Supplemental Material

Supplemental Text

Analysis of chimpanzee data using the chimpanzee MSY reference sequence

Among the species analysed here, chimpanzee is the only one in addition to human for which a high-quality MSY reference sequence exists (Hughes et al. 2010). In order to check if using the human reference sequence (Skaletsky et al. 2003) biased the obtained results for MSY, we mapped all chimpanzee data to the panTro4 reference using Stampy v1.0.23 (Lunter and Goodson 2011). For samples from the published dataset (Prado-Martinez et al. 2013), reads were extracted from MSY BAM files mapped to the human genome reference using the Picard SamToFastq tool (Wysoker et al. 2009). All chimpanzee samples from both datasets were analysed together, and mapping and other data processing steps including filtering were done as described in the main text, except that GATK v3.4-0 (DePristo et al. 2011) was used for local realignment, and in variant calling minimum mapping quality 50 was used.

Variant calling for the chimpanzee MSY phylogeny was done on regions previously defined (Hughes et al. 2010) as X-degenerate and human-orthologous (panTro4 ChrY:16731094-21597282; ChrY:21647020-23798644; ChrY:24047549-25629393; ChrY:25794387-26265354), totalling approximately 9 Mb, with mean coverage ranging from 17 × to 26.6 × (mean 22 ×) for our samples, and from 6.4 × to 18.6 × (mean 10.6 ×) for published (Prado-Martinez et al. 2013) samples. A total of 2,336,730 bp, including 12,127 variant sites, were left after filtering from the total of 19 chimpanzees.

Based on the chimpanzee reference sequence analysis we constructed a maximum parsimony tree (Supplemental Figure S7) and also estimated TMRCAs of the nodes labelled in the tree shown in Figure 3, obtaining very similar dates (Supplemental Table S5).

Comparison of custom-capture and published whole-genome sequence (WGS) datasets

A comparison of MSY sequence data obtained using custom enrichment and whole-genome sequencing was undertaken to investigate possible biases created by the capture approach. The capture probes were built on the human reference genome, therefore possibly enriching for regions of highest homology between great apes and humans. This is expected to affect the MSY regions the most, as autosomes and X Chromosome have diverged less over evolutionary time (Hughes 2010).

We analysed separately the capture and WGS data mapped to the human genome reference sequence for bonobos, chimpanzees, gorillas and orangutans using identical variant calling and filtering parameters, as described for the final merged MSY dataset. This procedure leads to somewhat different final lengths of sequence between the two sequencing approaches (Supplemental Table S3), mainly due to differences in read-depth, and also a further reduced length when data from both
approaches are merged into an overlapping set. We observe statistically significant differences between WGS and sequence-capture in the mean number of variant sites in each species. However, no significant differences are seen between capture and WGS samples for any of the species when these are extracted from the final merged dataset (Supplemental Table S3). Estimates of divergence from human for individual samples, whether based on sequence-capture, WGS, or the merged dataset, are very similar (Supplemental Table S4), showing that when overlapping MSY regions are retained then the datasets behave in the same way.

The obtained differences between capture and WGS data are likely due to a combination of factors such as inappropriate reference sequence, differences in read lengths and depth of coverage, and in the specific MSY regions retained in each analysis. Different regions of a chromosome may differ in mutation rate, as has been reported recently for MSY (Trombetta et al. 2015). The reference sequence effect can neither be overcome nor properly evaluated until high-quality MSY sequences for all species become available. Notably, when mapping chimpanzees to the chimpanzee reference, we see an increase in the total number of variants identified, but the fact that TMRCA estimates are only very slightly affected suggests a minor effect on the overall results and conclusions of our analysis.

**Concordance of genotype calls**

Overlap of some great-ape samples between datasets allowed an assessment of genotype concordance and therefore also gave an indication of data quality in our sequencing.

For mtDNA, GGG_Guy was sequenced both by us and within a published dataset (Xue et al. 2015), and PPA_Bono was sequenced by us and in a published dataset (Prado-Martinez et al. 2013). In each case, comparing respectively 15,453 and 15,447 bp, there were no discordant calls.

For MSY, PPA_Bono was sequenced by us and in a published dataset (Prado-Martinez et al. 2013), and showed no discordant calls out of the 54,695 variant sites used to build the cross-species phylogeny shown in Figure 4.

For autosomal data a total of 28 genotypes out of 14,024 variant sites differed for PPA_Bono between the datasets, suggesting an overall discordance rate ~0.2%.

**Relatedness analysis**

Relatedness is known to be a problem when using great-ape samples, in particular for captive-born individuals. For our samples we had no prior knowledge of possible relatedness, except for gorillas GGG_Nikumba and GGG_Tomoka, who have been reported to be father and son (Boyer et al. 1973). Also, some individuals were known to be closely related based on published genetic data (Prado-Martinez et al. 2013; Xue et al. 2015). In order to estimate the kinship coefficients between all samples, the software KING was used (Manichaikul et al. 2010). Among bonobos, no relatedness was identified. Among chimpanzees, a second-degree relationship was
identified between PTV_8 and PTV_Donald, but since their MSY sequences differ by 82 variants across the final 2,496,576 bp, both samples were retained in all MSY analyses. However, because no differences were found in the mtDNAs between the two, PTV_Donald was retained in the mtDNA tree, but removed from dating and calculations of genetic diversity. Among gorillas, the father-son relationship between GGG_Nikumba and GGG_Tomoka was confirmed. For other gorillas we obtained the same relationships as previously published (Prado-Martinez et al. 2013; Xue et al. 2015). Among orangutans, first-degree relationships were found between PPY_Thai and PPY_Temmy, and PAB_Sinjo and PAB_Babu.

**ADMiXTURE analysis**

Analysis of shared genetic components in autosomal data was done using the ADMiXTURE program (Alexander et al. 2009) with 10-fold cross-validation (CV) (Alexander and Lange 2011). In order to avoid biases from related individuals, the following samples were excluded: PTV_Donald, GGG_Tomoka, GGG_Bulera, GGG_Suzie, GGG_Oko, GGG_Kowali, GBB_UMurimo, GBB_Maisha, PPY_Temmy and PAB_Babu. Overall the results (Supplemental Figure S3) agree well with the PCAs (Figure 2; Supplemental Figure S1). The CV error is lowest for $k=1$ for bonobos, $k=3$ for chimpanzees, and $k=2$ for gorillas and orangutans (Supplemental Figure S4). For the final number of autosomal variants used for each species, see Supplemental Table S2.

**Ancestral states of MSY variants**

In order to define the ancestral states for the final filtered variants used in intraspecific phylogenetic tree construction (Figure 3), we used sequence data generated from the other species (including humans), as well as the phylogenetic information from the maximum parsimony tree extracted from the PHYLIP outfile.

First, final variant sites from the species to be rooted were called from other species using SAMTools (Li et al. 2009) as described above, filtered for strand bias and minimum depth $\geq 1$. For rooting the bonobo and chimpanzee trees, the allele matching gorillas or orangutans was preferred, and when missing data or non-matching alleles precluded this, the human allele was used. For gorillas, the orangutan allele was preferred and for orangutans the gorilla allele was preferred. If the sites were missing in the other species or alleles did not match, then the ancestral allele was assigned randomly.

