Supplementary Material for "**New Middle Miocene Ape (Primates: Hylobatidae) from Ramnagar, India Fills Major Gaps in the Hominoid Fossil Record**"

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1. Detailed Materials and Methods

Geological background

Outcrops of the Lower Siwalik Subgroup occur around the town of Ramnagar (figure 1), and are exposed in the southern limb of the Udhampur Syncline [51]. The southern limb of the Udhampur Syncline exhibits a continuous succession of the Siwalik Group trending N-NNE-S-SSW strike ridges [52] that are ~ 3146 m in thickness [53]. The Lower Siwalik Mansar Formation is subdivided into the lower Dodenal and the upper Ramnagar members, which have been equated to the Kamlial and Chinji formations of the Potwar Plateau, Pakistan, respectively [53-54]. However, fauna characteristic of the Kamlial Formation has yet to be recovered from Ramnagar [55], and the Ramnagar fauna has always been noted as similar to the Chinji Formation instead [52, 55-61]. Thus, the sedimentary deposits surrounding Ramnagar have been assigned to the Ramnagar Member of the Mansar Formation, Siwalik Group [53-54].

As previously documented [14-15, 52], the stratigraphic sequence of the study region is characterized by a repetitive sequence of major sandstones (~2-6 m thick) alternating with thick packages of reddish-brown mudstones/paleosols (~5-25 m thick) and thinner sandstones (<1 m thick) representing a successive series of fluvial channels (sandstones) and overbank/floodplain deposits (mudstones/paleosols). *Kapi* specimen VPL/RSP2 was surface collected from paleosol outcrops at the site of Sunetar 2 (figure 1). This discovery location is only ~110 m southeast from where the sivaladapid *Ramadapis sahnii* specimen VPL/RSP1 was also collected [14]. Stratigraphically, VPL/RSP2 was discovered ~10 m above VPL/RSP1, but both specimens are presumed to have been derived from the exposed 20 m thick sequence of paleosols that is bracketed by major sandstones. Sunetar 2 correlates well with Sunetar 1 that is richly fossiliferous and is exposed ~1.2 km northwest of the former [14]; additionally, Sunetar 2 is located ~4.65 km west of Rashole 3, the site where the *Sivapithecus indicus* specimen WIF/A 1825 was collected [15]. Based on preliminary mapping of the major sandstones in the Ramnagar region, the sandstone-bounded sequence at Rashole is either equivalent, or close to equivalent, to the sequence exposed at Sunetar 1 and 2, suggesting that *Sivapithecus*, *Kapi*, and *Ramadapis* likely co-occur at the same stratigraphic level. In either case, the same biochronological constraints assigned to Rashole can be applied to Sunetar 2; stratigraphically, both sites lie slightly below the rodent-bearing site of Dehari, which has been estimated to be ~13.6-13.2 Ma on the basis of currently identified, although fragmentary, time-sensitive micromammals [17, 62]. The collected Rashole and Sunetar macromammals *Dorcabune* cf. *anthracotherioides*, *Conohyus* cf. *sindiensis*, and *Sivapithecus indicus* also have well-established first appearance dates (FADs) on the Potwar Plateau (~13.6, 14.6, and 12.7 Ma, respectively) [11, 63]. In combination with the younger end of the chronological range of the micromammals currently identified from Dehari (~13.2 Ma), we suggest that an approximate age close to 13 Ma and an estimated range of anywhere between ~12.5-13.8 Ma is most reasonable for Sunetar and Rashole (see also [15]). This is also consistent with the tip-dating analysis estimate of 11.2-14.1 Ma (95% confidence intervals, mean = 12.8 Ma) independently derived from the phylogenetic position of *Ramadapis sahnii* from Sunetar 2 (14).

Samples

The taxonomic status and phyletic affinities of VPL/RSP2 (Vertebrate Paleontology Laboratory/Ramnagar Sunetar Primate-2) and H-GSP 8114/609 were assessed using a large comparative dataset of extinct and extant catarrhine taxa. Our higher-level taxonomy (i.e., family level and above) of fossil catarrhines follows ref. [6] and is provided in tables S2 and S4. Descriptions of VPL/RSP2 were facilitated by 3D surface scans rendered from µCT scans (Fig. 3; voxel resolution = 0.011 mm).

VPL/RSP2 corresponds to a right third lower molar (M_3) found at Sunetar 2, a site within the larger site complex of Sunetar located ~4.5 km S/SE of the town of Ramnagar, Jammu and Kashmir, India. Specimen H-GSP 8114/609 is a first lower molar (M_1) germ from the Manchar Formation in southern Pakistan and with an estimated age close to the Early/Middle Miocene boundary, ~16-17 Ma [38]. This specimen (along with a handful of other isolated teeth from the Manchar and Kamlial Formations) was referred to *Dionysopithecus* sp., a genus now recognized within the family Pliopithecidae (superfamily Pliopithecoidea), but with noted resemblances to East African Early Miocene taxa (dendropithecids and proconsulids) such as *Micropithecus*, *Proconsul*, and *Afropithecus* as well [38]. While VPL/RSP2 represented the main focus of this study, the affinities of H-GSP 8114/609 were reexamined given its proximity in time and space to the M_3 from Ramnagar and given that it is the most taxonomically informative specimen assigned to the Manchar and Kamlial Formation *Dionysopithecus* sp. hypodigm [37-39].

The comparative dataset comprises 332 molar teeth, including 71 fossil specimens from broad taxonomic categories (genera included in each category in parentheses): Propliopithecidae (*Aegyptopithecus* and *Propliopithecus*), Proconsulidae (*Ekembo*, *Equatorius*, *Kalepithecus*, *Otavipithecus*, *Proconsul,* and *Rangwapithecus*), Dendropithecidae (*Dendropithecus, Limnopithecus, Micropithecus,* and *Simiolus*), Pliopithecidae (*Anapithecus*, *Dionysopithecus*, *Egarapithecus*, *Epipliopithecus*, *Laccopithecus*, *Platodontopithecus*, *Plesiopithecus,* and *Pliopithecus*), and Hylobatidae (*Yuanmoupithecus* and *Bunopithecus*). Sample size details per taxonomic category and molar type are provided in tables S2 and S4. Fossil data were collected either on the original specimens or high-resolution casts located at the following institutions: American Museum of Natural History (AMNH), New York, USA; Museum of Comparative Zoology (MCZ), Cambridge, USA; New York University (NYU), New York, USA; Arizona State University (ASU), Tempe, USA.

Our extant sample included 151 hylobatid molars from all four living genera (*Hylobates*, *Hoolock*, *Nomascus*, and *Symphalangus*) and 110 hominid molars from all three living genera (*Pongo*, *Gorilla*, and *Pan*) (tables S2 and S4). All specimens in this sample were collected from skeletal collections at the following institutions: AMNH; MCZ; National Museum of Natural History (NMNH), Washington D.C., USA; Institute of Zoology (IOZ), Chinese Academy of Sciences, Beijing, China; Kunming Institute of Zoology (KIZ), Chinese Academy of Sciences, Kunming, China; Sun Yat-sen University (SYS), Guangzhou, China, and Museum für Naturkunde (ZMB), Berlin, Germany. Sex was not included as a variable in this study. No antimeres were included and if both the right and left sides of a given specimen and molar type were available, only the best preserved was analyzed.

Image data acquisition

All analyses were conducted on high-resolution images of the occlusal surface of teeth taken with either a Canon Digital Rebel XT camera with a 75–300 mm lens, Nikon D1H camera with an A/F micro-Nikkor 105 mm lens, or a Leica EZ 4D microscope built-in camera. Following protocols described elsewhere [64-65], each tooth was oriented independently, so that the buccal, and where possible, distal portion of the cervical line was perpendicular to the optical axis of the camera. A millimeter scale placed at the same horizontal plane as the cusp apices was included in each image for calibration when using the digital cameras, and both the camera and scale were leveled using standard bubble devices. The Leica EZ 4D was equipped with a built-in calibration tool such that no external scale was necessary. To test for error in orientation between observers and devices used, we calculated the maximum crown area of six hylobatid molars with different degrees of dental wear and preservation (including one molar with missing enamel on its mesial portion due to postmortem damage and whose enamel had therefore to be digitally reconstructed) photographed independently by AO (Canon Digital Rebel XT camera) and CG (Leica EZ 4D). Sessions between observers were separated by at least one year and the percentage difference was on average 2.79%.

All digital images of the molars were imported into Adobe® Photoshop CC 2017 to align the central groove with the y-axis and the main buccolingual groove with the x-axis. Right teeth were mirror-imaged to correspond to the left side and treated as such for landmark digitizing and analyses. When necessary, interproximal wear was corrected following ref. [66]. For standardization across specimens, linear measurements and breadth-length indices were collected from surface renderings or digital photos of VPL/RSP2 and H-GSP 8114/609 and used in comparisons across taxa. Measurements of these specimens were also taken in three dimensions (3D) using digital calipers, accounting for differences in the given descriptive measurements (3D) and those used for breadth-length indices (2D).

Geometric morphometric analysis

We used geometric morphometric techniques to quantify and visualize 2D dental shape variation in VPL/RSP2, H-GSP 8114/609 and our comparative sample. To do so, a methodological approach using homologous landmarks derived from ref. 18 was undertaken. As detailed in table S1 and figure S1, this approach included a total of 14 landmarks placed at the tips of the five main cusps (protoconid, metaconid, hypoconid, entoconid, and hypoconulid), at the intersection of main grooves, and at the intersection of the main grooves (or their projection) with the molar outline. Landmark digitizing was conducted by AO using TpsDig 232 software [67]. Intra-observer error in landmark digitizing is negligible, with further details described elsewhere [4, 68].

To minimize any taxonomic attributions based exclusively on size, we focused on shape variables in all morphometric analyses. Landmark data were imported into MorphoJ and superimposed using a generalized least-square Procrustes superimposition to remove the effects of translation, rotation, and scaling of the raw coordinate data. To test for any significant allometric component in the morphometric data, a multivariate regression of the Procrustes coordinates (dependent variables) vs. log centroid size (independent variable) was performed in MorphoJ and the relationship was found to be non-significant with size explaining only 1.22% of the shape variance in the M_3 analysis (p= 0.0602). Although allometric variation is stronger and statistically significant for M_1, only 6.99% of the shape variance can be explained by allometric effects (p<0.001).

Analyses were then performed on M_3 and M_1 separately. For each molar type, we first conducted a Principal Component Analysis (PCA) using the Procrustes coordinates to explore data point distribution in the shape space. Wireframe models were created within the software packages MorphoJ [20] and Morphologika2 [21] to visualize the extreme landmark configurations and determine the aspects of shape most correlated with the first and second principal components.

We also used Discriminant Function Analysis (DFA) pairwise tests, as implemented in MorphoJ, to investigate and visualize M_3 shape differences between VPL/RSP2 and each of the six major catarrhine groups included in our comparative sample (i.e., propliopithecids, proconsulids, dendropithecids, pliopithecids, hylobatids, and hominids). Procrustes distances were used to quantify the magnitude of these differences, with significance set at $p < 0.05$. It should be noted that this test differs from the classic DFA in that it allows comparisons between sample mean differences between pairs. We employed deformation grids to visualize shape deformations from the mean shape configuration (reference configuration) of each of our family-level taxonomic groups (i.e., proplioplithecids, proconsulids, dendropithecids, pliopithecids, hylobatids, and hominids) to the tooth shape of VPL/RSP2 (target configuration), as well as wireframes to compare VPL/RSP2 shape with that of group means (see figure S3). DFA pairwise tests were employed in the same manner for the M_1 sample to compare H-GSP 8114/609 to the mean shape of each family-level group as well (figure S5).

Finally, hierarchical phenetic trees were obtained from Procrustes distances by means of a neighbor-joining (NJ) cluster analysis with propliopithecids used as the outgroup at the root of the tree. Support values on the branches were quantified via a 10,000 replication bootstrap procedure. All analyses were performed in MorphoJ [20], SPSS v.25 (IBM Corp., Armonk, NY) and PAST v. 3.20 [69].

Phylogenetic analysis

In addition to general qualitative and 2D morphometric analyses, we conducted a parsimony analysis of 272 morphological characters to assess the phylogenetic position of *Kapi* and *Yuamnoupithecus* within the broader catarrhine radiation (see dataset S1). While both *Kapi* and *Yuanmoupithecus* are fragmentary and only represented by aspects of their dentition, sampling a broad number of characters and fossil taxa increases the probability of sampling critical cranial and postcranial morphologies that help drive polarity assessments of important features [70-72, 90-91]. In fact, multiple studies have demonstrated that increasing the number of characters in an analysis generally increases phylogenetic accuracy and that missing data is not a serious problem as long as character sampling is sufficiently robust [73-78]. Recent studies have affirmed that even fragmentary taxa can be phylogenetically informative and that fossil taxa, in particular, can be highly beneficial and influential in analyses due to their unique combinations of character states that affect resulting topologies [78, 90-91]. While caution is always necessary when analyzing very fragmentary taxa, and while it is true that they can act as wildcards in phylogenetic analyses and significantly reduce resolution [78], in our view the benefits of including fossil taxa, even those that are fragmentary, most often outweigh the potential negatives.

Thus, the morphological character matrix of ref. 19 was supplemented with eight new characters: seven characters derived from the results of our morphometric analyses presented above as well as recent discussions of hylobatid origins [7], and one body size character (as suggested by lower molar size, see dataset S1). In some cases, character states and scores differed from the datasets from which they were derived based on our independent qualitative and quantitative assessments of morphology (see dataset S1). *Kapi* and *Yuanmoupithecus* were scored and added to the matrix based on our own data and observations as well as information kindly provided by Terry Harrison and from the literature. All characters and character states are provided in dataset S1 and the matrix is provided as a Nexus file in dataset S2. In total, 272 characters scored for 49 taxa were included in the analysis, incorporating characters of the skull, dentition, and postcranium. *Kapi* and *Yuanmoupithecus* were scored for 16 and 38 available characters, respectively.

Characters were considered ordered whenever it can be assumed that a population likely passed through an intermediate state to get to an extreme state at either end of the character state transformation series. In these cases, ordering characters is a much more reasonable estimate of the evolutionary process (e.g., a population does not typically evolve from a small body mass to a large body mass without passing through an intermediate body mass through directional selection). Polymorphisms were coded as intermediate states between two fixed states whenever possible; simulations suggest that this coding system increases the accuracy of the resulting trees (79). All other characters were left unordered, and all characters were left unscaled so that all steps in the analysis were given equal weight.

The resulting matrix was analyzed using maximum parsimony optimization in the program TNT (80) using traditional search methods (subtree pruning and regrafting [SPR] and tree bisection and reconnection [TBR]). Heuristic searches were performed across 10,000 replicates. Bootstrap values (1000 replicates) were calculated to assess node support. A sample of platyrrhines (*Aotus*,(*Cebus*, *Saimiri*)) along with the primitive catarrhines *Catopithecus* and *Aegyptopithecus* were constrained as successive outgroups, with the ingroup composed of *Saadanius*, pliopithecids, Old World monkeys, dendropithecids, proconsulids, *Pliobates*, hylobatids, fossil hominids (*Sivapithecus*, *Kenyapithecus*, *Pierolapithecus*, *Hispanopithecus*, *Ouranopithecus*, *Lufengpithecus*, and *Oreopithecus*), and extant hominids (*Pongo*, *Gorilla*, and *Pan*). Broad-level taxonomy follows the main text [6].

