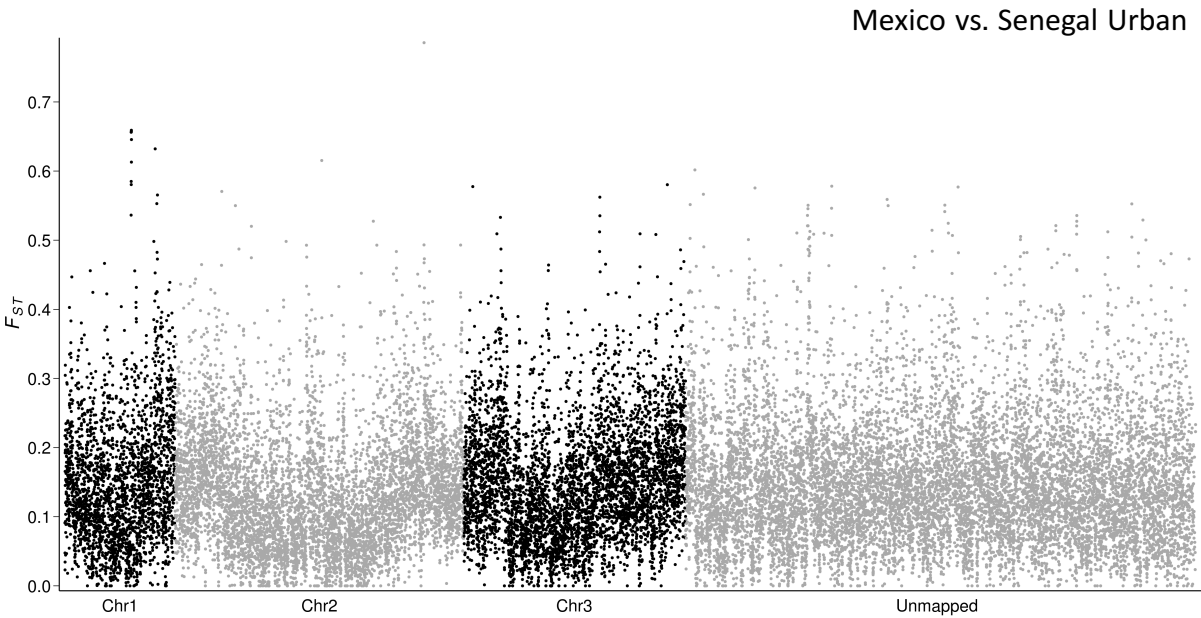
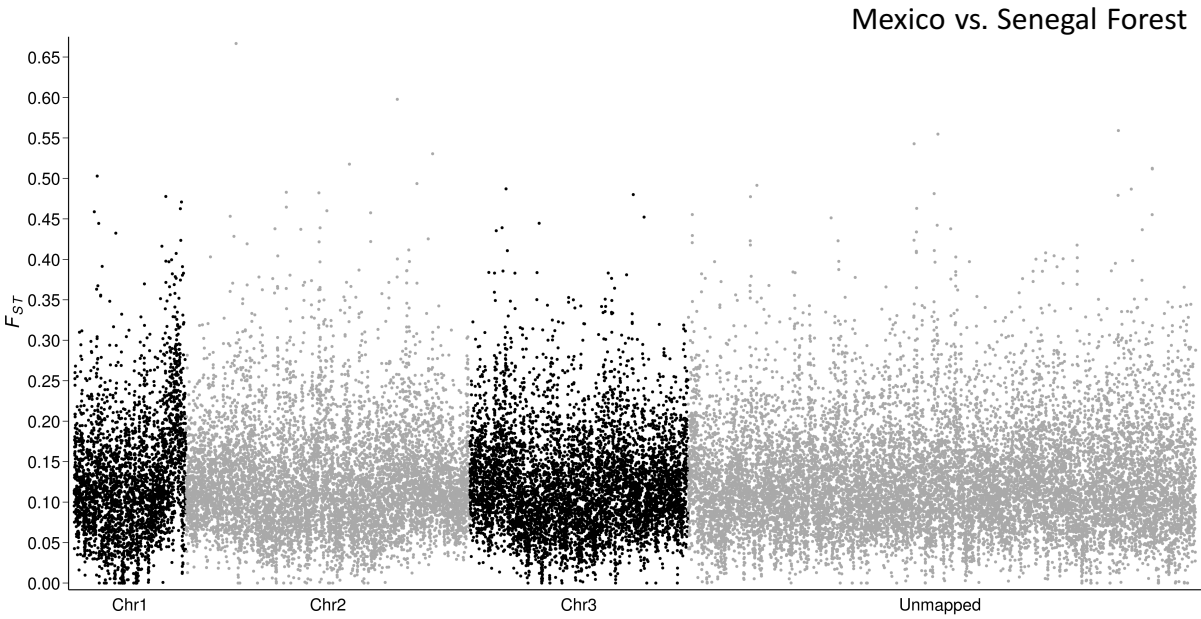