The allelic state defined using other species was checked against the reconstructed ancestral state from the PHYLIP output. If the defined allele did not match with the deepest rooting branches, but an allele from a different species did, then the ancestral state was changed and after checking all sites the maximum parsimony tree was constructed again. For all species this left a small proportion of sites (0.12-1.82% of variants) where the ancestral state was not supported by reconstructed states in the PHYLIP output.
Estimation of human-chimpanzee MSY divergence time based on sequence data

To ask if using the human MSY mutation rate was reasonable, we used it to estimate the divergence time of humans and chimpanzees. Human and chimpanzee samples were called and filtered together, yielding a total of 43,752 variants across 2,171,604 bp. Generation time differences were accounted for by averaging the per-nucleotide-per-year mutation rates. We used a Yule process speciation tree prior, a strict clock with normal distribution and HKY substitution model.

Supplemental References

Alexander DH, Lange K. 2011. Enhancements to the ADMIXTURE algorithm for individual ancestry estimation. *BMC bioinformatics* 12: 246.
Alexander DH, Novembre J, Lange K. 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Res* 19: 1655-1664.
Arora N, Nater A, van Schaik CP, Willems EP, van Noordwijk MA, Goossens B, Morf N, Bastian M, Knott C, Morrogh-Bernard H et al. 2010. Effects of Pleistocene glaciations and rivers on the population structure of Bornean orangutans (Pongo pygmaeus). *Proc Natl Acad Sci U S A* 107: 21376-21381.
Batini C, Lopes J, Behar DM, Calafell F, Jorde LB, van der Veen L, Quintana-Murci L, Spedini G, Destro-Bisol G, Comas D. 2011. Insights into the demographic history of African Pygmies from complete mitochondrial genomes. *Mol Biol Evol* 28: 1099-1110.
Bjork A, Liu W, Wertheim JO, Hahn BH, Worobey M. 2011. Evolutionary history of chimpanzees inferred from complete mitochondrial genomes. *Mol Biol Evol* 28: 615-623.
Boyer SH, Noyes AN, Boyer ML, Marr K. 1973. Hemoglobin alpha-3 chains in apes. Primary structures and the presumptive nature of back mutation in a normally silent gene. *J Biol Chem* 248: 992-1003.
Das R, Hergenrother SD, Soto-Calderon ID, Dew JL, Anthony NM, Jensen-Seaman ML. 2014. Complete mitochondrial genome sequence of the Eastern gorilla (Gorilla beringei) and implications for african ape biogeography. *J Hered* 105: 752-761.
DePristo MA, Banks E, Poplin R, Garimella KV, Maguire JR, Hartl C, Philippakis AA, del Angel G, Rivas MA, Hanna M et al. 2011. A framework for variation discovery and genotyping using next-generation DNA sequencing data. *Nat Genet* 43: 491-498.
Eriksson J, Siedel H, Lukas D, Kayser M, Erler A, Hashimoto C, Hohmann G, Boesch C, Vigilant L. 2006. Y-chromosome analysis confirms highly sex-biased dispersal and suggests a low male effective population size in bonobos (Pan paniscus). *Mol Ecol* 15: 939-949.
Hallast P, Batini C, Zadik D, Maisano Delser P, Wetton JH, Arroyo-Pardo E, Cavalleri GL, de Knijff P, Destro Bisol G, Dupuy BM et al. 2015. The Y-chromosome tree bursts into leaf: 13,000 high-confidence SNPs covering the majority of known clades. *Mol Biol Evol* 32: 661-673.
Hughes JF, Skaletsky H, Pyntikova T, Graves TA, van Daalen SK, Minx PJ, Fulton RS, McGrath SD, Locke DP, Friedman C et al. 2010. Chimpanzee and human
Y chromosomes are remarkably divergent in structure and gene content. *Nature* **463**: 536-539.

Hvilsom C, Carlsten F, Heller R, Jaffre N, Siegismund HR. 2014. Contrasting demographic histories of the neighboring bonobo and chimpanzee. *Primates* **55**: 101-112.

Karmin M, Saag L, Vicente M, Wilson Sayres MA, Jarve M, Talas UG, Rootsi S, Ilumae AM, Magi R, Mitt M et al. 2015. A recent bottleneck of Y chromosome diversity coincides with a global change in culture. *Genome Res* **25**: 459-466.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, Genome Project Data Processing S. 2009. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**: 2078-2079.

Lunter G, Goodson M. 2011. Stampy: a statistical algorithm for sensitive and fast mapping of Illumina sequence reads. *Genome Res* **21**: 936-939.

Ma X, Kelley JL, Eilertson K, Musharoff S, Degenhardt JD, Martins AL, Vinar T, Kosiol C, Siepel A, Gutenkunst RN et al. 2013. Population genomic analysis reveals a rich speciation and demographic history of orang-utans (Pongo pygmaeus and Pongo abelii). *PLoS One* **8**: e77175.

Manichaikul A, Mychaleckyj JC, Rich SS, Daly K, Sale M, Chen WM. 2010. Robust relationship inference in genome-wide association studies. *Bioinformatics* **26**: 2867-2873.

Nater A, Nietlisbach P, Arora N, van Schaik CP, van Noordwijk MA, Willems EP, Singleton I, Wich SA, Goossens B, Warren KS et al. 2011. Sex-biased dispersal and volcanic activities shaped phylogeographic patterns of extant Orangutans (genus: Pongo). *Mol Biol Evol* **28**: 2275-2288.

Oetjens MT, Shen F, Zou Z, Kidd JM. 2015. Inferring chimpanzee Y chromosome history and amplicon diversity from whole genome sequencing. *BioRxiv* doi: org/10.1101/029702.

Prado-Martinez J, Sudmant PH, Kidd JM, Li H, Kelley JL, Lorente-Galdos B, Veeramah KR, Woerner AE, O'Connor TD, Santpere G et al. 2013. Great ape genetic diversity and population history. *Nature* **499**: 471-475.

Skaletsky H, Kuroda-Kawaguchi T, Minx PJ, Cordum HS, Hillier L, Brown LG, Repping S, Pyntikova R, Ali J, Bieri T et al. 2003. The male-specific region of the human Y chromosome: a mosaic of discrete sequence classes. *Nature* **423**: 825-837.

Stone AC, Griffiths RC, Zegura SL, Hammer MF. 2002. High levels of Y-chromosome nucleotide diversity in the genus *Pan*. *Proc Natl Acad Sci U S A* **99**: 43-48.

Stone AC, Battistuzzi FU, Kubatko LS, Perry GH, Jr., Trudeau E, Lin H, Kumar S. 2010. More reliable estimates of divergence times in Pan using complete mtDNA sequences and accounting for population structure. *Philosophical Transactions of the Royal Society of London Series B, Biological sciences* **365**: 3277-3288.

Trombetta B, D’Atanasio E, Massaia A, Myres NM, Scozzari R, Cruciani F, Novelletto A. 2015. Regional differences in the accumulation of SNPs on the male-specific portion of the human Y chromosome replicate autosomal patterns: implications for genetic dating. *PLoS One* **10**: e0134646.

Wysoker A, Tibbetts K, Fennell T. 2009. Picard v1.86, available from http://picard.sourceforge.net/.
Xue Y, Prado-Martinez J, Sudmant PH, Narasimhan V, Ayub Q, Szpak M, Frandsen P, Chen Y, Yngvadottir B, Cooper DN et al. 2015. Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. *Science* **348**: 242-245.