2. Extended Description of VPL/RSP2 and Diagnosis of *Kapi ramnagarensis*

Extended Description

VPL/RSP2 corresponds to a relatively low-crowned M_3 with rounded corners from a catarrhine primate slightly smaller than *Hoolock* in molar size. VPL/RSP2 is mesiodistally longer than broad (breadth-length index of 0.79), indicating proportions within the range of extant hylobatids and most similar to those of proconsulids among fossil catarrhine taxa (mean breadth-length index of 0.77; range 0.68-0.85). It is considerably broader, on average, than those of pliopithecids (0.74; 62-87), and slightly broader than those of modern *Symphalangus* (0.75; 0.71-0.81), propliopithecids (0.75;

0.70-0.83), and dendropithecids (0.76; 0.71-0.83); however, it is relatively narrow compared to many modern gibbons (*Nomascus* = 0.85; 0.81-0.89, *Hoolock* = 0.84; 0.78-0.89, and *Hylobates* = 0.85; 0.77-0.92), as well as those of extinct *Yuanmoupithecus* (0.81) and *Bunopithecus* (0.82).

The crown of VPL/RSP2 is ovoid in occlusal outline, tapering distally such that its distal moiety is narrower than its mesial moiety. There are five well-developed cusps, arranged around the periphery of the crown. Cusps are low and conical in shape. The buccal wall of the crown shows some bulging and a moderately expressed semi-continuous buccal cingulum. The metaconid is the most voluminous (28% of total crown) and highest cusp, followed by the hypoconid and protoconid (25% and 22% of total crown area, respectively), which are subequal in elevation. The entoconid is similar in elevation to the hypoconid and protoconid, but relatively smaller in basal area (14% of total crown area). The hypoconulid is the smallest (11% of total crown area) of the five cusps. The hypoconulid is more distally placed relative to the hypoconid and entoconid and located slightly towards the buccal side of the midline of the crown.

The protocone has short but well-developed preprotocristid and postprotocristid. The metaconid is slightly mesial to the protoconid and has a short and rounded premetacristid. The metaconid and entoconid are widely spaced by a long postmetacristid. The hypoconid has a short prehypocristid (cristid obliqua) that is parallel to the long axis of the crown (rather than slightly oblique). Both the postentocristid and the posthypoconulid cristid are low and ill-defined, possibly due to moderate wear. The mesial fovea (i.e., trigonid basin) is long and rectangular, delimited distally by a well-differentiated hypometacristid and hypoprotocristid. The mesial marginal ridge is relatively sharp and well-developed. The distal fovea is intermediate in size but poorly defined.

The basal area of the trigonid is similar to the talonid. The talonid basin is expansive and has a simple Y-shaped groove pattern with no secondary wrinkling. A well-developed postcristid and hypoentocristid form the mesial-most portion of the distal fovea, separating it from the talonid basin. The metaconid is damaged, but there may be traces of a small mesostylid on the postmetacristid. A small tubercle is also present on the preprotocristid. There is no evidence of a pliopithecine triangle and no retention of the paraconid.

Extended Diagnosis and Comparisons with other taxa

Kapi ramnagarensis (VPL/RSP2) shares with hylobatids a number of synapomorphies: simple and low-crowned molars with rounded corners; peripherally arranged cusps; low conical cusps; absence of secondary wrinkling; weak crest development; expansive talonid basin; poorly defined distal fovea (but one that is intermediate in size vs. extant hylobatids that have a small/pit-like fovea); patterns of cusp proportions in which the protoconid, metaconid and hypoconid are roughly equal in basal area and more voluminous than the entoconid and hypoconulid; very small hypoconulid that is situated on the distal margin of the crown, slightly buccally but closer to the midline of the tooth; metaconid slightly mesial to protoconid; widely spaced metaconid and entoconid.

Compared to extant hylobatids, however, *K. ramnagarensis* exhibits: less inflated and slightly less peripherally oriented cusps, the presence of a moderately developed buccal cingulum (buccal cingulum expression ranges from absent to poorly developed in extant hylobatids with the exception of *Nomascus*, which can exhibit moderate expressions of these features as documented by Frisch [81] and Zhang et al. [5]), a well-defined and relatively long mesial fovea, better developed occlusal crests, a more elevated mesial marginal ridge; the presence of a small mesostylid (although a small to greatly pronounced mesostylid is common in some stem catarrhines and stem hominoids [39]); and a smaller breadth/length ratio with distal tapering.

Although early accounts suggested that pliopithecids and hylobatids were closely related [82-84], subsequent studies demonstrated that pliopithecids form a monophyletic group and that resemblances between the two clades were only superficial due to similarities in size and retention of primitive features [6-7, 31-33, 39]. Pliopithecids exhibit a combination of the following key lower molar features: presence of the pliopithecine triangle (although the pliopithecine triangle can be absent or weakly expressed in the M_1s of pliopithecoids, it is almost always present and well-developed in their M_3s [39]; buccal cusps that are shifted mesially relative to the lingual cusps; buccally positioned hypoconulid, which is almost in line with the two main buccal cusps (this is the general pattern seen in extinct catarrhines, but pliopithecids show this condition to an extreme); and very long and narrower lower molars (mean breadth-length index = 0.74).

Other features generally present in primitive catarrhines (e.g., propliopithecids, proconsulids, dendropithecids, pliopithecids) not observed in VPL/RSP2 include: retention of the paraconid, elevated occlusal crests and presence of secondary wrinkling, a well-developed buccal cingulum (which sometimes includes small accessory cuspules), a long and narrow talonid basin, a hypoconulid that is only slightly smaller than the hypoconid, higher crowned molars with tall, discrete cusps, a broad and well-defined distal fovea, and a prominent mesostylid.

More specifically, *K. ramnagarensis* differs from propliopithecid lower molars in the following features: more peripherally placed cusps, significantly reduced buccal flare, a relatively broad occlusal/talonid basin, shorter molar crown with increased bunodonty, hypoconid and entoconid more transversely aligned, metaconid typically larger than the protoconid, much larger mesial cusps compared to distal cusps (entoconid, hypoconid, and hypoconulid), a less extensive (mesiodistally) buccal cingulum that terminates more mesially (at the distal end of the hypoconid, at least on the M_3), a reduced (much smaller) and slightly more buccally positioned M_3 hypoconulid, more oval and less elongated lower M_3 crown, and the lack of a hypoconulid lobe on M_3.

Kapi ramnagarensis can be distinguished from dionysopithecine pliopithecids by: the absence of a paraconid, transversely aligned mesial and distal cusps with a transverse (rather than oblique) mesial crest between the protoconid and metaconid, a cristid obliqua that is oriented mesiodistally rather than slightly oblique, a comparatively reduced buccal cingulum with buccal cusps closer to the periphery of the tooth, a relatively broader talonid basin, a relatively shorter molar crown with increased bunodonty, the absence of a pliopithecine triangle or any crests associated with a pliopithecine triangle, metaconid typically larger than the protoconid, a relatively smaller entoconid-hypoconulid pair (and relatively larger mesial cusps compared to distal cusps), and an M_3 hypoconulid that is slightly buccal, but not connected to or in line with the other buccal cusps. The new Ramnagar ape can be distinguished from pliopithecine (*Pliopithecus* and *Epipliopithecus*) lower molars by: more transversely aligned mesial and distal cusps with a transverse mesial crest between the protoconid and metaconid, the metaconid a more oval (less elongated and rectangular) occlusal/crown outline, a relatively smaller hypoconulid-entoconid pair, more peripherally placed cusps creating a relatively broader occlusal basin that is devoid of any cresting, a shorter molar crown and cusps with increased bunodonty, a reduced buccal cingulum that terminates more mesially, the absence of a pliopithecine triangle or any crests associated with a pliopithecine triangle, and an M_3 hypoconulid that is only slightly buccal rather than connected to or in line with the other buccal cusps. *Kapi* differs in lower molar anatomy from crouzelines (*Plesiopliopithecus*, *Egarapithecus*, *Anapithecus*, *Barberapithecus*, and *Laccopithecus*) in the following features: a relatively shorter, broader occlusal outline with a more oval shaped (rather than elongated) M_3, transversely aligned mesial cusps with a transversely oriented crest (rather than oblique) between the protoconid and metaconid creating a transversely oriented mesial fovea, a mesially directed (rather than oblique) cristid obliqua, more peripherally placed cusps creating a relatively broad occlusal basin with no obvious crests or extensive enamel wrinkling (cresting/wrinkling also reduced in *Laccopithecus*), a mesiodistally reduced buccal cingulum, a shorter molar crown with increased bunodonty, more transversely aligned hypoconid and entoconid, the absence of a pliopithecine triangle or any crests associated with a pliopithecine triangle (also absent in *Laccopithecus* and possibly *Egarapithecus*), and an M_3 hypoconulid that is less buccally positioned than observed in most crouzelines (except *Laccopithecus*). While *Laccopithecus* shares with *Kapi* the absence of the plopithecine triangle, a somewhat reduced buccal cingulum (though still mesiodistally longer than in *Kapi*), and a less buccal hypoconulid than seen in most other pliopithecoids, it is easily diagnosed compared to *Kapi* by its elongated molar crowns, more mesially positioned buccal cusps relative to the lingual cusps, obliquely oriented mesial transverse crest and mesial fovea, more obliquely oriented cristid obliquid, and more internally placed cusps leading to a narrower and more restricted occlusal basin.

While *Kapi* is similar to the recently emended pliopithecid genus *Krishnapithecus* in its conical, uninflated, peripherally positioned cusps, reduced flare, and broad occlusal basin, *Kapi* differs *Krishnapithecus* in its overall smaller size, transversely aligned mesial and distal cusps, transversely aligned mesial transverse crest and mesial fovea, relatively low, bunodont crown and cusp height, lack of a pliopithecine triangle and any crests associated with the pliopithecine triangle, and presence of a moderately developed buccal cingulum.

Compared to pliopithecids, *Kapi* is less easily distinguished in lower molar morphology from dendropithecid and proconsulid taxa, which are less dentally specialized and more diverse. Still, there are clear, compelling, and diagnosable differences between *Kapi* and all well-established genera for which lower dentitions exist. *Kapi* differs from *Dendropithecus* in the following features: a relatively shorter and broader occlusal crown (on average) and more oval and less elongated/rectangular M_3, more peripherally placed cusps and less buccal flare, a relatively broader occlusal basin, more transversely aligned hypoconid and entoconid, a reduced buccal cingulum terminating more mesially (just distal to the hypoconid), less developed occlusal crests with shorter, more bunodont cusps, and an M_3 hypoconulid that is smaller and not as buccally positioned. *Kapi* contrasts with *Simiolus* in the following features: a relatively shorter and broader occlusal crown (on average), a relatively broad occlusal basin lacking any cresting or wrinkling, reduced occlusal flare and more peripherally placed cusps, more transversely aligned mesial and distal cusps, a reduced buccal cingulum terminating more mesially (just distal to the hypoconid), less developed occlusal shearing crests with shorter, more bunodont cusps, and an M_3 hypoconulid that is smaller and not as buccally positioned. *Kapi* is differentiated from *Micropithecus* by: more peripherally placed cusps and reduced occlusal flare, a more transverse mesial fovea (rather than oblique), a relatively broad occlusal basin lacking any cresting or wrinkling, a slightly reduced buccal cingulum terminating more mesially than in most *Micropithecus* specimens, but with overlap, and an M_3 hypoconulid that is smaller and not as buccally positioned. *Kapi* is distinguished from *Limnopithecus* by: more peripherally placed cusps and reduced occlusal flare, a relatively broader occlusal basin lacking any cresting or wrinkling, a reduced buccal cingulum terminating more mesially, a broader and relatively shorter M_3 crown (on average), and an M_3 hypoconulid that is typically not as buccally positioned.

Among proconsulids, *Kapi* is much smaller than all known genera except *Kalepithecus*. *Kapi* is most clearly differentiated in lower molar anatomy from *Kalepithecus* by its more conical cusps, more transversely aligned mesial and distal cusps, reduced buccal cingulum, much reduced occlusal flare, more peripherally placed cusps leading to a broader and more open talonid basin, and a reduced M_3 hypoconulid. *Kapi* is differentiated from *Kogolepithecus* by more transversely aligned hypoconid and entoconid, a reduced buccal cingulum, more peripherally placed cusps leading to a broader occlusal basin lacking clear cresting or wrinkling, and reduced occlusal flare. In addition to its smaller size, *Kapi* is generally differentiated from other proconsuline

(*Proconsul* and *Ekembo*) proconsulid lower molars by its shorter and broader M_3, reduced buccal cingulum, more peripherally placed occlusal cusps leading to a relatively broader occlusal basin, reduced occlusal flare, and a lack of noticeable wrinkling or cresting in and around the talonid basin. *Kapi* is distinct from nyanzapithecine proconsulids in its less inflated cusps, more transversely aligned mesial and distal cusps, reduced buccal cingulum terminating more mesially, a much broader occlusal basin lacking any substantial cresting and/or enamel wrinkling, shorter and broader occlusal outline and much less elongate M_3, more centrally placed M_3 hypoconulid. *Kapi* differs from known lower dentitions of afropithecine proconsulids (*Afropithecus*, *Morotopithecus*, *Heliopithecus*, *Nacholapithecus*, *Equatorius*, and *Otavipithecus*) in the following features: much smaller size, shorter and broader occlusal outline (at least in M_3), less inflated/more conical cusps and reduced occlusal flare, relatively broader and more open occlusal basin lacking crests or enamel wrinkling, more transversely aligned hypoconid and entoconid, and the presence of a moderately developed buccal cingulum (reduced to absent in most afropithecines, although *Kapi* is similar in development to that seen in *Otavipithecus*).

Kapi is most clearly differentiated from all known hominid genera by its much smaller size. In addition, its cusps tend to be less inflated and less bundont, the mesial fovea is relatively broad and long, the crown generally exhibits reduced flare, the broad occlusal basin lacks any cresting or wrinkling, a moderate buccal cingulum is present, and the hypoconid and entoconid are typically more transversely aligned, although overlapping the known range of variation among hominids. For a visual comparison of VPL/RSP2 with a sample of other taxa, see figure S2.

3. Extended Results and Discussion

2D GM analyses

Tables S3, S5, and S6 summarize the results of the PCAs, including the eigenvalues and percentage of the variance explained by each of the 24 principal components. Figure 3 of the main text illustrates the M_3 shape variation along the first two principal components, where PC 1 accounts for 25.1% of M_3 shape variation and PC 2 explains 10.8%.

Figure 3 shows a very clear gradient along PC 1, with hylobatids occupying almost exclusively negative values, hominids spanning both positive and negative values, and stem catarrhine/hominoid groups displaying positive values for PC 1. This distribution in the morphospace leads to nearly complete overlap among propliopithecids, proconsulids, dendropithecids, and pliopithecids along PC 1, and their strong separation from hylobatids and a number of crown hominid specimens as well. In fact, negative values on PC 1 are exclusive to crown hominoid specimens, and the vast majority of those specimens are crown hylobatids. Taxa in positive morphospace along PC 1 are characterized by longer and narrower molars with closely spaced protoconid, metaconid, entoconid and hypoconid due to the more central position of the buccal cusps (i.e., protoconid and hypoconid) and an overall shift of the four main cusps slightly more mesially. This relates both to overall increased crown flare in these taxa and a strong buccal cingulum in many cases as well. Positive values on PC 1 also have a large buccally positioned hypoconulid, a more skewed configuration of the talonid, more obliquely aligned mesial and distal cusps, and a narrow area formed by the Y-shaped groove pattern. PC 2 mainly differentiates propliopithecids from the other groups, which are widely spread in morphospace along this axis. Specimens at the positive end of PC 2 have molar crowns that exhibit less elongation and posterior tapering, while those at the negative end evince strong crown elongation and distal tapering. Other features loading on PC 2 seem to overlap with those on PC 1 and include differences in cusp position relative to the outline of the crown (i.e., flare), the position of the hypoconulid, and the relative positions of the buccal vs. lingual cusps. *Kapi* falls on negative PC 1 and negative PC 2, well within the range of variation observed among crown hylobatids and crown hominids to the exclusion of stem catarrhine/stem catarrhine groups, and plots closest to a number of hylobatid specimens. *Bunopithecus*, an extinct hylobatid from the Middle Pleistocene, plots exclusively within the hylobatid distribution, while *Yuanmoupithecus*, the earliest uncontested stem hylobatid known to date, falls within the small area of overlap among hylobatids, hominids, and dendropithecids. Interestingly, *Laccopithecus* falls exclusively within the distribution of extinct catarrhines, supporting the most common taxonomic placement of *Laccopithecus* with the Pliopithecoidea, despite early claims that it was a stem hylobatid [85-89].