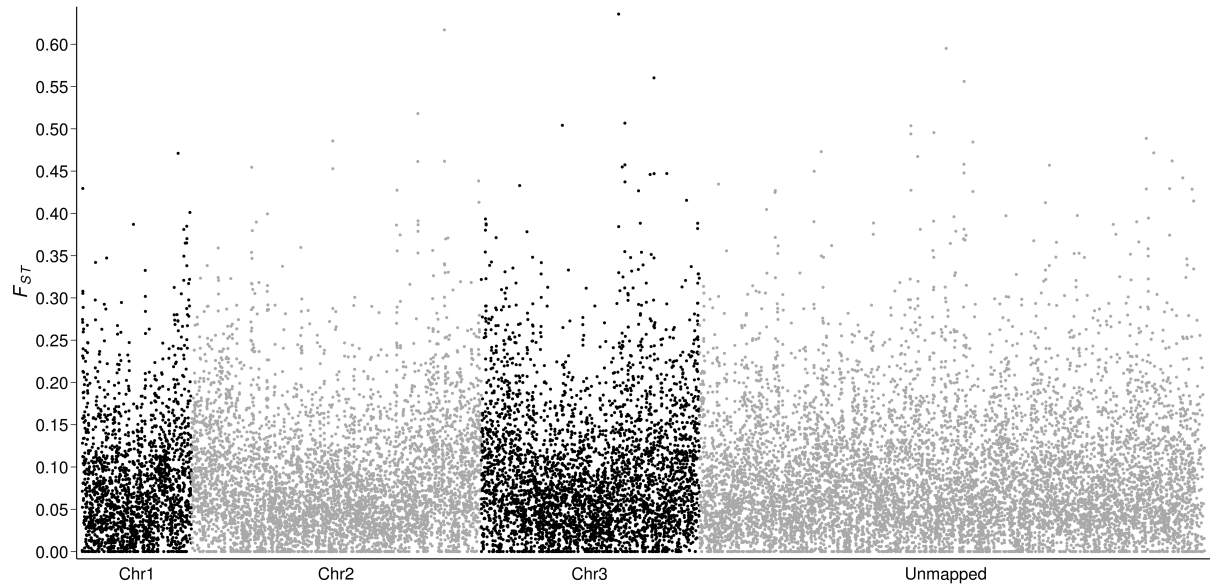


