Supplementary information

Table S1

Table S1. Non-human primate species and variables used in this study. BM: body mass; BrM: brain mass; PCTA: postcanine tooth area; DQ: dietary quality; *: <mark>values for</mark> *Pigathrix* sp. DQ = 1α + 2β + 3.5γ (α: percentage of leaves and structural parts of plants; β: percentage of fruit and reproductive parts of plants, including nuts and seeds; γ: percentage of animal items).

Species	BM [kg]	ECV [ml]	PCTA [mm^2]	DQ
Galago senegalensis	0.19 [1]	3.96 [1]	40.22 [3]	323 [6]
Lemur catta	2.21 [1]	22.90 [1]	79.04 [4]	158.5 [7]
Lepilemur mustelinus	0.77 [1]	9.56 [1]	30.82 [3]	110 [6]
Nycticebus coucang	0.65 [1]	10.13 [1]	84.95 [3]	164.5 [8]
Otolemur crassicaudatus	1.15 [1]	11.78 [1]	65.19 [3]	205 [6]
Perodicticus potto	0.84 [1]	12.42 [1]	83.84 [3]	223 [6]
Propithecus verreauxi	2.96 [1]	26.21 [1]	114.33 [3]	144 [7]
Tarsius (genus)	0.13 [1]	3.16 [1]	61.85 [3]	350 [6]
Alouatta caraya	5.38 [1]	52.63 [1]	125.29 [3]	130 [9]
Alouatta palliata	6.25 [1]	49.88 [1]	145.83 [3]	136.8 [10]
Alouatta seniculus	5.95 [1]	55.22 [1]	155.69 [3]	134.6 [11]
Aotus trivirgatus	0.99 [1]	16.85 [1]	44.71 [3]	177 [6]
Ateles geoffroyi	7.57 [1]	105.09 [1]	76.82 [3]	181.6 [12]
Brachyteles arachnoides	9.51 [2]	120.10 [2]	138.96 [3]	154.1 [13]
Cacajao calvus	3.17 [1]	76.00 [1]	61.51 [3]	201.6 [14]
Callicebus moloch	0.90 [2]	19.00 [2]	37.45 [3]	187 [6]
Callithrix jacchus	0.32 [1]	7.24 [1]	15.72 [5]	190 [15]
Callithrix pygmaea	0.12 [1]	4.17 [1]	10.05 [5]	183 [16]
Cebus apella	2.94 [1]	66.63 [1]	74.14 [3]	192.2 [17]
Chiropotes satanas	2.64 [2]	53.00 [2]	41.51 [3]	189.3 [18-19]
Lagothrix lagotricha	7.15 [1]	96.50 [1]	98.77 [3]	182.9 [20]
Leontopithecus rosalia	0.61 [1]	12.83 [1]	22.90 [5]	212.5 [21]
Pithecia pithecia	1.76 [1]	32.26 [1]	43.45 [3]	184 [6]
Saguinus oedipus	0.43 [1]	9.76 [1]	20.43 [5]	251 [6]
Saimiri sciureus	0.80 [1]	24.14 [1]	27.45 [3]	266 [22]
Cercocebus galeritus	7.44 [1]	99.07 [1]	163.33 [3]	179.8 [23]
Cercocebus torquatus	8.93 [1]	105.99 [1]	163.77 [3]	175.8 [24]
Cercopithecus ascanius	3.71 [1]	59.58 [1]	68.91 [3]	226.5 [25]
Cercopithecus cephus	3.59 [1]	65.26 [1]	79.85 [3]	247.5 [26]
Cercopithecus mitis	6.11 [1]	71.33 [1]	94.59 [3]	202.8 [25]
Cercopithecus mona	3.72 [1]	61.84 [1]	79.24 [3]	205 [6]
Cercopithecus neglectus	5.45 [1]	65.97 [1]	96.13 [3]	198 [6]
Cercopithecus nictitans	5.41 [2]	78.60 [2]	81.77 [3]	182.9 [27]
Chlorocebus aethiops	3.72 [1]	65.00 [1]	88.61 [3]	196 [28]
Colobus polykomos	9.10 [1]	73.83 [1]	129.59 [3]	134.6 [29]
Lophocebus albigena	7.36*	99.10 [2]	121.90 [3]	233.5 [30]
Macaca fascicularis	4.25 [1]	63.98 [1]	119.30 [3]	185.9 [31]
Macaca mulatta	6.79 [1]	88.98 [1]	140.58 [3]	138 [6]