The results of the PCA performed on the M_1 dataset are summarized in tables S5-S6. Figure S4 illustrates the distribution of the specimens and the relative placement of H-GSP 8114/609 along the first two principal components, where PC 1 and PC 2 account for 21.2% and 14.4% of M_1 shape variation, respectively. There is more overlap among groups in the M_1 PCA, consistent again with the suggestion that they are perhaps not as distinctive between taxa as are M_3s [27]. Hylobatids plot throughout negative PC 1 and the left-most portion of positive PC 1, while hominids are primarily located on positive

PC 1 with only a couple of specimens in negative PC 1 space. Stem catarrhine/hominoid taxa are spread across PC 1 and are primarily separated from crown hominoid taxa on PC 2; most propliopithecids, proconsulids, dendropithecids, and pliopithecids are found at the positive end of PC 2 and most hominids and hylobatids are found largely at the negative end. Proconsulids notably span both positive and negative PC 2 space, and dendropithecids cross into negative PC 2 space as well. Propliopithecids and pliopithecids plot exclusively in positive PC 2 space.

H-GSP 8114/609 plots on positive PC 1 and positive PC 2, in the area of overlap between dendropithecids, pliopithecids, and hominids, but to the exclusion of propliopithecids, proconsulids, and hylobatids. Specimens with negative loadings on PC 1 are characterized by narrower molar crowns with the entoconid and hypoconid more transversely aligned, increased distal tapering, a centrally positioned hypoconulid, and more peripherally placed cusps. The positive end of PC 1 appears associated with a relatively broader crown and occlusal basin, more centrally placed cusps, increased basal flare, a more mesially shifted hypoconid compared to entoconid, a more buccally positioned hypoconulid, and a lack of distal tapering. Specimens with positive PC 2 values exhibit centrally compressed cusp apices due primarily to the much more central position of the buccal cusps, more obliquely aligned buccal and lingual cusps, a much larger buccal cingulum and/or flare, and increased distal tapering. At the negative end of PC 2, M_1s show reduction of the buccal flare/cingulum, a broad occlusal basin, more transversely aligned buccal and lingual cusps, and less distal tapering.

Additional references cited in the Supplementary Materials

51. Gupta SS, Verma BC. 1988 Stratigraphy and vertebrate fauna of the Siwalik group, Mansar-Uttarbani section, Jammu district, Jammu and Kashmir. *J. Palaeontol. Soc. Ind.* **33**, 117-124.
52. Basu PK. 2004 Siwalik mammals of the Jammu Sub-Himalaya, India: an appraisal of their diversity and habitats. *Quatern. Int*. **117**, 105-118. (doi:10.1016/S1040-6182(03)00120-4)
53. Gupta SS. 2000 Lithostratigraphy and structure of the Siwalik succession and its relationship with the Murree succession around Ramnagar area, Udhampur Disrict, J & K. *Himal. Geol.* **21**, 53-61.
54. Gupta SS. 1997 Study and documentation of vertebrate fossils from the Siwalik Group of Jammu Sub-Himalayan foot hills. *Geol. Surv. Ind.* **129**, 5-7.
55. Nanda AC, Sehgal RK. 1993 Siwalik mammalian faunas from Ramnagar (J and K) and Nurpur (H.P.) and lower limit of *Hipparion*. *J. Geol. Soc. Ind*. **42**, 115-134.
56. Brown B, Gregory WK, Hellman M. 1924 On three incomplete anthropoid jaws from the Siwaliks, India. *Am. Mus. Novit*. **130,** 1-8.
57. Pilgrim GE. 1927 A *Sivapithecus* palate and other primate fossils from India. *Mem. Geol. Soc. Ind*. **14**, 1-26.
58. Colbert EH. 1935 Siwalik mammals in the American Museum of Natural History. *Trans. Am. Phil. Soc.* **26**, 1-40.
59. Gregory WK, Hellman M, Lewis GE. 1938 Fossil anthropoids of the Yale-Cambridge India expedition of 1935. *Carnegie Inst. Washington Publ*. **495**, 1-27.
60. Vasishat RN, Gaur R, Chopra SRK. 1978 Geology, fauna and palaeoenvironment of Lower Sivalik deposits around Ramnagar, India. *Nature* **275**, 736-737.
61. Gaur R, Chopra SRK. 1983 Palaeoecology of the middle Miocene Siwalik sediments of a part of Jammu and Kashmir State, India. *Palaeogeogr. Palaeocl.* **43**, 313-327.
62. Parmar V, Prasad GVR. 2006 Middle Miocene rhizomyid rodent (Mammalia) from the Lower Siwalik Subgroup of Ramnagar, Udhampur District, Jammu and Kashmir, India. *Neu. Jah. Geol. Palaeontol.* **6**, 371-384.
63. Barry JC, *et al.* 2013 The Neogene Siwaliks of the Potwar Plateau, Pakistan. In *Fossil Mammals of Asia: Neogene Biostratigraphy and Chronology* (eds. X Wang, LJ Flynn, M Fortelius), pp. 373-399. New York: Columbia University Press.
64. Bailey SE. 2002 *Neandertal dental morphology: implications for modern human origins*. Ph.D. Thesis, Arizona State Univ.
65. Pilbrow VC. 2003 *Dental variation in African apes with implications for understanding patterns of variation in species of fossil apes.* Ph.D. Thesis, New York Univ.
66. Wood BA, Engleman CA. 1988 Analysis of the dental morphology of Plio-Pleistocene hominids, V. Maxillary postcanine tooth morphology. *J Anat.* **161,** 1–35.
67. Rohlf FJ. 2016 TpsDig232. TpsSeries, Stony Brook Univ.
68. Ortiz A, Villamil CI, Kimock CM, He K, Harrison T. 2017 Tracking hylobatid taxonomic diversity from molar morphometrics. *Am. J. Phys. Anthropol.* **S64**: 306.
69. Hammer Ø, Harper DAT, Ryan PD. 2001 PAST: Paleontological Statistics Software Package for Education and Data Analysis. *Palaeontol. Electron*. **4,** 1-9. (http://palaeo-electronica.org/2001_1/past/issue1_01.htm)

70. Gatesy J, O'Leary MA. 2001 Deciphering whale origins with molecules and fossils. *Trends Ecol. Evol.* **16**, 562-570. (doi:10.1016/S0169-5347(01)02359-X)
71. Gatesy J, Amato G, Norell M, DeSalle R, Hayashi C. 2003 Combined support for wholesale taxic atavism in Gavailine Crocodylians. *Systematic Biol.* **52**, 403-422. (doi: 10.1080/10635150390197037)
72. Springer MS, Teeling EC, Madsen O, Stanhope MJ, de Jong WW. 2001 Integrated fossil and molecular data reconstruct bat echolocation. *Proc. Natl. Acad. Sci. USA* **98**, 6241-6246. (doi:10.1073/pnas.111551998)
73. Wiens JJ. 1998 Does adding characters with missing data increase or decrease phylogenetic accuracy? *Systematic Biol*. **47**, 625-640.
74. Wiens JJ. 2003 Incomplete taxa, incomplete characters, and phylogenetic accuracy: is there a missing data problem? *J. Vertebr. Paleontol.* **23**, 297-310. (doi:10.1671/0272-4634(2003)023[0297:ITICAP]2.0.CO;2)
75. Wiens JJ. 2003 Missing data, incomplete taxa, and phylogenetic accuracy. *Systematic Biol*. 52, 528-538. (doi:10.1080/10635150390218330)
76. Wiens JJ. 2006 Missing data and the design of phylogenetic analyses. *J. Biomed. Inform*. **39**, 34-42. (doi:10.1016/j.jbi.2005.04.001)
77. Wiens JJ, Morrill MC. 2011 Missing data in phylogenetic analysis: reconciling results from simulations and empirical data. *Systematic Biol*. **60**, 719-731. (doi:10.1093/sysbio/syr025)
78. Pattinson DJ, Thompson RS, Piotrowski AK, Asher RJ. 2015 Phylogeny, paleontology, and primates: do incomplete fossils bias the tree of life? *Systematic Biol.* **64**, 169-186. (doi:10.1093/sysbio/syu077)
79. Wiens JJ. 2000 Coding morphological variation within species and higher taxa for phylogenetic analysis. In *Phylogenetic Analysis of Morphological Data* (ed. JJ Wiens), pp. 115-145. Washington, DC: Smithsonian Institution Press.
80. Goloboff PA, Farris JS, Nixon KC. 2008 TNT, a free program for phylogenetic analysis. *Cladistics* **24**, 774-786. (doi:10.1111/j.1096-0031.2008.00217.x)
81. Frisch JE. 1965 Trends in the evolution of the hominoid dentition. *Bibliotheca Primatologica Basel* **3**, 1-130.
82. Simons EL. 1972 *Primate evolution: an introduction to man's place in nature*. New York: MacMillan.
83. Simons EL, Fleagle JG. 1973 The history of extinct gibbon-like primates. *Gibbon Siamang* **2**, 121–148.
84. Wu R, Pan Y. 1985 Preliminary observation on the cranium of *Laccopithecus robustus* from Lufeng, Yunnan with reference to its phylogenetic relationship. *Acta Anthropol. Sinica* **4**, 7–12.
85. Pan Y. 1988 Small fossil primates from Lufeng, a latest Miocene site in Yunnan Province, China. *J. Hum. Evol.* 17, 359–366.
86. Tyler DE. 1991 The problems of the Pliopithecidae as a hylobatid ancestor. *Hum. Evol.* **8**, 73–80.
87. Tyler DE. 1993 The evolutionary history of the gibbon. In *Evolving Landscapes and Evolving Biotas of East Asia since the Mid-Tertiary* (ed. NG Jablonski), pp, 228–240. Hong Kong: University of Hong Kong.

88. Nisbett RA, Ciochon RL. 1993 Primates in northern Viet Nam: a review of the ecology and conservation status of extant species, with notes on Pleistocene localities. *Int. J. Primatol.* **14**, 765–795.
89. Jablonski NG, Chaplin G. 2009 The fossil record of gibbons. In *The Gibbons* (eds. S Lappan, DJ Whittaker), pp. 111–130. New York: Springer.
90. Koch NM, Parry LA. 2020 Death is on our side: paleontological data drastically modify phylogenetic hypotheses. *Sys. Biol.* https://doi.org/10.1101/723882
91. Asher RJ, Smith MR, Rankin A, Emry RJ. 2019. Congruence, fossils and the evolutionary tree of rodents and lagomorphs. R. Soc. Open Sci. **6**, 190387. http://dx.doi.org/10.1098/rsos.190387

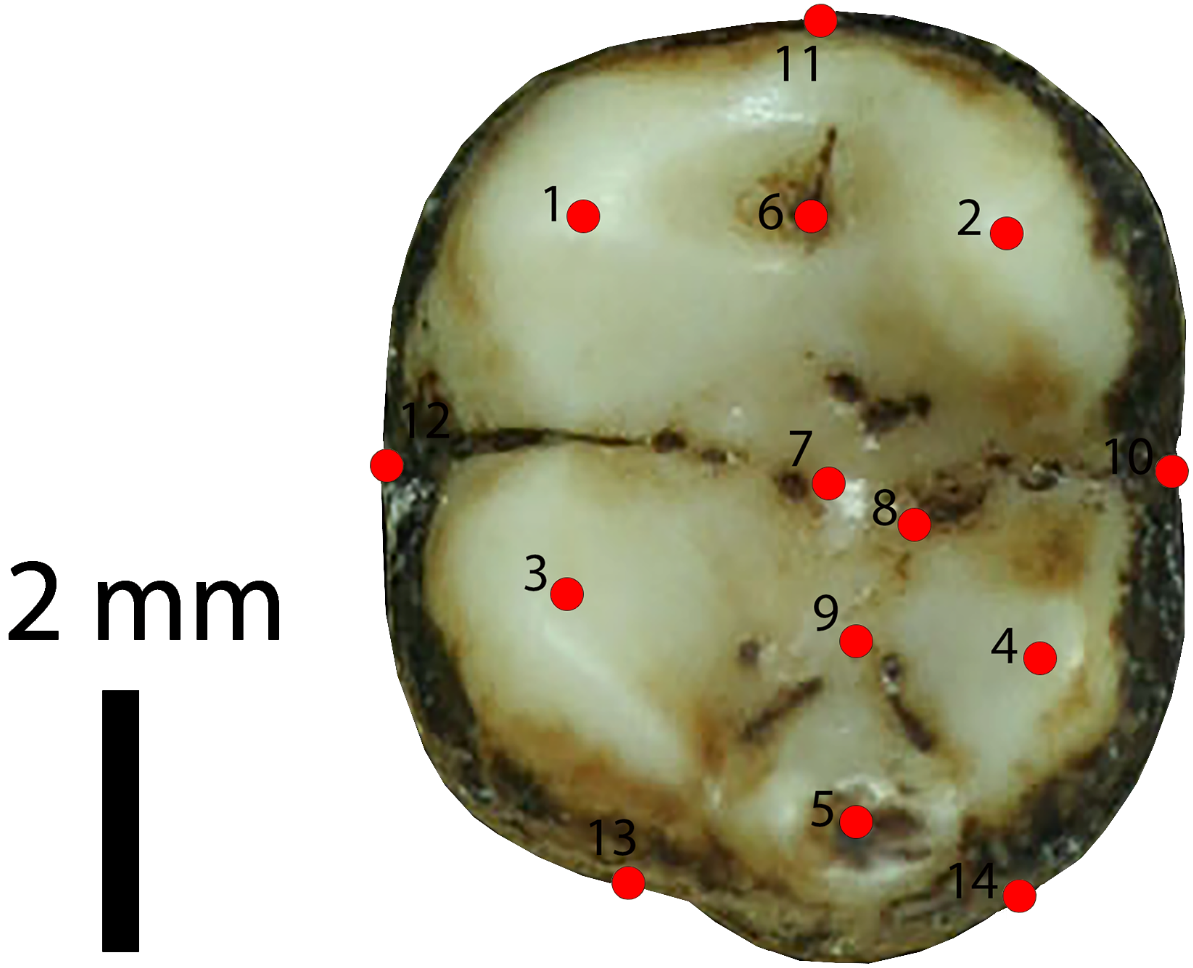

Figure S1. Protocol used in comparative analyses of catarrhine lower molars by means of 14 landmark 2D geometric morphometrics. Specimen depicted is a left M_3 of *Hoolock leuconedys*. See also Table S1.

Landmark	Description
1	Tip of the mesiobuccal cusp or protoconid
2	Tip of the mesiolingual cusp or metaconid
3	Tip of the distobuccal cusp or hypoconid
4	Tip of the distolingual cusp or entoconid
5	Tip of the hypoconulid or cusp 5
6	Center of the mesial fovea
7	Point where the central groove is crossed by the mesiobuccal groove
8	Point where the central groove is crossed by the lingual groove
9	Point where the central groove is intersected by the distobuccal groove (beginning of cusp 5)
10	Point where the dental outline is intersected by the lingual groove
11	The most mesial point of the occlusal outline opposite the mesial fovea
12	Point where the dental outline is intersected by the mesiobuccal groove
13	Point where the dental outline is intersected by the distobuccal groove
14	Point where the dental outline is intersected by the distal prolongation of the central groove

Notes: Landmark definitions based on ref 18.

