Supporting Information for

Beyond the mouse model: A transdisciplinary approach to the genetics of hominid dental evolution

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Table S1. Sample of extant Old World Monkeys used in this study.

Subfamily	Genus and Species	N	Museum
Cercopithecinae	*Cercopithecus mitis*	55	American Museum of Natural History[1]
		2	Cleveland Museum of Natural History[2]
		1	Museum of Vertebrate Zoology[3]
		37	National Museum of Natural History[4]
	Macaca fascicularis	87	American Museum of Natural History[1]
		5	Cleveland Museum of Natural History[2]
		5	Museum of Vertebrate Zoology[3]
	Macaca mulatta	3	Museum of Vertebrate Zoology[3]
		73	National Museum of Natural History[4]
	Papio hamadryas	4	American Museum of Natural History[1]
		27	Cleveland Museum of Natural History[2]
		55	National Museum of Natural History[4]
		41	Museum of Vertebrate Zoology[3]
	Theropithecus gelada	4	American Museum of Natural History[1]
		1	Cleveland Museum of Natural History[2]
		5	National Museum of Natural History[4]
Colobinae	*Colobus guereza*	53	American Museum of Natural History[1]
		4	Cleveland Museum of Natural History[2]
		68	National Museum of Natural History[4]
	Nasalis larvatus	28	American Museum of Natural History[1]
		2	Cleveland Museum of Natural History[2]
	Presbytis melalophos	58	American Museum of Natural History[1]
		25	National Museum of Natural History[4]
	Presbytis rubicunda	36	American Museum of Natural History[1]
		44	National Museum of Natural History[4]
	Total	**723**	

[1] New York City, New York, USA; [2] Cleveland, Ohio, USA; [3] Berkeley, California, USA; [4] Washington, District of Columbia, USA

Table S2. Descriptive statistics of PMM and MMC extant Old World primates (Cercopithecidae and Hominidae).

	Species	Trait	N	Mean	SD	CV
Cercopithecinae	*Cercopithecus mitis*	PMM	88	1.22	0.08	0.525
		MMC	85	1.10	0.06	0.327
	Macaca fascicularis	PMM	94	1.39	0.08	0.460
		MMC	77	1.42	0.10	0.704
	Macaca mulatta	PMM	75	1.42	0.07	0.345
		MMC	67	1.50	0.12	0.960
	Papio hamadryas	PMM	104	1.49	0.08	0.430
		MMC	63	1.52	0.10	0.658
	Theropithecus gelada	PMM	9	1.58	0.09	0.513
		MMC	8	1.60	0.13	1.056
Colobinae	*Colobus guereza*	PMM	118	1.06	0.07	0.462
		MMC	118	1.35	0.07	0.363
	Nasalis larvatus	PMM	27	1.25	0.06	0.288
		MMC	28	1.41	0.09	0.574
	Presbytis melalophos	PMM	80	1.09	0.08	0.587
		MMC	78	1.12	0.08	0.571
	Presbytis rubicunda	PMM	77	1.04	0.06	0.346
		MMC	77	1.12	0.05	0.223
Hominoidea	*Gorilla gorilla*	PMM	45	1.50	0.06	0.240
		MMC	41	1.11	0.07	0.441
	Homo sapiens	PMM	25	1.58	0.10	0.633
		MMC	31	0.98	0.07	0.500
	Pan paniscus	PMM	37	1.49	0.10	0.671
		MMC	32	0.96	0.06	0.375
	Pan troglodytes	PMM	59	1.49	0.08	0.430
		MMC	54	0.99	0.05	0.253
	Pongo pygmaeus	PMM	10	1.30	0.07	0.377
		MMC	8	0.99	0.05	0.253

Table S3. Spearman correlation between PMM and MMC for extant primates.

Species	p value	Spearman rho
Cercopithecus mitis	0.6137	0.0568
Colobus guereza	0.3906	-0.0818
Gorilla gorilla	0.7616	-0.0489
Homo sapiens	0.3467	-0.2161
Macaca fascicularis	0.5622	-0.0683
Macaca mulatta	0.1854	-0.1636
Nasalis larvatus	0.9516	0.0131
Papio hamadryas	0.3871	0.1176
Pan paniscus	0.0234	-0.4127*
Pan troglodytes	0.2971	0.1445
Pongo pygmaeus	0.7033	0.1667
Presbytis melalophos	0.2777	0.1259
Presbytis rubicunda	0.1079	0.1884
Theropithecus gelada	0.9063	-0.0714

*Significantly correlated.

