Sample	Ancestral N_e	Time in past of first size change (years)	N_e after first change	Time in past of second size change (years)	N_e after second change
1st side of cline (12 haplotypes)	33,191	539,816	50,716	39,023	8,132
2nd side of cline (16 haplotypes)	32,676	743,772	45,321	38,741	10,659
2nd side of cline (downsampled to 12 haplotypes)	32,809	648,295	47,507	48,996	11,808
All western lowland samples (downsampled to 12 haplotypes)	32,542	746,901	46,144	29,060	9,014

Table S2: Three-epoch demographic model results from *∂α∂i* for individuals on either side of a putative cline.
Inferences based on subsets of the western lowland gorilla samples, using the 8x data. Samples on the 1st side of cline: KB3782, KB3784, KB5792, KB5852, KB7973, X00109. Samples on the 2nd side of cline: A930, A931, A933, A936, A937, A962, KB6039, X00108.

Table S3: CLR Window

GO ID	Term	p-value
GO:0035725	sodium ion transmembrane transport	0.00039
GO:0006166	purine ribonucleoside salvage	0.00077
GO:0050909	sensory perception of taste	0.00188
GO:2000736	regulation of stem cell differentiation	0.00512
GO:0030157	pancreatic juice secretion	0.00519
GO:0046541	saliva secretion	0.00519
GO:0090257	regulation of muscle system process	0.00544
GO:0051983	regulation of chromosome segregation	0.00582
GO:0060964	regulation of gene silencing by miRNA	0.00685
GO:0086012	membrane depolarization during cardiac muscle cell action potential	0.00685
GO:0086019	cell-cell signaling involved in cardiac conduction	0.00685
GO:1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	0.00685
GO:2000270	negative regulation of fibroblast apoptotic process	0.00685
GO:0030071	regulation of mitotic metaphase/anaphase transition	0.00739
GO:0050709	negative regulation of protein secretion	0.00739
GO:0019319	hexose biosynthetic process	0.00825

Table S4: Top enriched GO terms from TopGo.
Results based on the Fisher's exact test and the elimination method by Alexa et al. (2006). All genes in regions with $p < 10^{-3}$ were included. The 16 terms with $p < 0.01$ are listed.

Alexa A, Rahnenfuhrer J, Lengauer T. 2006. Improved scoring of functional groups from gene expression data by decorrelating GO graph structure. Bioinformatics. 22(13):1600-1607.

Paper	Method	Data	Cross River-Western split time (kyr)	Cross River-Western split time (kyr, adjusted)	Western-Eastern split time (kyr)	Western-Eastern split time (kyr, adjusted)	Migration
Thalmann et al, 2011	ABC	8 micro-satellite loci	17.8				4.5 migrants per generation, symmetric
Becquet et al, 2007	MIMMAR	15 loci			92	171	M=0.87, symmetric
Scally et al, 2012	Custom-IM	Genome wide, reduced representation			500	429	0.2 migrants per generation, symmetric
Prado-Martinez et al, 2013	PSMC	Genome wide	80	114	150	214	none
Mailund et al, 2012	CoalHMM	95 loci (10Mbp interval between locus)				450	gene flow ended 150kr ago
Thalmann et al, 2007	IM	16 loci			78*	107	more gene flow from eastern to western gorilla after initial split at around 0.9-1.6 mya, no gene flow until 78 kyr ago
This study	G-PHOCS	25,573 loci		68		261	Western --> Eastern, 0.37 migrants per generation

Table S5: Comparison of published estimates of gorilla population split times.
Values from each study are adjusted to match the generation time and mutation rates employed in this study. A mutation rate adjustment is not performed for Thalmann et al (2011), which is based on microsatellites. We note that Thalmann et al (2007) report a range of split time values under several different models, with population split times ranging from 78 kya (without subsequent gene flow) to 1.6 mya, with some models including Eastern to Western migration.