Table S1. List of landmarks used in the 2D geometric morphometric analyses of occlusal morphology.

Specimen number	Family	Genus and species	Fossil/Extant
DPC 1027	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
DPC 2806	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
YPM 21032	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
DPC 1028	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
DPC 5392	Propliopithecidae	*Propliopithecus ankeli*	Fossil
DPC 1069	Propliopithecidae	*Propliopithecus chirobates*	Fossil
BM(NH).M 16650	Dendropithecidae	*Dendropithecus macinnesi*	Fossil
KNM-RU 2015	Dendropithecidae	*Dendropithecus macinnesi*	Fossil
KNM-ZP 01669b	Dendropithecidae	*Dendropithecus sp. indet.*	Fossil
KNM-SO 444	Dendropithecidae	*Limnopithecus evansi*	Fossil
KNM-ZP 01675	Dendropithecidae	*Limnopithecus sp. indet.*	Fossil
KNM-MB 9767	Dendropithecidae	*Micropithecus leakeyorum*	Fossil
KNM-WK 16960	Dendropithecidae	*Simiolus enjiessi*	Fossil
KNM-RU 7290	Proconsulidae	*Ekembo heseloni*	Fossil
KNM-RU 1674	Proconsulidae	*Ekembo nyanzae*	Fossil
KNM-RU 1947	Proconsulidae	*Ekembo nyanzae*	Fossil
KNM-SO 378	Proconsulidae	*Kalepithecus songhorensis*	Fossil
BER I	Proconsulidae	*Otavipithecus namibiensis*	Fossil
KNM-SO 396	Proconsulidae	*Proconsul major*	Fossil
KNM-SO 463	Proconsulidae	*Rangwapithecus gordoni*	Fossil
RUD 98	Pliopithecidae	*Anapithecus hernyaki*	Fossil
IPS 2943	Pliopithecidae	*Egarapithecus narcisoi*	Fossil
Naturhistorisches Museum (Basel), Individual III	Pliopithecidae	*Epipliopithecus vindobenensis*	Fossil
Naturhistorisches Museum (Basel), Individual I	Pliopithecidae	*Epipliopithecus vindobenensis*	Fossil
PA 880	Pliopithecidae	*Laccopithecus robustus*	Fossil
PA 870	Pliopithecidae	*Platodontopithecus jianghuaiensis*	Fossil
MNHN Chantrei Deperet, La Grive	Pliopithecidae	*Pliopithecus antiquus*	Fossil
Goriach (H30), Joanneum 3675	Pliopithecidae	*Pliopithecus platydon*	Fossil
MNHN Sansan (H2)	Pliopithecidae	*Pliopithecus* sp. indet.	Fossil
AMNH 18534	Hylobatidae	*Bunopithecus sericus*	Fossil
VPL/RSP-2	Hylobatidae	*Kapi ramnagarensis*	Fossil
YML 112-1x	Hylobatidae	*Yuanmoupithecus xiaoyuan*	Fossil
AMNH 112688	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112697	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112698	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112702	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112703	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 83413	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 83415	Hylobatidae	*Hoolock hoolock*	Extant

AMNH 83417	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112671	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112674	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112680	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112683	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112719	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112720	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112960	Hylobatidae	*Hoolock leuconedys*	Extant
KIZ 014035	Hylobatidae	*Hoolock leuconedys*	Extant
USNM 257988	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 102773	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102774	Hylobatidae	*Hylobates agilis*	Extant
AMNH 106571	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102161	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102200	Hylobatidae	*Hylobates agilis*	Extant
AMNH 106572	Hylobatidae	*Hylobates agilis*	Extant
AMNH 106578	Hylobatidae	*Hylobates agilis*	Extant
AMNH 106678	Hylobatidae	*Hylobates agilis*	Extant
AMNH 106679	Hylobatidae	*Hylobates agilis*	Extant
AMNH 103442	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 103441	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 103665	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 106053	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 103243	Hylobatidae	*Hylobates klossii*	Extant
MCZ 41546	Hylobatidae	*Hylobates lar*	Extant
AMNH 54662	Hylobatidae	*Hylobates lar entelloides*	Extant
AMNH 101695	Hylobatidae	*Hylobates lar entelloides*	Extant
USNM 083262	Hylobatidae	*Hylobates lar entelloides*	Extant
USNM 111970	Hylobatidae	*Hylobates lar entelloides*	Extant
USNM 111989	Hylobatidae	*Hylobates lar entelloides*	Extant
USNM 124232	Hylobatidae	*Hylobates lar entelloides*	Extant
USNM 296922	Hylobatidae	*Hylobates lar entelloides*	Extant
USNM 296923	Hylobatidae	*Hylobates lar entelloides*	Extant
AMNH 102093	Hylobatidae	*Hylobates moloch*	Extant
AMNH 41342	Hylobatidae	*Hylobates moloch*	Extant
ZMB 7808	Hylobatidae	*Hylobates muelleri*	Extant
AMNH 103403	Hylobatidae	*Hylobates muelleri*	Extant
AMNH 103723	Hylobatidae	*Hylobates muelleri*	Extant
AMNH 106782	Hylobatidae	*Hylobates muelleri*	Extant
AMNH 106327	Hylobatidae	*Hylobates muelleri*	Extant
USNM 198268	Hylobatidae	*Hylobates muelleri funereus*	Extant
USNM 241019	Hylobatidae	*Hylobates pileatus*	Extant
USNM 296920	Hylobatidae	*Hylobates pileatus*	Extant
ZMB 7814	Hylobatidae	*Hylobates* sp. indet.	Extant
ZMB 7860	Hylobatidae	*Hylobates* sp. indet.	Extant
ZMB 7825	Hylobatidae	*Hylobates* sp. indet.	Extant

ZMB 7819	Hylobatidae	*Hylobates* sp. indet.	Extant
MCZ 38115	Hylobatidae	*Nomascus concolor*	Extant
MCZ 38116	Hylobatidae	*Nomascus concolor*	Extant
KIZ 000170	Hylobatidae	*Nomascus concolor*	Extant
KIZ 000391	Hylobatidae	*Nomascus concolor*	Extant
KIZ 003192	Hylobatidae	*Nomascus concolor*	Extant
KIZ 009643	Hylobatidae	*Nomascus concolor*	Extant
KIZ 0106167	Hylobatidae	*Nomascus concolor*	Extant
KIZ 012168	Hylobatidae	*Nomascus concolor*	Extant
USNM 464992	Hylobatidae	*Nomascus concolor*	Extant
AMNH 87252	Hylobatidae	*Nomascus gabriellae*	Extant
SYS 1	Hylobatidae	*Nomascus hainanus*	Extant
IOZ 14517	Hylobatidae	*Nomascus leucogenys*	Extant
IOZ 18071	Hylobatidae	*Nomascus leucogenys*	Extant
KIZ 000175	Hylobatidae	*Nomascus leucogenys*	Extant
USNM 240490	Hylobatidae	*Nomascus leucogenys*	Extant
AMNH 102195	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102196	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102197	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102720	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102724	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102725	Hylobatidae	*Symphalangus syndactylus*	Extant
USNM 395514	Hylobatidae	*Symphalangus syndactylus*	Extant
USNM 519573	Hylobatidae	*Symphalangus syndactylus*	Extant
MCZ 27831	Hylobatidae	*Symphalangus syndatylus*	Extant
MCZ 17684	Hominidae	*Gorilla gorilla*	Extant
MCZ 38326	Hominidae	*Gorilla gorilla*	Extant
MCZ 46325	Hominidae	*Gorilla gorilla*	Extant
ZMB 30941	Hominidae	*Gorilla gorilla*	Extant
ZMB 31626	Hominidae	*Gorilla gorilla*	Extant
AMNH 115609	Hominidae	*Gorilla gorilla*	Extant
AMNH 167325	Hominidae	*Gorilla gorilla*	Extant
AMNH 167326	Hominidae	*Gorilla gorilla*	Extant
AMNH 167327	Hominidae	*Gorilla gorilla*	Extant
AMNH 167328	Hominidae	*Gorilla gorilla*	Extant
AMNH 167332	Hominidae	*Gorilla gorilla*	Extant
AMNH 167337	Hominidae	*Gorilla gorilla*	Extant
AMNH 167338	Hominidae	*Gorilla gorilla*	Extant
AMNH 167339	Hominidae	*Gorilla gorilla*	Extant
AMNH 167672	Hominidae	*Gorilla gorilla*	Extant
AMNH 170363	Hominidae	*Gorilla gorilla*	Extant
AMNH 200503	Hominidae	*Gorilla gorilla*	Extant
AMNH 200506	Hominidae	*Gorilla gorilla*	Extant
AMNH 201472	Hominidae	*Gorilla gorilla*	Extant
AMNH 214104	Hominidae	*Gorilla gorilla*	Extant
AMNH 214107	Hominidae	*Gorilla gorilla*	Extant

AMNH 214111	Hominidae	*Gorilla gorilla*	Extant
AMNH 214113	Hominidae	*Gorilla gorilla*	Extant
AMNH 235603	Hominidae	*Gorilla gorilla*	Extant
AMNH 54089	Hominidae	*Gorilla gorilla*	Extant
AMNH 54090	Hominidae	*Gorilla gorilla*	Extant
AMNH 90194	Hominidae	*Gorilla gorilla*	Extant
ZMB 31277	Hominidae	*Gorilla gorilla*	Extant
ZMB 31435	Hominidae	*Gorilla gorilla*	Extant
ZMB 83546	Hominidae	*Gorilla gorilla*	Extant
ZMB 83561	Hominidae	*Gorilla gorilla*	Extant
AMNH 51376	Hominidae	*Pan troglodytes*	Extant
MCZ 9493	Hominidae	*Pan troglodytes*	Extant
MCZ 6244	Hominidae	*Pan troglodytes*	Extant
AMNH 119227	Hominidae	*Pan troglodytes*	Extant
AMNH 167342	Hominidae	*Pan troglodytes*	Extant
AMNH 167346	Hominidae	*Pan troglodytes*	Extant
AMNH 183130	Hominidae	*Pan troglodytes*	Extant
AMNH 51204	Hominidae	*Pan troglodytes*	Extant
AMNH 51376	Hominidae	*Pan troglodytes*	Extant
AMNH 51377	Hominidae	*Pan troglodytes*	Extant
AMNH 51394	Hominidae	*Pan troglodytes*	Extant
AMNH 81854	Hominidae	*Pan troglodytes*	Extant
AMNH 89353	Hominidae	*Pan troglodytes*	Extant
AMNH 89406	Hominidae	*Pan troglodytes*	Extant
AMNH 90293	Hominidae	*Pan troglodytes*	Extant
MCZ 37518	Hominidae	*Pongo pygmaeus*	Extant
MCZ 37519	Hominidae	*Pongo pygmaeus*	Extant
AMNH 19548	Hominidae	*Pongo pygmaeus*	Extant
AMNH 28253	Hominidae	*Pongo pygmaeus*	Extant
USNM 142169	Hominidae	*Pongo pygmaeus*	Extant
USNM 142191	Hominidae	*Pongo pygmaeus*	Extant
USNM 142195	Hominidae	*Pongo pygmaeus*	Extant
ZMB 6954	Hominidae	*Pongo pygmaeus*	Extant
ZMB 6957	Hominidae	*Pongo pygmaeus*	Extant
ZMB 83509	Hominidae	*Pongo pygmaeus*	Extant

Table S2. List of catarrhine M_3 specimens included in this study.

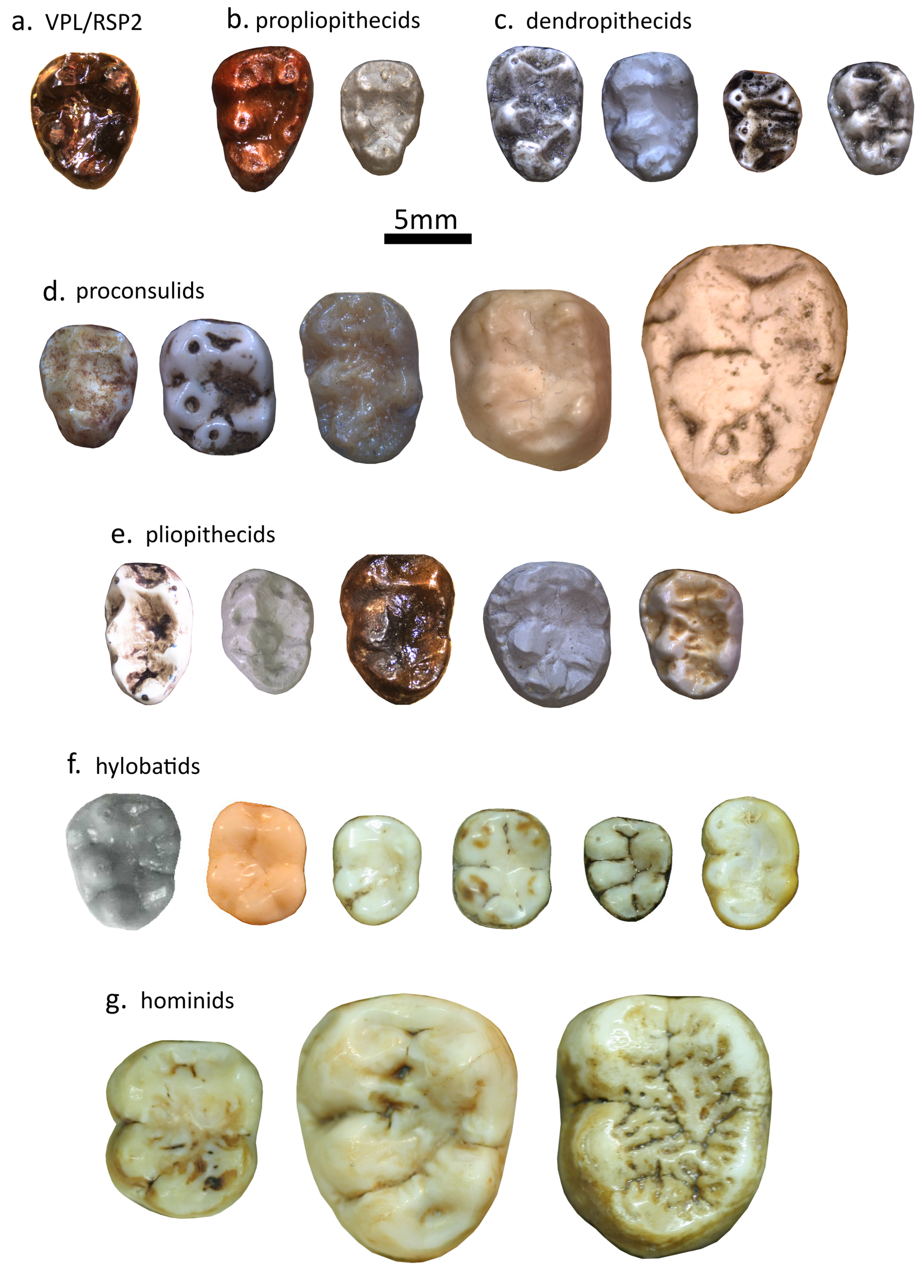

Figure S2. *Kapi ramnagarensis* gen. et sp. nov. in occlusal view compared to a sample of extinct and extant catarrhines. All specimens are M_3s and are visualized with the buccal side to the left (right molars mirror-imaged and identified with *). **a,** VPL/RSP2 from Ramnagar, India; **b,** propliopithecids (left to right): *Aegyptopithecus zeuxis* (DPC 2806), *Propliopithecus chirobates* (DPC 1069); **c,** dendropithecids (left to right): *Dendropithecus* sp. indet. *(*KNM-ZP 01669b*), *Limnopithecus evansi (*KNM-SO 444*), *Micropithecus leakeyorum* (KNM-MB 9767*), *Simiolus enjiessi* (KNM-WK 16960)*; **d,** proconsulids (left to right): *Kalepithecus songhorensis* (KNM-SO 378*), *Ekembo heseloni* (KNM-RU 7290), *Rangwapithecus gordoni* (KNM-SO 463*), *Otavipithecus namibiensis* (BERI*), *Proconsul major* (KNM-SO 396); **e,** pliopithecids (left to right): *Egarapithecus narcisoi* (IPS 2943*), *Epipliopithecus vindobenensis* (Naturhistorisches Museum, Basel, Individual I), *Laccopithecus robustus* (PA 880), *Platodontopithecus jianghuaiensis* (PA 870), *Pliopithecus antiquus* (MNHN Chantrei Deperet, La Grive*); **f,** hylobatids (left to right): *Yuanmoupithecus* (YML 112-1x; image from Pan, 2006), *Bunopithecus sericus* (AMNH 18534), *Nomascus leucogenys* (NMNH 240490), *Hoolock hoolock* (AMNH 83413), *Hylobates moloch* (AMNH 103442), *Symphalangus syndactylus* (USNM 519573*); **g,** hominids (from left to right*): Pan troglodytes* (AMNH 167342), *Gorilla gorilla* (AMNH 167338), *Pongo pygmaeus* (NMNH 142195).

