

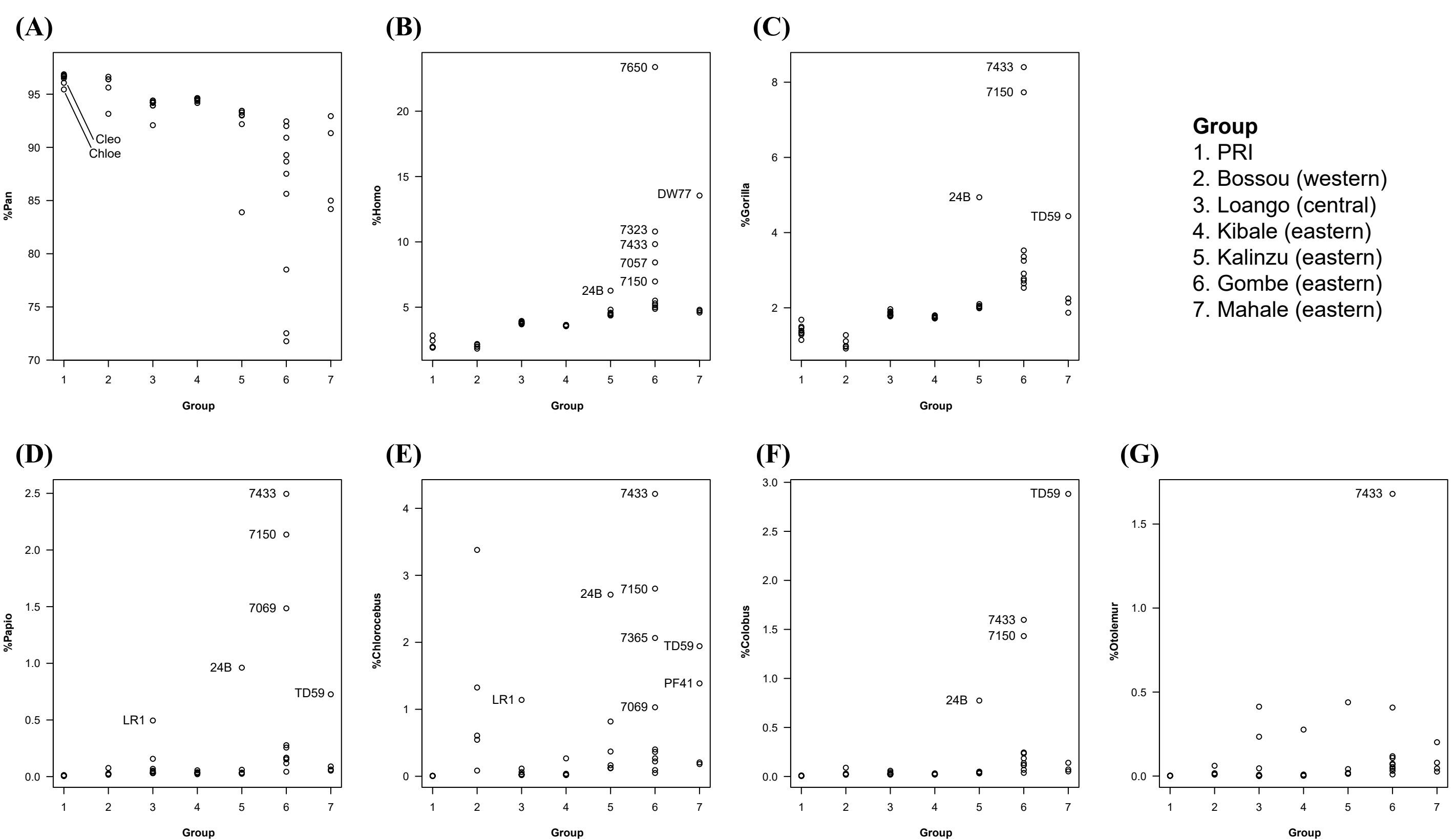


Fig. S1 BBsplit results for detection of contamination by human and prey primates. Each circle is corresponding to a sample. **(A)** %*Pan* (chimpanzee). **(B)** %*Homo* (human). **(C)** %*Gorilla* (gorilla). **(D)** %*Papio* (baboon). **(E)** %*Chlorocebus* (guenon). **(F)** %*Colobus* (colobus). **(G)** %*Otolemur* (galago).

