

Supplementary Figures

1. CHAPTER ONE

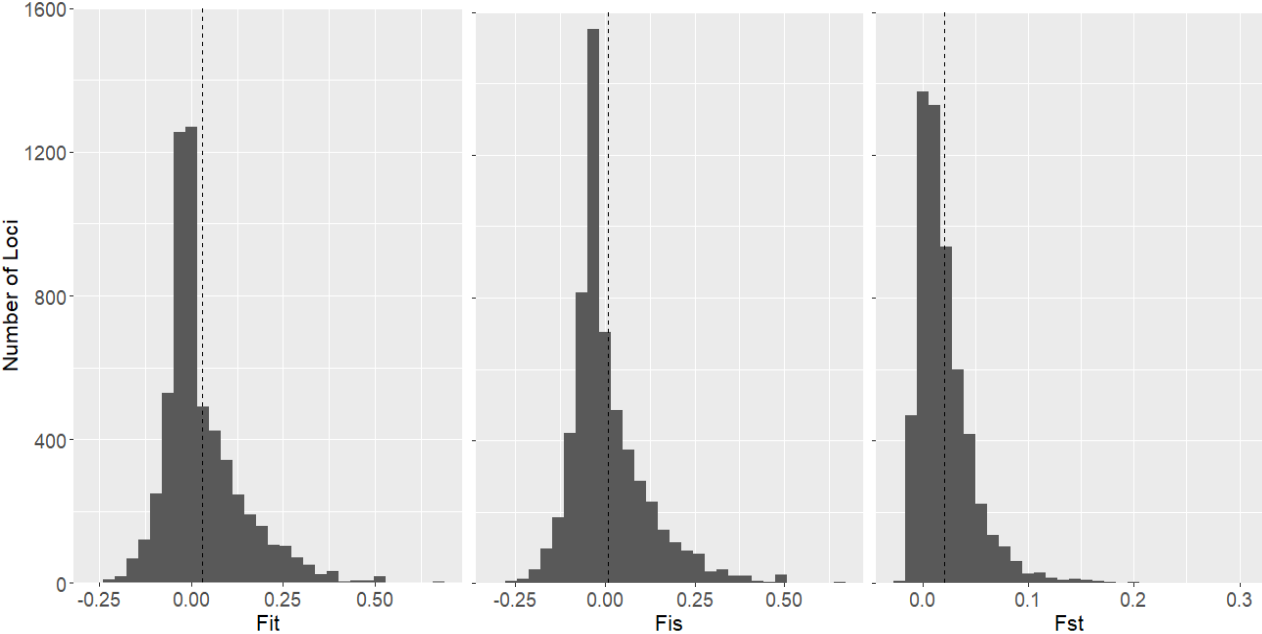


Figure S1.1. Distribution of F-statistics per locus over all populations, as calculated in Genepop v4.2. Dashed line indicates mean value.

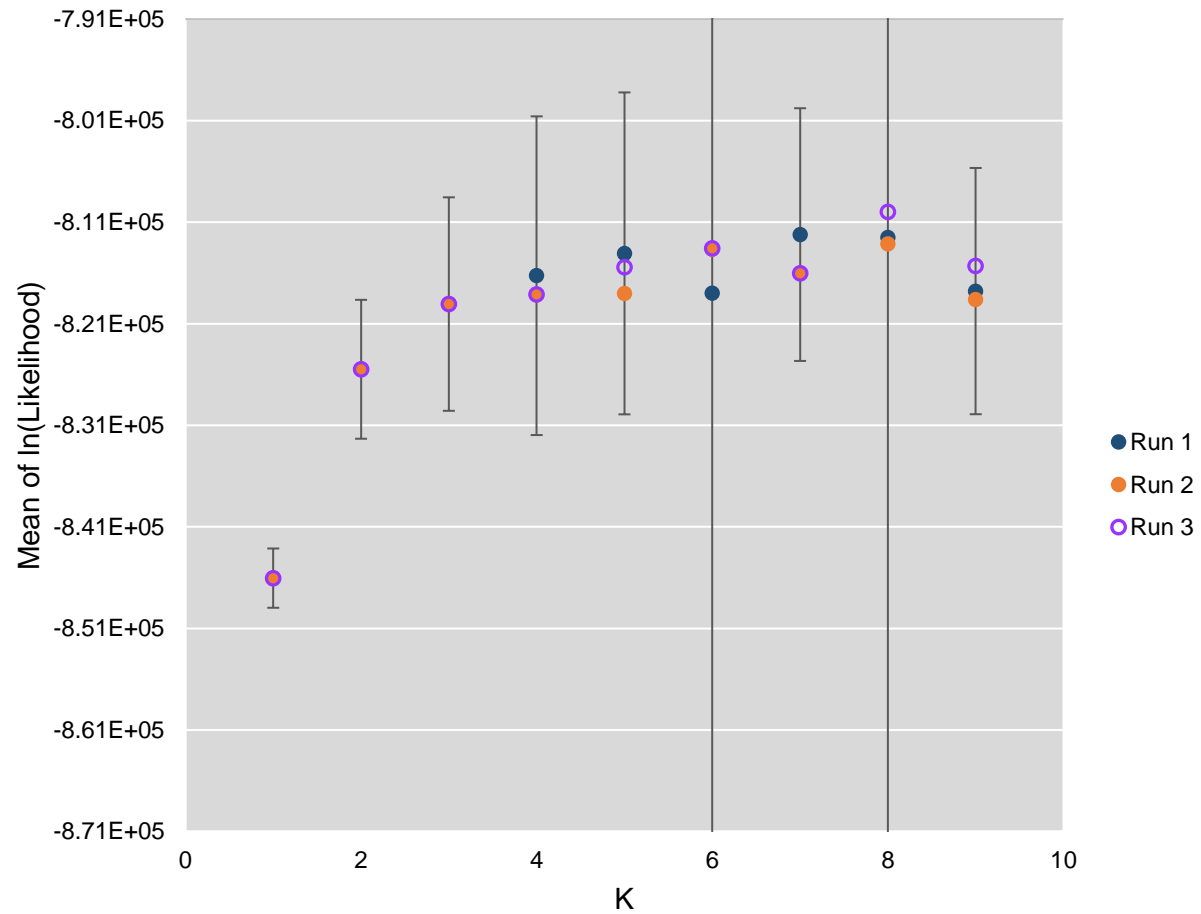


Figure S1.2. Mean log likelihoods produced by STRUCTURE for each value of K, with error bars representing variance of the $\ln(\text{Likelihood})$.

2. CHAPTER TWO

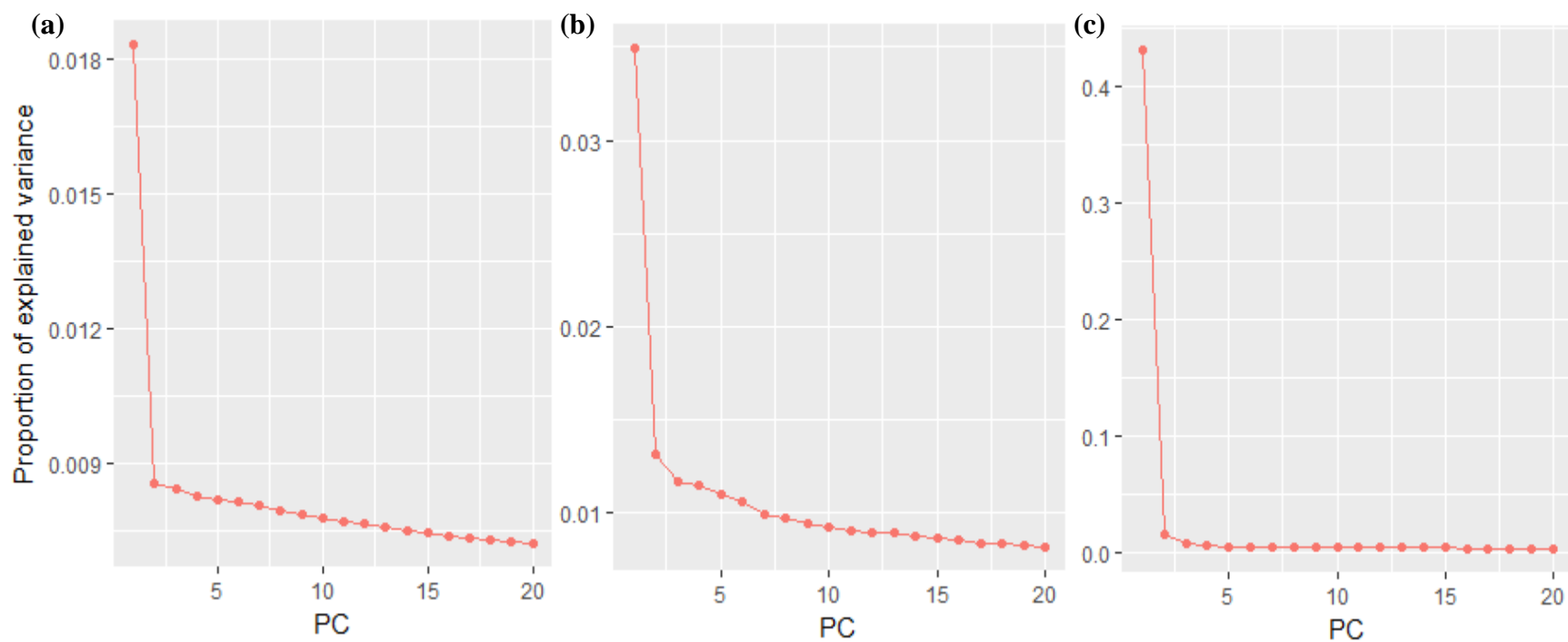


Figure S2.1. Scree plots of the first 20 principal components (PCs) for PCAdapt outlier analysis in the **(a)** eastern population, **(b)** western population, and **(c)** full data set.

