surface models. The polyline tool in the software module IMEdit was applied to
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        interactively mark and fit closed polylines onto the models surfaces along the perimeter of wear
        facets in each tooth crown. By re-triangulation of the crown surfaces, the polylines became
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        integrated into the surface models. For To measureing each wear facet area, triangles were selected
        up to each polyline curve, grouped and color-coded following the occlusal compass<sup>243,5059</sup>. The area
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       measurement tool in IMEdit was used to compute area in mm<sup>2</sup> for each wear facet. Wear facet areas
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        were summarized summed for chewing cycle power stroke phases 47,5356,62. Buccal Phase 1 (BPh I),
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        lingual Phase 1 (LPh I) and Phase 2 (Ph II) facet area data were grouped for comparing percentage
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        distribution of wear. In respect of comparing To compare power stroke movements only, flat worn
       areas on cusp tips, identified as tip crushing areas<sup>52</sup> areas<sup>61</sup>, were excluded from measuring because
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       this type of tissue loss usually results from puncture-crushing activity \frac{56,6247,53}{} and is not attributable
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with certainty to one of the two power stroke phases. Percentage results are illustrated in ternary 360 361 plots. Each corner of the triangle represents 100% of one variable. Accordingly, a sample with an 362 equal distribution of wear facet areas will be placed in the center of the triangle. The plots were generated using the ggtern package v.2.2.2⁵⁴-2⁶³ in R v.3.4⁶⁴⁵⁵. The R package RVAideMemoire 0.9-363 66⁶⁵⁵⁶ was used to perform one-way permutational multivariate analysis of variance 364 (PERMANOVA) on the three variables (BPh I, LPh I and Ph II) distinctly separately for the 365 366 maxillary and mandibular molar samples. A Bray-Curtis similarity matrix was calculated based on a 367 9999 permutations parameter. For both upper and lower molars the test was significant (p<0.05), with values for the pseudo-F model of 18.78 and 13.98 and R² coefficients of 0.53 and 0.57. 368 respectively. Post-hoc PERMANOVA pairwise comparisons were run with a false discovery rate 369 370 (FDR) correction (Supplementary Table 5). 371 372 **3D tooth tissue proportions**. Premolar and molar crowns and roots were digitally isolated at the 373 cervix along the best-fit plane and surface rendering was performed using unconstrained smoothing 374 for visualization, while constrained smoothing was applied for the quantitative analyses. For the 375 molar teeth, seven linear, surface, and volumetric variables describing tooth tissue proportions were digitally measured or calculated on the molars: Ve, the volume of the enamel cap (mm³); Vcdp; the 376 volume of the crown dentine+pulp (mm³); Vc, the total crown volume; SEDJ, the surface area of 377 the enamel-dentine junction (mm²); Vcdp/Vc, the percent of the crown volume that is dentine and 378 379 pulp (%); 3D AET (=Ve/SEDJ), the three-dimensional average enamel thickness (mm); 3D RET (=3D AET/Vcdp^{1/3}*100), the scale-free three-dimensional relative enamel thickness (see 380 381 methodological details in the refs. 242,2836,6657). For both premolars and molars, the following parameters were also calculated: LEA, the lateral enamel surface area (mm²)⁶⁷⁵⁸; RA, the total root 382 surface area (mm²)⁵⁸; CRR (=LEA/RA*100), the crown-root ratio (%) (see Figure 4, 383 384 Supplementary Figures 2-3 and Supplementary Tables 3,4,7,8). Because of its the advanced degree 385 of occlusal wear in Sangiran 6a-degree, only crown-root proportions were assessed for the 386 mandibular fourth premolar of Sangiran 6a. 387 Intra- and interobserver accuracy tests for accuracy of the measures run by two observers provided differences <5%. Adjusted Z-score analyses 68,6959,60 were performed on three tooth crown 388 tissue proportions parameters (Vcdp/Vc, 3D AET and 3D RET) for the robust Indonesian hominid 389 390 maxillary (Trinil 11620, Trinil 11621 and SMF-8898) and mandibular molars (Arjuna 9, FS-77, 391 SMF-8855, SMF-8864, SMF-8865, SMF-8879 and SMF-10055) and were compared with some 392 extant and fossil hominid samples (Supplementary Figure <u>17-18</u> and Supplementary Table 8). This 393 statistical test was also applied for the CRR parameter on the maxillary molars Trinil 11620 and 394 Trinil 11621, on the mandibular fourth premolar of Sangiran 6a and on the molars of Sangiran 6a

and Arjuna 9 preserving complete roots (Figure 4, Supplementary Figure 3 and Supplementary Table 119). This statistical method allows the comparison of unbalanced samples, which is often the case when dealing with the fossil record, using the Student's t inverse distribution following the formula: [(x-m)/(s*sqrt(1+1/n)]/(Student.t.inverse(0.05;n-1)), where x is the value of the variable (e.g., Vedp/Ve of Arjuna 9 M2); m is the mean of the same variable for a comparative sample (e.g., Vedp/Ve of of MH); n is the size of the comparative sample (e.g., 41 individuals); and s is the standard deviation of the comparative sample (e.g., sd: 3.93).

