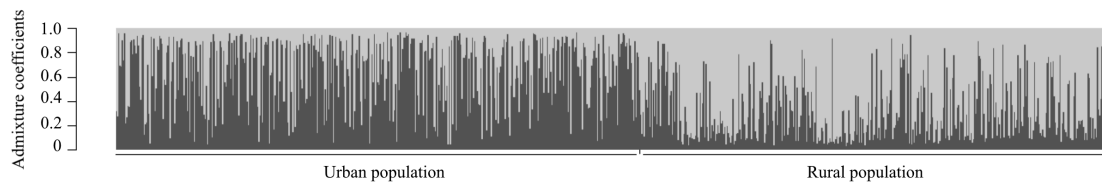


1

2 **S4a Figure:** Changes in K values from the mean log-likelihood probabilities (right axis) and plot
 3 of mean likelihood $L(K)$ and variance per K value (left axis) from STRUCTURE runs where
 4 inferred clusters (K) ranged from 1 to 10.



5

6 **S4b Figure:** Output of clustering analysis by STRUCTURE software for two clusters ($K=2$) of the
 7 849 trees, using fourteen microsatellite markers, grouped by origin (urban trees; rural trees). Each
 8 vertical bar represents one individual and shows its inferred cluster membership; black and gray
 9 colors correspond each to one cluster. If both colors are present, the haplotype consists of a mixture
 10 of markers assigned to both black and gray clusters. The samples from the urban area and rural area
 11 were assigned in different proportions to each cluster. Using an assignment probability threshold
 12 of 0.8, 41% and 8% of individuals from the urban population were respectively assign to the black
 13 and gray clusters (51% were presenting intermediate genotypes) and 5% and 45% of individuals
 14 from the rural population were respectively assigned to the black and grey clusters (50% were
 15 presenting intermediate genotypes).