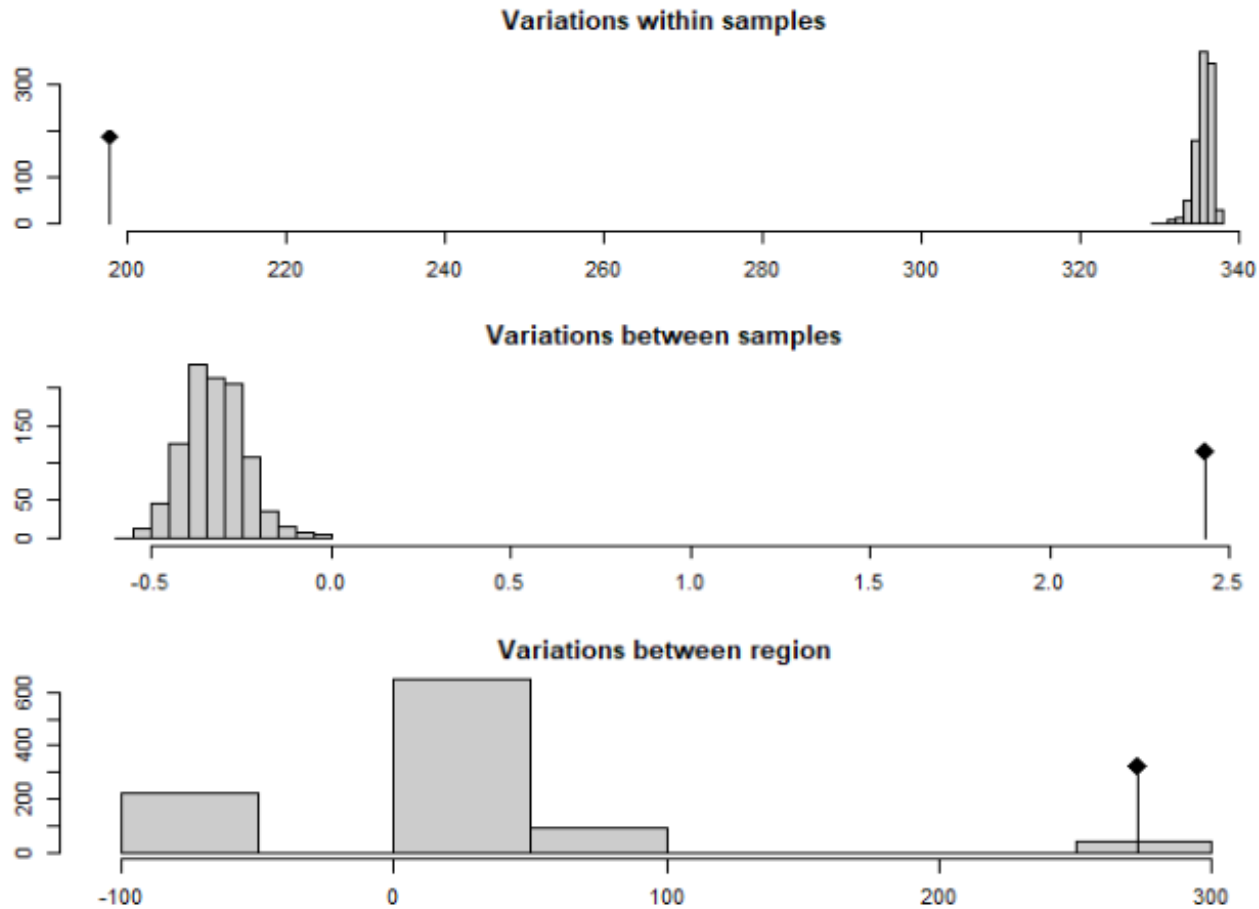


Figure S2.2. Histograms from the AMOVA showing the distribution of the randomized strata, with points representing the observed data. The strata are the eastern and western populations (“region”) and subpopulations (“sample”).

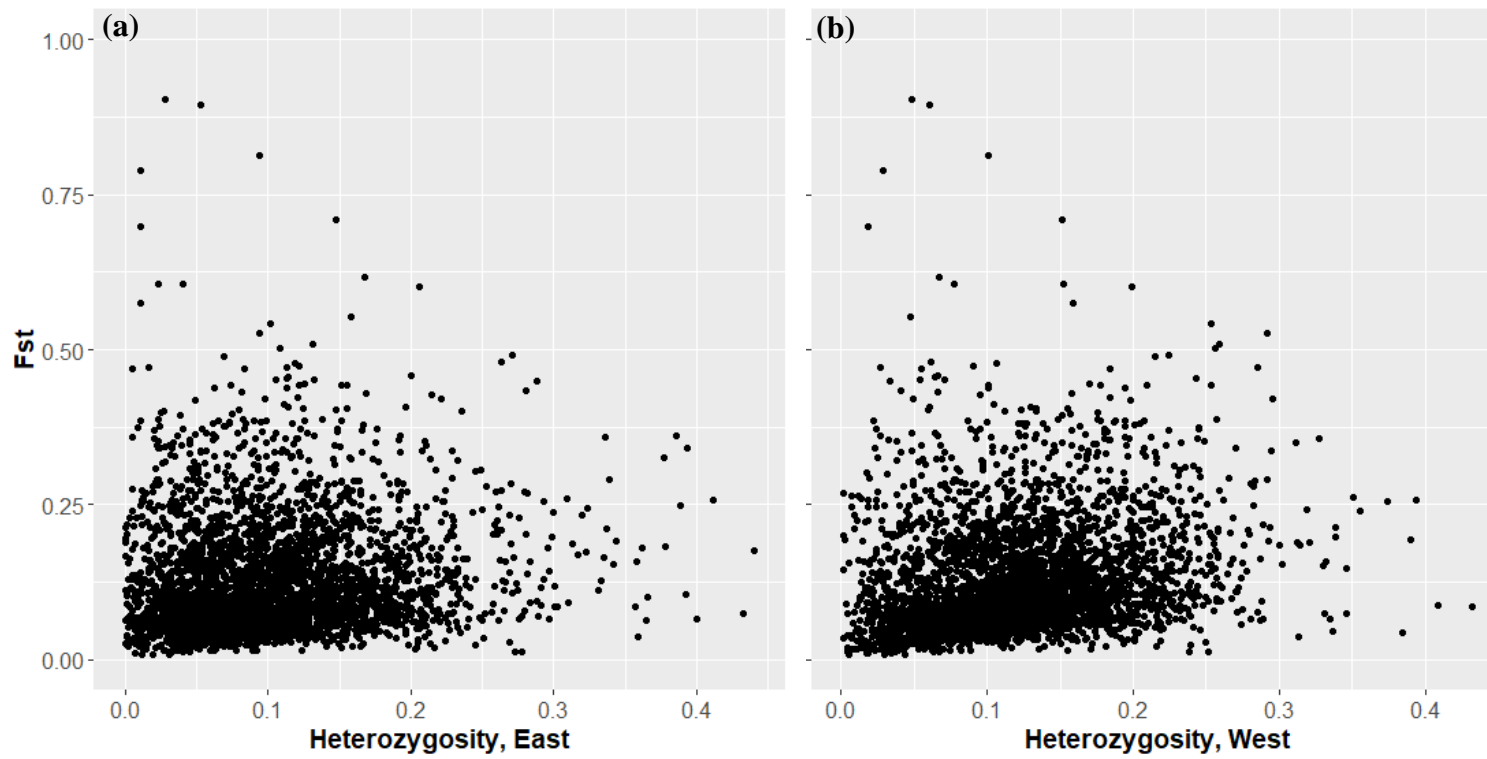


Figure S2.3. Each weighted average F_{st} from the full data set plotted against the corresponding weighted average H_o in the (a) eastern and (b) western population.