Supplementary Figures

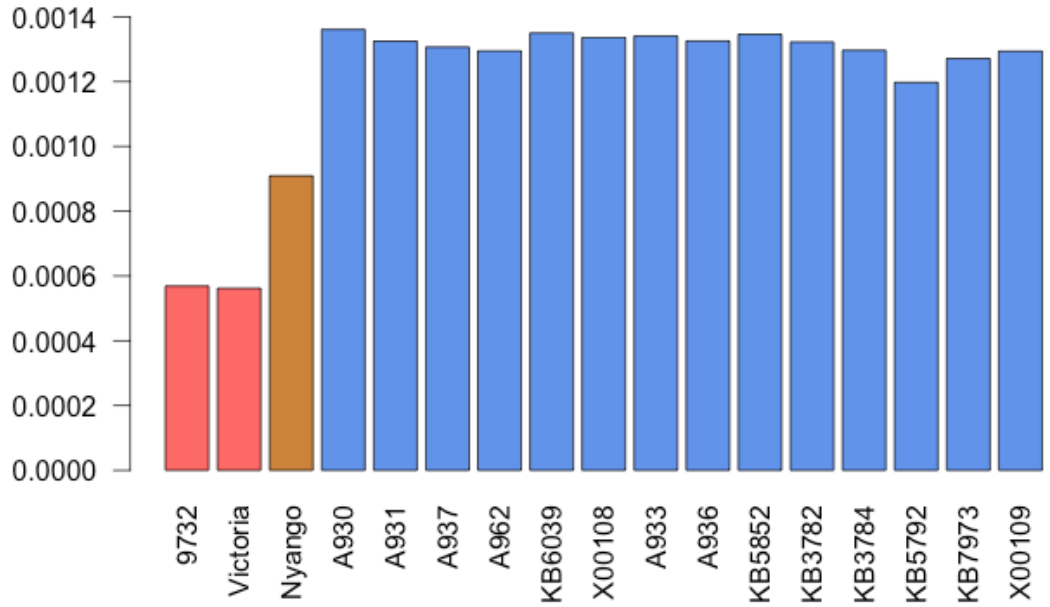


Figure S1: Genome wide heterozygosity values.
Heterozygosity was calculated along the autosomes for each sample based on the 8x coverage masks. Samples are colored based on species: eastern lowland (red), Cross River (yellow), and western lowland (blue).

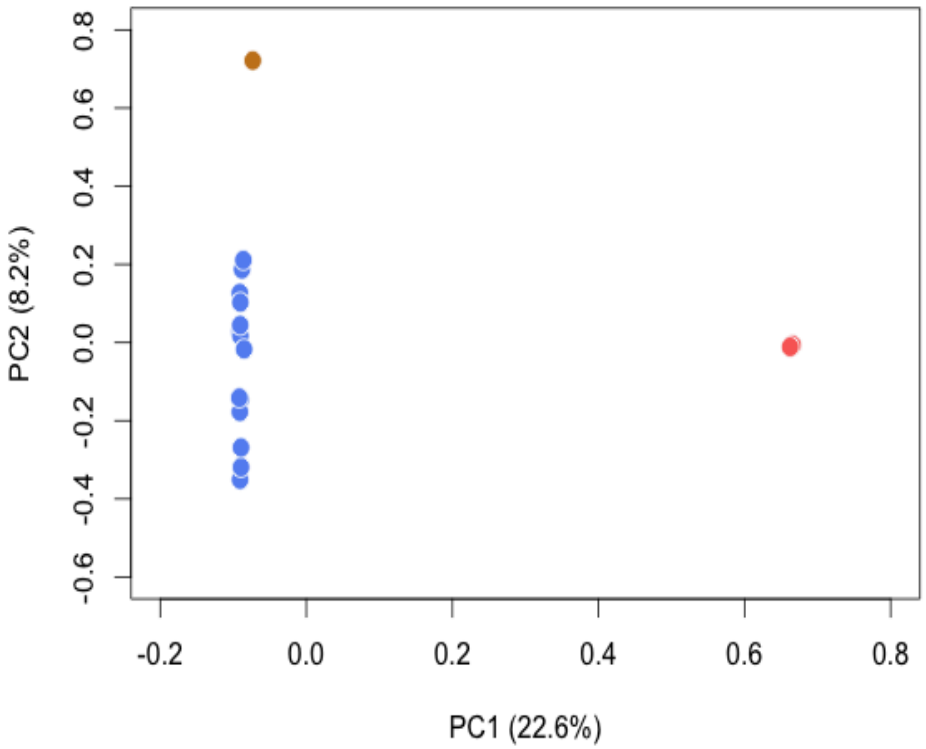


Figure S2: PCA of three gorilla species. Colors indicate species: Cross River (brown), western lowland (blue), and eastern lowland (red). Data was thinned to include 20% of the total number of intersecting SNPs. Percentages indicate the percent of variance explain by each principle component.

