

Supplementary Figures

Limited introgression from non-native commercial strains and signatures of adaptation in the key pollinator *Bombus terrestris*

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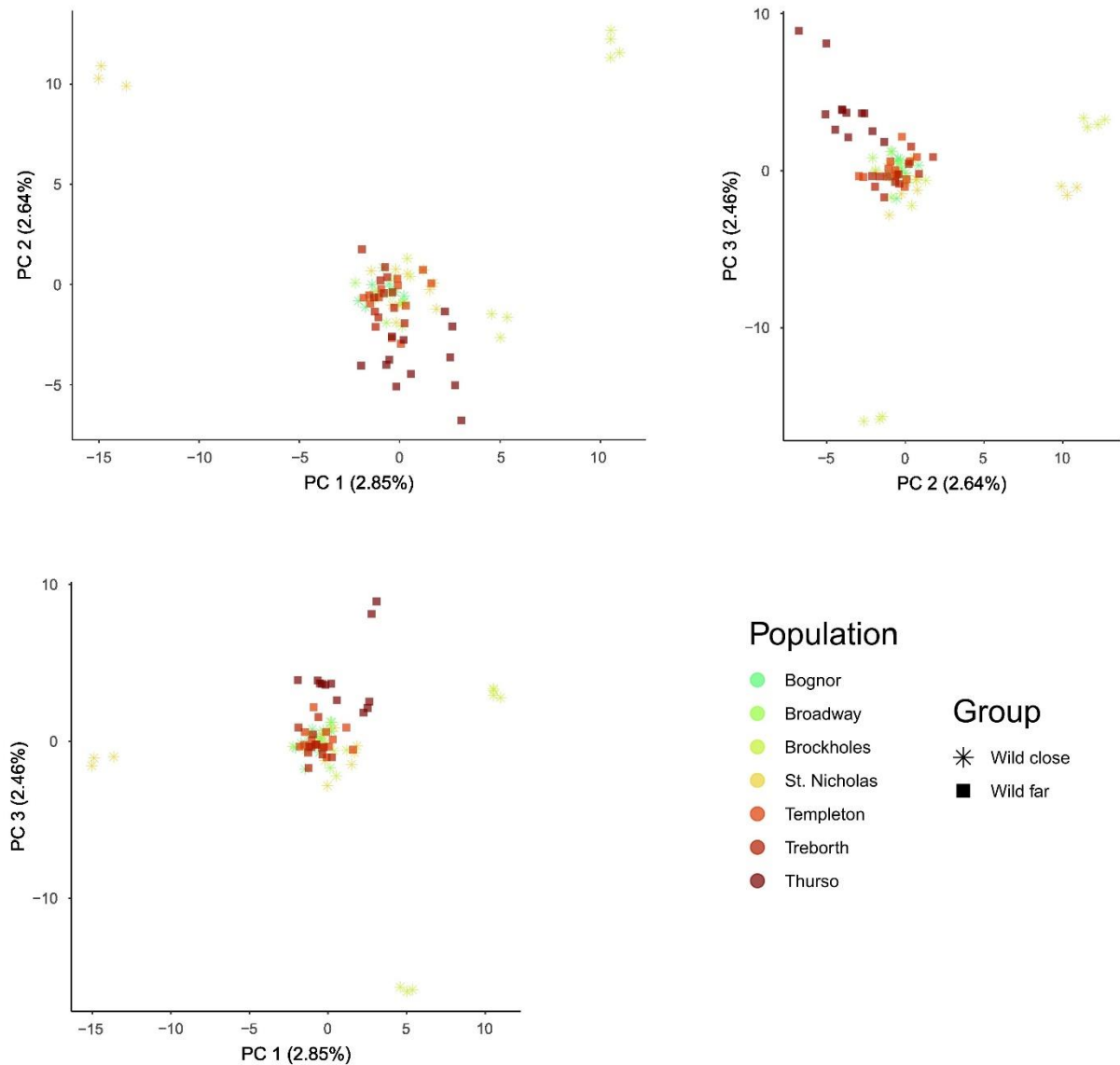
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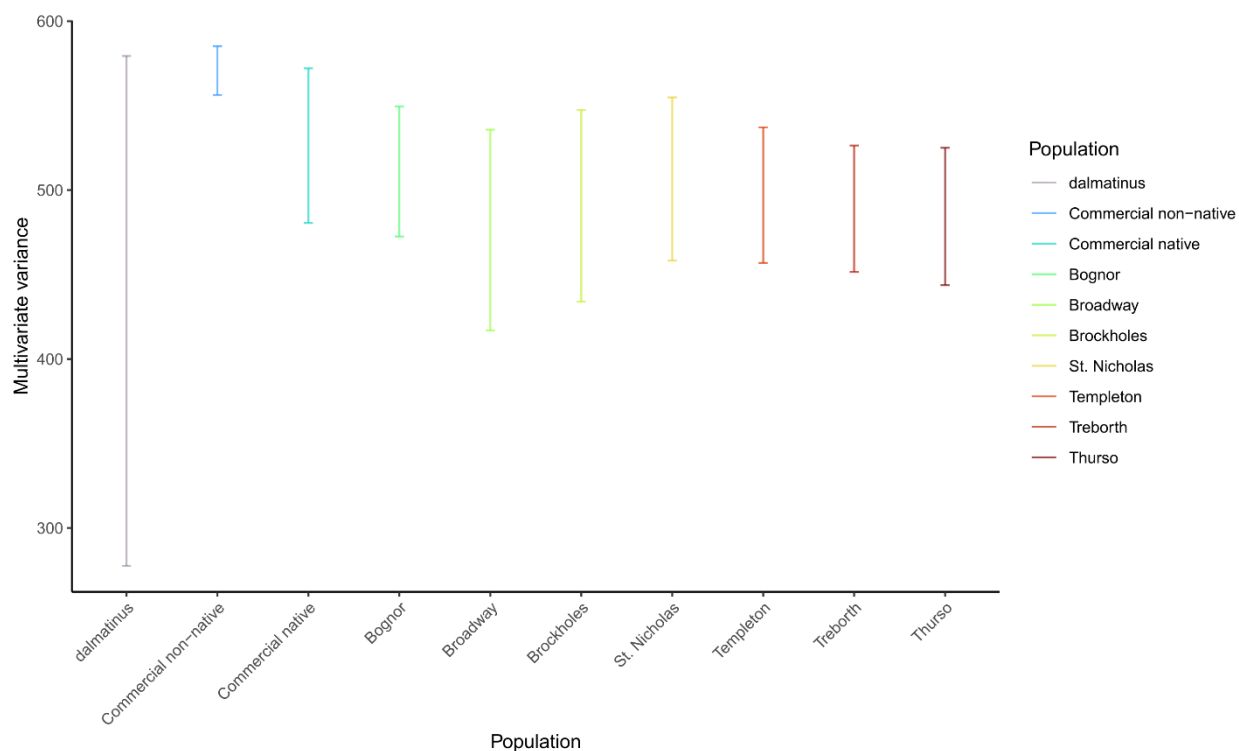
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Supplementary Figure S1