Macaca nemestrina	8.82 [1]	105.59 [1]	157.72 [3]	195 [6]
Macaca nigra	7.68 [1]	94.90 [1]	131.64 [3]	245.85 [32]
Macaca sylvanus	12.01 [1]	93.20 [1]	98.11 [3]	129 [33]
Nasalis larvatus	14.56 [1]	92.30 [1]	127.07 [3]	145 [34]
Papio cynocephalus	17.15 [1]	163.19 [1]	307.05 [3]	163 [6]
Pliocolobus badius	8.29 [1]	63.59 [1]	118.19 [3]	144.5 [35]
Presbitys comata	6.70 [1]	80.30 [1]	82.57 [3]	125 [36]
Pygathrix nemaeus	9.72 [1]*	97.20 [1]*	123.39 [3]	118 [37]
Rhinopithecus roxellana	12.25 [2]	121.70 [2]	176.36 [3]	160 [38]
Theropithecus gelada	15.35 [1]	133.33 [1]	244.24 [3]	117 [6]
Trachypithecus cristatus	6.39 [1]	57.86 [1]	98.08 [3]	132 [6]
Trachypithecus johnii	11.60 [1]	84.60 [1]	115.88 [3]	132 [6]
Gorilla gorilla	120.10 [1]	490.41 [1]	669.94 [3]	173.2 [27]
Hylobates lar	5.60 [1]	101.97 [1]	87.60 [3]	232 [39]
Hylobates moloch	5.82 [2]	113.70 [2]	100.64 [3]	175 [40]
Pan paniscus	39.10 [1]	341.29 [1]	221.50 [3]	164 [41]
Pan troglodytes	44.97 [1]	368.35 [1]	306.73 [3]	194.6 [27]
Pongo pygmaeus	58.54 [1]	377.38 [1]	434.34 [3]	178 [6]

Table S2

Table S2. Descriptive statistics for the extinct hominin species analyzed in this study ($\overline{x}$: mean; N: sample size, in brackets). BM: body mass; BrM: brain mass; PCTA: postcanine tooth area; LP: Lower Pleistocene; MP: Middle Pleistocene. (*): MD values for P^4, M^1 and M^2 were measured on a photograph.

	BM [kg]	BrM [g]	PCTA [mm^2]
A. afarensis	38 (–) [42]	457.8 (4) [48]	499.0 (P^4=11, M^1=6, M^2=8) [56]
A. africanus	35.5 (–) [42]	448.1 (7) [49]	527.2 (P^4=15, M^1=24, M^2=23) [57]
A. garhi	–	445.8 (1) [50]	674.9 (P^4=1, M^1=1, M^2=1) [50]
P. boisei	41.5 (–) [42]	476.2 (7) [51]	712.6 (P^4=6, M^1=10, M^2=8) [58, 59]
P. robustus	36 (–)[42]	470.9 (1) [52]	569.2 (P^4=22, M^1=26, M^2=23) [57]
A. sediba	33 (1) [43]	437.1 (1) [43]	442.9 (P^4=1, M^1=1, M^2=1) [43]
H. habilis	34.5 (–) [42]	610.8 (5) [51]	457.4 (P^4=9, M^1=13, M^2=8) [58, 60]
H. rudolfensis	55.5 (–) [42]	735.8 (1) [51]	613.3 (P^4=1, M^1=1, M^2=1) [58]
H. georgicus	43.4 (3) [44]	654.5 (4) [53-55]	405.3 (P^4=2, M^1=2, M^2=2) [53, 61]
H. ergaster	61.7 (5) [45]	860.6 (4) [45]	434.2 (P^4=2, M^1=3, M^2=4) [58, 62]
H. erectus (LP)	–	842.6 (7) [45]	420.8 (P^4=4, M^1=3, M^2=3) [62]
H. erectus (MP)	56.2 (2) [45]	1082.5 (17) [45]	365 (P^4=11, M^1=7, M^2=8) [62]
H. heidelbergensis	62 (–) [45]	1161.7 (9) [45]	377.8 (P^4=8, M^1=9, M^2=9) [62]
H. rhodesiensis	65.8 (7) [45]	1053.3 (5) [45]	410.3 (P^4=1, M^1=1, M^2=1) [62]
H. neanderthalensis	74.4 (21) [45]	1414.3 (16) [45]	331.1 (P^4=20, M^1=20, M^2=19) [62]
H. floresiensis	36 (1) [46]	413.8 (1) [46]	347.1 (P^4=1, M^1=1, M^2=1) [46] (*)
H. sapiens	65.8 (81) [47]	1462.7 (37) [45]	320.2 (P^4=27, M^1=38, M^2=28) [47, 63]