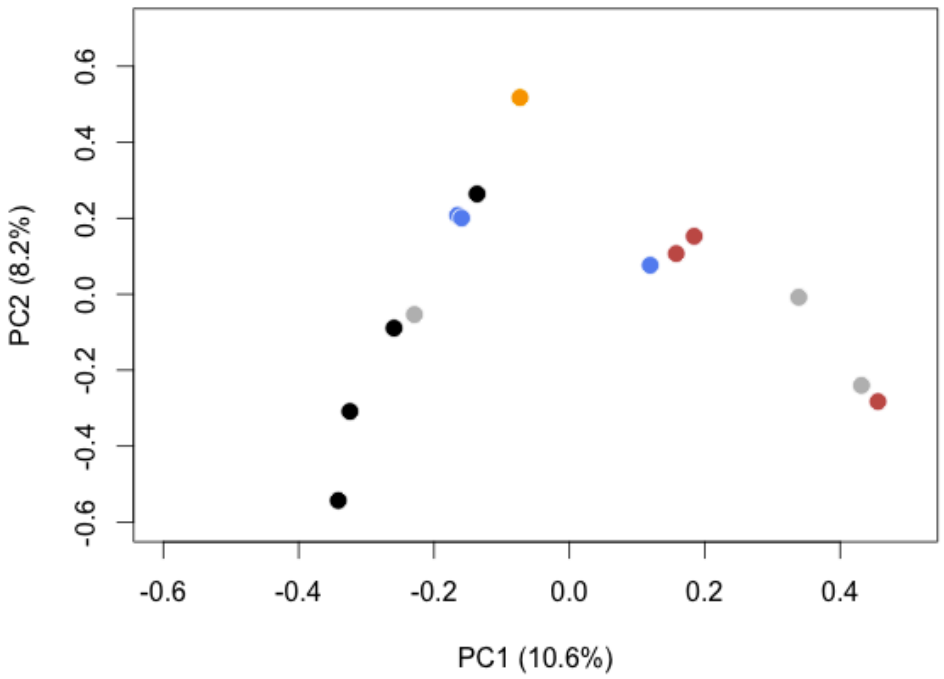
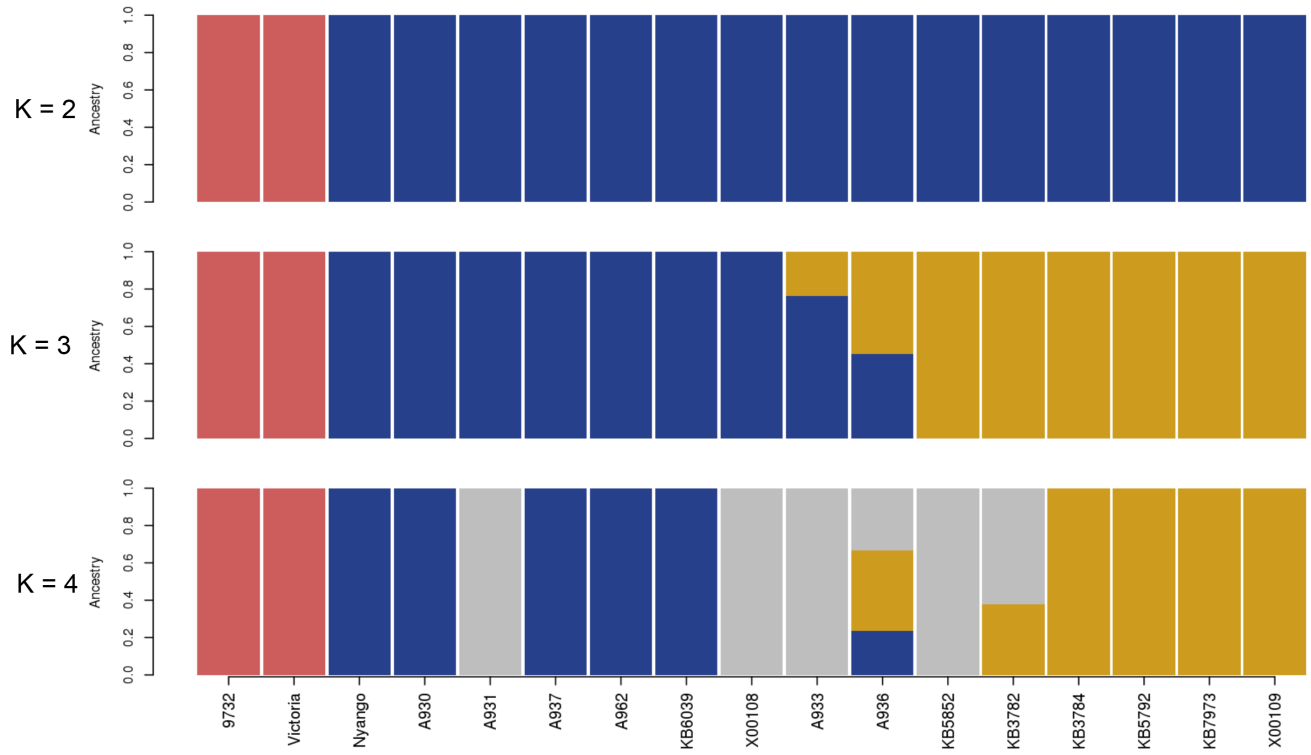