A - Mean F_{ST} values for 1000bp non-overlapping windows for each population pairwise comparison.

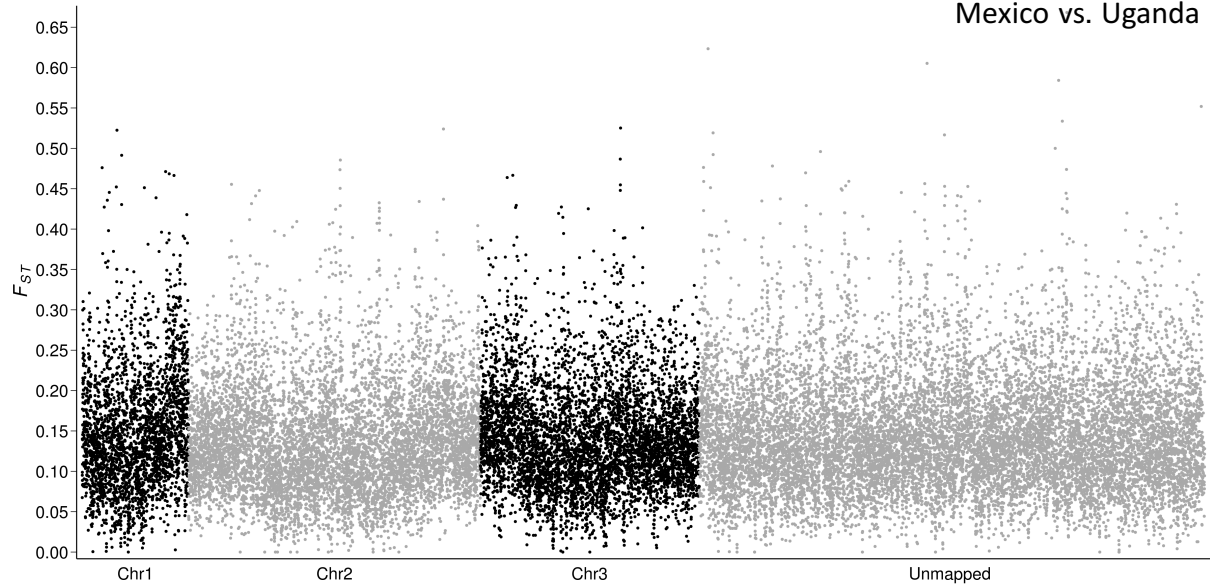
The x-axis represents a physical map (bp) made by arranging scaffolds along the genetic map with scaffolds mapping to the same genetic map position being ordered randomly. Scaffolds according to Juneja et al (2015 PLoS Pathogens. 11: e1004765). All positions with less than 10 individuals in each population comparison were excluded. Only windows contained at least 10 SNPs were plotted.