Zsurka G, Kudina T, Peeva V, Hallmann K, Elger CE, Khrapko K, Kunz WS. 2010. Distinct patterns of mitochondrial genome diversity in bonobos (Pan paniscus) and humans. *BMC Evol Biol* **10**: 270.
Supplemental Table S1: Great-ape and human individuals sequenced and analysed in this study.

| Species                      | Common name          | Name       | Name in figures | Sex | Studbook ID | Geographic origin/patient/birth origin | MSY/mtD NA lineage | Ref |
|------------------------------|----------------------|------------|-----------------|-----|-------------|----------------------------------------|-------------------|-----|
| *Pan paniscus*               | Bonobo               | Bono       | PPA_Bono        | M   | 102         | Wild born                             | na                |     |
| *P. paniscus*                | Bonobo               | PPA2       | PPA_PPA2        | M   | na          | Captive born                           | na                |     |
| *P. paniscus*                | Bonobo               | Masikini   | PPA_Masikini    | M   | 54          | Wild born                             | na                |     |
| *Pan troglodytes troglodytes*| Central chimpanzee   | Moritz     | PTT_Moritz      | M   | 10920       | Nigeria, wild born                     | na                |     |
| *P. t. troglodytes/ *Pan troglodytes verus* | Tommy | PTT/PTV_Tommy |               | M   | na          | Wild born?                            | na                |     |
| *P. t. schweinfurthii*       | Eastern chimpanzee   | Bobby      | PTS_Bobby       | M   | na          | Wild born?                            | na                |     |
| *P. t. verus*                | Western chimpanzee   | PTR7 - Johnny | PTV_7          | M   | na          | Captive born                          | na                |     |
| *P. t. verus*                | Western chimpanzee   | Buttons    | PTV_Buttons     | M   | 10411       |                                       | na                |     |
| *P. t. verus*                | Western chimpanzee   | NA03450    | PTV_NA03450     | M   | na          | Coriell Institute for Medical Research | na                |     |
| *P. t. verus*                | Western chimpanzee   | PTR8 - Carl | PTV_8          | M   | na          | Captive born                          | na                |     |
| *P. t. verus* / *P. t. elliotti* | hybrid | EB176JC  | PTE/PTV_EB176JC | M   | na          | ECACC cell line no. 89072704           | na                |     |
| *Gorilla gorilla gorilla*    | Western lowland gorilla | Fritz | GGG_Fritz      | M   | 253         | Cameroon, wild born                    | na                |     |
| *G. gorilla gorilla*         | Western lowland gorilla | Tomoka | GGG_Tomoka    | M   | 122         | Captive born                          | na                |     |
| *G. g. gorilla*              | Western lowland gorilla | Guy | GGG_Guy        | M   | 5           | Cameroon, wild born                    | na                |     |
| *G. g. gorilla*              | Western lowland gorilla | Nikumba | GGG_Nikumba    | M   | 42          | Republic of the Congo (?) , wild born  | na                |     |
| *Pongo abelii*               | Sumatran orangutan   | Sinjo      | PAB_Sinjo       | M   | 1007        | Captive born                          | na                |     |
| *P. abelii*                  | Sumatran orangutan   | Duapuluh   | PAB_Duapuluh    | M   | 2810        | Captive born                          | na                |     |
| *P. abelii*                  | Sumatran orangutan   | ppy10      | PAB_ppy10      | M   | na          | Captive born                          | na                |     |
| *P. pygmaeus*                | Bornean orangutan    | Thai       | PPY_Thai       | M   | 2861        | Captive born                          | na                |     |

**Human samples used for MSY**

| Homo sapiens | Human GRC13292546 | HSA_A00 | M | Mbo | A00 | 1 |
|--------------|-------------------|---------|---|-----|-----|---|
| H. sapiens   | Human bkl-2       | HSA_A0  | M | Bakola | A0-L896 | 2 |
| Specie               | Sample       | Code          | Haplotype | Gender | Language | Code          | Population | Birth Type | Notes   |
|---------------------|--------------|---------------|-----------|--------|----------|---------------|-------------|------------|---------|
| *H. sapiens*        | Human        | eng-GB1778    | HSA_A1a   | M      | English  | A1a-M31       |             |            |         |
| *H. sapiens*        | Human        | bak-41        | HSA_A2    | M      | Baka     | A2-M14        |             |            |         |
| *H. sapiens*        | Human        | bak-25        | HSA_B2a   | M      | Baka     | B2a-M152      |             |            |         |
| *H. sapiens*        | Human        | nep-0273      | HSA_C5    | M      | Nepalese | C5-M365       |             |            |         |
| *H. sapiens*        | Human        | bav-13        | HSA_E1b   | M      | Bavarian | E1b1b1c-M123 |             |            |         |
| *H. sapiens*        | Human        | ire-55        | HSA_R1b   | M      | Irish    | R1b1b2-M222   |             |            |         |

**Human samples used for mtDNA**

| Specie               | Sample       | Code          | Haplotype | Gender | Language | Code          | Population | Birth Type | Notes   |
|---------------------|--------------|---------------|-----------|--------|----------|---------------|-------------|------------|---------|
| *H. sapiens*        | Human        | eng-O109      | HSA_H     | M      | English  | H             |             |            |         |
| *H. sapiens*        | Human        | CHB-NA18636   | HSA_M     | M      | Chinese (CHB) | M            |             |            |         |
| *H. sapiens*        | Human        | CHB-NA18611   | HSA_A     | M      | Chinese (CHB) | A            |             |            |         |
| *H. sapiens*        | Human        | CHB-NA18562   | HSA_D     | M      | Chinese (CHB) | D            |             |            |         |
| *H. sapiens*        | Human        | ork-565       | HSA_U4    | M      | Orcadian | U4            |             |            |         |
| *H. sapiens*        | Human        | YRI-NA18501   | HSA_L1    | M      | Yoruba (YRI) | L1           |             |            |         |
| *H. sapiens*        | Human        | YRI-NA18856   | HSA_L2    | M      | Yoruba (YRI) | L2           |             |            |         |
| *H. sapiens*        | Human        | H079          | HSA_L0    | M      | Mbuti    | L0a           |             |            |         |

