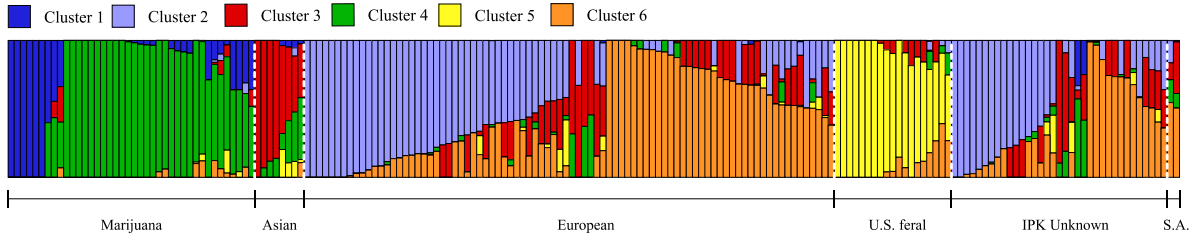
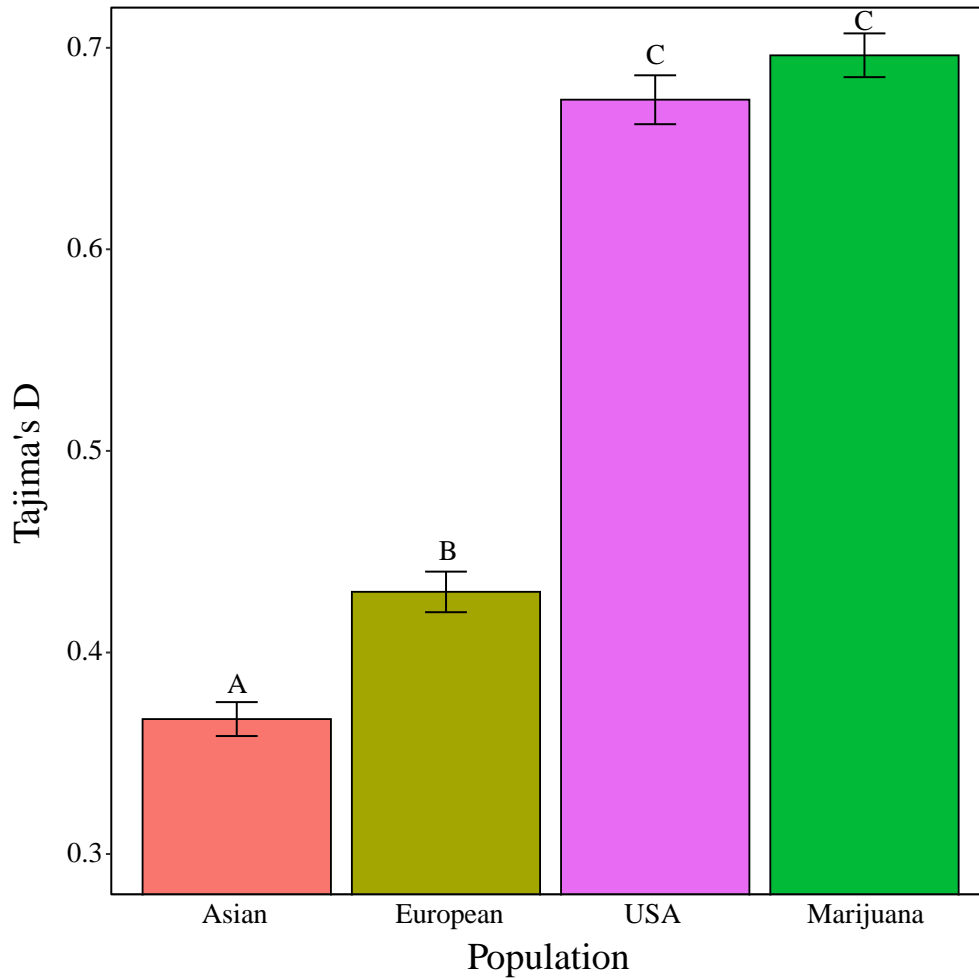


1 **Supplemental Figure 1.** Cross validation (CV) errors calculated by ADMIXTURE for K values
2 1-10. K = 6 exhibited the lowest cross validation error.