Enamel thickness distribution cartographies. The 3D topographic mapping of the site-specific enamel thickness variation was <u>realized generated</u> from the segmented enamel and crown dentine components of unworn to only slightly worn teeth and rendered using chromatic scales <u>70-7461-65</u>. A rainbow chromatic scale was also used to illustrate gradual variation of enamel thickness, ranging from the thickest (in red) to the thinnest (in blue) (Figure 3).

Geometric morphometric analyses. 3D geometric morphometric (GM) analyses were conducted on the virtual surfaces of the EDJ of the maxillary molars and mandibular fourth premolar and molars. The landmarks were set along the marginal outline of the EDJ occlusal basin⁶⁵ basin⁷⁴. For the maxillary molars, six landmarks were set: three at the apex of the paracone, protocone and metacone dentine horns, and three at each intermediate lowest point between two horns along the dentine marginal ridges and oblique crest. For the lower fourth premolar, eight landmarks were put placed on the EDJ surface: four at the apex of the protoconid, metaconid, entoconid and hypoconid dentine horns and four at each intermediate lowest point between two horns along the dentine marginal ridge. For the mandibular molars, seven landmarks were placed: four at the apex of the protoconid, metaconid, entoconid and hypoconid dentine horns and three at each intermediate lowest point between two horns along the dentine marginal ridge (located by translating the cervical plane occlusally), except between the two distal horns (because of the variable presence of the hypoconulid, notably in modern humans, this latter cusp and the distal marginal ridge were not considered). While the specimen Trinil 11620 is virtually unworn, the protocone dentine horn apex of Trinil 11621 is affected by wear. It was thus reconstructed based on the intact height and morphology of the paracone, as well as on those of the mesial dentine horns of Trinil 11620. A similar procedure was applied to reconstruct the buccal dentine horns of Sangiran 5 and Sangiran 6a (Figure 1). We also conducted GM analyses on the pulp chamber shape, setting similarly located landmarks on the cavity roof of the maxillary and mandibular molars, but not on that of the lower premolar because of a lack of expression of the distal cusps on its pulp chamber. We performed generalized Procrustes analyses, principal component analyses (PCA) and between-group principal

- 430 component analyses (bgPCA) based on the Procrustes shape eoordinates 66-coordinates and using
- genera as groups (Figures 5-6 and Supplementary 8-10 and 12-14). The robust Indonesian hominid
- specimens were included a posteriori in the bgPCA. The analyses were performed using the
- package ade4 v.1.7- 6^{67} - 6^{76} for R v.3.46455. Allometry was tested using multiple regressions in
- which the <u>explanatory explicative</u>-variable is the centroid size and the dependent variables are the
- PC and bgPC scores. In all PCA and bgPCA, the first components only show a weak allometric
- signal $(0.00 < R^2 < 0.30)$, the differences between specimens thus mostly representing shape-variation.
- In order to statistically assess the taxonomic affinities of the robust Indonesian hominid molars, we
- 438 used a supervised classification method by Support Vector Machine (SVM). Compared with linear
- discriminant analyses (LDA) and quadratic discriminant analyses (QDA), SVM makes no
- 440 assumptions about the data, meaning it is a very flexible and powerful method $\frac{7869}{}$. SVM tests were
- performed on the PC scores from each GM analysis on the first number of PCs representing needed
- 442 <u>to achieve</u> more than 95% of the total variability (i.e., 6 to 11 first PCs) (Supplementary Tables 5
- and $\frac{10}{11}$). Leave-2-out cross-validations were run in order to validate the model (predictive
- accuracy) of classification for the groups including hominins (*Homo*) on the one hand and apes
- (Ponginae-*Lufengpithecus*) on the other hand. Then, we'We then tested the attribution of the
- Indonesian fossil hominid specimens included in the GM analyses (Arjuna 9, Sangiran 5, Sangiran
- 447 6a, FS-77, SMF-8855, SMF-8864, SMF-8865, SMF-8879, SMF-8898, SMF-10055, Trinil 11620,
- 448 Trinil 11621) with respect to the model.