**Great ape samples from published datasets**

| Specie               | Sample       | Code          | Haplotype | Gender | Language | Code          | Population | Birth Type | Notes   |
|---------------------|--------------|---------------|-----------|--------|----------|---------------|-------------|------------|---------|
| *P. paniscus*       | Bonobo       | Desmond       | PPA_Desmond | M      | Wild born | na            |             |            |         |
| *P. paniscus*       | Bonobo       | Bono          | PPA_Bono   | M      | Wild born | na            |             |            |         |
| *P. paniscus*       | Bonobo       | LB502         | PPA_LB502  | F      | Captive born | na        |             |            |         |
| *P. paniscus*       | Bonobo       | Hortense      | PPA_Hortense | F      | Wild born | na            |             |            |         |
| *P. paniscus*       | Bonobo       | Kosana        | PPA_Kosana | F      | Wild born | na            |             |            |         |
| *P. paniscus*       | Bonobo       | Dzeeta        | PPA_Dzeeta | F      | Wild born | na            |             |            |         |
| *P. paniscus*       | Bonobo       | Hermien       | PPA_Hermien | F      | Wild born | na            |             |            |         |
| Species               | Status                        | Name         | Sex  | Age | Birth Method | Notes |
|-----------------------|-------------------------------|--------------|------|-----|--------------|-------|
| *P. paniscus*         | Bonobo                        | Catherine    | F    | 55  | Wild born    | na    |
| *P. paniscus*         | Kombote                       | PPA_Kombote  | F    | 56  | Wild born    | na    |
| *P. paniscus*         | Chipita                       | PPA_Chipita  | F    | 220 | Wild born    | na    |
| *P. paniscus*         | Natalie                       | PPA_Natalie  | F    | 46  | Wild born    | na    |
| *P. paniscus*         | Salonga                       | PPA_Salonga  | F    | 52  | Captive born | na    |
| *P. paniscus*         | Kumbuka                       | PPA_Kumbuka  | F    | 260 | Captive born | na    |
| *P. t. troglodytes*   | Central chimpanzee            | Vaillant     | M    | na  | Wild born    | na    |
| *P. t. troglodytes*   | Doris                         | PTT_Doris    | F    | na  | Wild born    | na    |
| *P. t. troglodytes*   | Julie                         | PTT_Julie    | F    | 10306 | Wild born | na    |
| *P. t. schweinfurthii*| Eastern chimpanzee            | Vincent      | M    | Ch-045 | Wild born | na    |
| *P. t. schweinfurthii*| Kidongo                       | PTS_Kidongo  | F    | N/A | Wild born    | na    |
| *P. t. schweinfurthii*| Nakuu                         | PTS_Nakuu    | F    | N/A | Wild born    | na    |
| *P. t. verus*         | Bosco                         | PTV_Bosco    | M    | 215 | Wild born    | na    |
| *P. t. verus*         | Koby                          | PTV_Koby     | M    | 650 | Wild born    | na    |
| *P. t. verus*         | Clint                         | PTV_Clint    | M    | C0471 | Captive born | na    |
| *P. t. verus*         | Donald                        | PTV_Donald   | M    | C0551 | Captive born | na    |
| *P. t. elliotti*      | Nigeria-Cameroon chimpanzee  | Akwaya-Jean  | M    | LWC2 | Wild born    | na    |
| *P. t. elliotti*      | Basho                         | PTE_Basho    | M    | LWC8 | Wild born    | na    |
| *P. t. elliotti*      | Damian                        | PTE_Damian   | M    | LWC12 | Wild born  | na    |
| *P. t. elliotti*      | Koto                          | PTE_Koto     | M    | LWC24 | Wild born  | na    |
| *P. t. elliotti*      | Taweh*                        | PTE_Taweh    | M    | LWC43 | Wild born  | na    |
| *P. t. elliotti*      | Banyo                         | PTE_Banyo    | F    | LWC7 | Wild born    | na    |
| Species                  | Subspecies                  | Population | Sex | Birth Year | Status   | Age |
|-------------------------|-----------------------------|------------|-----|------------|----------|-----|
| *P. t. ellioti*         | Nigeria-Cameroon chimpanzee| Julie      | F   | LWC21      | Wild born| na  |
| *P. t. ellioti*         | Nigeria-Cameroon chimpanzee| Kopongo    | F   | LWC23      | Wild born| na  |
| *P. t. ellioti*         | Nigeria-Cameroon chimpanzee| Paquita    | F   | LWC038     | Wild born| na  |
| *P. t. ellioti*         | Nigeria-Cameroon chimpanzee| Tobi       | F   | LWC046     | Wild born| na  |
| *G. beringei graueri*   | Eastern lowland gorilla     | M'kubwa    | M   | 9907       | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Kaisi      | M   | 9909       | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Ntabwoba   | M   | na         | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Victoria   | F   | 9919       | Captive born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Dunia      | F   | na         | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Itebero    | F   | na         | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Pinga      | F   | na         | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Serufuli   | F   | na         | Wild born| na  |
| *G. b. graueri*         | Eastern lowland gorilla     | Tumani     | F   | na         | Wild born| na  |
| *G. b. beringei*        | Mountain gorilla            | Imfura     | M   | na         | Wild born| na  |
| *G. b. beringei*        | Mountain gorilla            | Kaboko     | M   | na         | Wild born| na  |
| *G. b. beringei*        | Mountain gorilla            | Zirikana   | M   | na         | Wild born| na  |
| *G. b. beringei*        | Mountain gorilla            | Maisha     | F   | na         | Wild born| na  |
| *G. b. beringei*        | Mountain gorilla            | Tuck       | F   | na         | Wild born| na  |
| *G. b. beringei*        | Mountain gorilla            | Turimaso   | F   | na         | Wild born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Azizi      | M   | 1459       | Captive born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Banjo      | M   | 255        | Wild born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Abe        | M   | 52         | Wild born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Tzambo     | M   | 440        | Wild born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Kowali     | F   | 663        | Captive born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Bulera     | F   | 1120       | Captive born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Suzie      | F   | 636        | Wild born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Kokamo     | F   | 1049       | Captive born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Mimi       | F   | 241        | Wild born| na  |
| *G. g. gorilla*         | Western lowland gorilla     | Dian       | F   | 1091       | Captive born| na  |
| Species            | Common Name                        | Gender | Call Number | Birth Location                  | Gender | Born Location | References          |
|--------------------|------------------------------------|--------|-------------|---------------------------------|--------|---------------|---------------------|
| G. g. gorilla      | Western lowland gorilla            | Delphi | GGG_Delphi  | F                               | 230    | Wild born     | 1 – Karmin et al. 2015; 2 – Hallast et al. 2015 |
| G. g. gorilla      | Western lowland gorilla            | Sandra | GGG_Sandra  | F                               | 969    | Captive born  | 3 – Batini et al. 2011; 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Coco   | GGG_Coco    | F                               | 1351   | Wild born     | 5 – Xue et al. 2015 |
| G. g. gorilla      | Western lowland gorilla            | Kolo   | GGG_Kolo    | F                               | 936    | Captive born  | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Amani  | GGG_Amani   | F                               | 899    | Captive born  | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Akiba Beri | GGG_Akiba_Beri | F                     | 1926   | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Choomba | GGG_Choomba | F                               | 180    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Paki   | GGG_Paki    | F                               | 191    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Anthal | GGG_Anthal  | F                               | 1930   | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Katie  | GGG_B650_Katie | F                           | 498    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Carolyn | GGG_Carolyn | F                       | 3      | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Porta  | GGG_Porta   | F                               | 64     | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Vila   | GGG_Vila    | F                               | 80     | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Helen  | GGG_Helen   | F                               | 96     | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Oko    | GGG_OKo     | F                               | 192    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Dolly  | GGG_Dolly   | F                               | 195    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. gorilla      | Western lowland gorilla            | Katie  | GGG-KB4986_Katie | F                     | 498    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| G. g. diehli       | Cross River gorilla                | Nyango | GGD_Nyango  | F                               | 9941   | Wild born     | 4 – Prado-Martinez et al. 2013 |
| P. abelii          | Sumatran orangutan                 | Buschi | PAB_Buschi  | M                               | 498    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| P. abelii          | Sumatran orangutan                 | Elsi   | PAB_Elsi    | F                               | 446    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| P. abelii          | Sumatran orangutan                 | Kiki   | PAB_Kiki    | F                               | 154    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| P. abelii          | Sumatran orangutan                 | Dunja  | PAB_Dunja   | F                               | 1302   | Captive born  | 4 – Prado-Martinez et al. 2013 |
| P. abelii          | Sumatran orangutan                 | Babu   | PAB_Babu    | F                               | 511    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| P. pygmaeus        | Bornean orangutan                  | Napoleon | PPY_Napoleon | M               | 898    | Wild born     | 4 – Prado-Martinez et al. 2013 |
| P. pygmaeus        | Bornean orangutan                  | Nonja  | PPY_Nonja   | F                               | 1581   | Captive born  | 4 – Prado-Martinez et al. 2013 |
| P. pygmaeus        | Bornean orangutan                  | Temmy  | PPY_Temmy   | F                               | 1852   | Captive born  | 4 – Prado-Martinez et al. 2013 |
| P. pygmaeus        | Bornean orangutan                  | Sari   | PPY_Sari    | F                               | 1097   | Captive born  | 4 – Prado-Martinez et al. 2013 |
| P. pygmaeus        | Bornean orangutan                  | Tilda  | PPY_Tilda   | F                               | 1452   | Wild born     | 4 – Prado-Martinez et al. 2013 |