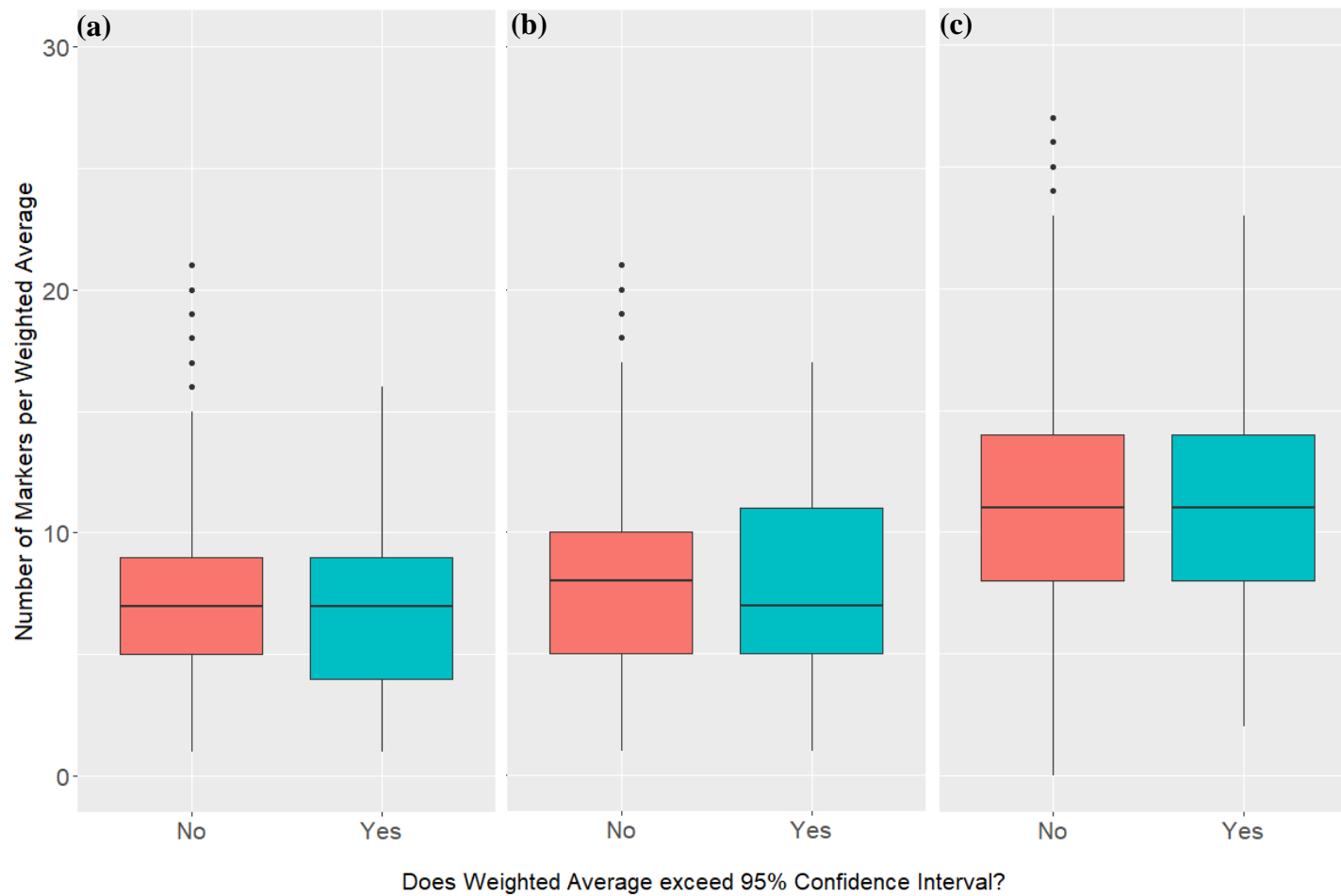
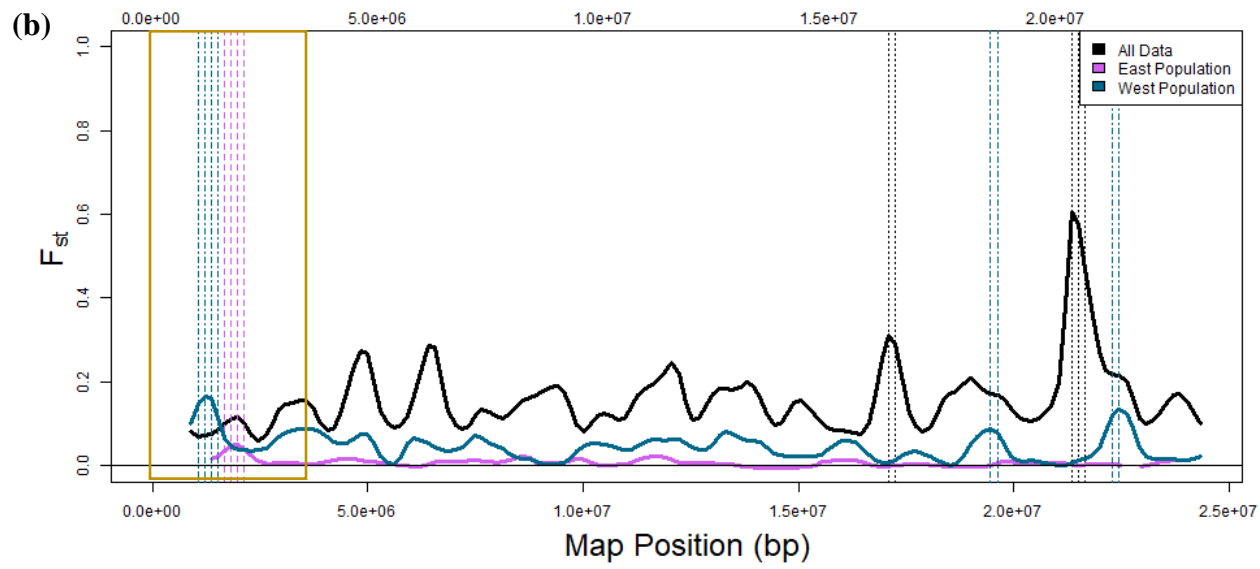
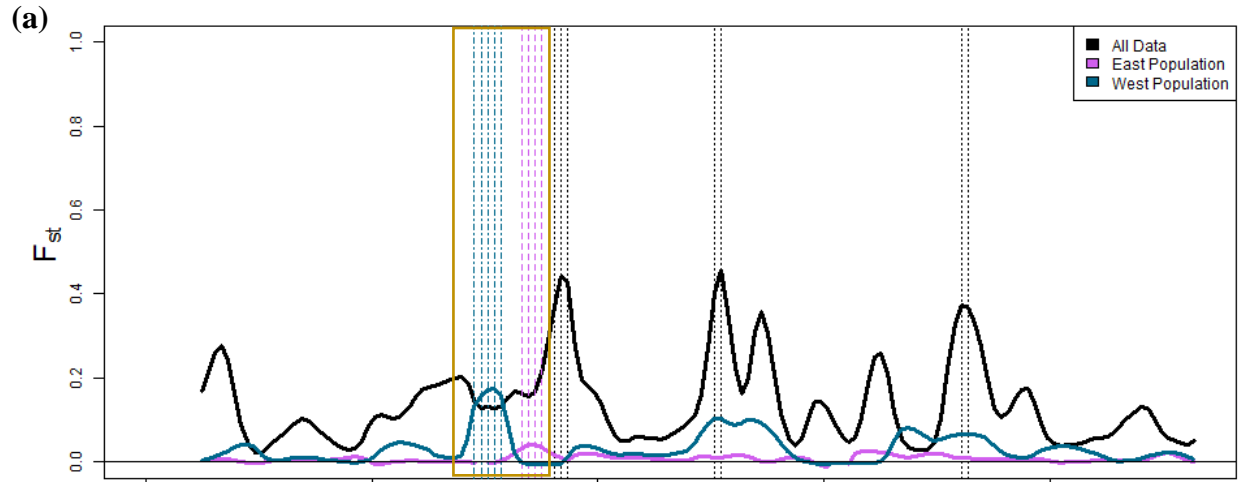


Figure S2.4. Boxplot of the number of markers (RAD loci) per weighted average F_{st} , for weighted averages that did (blue) and did not (red) exceed the 95% confidence interval, in the (a) eastern population, (b) western population, and (c) full data set.



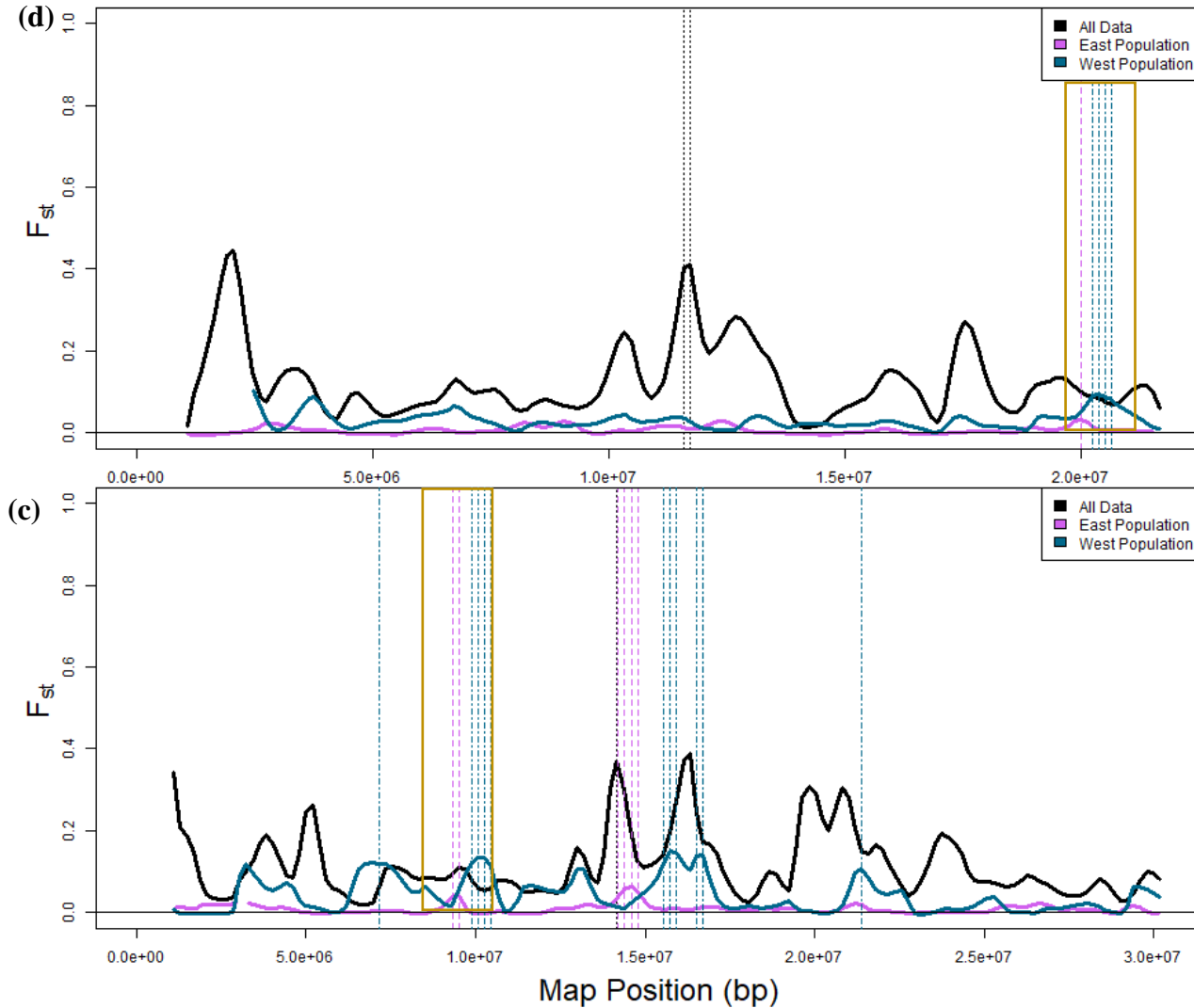


Figure S2.5. Kernel-smoothing weighted average F_{st} along Atlantic cod linkage groups (a) 2, (b) 9, (c) 16, and (d) 22, where genomic regions of elevated divergence in the eastern and western populations are in close proximity to one another (marked by yellow box). Dashed lines mark the positions of weighted averages which exceeded the 95% confidence interval, indicative of outlier regions.