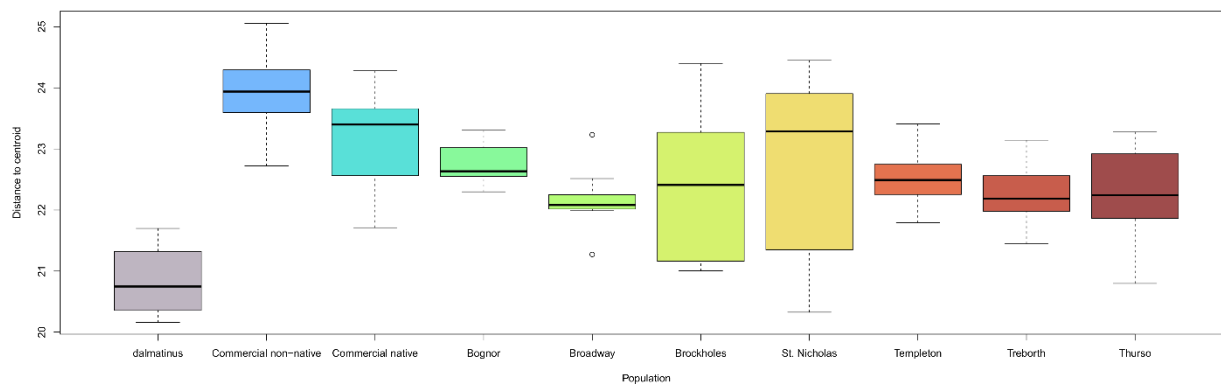
Supplementary Figure S1. Score plots along the first three principal components (from left to right: PC1 vs PC2, PC1 vs PC3, PC2 vs PC3) of a PCA performed on the wild samples only.