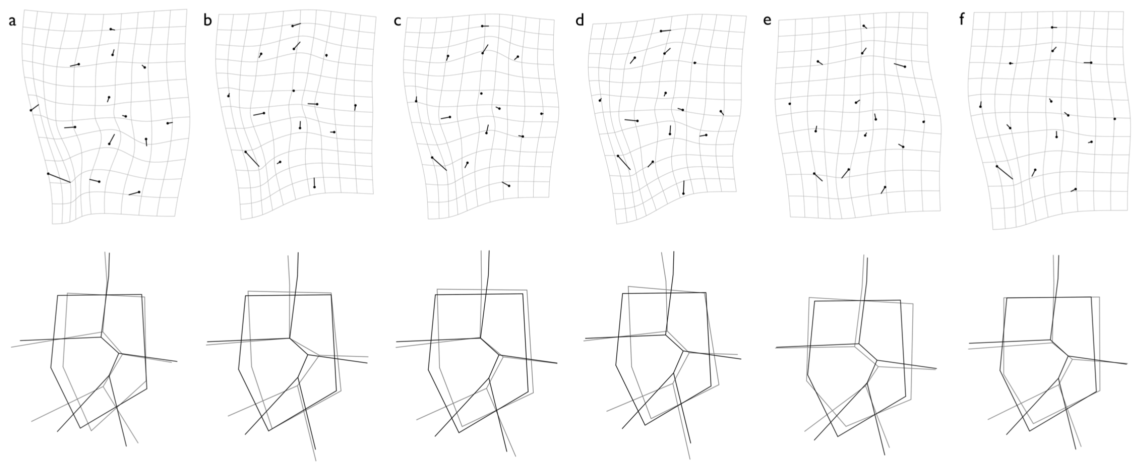

Figure S3. Deformation grids (top row) and wireframes (bottom row) based on 14 homologous landmarks (14L) comparing VPL/RSP2 with: **a,** propliopithecids; **b,** proconsulids; **c,** dendropithecids; **d,** pliopithecids; **e,** hylobatids; and **f,** hominids. Deformation grids show shape deformations from the M3 mean shape (reference configuration) of each of the five major taxonomic groups analyzed to the M3 shape of VPL/RSP2 (target configuration), with vectors indicating the direction of change from the reference to the target shape coordinate locations. Wireframes compare the M3 configuration of VPL/RSP2 (in black) with mean shapes of extant and extinct catarrhine taxa (in gray). Procrustes distances for a (0.16), b (0.15), c (0.14), d (0.16), e (0.11), and f (0.12); *p*-values non-significant.

Specimen	PC1	PC2	PC3	PC4	PC5	PC6
Kapi VPL/RSP2	-0.0181	-0.0283	0.0371	0.0152	-0.0081	0.0215
Dendropithecus KNM-RU 2015	0.0740	0.0431	0.0091	-0.0103	0.0270	0.0144
Dendropithecus KNM-ZP 01669	0.0269	0.0487	0.0055	0.0718	-0.0685	0.0017
Dendropithecus KNM-RU 16650	0.0147	0.0549	0.0182	0.0507	-0.0090	-0.0169
Limnopithecus KNM-SO 444	0.0421	-0.0477	-0.0152	0.0579	0.0017	0.0323
Limnopithecus KNM-ZP 01675	0.0539	0.0161	0.0282	0.0174	-0.0090	0.0080
Micropithecus KNM MB 9767	0.0809	-0.0048	0.0025	-0.0632	-0.0108	0.0174
Simiolus KNM-WK 16960	0.1208	-0.0614	-0.0093	0.0333	0.0386	-0.0018
Bunopithecus AMNH 18534	-0.1091	0.0064	0.0421	0.0673	0.0196	0.0154
Hoolock AMNH 112671	-0.1677	0.0668	-0.0160	0.0526	-0.0106	0.0465
Hoolock AMNH 112674	-0.0338	-0.0207	0.0057	-0.0088	0.0127	0.0040
Hoolock AMNH 112680	-0.0717	0.0212	0.0348	0.0075	0.0086	0.0202
Hoolock AMNH 112683	-0.0679	0.0170	0.0486	0.0233	0.0065	0.0424
Hoolock AMNH 112688	-0.0211	0.0384	0.0062	0.0025	0.0311	-0.0041
Hoolock AMNH 112697	-0.1222	-0.0724	0.0476	0.0254	-0.0107	-0.0422
Hoolock AMNH 112698	-0.0609	-0.0202	0.0517	0.0367	-0.0301	0.0016
Hoolock AMNH 112702	-0.0907	0.0349	0.0039	-0.0131	0.0090	0.0125
Hoolock AMNH 112703	-0.0487	0.0038	0.0178	-0.0026	0.0509	0.0438
Hoolock AMNH 112719	-0.0547	0.0030	-0.0022	-0.0064	-0.0121	0.0129
Hoolock AMNH 112720	-0.0224	-0.0011	0.0473	-0.0106	0.0224	0.0289
Hoolock AMNH 112960	0.0375	-0.0188	0.0513	-0.0816	0.0124	0.0001
Hoolock AMNH 83413	-0.0702	0.0473	0.0449	-0.0151	-0.0217	-0.0113
Hoolock AMNH 83415	-0.0436	-0.0712	0.0038	0.0136	0.0000	-0.0326
Hoolock AMNH 83417	-0.0681	0.0145	0.0318	0.0393	-0.0265	0.0365
Hoolock KIZ 014035	-0.0642	-0.0413	0.0433	0.0480	0.0186	-0.0013
Hoolock USNM 257988	-0.0539	-0.1388	-0.0122	0.0471	-0.0136	-0.0040
Hylobates AMNH 101695	-0.0597	-0.0661	0.0313	0.0181	-0.0194	-0.0080
Hylobates AMNH 102093	-0.0442	-0.0768	0.0062	-0.0087	-0.0239	0.0254
Hylobates AMNH 102161	-0.0125	0.0258	0.0092	-0.0479	0.0103	-0.0012
Hylobates AMNH 102200	-0.0076	-0.0442	-0.0576	-0.0316	0.0323	0.0297
Hylobates AMNH 102773	-0.0473	-0.0398	-0.0731	-0.0472	0.0567	-0.0160
Hylobates AMNH 102774	-0.0539	0.0333	-0.0274	-0.0681	0.0280	0.0258
Hylobates AMNH 103243	-0.0927	-0.0214	0.0244	0.0392	-0.0117	0.0045
Hylobates AMNH 103403	-0.0468	-0.0006	0.0007	-0.0618	0.0337	0.0056
Hylobates AMNH 103441	-0.0792	0.0427	-0.0333	-0.0499	0.0394	-0.0221
Hylobates AMNH 103442	0.0132	0.0176	-0.0111	-0.0673	0.0141	-0.0224
Hylobates AMNH 103665	0.0359	-0.0038	0.0226	-0.0697	-0.0326	0.0101
Hylobates AMNH 103723	-0.0914	0.0001	0.0094	0.0134	-0.0518	-0.0088
Hylobates AMNH 106053	-0.0815	-0.0255	0.0141	-0.0199	-0.0232	-0.0140
Hylobates AMNH 106327	-0.0245	-0.0611	0.0468	-0.0263	-0.0127	-0.0266
Hylobates AMNH 106571	-0.1073	0.0007	-0.1018	0.0173	-0.0006	0.0331
Hylobates AMNH 106572	-0.0196	-0.0044	-0.0027	-0.0464	-0.0089	-0.0215
Hylobates AMNH 106578	-0.0151	0.0124	-0.0227	-0.0508	0.0040	-0.0085
Hylobates AMNH 106678	-0.0039	-0.0298	-0.0352	-0.0381	0.0060	0.0026
Hylobates AMNH 106679	-0.0394	0.0458	-0.0747	0.0045	-0.0074	-0.0001

Hylobates AMNH 106782	-0.0617	-0.0794	0.0441	-0.0486	-0.0049	-0.0360
Hylobates AMNH 41342	-0.0829	-0.0526	0.0194	-0.0187	-0.0472	0.0197
Hylobates AMNH 54662	-0.0067	-0.0020	0.0098	-0.0575	-0.0014	-0.0005
Hylobates MCZ 41546	-0.0123	0.0247	0.0068	-0.0569	0.0223	0.0373
Hylobates USNM 083262	-0.0590	-0.0612	0.0361	0.0065	-0.0435	0.0203
Hylobates USNM 111970	-0.0204	-0.0191	0.0266	0.0057	-0.0356	0.0033
Hylobates USNM 111989	-0.0456	-0.0002	-0.0826	0.0206	0.0140	0.0001
Hylobates USNM 124232	-0.0515	-0.0369	0.0456	0.0070	0.0304	0.0088
Hylobates USNM 198268	-0.0405	-0.0177	-0.0297	-0.0114	0.0092	-0.0235
Hylobates USNM 241019	-0.0059	-0.0452	0.0197	-0.0892	0.0278	-0.0143
Hylobates USNM 296920	-0.0362	-0.0289	-0.0415	0.0391	0.0144	-0.0173
Hylobates USNM 296922	-0.0498	0.0413	-0.0077	-0.0364	0.0004	0.0089
Hylobates USNM 296923	-0.0884	-0.0339	0.0078	0.0388	0.0140	0.0168
Hylobates ZMB 7814	-0.0777	0.0157	0.0176	-0.0155	-0.0351	0.0042
Hylobates ZMB 7819	0.0221	-0.0734	-0.0308	-0.0266	-0.0234	-0.0029
Hylobates ZMB 7825	-0.0474	0.0214	-0.0084	0.0004	-0.0014	0.0169
Hylobates ZMB 7860	-0.0752	-0.0049	-0.0339	0.0108	-0.0176	-0.0307
Hyobates ZMB 7808	-0.1112	0.0340	0.0352	-0.0115	0.0179	0.0405
Nomascus KIZ000175	-0.0951	-0.0616	-0.0379	0.0636	-0.0316	-0.0198
Nomascus AMNH 87252	-0.0515	0.0316	0.0312	-0.0230	0.0273	0.0395
Nomascus IOZ 14517	-0.0805	-0.0128	0.0167	0.0380	0.0678	-0.0080
Nomascus IOZ 18071	-0.0508	0.0117	0.0014	0.0284	0.0313	-0.0427
Nomascus KIZ 000170	-0.0609	-0.0442	-0.0068	0.0189	0.0196	0.0025
Nomascus KIZ 000391	0.0061	-0.0193	-0.0306	0.0097	0.0151	0.0002
Nomascus KIZ 003192	-0.0613	-0.0073	0.0062	-0.0133	0.0427	0.0153
Nomascus KIZ 009643	-0.0628	-0.0078	0.0021	-0.0014	0.0401	-0.0231
Nomascus KIZ 0106167	-0.0653	-0.0654	-0.0206	-0.0100	0.0113	-0.0271
Nomascus KIZ 012168	0.0067	-0.0373	-0.0471	-0.0088	0.0343	-0.0198
Nomascus MCZ 38115	-0.0369	0.0331	0.0504	-0.0072	-0.0226	0.0147
Nomascus MCZ 38116	-0.0556	-0.0147	-0.0183	0.0172	-0.0007	0.0115
Nomascus SYS1	-0.1167	0.1150	-0.0007	0.0547	0.0656	0.0281
Nomascus USNM 240490	-0.0227	0.0417	-0.0327	-0.0337	-0.0257	0.0091
Nomascus USNM 464992	-0.0679	-0.0538	-0.0554	0.0391	-0.0090	-0.0020
Symphalangus AMNH 102195	-0.0076	0.0733	-0.1379	-0.0236	-0.0429	0.0396
Symphalangus AMNH 102196	-0.0178	0.0042	-0.0440	0.0252	-0.0010	0.0487
Symphalangus AMNH 102197	0.0168	0.0235	-0.0840	0.0564	-0.0210	0.0233
Symphalangus AMNH 102720	0.0543	0.0253	-0.0146	-0.0270	0.0009	0.0300
Symphalangus AMNH 102724	0.0341	0.0304	-0.0204	-0.0207	-0.0343	0.0122
Symphalangus AMNH 102725	0.0173	0.0318	-0.0370	0.0384	-0.0521	0.0360
Symphalangus MCZ 27831	-0.0349	0.0165	-0.0357	0.0100	-0.0290	0.0197
Symphalangus USNM 395514	-0.0239	-0.0540	-0.0140	0.0391	-0.0233	0.0116
Symphalangus USNM 519573	0.0502	0.0261	-0.0448	-0.0127	-0.0544	0.0433
Yuanmoupithecus YML 112-1x	0.0340	-0.0039	-0.0220	0.0318	0.0185	0.0744
Anapithecus RUD 98	0.0645	-0.0861	0.0708	0.1061	-0.0202	-0.0015
Egarapithecus IPS 2943	0.0890	-0.0600	0.0203	-0.0116	-0.0760	0.0739
Epipliopithecus NM (Basel) Ind I	0.1105	-0.0010	0.0120	0.0229	0.0284	0.0057
Epipliopithecus NM (Basel) Ind III	0.1771	-0.0160	0.0321	-0.0040	0.0031	0.0148
Laccopithecus PA 880	0.0984	-0.0513	0.0335	0.0667	0.0527	0.0007