Table S3

Table S3. Descriptive statistics of regression analyses of brain mass (BrM, in g) on body mass (BM, in kg) and of body mass on postcanine tooth area (PCTA, in mm^2) for primate groups. RMA: Reduced Major Axis; OLS: Ordinary Least Squares; N: sample size; r: coefficient of correlation; β_0: Y–intercept; β_1: slope; [CI 95%]: 95% confidence interval for the slope; H_0 (b=0): null hypothesis for slope zero; H_0 (b=1; b=2/3): null hypothesis for slope values expected from geometric scaling (isometry); H_0 (b=3/4) and H_0 (b=1/2): null hypothesis for slope values expected from elastic similarity (allometry); n.s.: non-significant t-test value for comparison of slopes (p > 0.05).

logBrM-logBM		N	r	β_0	β_1 [CI 95%]	$H_0(\beta_1=0)$	$H_0(\beta_1=1)$	$H_0(\beta_1=3/4)$
All primates	RMA	71	0.973	1.220	0.902 [0.842-0.956]	<0.0001	<0.0001	<0.0001
	OLS	71	0.973	1.240	0.877 [0.815-0.936]	<0.0001	<0.0001	<0.0001
Non-human primates	RMA	56	0.972	1.257	0.787 [0.739-0.829]	<0.0001	<0.0001	n.s.
	OLS	56	0.972	1.207	0.765 [0.719-0.808]	<0.0001	<0.0001	n.s.
Prosimians	RMA	8	0.993	1.114	0.687 [0.634-0.734]	<0.0001	<0.0001	<0.05
	OLS	8	0.993	1.113	0.682 [0.642-0.743]	<0.0001	<0.0001	<0.05
Anthropoids	RMA	48	0.97	1.322	0.723 [0.691-0.774]	<0.0001	<0.0001	n.s.
	OLS	48	0.97	1.338	0.705 [0.691-0.774]	<0.0001	<0.0001	n.s.
Platyrrhines	RMA	17	0.967	1.317	0.774 [0.692-0.855]	<0.0001	<0.0005	n.s.
	OLS	17	0.967	1.323	0.748 [0.668;0.837]	<0.0001	<0.0001	n.s.
Catarrhines	RMA	31	0.936	1.361	0.684 [0.599-0.763]	<0.0001	<0.0001	n.s.
	OLS	31	0.936	1.404	0.640 [0.563-0.751]	<0.0001	<0.0001	n.s.
Cercopithecoids	RMA	25	0.656	1.433	0.581 [0.440-0.706]	<0.0001	<0.0001	<0.005
	OLS	25	0.656	1.529	0.470 [0.342-0.609]	<0.0001	<0.0001	<0.005
Hominoids	RMA	6	0.991	1.643	0.540 [0.471-0.781]	<0.0002	<0.0005	n.s.
	OLS	6	0.991	1.65	0.535 [0.459-0.768]	<0.0002	<0.0005	n.s.
Extinct hominins	RMA	15	0.938	0.19	1.581 [1.321-1.847]	<0.0001	<0.0001	<0.0001
	OLS	15	0.938	0.356	1.489 [1.205-1.786]	<0.0001	<0.0001	<0.0001
Homo	RMA	10	0.9	0.317	1.519 [0.854-1.940]	<0.0001	n.s.	<0.05
	OLS	10	0.900	0.579	1.367 [0.828-1.906]	<0.0005	n.s.	<0.05
logBM-logPCTA		N	r	β_0	β_1 [CI 95%]	$H_0(\beta_1=0)$	$H_0(\beta_1=2/3)$	$H_0(\beta_1=1/2)$
All primates	RMA	71	0.917	1.620	0.583 [0.518-0.650]	<0.0001	<0.05	<0.0001
	OLS	71	0.917	1.660	0.534 [0.448-0.616]	<0.0001	<0.05	<0.0001
Non-human primates	RMA	56	0.883	1.633	0.539 [0.461-0.627]	<0.0001	<0.01	n.s.
	OLS	56	0.883	1.671	0.475 [0.369-0.585]	<0.0001	<0.01	n.s.
Prosimians	RMA	8	-	-	-	n.s.	-	-
	OLS	8	-	-	-	n.s.	-	-
Anthropoids	RMA	48	0.961	1.526	0.627 [0.580-0.663]	<0.0001	<0.05	<0.001
	OLS	48	0.961	1.554	0.602 [0.561-0.643]	<0.0001	<0.05	<0.005
Platyrrhines	RMA	17	0.959	1.531	0.643 [0.549;0.720]	<0.0001	n.s.	<0.0005
	OLS	17	0.959	1.538	0.616 [0.529;0.698]	<0.0001	n.s.	<0.0001
Catarrhines	RMA	31	0.912	1.515	0.633 [0.506-0.711]	<0.0001	n.s.	<0.05
	OLS	31	0.912	1.570	0.577 [0.500-0.689]	<0.0001	n.s.	<0.05
Cercopithecoids	RMA	25	0.764	1.404	0.774 [0.591-0.973]	<0.0001	n.s.	n.s.
	OLS	25	0.764	1.563	0.592 [0.372-0.837]	<0.0001	n.s.	n.s.
Hominoids	RMA	6	0.980	1.464	0.635 [0.267-0.774]	<0.001	n.s.	n.s.
	OLS	6	0.980	1.482	0.622 [0.264-0.758]	<0.001	n.s.	n.s.
Extinct hominins	RMA	15	-0.471	4.104	-0.817 [-1.175 — -0.463]	n.s.	n.s.	-
	OLS	15	-0.471	3.290	-0.385 [-0.759 — -0.078]	n.s.	n.s.	-
Homo	RMA	10	-	-	-	n.s.	-	-
	OLS	10	-	-	-	n.s.	-	-