Figure S3: PCA of western lowland gorilla.
PCA of 14 western lowland gorillas based on 8x sequencing data. Colors indicate geographical origin: Equatorial Guinea (orange), Cameroon (blue), Congo (red), captive born (black), unknown origin (grey). Percentages indicate the percent of variance explained by each principle component.

A.



B.

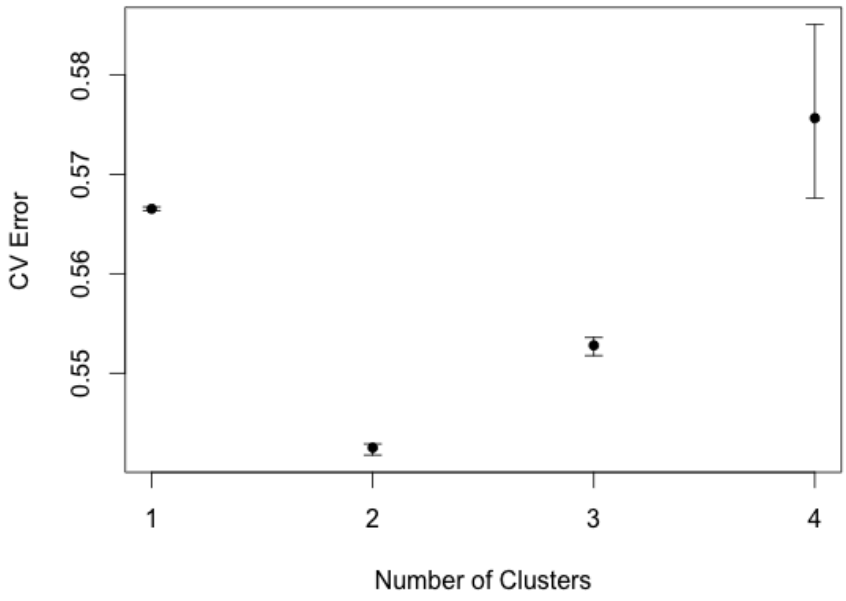
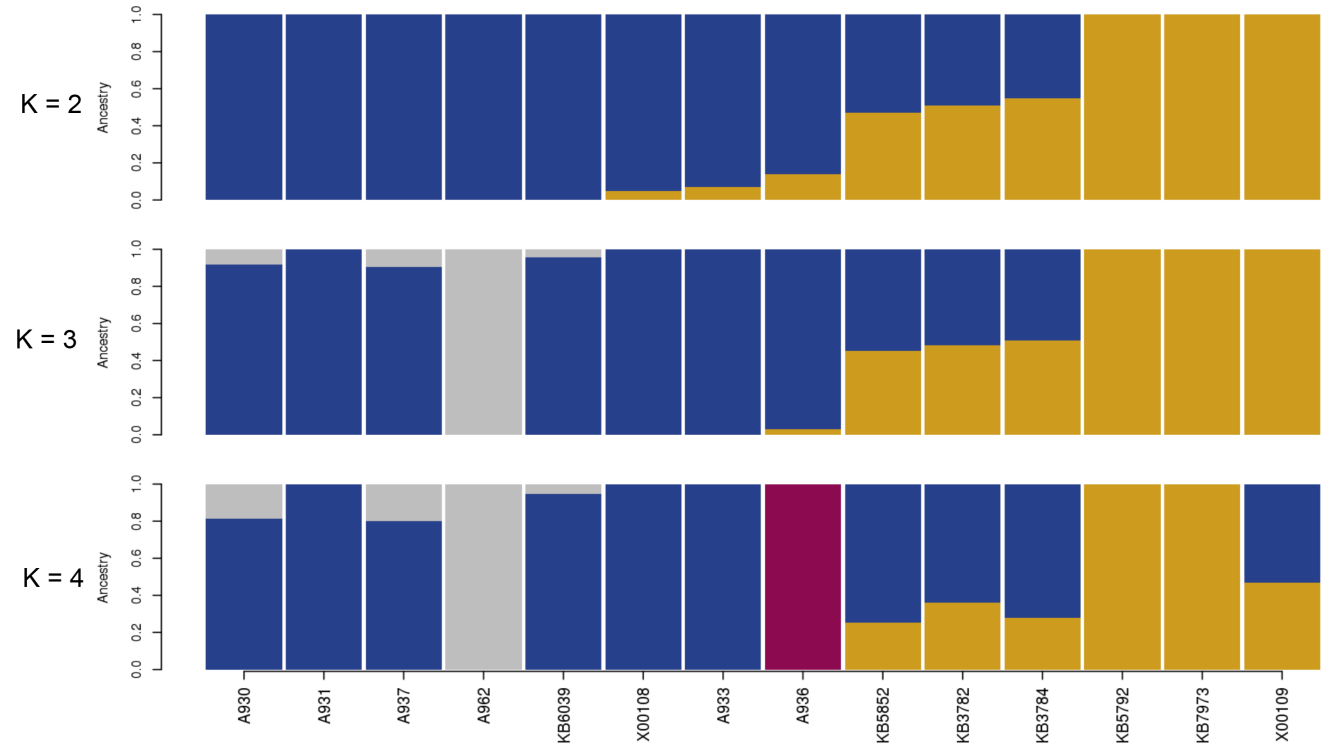