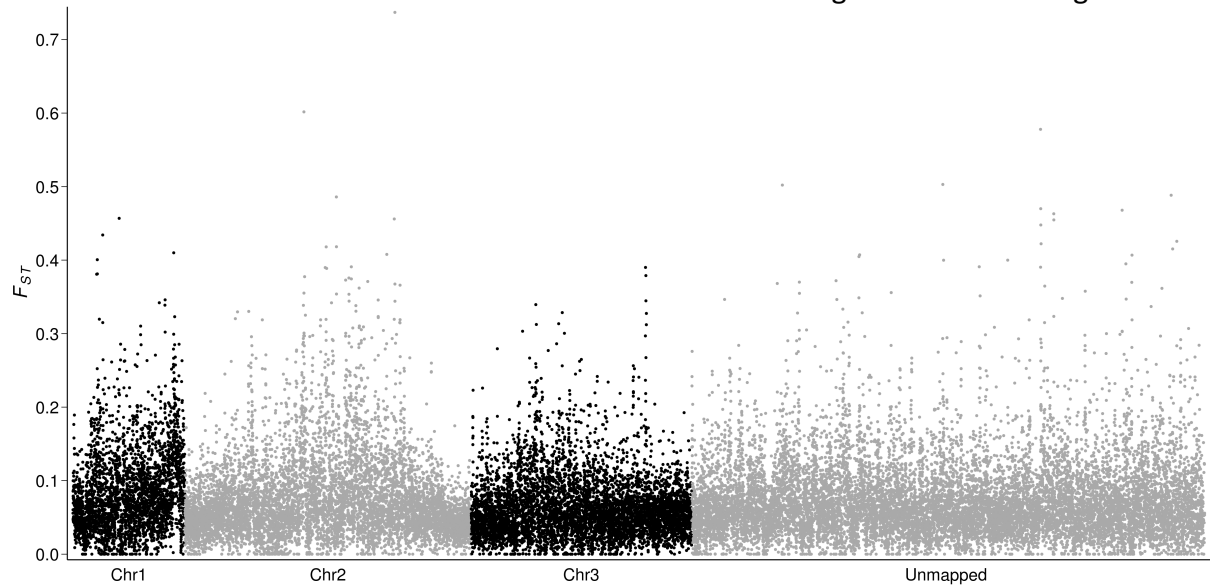
Mexico vs. Sri Lanka



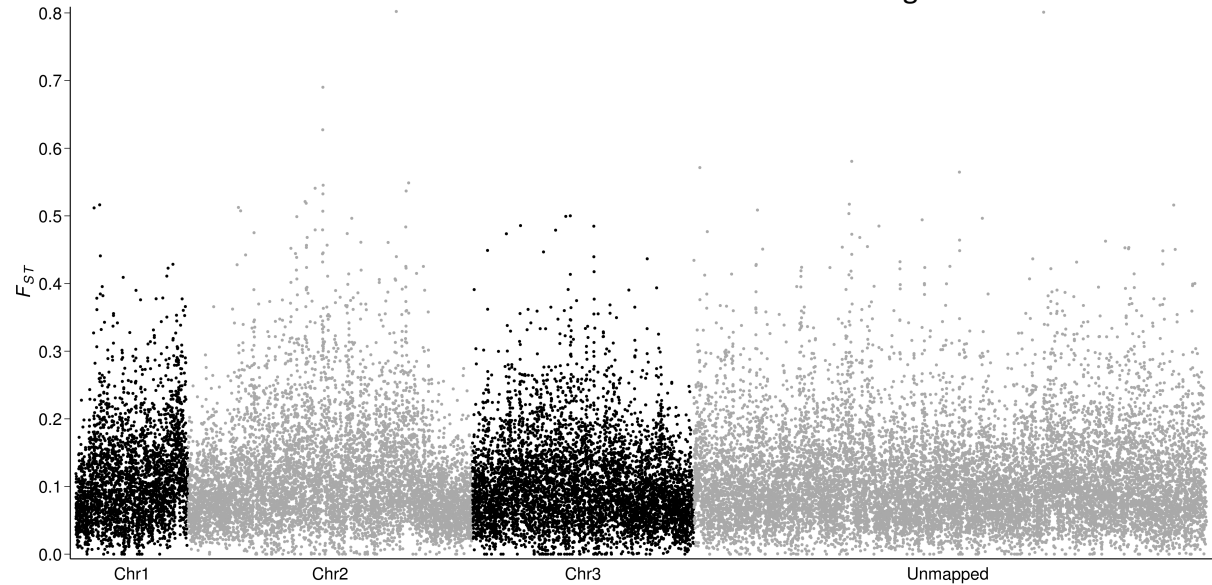
Mexico vs. Uganda



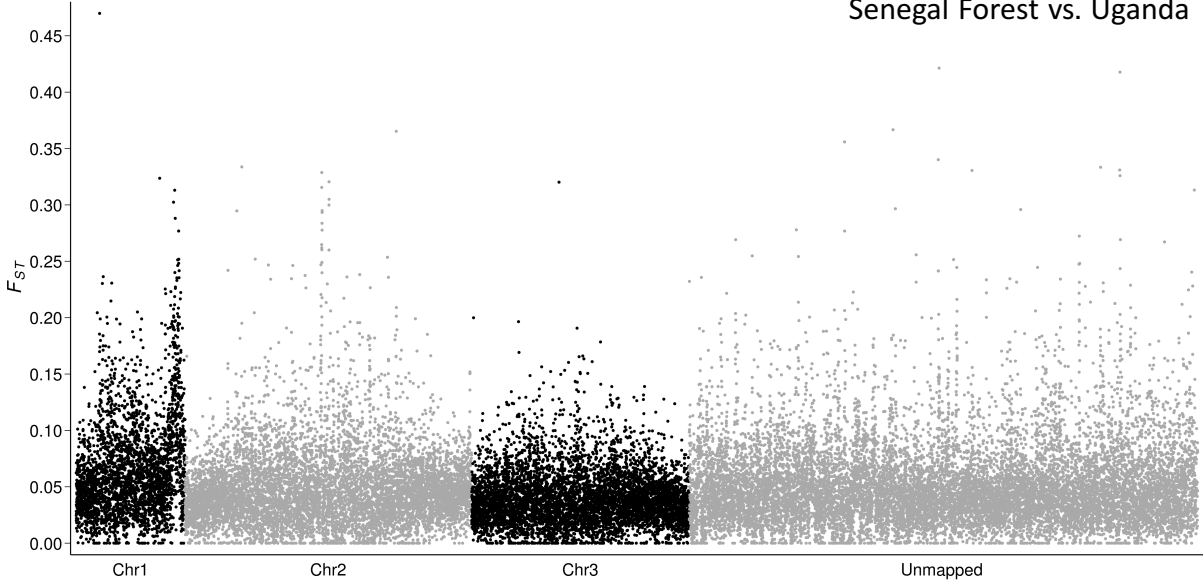
Senegal Forest vs. Senegal Urban



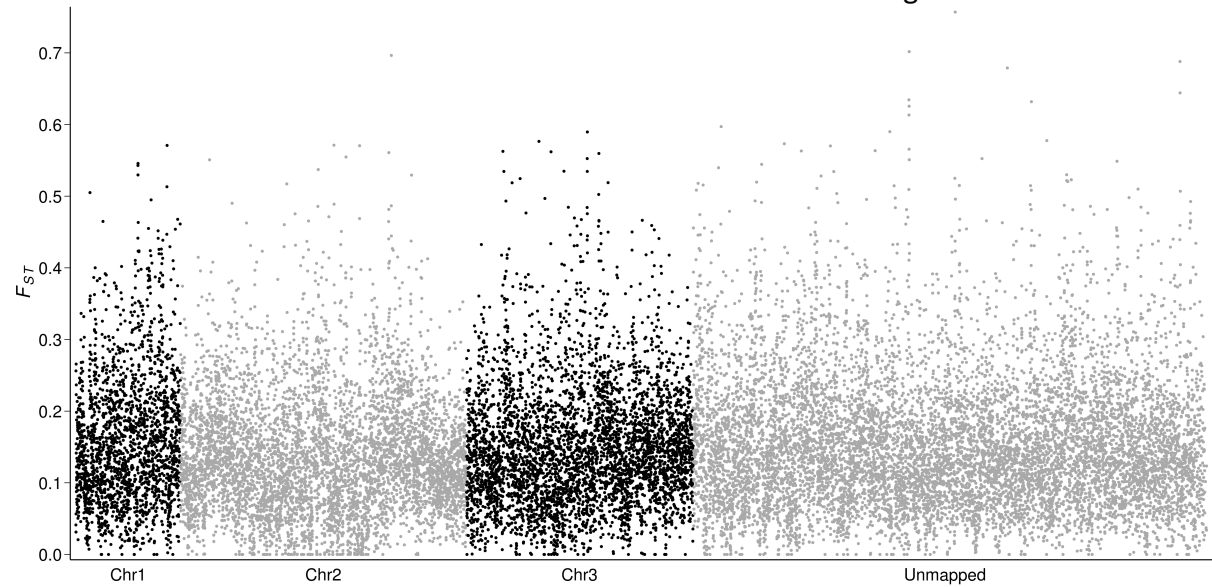