Table S4

Table S4. Descriptive statistics of regression analyses of postcanine tooth area (PCTA) on brain mass (BrM) in several primate groups. For legend see Table S3; res: size-adjusted residuals from the equations for logPCTA and logBrM on logBM.

logBrM-logPCTA		N	r	β_0	β_1 [CI 95%]	H_0 (β_1=0)	H_0 (β_1=isom)
All primates	RMA	73	0.884	0.831	0.646 [0.555-0.734]	<0.0001	*n.s.*
	OLS	73	0.884	0.978	0.571 [0.477-0.666]	<0.0001	<0.05
Non-human primates	RMA	56	0.668	0.773	0.684 [0.564-0.809]	<0.0001	n.s.
	OLS	56	0.668	0.989	0.559 [0.408-0.715]	<0.0001	n.s.
Prosimians	RMA	8	-	-	-	ns	-
	OLS	8	-	-	-	ns	-
Anthropoids	RMA	48	0.927	-0.448	1.160 [1.056-1.277]	<0.0001	<0.0001
	OLS	48	0.927	-0.280	1.075 [0.935-1.123]	<0.0001	<0.0001
Platyrrhines	RMA	17	0.882	0.437	0.831 [0.635-0.974]	<0.0001	n.s.
	OLS	17	0.882	0.587	0.732 [0.565-0.878]	<0.0001	n.s.
Catarrhines	RMA	31	0.894	0.255	0.926 [0.710-1.093]	<0.0001	<0.001
	OLS	31	0.894	0.454	0.828 [0.631-1.031]	<0.0001	*n.s.*
Cercopithecoids	RMA	25	0.869	-0.505	1.333 [1.143-1.548]	<0.0001	<0.0001
	OLS	25	0.869	-0.167	1.158 [0.929-1.521]	<0.0001	<0.0001
Hominoids	RMA	6	0.951	-0.465	1.174 [0.903-1.528]	<0.005	n.s.
	OLS	6	0.951	-0.327	1.117 [0.757-1.407]	<0.005	n.s.
Extinct hominins	RMA	15	-0.645	4.211	-0.547 [-0.713 – -0.387]	<0.001	n.s.
	OLS	15	-0.645	3.658	-0.353 [-0.568 – -0.157]	<0.002	n.s.
Homo	RMA	11	-	-	-	n.s.	-
	OLS	11	-	-	-	n.s.	-
Homo without *H. floresiensis*	RMA	10	-0.751	4.407	-0.604 [-0.897– -0.247]	<0.02	ns
	OLS	10	-0.751	3.96	-0.436[-0.695;-0.083]	<0.02	ns
logPCTA$_{BMres}$ on logBrM$_{BMres}$		N	r	β_0	β_1[CI 95%]	H_0(β_1=0)	H_0(β_1=isom)
All Primates	OLS	71	-	-	-	n.s.	-
Non-human Primates	OLS	56	-	-	-	n.s.	-
Prosimii	OLS	8	0.811	0.407	1.791 [0.489-3.084]	<0.05	n.s.
Anthropoids	OLS	48	-0.301	-0.073	-0.227 [-0.441 – -0.013]	<0.05	<0.005
Platyrrhines	OLS	17	-0.697	-0.071	-0.588 [-0.922 – -0.225]	<0.005	<0.05
Catarrhines	OLS	31	-	-	-	n.s.	-
Cercopithecoids	OLS	25	-	-	-	n.s.	-
Hominoids	OLS	6	-	-	-	n.s.	-
Extinct hominins	OLS	15	-0.810	0.252	-1.146 [-1.646 – -0.651]	<0.005	n.s.
Homo	OLS	10	-0.650	0.162	-0.779 [-1.521 – -0.037]	<0.05	n.s.
logPCTA$_{DQres}$ on logBrM$_{DQres}$		N	r	β_0	β_1[CI 95%]	H_0(β_1=0)	H_0(β_1=isom)
Non-human Primates	OLS	56	0.791	0.000	0.543 [0.429-0.658]	<0.0001	<0.05
Prosimians	OLS	8	0.713	0.441	0.838 [0.016-1.660]	<0.05	n.s.
Anthropoids	OLS	48	0.902	-0.063	0.736 [0.632-0.841]	<0.0001	n.s.
Platyrrhines	OLS	17	0.824	-0.124	0.625 [0.389-0.861]	<0.0001	n.s.
Catarrhines	OLS	31	0.882	-0.037	0.724 [0.576-0.871]	<0.0001	n.s.
Cercopithecoids	OLS	25	0.813	-0.029	0.741 [0.511-0.970]	<0.0001	n.s.
Hominoids	OLS	6	0.914	-0.382	1.154 [0.443-1.866]	<0.02	n.s.