Table S4. Sample of extinct Old World Monkey specimens and taxonomic categories.

Family	Subfamily	Species	N	Reference
Cercopithecidae	Cercopithecinae	*Papio hamadryas ssp.*	6	*1*
		Pliopapio alemui	5	*2*
		Theropithecus oswaldi cf. darti	8	*3*
	Colobinae	*Colobus sp.*	25	*1*
		Kuseracolobus aramisi	3	*2*
		Paracolobus enkorikae	6	*4*
Victoriapithecidae	Victoriapithecinae	*Victoriapithecus macinnesi*	3	*5*
		Total	**56**	

Table S5. Descriptive statistics for PMM and MMC of extinct Old World Monkeys.

Species	Trait	N	Mean	SD	CV
Colobus sp.	PMM	17	1.33	0.11	0.910
	MMC	12	1.31	0.05	0.191
Kuseracolobus aramisi	PMM	1	1.39	NA	NA
	MMC	1	1.46	NA	NA
Papio hamadryas ssp.	PMM	6	1.42	0.20	2.817
	MMC	4	1.65	0.14	1.188
Paracolobus enkorikae	PMM	2	1.27	0.17	2.276
	MMC	3	1.32	0.11	0.917
Pliopapio alemui	PMM	1	1.56	NA	NA
	MMC	1	1.38	NA	NA
Theropithecus oswaldi cf. *darti*	PMM	8	1.56	0.17	1.853
	MMC	8	1.72	0.14	1.140
Victoriapithecus macinnesi	PMM	3	1.20	0.12	1.200
	MMC	3	1.41	0.06	0.255

Table S6. Sample of extant apes and humans.

Species	N	Museum
Gorilla gorilla	45	Cleveland Museum of Natural History[1]
Homo sapiens	46	Hearst Museum of Anthropology[2]
Pan paniscus	39	Royal Museum of Central Africa[3]
Pan troglodytes	59	Cleveland Museum of Natural History[1]
Pongo pygmaeus	10	Cleveland Museum of Natural History[1]
Total	**199**	

[1] Cleveland, Ohio, USA; [2] Berkeley, California, USA; [3] Tervuren, Belgium

Table S7: Extinct hominoid taxa studied.

	Genus	**Species**	**N**	**Reference**
extinct Hominidae	*Ardipithecus*	*ramidus**	3	*6*
	Australopithecus	*afarensis**	16	*6, 8*
		*africanus**	10	*6*
		*anamensis**	4	*6, 9*
		*boisei**	7	*10*
		*garhi**	2	*6*
		*robustus**	13	*6*
	Homo	*antecessor*	3	*11*
		erectus	15	*10, 12-17*
		heidelbergensis	3	*18, 19*
		*neanderthalensis**	11	*20*
		sapiens (archaic)*	2	*6*
		sp. (Dmanisi)	2	*21, 22*
		sp.(Sima)	24	*23, 24*
other extinct hominoids†	*Afropithecus*	*turkanensis*	1	*25*
	Ankarapithecus	*meteai*	1	*26*
	Dryopithecus	*sp.**	6	*6*
	Griphopithecus	*alpani*	1	*27*
	Kenyapithecus	*africanus*	3	*28-30*
	Khoratpithecus	*piriyai*	1	*31*
	Limnopithecus	*legetet*	4	*32, 33*
	Micropithecus	*clarki*	2	*32*
	Ouranopithecus	*macedoniensis*	4	*34*
	Proconsul	*africanus*	4	*33, 35*
		heseloni	6	*36*
		major	6	*35-37*
		nyanzae	5	*33, 35, 36*
	Rangwapithecus	*gordoni*	3	*38, 39*
	Sivapithecus	*indicus*	3	*35, 40*
Total			**165**	

*includes data from Suwa and colleagues (*6*) and references therein.
†see controversies over familial designations in Hartwig (*7*).