Senegal Forest vs. Sri Lanka



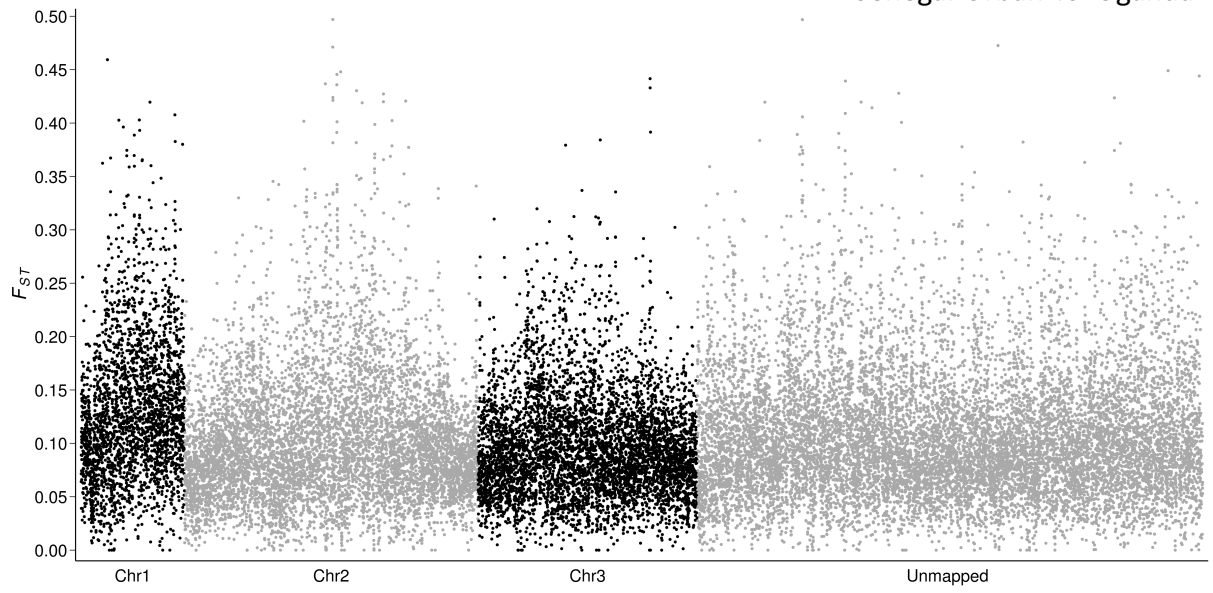
Senegal Forest vs. Uganda



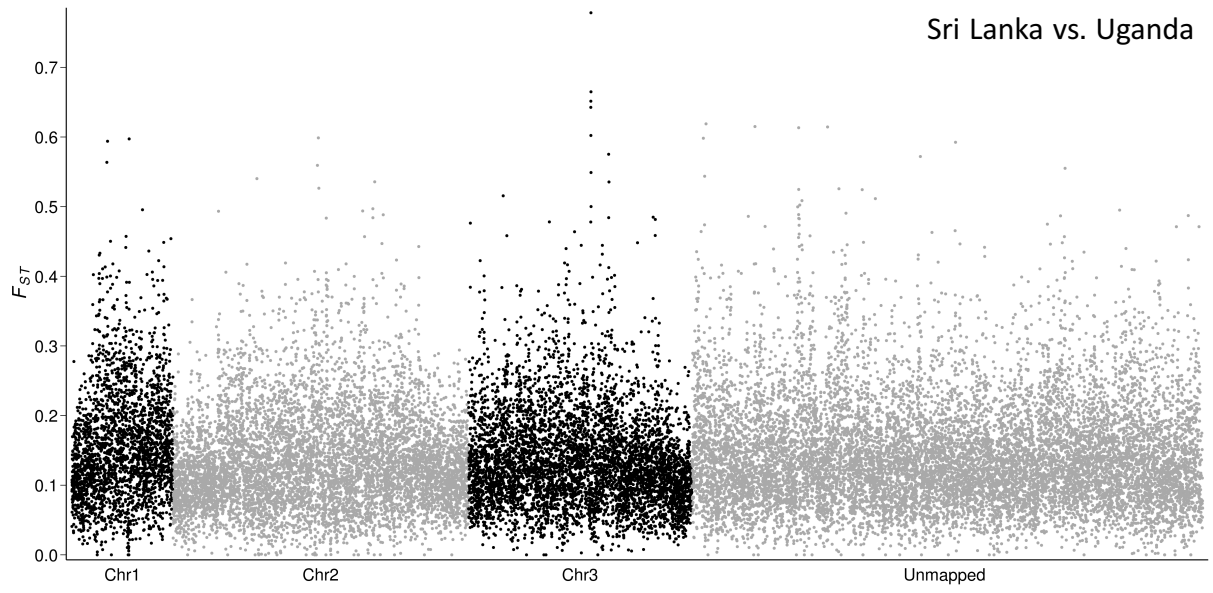
Senegal Urban vs. Sri Lanka



Senegal Urban vs. Uganda

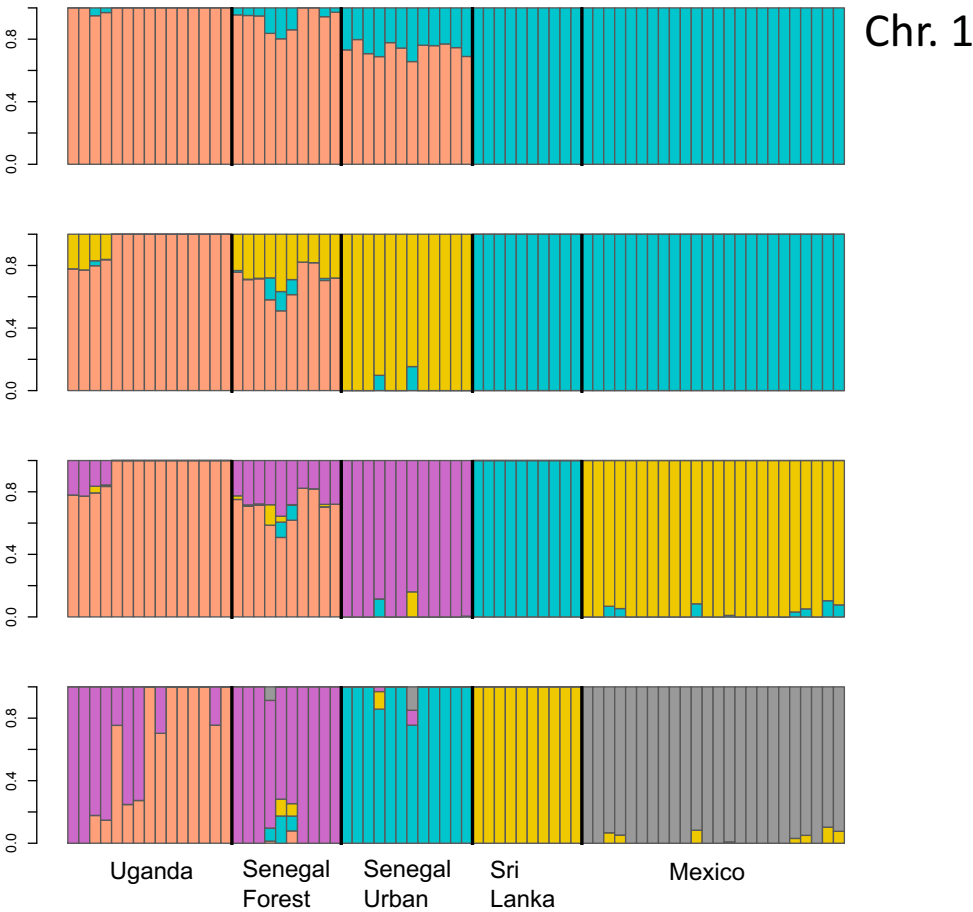