Supplementary Figure S2



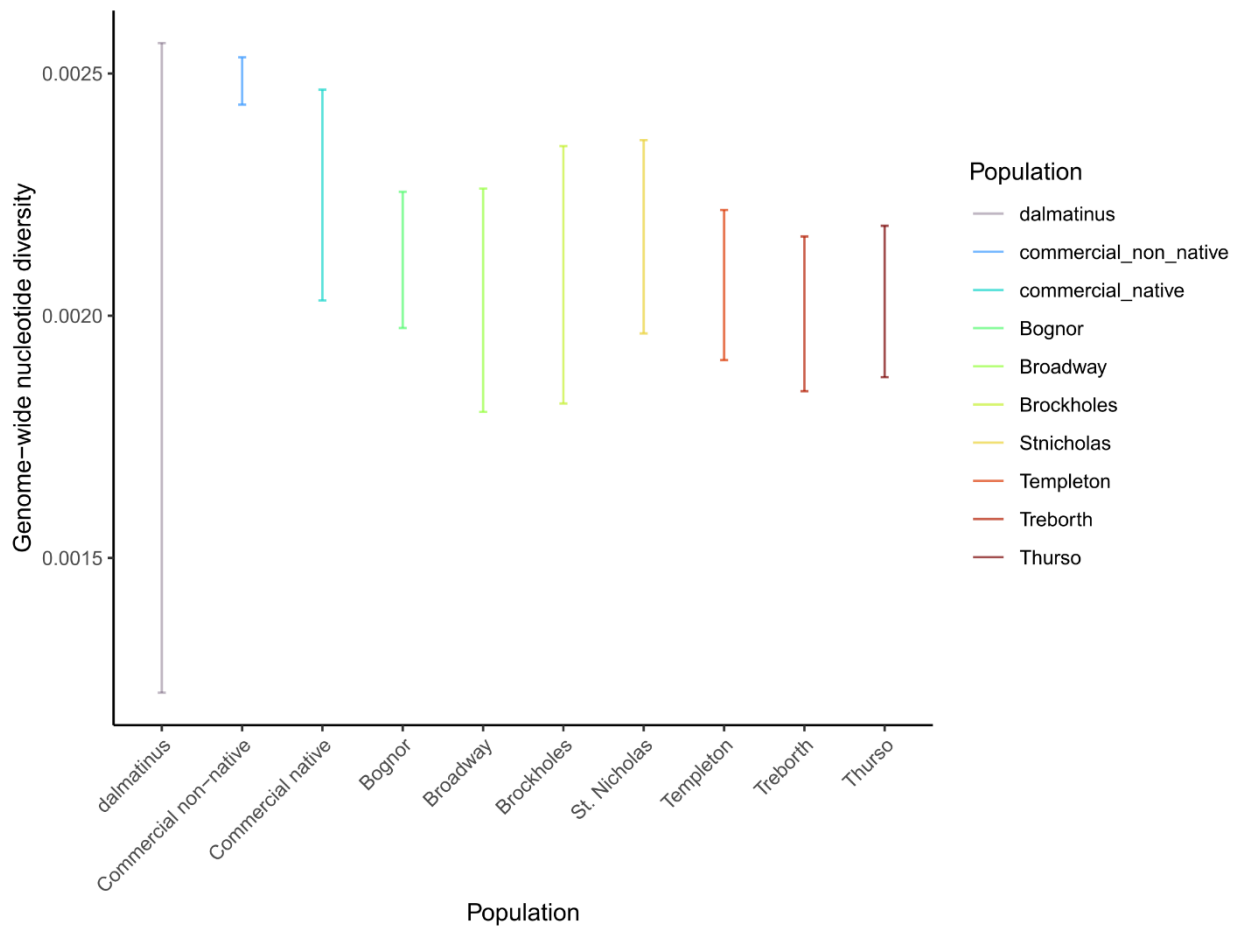
Supplementary Figure S2. Confidence intervals for multivariate variance of each population using all principal components.