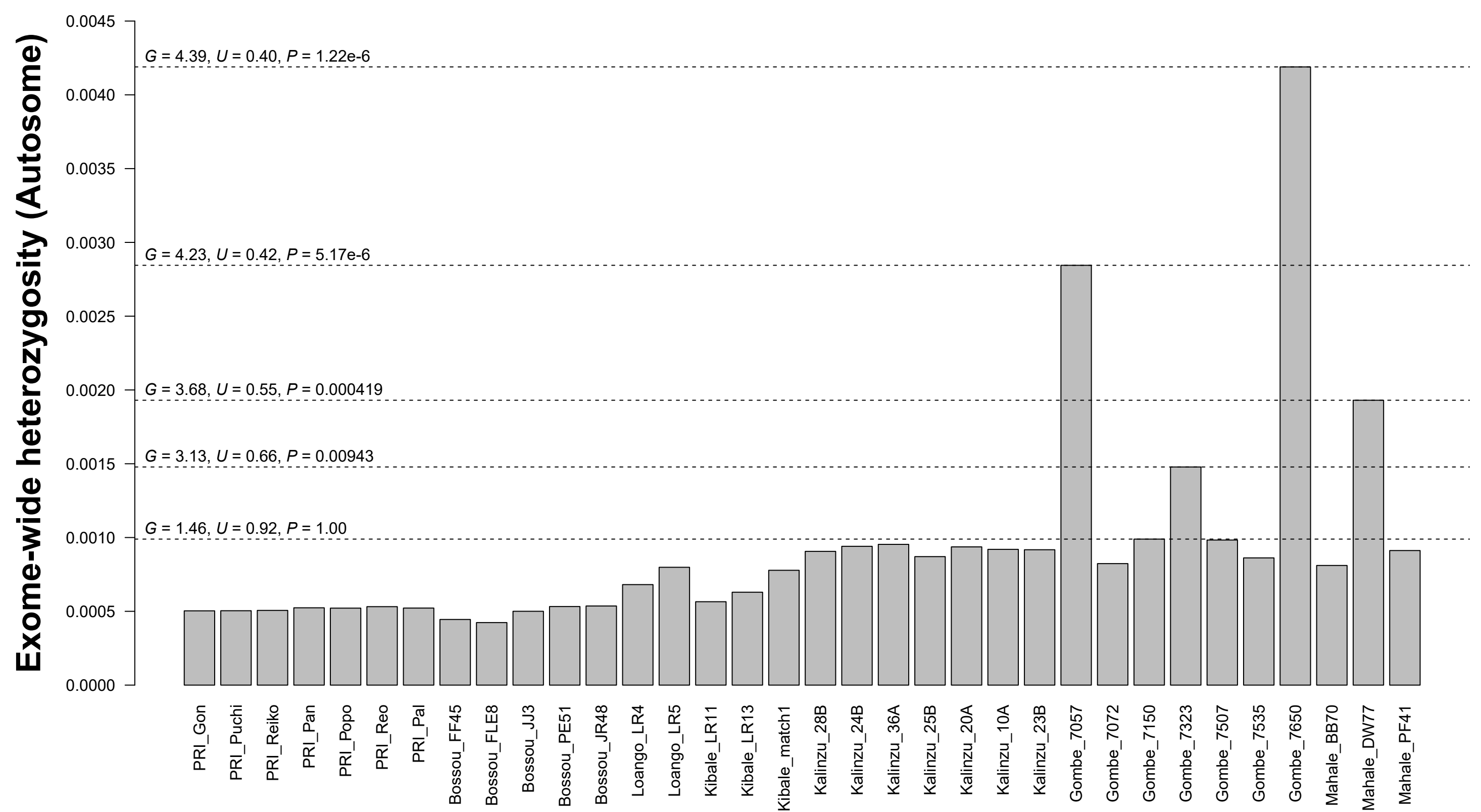


Fig. S2 Autosomal exome-wide heterozygosity, $H(A)$, and detection of possible human and prey contamination in feces. Horizontal dashed line shows the stepwise maximum values and statistics (G , U , and P) of Grubbs test for detecting outliers. The top four $H(A)$ values (<0.0014) were considered outliers ($P < 0.05$).