Data availability. The authors declare that all data supporting the findings of this study are

available within the paper [and its supplementary Supplementary information files].

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Competing interests

The authors declare no competing interests.

Additional Information

- **Supplementary Information information** is available in the online version of the paper.
- Reprints and permissions information is available at www.nature.com/reprints.
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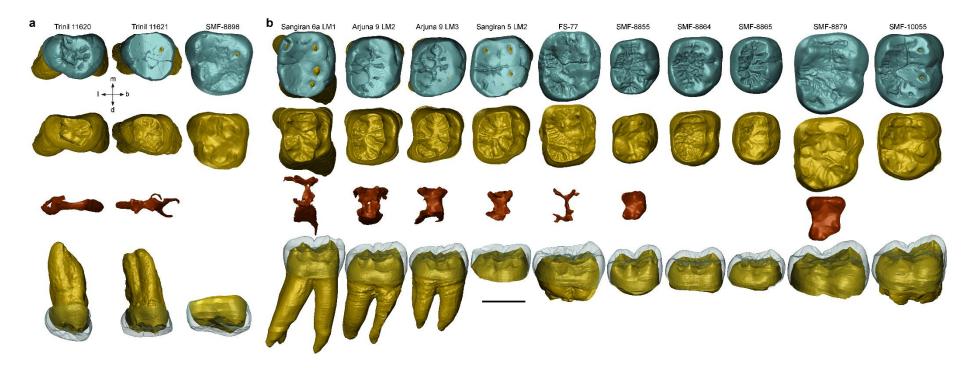


Figure 1 | Virtual rendering of the Indonesian hominid teeth examined for taxonomic reassessment. a, Maxillary molars. b, Mandibular molars (Supplementary Table 1). From the top, the rows shows: the external occlusal morphology, the occlusal dentine, the occlusal pulp cavity and the buccal view EDJ with the overlain semi-transparent enamel cap in buccal view. In the bottom row, the EDJ is visible through the enamel imaged in semi-transparency. For SMF-8879, only the crown is imaged. For Trinil 11621, Sangiran 5 and 6a, the worn dentine horn apices were reconstructed following the morphology of the other well-preserved cusps (see Methods). b, buccal; d, distal; l, lingual; m, mesial. Scale bar, 10 mm.

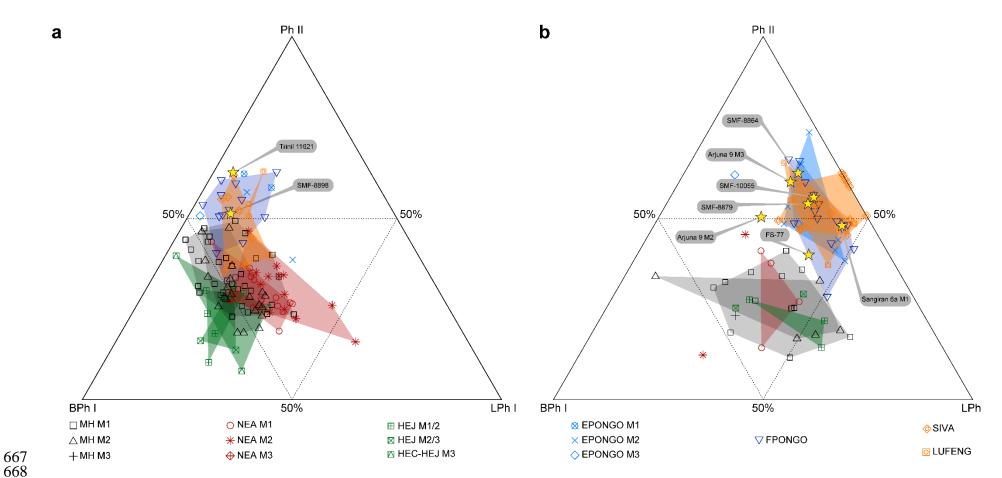


Figure 2 | **Occlusal Fingerprint Analyses**. **a, b**, Ternary diagram showing the proportions (in %) of relative wear areas of buccal phase I (BPh I), lingual phase I (LPh I), and phase II (Ph II) facets for the Indonesian fossil hominid maxillary (**a**) and mandibular (**b**) molars examined for taxonomic reassessment (Supplementary Table 1) compared with fossil and extant hominid specimens/samples. Each base of the triangle represents a ratio of 0% while the vertices correspond to a percentage of 100%. EPONGO, extant *Pongo*; FPONGO, fossil *Pongo*; HEC, *H. erectus* from China; HEJ, *H. erectus* from Java; LUFENG, *Lufengpithecus*; MH, modern humans; NEA, Neanderthals; SIVA, *Sivapithecus* (Supplementary Table 2).