Table S5

Table S5. Descriptive statistics of regression analyses of dietary quality (DQ) postcanine tooth area (PCTA, in mm^2) in several primate groups. Res: size-adjusted residuals from the equations for logPCTA and logDQ on logBM and logBrM respectively.

logDQ-logPCTA		N	r	β_0	β_1 [CI 95%]	$H_0(\beta_1=0)$
Non-human primates	RMA	56	-0.35	2.871	-0.318[-0.401 – -0,190]	<0.01
	OLS	56	-0.35	2.467	-0.112[-0.179 – -0.013]	<0.01
Prosimians	RMA	8	-	-	-	n.s.
	OLS	8	-	-	-	n.s.
Anthropoids	RMA	48	-0.41	2.764	-0.264[-0.331 – -0.158]	<0.005
	OLS	48	-0.41	2.456	-0.108[-0.158 – -0.035]	<0.005
Platyrrhines	RMA	17	-0.70	2.659	-0.234[-0.322 – -0.134]	<0.002
	OLS	17	-0.70	2.538	-0.163[-0.258 – -0.035]	<0.002
Catarrhines	RMA	31	-	-	-	n.s.
	OLS	31	-	-	-	n.s.
Cercopithecoids	RMA	25	-	-	-	n.s.
	OLS	25	-	-	-	n.s.
Hominoids	RMA	6	-	-	-	n.s.
	OLS	6	-	-	-	n.s.
logDQ$_{BMres}$ on logPCTA$_{BMres}$		N	r	β_0	β_1[CI 95%]	$H_0(\beta_1=0)$
Non-human primates	OLS	56	-	-	-	n.s.
Prosimians	OLS	8	0.797	-0.14	0.526[0.128-0.924]	<0.02
Anthropoids	OLS	48	-	-	-	n.s.
Platyrrhines	OLS	17	-0.60	-0.05	-0.369[-0.642– -0.096]	<0.02
Catarrhines	OLS	31	-	-	-	n.s.
Cercopithecoids	OLS	25	-	-	-	n.s.
Hominoids	OLS	6	-	-	-	n.s.
logDQ$_{BrMres}$ on logPCTA$_{BrMres}$		N	r^2	β_0	β_1[CI 95%]	$H_0(\beta_1=0)$
Non-human primates	OLS	56	-	-	-	n.s.
Prosimians	OLS	8	0.592	-0.19	0.700[0.235-1.165]	<0.05
Anthropoids	OLS	48	0.109	-0.01	-0.186[-0.339– -0.033]	<0.05
Platyrrhines	OLS	17	0.549	-0.05	-0.314[-0.457– -0.171]	<0.001
Catarrhines	OLS	31	-	-	-	n.s.
Cercopithecoids	OLS	25	-	-	-	n.s.
Hominoids	OLS	6	-	-	-	n.s.

Table S6

Table S6. Descriptive statistics of the regressions adjusted for Primates after independent contrasts analyses using the Phylogenetic Generalized Least-Squares (PGLS) method. α: estimated parameter used to indicate the strength of the evolutionary constraint.