Notes for Table S7: The fossil hominoid linear dental metric data are from G. Suwa and T. White, following (*6*) and references therein, and from fossil descriptions in the literature. Data were collected for a specimen only if all measurements needed to calculate MMC and PMM values were preserved from the same side of the dentition. Where measurements for both sides were reported, only the left side measurements were collected. Measurements reported as estimates were not collected. The limited and unequal representation of fossil taxa in our sample is the result of the relatively incomplete fossil material available, precluding the collection of the multiple metrics required to describe the MMC and PMM phenotypes. Specimens from Kelley et al. (*41*) described as *Equatorius africanus* by the authors are included here as *Kenyapithecus africanus* (following *42*). Specimens from Pickford et al. (*36*) described as *Ugandapithecus major* by the authors are included here as *Proconsul major* (*43*). Only *Homo* specimens with a clearly defined taxonomic affinity were included (e.g., OH 7 and OH 13, for which taxonomic affinity remains debated, were excluded). The Dmanisi mandible (D211) was excluded as it was deemed potentially unrepresentative of the Dmanisi sample in terms of molar proportions (*18*).

Table S8. Descriptive statistics for MMC and PMM of extinct hominoids used in this study with taxon sample sizes greater than two. See Table S7 for a complete list with references (all data were culled from published literature).

Species	Trait	N	Mean	SD	CV
Ardipithecus ramidus	PMM	3	1.68	0.05	0.149
	MMC	3	1.16	0.02	0.034
Australopithecus afarensis	PMM	14	1.51	0.07	0.325
	MMC	12	1.15	0.06	0.313
Australopithecus africanus	PMM	8	1.48	0.05	0.169
	MMC	5	1.15	0.09	0.704
Au. anamensis	PMM	2	1.59	0.13	1.063
	MMC	3	1.17	0.08	0.547
Australopithecus boisei	PMM	5	1.31	0.07	0.374
	MMC	7	1.22	0.10	0.820
Australopithecus robustus	PMM	12	1.43	0.08	0.448
	MMC	9	1.16	0.06	0.310
Homo erectus	PMM	11	1.51	0.08	0.424
	MMC	9	0.98	0.12	1.469
Homo heidelbergensis	PMM	2	1.62	0.11	0.747
	MMC	3	1.03	0.04	0.155
Homo neanderthalensis	PMM	11	1.61	0.10	0.621
	MMC	8	0.98	0.06	0.367
Homo sp.(Sima)	PMM	18	1.57	0.08	0.408
	MMC	17	1.02	0.08	0.627
Ouranopith. macedoniensis	PMM	4	1.60	0.09	0.506
	MMC	4	1.30	0.06	0.277
Proconsul africanus	PMM	3	1.55	0.12	0.929
	MMC	3	1.36	0.01	0.007
Proconsul heseloni	PMM	6	1.63	0.11	0.742
	MMC	4	1.38	0.09	0.587
Proconsul major	PMM	4	1.55	0.06	0.232
	MMC	5	1.44	0.08	0.444
Proconsul nyanzae	PMM	5	1.49	0.19	2.423
	MMC	4	1.45	0.08	0.441
Rangwapithecus gordoni	PMM	3	1.53	0.14	1.281
	MMC	3	1.31	0.21	3.366

Table S9. Results from single-trait phylogenetic generalized least squares regressions of MMC and PMM.*

Trait	Pagel's λ	Lower 95% CI	Upper 95% CI
Cercopithecoids Only			
MMC	0.90	0.81	0.99
PMM	0.91	0.79	1.00
P4 Crown Area: M1 Crown Area	0.63	0.40	0.85
P4 Length : M1 Length	0.82	0.66	0.96
M1 Crown Area	0.97	0.93	0.99
PMMw	0.84	0.71	0.97
MMCw	0.91	0.80	0.99
P4 Length	0.97	0.91	1.00
M1 Length	0.98	0.95	1.00
M2 Length	0.98	0.95	1.00
M2 Width	0.97	0.93	0.99
M3 Length	0.98	0.95	1.00
Cercopithecoids + Hominoids (without humans)			
MMC	0.88	0.80	0.96
PMM	0.92	0.86	0.98
P4 Crown Area: M1 Crown Area	0.69	0.52	0.87
P4 Length : M1 Length	0.84	0.73	0.95
M1 Crown Area	0.98	0.96	0.99
PMMw	0.75	0.59	0.90
MMCw	0.81	0.69	0.93
P4 Length	0.97	0.94	0.99
M1 Length	0.98	0.96	0.99
M2 Length	0.99	0.98	1.00
M2 Width	0.98	0.96	0.99
M3 Length	0.98	0.96	0.99

*Pagel's λ is understood to be a measure of phylogenetic signal. A value of 1 indicates that trait values vary in accordance with the phylogenetic tree space, in turn indicating that traits are changing across the tree in a manner consistent with a Brownian motion model of evolution. P4 = fourth mandibular premolars. M1, 2, or 3 = first, second, or third mandibular molar. Length = mesiodistal breadth of the crown. Width = buccolingual breadth of the crown. PMMw = PMM calculated with widths rather than lengths. MMCw = MMC calculated with widths rather than lengths.