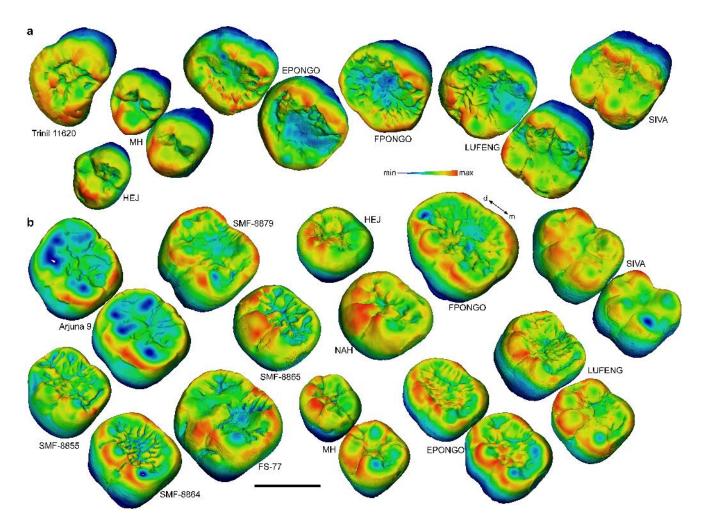


Figure 3 | **Enamel thickness cartographies. a**, Maxillary molars, **b**, Mandibular molars. The Indonesian hominid teeth (Supplementary Table 1) are compared with fossil and extant hominid specimens. EPONGO, extant *Pongo*; FPONGO, fossil *Pongo*; HEJ, *H. erectus* from Java; LUFENG, *Lufengpithecus*; MH, modern humans; NAH, North African late Early Pleistocene *Homo*; SIVA, *Sivapithecus* (Supplementary Table 2). Independently from Irrespective of their original side, all specimens are displayed as right antimeres in a slightly oblique occlusal perspective. Scale bar, 10 mm.

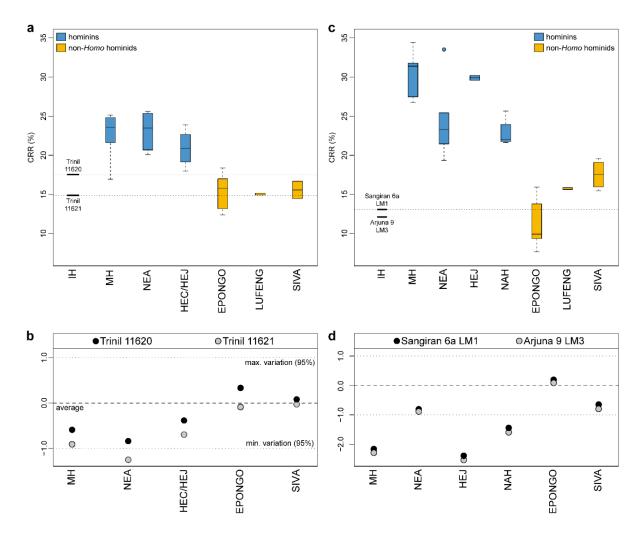


Figure 4 | **Molar crown-root proportions. a, b**, The crown-root ratio (CRR, in %) and its adjusted Z-score statistics for the Indonesian hominid (IH) maxillary molars from Trinil compared with fossil and extant hominid specimens/samples. **c, d**, Similar comparative analyses for the mandibular molars of Sangiran 6a and Arjuna 9 (Supplementary Table 1). EPONGO, extant *Pongo*; HEC, *H. erectus* from China; HEJ, *H. erectus* from Java; LUFENG, *Lufengpithecus*; MH, modern humans; NAH; North African late Early *Homo*; NEA, Neanderthals; SIVA, *Sivapithecus* (Supplementary Table 2).