Figure S4: Admixture results for the three gorilla subspecies.
A: Population membership inferred from ADMIXTURE with 2 - 4 populations. **B**: Cross Validation Error from ADMIXTURE analyses on three gorilla subspecies. CV error is estimated for 10 independent runs, and the results from run with the CV error is shown in A.

A.



B.

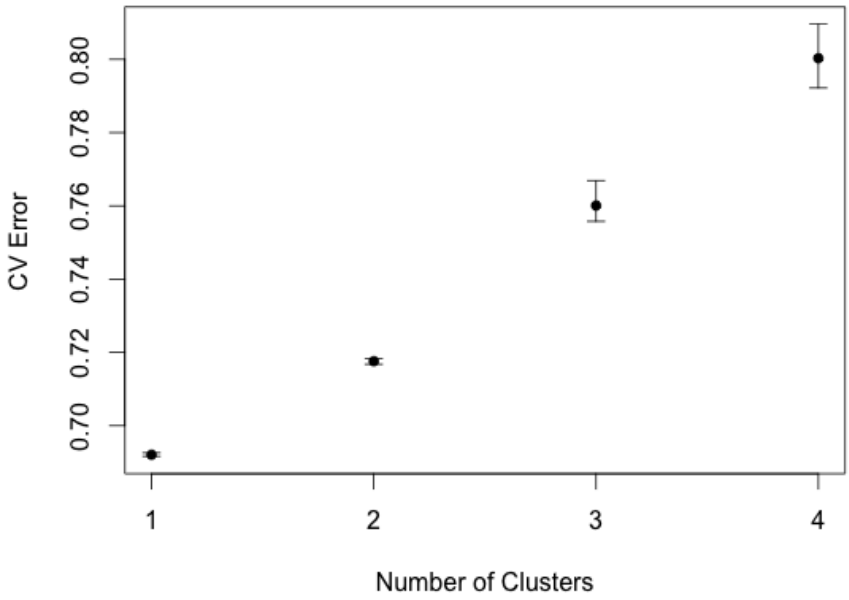


Figure S5: Admixture assignment and CV Error for 14 western lowland gorillas.
A: Population membership inferred from ADMIXTURE with 2 - 4 populations. **B**: Cross Validation Error from ADMIXTURE analyses on three gorilla subspecies. CV error is estimated for 10 independent runs, and the results from the runs with the lowest error is shown in A.