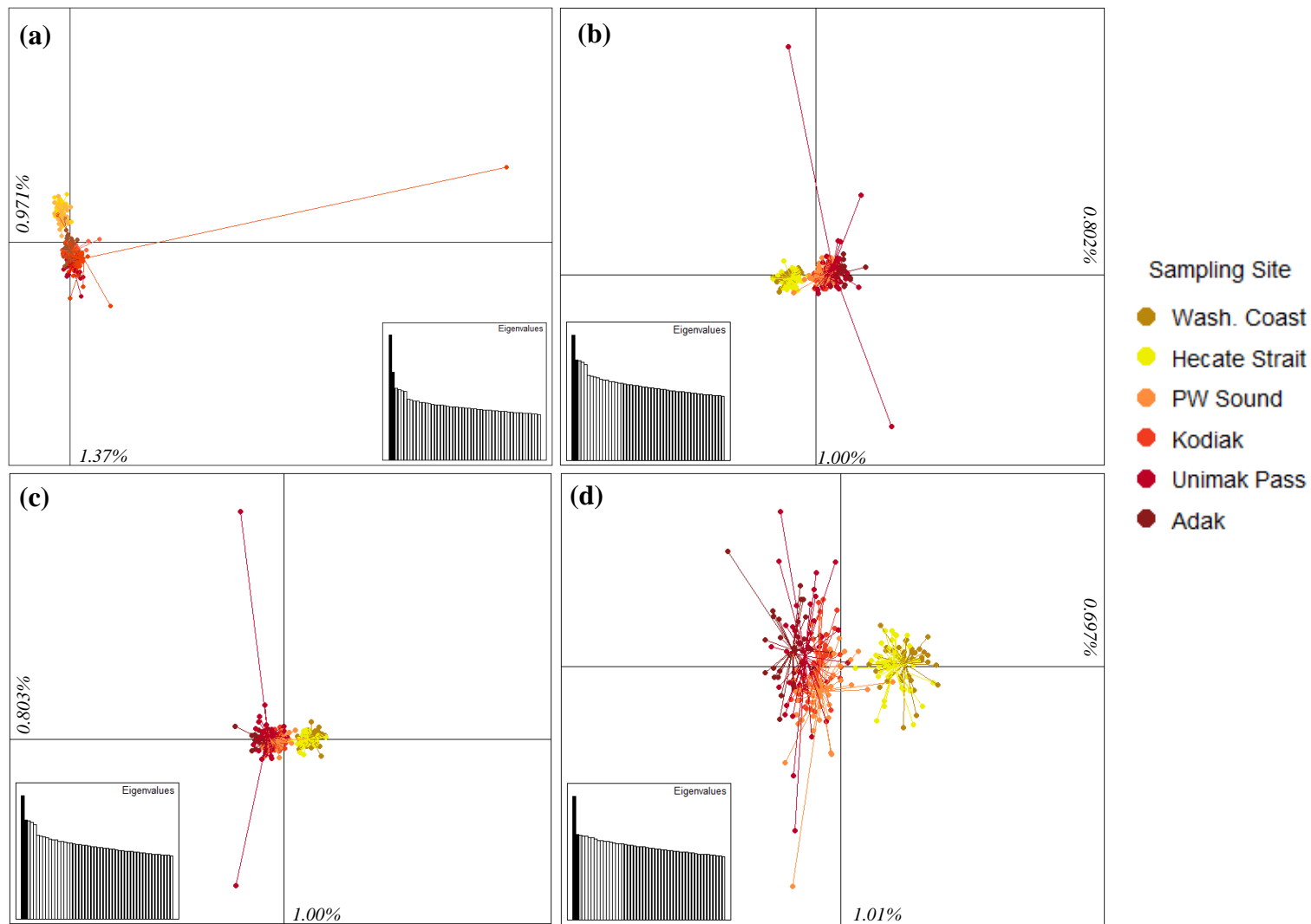


Figure S2.6. Principal component analyses on neutral loci for the eastern population, with (a) all Unimak Pass individuals, and after removing (b) one Unimak Pass individual, (c) three Unimak Pass individuals, and (d) five Unimak Pass individuals (matching **Figure 2.12c**). Inset displays eigenvalues for up to fifty principal components; percent of variation explained by each principal component is labeled on the appropriate axis.

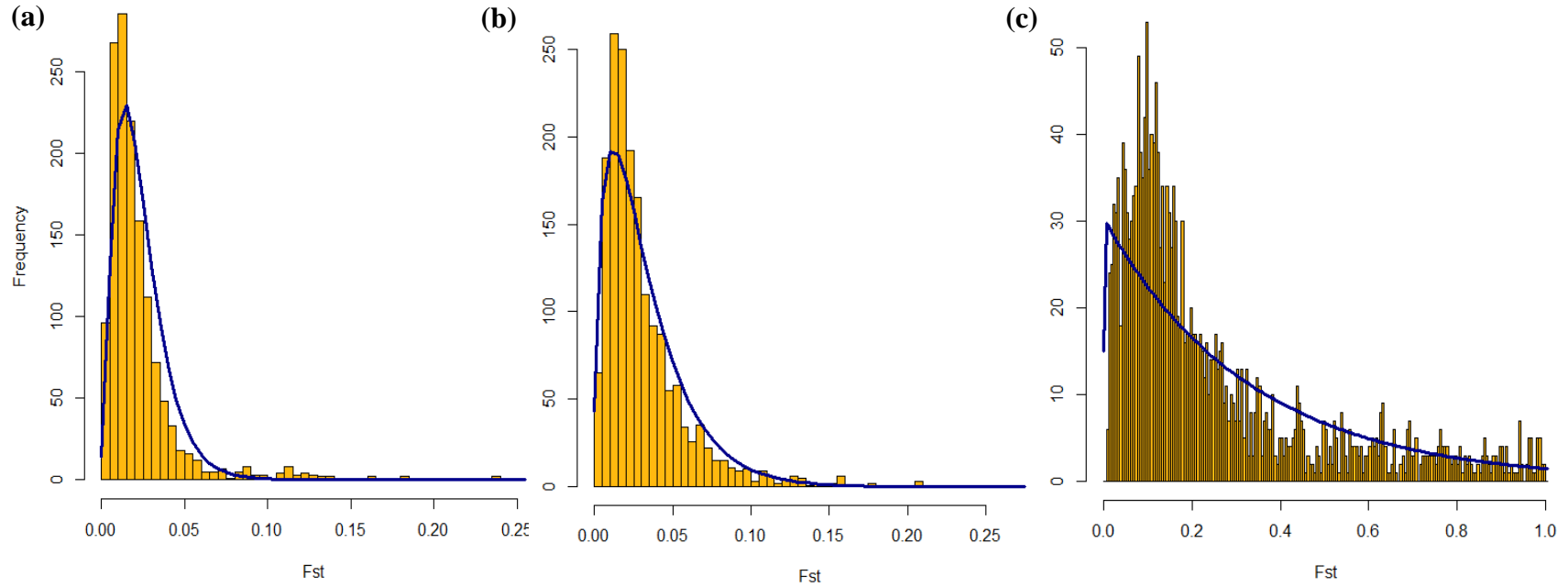
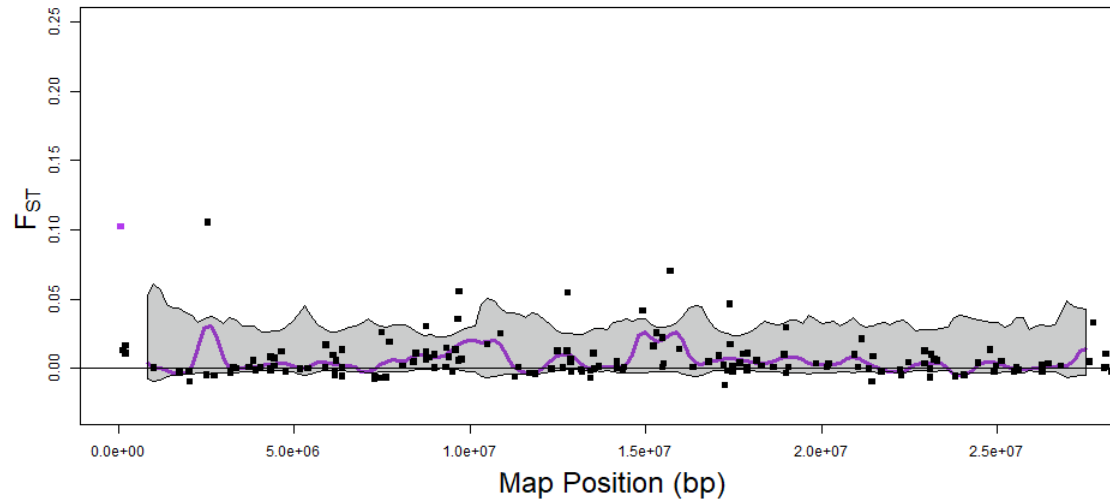