Supplementary Figure S3



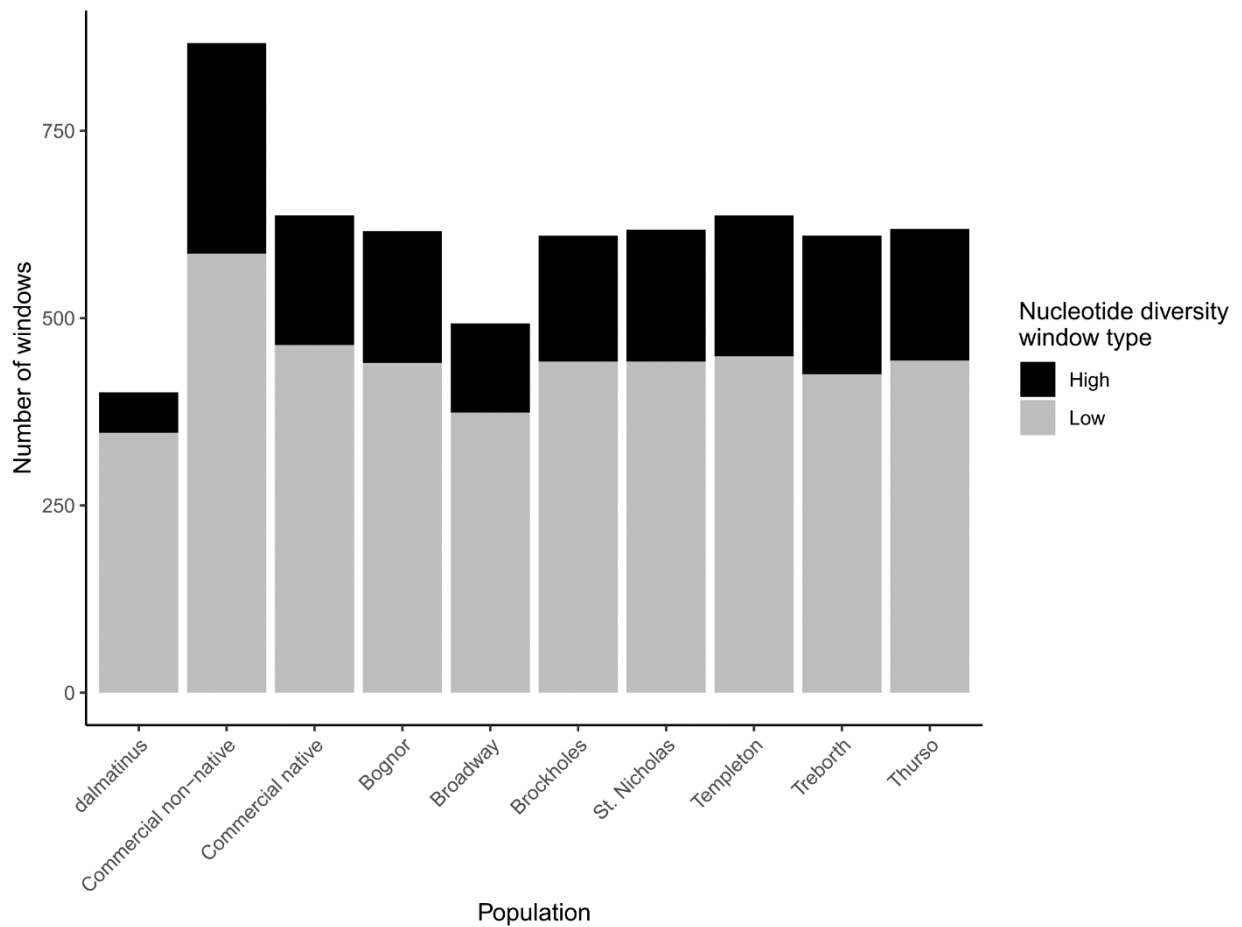
Supplementary Figure S3. Distance from centroid obtained using the PERMDISP2 procedure as implemented in the R package *vegan* on the full set of principal components obtained from genetic data.