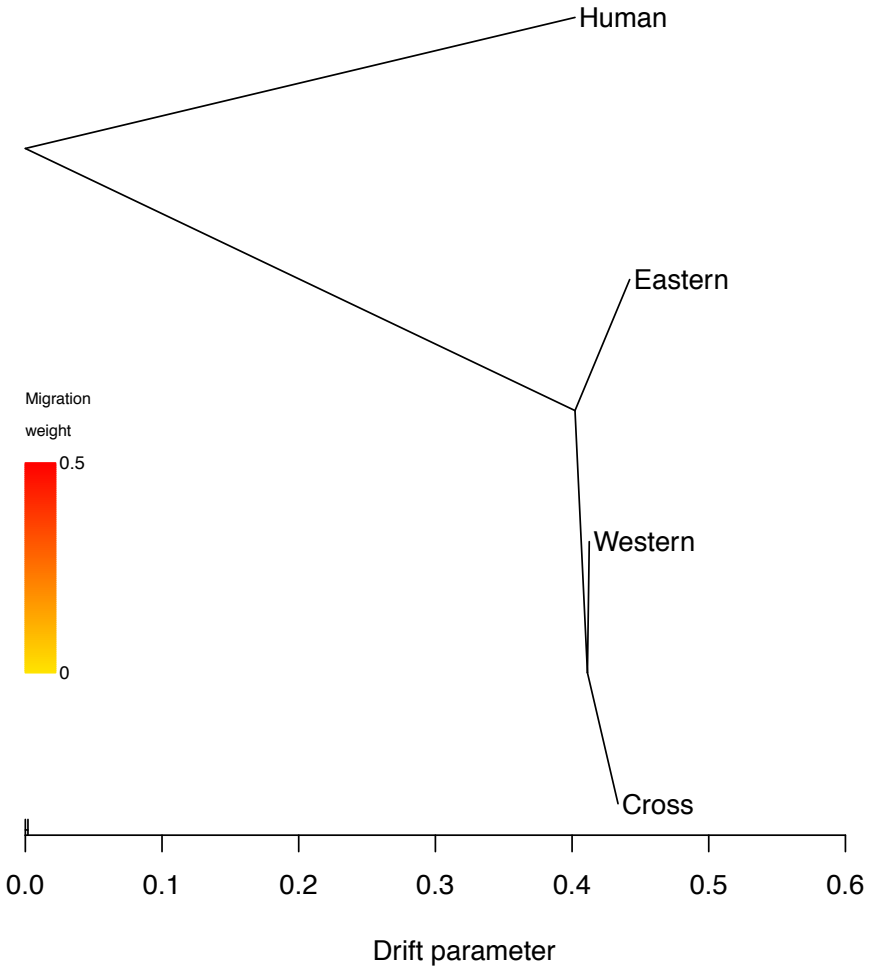
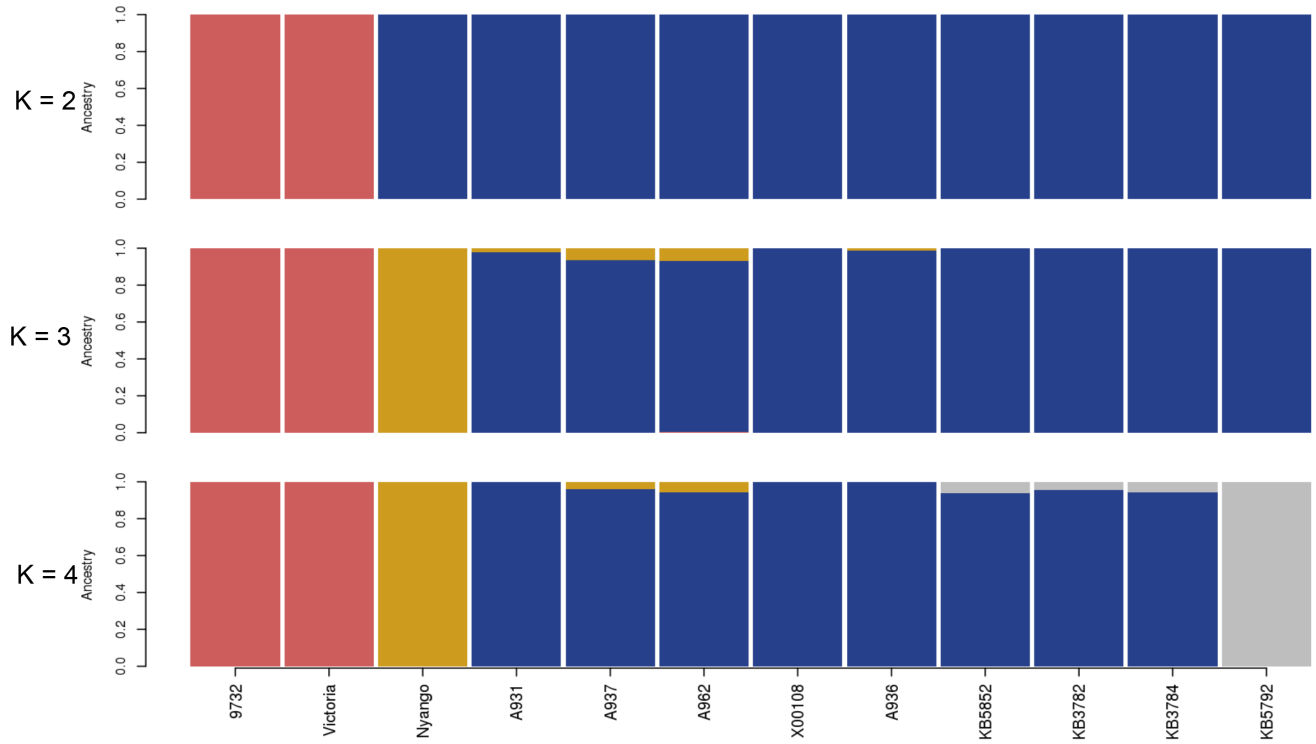