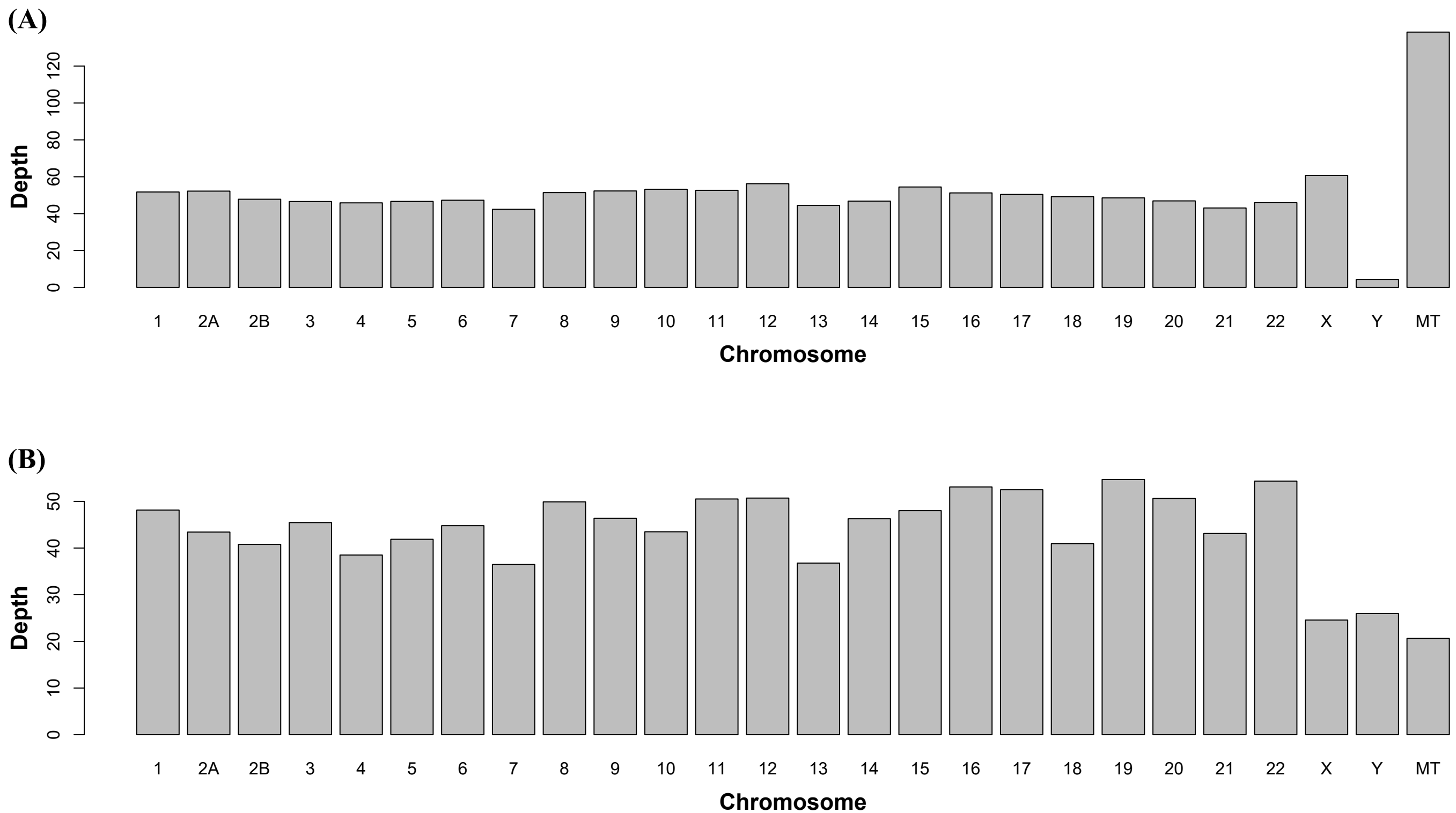


Fig. S3 Examples of sequencing depth for each chromosome and mitochondrial genome. Coding sequences of autosomes (chromosome 1, 2A, 2B, 3, ..., 22) were sequenced uniformly. Mitochondrial genome depth was sample-dependent. **(A)** Female chimpanzee, Jire (JR48, Bossou). X chromosome sequencing occurred at the level of autosomes, whereas Y chromosome sequencing was minimal. **(B)** Male chimpanzee, Jeje (JJ3, Bossou). X and Y chromosome sequencing was almost equal at half the level of autosomes.