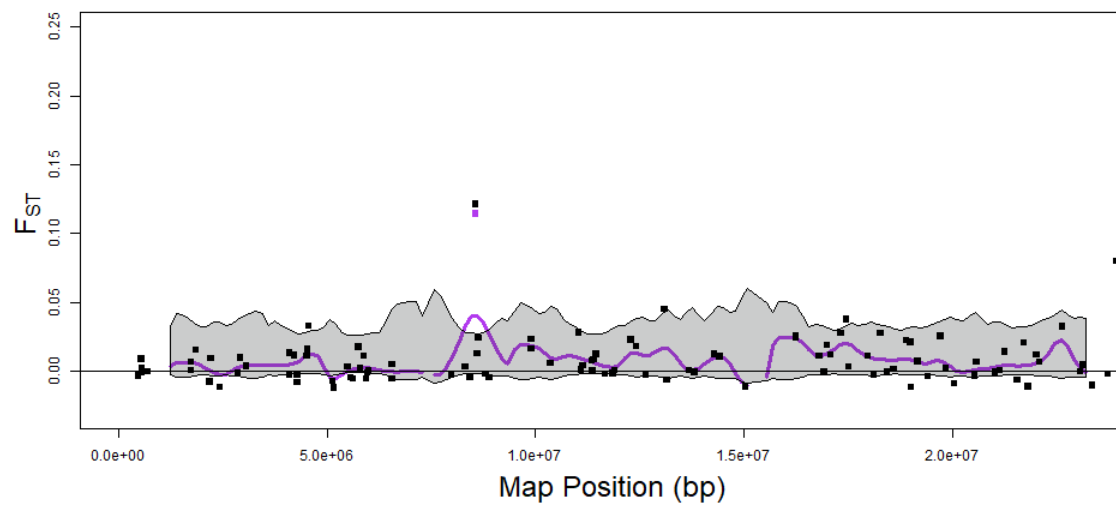
Figure S2.7. OutFLANK's empirical distribution of per locus F_{st} without sample size correction, with line indicating smoothed distribution of null model, for the **(a)** eastern population, **(b)** western population, and **(c)** full data set.

Figure S2.8. Kernel-smoothing average F_{st} in the eastern population, overlaid with per-locus F_{st} (points). Points colored purple indicate an outlier locus. Gray shading indicates the limits of the 95% confidence interval. Each linkage group (1 – 23) was plotted independently. Breaks in the kernel-smoothing average are the result of data removed during filtering for low marker density.

