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; \*: values for *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 [mm²] | DQ |
|--------------------------|---------|----------|-------------|----|
| *Galago senegalensis*    | 0.19    | 3.96     | 40.22       | 323| [6]|
| *Lemur catta*            | 2.21    | 22.90    | 79.04       | 158.5| [7]|
| *Lepilemur mustelinus*   | 0.77    | 9.56     | 30.82       | 110| [6]|
| *Nycticebus coucang*     | 0.65    | 10.13    | 84.95       | 164.5| [8]|
| *Otolemur crassicaudatus*| 1.15    | 11.78    | 65.19       | 205| [6]|
| *Perodicticus potto*     | 0.84    | 12.42    | 83.84       | 223| [6]|
| *Propithecus verreauxi*  | 2.96    | 26.21    | 114.33      | 144| [7]|
| *Tarsius* (genus)        | 0.13    | 3.16     | 61.85       | 350| [6]|
| *Alouatta caraya*        | 5.38    | 52.63    | 125.29      | 130| [9]|
| *Alouatta palliata*      | 6.25    | 49.88    | 145.83      | 136.8| [8]|
| *Alouatta seniculus*     | 5.95    | 55.22    | 155.69      | 134.6| [11]|
| *Aotus trivirgatus*      | 0.99    | 16.85    | 44.71       | 177| [6]|
| *Ateles geoffroyi*       | 7.57    | 105.09   | 181.6       | 181| [12]|
| *Brachyteles arachnoides*| 9.51    | 120.10   | 154.1       | 189.3| [13]|
| *Cacajao calvus*         | 3.17    | 76.00    | 201.6       | 201| [14]|
| *Callicebus moloch*      | 0.90    | 19.00    | 37.45       | 187| [6]|
| *Callithrix jacchus*     | 0.32    | 7.24     | 15.72       | 190| [15]|
| *Callithrix pygmaea*     | 0.12    | 4.17     | 10.05       | 183| [16]|
| *Cebus apella*           | 2.94    | 66.63    | 74.14       | 192| [17]|
| *Chiropotes satanas*     | 2.64    | 53.00    | 41.51       | 189.3| [18-19]|
| *Lagothricha lagotricha* | 7.15    | 96.50    | 98.77       | 182| [20]|
| *Leontopithecus rosalia* | 0.61    | 12.83    | 22.90       | 212.5| [21]|
| *Pithecia pithecia*      | 1.76    | 32.26    | 43.45       | 184| [6]|
| *Saguinus oedipus*       | 0.43    | 9.76     | 20.43       | 251| [6]|
| *Saimiri sciureus*       | 0.80    | 24.14    | 27.45       | 266| [22]|
| *Cercocetus galeritus*   | 7.44    | 99.07    | 163.33      | 179.8| [23]|
| *Cercocetus torquatus*   | 8.93    | 105.99   | 163.77      | 175.8| [24]|
| *Cercopithecus ascanius* | 3.71    | 59.58    | 68.91       | 226.5| [25]|
| *Cercopithecus cephus*   | 3.59    | 65.26    | 79.85       | 247.5| [26]|
| *Cercopithecus mitis*    | 6.11    | 71.33    | 94.59       | 202.8| [25]|
| *Cercopithecus mona*     | 3.72    | 61.84    | 79.24       | 205| [6]|
| *Cercopithecus neglectus*| 5.45    | 65.97    | 96.13       | 198| [6]|
| *Cercopithecus nictitans*| 5.41    | 78.60    | 81.77       | 182.9| [27]|
| *Chlorocebus aethiops*   | 3.72    | 60.01    | 88.61       | 196| [28]|
| *Colobus polykomos*      | 9.10    | 73.83    | 129.59      | 134.6| [29]|
| *Lophocebus albigena*    | 7.36*   | 99.10    | 121.90      | 233.5| [30]|
| *Macaca fascicularis*    | 4.25    | 63.98    | 119.30      | 185.9| [31]|
| *Macaca mulatta*         | 6.79    | 88.98    | 140.58      | 138| [6]|

Supplementary information
| Species                      | Value 1  | Value 2  | Value 3  | Value 4  |
|------------------------------|----------|----------|----------|----------|
| *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 (\(\bar{x}\): 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.