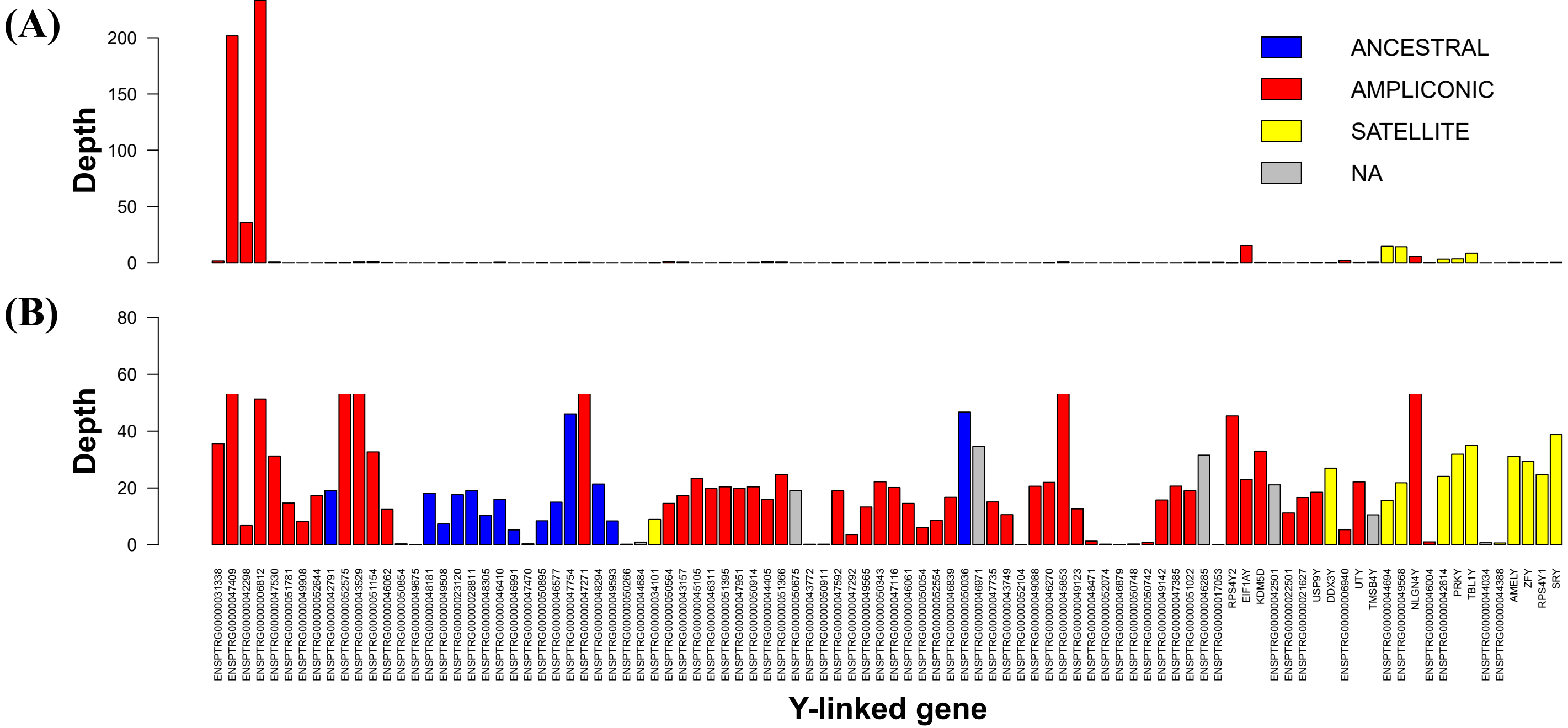


Fig. S4 Examples of sequencing depth for each Y-linked gene. **(A)** Female chimpanzee, Jire (JR48, Bossou). Some ampliconic and satellite genes were sequenced. **(B)** Male chimpanzee, Jeje (JJ3, Bossou). Most of Y-linked genes were sequenced uniformly.