Table S10. Results from Morphological Disparity Through Time analysis for extant catarrhine taxa measured in this study.*

Trait	MDI	p-value
Cercopithecoids + Hominoids (without humans)		
MMC	-0.107	0.093
PMM	-0.126	0.074
P4 Crown Area: M1 Crown Area	-0.249	<0.001
P4 Length : M1 Length	-0.218	0.001
M1 Crown Area	0.042	0.351
PMMw	-0.250	<0.001
MMCw	0.033	0.381

*MDI = morphological disparity index. P4 = fourth mandibular premolars. M1, 2, or 3 = first, second, or third mandibular molar. Length = mesiodistal breadth of the crown. Width = buccolingual breadth of the crown. PMMw = PMM calculated with widths rather than lengths. MMCw = MMC calculated with widths rather than lengths.

Table S11. Divergence dates inferred from *10kTrees* dataset, with published ranges from other molecular studies.

Node	Divergence	*10kTrees* Consensus Date	Published Range	Source(s)
1	Hominoidea/Cercopithecoidea	30.00 Ma	38 – 20 Ma	*44*, *45*
2	Cercopithecinae/Colobinae	21.41 Ma	22.9 – 13.22 Ma	*44 – 47*
3	Papionini/Cercopithecini	14.88 Ma	15.0 – 9.2 Ma	*44 – 46*
4	*Macaca*/*Papio*	7.08 Ma	10.9 – 6.7 Ma	*44, 45, 47*
5	*Papio*/*Theropithecus*	5.77 Ma	4.7 – 3.4 Ma	*44*
6	*M. mulatta*/*M. fascicularis*	5.05 Ma	5.5 – 3.3 Ma	*44, 48*
7	Colobini/Presbytini	15.44 Ma	15.1 – 9.2 Ma	*44, 47*
8	*Presbytis*/*Nasalis*	13.31 Ma	11.2 – 6.5 Ma	*44, 47*
9*	*Pr. melalophos*/*Pr. rubicunda*	1.31 Ma	2.5 – 0.9 Ma	*49 – 51*
10	Homininae/Ponginae	15.13 Ma	19.7 – 13.5 Ma	*44*
11	*Gorilla* from *Pan*/Hominidae	8.65 Ma	10.1 – 6.6 Ma	*44, 45*
12	*Pan*/Hominidae	6.18 Ma	8.0 – 5.4 Ma	*44*
13	*Pa. troglodytes*/*Pa. paniscus*	2.33 Ma	3.2 – 1.3 Ma	*44, 45*

