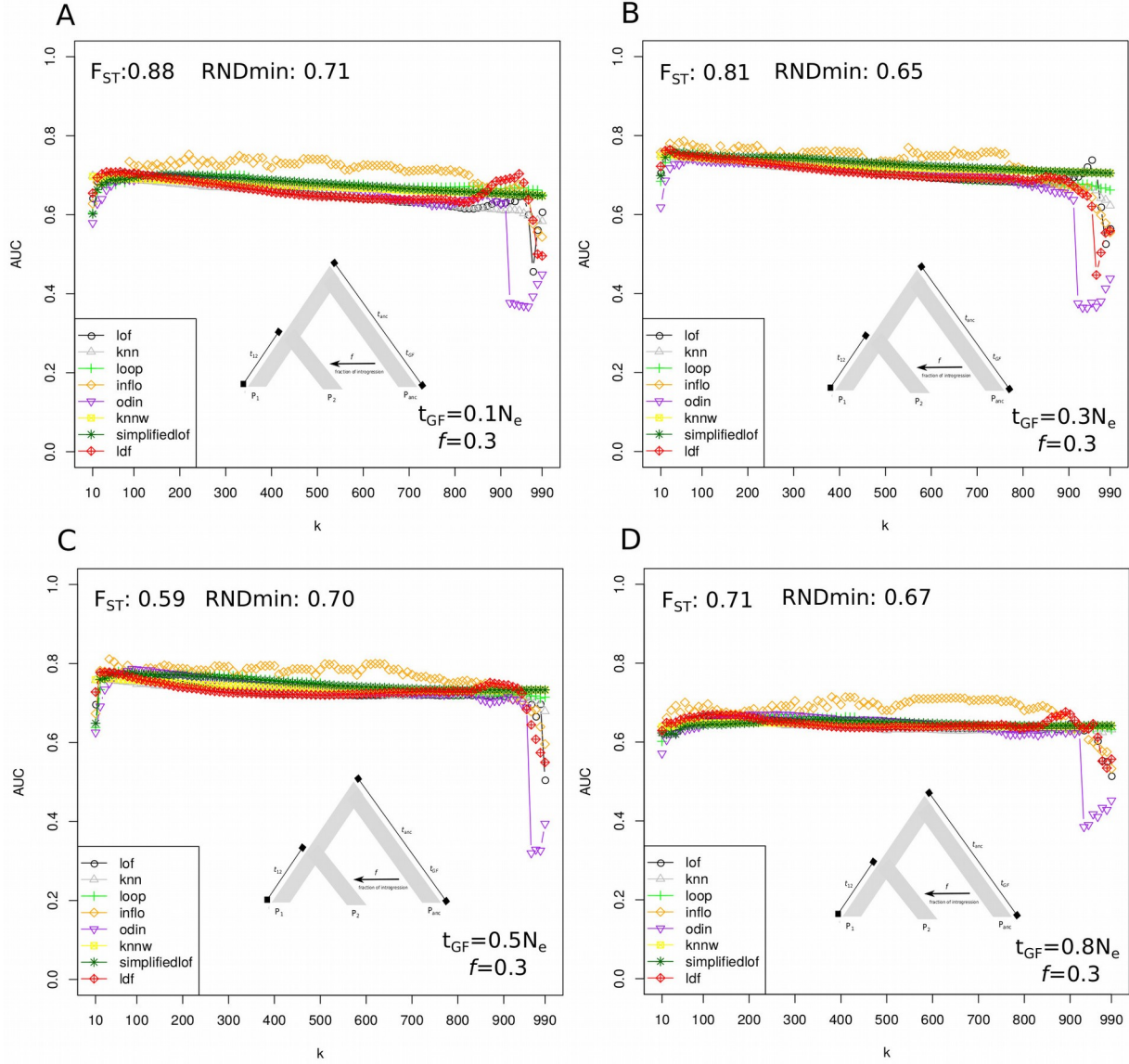


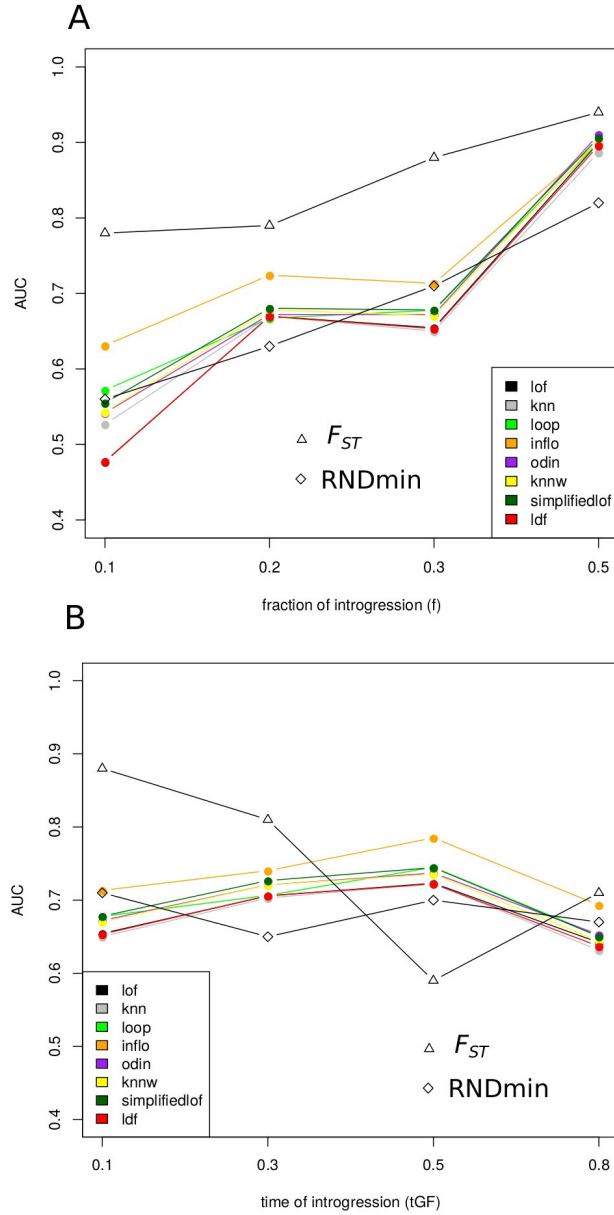
Supplementary Material

Genome Scans for Selection and Introgression based on k -
Nearest Neighbor Techniques

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Supplementary Figure S1: Introgression. Varying the time of gene-flow (t_{GF}) and using d_{xy} as features. The results for the k NN-based methods using d_{xy} as features shown for 100 sequentially sampled k 's ($k=[1, 10, \dots, 990, 1000]$). The coalescent times are $t_{12}=1N_e$ and $t_{anc}=2N_e$ generations ago. Recombination rate is set to $r=0.01$ in all simulations. The outcome of the k NN-based methods are compared to F_{ST} and $RNDmin$. The time of gene-flow is set to **A.** $t_{GF}=0.1N_e$ **B.** $t_{GF}=0.3N_e$ **C.** $t_{GF}=0.5N_e$ and **D.** $t_{GF}=0.8N_e$ generations ago.



Supplementary Figure S2: Detecting introgression with a computed k and using d_{xy} as features. The accuracy of the kNN -methods using d_{xy} as features compared to F_{ST} and $RNDmin$. Recombination rate is set to $r=0.01$ in all simulations. **A.** Varying the fraction of introgression ($f=[0.1, 0.2, 0.3, 0.5]$) **B.** Varying the time of gene-flow ($t_{GF}=[0.1, 0.3, 0.5, 0.8]$).