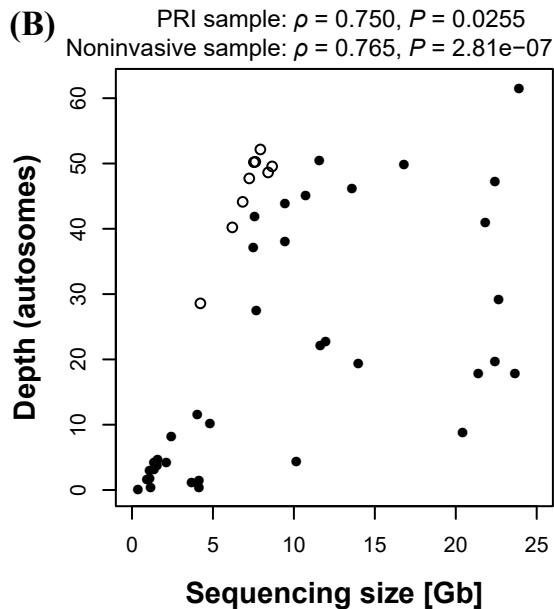
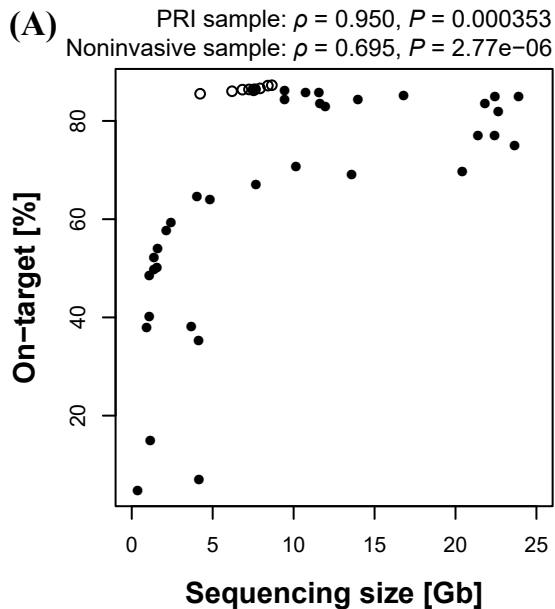


Fig. S5 Relationship between sequence size and various statistics. Sequencing size was positively correlated with **(A)** on-target proportion (saturated at around 80%) and **(B)** sequencing depth. Open circles: PRI samples. Closed circles: noninvasive samples.

