**Supplementary Figure S1**

Known relationships among *Pan troglodytes verus* individuals sequenced in this study. (A) Relationships among individuals of the BPRC (Biomedical Primate Research Centre) sample, constituted of 15 isolated individuals (all females), and 35 individuals related through five separate genealogies. All individuals were Sanger sequenced for the three *NAT* genes (*NAT1*, *NAT2*, and *NATP*), except those shown in white, orange and blue, due to DNA unavailability; genotypes of individuals that were unambiguously deduced from their descendants are shown in blue (inferred for the three *NAT* genes) or orange (inferred only for *NATP*), while those in white could not be inferred. Genotypes used in the analyses of diversity included those of the founders, shown in yellow (genotypes of the three *NAT* genes sequenced), in blue, or in orange, and those of two descendants, Oscar (in beige, genotypes of the three *NAT* genes sequenced), and Annaclara (in gray, only included for *NAT1* and *NAT2* as the corresponding genotype of Gerrit at *NAT1* and *NAT2* could not be inferred from his descendants). *NAT* genotypes of individuals in green (sequenced) were only used to infer their parents’ genotypes and were not included in the analyses of diversity. (B) Relationships among individuals of the CARTA (Center for Academic Research and Training in Anthropogeny) sample. The CARTA complete sample is constituted of 10 unrelated individuals (6 females, 2 males, and 2 individuals of unknown sex, represented by polygons), and 16 individuals related through two separate genealogies. All individuals in purple were Sanger sequenced for the three *NAT* genes. (C) The two unrelated individuals from the Basel zoo, that were also Sanger sequenced for the three *NAT* genes, were included in the analyses in the San Diego samples (Supplementary File S1).

**Supplementary Figure S2**

Median-joining network of *NAT1* haplotypes in the *Pan* genus and divergence from other hominoid species (human, gorilla and orangutan), represented by their reference sequence (GRC37/hg19, gorGor4 and ponAbe2). Positions are numbered according to the human cds (Supplementary Table S3); non-synonymous mutations are shown in red bold type, synonymous mutations in blue. A black arrow points to the inferred recurrent substitution in the median joining network at position 18’080’085 (position 529 in cds), which is characterized by a C in humans and gorillas and an A in chimpanzees, bonobos and orangutans.

**Supplementary Figure S3**

Median-joining network of *NAT2* haplotypes in the *Pan* genus and divergence from other hominoid species (human, gorilla and orangutan), represented by their reference sequence (GRC37/hg19, gorGor4 and ponAbe2). Positions are numbered according to the human cds (Supplementary Table S4); non-synonymous mutations are shown in red bold type, synonymous mutations in blue. Positions that mark substitution divergence between some species but are polymorphic in another species are indicated by a star. The red arrow points to a shared non-synonymous polymorphism (C/T) between humans and Western common chimpanzees at position 18’258’091 (578 in cds). Black arrows point to inferred multiple or recurrent substitutions in the median joining network.

**Supplementary Figure S4**

Median-joining network of *NATP* haplotypes in the *Pan* genus and divergence from other hominoid species (human, gorilla and orangutan), represented by their reference sequence (GRC37/hg19, gorGor4 and ponAbe2). Positions (+ 18’220’000) are numbered according to the human reference sequence (Supplementary Table S5). Due to undefined states, several sequence stretches were not considered for median-joining network construction (Supplementary Table S5). Positions that mark substitution divergence between some species but are polymorphic in another species are indicated by a star. Blue arrows point to shared polymorphisms between species: a shared T/A polymorphism between humans and chimpanzees (all sub-species but Western common chimpanzees) at position 18’228’285; a shared G/A polymorphism between bonobos and *P.t. schweinfurthii* at position 18’228’659; a shared G/A polymorphism between humans and *P.t. troglodytes* at position 18’228’661; a shared T/C polymorphism between *P.t. ellioti* and *Gorilla gorilla* at position 18’228’959. Black arrows point to inferred multiple, recurrent or coincidental substitutions in different species or sub-species at a position in the network.

**Supplementary Figure S5**

Nucleotide diversity (*π* x 10-3) at the three *NAT* genes in the two *Gorilla* and the two *Pongo* species. The dotted lines were added to the graphs to highlight inter-locus variation.

**Supplementary Figure S6**

Expected heterozygosity (*h*) and nucleotide diversity (*π* x 10-3) at the three *NAT* genes in modern human populations. Each dot represents a population (listed in Supplementary Table S7), color-coded according to continental origin.