Fig. S3. Hominoid species tree based on 292 single-copy, presumably neutral, and independent loci.

Shown are the inferred phylogenetic relationships among the extant human (H), chimpanzee (C), gorilla

(G), and orangutan (O) lineages along with estimated ancestral effective population sizes (N_{HC}, N_{HCG}, and

N_{HCGO}) and speciation times (τ_{H-C}, τ_{HC-G}, and τ_{HCG-O}) in millions of years ago (Mya). Species tree topology

and population genetic parameters were obtained from multi-locus coalescent analyses implemented in

the Bayesian program BPP2.2 (Yang 2012).