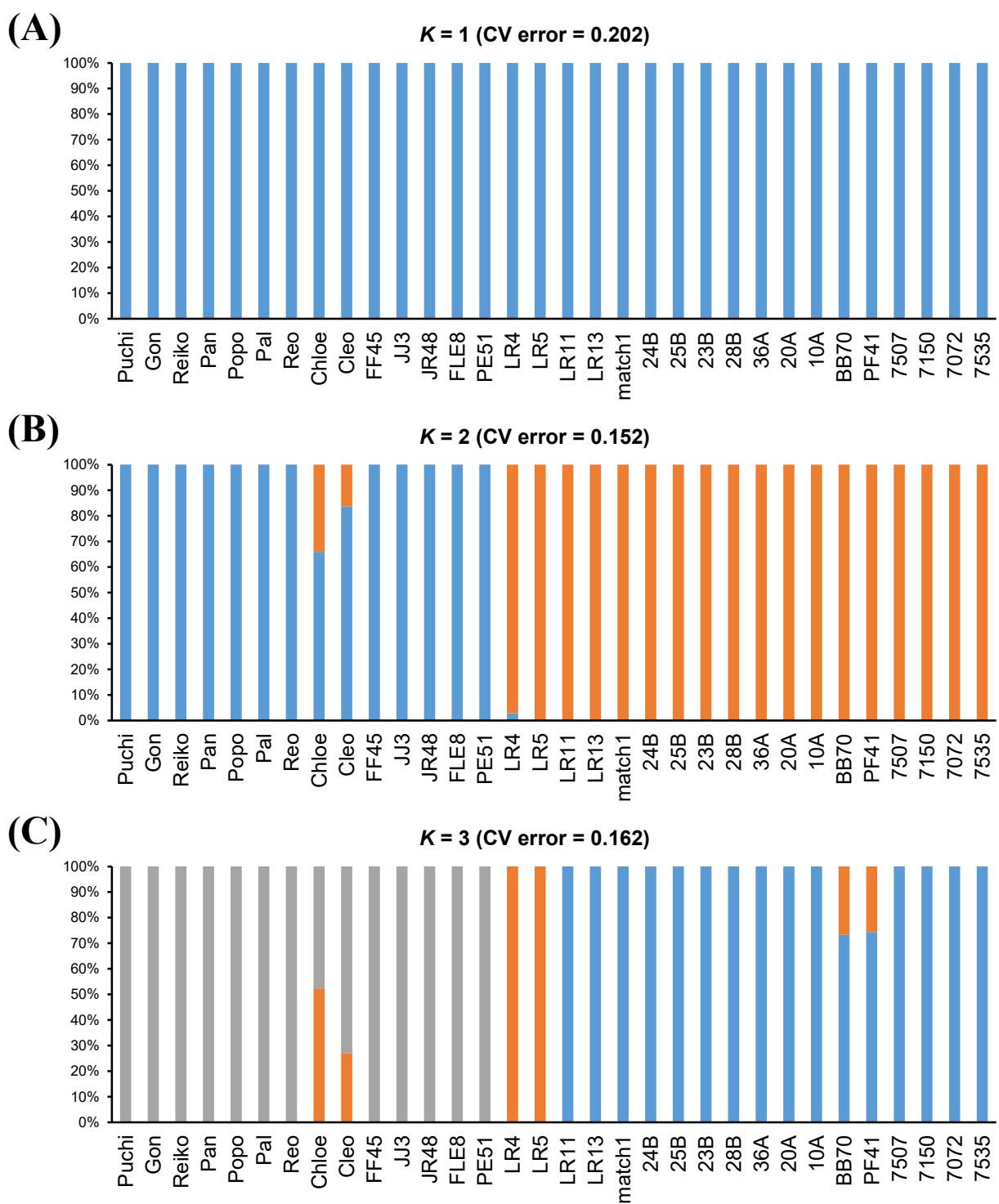


Fig. S6 ADMIXTURE results. Each color in barplots indicates an estimated ancestry. K : the number of populations. CV: cross-validation. **(A)** $K = 1$. **(B)** $K = 2$. **(C)** $K = 3$. **(D)** $K = 4$. **(E)** $K = 5$. **(F)** $K = 6$. **(G)** $K = 7$.