Supporting Information, Figures

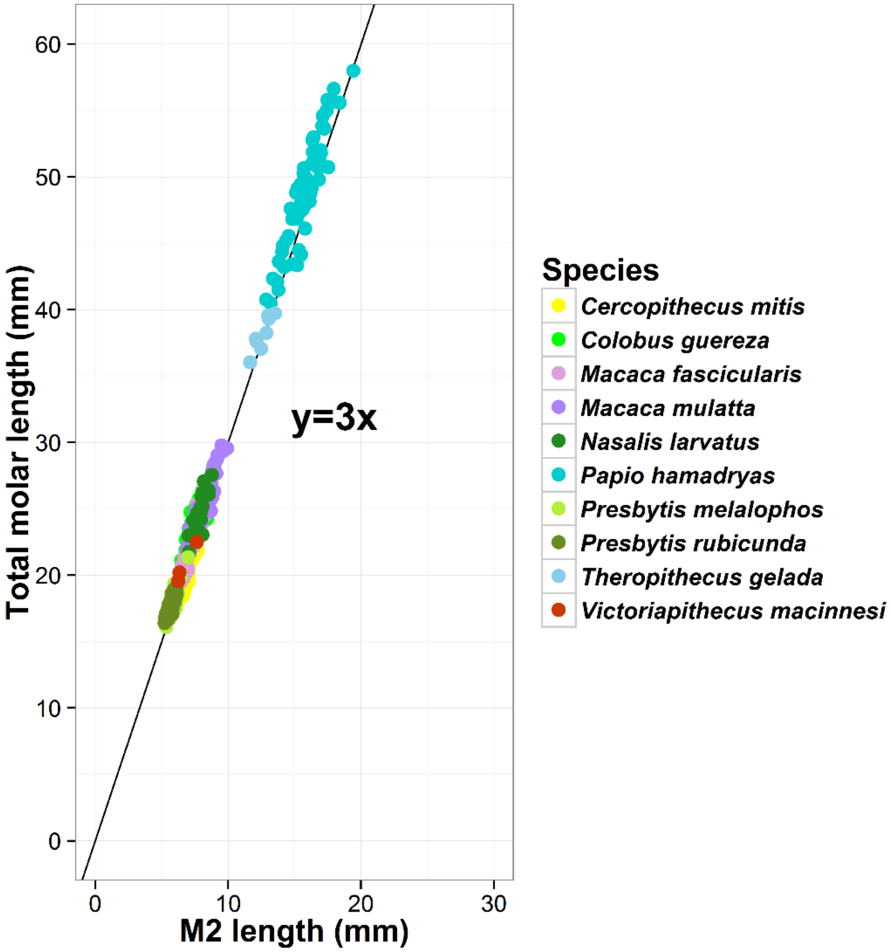

Fig. S1. Correlation of mandibular M2 mesiodistal length with the mesiodistal length of the total molar row length (M1+M2+M3).