Platodontopithecus PA 870	0.0399	0.0793	0.0603	0.0400	0.0148	0.0134
Pliopithecus Goriach (H30)	0.0745	0.0068	0.0515	0.0777	0.0241	0.0404
Pliopithecus La Grive	0.0583	-0.0625	0.0611	-0.0189	0.0504	0.0340
Pliopithecus MNHN Sansan (H2)	0.1549	-0.0398	0.0885	-0.0302	0.0256	-0.0057
Ekembo KNM-RU 1674	0.0562	0.0264	0.0565	0.0322	-0.0095	0.0046
Ekembo KNM-RU 1947	0.0958	0.0027	-0.0089	-0.0235	0.0406	0.0283
Ekembo KNM-RU 7290	0.1512	-0.0249	0.0071	-0.0237	0.0426	0.0357
Kalepithecus KNM-SO 378	0.0645	0.0309	0.0500	0.0396	0.0211	0.0231
Otavipithecus BER I	0.0475	-0.0527	0.0408	-0.0030	0.0066	0.0188
Proconsul KNM-SO 396	0.0813	-0.0366	0.0275	0.0366	-0.0171	-0.0125
Rangwapithecus KNM-SO 463	0.1469	-0.0174	0.0501	0.0109	-0.0243	0.0646
Aegyptopithecus DPC 1027	0.0801	0.0161	0.0183	0.0615	0.0678	-0.0425
Aegyptopithecus DPC 2806	0.0700	0.0047	-0.0137	0.0749	-0.0171	-0.0315
Aegyptopithecus YPM 21032	0.0749	0.0550	0.0843	0.0685	-0.0396	-0.0396
Aegytopithecus DPC 1028	0.0514	0.0724	0.0036	0.0769	0.0261	-0.0182
Propliopithecus DPC 1069	0.0118	0.0440	-0.0430	0.0684	-0.0008	-0.0604
Propliopithecus DPC 5392	0.0171	0.0765	0.0257	0.1068	0.0243	-0.0756
Gorilla MCZ 17684	0.0546	0.0050	-0.0175	-0.0038	-0.0450	-0.0448
Gorilla MCZ 38326	0.0500	-0.0127	-0.0634	-0.0249	-0.0461	-0.0065
Gorilla MCZ 46325	0.0246	-0.0336	-0.0673	-0.0273	-0.0033	0.0307
Gorilla ZMB 30941	0.0314	0.0395	-0.0422	0.0187	0.0136	-0.0489
Gorilla ZMB 31626	0.0657	-0.0037	0.0108	-0.0542	-0.0184	-0.0389
Gorilla AMNH 115609	0.0350	0.0407	-0.0280	0.0122	-0.0236	-0.0133
Gorilla AMNH 167325	0.0688	0.0086	-0.0672	0.0364	-0.0036	0.0574
Gorilla AMNH 167326	0.0421	-0.0679	-0.0658	0.0113	0.0083	-0.0143
Gorilla AMNH 167327	0.0150	0.0419	-0.0343	0.0205	0.0258	-0.0282
Gorilla AMNH 167328	0.0177	-0.0105	-0.0202	0.0128	-0.0394	-0.0395
Gorilla AMNH 167332	0.0296	0.0246	-0.0357	-0.0161	-0.0383	0.0044
Gorilla AMNH 167337	0.0209	-0.0018	-0.0797	-0.0020	-0.0114	0.0218
Gorilla AMNH 167338	0.0285	-0.0107	-0.0461	0.0066	0.0124	-0.0089
Gorilla AMNH 167339	0.0422	-0.0900	-0.0442	0.0296	0.0222	0.0196
Gorilla AMNH 167672	0.0503	0.0031	-0.0380	0.0104	0.0163	-0.0103
Gorilla AMNH 170363	-0.0395	0.0131	-0.0324	-0.0463	0.0601	0.0026
Gorilla AMNH 200503	0.0517	0.0100	-0.0159	0.0104	-0.0375	0.0216
Gorilla AMNH 200506	0.0524	0.0407	-0.0402	-0.0128	-0.0272	-0.0256
Gorilla AMNH 201472	0.0072	-0.0079	-0.0636	0.0301	0.0098	-0.0603
Gorilla AMNH 214104	0.0567	0.0144	-0.0374	-0.0163	-0.0554	-0.0692
Gorilla AMNH 214107	0.0405	0.0524	-0.0038	0.0124	-0.0008	0.0006
Gorilla AMNH 214111	0.0674	0.0007	0.0440	-0.0307	-0.0047	0.0048
Gorilla AMNH 214113	0.0182	-0.0184	-0.0452	-0.0446	-0.0022	-0.0376
Gorilla AMNH 235603	0.0948	0.0277	-0.0267	0.0160	0.0366	-0.0193
Gorilla AMNH 54089	0.0498	0.0123	0.0268	-0.0229	-0.0004	-0.0306
Gorilla AMNH 54090	0.0203	-0.0486	-0.0133	-0.0182	-0.0022	-0.0348
Gorilla AMNH 90194	0.0567	-0.0703	-0.0106	-0.0659	0.0128	0.0018
Gorilla ZMB 31277	0.0897	-0.0179	-0.0655	-0.0217	-0.0097	-0.0267
Gorilla ZMB 31435	0.0542	-0.0149	-0.0205	-0.0230	-0.0383	-0.0696
Gorilla ZMB 83546	-0.0376	0.0161	-0.0294	0.0070	0.0136	-0.0370
Gorilla ZMB 83561	0.0155	0.0203	-0.0264	0.0133	0.0205	-0.0097

Pan AMNH 51376	0.0163	0.0736	0.0308	-0.0558	-0.0177	-0.0126
Pan MCZ 9493	-0.0027	0.0038	0.0442	-0.0408	-0.0268	-0.0099
Pan MCZ 6244	0.0216	0.0275	0.0171	0.0575	0.0109	-0.0139
Pan AMNH 119227	-0.0157	0.0470	0.0269	-0.0336	-0.0094	0.0243
Pan AMNH 167342	-0.0411	-0.0011	0.0093	-0.0426	-0.0173	-0.0109
Pan AMNH 167346	-0.0721	0.0491	0.0802	-0.0521	0.0404	-0.0233
Pan AMNH 183130	0.0184	0.0002	0.0251	-0.0267	0.0559	-0.0324
Pan AMNH 51204	-0.0549	0.0210	0.0241	-0.0120	-0.0771	0.0182
Pan AMNH 51376	0.0056	0.0796	0.0286	-0.0478	-0.0134	-0.0113
Pan AMNH 51377	-0.0071	0.0092	0.0385	-0.0209	-0.0179	-0.0564
Pan AMNH 51394	-0.0921	0.0176	0.0449	-0.0287	0.0104	-0.0248
Pan AMNH 81854	-0.0296	0.0344	0.0513	-0.0505	-0.0404	-0.0121
Pan AMNH 89353	-0.0048	-0.0027	0.0540	-0.0722	-0.0158	-0.0187
Pan AMNH 89406	-0.0065	0.0255	0.0503	-0.0475	-0.0201	-0.0327
Pan AMNH 90293	-0.0595	0.0192	0.0640	-0.0033	-0.0094	0.0112
Pongo MCZ 37518	0.0191	-0.0115	-0.0375	-0.0118	0.0534	0.0370
Pongo MCZ 37519	0.0227	0.0469	-0.0155	-0.0154	0.0650	0.0023
Pongo AMNH 19548	0.0281	-0.0379	0.0302	0.0139	0.0124	-0.0179
Pongo AMNH 28253	0.0413	0.0518	-0.0101	0.0078	0.0006	-0.0407
Pongo USNM 142169	0.0301	0.0404	0.0039	0.0211	0.0031	-0.0139
Pongo USNM 142191	0.1151	0.0578	0.0030	-0.0421	0.0106	0.0245
Pongo USNM 142195	0.0152	0.0197	0.0485	0.0205	-0.0556	0.0056
Pongo ZMB 6954	0.0809	-0.0072	-0.0234	-0.0227	-0.0042	0.0228
Pongo ZMB 6957	0.0348	0.0526	0.0211	-0.0034	-0.0475	0.0125

Table S3. Results of M_3 PCA including PC scores by specimen for the first 6 PCs.

Specimen number	Family	Genus and species	Fossil/Extant
H-GSP 8114-609	Incertae sedis	*"Dionysopithecus" sp. indet.*	Fossil
DPC 1112	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
YPM 21032	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
DPC 1028	Propliopithecidae	*Aegyptopithecus zeuxis*	Fossil
DPC 1069	Propliopithecidae	*Propliopithecus chirobates*	Fossil
DPC 1106	Propliopithecidae	*Propliopithecus chirobates*	Fossil
DPC 1029	Propliopithecidae	*Propliopithecus sp. indet.*	Fossil
KNM-RU 2015	Dendropithecidae	*Dendropithecus macinnesi*	Fossil
KNM-RU 1850	Dendropithecidae	*Dendropithecus macinnesi*	Fossil
KNM-RU 1727	Dendropithecidae	*Dendropithecus macinnesi*	Fossil
KNM-RU 900	Dendropithecidae	*Dendropithecus macinnesi*	Fossil
KNM-ZP 01669	Dendropithecidae	*Dendropithecus sp. indet.*	Fossil
KNM-KO 8	Dendropithecidae	*Limnopithecus legetet*	Fossil
KNM-ZP 01675	Dendropithecidae	*Limnopithecus sp. indet.*	Fossil
KNM-LG 920	Dendropithecidae	*Micropithecus clarki*	Fossil
KNM-ZP 10670	Dendropithecidae	*Micropithecus sp. indet.*	Fossil
KNM-WK 16960	Dendropithecidae	*Simiolus enjiessi*	Fossil
KNM-RU 7290	Proconsulidae	*Ekembo heseloni*	Fossil
KNM-RU 1678	Proconsulidae	*Ekembo heseloni*	Fossil
KNM-RU 2036	Proconsulidae	*Ekembo heseloni*	Fossil
KNM-MB 20573	Proconsulidae	*Equatorius*	Fossil
KNM-NC 9740	Proconsulidae	*Equatorius africanus*	Fossil
KNM-TH 28860	Proconsulidae	*Equatorius africanus*	Fossil
KNM-SO 378	Proconsulidae	*Kalepithecus*	Fossil
BER I	Proconsulidae	*Otavipithecus*	Fossil
KNM-RU 1706	Proconsulidae	*Proconsul africanus*	Fossil
KNM-SO 396	Proconsulidae	*Proconsul major*	Fossil
KNM-SO 464	Proconsulidae	*Rangwapithecus gordoni*	Fossil
TF 2451	Pliopithecidae	*"Dionysopithecus" orientialis*	Fossil
PA 1054	Pliopithecidae	*Dionysopithecus shuangouensis*	Fossil
PA 1243	Pliopithecidae	*Dionysopithecus shuangouensis*	Fossil
PA 1251	Pliopithecidae	*Dionysopithecus shuangouensis*	Fossil
PA 1224	Pliopithecidae	*Platodontopithecus jianghuaiensis*	Fossil
PA 1225	Pliopithecidae	*Platodontopithecus jianghuaiensis*	Fossil
PA 1226	Pliopithecidae	*Platodontopithecus jianghuaiensis*	Fossil
Sa 999 (MNHN)	Pliopithecidae	*Plesiopithecus auscitanensis*	Fossil
IPS 41719	Pliopithecidae	*Pliopithecus canmatensis*	Fossil
Goriach (H24)	Pliopithecidae	*Pliopithecus platydon*	Fossil
Goriach (H30), Joanneum 3675	Pliopithecidae	*Pliopithecus platydon*	Fossil
Goriach (H32), Joanneum 2100	Pliopithecidae	*Pliopithecus platydon*	Fossil
AMNH 19400	Hylobatidae	*Hoolock sp. indet.*	Extant
AMNH 112689	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112691	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112699	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112700	Hylobatidae	*Hoolock hoolock*	Extant

AMNH 112703	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 83414	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 83424	Hylobatidae	*Hoolock hoolock*	Extant
AMNH 112669	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112671	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112677	Hylobatidae	*Hoolock leuconedys*	Extant
AMNH 112965	Hylobatidae	*Hoolock leuconedys*	Extant
KIZ 011796	Hylobatidae	*Hoolock leuconedys*	Extant
KIZ 011345	Hylobatidae	*Hoolock sp. indet.*	Extant
USNM 111990	Hylobatidae	*Hoolock sp. indet.*	Extant
KIZ 011338	Hylobatidae	*Hoolock tianxing*	Extant
MCZ 26474	Hylobatidae	*Hoolock tianxing*	Extant
AMNH 102161	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102162	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102200	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102473	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102474	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102775	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102776	Hylobatidae	*Hylobates agilis*	Extant
AMNH 102777	Hylobatidae	*Hylobates agilis*	Extant
AMNH 106679	Hylobatidae	*Hylobates agilis*	Extant
USNM 113177	Hylobatidae	*Hylobates agilis*	Extant
AMNH 103442	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 103443	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 103454	Hylobatidae	*Hylobates albibarbis*	Extant
AMNH 103353	Hylobatidae	*Hylobates klossiii*	Extant
AMNH 43063	Hylobatidae	*Hylobates lar*	Extant
AMNH 43064	Hylobatidae	*Hylobates lar*	Extant
AMNH 54662	Hylobatidae	*Hylobates lar*	Extant
AMNH 54966	Hylobatidae	*Hylobates lar*	Extant
KIZ 003147	Hylobatidae	*Hylobates lar*	Extant
USNM 83262	Hylobatidae	*Hylobates lar*	Extant
USNM 296922	Hylobatidae	*Hylobates lar*	Extant
AMNH 102026	Hylobatidae	*Hylobates moloch*	Extant
AMNH 106788	Hylobatidae	*Hylobates moloch*	Extant
AMNH 130172	Hylobatidae	*Hylobates moloch*	Extant
AMNH 200853	Hylobatidae	*Hylobates moloch*	Extant
ZMB 7835	Hylobatidae	*Hylobates muelleri*	Extant
ZMB 7804	Hylobatidae	*Hylobates muelleri*	Extant
USNM 198268	Hylobatidae	*Hylobates muelleri*	Extant
USNM 198271	Hylobatidae	*Hylobates muelleri*	Extant
USNM 198272	Hylobatidae	*Hylobates muelleri*	Extant
USNM 198843	Hylobatidae	*Hylobates muelleri*	Extant
UNSM 201556	Hylobatidae	*Hylobates pileatus*	Extant
USNM 253405	Hylobatidae	*Hylobates pileatus*	Extant
ZMB 7819	Hylobatidae	*Hylobates sp. indet.*	Extant
AMNH 100048	Hylobatidae	*Hylobates sp. indet.*	Extant
MCZ 38114	Hylobatidae	*Nomascus concolor*	Extant

MCZ 38115	Hylobatidae	*Nomascus concolor*	Extant
IOZ 17927	Hylobatidae	*Nomascus concolor*	Extant
IOZ 17929	Hylobatidae	*Nomascus concolor*	Extant
KIZ 000170	Hylobatidae	*Nomascus concolor*	Extant
KIZ 000391	Hylobatidae	*Nomascus concolor*	Extant
KIZ 010122	Hylobatidae	*Nomascus concolor*	Extant
KIZ 010122-LS980628	Hylobatidae	*Nomascus concolor*	Extant
KIZ 024165	Hylobatidae	*Nomascus concolor*	Extant
USNM 320787	Hylobatidae	*Nomascus concolor*	Extant
USNM 464992	Hylobatidae	*Nomascus concolor*	Extant
USNM 257996	Hylobatidae	*Nomascus gabriellae*	Extant
IOZ 14524	Hylobatidae	*Nomascus leucogenys*	Extant
IOZ 14525	Hylobatidae	*Nomascus leucogenys*	Extant
KIZ 000173	Hylobatidae	*Nomascus leucogenys*	Extant
KIZ 000175	Hylobatidae	*Nomascus leucogenys*	Extant
USNM 296921	Hylobatidae	*Nomascus leucogenys*	Extant
ZMB 38586	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102189	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102193	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 102722	Hylobatidae	*Symphalangus syndactylus*	Extant
MCZ 36031	Hylobatidae	*Symphalangus syndactylus*	Extant
AMNH 115609	Hominidae	*Gorilla gorilla*	Extant
AMNH 167326	Hominidae	*Gorilla gorilla*	Extant
AMNH 167328	Hominidae	*Gorilla gorilla*	Extant
AMNH 167333	Hominidae	*Gorilla gorilla*	Extant
AMNH 167334	Hominidae	*Gorilla gorilla*	Extant
AMNH 167337	Hominidae	*Gorilla gorilla*	Extant
AMNH 167338	Hominidae	*Gorilla gorilla*	Extant
AMNH 167339	Hominidae	*Gorilla gorilla*	Extant
AMNH 200506	Hominidae	*Gorilla gorilla*	Extant
AMNH 235603	Hominidae	*Gorilla gorilla*	Extant
AMNH 54089	Hominidae	*Gorilla gorilla*	Extant
AMNH 54090	Hominidae	*Gorilla gorilla*	Extant
AMNH 54091	Hominidae	*Gorilla gorilla*	Extant
AMNH 90194	Hominidae	*Gorilla gorilla*	Extant
ZMB 31435	Hominidae	*Gorilla gorilla*	Extant
ZMB 83546	Hominidae	*Gorilla gorilla*	Extant
AMNH 119227	Hominidae	*Pan troglodytes*	Extant
AMNH 167342	Hominidae	*Pan troglodytes*	Extant
AMNH 167345	Hominidae	*Pan troglodytes*	Extant
AMNH 183130	Hominidae	*Pan troglodytes*	Extant
AMNH 201239	Hominidae	*Pan troglodytes*	Extant
AMNH 35199	Hominidae	*Pan troglodytes*	Extant
AMNH 3550	Hominidae	*Pan troglodytes*	Extant
AMNH 5094	Hominidae	*Pan troglodytes*	Extant
AMNH 51204	Hominidae	*Pan troglodytes*	Extant
AMNH 51208	Hominidae	*Pan troglodytes*	Extant
AMNH 51211	Hominidae	*Pan troglodytes*	Extant