| Species          | BM [kg] | BrM [g]   | PCTA [mm\(^2\)] |
|------------------|---------|-----------|------------------|
| *A. afarensis*   | 38 (–)  | 457.8 (4) | 499.0 (P\(^4\)=11, M\(^1\)=6, M\(^2\)=8) [56] |
| *A. africanus*   | 35.5 (–)| 448.1 (7) | 527.2 (P\(^4\)=15, M\(^1\)=24, M\(^2\)=23) [57] |
| *A. garhi*       | –       | 445.8 (1) | 674.9 (P\(^4\)=1, M\(^1\)=1, M\(^2\)=1) [50] |
| *P. boisei*      | 41.5 (–)| 476.2 (7) | 712.6 (P\(^4\)=6, M\(^1\)=10, M\(^2\)=8) [58, 59] |
| *P. robustus*    | 36 (–)[42]| 470.9 (1) | 569.2 (P\(^4\)=22, M\(^1\)=26, M\(^2\)=23) [57] |
| *A. sediba*      | 33 (1)  | 437.1 (1) | 442.9 (P\(^4\)=1, M\(^1\)=1, M\(^2\)=1) [43] |
| *H. habilis*     | 34.5 (–)| 610.8 (5) | 457.4 (P\(^4\)=9, M\(^1\)=13, M\(^2\)=8) [58, 60] |
| *H. rudolfensis* | 55.5 (–)| 735.8 (1) | 613.3 (P\(^4\)=1, M\(^1\)=1, M\(^2\)=1) [58] |
| *H. georgicus*   | 43.4 (3)[44]| 654.5 (4) | 405.3 (P\(^4\)=2, M\(^1\)=2, M\(^2\)=2) [53, 61] |
| *H. ergaster*    | 61.7 (5)[45]| 860.6 (4) | 434.2 (P\(^4\)=2, M\(^1\)=3, M\(^2\)=4) [58, 62] |
| *H. erectus* (LP)| –       | 842.6 (7) | 420.8 (P\(^4\)=4, M\(^1\)=3, M\(^2\)=3) [62] |
| *H. erectus* (MP)| 56.2 (2)[45]| 1082.5 (17) | 365 (P\(^4\)=11, M\(^1\)=7, M\(^2\)=8) [62] |
| *H. heidelbergensis* | 62 (–)[45]| 1161.7 (9) | 377.8 (P\(^4\)=8, M\(^1\)=9, M\(^2\)=9) [62] |
| *H. rhodesiensis* | 65.8 (7)[45]| 1053.3 (5) | 410.3 (P\(^4\)=1, M\(^1\)=1, M\(^2\)=1) [62] |
| *H. neanderthalensis* | 74.4 (21)[45]| 1414.3 (16) | 331.1 (P\(^4\)=20, M\(^1\)=20, M\(^2\)=19) [62] |
| *H. floresiensis* | 36 (1)[46]| 413.8 (1) | 347.1 (P\(^4\)=1, M\(^1\)=1, M\(^2\)=1) [46] (*) |
| *H. sapiens*     | 65.8 (81)[47]| 1462.7 (37) | 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 mm²) for primate groups. RMA: Reduced Major Axis; OLS: Ordinary Least Squares; N: sample size; r: coefficient of correlation; \( \beta_0 \): Y–intercept; \( \beta_1 \): slope; [CI 95%]: 95% confidence interval for the slope; \( H_0 (b=0) \): null hypothesis for slope zero; \( H_0 (b=1) = 1/2 \): 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   | \( \beta_0 \) | \( \beta_1 \) [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. |
| Platyrhines | 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. |
| Cercopithecoïds | 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   | \( \beta_0 \) | \( \beta_1 \) [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 |
| Platyrhines | 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 |
| Cercopithecoïds | 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. 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    | β₀   | β₁ [CI 95%] | H₀ (β₁=0) | H₀ (β₁=0.5) |
|----------------------|-----|------|------|-------------|-----------|-------------|
| 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.      |
| Cercopithecoidea     | 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   |
| Hominoidea           | 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. floreisins | 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_{size} on logBrM_{size} | N   | r    | β₀   | β₁ [CI 95%] | H₀ (β₁=0) | H₀ (β₁=0.5) |
|----------------------------------|-----|------|------|-------------|-----------|-------------|
| All Primates                     | OLS| 71   | -    | -           | n.s.      | -           |
| Non-human Primates               | OLS| 56   | -    | -           | n.s.      | -           |
| Prosimians                       | 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.      | -           |
| Cercopithecoidea                 | OLS| 25   | -    | -          | n.s.      | -           |
| Hominoidea                       | 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_{size} on logBrM_{size} | N   | r    | β₀   | β₁ [CI 95%] | H₀ (β₁=0) | H₀ (β₁=0.5) |
|----------------------------------|-----|------|------|-------------|-----------|-------------|
| Homo                             | OLS| 56   | 0.791| 0.000       | 0.543 [0.429-0.658] | <0.0001 | <0.05      |
| Non-human Primates               | OLS| 8    | 0.713| 0.441       | 0.838 [0.016-1.660] | <0.05  | n.s.      |
| Prosimians                       | OLS| 48   | 0.902| -0.063      | 0.736 [0.632-0.841] | <0.001  | n.s.      |
| Anthropoids                      | OLS| 17   | 0.824| -0.124      | 0.625 [0.389-0.861] | <0.001  | n.s.      |
| Platyrrhines                     | OLS| 31   | 0.882| -0.037      | 0.724 [0.576-0.871] | <0.001  | n.s.      |
| Catarrhines                      | OLS| 25   | 0.813| -0.029      | 0.741 [0.511-0.970] | <0.001  | n.s.      |
| Cercopithecoidea                 | OLS| 6    | 0.914| -0.382      | 1.154 [0.443-1.866] | <0.02  | n.s.      |