Supplementary Figure S4



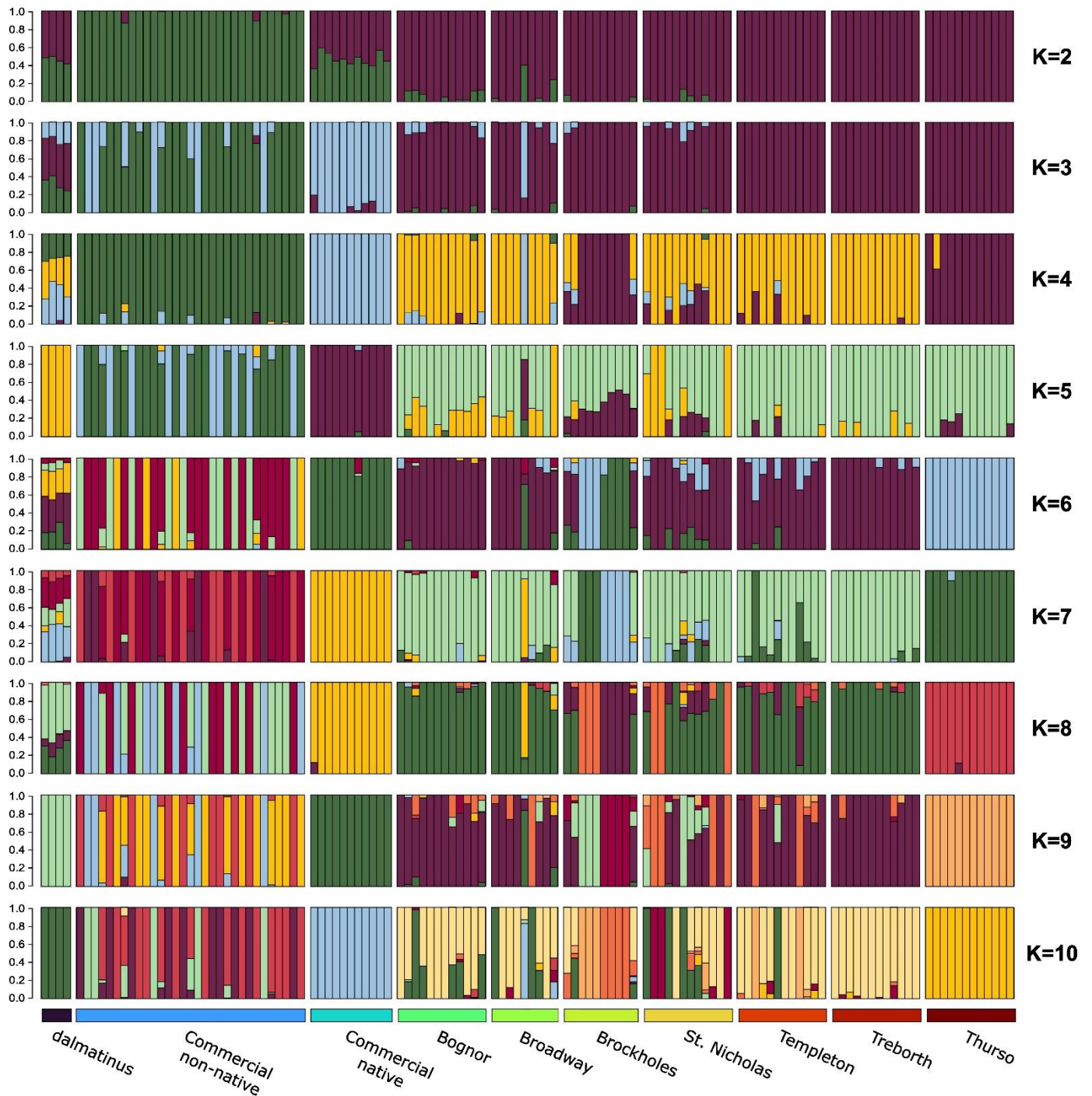
Supplementary Figure S4. Bootstrapped 95% confidence intervals for genome-wide nucleotide diversity. The wide confidence interval for *dalmatinus* can be explained by the small number of individuals in this sample.

