Table 1. Summarized information about total sample size, sex, age at death, and provenance of each taxon.

| Species | *Total n* | Sex[a] M/F/? | Age[b] I/J/A/? | Malleus/Incus/ Stapes | Provenance[c] W/Z/? |
|---|---|---|---|---|---|
| *Homo sapiens* | 57 | 17/12/28 | 0/11/46/0 | 39/43/19 | - |
| *Pan paniscus* | 1 | 0/1/0 | 0/1/0/0 | 1/1/1 | 1/0/0 |
| *Pan troglodytes* | 30 | 11/8/7 | 1/13/13/3 | 21/18/10 | 24/5/1 |
| *Gorilla beringei* | 3 | 1/1/1 | 0/2/1/0 | 3/3/2 | 3/0/0 |
| *Gorilla gorilla* | 13 | 3/7/3 | 1/5/6/1 | 13/10/5 | 11/1/1 |
| *Pongo* sp. | 15 | 6/3/6 | 4/2/5/4 | 11/11/5 | 7/4/4 |
| *Symphalangus syndactylus* | 5 | 0/2/3 | 0/3/2/0 | 5/4/3 | 5/0/0 |

[a] Sex: male (M) / female (F) / unknown (?).

[b] Age: infant (I), M1 un-erupted / juvenile (J), M1 but not M3 erupted / adult (A), M3 erupted/ unknown (?).

[c] Provenance: wild (W) / zoo (Z) / unknown (?).

Table 2. Malleus: *P*-values of malleus mean shape differences among hominoid species.[a]

| | *P. troglodytes* (*n*=21) | *G. beringei* (*n*=3) | *G. gorilla* (*n*=13) | *Pongo* sp. (*n*=11) | *S. syndactylus* (*n*=5) |
|---|---|---|---|---|---|
| *H. sapiens* (*n*=39) | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| *P.troglodytes* (*n*=21) | - | <0.001 | <0.001 | <0.001 | <0.001 |
| *G. beringei* (*n*=3) | | - | 0.001 | 0.003 | 0.03 |
| *G. gorilla* (*n*=13) | | | - | <0.001 | <0.001 |
| *Pongo* sp. (*n*=11) | | | | - | 0.004 |

[a] *P. paniscus* not included since sample size *n*=1

Table 3. Malleus: mean scores of the first three principal components.

| *Species* | PC 1 | PC 2 | PC 3 |
|---|---|---|---|
| *H. sapiens* | 0.051 | -0.001 | -0.001 |
| *P. paniscus* | -0.025 | 0.037 | 0.052 |
| *P. troglodytes* | -0.03 | 0.022 | 0.043 |
| *G. beringei* | -0.044 | -0.023 | -0.001 |
| *G. gorilla* | -0.039 | -0.062 | 0.011 |
| *Pongo* sp. | -0.037 | 0.037 | -0.035 |
| *S. syndactylus* | -0.06 | -0.005 | -0.083 |

Table 4. Malleus: ancestral coordinate estimation of the first three principal components.[a]

| Taxon | PC 1 | s.e.m. | PC 2 | s.e.m. | PC 3 | s.e.m. |
|---|---|---|---|---|---|---|
| Hominidae | -0.030 | 0.004 | 0.008 | 0.005 | -0.021 | 0.004 |
| Homininae | -0.016 | 0.006 | -0.003 | 0.007 | 0.008 | 0.005 |
| *Gorilla* | -0.039 | 0.004 | -0.039 | 0.004 | 0.005 | 0.003 |
| *Pan* | -0.023 | 0.004 | 0.024 | 0.005 | 0.041 | 0.004 |
| Hominini | -0.007 | 0.006 | 0.004 | 0.007 | 0.014 | 0.005 |

[a] s.e.m. standard error of mean

Table 5. Incus: *P*-values of incus mean shape differences among hominoid species.[a]

| | *P. troglodytes* (*n*=18) | *G. beringei* (*n*=3) | *G. gorilla* (*n*=10) | *Pongo* sp. (*n*=11) | *S. syndactylus* (*n*=4) |
|---|---|---|---|---|---|
| *H. sapiens* (*n*=43) | <0.001 | <0.001 | <0.001 | <0.001 | <0.001 |
| *P.troglodytes* (*n*=18) | - | <0.001 | <0.001 | <0.001 | <0.001 |
| *G. beringei* (*n*=3) | | - | 0.01 | 0.003 | 0.057 (n.s.) |
| *G. gorilla* (*n*=10) | | | - | <0.001 | 0.001 |
| *Pongo* sp. (*n*=11) | | | | - | 0.014 |