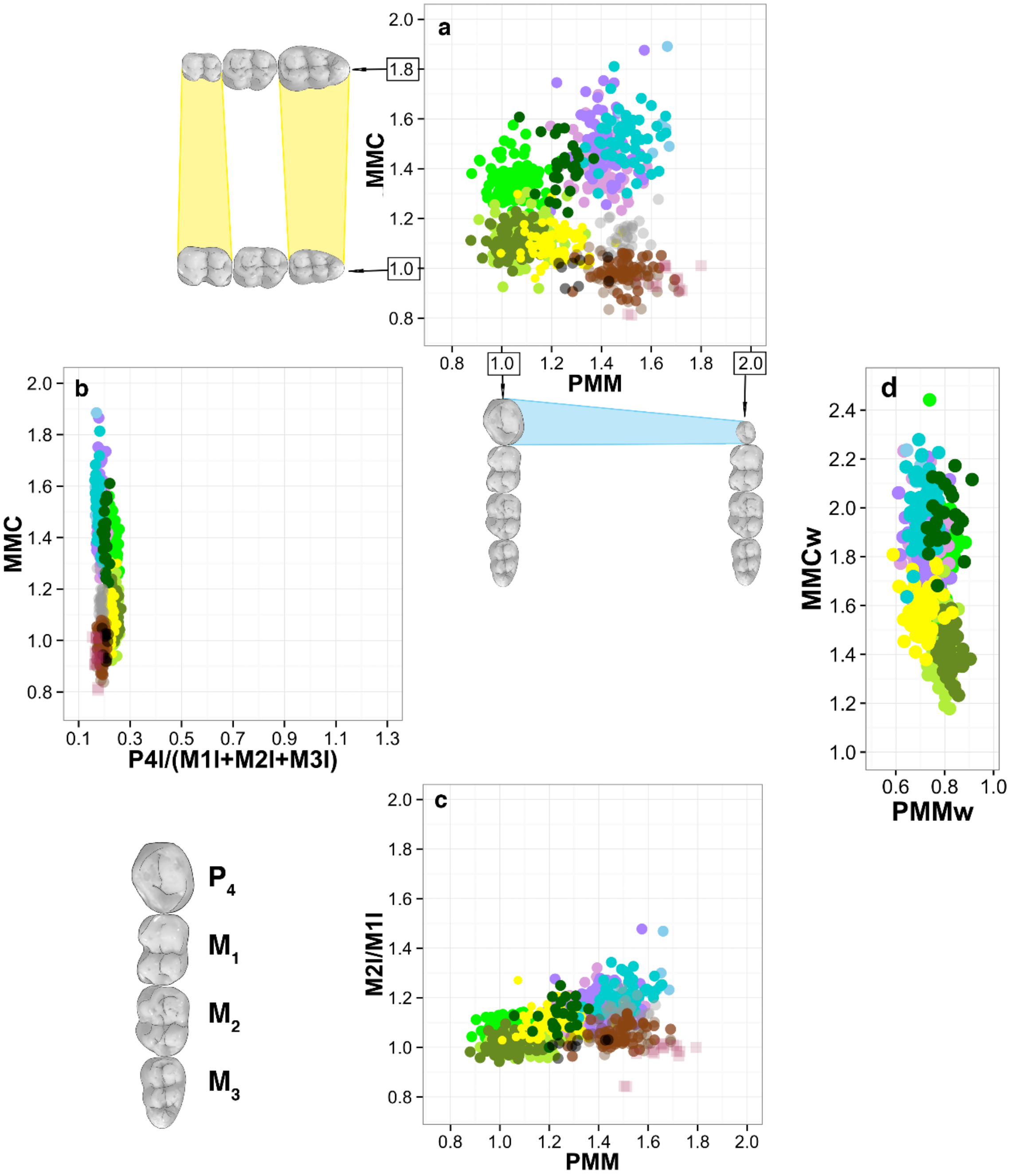

Fig. S2. PMM and MMC compared to other methods for capturing the GP within and between the premolar and molar genetic modules across Old World primates; a) PMM and MMC for all extant taxa presented in Figures 1b and 2a, following those same color schemes; b) MMC plotted against the mesiodistal length of P4 divided by the sum of the mesiodistal lengths of the three molars (note that the taxonomic pattern is reversed because the denominator is larger than the numerator, unlike the other ratios); c) the PMM plotted against the mesiodistal length of M2/M1; d) PMM and MMC calculated with buccolingual widths instead of mesiodistal lengths. These other ratios return the same pattern of relationships between taxa, but the PMM and MMC in a) yields the best discrimination.

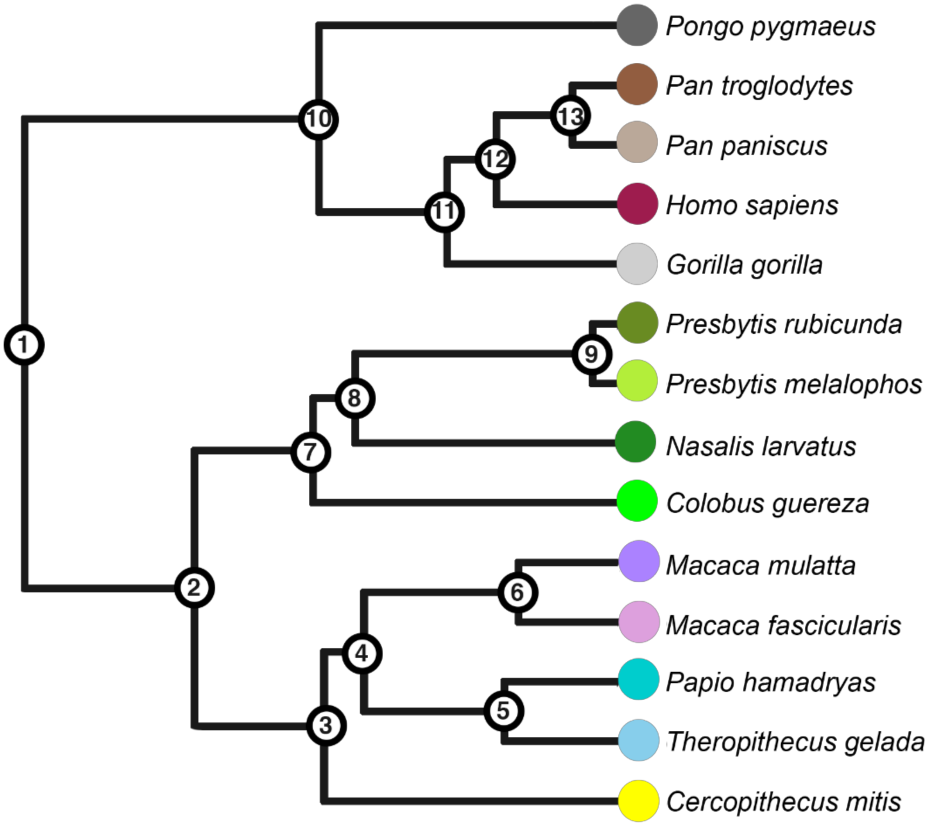

Fig. S3. Consensus molecular chronogram used in the phylogenetic analysis. See Supplementary Table 9 for molecular divergence dates and their literary source.