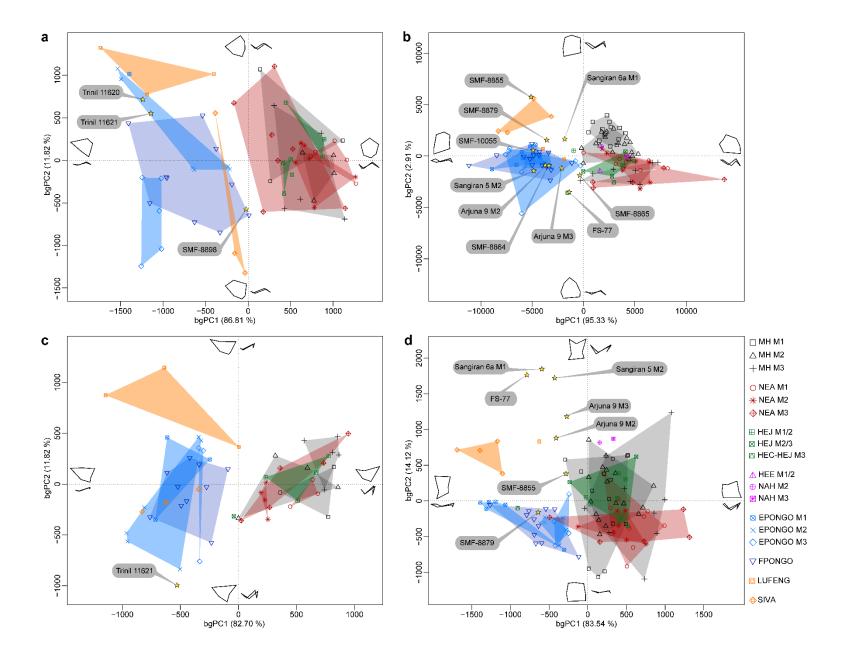


Figure 5 | **Geometric morphometric analyses of the EDJ and pulp chamber. a, b**, Between-group principal component analyses (bgPCA) of the 3D landmarks Procrustes-registered shape coordinates of the Indonesian hominid maxillary (a) and mandibular (b) molar EDJs (Supplementary Table 1) compared with fossil and extant hominid specimens/samples. c, d, bgPCA of the underlying maxillary (c) and mandibular (d) pulp cavity. The wireframes at the end of the axes illustrate the extreme morphological variation trends along each bgPC in occlusal (mesial aspect upward) and buccal views (mesial aspect rightward). EPONGO, extant *Pongo*; FPONGO, fossil *Pongo*; HEC, *H. erectus* from China; HEE, *H. erectus/ergaster* from Eritrea; HEJ, *H. erectus* from Java; LUFENG, *Lufengpithecus*; MH, modern humans; NAH, North African late Early Pleistocene *Homo*; NEA, Neanderthals; SIVA, *Sivapithecus* (Supplementary Table 2).

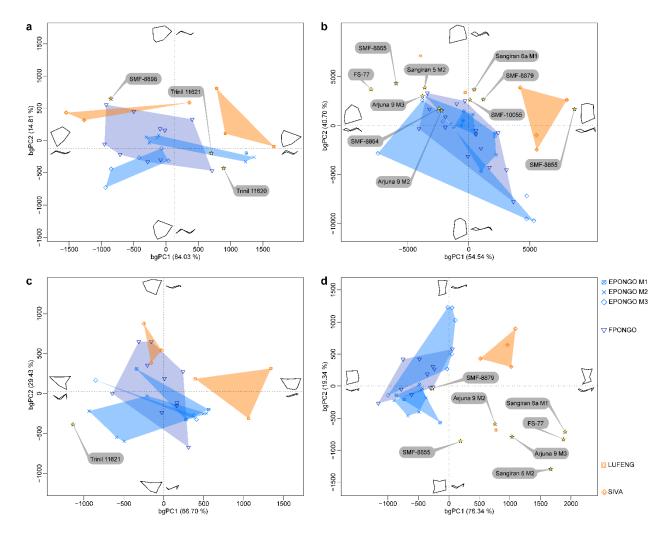


Figure 6 | Geometric morphometric analyses of the EDJ and pulp chamber in non-*Homo* hominids. a, b, Between-group principal component analyses (bgPCA) of the 3D landmarks Procrustes-registered shape coordinates of the Indonesian hominid maxillary (a) and mandibular (b) molar EDJs (Supplementary Table 1) compared with fossil and extant non-*Homo* hominid samples. c, d, bgPCA of the underlying maxillary (c) and mandibular (d) pulp cavity. The wireframes at the end of the axes illustrate the extreme morphological variation trends along each bgPC in occlusal (mesial aspect upward) and buccal views (mesial aspect rightward). EPONGO, extant *Pongo*; FPONGO, fossil *Pongo*;

707 LUFENG, *Lufengpithecus*; SIVA, *Sivapithecus* (Supplementary Table 2).