AMNH 51377	Hominidae	*Pan troglodytes*	Extant
AMNH 51382	Hominidae	*Pan troglodytes*	Extant
AMNH 51386	Hominidae	*Pan troglodytes*	Extant
AMNH 51392	Hominidae	*Pan troglodytes*	Extant
AMNH 89352	Hominidae	*Pan troglodytes*	Extant
AMNH 89353	Hominidae	*Pan troglodytes*	Extant
AMNH 89406	Hominidae	*Pan troglodytes*	Extant
AMNH 89407	Hominidae	*Pan troglodytes*	Extant
AMNH 90191	Hominidae	*Pan troglodytes*	Extant
AMNH 90293	Hominidae	*Pan troglodytes*	Extant
AMNH 19548	Hominidae	*Pongo pygmaeus*	Extant
AMNH 18010	Hominidae	*Pongo pygmaeus*	Extant
AMNH 19180	Hominidae	*Pongo pygmaeus*	Extant
AMNH 202511	Hominidae	*Pongo pygmaeus*	Extant
AMNH 28253	Hominidae	*Pongo pygmaeus*	Extant
AMNH 35549	Hominidae	*Pongo pygmaeus*	Extant
AMNH 80008	Hominidae	*Pongo pygmaeus*	Extant
USNM 142170	Hominidae	*Pongo pygmaeus*	Extant
USNM 142191	Hominidae	*Pongo pygmaeus*	Extant
USNM 142195	Hominidae	*Pongo pygmaeus*	Extant
USNM 142196	Hominidae	*Pongo pygmaeus*	Extant
USNM 142200	Hominidae	*Pongo pygmaeus*	Extant
USNM 142169	Hominidae	*Pongo pygmaeus*	Extant
USNM 145319	Hominidae	*Pongo pygmaeus*	Extant
ZMB 67173	Hominidae	*Pongo pygmaeus*	Extant
ZMB 6954	Hominidae	*Pongo pygmaeus*	Extant
ZMB 6957	Hominidae	*Pongo pygmaeus*	Extant

Table S4. List of catarrhine M_1 specimens included in this study.

M_3 Analysis			
PC	**Eigenvalue**	**% variance**	**SUM Variance**
1	0.0038	25.08%	25.08%
2	0.0017	10.84%	35.91%
3	0.0016	10.32%	46.23%
4	0.0015	9.60%	55.82%
5	0.0009	5.76%	61.59%
6	0.0008	5.08%	66.66%
7	0.0006	3.96%	70.62%
8	0.0006	3.64%	74.26%
9	0.0005	3.22%	77.47%
10	0.0004	2.87%	80.34%
11	0.0004	2.59%	82.92%
12	0.0003	2.27%	85.19%
13	0.0003	2.19%	87.39%
14	0.0003	2.11%	89.50%
15	0.0003	1.71%	91.21%
16	0.0002	1.45%	92.66%
17	0.0002	1.40%	94.05%
18	0.0002	1.25%	95.30%
19	0.0002	1.15%	96.45%
20	0.0002	0.99%	97.44%
21	0.0001	0.84%	98.28%
22	0.0001	0.80%	99.08%
23	0.0001	0.62%	99.70%
24	0.0000	0.31%	100.00%

M_1 Analysis			
PC	**Eigenvalue**	**% variance**	**SUM Variance**
1	0.0021	21.19%	21.19%
2	0.0014	14.38%	35.56%
3	0.0008	8.62%	44.18%
4	0.0007	7.58%	51.75%
5	0.0006	6.06%	57.81%
6	0.0005	5.17%	62.98%

7	0.0004	4.35%	67.33%
8	0.0004	3.96%	71.28%
9	0.0004	3.81%	75.09%
10	0.0003	3.37%	78.46%
11	0.0003	3.07%	81.54%
12	0.0003	2.55%	84.08%
13	0.0002	2.38%	86.47%
14	0.0002	1.91%	88.37%
15	0.0002	1.85%	90.22%
16	0.0002	1.60%	91.82%
17	0.0001	1.40%	93.22%
18	0.0001	1.33%	94.55%
19	0.0001	1.27%	95.82%
20	0.0001	1.12%	96.93%
21	0.0001	1.01%	97.94%
22	0.0001	0.94%	98.88%
23	0.0001	0.65%	99.52%
24	0.0000	0.48%	100.00%

Table S5. Principal Components loadings and Eigenvalues for 14L 2D GM analyses of M_3 and M_1 specimens.

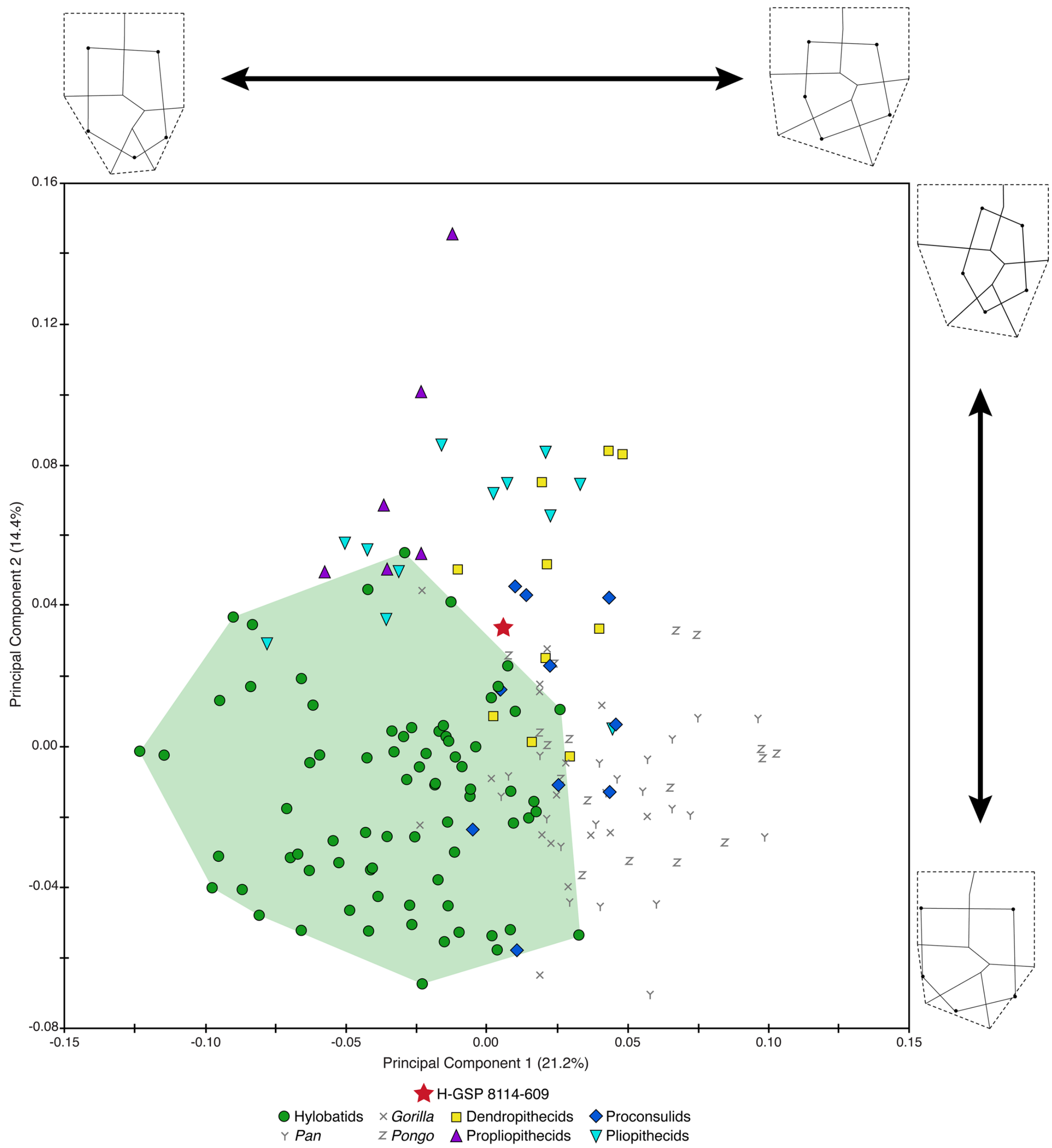

Figure S4. PCA resulting from 2D morphometric analysis of overall M_1 crown shape characterized by 14 homologous landmarks (see wireframes; cusps=black circles). H-GSP 8114-609 *Dionysopithecus* sp. plots within the area of overlap between multiple stem and crown catarrhine/hominoid families, but outside the distribution of hylobatid specimens (=green polygon).

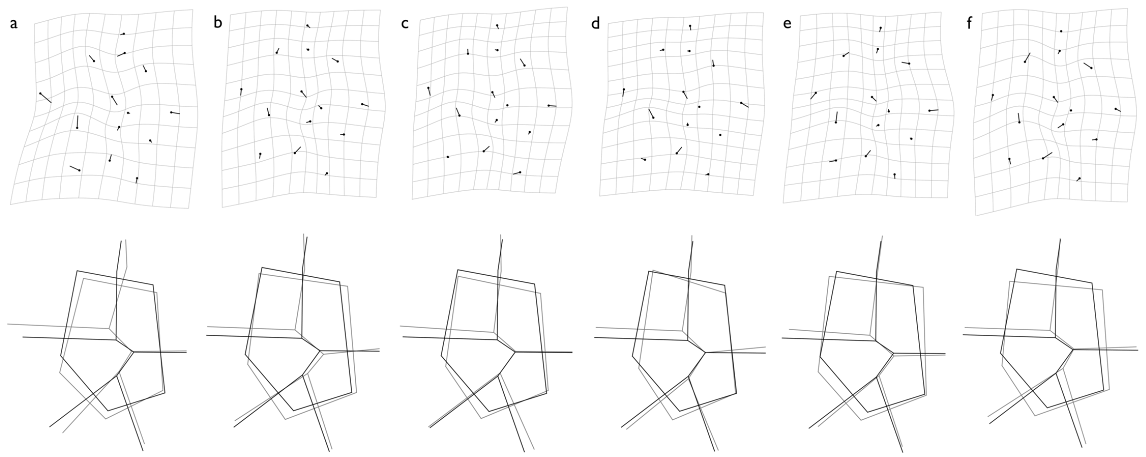

Figure S5. Deformation grids (top row) and wireframes (bottom row) based on 14 homologous landmarks (14L) comparing H-GSP 8114-609 ("*Dionysopithecus*" sp. indet.) with: **a,** propliopithecids; **b,** proconsulids; **c,** dendropithecids; **d,** pliopithecids; **e,** hylobatids; and **f,** hominids. Deformation grids show shape deformations from the M_1 mean shape (reference configuration) of each of the five major taxonomic groups analyzed to the M_1 shape of H-GSP 8114-609 (target configuration), with vectors indicating the direction of change from the reference to the target shape coordinate locations. Wireframes compare the M_1 configuration of H-GSP 8114-609 (in black) with mean shapes of extant and extinct catarrhine taxa (in gray). Procrustes distances for a (0.15), b (0.10), c (0.10), d (0.10), and e (0.12); and f (0.12); *p*-values non-significant.

Specimen	PC1	PC2	PC3	PC4	PC5	PC6
Dendropithecus KNM-RU 1727	0.0214	0.0518	0.0063	0.0386	0.0073	0.0070
Dendropithecus KNM-RU 1850	0.0482	0.0831	0.0276	0.0364	0.0180	0.0147
Dendropithecus KNM-RU 2015	-0.0103	0.0503	0.0376	-0.0043	-0.0183	-0.0103
Dendropithecus KNM-RU 900	0.0196	0.0751	-0.0231	0.0002	0.0189	-0.0147
Dendropithecus KNM-ZP 01669	0.0295	-0.0028	-0.0093	-0.0380	0.0398	-0.0165
Limnopithecus KNM-KO 8	0.0400	0.0335	-0.0131	0.0261	0.0027	0.0161
Limnopithecus KNM-ZP 01675	0.0433	0.0840	0.0267	0.0326	0.0337	-0.0005
Micropithecus KNM-LG 920	0.0023	0.0087	0.0203	-0.0008	0.0059	-0.0222
Micropithecus KNM-ZP 01670	0.0160	0.0013	0.0195	0.0232	0.0000	-0.0449
Simiolus KNM-WK 16960	0.0209	0.0252	0.0495	0.0355	-0.0036	-0.0301
"*Dionysopithecus*" H-GSP 8114-609	0.0059	0.0340	0.0226	-0.0303	-0.0134	0.0074
Hoolock AMNH 112669	-0.0137	-0.0452	0.0538	-0.0105	-0.0172	0.0049
Hoolock AMNH 112671	-0.0425	-0.0032	-0.0624	-0.0358	-0.0163	0.0215
Hoolock AMNH 112677	-0.0295	0.0029	-0.0304	-0.0304	-0.0009	0.0167
Hoolock AMNH 112689	0.0260	0.0106	-0.0505	-0.0176	0.0298	0.0261
Hoolock AMNH 112691	0.0016	0.0139	-0.0303	-0.0304	-0.0235	0.0388
Hoolock AMNH 112699	-0.0144	0.0029	-0.0066	-0.0189	0.0308	0.0274
Hoolock AMNH 112700	0.0149	-0.0202	-0.0370	-0.0358	0.0298	0.0359
Hoolock AMNH 112703	-0.0154	0.0060	-0.0398	-0.0012	-0.0168	-0.0028
Hoolock AMNH 112965	-0.0173	-0.0378	0.0148	-0.0232	-0.0312	0.0149
Hoolock AMNH 19400	-0.0127	0.0411	-0.0136	-0.0146	-0.0071	-0.0014
Hoolock AMNH 83414	0.0041	0.0171	-0.0551	-0.0333	0.0478	0.0030
Hoolock AMNH 83424	-0.0088	-0.0057	-0.0134	-0.0235	0.0282	0.0029
Hoolock KIZ 011338	-0.0617	0.0118	-0.0174	-0.0126	0.0082	0.0311
Hoolock KIZ 011345	-0.0710	-0.0176	-0.0069	-0.0204	-0.0034	0.0365
Hoolock KIZ 011796	-0.0658	0.0193	-0.0390	0.0343	-0.0349	0.0057
Hoolock MCZ 26474	-0.0291	0.0551	-0.0085	-0.0141	0.0417	0.0090
Hoolock USNM 111990	-0.0659	-0.0522	-0.0077	-0.0051	-0.0095	-0.0061
Hylobates AMNH 100048	-0.0671	-0.0305	0.0992	-0.0059	0.0292	-0.0098
Hylobates AMNH 102026	-0.0135	0.0016	0.0066	0.0063	-0.0221	0.0111
Hylobates AMNH 102161	0.0176	-0.0185	-0.0176	-0.0005	0.0195	0.0089
Hylobates AMNH 102162	-0.0114	-0.0300	-0.0316	0.0016	-0.0024	0.0414
Hylobates AMNH 102200	-0.0697	-0.0315	0.0092	0.0251	0.0259	0.0148
Hylobates AMNH 102473	-0.0150	-0.0554	-0.0519	0.0072	-0.0372	-0.0042
Hylobates AMNH 102474	-0.0975	-0.0401	0.0172	-0.0162	-0.0177	-0.0111
Hylobates AMNH 102775	-0.1146	-0.0024	-0.0480	-0.0379	-0.0649	0.0256
Hylobates AMNH 102776	-0.0139	-0.0214	0.0031	-0.0197	0.0069	0.0139
Hylobates AMNH 102777	-0.0229	-0.0674	0.0530	-0.0119	-0.0066	0.0089
Hylobates AMNH 103353	-0.0239	-0.0057	-0.0035	-0.0168	0.0138	0.0021
Hylobates AMNH 103442	-0.0413	-0.0350	-0.0416	-0.0098	-0.0441	0.0125
Hylobates AMNH 103443	-0.1232	-0.0013	0.0038	-0.0028	-0.0047	0.0243
Hylobates AMNH 103454	0.0085	-0.0127	-0.0364	0.0316	0.0186	-0.0012
Hylobates AMNH 106679	0.0084	-0.0520	-0.0077	-0.0545	0.0149	-0.0073
Hylobates AMNH 106788	0.0168	-0.0156	-0.0069	-0.0033	0.0101	-0.0330
Hylobates AMNH 130172	-0.0284	-0.0093	-0.0112	-0.0168	-0.0043	0.0087
Hylobates AMNH 200853	-0.0060	-0.0141	-0.0096	-0.0105	-0.0166	-0.0156
Hylobates AMNH 43063	-0.0948	0.0131	-0.0599	0.0010	0.0336	-0.0136