Primates		N	α	r	β_0	β_1 [CI 95%]	se	H_0 ($\beta_1=0$)	H_0 ($\beta_1=isom$)	H_0 ($\beta_1=0.75$)
logBrM on logBM	PGLS	56	0.95	0.94	1.21	0.69 [0.62-0.76]	0.035	<0.0001	<0.0001	n.s.
logPCTA on logBM	PGLS	56	-	-	-	-	-	n.s.	-	-
logPCTA on logBrM	PGLS	56	0.50	0.78	0.98	0.69 [0.54-0.84]	0.076	<0.0001	<0.0001	-
logDQ on logBM	PGLS	56	3.51	-0.44	2.30	-0.10 [-0.24 – -0.64]	0.028	<0.05	-	-
logDQ on logBrM	PGLS	56	-	-	-	-	-	n.s.	-	-
logDQ on logPCTA	PGLS	56	2.63	-0.28	2.50	-0.12 [-0.04 – -0.62]	0.057	<0.05	-	-

Primates		N	α	r	β_0	β_1	se	H_0 ($\beta_1=0$)	H_0 ($\beta_1=isom$)	H_0 ($\beta_1=0.75$)
logPCTA$_{BMres}$ on logBrM$_{BMres}$	PGLS	56	-	-	-	-	-	n.s.	-	-
logDQ$_{BMres}$ on logBrM$_{BMres}$	PGLS	56	-	-	-	-	-	n.s.	-	-
logDQ$_{BMres}$ on logPCTA$_{BMres}$	PGLS	56	-	-	-	-	-	n.s.	-	-
logDQ$_{BrMres}$ on logPCTA$_{BrMres}$	PGLS	56	-	-	-	-	-	n.s.	-	-

Body and brain size

BM, BrM and ECV values for extant primates and fossil hominins were taken from the bibliography (Tables S1 and S2). For those species in which brain size was expressed in the literature as endocranial volumes (ECV, in cm^3), BrM was calculated using the following formula:

BrM = 1.036 ECV [1].

The sample analyzed of *H. sapiens* includes only Late Pleistocene specimens from Europe and the Near East (see Table S2).

Postcanine tooth size

Following previous studies, PCTA was estimated by summing the occlusal areas of three maxillary teeth, the fourth premolar (P^4) and the first and second molars (M^1 and M^2). The area of each tooth was obtained multiplying its mesiodistal length (MD) by its buccolingual breadth (BL). Most measurements were collected from the seminal work of Swindler [3] on the dentition of primates. The database was completed with metric data of *Lemur catta* [4] and Callitrichinae [5]. The measurements for fossil hominin crania were taken from several bibliographic sources (Table S2). The only exception was holotype LB-1 of *Homo floresiensis,* whose MD values for P^4, M^1 and M^2 were measured on a photograph [ref. 46: Fig. 1]. It is worth making clear that after measuring the buccolingual dimensions of selected teeth for fossil *Homo* on published photographs [64, 65], the differences with the measurements obtained from the bibliography were of <0.1 mm in all cases.

It could be argued, however, that the use of only three teeth of the postcanine dentition could introduce a source of error and bias in our analyses, except for those constructed within a narrow taxonomy. For example, if M^1:M^3 size ratio is compared between platyrrhines and cercopithecoids, it is apparent that New World monkeys devote relatively little area to the M^3 in comparison to Old World monkeys. This is particularly evident in callitrichids, which mostly lack an M^3, accounting the M^1 and M^2 for 100% of the molar area. In contrast, the M^3 represents a substantial proportion of total molar area in the catarrhines, reaching >33% in some species. This is a potential source of fluctuation for the slopes adjusted when different primate clades are involved (i.e., the slopes would not only reflect differences in tooth size relative to body size, but also tooth sizes relative to teeth not included in the calculation of postcanine tooth area). However, the reason for analyzing exclusively the area of P^4, M^1 and M^2 is that McHenry [66] used these teeth for calculating the molarization coefficient and measurements for a high number of primate species are available. In contrast, the use of other postcanine teeth would have resulted in a substantial decrease of sample size. In addition, the first molar is usually placed at 7:10 of the jaw lever arm, the point where the maximum bite force is exerted during chewing, while the fourth premolar and the second molar are situated immediately before and after it, respectively, which means that these teeth are also crucial for mastication [66]. Finally, we are aware that teeth are complex structures and the use of postcanine tooth area oversimplifies a number of histological, morphological and topological aspects that play a key role in food processing. However, there is a vast number of meta-analyses in which this type of variables (i.e., body size, brain size and tooth size) have been used (e.g., for the specific case of postcanine tooth area [67].

Dietary Quality

Dietary quality (DQ) was defined as follows:

DQ = 1α + 2β + 3.5γ [68],

where α is the percentage of leaves and structural parts of plants in the diet, β is the percentage of fruit and reproductive parts of plants (including nuts and seeds), and γ is the percentage of animal items. In this way, DQ reflects the dietary contribution of those foodstuffs considered in more traditional dietary categories (i.e., folivores, frugivores and faunivores). DQ was estimated for primate species using data on diet composition published in a number of studies (see Table S1). This variable measures some physical properties of foodstuffs, for example those derived from fiber contents, but others (e.g., toughness and hardness) are not clearly reflected in DQ values. However, DQ has been widely used in this type of approaches, including some recent studies [e.g., 69, 70].