β: Wald statistic from logtransformed regression analyses. β₀: Wald statistic from raw regression analyses.
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   | $\beta_0$ | $\beta_1$ [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   | $\beta_0$ | $\beta_1$ [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$^2$ | $\beta_0$ | $\beta_1$ [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   | β₀  | β₁ [CI 95%]     | se  | H₀ (β₁=0) | H₀ (β₁=isom) | H₀ (β₁=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  | -   | -   | -             | -   | -          | -            | -            |
| 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| -   | 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   | β₀  | β₁ [CI 95%]     | se  | H₀ (β₁=0) | H₀ (β₁=isom) | H₀ (β₁=0.75) |
|----------|----|-----|-----|-----|----------------|-----|------------|--------------|--------------|
| logPCTA_bMres on logBM | PGLS | 56  | -   | -   | -             | -   | -          | n.s.         | -            |
| logDQ_bMres on logBM   | PGLS | 56  | -   | -   | -             | -   | -          | n.s.         | -            |
| logDQ_bMres on logBrM  | PGLS | 56  | -   | -   | -             | -   | -          | n.s.         | -            |
| logPCTA_bMres on logPCTA | PGLS | 56  | -   | -   | -             | -   | -          | n.s.         | -            |
| logDQ_bMres on logPCTA | PGLS | 56  | -   | -   | -             | -   | -          | n.s.         | -            |
| logPCTA_bMres | 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:

$$\text{BrM} = 1.036 \times \text{ECV}[1].$$

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:

$$\text{DQ} = 1\alpha + 2\beta + 3.5\gamma[68],$$
where $\alpha$ is the percentage of leaves and structural parts of plants in the diet, $\beta$ is the percentage of fruit and reproductive parts of plants (including nuts and seeds), and $\gamma$ 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) have 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 $X_1-X_2$, $X_3-X_4$, $X_5-X_6$, and $X_7-X_8$ will be independent of each other. For example, the difference $X_1-X_2$ will depend exclusively on the evolutionary events that took place in branches 1 and 2, while the difference $X_3-X_4$ 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 $((X_1+X_2)/2) - ((X_3+X_4)/2)$ is independent from the difference $((X_5+X_6)/2) - ((X_7+X_8)/2)$ 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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Figure S1. Phylogeny used in this study. 10kTrees Project (Primates: Consensus tree)
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]).