Hylobates AMNH 43064	-0.0900	0.0368	-0.0851	0.0003	0.0219	-0.0378
Hylobates AMNH 54662	-0.0256	-0.0256	-0.0136	-0.0243	0.0329	-0.0293
Hylobates AMNH 54966	-0.0182	-0.0105	-0.0135	-0.0077	-0.0031	0.0151
Hylobates KIZ 003147	-0.0832	0.0347	-0.0355	-0.0625	0.0115	-0.0158
Hylobates USNM 083262	-0.0267	0.0054	-0.0232	0.0351	-0.0375	-0.0143
Hylobates USNM 113177	-0.0266	-0.0505	-0.0441	0.0058	-0.0280	0.0044
Hylobates USNM 198268	0.0037	-0.0577	0.0497	-0.0005	-0.0320	-0.0215
Hylobates USNM 198271	-0.0098	-0.0527	0.0462	0.0009	0.0274	-0.0094
Hylobates USNM 198272	-0.0630	-0.0352	0.0028	0.0169	-0.0327	0.0420
Hylobates USNM 198843	-0.0112	-0.0029	-0.0296	-0.0039	0.0193	-0.0112
Hylobates USNM 201556	-0.0329	-0.0015	0.0532	0.0174	0.0285	-0.0089
Hylobates USNM 253405	-0.0838	0.0171	0.0266	0.0265	0.0074	0.0172
Hylobates USNM 296922	-0.0487	-0.0465	-0.0260	0.0444	0.0215	-0.0577
Hylobates ZMB 7804	0.0327	-0.0535	0.0100	0.0112	0.0314	-0.0138
Hylobates ZMB 7819	-0.0420	-0.0524	-0.0007	0.0175	-0.0203	0.0168
Hylobates ZMB 7835	-0.0868	-0.0406	-0.0203	-0.0067	0.0213	-0.0458
Nomascus IOZ 14524	-0.0169	0.0044	0.0247	-0.0376	-0.0068	0.0255
Nomascus IOZ 14525	-0.0058	-0.0121	0.0438	-0.0194	0.0478	0.0029
Nomascus IOZ 17927	-0.0430	-0.0244	0.0661	0.0070	-0.0398	0.0062
Nomascus IOZ 17929	-0.0525	-0.0329	0.0538	0.0369	-0.0181	-0.0183
Nomascus KIZ 000170	-0.0274	-0.0450	0.0428	0.0107	-0.0264	0.0222
Nomascus KIZ 000173	-0.0215	-0.0019	0.0137	-0.0036	-0.0071	0.0423
Nomascus KIZ 000175	-0.0184	-0.0108	0.0240	-0.0314	-0.0093	0.0187
Nomascus KIZ 000391	-0.0546	-0.0267	-0.0043	0.0174	-0.0071	0.0036
Nomascus KIZ 010122	-0.0422	0.0447	-0.0149	0.0180	0.0406	0.0276
Nomascus KIZ 010122-LS980628	-0.0593	-0.0024	-0.0131	0.0213	0.0342	-0.0058
Nomascus KIZ 024165	-0.0406	-0.0345	0.0027	-0.0158	-0.0072	0.0143
Nomascus MCZ 38114	0.0075	0.0230	0.0214	-0.0557	0.0310	0.0004
Nomascus MCZ 38115	0.0095	-0.0217	0.0111	-0.0335	-0.0106	-0.0110
Nomascus USNM 257996	-0.0354	-0.0255	-0.0188	-0.0054	0.0255	-0.0063
Nomascus USNM 296921	-0.0808	-0.0479	0.0364	0.0167	-0.0059	0.0063
Nomascus USNM 320787	-0.0952	-0.0311	-0.0012	0.0269	-0.0134	-0.0056
Nomascus USNM 464992	-0.0628	-0.0046	0.0257	-0.0028	0.0240	0.0210
Symphalangus AMNH 102189	0.0101	0.0100	0.0115	-0.0113	0.0426	-0.0016
Symphalangus AMNH 102193	0.0019	-0.0537	0.0263	0.0315	0.0431	0.0246
Symphalangus AMNH 102722	-0.0337	0.0044	-0.0082	-0.0277	0.0376	-0.0222
Symphalangus MCZ 36031	-0.0039	0.0000	0.0037	0.0072	0.0809	-0.0113
Symphalangus ZMB 38586	-0.0386	-0.0425	0.0505	0.0217	0.0080	0.0070
Dionysopithecus PA 1054	-0.0504	0.0579	0.0491	-0.0395	-0.0128	0.0039
Dionysopithecus PA 1243	0.0024	0.0720	0.0192	-0.0190	0.0383	0.0051
Dionysopithecus PA 1251	0.0073	0.0749	-0.0020	-0.0619	0.0104	-0.0184
Dionysopithecus TF 2451	0.0447	0.0051	0.0107	0.0133	0.0210	-0.0300
Platodontopithecus PA 1224	0.0332	0.0746	0.0037	-0.0360	-0.0030	0.0105
Platodontopithecus PA 1225	0.0226	0.0657	0.0431	-0.0441	-0.0025	0.0382
Platodontopithecus PA 1226	0.0209	0.0837	0.0164	-0.0553	-0.0151	0.0092
Plesiopithecus MNHN Sa 999	-0.0780	0.0293	0.0236	-0.0069	0.0070	-0.0200
Pliopithecus Goriach (H24)	-0.0160	0.0858	0.0090	0.0102	-0.0414	0.0179
Pliopithecus Goriach (H30)	-0.0312	0.0499	0.0242	-0.0159	-0.0094	-0.0322
Pliopithecus Goriach (H32)	-0.0357	0.0363	0.0168	-0.0304	-0.0473	-0.0906

Pliopithecus IPS 41719	-0.0424	0.0560	0.0516	0.0031	-0.0081	-0.0045
Ekembo KNM-RU 1678	0.0225	0.0230	0.0268	-0.0231	-0.0111	0.0108
Ekembo KNM-RU 7290	0.0047	0.0162	0.0008	-0.0291	-0.0208	0.0003
Equatorius KNM-MB 20573	0.0107	-0.0578	-0.0277	0.0067	-0.0316	-0.0039
Equatorius KNM-NC 9740	-0.0050	-0.0235	0.0470	0.0023	-0.0210	-0.0387
Equatorius KNM-TH 28860	0.0101	0.0455	0.0340	0.0005	-0.0162	-0.0186
Kalepithecus KNM-SO 378	0.0435	0.0423	0.0326	-0.0209	0.0047	-0.0094
Otavipithecus BER I	0.0459	0.0063	0.0314	-0.0244	-0.0056	0.0112
Proconsul KNM-RU 1706	0.0437	-0.0129	0.0296	0.0162	-0.0239	-0.0135
Proconsul KNM-RU 2036	0.0255	-0.0109	0.0134	0.0022	0.0255	-0.0028
Proconsul KNM-SO 396	0.0140	0.0430	-0.0171	0.0008	-0.0175	0.0004
Rangwapithecus KNM-SO 464	0.0049	0.0162	0.0219	0.0164	0.0379	0.0108
Aegyptopithecus YPM 21032	-0.0233	0.0547	-0.0461	0.0571	-0.0004	-0.0313
Aegytopithecus DPC 1028	-0.0233	0.1007	-0.0001	0.0554	-0.0408	-0.0051
Aegytopithecus DPC 1112	-0.0366	0.0685	0.0063	0.0285	-0.0273	0.0013
Propliopithecus DPC 1029	-0.0122	0.1455	-0.0531	0.0573	-0.0403	-0.0175
Propliopithecus DPC 1069	-0.0575	0.0495	-0.0318	0.0239	-0.0279	-0.0102
Propliopithecus DPC 1106	-0.0354	0.0503	-0.0095	-0.0166	-0.0117	-0.0288
Gorilla AMNH 115609	0.0409	0.0117	0.0272	0.0392	0.0110	-0.0184
Gorilla AMNH 167326	0.0228	-0.0275	-0.0097	0.0372	0.0279	0.0197
Gorilla AMNH 167328	0.0289	-0.0398	-0.0052	0.0395	0.0374	0.0164
Gorilla AMNH 167333	0.0570	-0.0198	-0.0048	-0.0145	0.0068	0.0123
Gorilla AMNH 167334	0.0189	-0.0649	-0.0081	0.0254	-0.0116	0.0005
Gorilla AMNH 167337	-0.0237	-0.0223	-0.0137	0.0154	0.0023	0.0072
Gorilla AMNH 167338	0.0370	-0.0252	-0.0093	0.0271	0.0099	0.0288
Gorilla AMNH 167339	0.0196	-0.0250	0.0164	0.0242	0.0088	0.0385
Gorilla AMNH 200506	0.0188	0.0156	-0.0131	-0.0069	0.0143	0.0383
Gorilla AMNH 235603	0.0189	0.0177	-0.0149	-0.0007	0.0086	0.0205
Gorilla AMNH 54089	0.0016	-0.0090	-0.0039	0.0130	-0.0092	-0.0135
Gorilla AMNH 54090	0.0281	-0.0046	0.0110	0.0296	-0.0112	0.0069
Gorilla AMNH 54091	0.0215	0.0278	0.0146	0.0424	-0.0086	0.0179
Gorilla AMNH 90194	0.0439	-0.0244	-0.0119	0.0299	0.0356	0.0122
Gorilla ZMB 31435	0.0248	-0.0137	-0.0178	0.0614	0.0257	0.0246
Gorilla ZMB 83546	-0.0230	0.0444	0.0026	0.0875	0.0454	0.0300
Pan AMNH 119227	0.0213	-0.0204	-0.0162	0.0337	-0.0069	-0.0133
Pan AMNH 167342	0.0051	-0.0141	-0.0278	0.0029	-0.0033	0.0012
Pan AMNH 167345	0.0077	-0.0083	-0.0056	-0.0284	0.0134	-0.0075
Pan AMNH 183130	0.0963	0.0080	-0.0057	0.0084	-0.0406	0.0384
Pan AMNH 201239	0.0987	-0.0256	-0.0470	0.0141	-0.0035	-0.0133
Pan AMNH 35199	0.0554	-0.0126	0.0247	-0.0391	0.0058	0.0061
Pan AMNH 3550	0.0603	-0.0446	-0.0304	0.0558	0.0042	0.0068
Pan AMNH 5094	0.0580	-0.0704	-0.0391	0.0229	-0.0244	-0.0388
Pan AMNH 51204	0.0189	-0.0025	-0.0304	0.0022	-0.0303	0.0285
Pan AMNH 51208	0.0264	-0.0283	-0.0182	-0.0270	-0.0212	-0.0116
Pan AMNH 51211	0.0403	-0.0453	-0.0065	-0.0722	0.0017	-0.0057
Pan AMNH 51377	0.0659	0.0022	0.0084	0.0220	-0.0333	-0.0010
Pan AMNH 51382	0.0750	0.0082	0.0009	0.0236	0.0035	0.0193
Pan AMNH 51386	0.0295	-0.0441	-0.0006	0.0178	-0.0184	-0.0246
Pan AMNH 51392	0.0723	-0.0194	-0.0223	-0.0156	-0.0109	-0.0009

Pan AMNH 89352	0.0388	-0.0220	0.0140	-0.0265	0.0109	-0.1035
Pan AMNH 89353	0.0571	-0.0036	-0.0189	-0.0053	-0.0119	-0.0341
Pan AMNH 89406	0.0400	-0.0046	-0.0471	-0.0125	0.0398	-0.0178
Pan AMNH 89407	0.0658	-0.0176	-0.0282	-0.0342	-0.0419	0.0103
Pan AMNH 90191	0.0424	-0.0131	-0.0357	0.0183	-0.0099	-0.0272
Pan AMNH 90293	0.0463	-0.0091	-0.0344	0.0185	-0.0024	-0.0028
Pongo AMNH 19548	0.0358	-0.0153	0.0199	0.0124	-0.0249	-0.0185
Pongo AMNH 18010	0.0293	0.0022	-0.0324	-0.0023	0.0237	-0.0054
Pongo AMNH 19180	0.0676	-0.0329	-0.0091	-0.0156	-0.0254	-0.0264
Pongo AMNH 202511	0.0652	-0.0117	-0.0008	-0.0207	0.0021	-0.0239
Pongo AMNH 28253	0.0262	-0.0091	0.0265	0.0398	-0.0308	-0.0018
Pongo AMNH 35549	0.0846	-0.0272	-0.0057	0.0142	-0.0027	0.0024
Pongo AMNH 80008	0.0339	-0.0365	-0.0071	-0.0325	-0.0067	-0.0027
Pongo USNM 142170	0.0215	0.0004	0.0235	0.0219	-0.0009	0.0015
Pongo USNM 142191	0.0746	0.0317	0.0027	0.0151	-0.0143	-0.0086
Pongo USNM 142195	0.0672	0.0330	0.0132	-0.0085	0.0012	0.0035
Pongo USNM 142196	0.0077	0.0259	0.0236	0.0003	-0.0123	-0.0192
Pongo USNM 142200	0.0975	-0.0007	0.0200	-0.0211	-0.0291	0.0348
Pongo USNM 142169	0.0506	-0.0325	0.0420	0.0078	0.0128	0.0185
Pongo USNM 145319	0.0980	-0.0033	0.0021	-0.0249	-0.0290	0.0190
Pongo ZMB 67173	0.0188	0.0040	-0.0046	0.0110	0.0024	-0.0123
Pongo ZMB 6954	0.1029	-0.0020	-0.0131	-0.0437	0.0041	0.0037
Pongo ZMB 6957	0.0240	0.0236	0.0064	0.0129	-0.0246	0.0241

Table S6. Results of M_1 PCA including PC scores by specimen for the first 6 PCs.