In addition, we must recognize that our analyses may oversimplify the relationship between tooth size and food type by focusing exclusively on dietary quality. The reason is that enamel thickness and tooth morphology and topology may reflect a balance between the need to fracture foods without fracturing the tooth itself: for example, the large teeth of *Paranthropus* could have been used for processing foodstuffs with quite divergent mechanical properties, which opens the possibility that tooth morphology reflects "fallback" food items rarely consumed instead of the most commonly masticated items [71-74].

Phylogenetic Control

The procedure used of Phylogenetic Generalized Least-Squares (PGLS) works as follows [75]: imagine eight species showing the phylogenetic relationship depicted in Figure S2. Two phenotypic traits (X, Y; for example, body mass and brain volume) has been measured in each of these species for analyzing the relationship between the traits. The problem is that it is not possible to assume that the measurements taken in any species will be independent from those obtained in others, as they may be subject to phylogenetic inertia.

The method of phylogenetic contrasts consists of transforming the original metric variables into new variables (CX, CY), which preserve the same covariance as the original ones. According to the tree topology of the hypothetical phylogeny analyzed (Fig. S1), the differences X1-X2, X3-X4, X5-X6, and X7-X8 will be independent of each other. For example, the difference X1-X2 will depend exclusively on the evolutionary events that took place in branches 1 and 2, while the difference X3-X4 will be the result of those that account for branches 3 and 4. Given that both sets of events are independent, this situation guarantees data independence for statistical analyses.

According to this reasoning and deepening into the tree nodes, we can affirm that the difference [(X1+X2)/2] – [(X3+X4)/2] is independent from the difference [(X5+X6)/2] – [(X7+X8)/2] and thus, the original variable X (with N species) is finally transformed in CX (with N-1 cases, dots in Fig. 1). The same procedure is applied to the variable Y for transforming it in CY. Given that the method ensures that cov(X,Y) = cov(CX,CY), this implies that if the original variables were correlated the new contrasts will show also a statistical correlation [for technical details, see ref. 76], but now it is guaranteed that the cases studied are independent (i.e., free of phylogenetic inertia).

COMPARE calculates the relationship between traits, while also taking phylogeny and within-taxon variation into account. As with estimation of ancestral states, weights are a function of the within-species variation, the phylogeny, and the model of character evolution.

Among other things, the PGLS method implemented in COMPARE assumes that:

1. - Character evolution can be described using a model of phenotypic evolution, which leads to either a linear or an exponential increase in between-taxon divergence with phylogenetic distance. Exponential models are appropriate for evolution under some

constraints (e.g., stabilizing selection about a fixed optimum). A linear model (e.g., Brownian motion) is approximated by setting the constraint to zero. This is more commonly used in population genetics for describing the evolution of characters undergoing random genetic drift, or directional selection when the direction of selection is shifting back and forth at random.

2. - Expected similarities and differences between all taxa (including hypothetical ancestors) are known. These similarities or differences will be obtained directly from the phylogeny as part of the calculations.

3. - Standard errors of the measurements for each taxon are available, and they adequately represent within-species variation in the trait.

4. - Relationships between traits are well described by a generalized least-squares model regression or correlation.