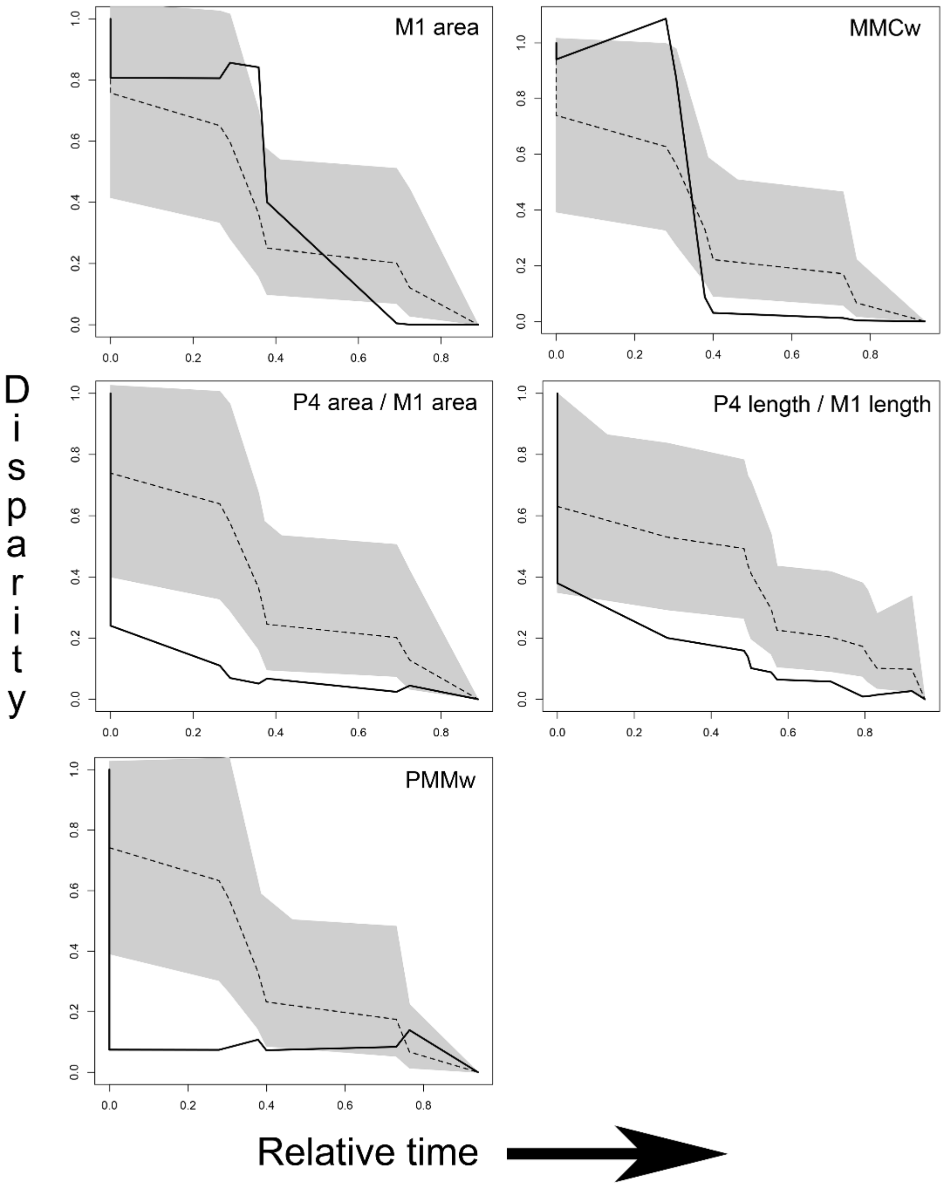

Fig. S4. Disparity through time results of dental traits to compare with PMM and MMC presented in Figure 3 of the main text. Dotted lines indicate the predicted disparity values and shaded areas the 95% confidence intervals. Solid lines indicate actual trait values. Values near 0 indicate that a particular clade contains little of the overall variation, and that variation in the trait is partitioned between subclades rather than within them. Values near 1.0 suggest that a clade contains a large amount of that variation, and that clades may overlap in trait space. As shown in Figure 3, PMM and MMC, trait values fall significantly below expected values beginning in the mid-Miocene, indicating trait partitioning between subfamilies within Primates. Two of the traits shown here in the top row yield a similar pattern, but these composite traits include significant pleiotropic effects with body size, and the pattern may well reflect the shift in body size variation rather than possible selection on dental patterns. The other three traits do not vary significantly across the clades.

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