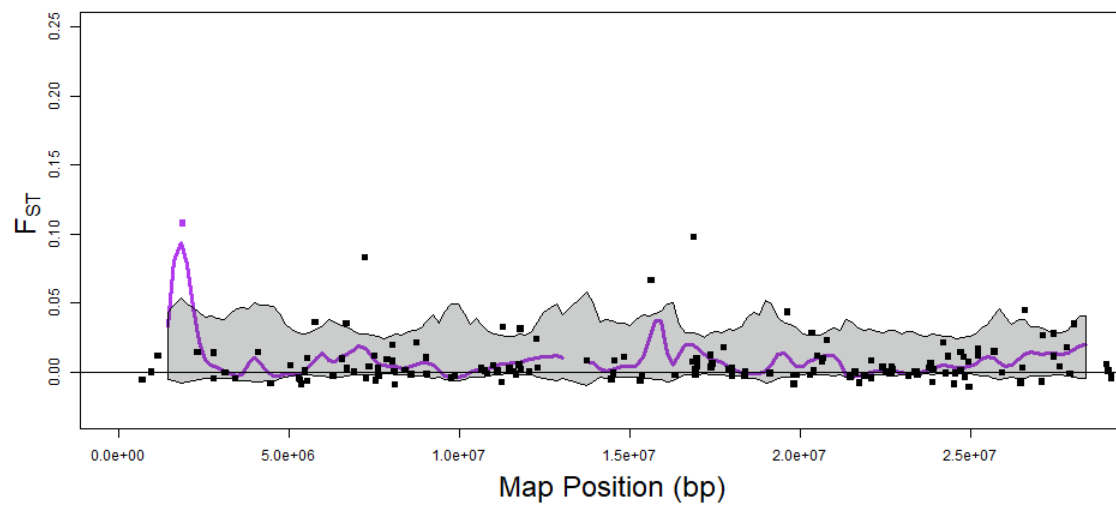
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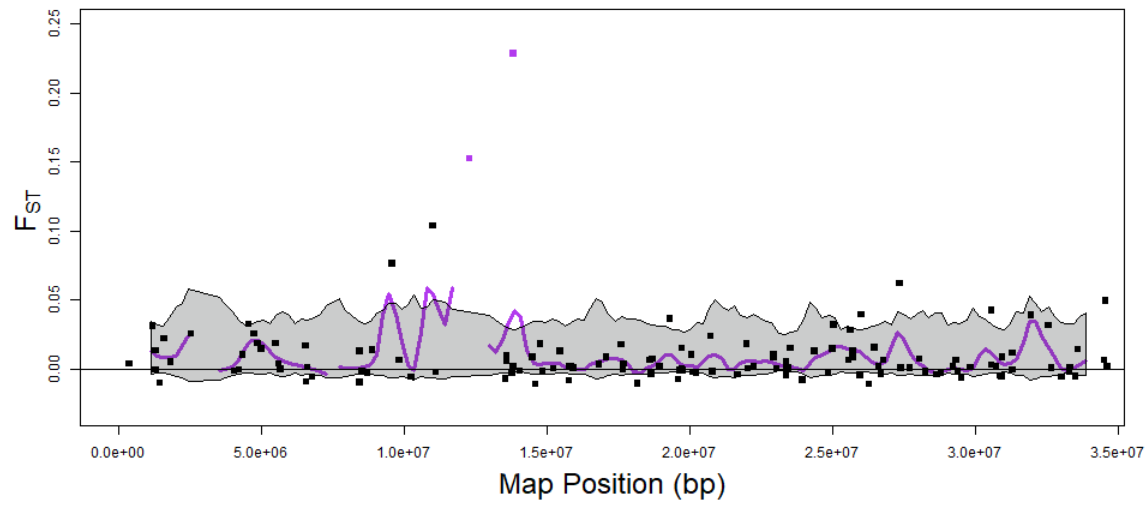
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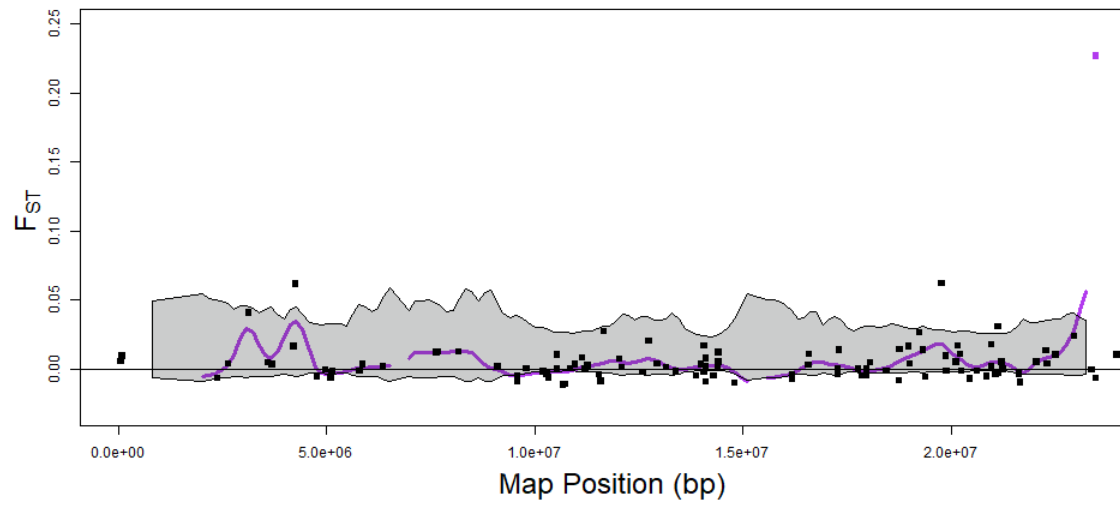
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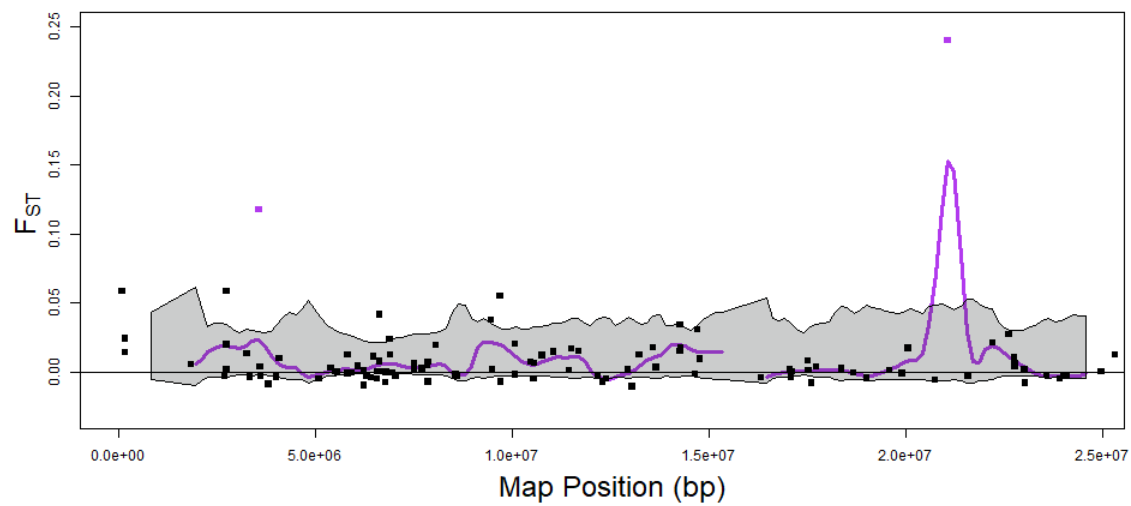
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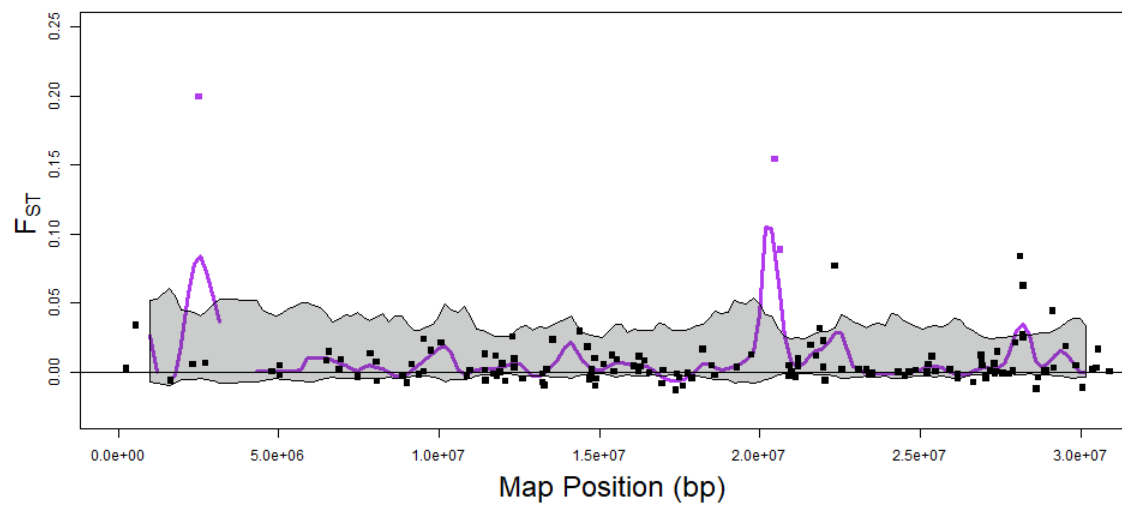
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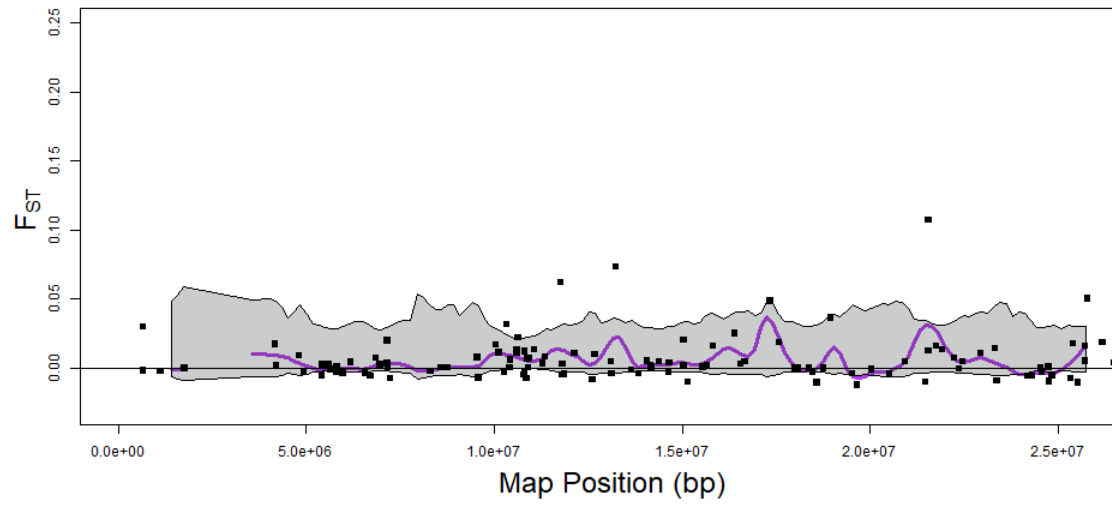
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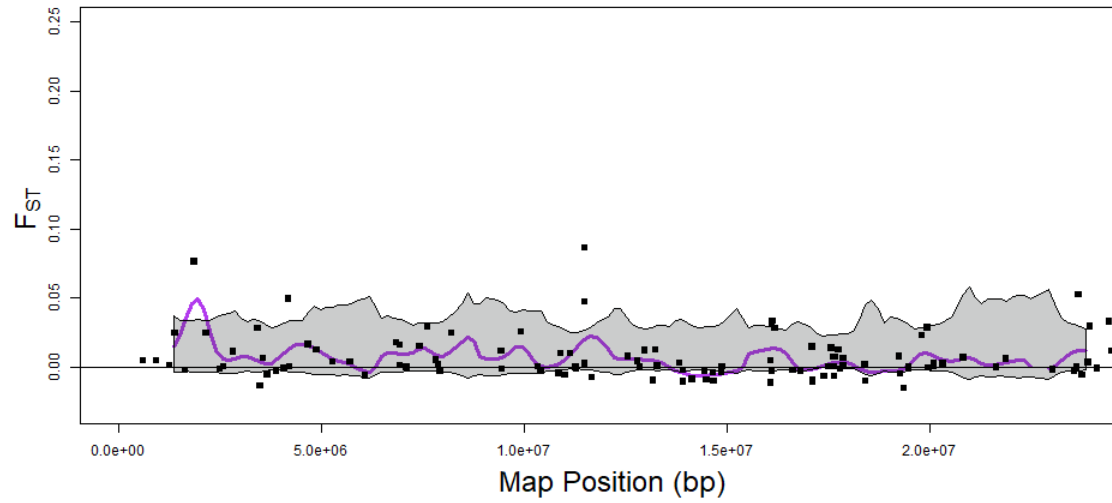