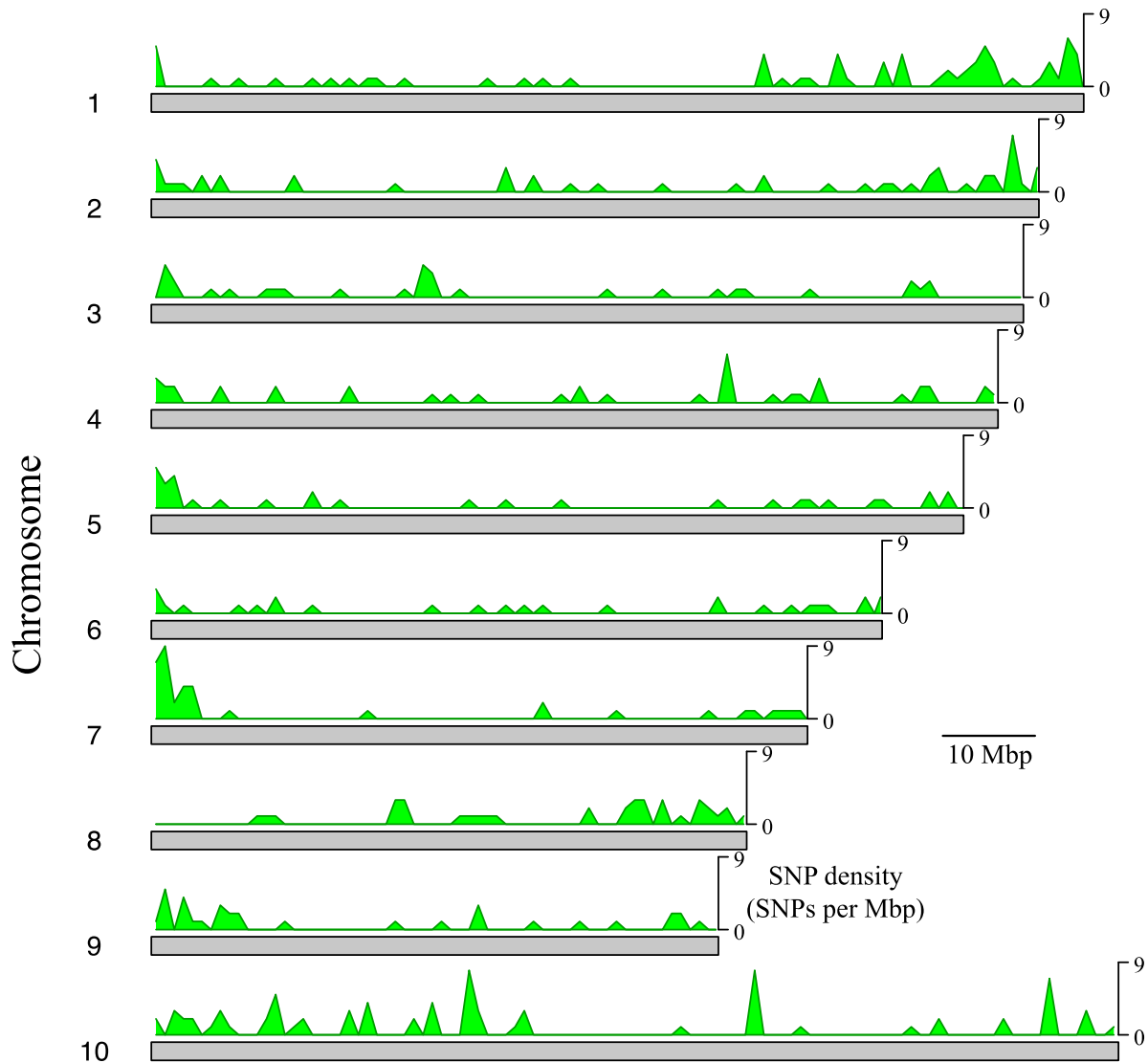
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13 **Supplemental Figure 2.** Stacked bar plots representing ADMIXTURE results showing individual
14 ancestry likelihoods assuming $K = 6$.
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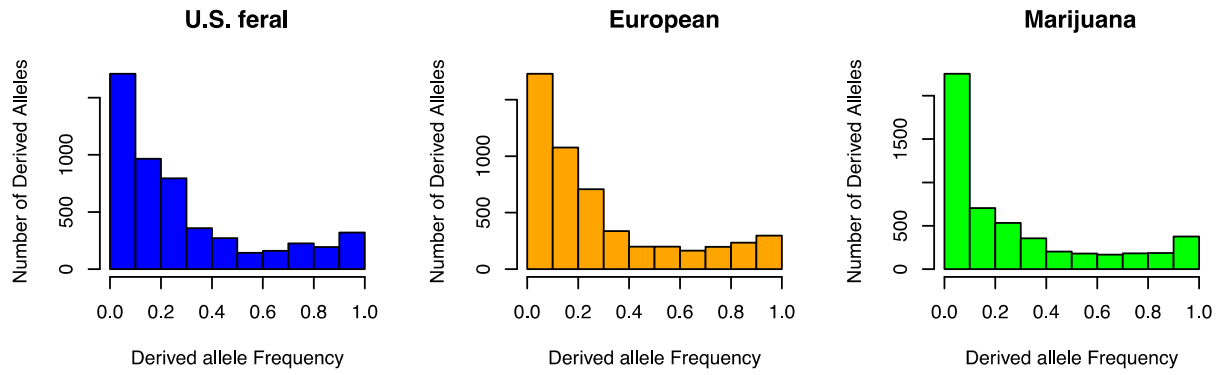


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45 **Supplemental Figure 3.** Bar plots showing the comparisons of mean Tajima's D (\pm standard
46 error) across the Asian, European, U.S. feral and Marijuana sub-populations at the 7540 single
47 copy orthologs. Letters above bars indicate significance of Tukey adjusted post-hoc pairwise
48 comparisons such that different letters indicate significant differences ($p < 0.05$).
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52 **Supplemental Figure 4.** SNP density plot depicting the locations of derived alleles showing
53 evidence for species wide selection. Shown are horizontal grey bars representing the ten *C. sativa*
54 chromosomes with local green density plots that depict the number of species wide high frequency
55 derived alleles in 1 megabase intervals.

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66 **Supplemental Figure 5.** Individual derived allele frequency spectrums for the U.S. feral,
67 European and Marijuana sub-populations respectively.

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