[a] n.s. not significant; *P. paniscus* not included since sample size *n*=1

Table 6. Incus: mean scores of the first three principal components.

| *Species* | PC 1 | PC 2 | PC 3 |
|---|---|---|---|
| *H. sapiens* | -0.048 | 0.006 | -0.012 |
| *P. paniscus* | 0.024 | 0.037 | 0.043 |
| *P. troglodytes* | 0.071 | 0.053 | -0.009 |
| *G. beringei* | 0.019 | -0.050 | -0.012 |
| *G. gorilla* | 0.052 | -0.079 | -0.013 |
| *Pongo* sp. | 0.010 | -0.030 | 0.047 |
| *S. syndactylus* | 0.005 | 0.004 | 0.063 |

Table 7. Incus: ancestral coordinate estimation of the first three principal components.[a]

| Taxon | PC 1 | s.e.m. | PC 2 | s.e.m. | PC 3 | s.e.m. |
|---|---|---|---|---|---|---|
| Hominidae | 0.012 | 0.006 | -0.012 | 0.005 | 0.027 | 0.005 |
| Homininae | 0.015 | 0.008 | -0.009 | 0.007 | 0.006 | 0.006 |
| *Gorilla* | 0.034 | 0.005 | -0.060 | 0.004 | -0.011 | 0.004 |
| *Pan* | 0.040 | 0.006 | 0.037 | 0.005 | 0.015 | 0.005 |
| Hominini | 0.011 | 0.008 | 0.004 | 0.007 | 0.005 | 0.006 |

[a] s.e.m. standard error of mean

Table 8. Stapes: *P*-values of stapes mean shape differences among hominoid species.[a]

| | *P. troglodytes* (*n*=10) | *G. beringei* (*n*=2) | *G. gorilla* (*n*=5) | *Pongo* sp. (*n*=5) | *S. syndactylus* (*n*=3) |
|---|---|---|---|---|---|
| *H. sapiens* (*n*=19) | <0.001 | 0.009 | <0.001 | <0.001 | <0.001 |
| *P. troglodytes* (*n*=10) | - | 0.089(n.s) | 0.037 | <0.001 | 0.002 |
| *G. beringei* (*n*=2) | | - | 0.619(n.s) | 0.188(n.s.) | 0.199 (n.s.) |
| *G. gorilla* (*n*=5) | | | - | 0.007 | 0.017 |
| *Pongo* sp. (*n*=5) | | | | - | 0.137 |

[a] n.s. not significant; *P. paniscus* not included since sample size *n*=1

Table 9. Stapes: mean scores of the first three principal components.

| *Species* | PC 1 | PC 2 | PC 3 |
|---|---|---|---|
| *H. sapiens* | -0.055 | -0.009 | -0.013 |
| *P. paniscus* | 0.046 | 0.05 | -0.009 |
| *P. troglodytes* | -0.006 | 0.011 | 0.009 |
| *G. beringei* | 0.041 | -0.02 | 0.015 |
| *G. gorilla* | 0.044 | 0.021 | 0.006 |
| *Pongo* sp. | 0.086 | -0.015 | 0.03 |
| *S. syndactylus* | 0.111 | 0.005 | -0.014 |

Table 10. Stapes: ancestral coordinate estimation of the first three principal components.[a]

| Taxon | PC 1 | s.e.m. | PC 2 | s.e.m. | PC 3 | s.e.m. |
|---|---|---|---|---|---|---|
| Hominidae | 0.055 | 0.006 | 0.000 | 0.005 | 0.007 | 0.002 |
| Homininae | 0.020 | 0.008 | 0.006 | 0.007 | 0.002 | 0.003 |
| *Gorilla* | 0.041 | 0.005 | 0.001 | 0.004 | 0.010 | 0.002 |
| *Pan* | 0.018 | 0.006 | 0.026 | 0.005 | 0.000 | 0.002 |
| Hominini | 0.008 | 0.008 | 0.008 | 0.007 | -0.001 | 0.003 |

[a] s.e.m. standard error of mean