* - according to Prado-Martinez et al. 2013, Taweh seems to have two X Chromosomes plus a portion of the Y Chromosome, therefore in this study only autosomal regions were used from this sample; na – not available.
### Supplemental Table S2: Summary of variants and sequenced regions.

|                | N  | Final length | S    | Recurrent sites (%) |
|----------------|----|--------------|------|---------------------|
| **MSY (hg19)** |    |              |      |                     |
| All samples    | 51 | 750,616      | 54,611 | na                  |
| Humans         | 8  | 3,587,037    | 3544  | na                  |
| Chimpanzees    | 19 | 2,496,576    | 12,208| 68 (0.56%)          |
| Bonobos        | 4  | 3,637,523    | 3284  | 0 (0%)              |
| Chimpanzees and bonobos | 23 | 2,340,169 | 18,753 | na |
| Gorillas       | 13 | 2,043,299    | 1262  | 4 (0.32%)           |
| Orangutans     | 6  | 2,348,840    | 2476  | 8 (0.32%)           |
| **MSY (PanTro4)** |    |              |      |                     |
| Chimpanzees    | 19 | 2,336,730    | 12,127| 87 (0.72%)          |
| **ChrX**       |    |              |      |                     |
| Chimpanzees    | 19 | 211,364      | 1070  | na                  |
| Bonobos        | 4  | 268,948      | 220   | na                  |
| Gorillas       | 14 | 72,837       | 171   | na                  |
| Orangutans     | 6  | 247,819      | 890   | na                  |
| **Autosomal**  |    |              |      |                     |
| Chimpanzees    | 33 | 3,666,900    | 27,376| na                  |
| Bonobos        | 15 | 5,092,536    | 13,996| na                  |
| Gorillas       | 48 | 2,627,902    | 10,069| na                  |
| Orangutans     | 14 | 5,364,020    | 48,109| na                  |

N - sample size; S – number of variable sites; na – not available.
Supplemental Table S3: Comparison of MSY data based on custom-capture and whole-genome sequencing.

| Dataset* | N | Final length | Mean no. of REF sites | Mean no. of ALT sites | Mean divergence from human | p-value** |
|----------|---|---------------|----------------------|----------------------|---------------------------|-----------|
| **Bonobos** | | | | | | |
| WGS      | 2 | 3,994,211     | 3,933,780            | 60,431               | 1.513                     | 0.003 (WGS vs capt.) |
| capture  | 3 | 3,799,793     | 3,743,280            | 56,513               | 1.487                     | 0.406 (capt. vs merged) |
| merged   | 4 | 3,637,523     | 3,583,692            | 53,831               | 1.480                     | <0.0001 (WGS vs merged) |
| merged-WGS | 2 | 3,637,523     | 3,583,681            | 53,843               | 1.480                     | 0.949 (merged-WGS vs merged-capt.) |
| merged-capture | 3 | 3,637,523 | 3,583,702 | 53,821 | 1.479 |
| **Chimpanzees** | | | | | | |
| WGS      | 11 | 3,075,888     | 3,032,804            | 43,084               | 1.401                     | <0.0001 (WGS vs capt.) |
| capture  | 8 | 3,297,041     | 3,247,697            | 49,344               | 1.497                     | <0.0001 (capt. vs merged) |
| merged   | 19 | 2,496,576     | 2,460,684            | 35,892               | 1.438                     | <0.0001 (WGS vs merged) |
| merged-WGS | 11 | 2,496,576 | 2,460,712 | 35,864 | 1.436 |
| merged-capture | 8 | 2,496,576 | 2,460,645 | 35,931 | 1.439 |
| **Gorillas** | | | | | | |
| WGS      | 10 | 2,071,756     | 2,031,405            | 40,351               | 1.948                     | <0.0001 (WGS vs capt.) |
| capture  | 4 | 2,789,895     | 2,732,957            | 56,938               | 2.041                     | <0.0001 (capt. vs merged) |
| merged   | 14 | 2,043,299     | 2,003,432            | 39,867               | 1.951                     | 0.803 (WGS vs merged) |
| merged-WGS | 10 | 2,043,299 | 2,003,437 | 39,862 | 1.951 |
| merged-capture | 4 | 2,043,299 | 2,003,421 | 39,878 | 1.952 |
| **Orangutans** | | | | | | |
| WGS      | 2 | 2,850,916     | 2,709,102            | 141,815              | 4.974                     | <0.0001 (WGS vs capt.) |
| capture  | 4 | 2,537,735     | 2,426,470            | 111,266              | 4.384                     | 0.018 (capt. vs merged) |
| merged   | 6 | 2,348,840     | 2,246,887            | 101,954              | 4.341                     | <0.0001 (WGS vs merged) |
| merged-WGS | 2 | 2,348,840 | 2,246,865 | 101,975 | 4.341 |
| merged-capture | 4 | 2,348,840 | 2,246,897 | 101,943 | 4.340 |

* - WGS - whole-genome sequenced samples; capture - samples sequenced using custom-capture approach (current study); merged - WGS and capture samples analysed together to obtain overlapping sites that were used in all analysis undertaken; merged-WGS/merged-capture - WGS/capture samples extracted from the final merged dataset

** - chi square with Yates correction
Supplemental Table S4: Comparison of individual sample data based on custom-capture and whole-genome sequencing.

