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.
Senegal Forest vs. Sri Lanka

Senegal Forest vs. Uganda

Senegal Urban vs. Sri Lanka
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 \((K=2\text{–}5)\), and is inferred from all sites in our dataset.
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.