Supplementary Figure S2. Optimal number of genetic clusters in the wild Ugandan *C. canephora* set according to the admixture model with correlated alleles implemented in Structure. a The log-likelihood of the data [lnP(X)] averaged over 10 consecutive Structure runs for K = 2 to 7, with error bars representing ± standard deviation. b Evanno's ΔK statistic plotted against K.

Structure analysis revealed a maximum ΔK value for K = 3 suggesting the split into three main clusters, but it is worth noting that for K = 4, ΔK value is above zero indicating that the genetic structure produced by dividing all genotypes into 4 groups is also likely.