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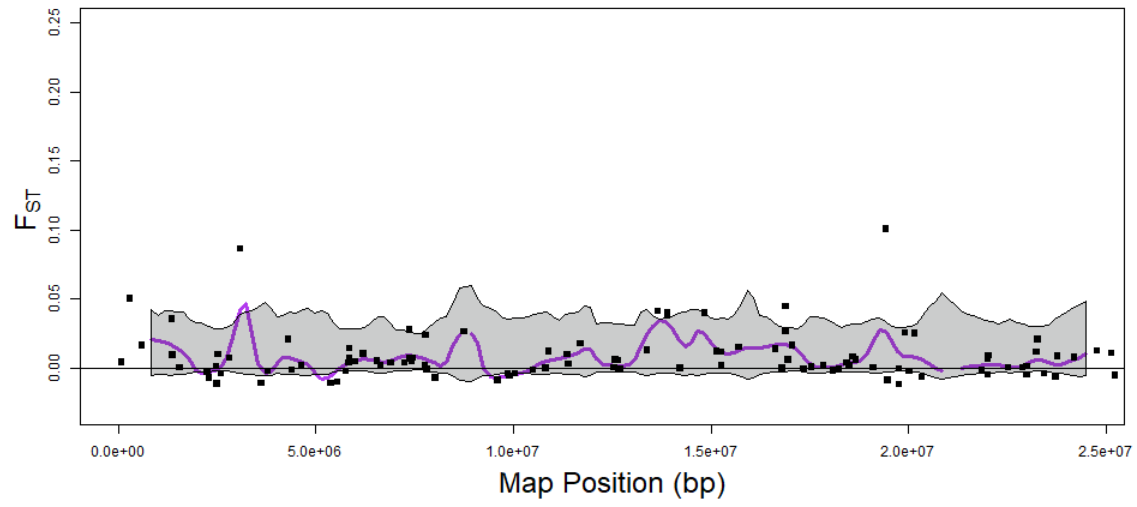
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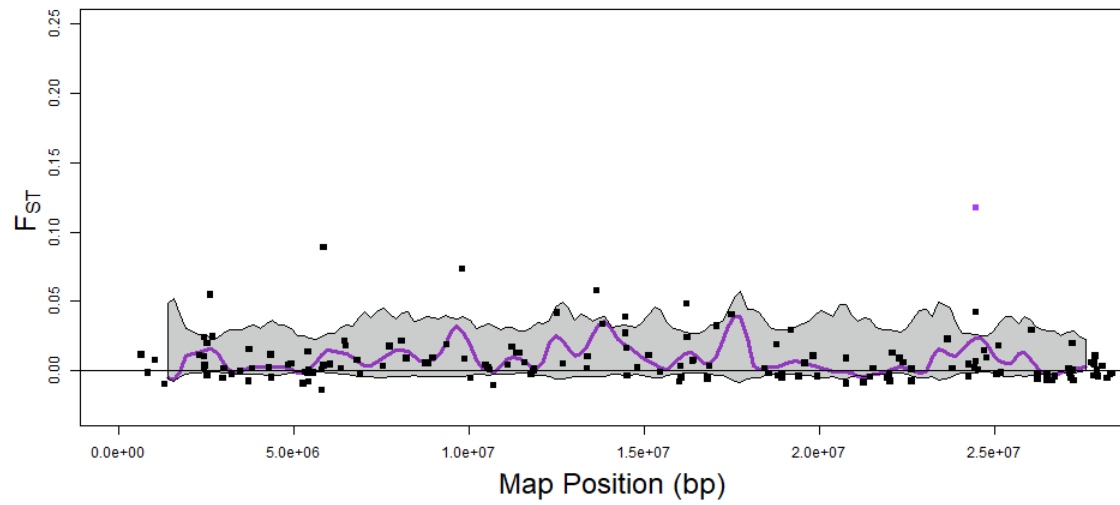
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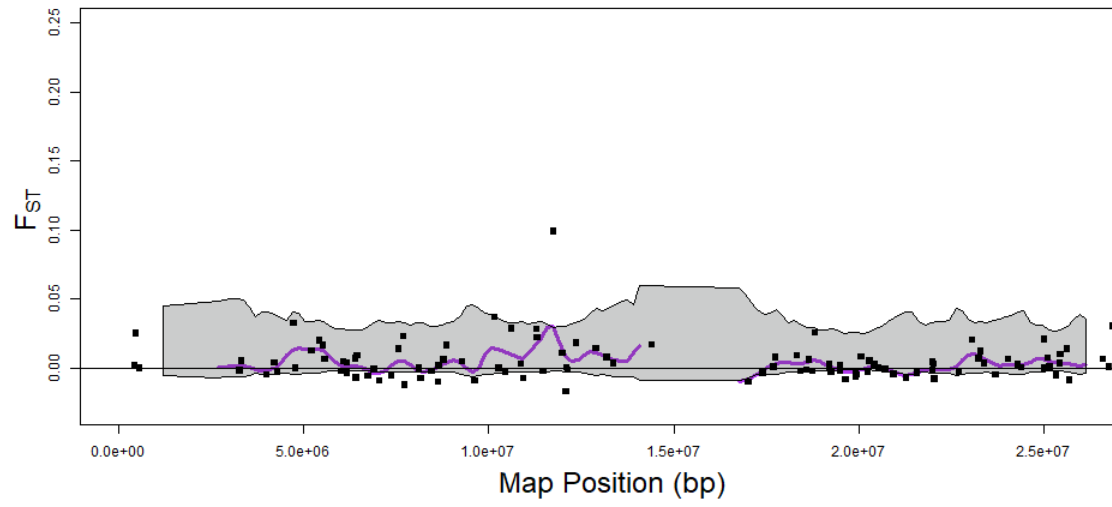
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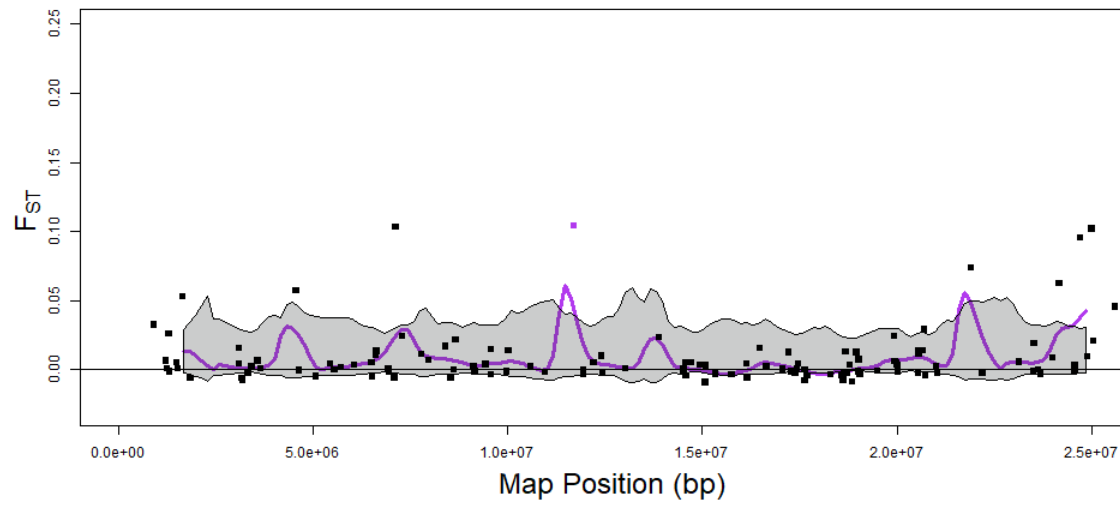
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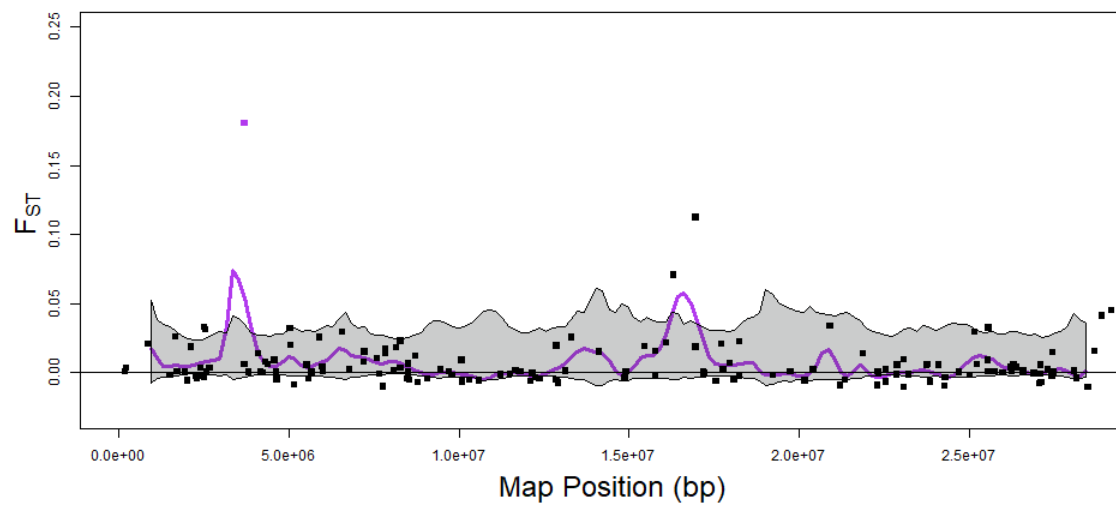
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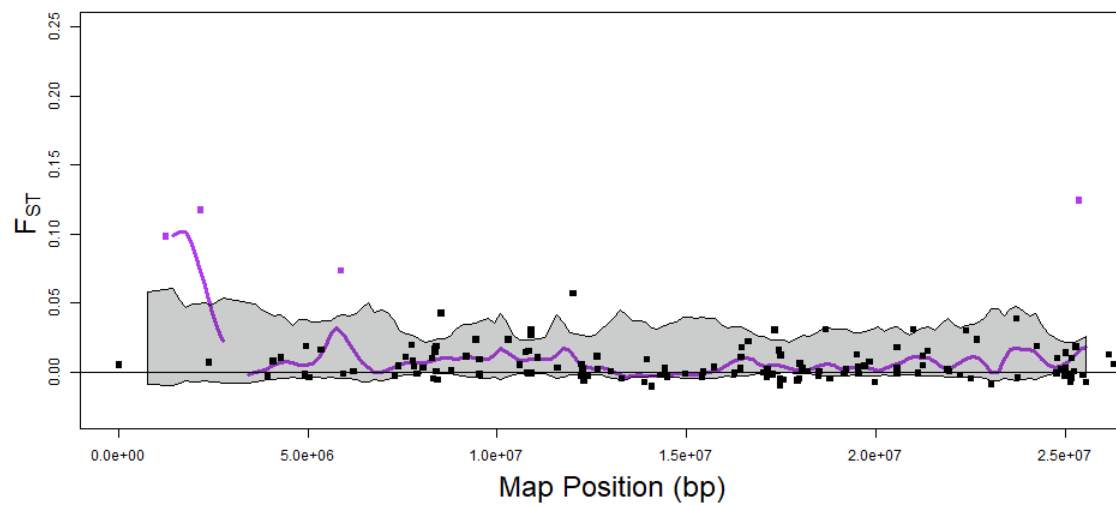