| Sample            | Dataset | Final length | Fixed differences | Variant sites (REF calls) | Variant sites (ALT calls) | Divergence from human | Dataset    | Final length | Fixed differences | Variant sites (REF calls) | Variant sites (ALT calls) | Divergence from human |
|-------------------|---------|--------------|-------------------|---------------------------|---------------------------|-----------------------|------------|--------------|-------------------|---------------------------|---------------------------|------------------------|
| **Bonobos**       |         |              |                   |                           |                           |                       |            |              |                   |                           |                           |                        |
| PPA_Desmond       | WGS     | 3,994,211    | 58,668            | 1706                      | 1767                      | 1.513                 | merged-WGS | 3,637,523    | 52,259            | 1684                      | 1600                      | 1.481                  |
| PPA_Bono          | WGS     | 3,994,211    | 58,668            | 1714                      | 1759                      | 1.513                 | merged-WGS | 3,637,523    | 52,259            | 1717                      | 1567                      | 1.480                  |
| PPA_PPA2          | capture | 3,799,793    | 56,323            | 186                       | 196                       | 1.487                 | merged-capt.| 3,637,523    | 52,259            | 1717                      | 1567                      | 1.480                  |
| PPA_Masikini      | capture | 3,799,793    | 56,323            | 194                       | 188                       | 1.487                 | merged-capt.| 3,637,523    | 52,259            | 1725                      | 1559                      | 1.480                  |
| **Chimpanzees**   |         |              |                   |                           |                           |                       |            |              |                   |                           |                           |                        |
| PTE_Akwaya_Jean   | WGS     | 3,075,888    | 41,113            | 5420                      | 2065                      | 1.404                 | merged-WGS | 2,496,576    | 32,086            | 3830                      | 3828                      | 1.439                  |
| PTE_Basho         | WGS     | 3,075,888    | 41,113            | 5575                      | 1910                      | 1.399                 | merged-WGS | 2,496,576    | 32,086            | 8511                      | 3697                      | 1.433                  |
| PTE_Damian        | WGS     | 3,075,888    | 41,113            | 5426                      | 2059                      | 1.404                 | merged-WGS | 2,496,576    | 32,086            | 8383                      | 3825                      | 1.438                  |
| PTE_Koto          | WGS     | 3,075,888    | 41,113            | 5421                      | 2064                      | 1.404                 | merged-WGS | 2,496,576    | 32,086            | 8380                      | 3828                      | 1.439                  |
| PTS_Vincent       | WGS     | 3,075,888    | 41,113            | 5563                      | 1922                      | 1.399                 | merged-WGS | 2,496,576    | 32,086            | 8448                      | 3760                      | 1.436                  |
| PTS_Bwambale      | WGS     | 3,075,888    | 41,113            | 5608                      | 1877                      | 1.398                 | merged-WGS | 2,496,576    | 32,086            | 8487                      | 3721                      | 1.434                  |
| PTT_Vaillant      | WGS     | 3,075,888    | 41,113            | 5546                      | 1939                      | 1.400                 | merged-WGS | 2,496,576    | 32,086            | 8495                      | 3713                      | 1.434                  |
| PTV_Bosco         | WGS     | 3,075,888    | 41,113            | 5526                      | 1959                      | 1.400                 | merged-WGS | 2,496,576    | 32,086            | 8414                      | 3794                      | 1.437                  |
| PTV_Koby          | WGS     | 3,075,888    | 41,113            | 5524                      | 1961                      | 1.400                 | merged-WGS | 2,496,576    | 32,086            | 8412                      | 3796                      | 1.437                  |
| PTV_Clint         | WGS     | 3,075,888    | 41,113            | 5520                      | 1965                      | 1.401                 | merged-WGS | 2,496,576    | 32,086            | 8402                      | 3806                      | 1.438                  |
| PTV_Donald        | WGS     | 3,075,888    | 41,113            | 5527                      | 1958                      | 1.400                 | merged-WGS | 2,496,576    | 32,086            | 8413                      | 3795                      | 1.437                  |
| PTT/PTV_Tommy     | capture | 3,297,041    | 44,404            | 6563                      | 5046                      | 1.500                 | merged-capt.| 2,496,576    | 32,086            | 8206                      | 4002                      | 1.445                  |
| PTV_7             | capture | 3,297,041    | 44,404            | 6694                      | 4915                      | 1.496                 | merged-capt.| 2,496,576    | 32,086            | 8404                      | 3804                      | 1.438                  |
| PTT_Moritz        | capture | 3,297,041    | 44,404            | 6551                      | 5058                      | 1.500                 | merged-capt.| 2,496,576    | 32,086            | 8193                      | 4015                      | 1.446                  |
| PTS_Bobby         | capture | 3,297,041    | 44,404            | 6767                      | 4842                      | 1.494                 | merged-capt.| 2,496,576    | 32,086            | 8483                      | 3725                      | 1.434                  |
| PTE/PTV_EB176JC   | capture | 3,297,041    | 44,404            | 6696                      | 4913                      | 1.496                 | merged-capt.| 2,496,576    | 32,086            | 8406                      | 3802                      | 1.437                  |
| PTV.Buttons       | capture | 3,297,041    | 44,404            | 6689                      | 4920                      | 1.496                 | merged-capt.| 2,496,576    | 32,086            | 8400                      | 3808                      | 1.438                  |
| PTV_NA03450       | capture | 3,297,041    | 44,404            | 6699                      | 4910                      | 1.496                 | merged-capt.| 2,496,576    | 32,086            | 8410                      | 3798                      | 1.437                  |
| PTV_8             | capture | 3,297,041    | 44,404            | 6693                      | 4916                      | 1.496                 | merged-capt.| 2,496,576    | 32,086            | 8403                      | 3805                      | 1.438                  |
### Gorillas

| Gorillas   | Method | Length (bp) | Repeat (bp) | Contig (bp) | N50 (bp) | Phred (bp) |
|------------|--------|-------------|-------------|-------------|----------|------------|
| GBG_Mkubwa | WGS    | 2,071,756   | 39,991      | 851         | 353      | 1.947      |
| GBG_Kaisi  | WGS    | 2,071,756   | 39,991      | 841         | 363      | 1.948      |
| GGG_Azizi  | WGS    | 2,071,756   | 39,991      | 848         | 356      | 1.947      |
| GGG_Banjo  | WGS    | 2,071,756   | 39,991      | 813         | 391      | 1.949      |
| GGG_Abe    | WGS    | 2,071,756   | 39,991      | 827         | 377      | 1.948      |
| GGG_Tzambo | WGS    | 2,071,756   | 39,991      | 870         | 334      | 1.946      |
| GBB_Imfura | WGS    | 2,071,756   | 39,991      | 848         | 356      | 1.947      |
| GBB_Kaboko | WGS    | 2,071,756   | 39,991      | 850         | 354      | 1.947      |
| GBB_Zirikana | WGS | 2,071,756 | 39,991 | 850 | 354 | 1.947 |
| GBG_Ntabwoba | WGS | 2,071,756 | 39,991 | 842 | 362 | 1.948 |
| GGG_Fritz  | capture| 2,789,895   | 56,651      | 446         | 293      | 2.041      |
| GGG_Tomoka | capture| 2,789,895   | 56,651      | 469         | 270      | 2.040      |
| GGG_Guy    | capture| 2,789,895   | 56,651      | 419         | 320      | 2.042      |
| GGG_Nikumba| capture| 2,789,895   | 56,651      | 475         | 264      | 2.040      |

### Orangutans

| Orangutans | Method | Length (bp) | Repeat (bp) | Contig (bp) | N50 (bp) | Phred (bp) |
|------------|--------|-------------|-------------|-------------|----------|------------|
| PAB_Buschi | WGS    | 2,850,916   | 140,215     | 1502        | 1565     | 4.973      |
| PPP_Napoleon | WGS | 2,850,916 | 140,215 | 1433 | 1634 | 4.976 |
| PAB_Sinjo  | capture| 2,537,735   | 110,006     | 1327        | 1221     | 4.383      |
| PAB_Duapuluh | capture | 2,537,735 | 110,006 | 1319 | 1229 | 4.383 |
| PAB_ppy10  | capture| 2,537,735   | 110,006     | 1331        | 1217     | 4.383      |
| PPP_Thai   | capture| 2,537,735   | 110,006     | 1177        | 1371     | 4.389      |

* - WGS - whole-genome sequenced sample; capture - sample sequenced using custom-capture approach (this study); merged - WGS and capture samples analysed together to obtain overlapping sites that were used in all analysis undertaken; merged-WGS/merged-capt. - WGS/capture samples extracted from the final merged dataset.
Supplemental Table S5: TMRCA estimates for nodes in the chimpanzee MSY phylogeny based on the chimpanzee reference sequence.