Supplementary Figure S5



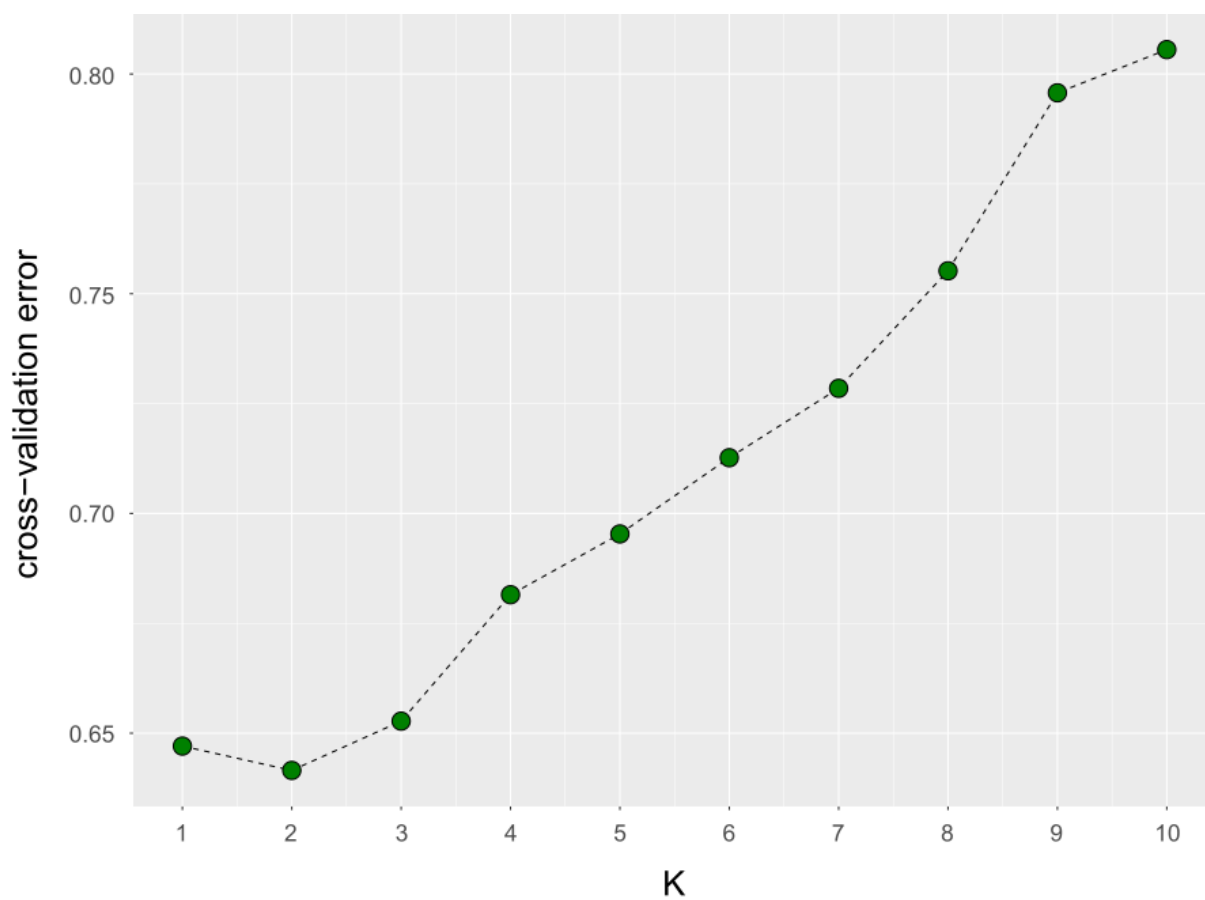
Supplementary Figure S5. Number of high or low nucleotide diversity windows for each population. These are the windows whose 95% confidence interval obtained by bootstrapping in the sliding window analysis did not overlap the bootstrapped genome-wide 95% confidence interval for the population they belonged to.