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Cercopithecus_mitis
Cercopithecus_nictitans
Cercopithecus_ascanius
Cercopithecus_cephus
Cercopithecus_mona
Cercopithecus_neglectus
Chlorocebus_aethiops
Cercocebus_galeritus
Cercocebus_torquatus
Lophocebus_albigena
Theropithecus_gelada
Papio_cynocephalus
Macaca_nigra
Macaca_nemestrina
Macaca_fascicularis
Macaca_mulatta
Macaca_sylvanus
Colobus_polykomos
Piliocolobus_badius
Nasalis_larvatus
Pygathrix_nemaeus
Rhinopithecus_roxellana
Trachypithecus_johnii
Trachypithecus_cristatus
Presbytis_comata
Hylobates_moloch
Hylobates_lar
Gorilla_gorilla_gorilla
Pan_paniscus
Pan_troglodytes_troglodytes
Pongo_pygmaeus
Alouatta_palliata
Alouatta_caraya
Alouatta_seniculus
Ateles_geoffroyi
Brachyteles_arachnoides
Lagothrix_lagotricha
Aotus_trivirgatus
Callithrix_pygmaea
Callithrix_jacchus
Leontopithecus_rosalia
Saguinus_oedipus
Cebus_apella
Saimiri_sciureus
Cacajao_calvus
Chiropotes_satanas
Pithecia_pithecia
Callicebus_moloch
Tarsius_syrichta
Lepilemur_mustelinus
Propithecus_verreauxi
Lemur_catta
Perodicticus_potto
Nycticebus_coucang
Galago_senegalensis
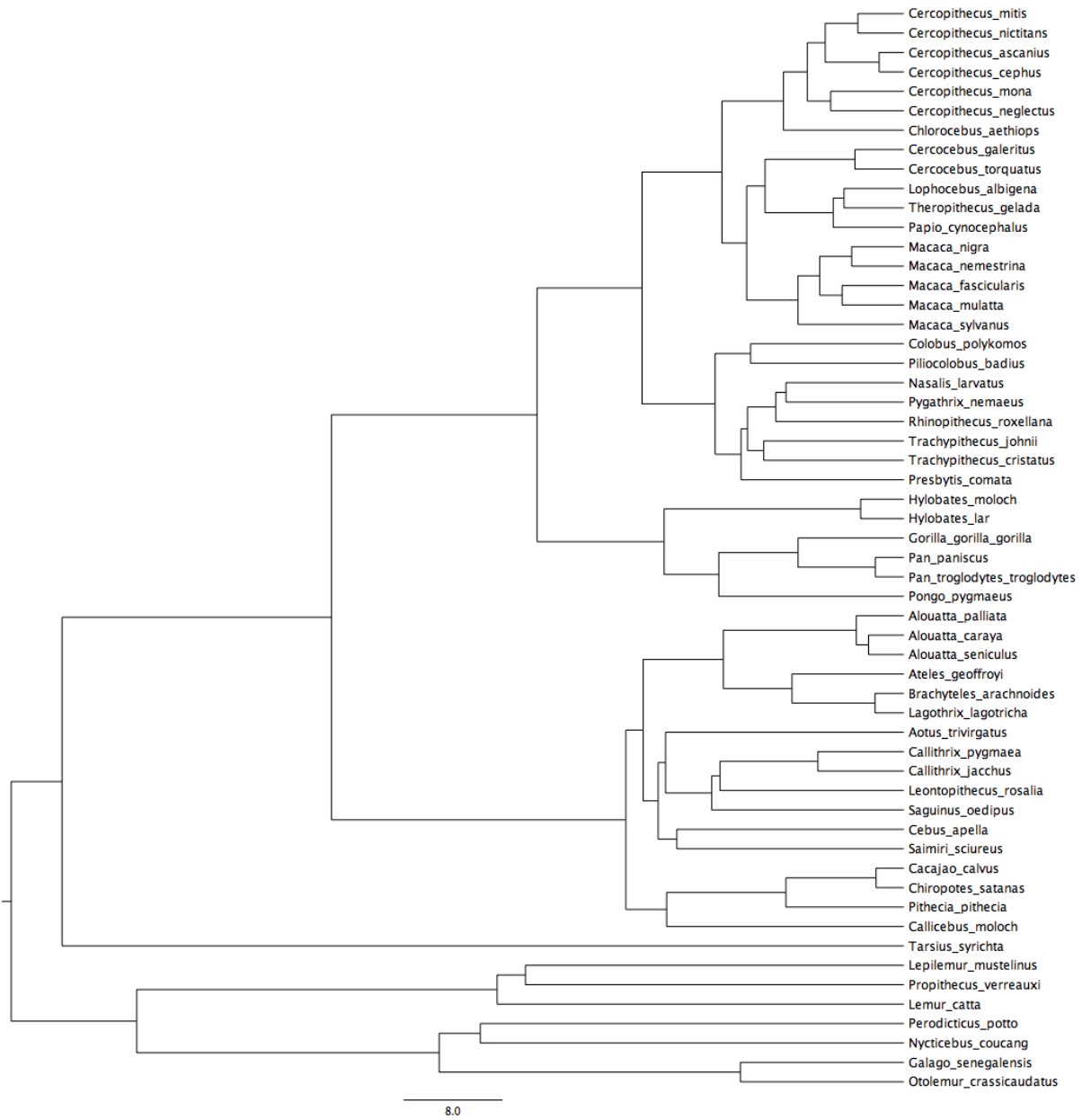Otolemur_crassicaudatus

8.0

Figure S2. A hypothetical, highly symmetrical phylogeny for eight species from which independent contrasts between taxa can be defined. The tree shows a radiation that gives rise to four pairs of closely related species (modified from Felsenstein [77]).