| MSY (PanTro4) | N  | S    | TMRCA/KYA (95% HPD interval) |
|---------------|----|------|------------------------------|
| Chimpanzee root | 19 | 12,127 | 1,225 (1,084-1,390) |
| PTT (1)       | 2  | 166   | 27.8 (22.5-33.4)          |
| PTT (2)       | 17 | 6252  | 486 (428-551)             |
| PTS/PTE/PTV (3) | 16 | 4727  | 439 (387-498)             |
| PTE/PTV (4)   | 13 | 2929  | 370 (326-420)             |
| PTS (5)       | 3  | 560   | 82.8 (71.2-95.8)          |
| PTE (6)       | 4  | 919   | 146 (128-168)             |
| PTE (7)       | 3  | 29    | 4.0 (2.6-5.7)             |
| PTV (8)       | 9  | 243   | 16.6 (13.7-19.6)          |

Numbers in parentheses in the ‘Node’ column refer to numbered nodes in the trees in Figure 3; for abbreviations in the same column, refer also to Figure 3; N – number of individuals; S – number of variable sites; TMRCA – time to most recent common ancestor; HPD – highest posterior density.
Supplemental Table S6: Comparison of MSY- and mtDNA-based TMRCA estimates in this study with those from other studies.

| Locus     | Node       | N (ours) | TMRCA/KYA (95% HPD)(ours) | TMRCA/KYA (95% HPD, SD or 95% CI)* (literature estimate) | N (literature) | Data type                                      | Ref |
|-----------|------------|----------|---------------------------|----------------------------------------------------------|---------------|-----------------------------------------------|-----|
| MSY       | PPA root   | 4        | 341.1 (312.4-371.9)       | 500 (230-770)                                            | 7             | 23 SNPs/indels in ~3kb                        | 1   |
| PTR root  | 19         |          | 1,174.5 (1,079.7-1,275.6) | 720 (370-1,070)                                          | 101           | 23 SNPs/indels in ~3kb                        | 1   |
| PTE/PTV   | 16         |          | 413 (364-468)             | 423 (313-542)                                            | 9             | 7752 SNPs                                    | 3   |
| PTE/PTV   | 13         |          | 360.2 (330.3-392.3)       | 371 (211-524)                                            | 6             | 7752 SNPs                                    | 3   |
| PTS (5)   | 3          |          | 77.2 (68.3-86.2)          | 93 (37-158)                                              | 2             | 7752 SNPs                                    | 3   |
| PTE (6)   | 4          |          | 151.9 (137.1-167.2)       | 150 (62-249)                                             | 4             | 7752 SNPs                                    | 3   |
| PTV (8)   | 9          |          | 13.5 (11.3-15.8)          | 12 (4.0-21)                                              | 2             | 7752 SNPs                                    | 3   |
| GGO root  | 13         |          | 104.6 (94.5-116)          | 142                                                      | 5             | 630 SNPs                                    | 4   |
| GBB (5)   | 3          |          | 0.44 (0.08-0.97)          | 0.73                                                     | 3             | 630 SNPs                                    | 4   |
| GBG/GBB (4)** | 6 |          | 31.4 (26-37.1)            | 45                                                       | 4             | 630 SNPs                                    | 4   |
| Pongo root| 6          |          | 320.4 (293.3-349.7)       | 168 (38-375)                                             | 115           | 4 SNPs, 11 STRs                              | 5   |
| PAB       | 4          |          | 9.5 (7.4-11.6)            | 4.2 (1.3-7.8)                                            | 40            | 4 SNPs, 11 STRs                              | 5   |
| PTV (8)   | 9          |          | 13.5 (11.3-15.8)          | 12 (4.0-21)                                              | 2             | 7752 SNPs                                    | 3   |
| mtDNA     | PPA root   | 4        | 307 (240.5-376.4)         | 410 (363-547)                                            | 34            | 470bp HVRI                                  | 2   |
| PTR root  | 18         |          | 920.5 (811-1,034.3)       | 830 (640-1,040)                                          | 10            | 15,441bp                                    | 8   |
| PTT (1)   | 6          |          | 323.6 (265.9-387.9)       | 230 (160-310)                                            | 3             | 15,441bp                                    | 8   |
| PTE/PTV   | 11         |          | 452.2 (383.8-525.6)       | 410 (320-520)                                            | 7             | 15,441bp                                    | 8   |
| Node | N  | Number of individuals | TMRCA (95% HPD) | Number of genes | Length (bp) |
|------|----|-----------------------|-----------------|-----------------|-------------|
| PTS (4) | 3 | 103.7 (73.3-137.8) | 508 (301-715) | complete mtDNA | 14,501bp |
|       |    | 80 (51–113) | 376 (239–511) | 12 protein-coding genes (10,869bp) | 3 |
|       |    | 144 (53-242) | 455 (195-719) | 4 complete mtDNA | 9 |
|       |    | 157 (83–242) | 6 | 12 protein-coding genes (10,869bp) | 3 |
|       |    | 101 (61–149) | 2 | complete mtDNA | 9 |
|       |    | 125 (50-204) | 4 | 12 protein-coding genes (10,869bp) | 3 |
|       |    | 289 (179–413) | 17 | 14,501bp | 7 |
|       |    | 32 (8-61) | 2 | 12 protein-coding genes (10,869bp) | 3 |
| PTE (6) | 4 | 105 (73.1-139.7) | 532x (195-719) | 12 protein-coding genes (10,869bp) | 3 |
|       |    | 157 (83–242) | 6 | complete mtDNA | 9 |
|       |    | 101 (61–149) | 2 | complete mtDNA | 9 |
|       |    | 125 (50-204) | 4 | 12 protein-coding genes (10,869bp) | 3 |
|       |    | 289 (179–413) | 17 | 14,501bp | 7 |
|       |    | 32 (8-61) | 2 | 12 protein-coding genes (10,869bp) | 3 |
| PTV (7) | 7 | 375.7 (311.8-443.5) | 1,890 (1,440-2,390) | complete mtDNA | 15,599bp |
|       |    | 1,340 | 3 |
|       |    | 404 (284-531) | 74 | complete mtDNA | 4 |
|       |    | 15,599bp | 10 |
| GGO root | 13 | 1,613.9 (1,428.2-1,802.7) | 3,600 (2,300-5,000) | 123 bp from HVRI | 11 |
|       |    | 1,330 | 217 | 3 genes (1,355bp) | 5 |
|       |    | 404 (284-531) | 74 | complete mtDNA | 4 |
|       |    | 15,599bp | 10 |
| GGG (1) | 8 | 293.2 (231.2-358.6) | 3,500 (2,310-4,750) | 82 SNPs from HVRI | 12 |
|       |    | 3,670 | 76 | 3 genes (1,355bp) | 5 |
|       |    | 3,990 (3,010-5,090) | 2 | 15,599bp | 10 |
|       |    | 3,120 | 64 | 82 SNPs from HVRI | 12 |
|       |    | 176 (72-322) | 211 | 323 bp from HVRI | 11 |
| Pongo root | 6 | 2,550.8 (2,354-2,754) | 3,500 (2,310-4,750) | 82 SNPs from HVRI | 12 |
|       |    | 3,670 | 76 | 3 genes (1,355bp) | 5 |
|       |    | 3,990 (3,010-5,090) | 2 | 15,599bp | 10 |
|       |    | 3,120 | 64 | 82 SNPs from HVRI | 12 |
|       |    | 176 (72-322) | 211 | 323 bp from HVRI | 11 |
|       |    | 178 (75-305) | 52 | 3 genes (1,355bp) | 5 |
| PAB | 4 | 692 (592.4-798.4) | 3,500 (2,310-4,750) | 82 SNPs from HVRI | 12 |
|       |    | 3,120 | 64 | 3 genes (1,355bp) | 5 |
|       |    | 176 (72-322) | 211 | 323 bp from HVRI | 11 |
|       |    | 178 (75-305) | 52 | 3 genes (1,355bp) | 5 |
| PPY | 2 | 25.9 (8.9-47.2) | 176 (72-322) | 323 bp from HVRI | 11 |
|       |    | 178 (75-305) | 52 | 3 genes (1,355bp) | 5 |