Supplementary Figure S6

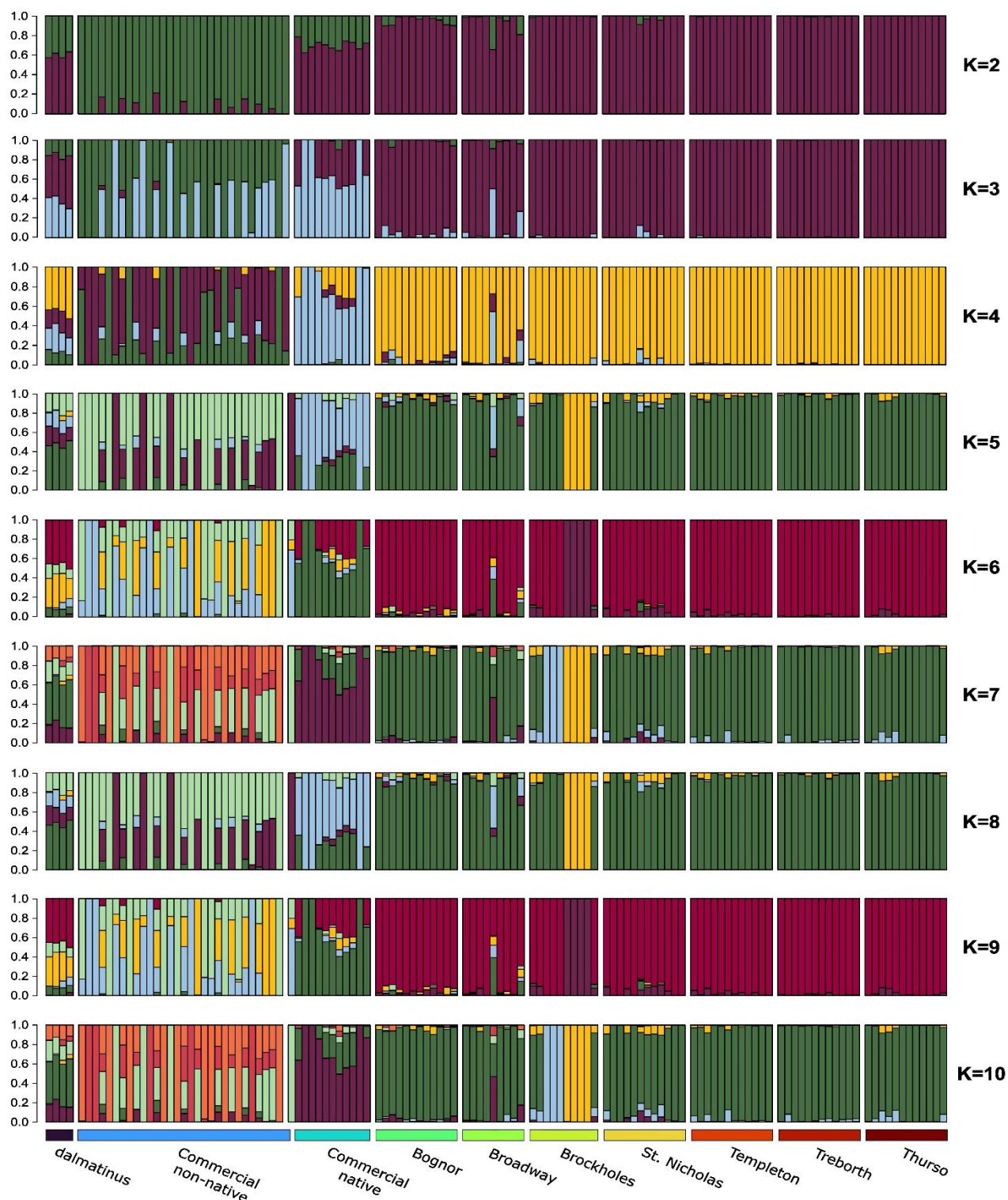


Supplementary Figure S6. Genetic clustering and individual ancestry at K ranging from 2 to 10 inferred by Admixture.

Supplementary Figure S7

**Supplementary Figure S7.** Cross-validation error plot of the Admixture analysis.

Supplementary Figure S8



Supplementary Figure S8. Individual coancestry inferred by the hierarchical Bayesian model implemented in the program Entropy for K ranging from 2 to 10.