Figure S6: Four-population phylogeny as inferred by TreeMix (Pickrell and Pritchard, 2012). The tree was inferred using reference-free genotypes obtained using BSNP at putatively unlinked neutrally evolving loci.

A.



B.

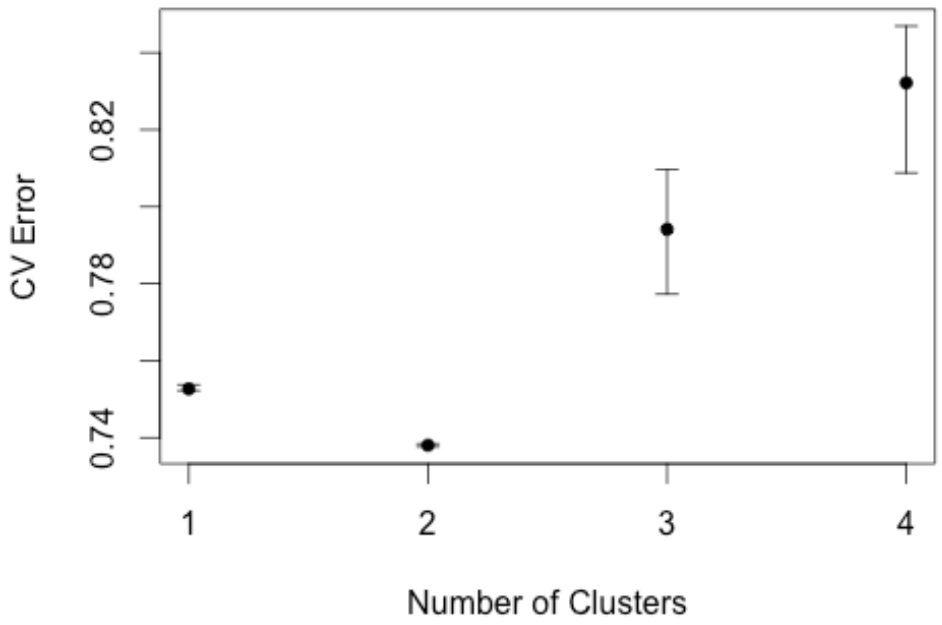


Figure S7: Admixture analysis for subset of samples used in G-PhoCS analysis.
Results are based on reference-free genotypes obtained using BSNP at putatively unlinked neutrally evolving loci.