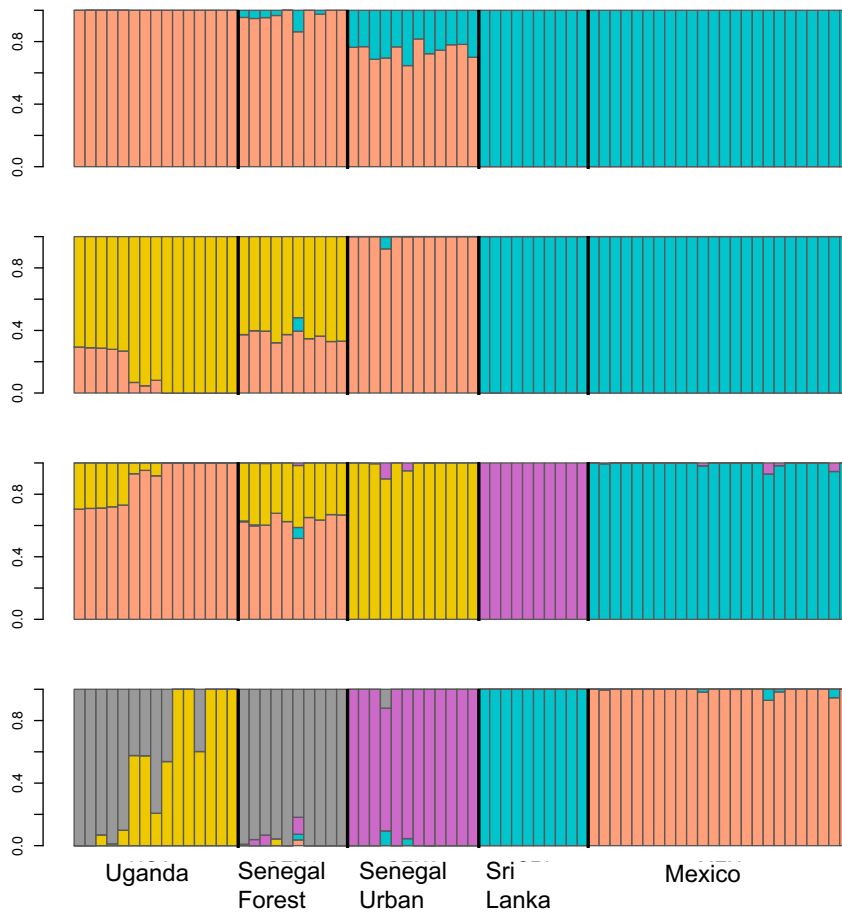
Sri Lanka vs. Uganda



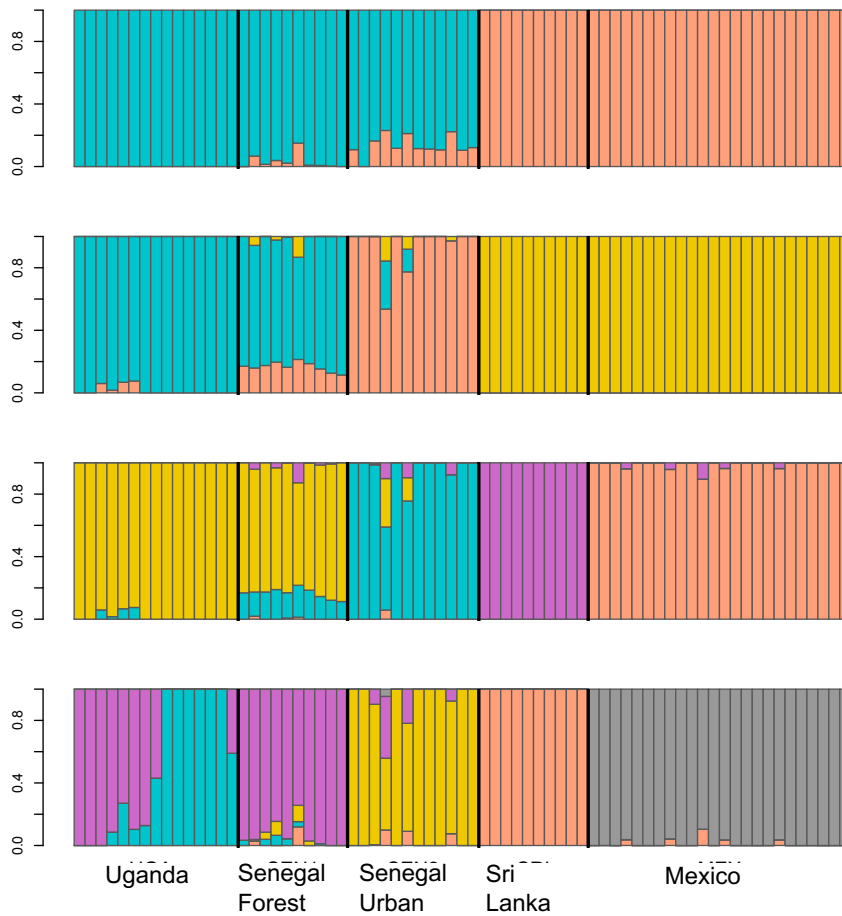
B - Ancestry proportions for *Ae. aegypti* individuals from five populations
calculated for each of the chromosomes separately.

Ancestry is conditional on the number of genetic clusters ($K=2-5$), and is inferred from all sites in our dataset.





Chr. 2



Chr. 3

C - Principal components analysis of *Ae. aegypti* exome sequences from five populations calculated for each chromosome separately.

The PCA was calculated from a covariance matrix calculated from all variants in the dataset and accounting for genotype uncertainty. The percentage of the variance explained by each component is shown on the top of the plot.