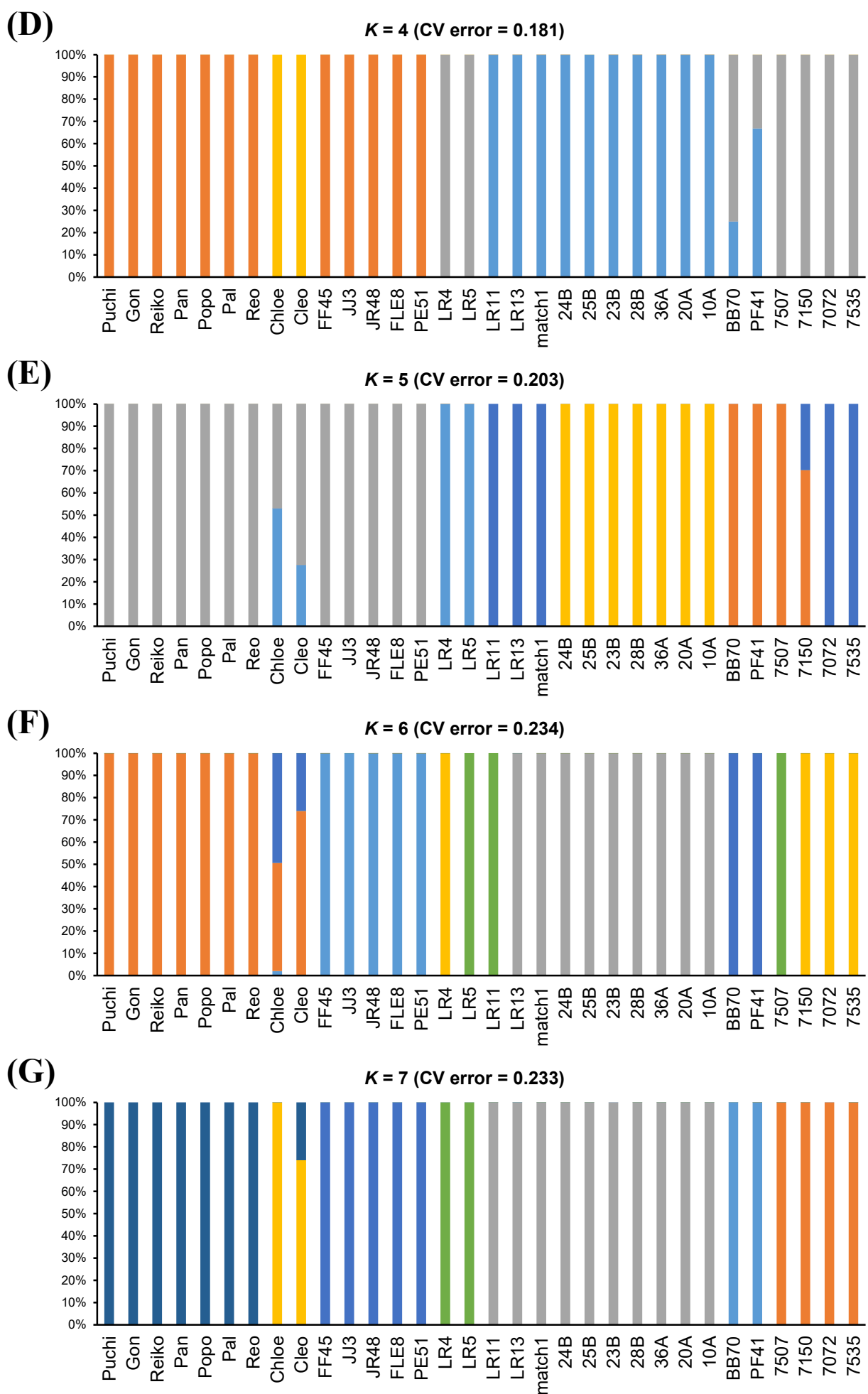


Fig. S6 Continued.

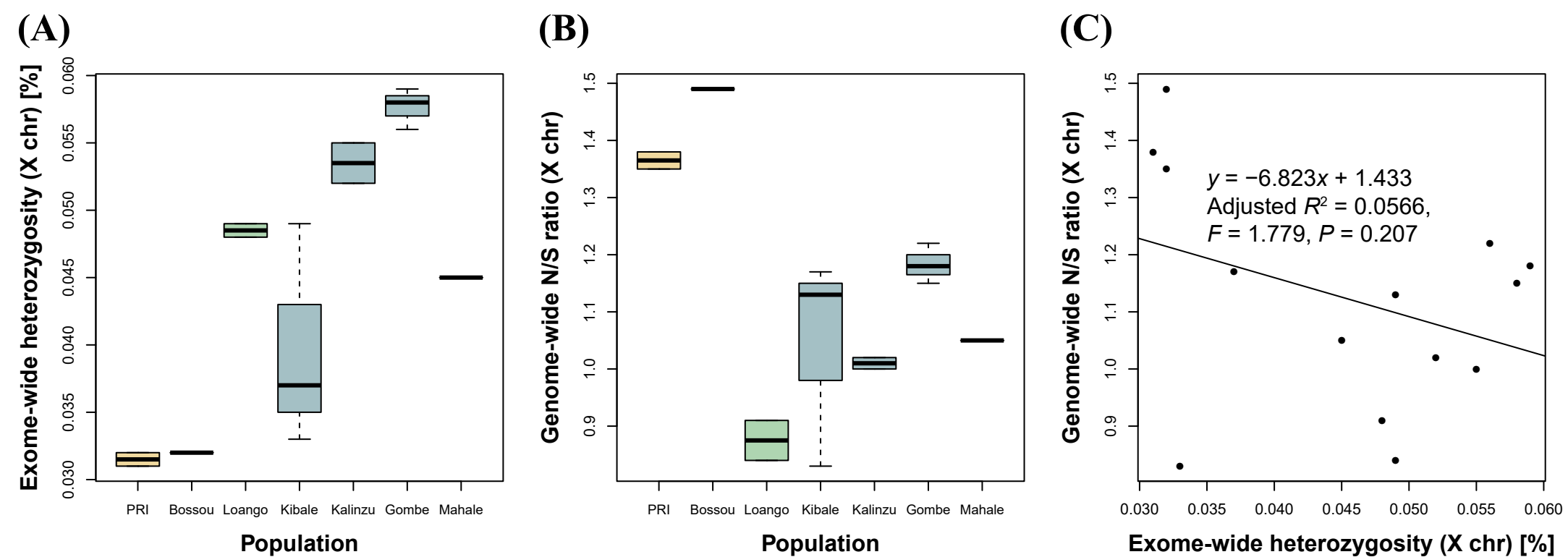
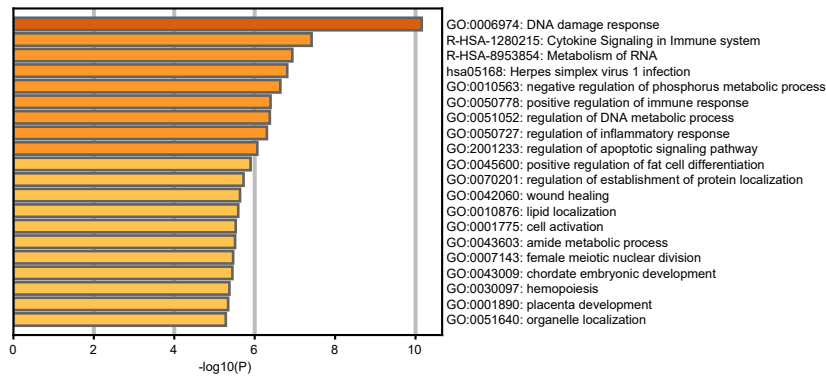
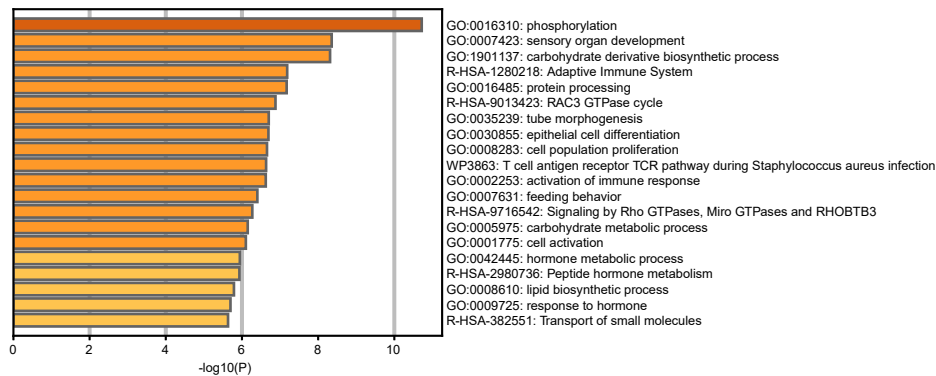