Numbers in parentheses in the ‘Node’ columns refer to numbered nodes in the trees in Figure 3; for abbreviations in the same column, refer also to Figure 3; N – number of individuals; TMRCA – time to most recent common ancestor; HPD – highest posterior density; SD – standard deviation, CI – confidence interval. Refs.: 1 – Stone et al. 2002; 2 – Eriksson et al. 2006; 3 – Oetjens et al. 2015; 4 – Xue et al. 2015; 5 – Nater et al. 2011; 6 – Zsurka et al. 2010; 7 – Hvilsom et al. 2013; 8 – Stone et al. 2010; 9 – Bjork et al. 2011; 10 – Das et al. 2014; 11 – Arora et al. 2010; 12 – Ma et al. 2013

* - green text - TMRCA estimate in the same order as ours; blue text - literature estimate is an order higher; orange text - literature estimate is an order lower

** - comparable node chosen from the datasets
Supplemental Table S8: Filtering parameters for great ape MSY, ChrX, autosomal and mtDNA sequences.

| Filter                        | MSY/ChrX | Autosomal | mtDNA |
|-------------------------------|----------|-----------|-------|
| Indels removed                | yes      | yes       | no    |
| Minimum QUAL                  | 33       | 33        | No    |
| Minimum depth (DP)            | 3        | 6         | 3     |
| Strand bias (SP)              | p<0.05   | p<0.05    | p<0.05|
| SnpGap                        | 5        | 5         | no    |
| Remove heterozygous calls     | Yes      | No        | Yes   |
| Minimum PL difference*        | No       | 21        | No    |
| Missing data per sample       | None allowed | None allowed | None allowed |
| and per site                  |          |           |       |

* calls where the minimum difference between genotype likelihoods was less than 21 were removed.
Supplemental Table S14: TMRCA estimates for nodes in the great-ape mtDNA phylogenies based on the coding region mutation rate.

| mtDNA coding region | N | TMRCA/KYA (95% HPD interval) |
|---------------------|---|-------------------------------|
| Human root          | 8 | 206 (146-286)                 |
| Bonobo root         | 4 | 337 (237-464)                 |
| PPA (1)             | 3 | 8.3 (1.3-19.2)                |
| Chimpanzee root     | 18| 922 (678-1,228)               |
| PTT (2)             | 2 | 53.4 (28.4-85.1)              |
| PTT (1)             | 6 | 347 (248-470)                 |
| PTT/PTS (3)         | 5 | 265 (188-362)                 |
| PTE/PTV (5)         | 11| 450 (329-606)                 |
| PTS (4)             | 3 | 125 (84-177)                  |
| PTE (6)             | 4 | 128 (86-181)                  |
| PTV (7)             | 7 | 392 (285-530)                 |
| Gorilla root        | 13| 1,735 (1,277-2,301)           |
| GGG (1)             | 8 | 346 (246-474)                 |
| GGG (2)             | 7 | 113 (73-164)                  |
| GBG (5)             | 2 | 4.7 (0.08-13.9)               |
| GBB (4)             | 3 | 8.9 (1.5-19.9)                |
| GBG/GBB (3)         | 5 | 234 (160-327)                 |
| Orangutan root      | 6 | 3,609 (2,617-4,888)           |
| PAB                 | 4 | 837 (619-1,137)               |
| PPY                 | 2 | 28.4 (11.4-50.7)              |

Numbers in parentheses in the ‘Node’ columns refer to numbered nodes in the trees in Figure 3; for abbreviations in the same column, refer also to Figure 3; N – number of individuals; TMRCA – time to most recent common ancestor; HPD – highest posterior density.
Supplemental Figure S1: PCA of autosomal SNP variation in sequenced bonobos and orangutans.
PCA plots based on autosomal SNP variation in (A) the 3 bonobos sequenced here (crosses), plus 12 published bonobos (Prado-Martinez et al. 2013) (circles); (B) the same samples as (a) with the addition of 25 published chimpanzees (Prado-Martinez et al. 2013) and the 8 chimpanzees sequenced here and also represented in Figure 2A (crosses); and (C) the 4 orangutans sequenced here (crosses), plus 10 published individuals (Prado-Martinez et al. 2013) of known sub-species status (circles). Abbreviations for species/subspecies names are as in the legend to Figure 3.
Supplemental Figure S2: PCA of X-Chromosomal SNP variation in chimpanzees.
PCA plot based on X-Chromosomal SNP variation in the 8 chimpanzee males sequenced here (crosses), plus 11 published males (Prado-Martinez et al. 2013) of known sub-species status (circles). Considering the two inter-subspecies hybrids, the X Chromosome of EB176JC clusters with *P. t. elliotti* which, together with the MSY and mtDNA results, is consistent with first-generation hybrid status. The X Chromosome of the other hybrid, Tommy, lies between the PTV cluster and the group of PTT/PTS samples, and the nature of his hybrid status is less clear. Abbreviations for species/subspecies names are as in the legend to Figure 3.
**Supplemental Figure S3: Model-based estimation of ancestry in great apes using ADMIXTURE.**
All individuals (columns) are grouped into different clusters (\(k=2\) to \(k=5\), rows) coloured according to their shared genetic structure. Names of great-ape males sequenced in this study are in red.
Supplemental Figure S4: Cross-validation error in ADMIXTURE analysis.
Supplemental Figure S5: Location and extent of sequenced chimpanzee MSY-orthologous regions compared to the chimpanzee reference sequence.

(A) Schematic representation of the chimpanzee Y Chromosome (Hughes et al. 2010) showing blocks of different sequence classes. (B) The analysed sub-regions of chimpanzee MSY, shown as plots of read depth against chromosome position. In each plot the y-axis ranges from zero to 150 ×. Sample size (N) is given to the left, and the extent of sequence obtained (bp) to the right. Chimpanzees carry two distinct structural variant sequences (Ptr1 and 2) differing by a large deletion highlighted by a magenta bar; the gaps indicated by the green bars correspond to large blocks that are absent from the human reference sequence. The Ptr2-specific retention of a sequence block indicated in Figure 1 is not visible here since it does not exist in the chimpanzee reference sequence. (C) Locations of single-copy MSY genes (Hughes et al. 2010) shown as triangles (not drawn to scale) pointing in the direction of transcription. Three of these genes, functional in humans, are reported to be pseudogenes in chimpanzees (Bellott et al. 2014), and are indicated by unfilled triangles.
Supplemental Figure S6: MSY phylogeny for chimpanzees and bonobos combined. Species/subspecies names and names of individuals are given at the tips of branches as in Figure 3C and D.
Supplemental Figure S7: Comparison of chimpanzee MSY phylogenies, based on mapping to chimpanzee and human reference sequences. (A) Chimpanzee, and (B) human reference sequence mapping. Species/subspecies names and names of individuals are given at the tips of branches as in Figure 3D.
Supplemental Figure S8: Great-ape MSY phylogenies containing named branches. (A) Bonobos. Refer to Table S9 to find variants on specific numbered branches; (B) Chimpanzees mapped to human genome reference (see Table S10); (C) Gorillas (see Table S11); (D) Orangutans (see Table S12); (E) Chimpanzees mapped to chimpanzee genome reference (see Table S13).