Fig. S7 Relationship between exome heterozygosity and the genome-wide N/S ratio in X chromosomes. **(A–C)** The trends were similar to those observed for autosomes (refer to **Fig. 5**).

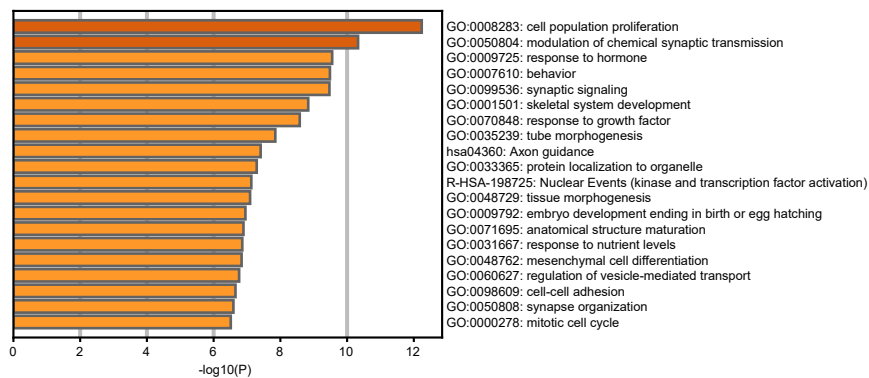
(A) Kibale



(B) Kalinzu



(C) Gombe



(D) Mahale

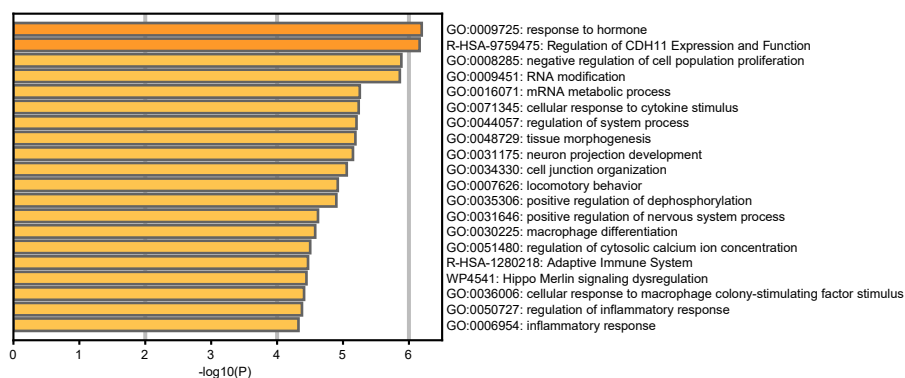


Fig. S8 Results of functional enrichment analysis by Metascape. Top terms are shown. **(A)** Kibale population. **(B)** Kalinzu population. **(C)** Gombe population. **(D)** Mahale population.