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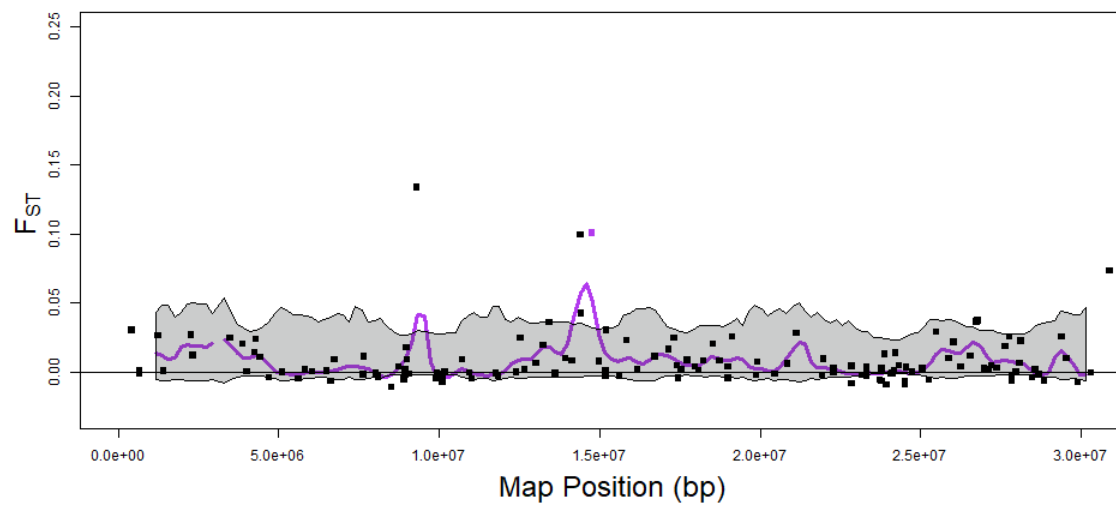
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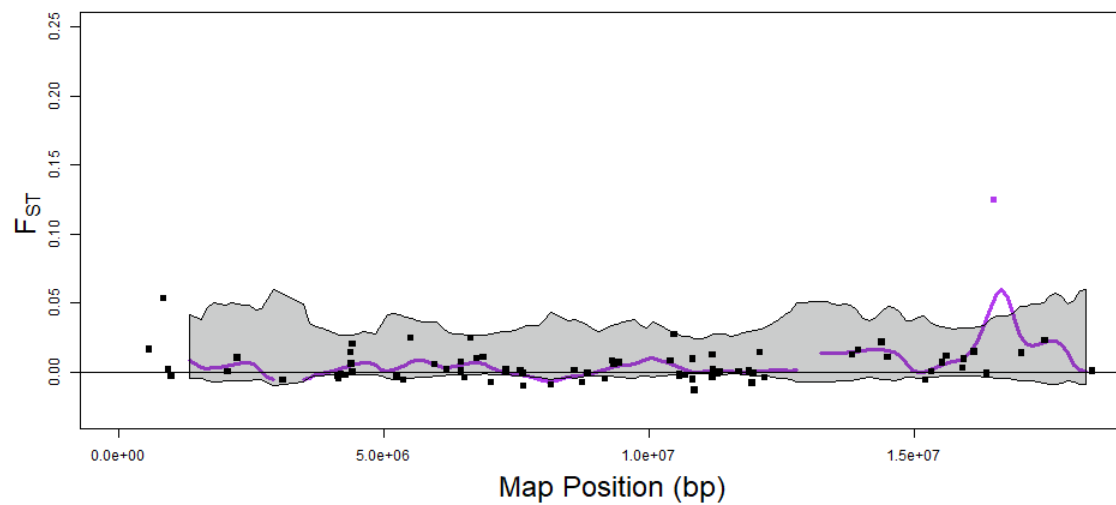
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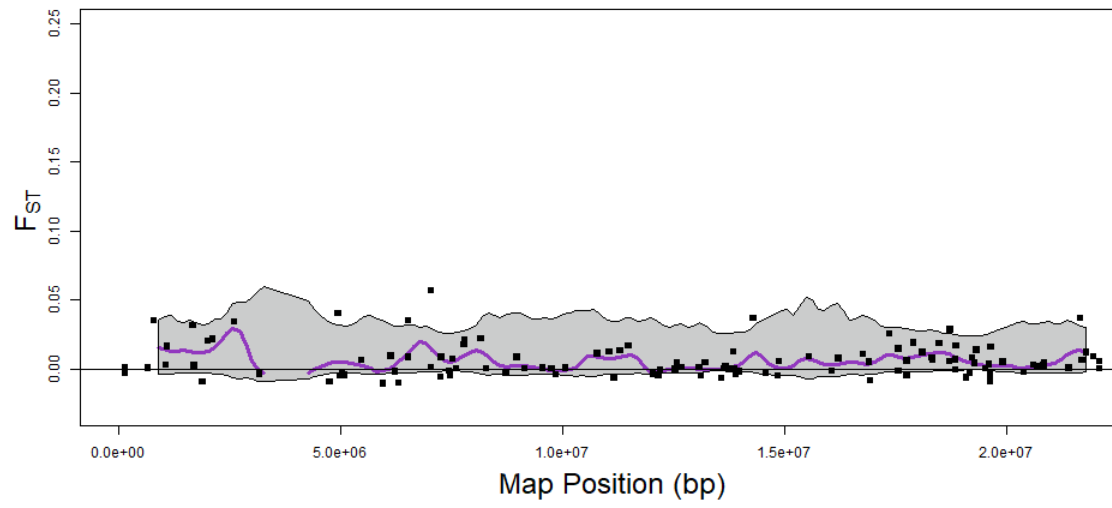
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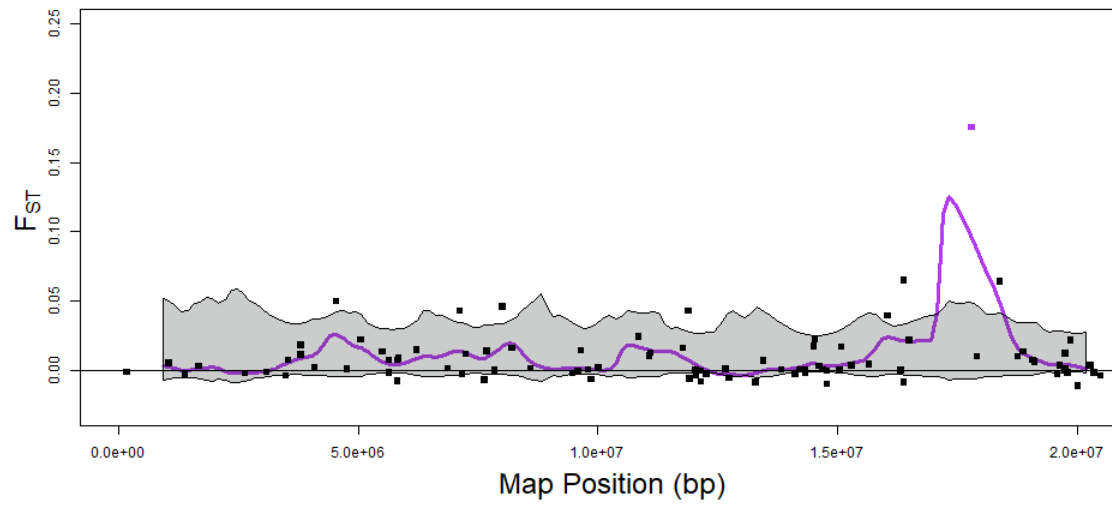
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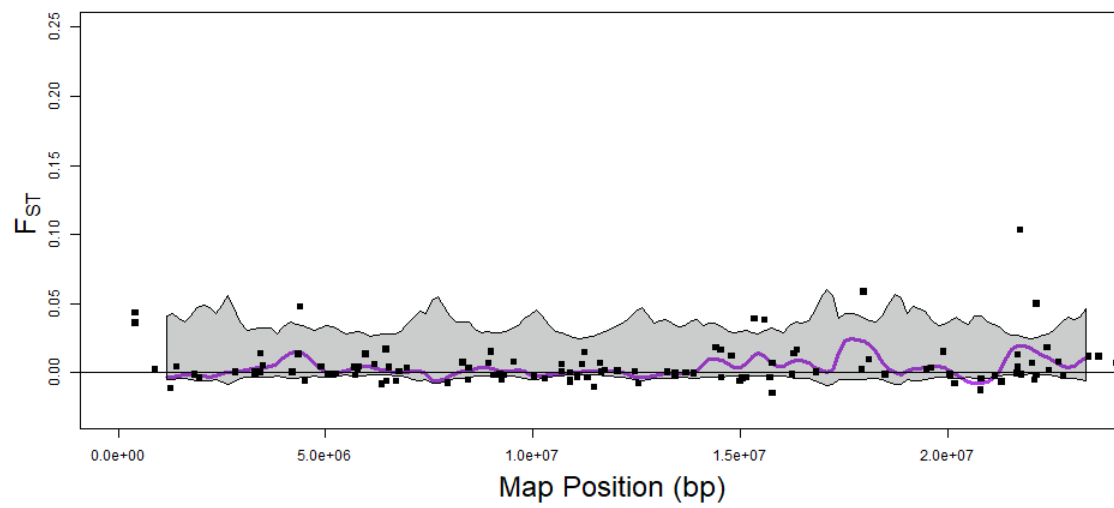
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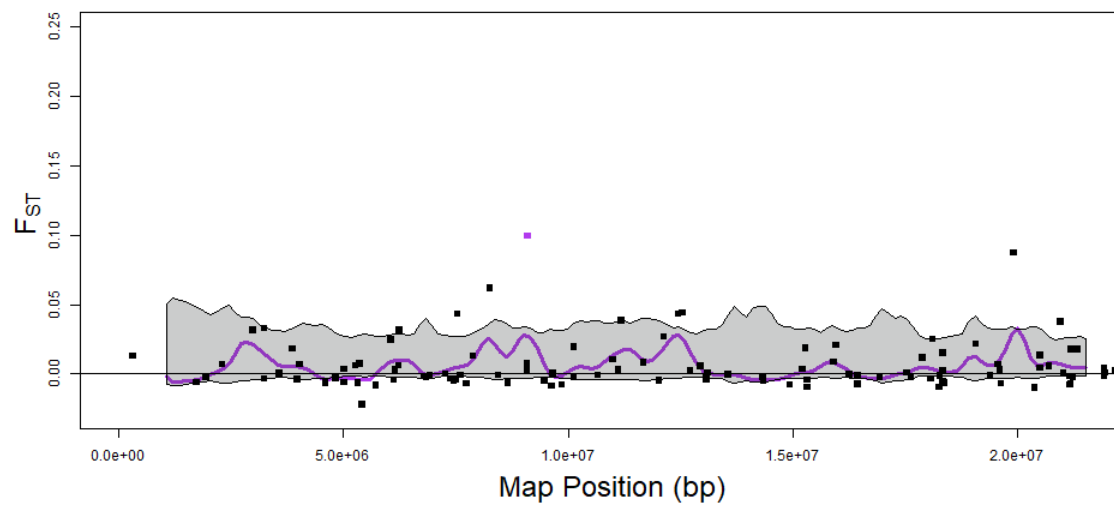
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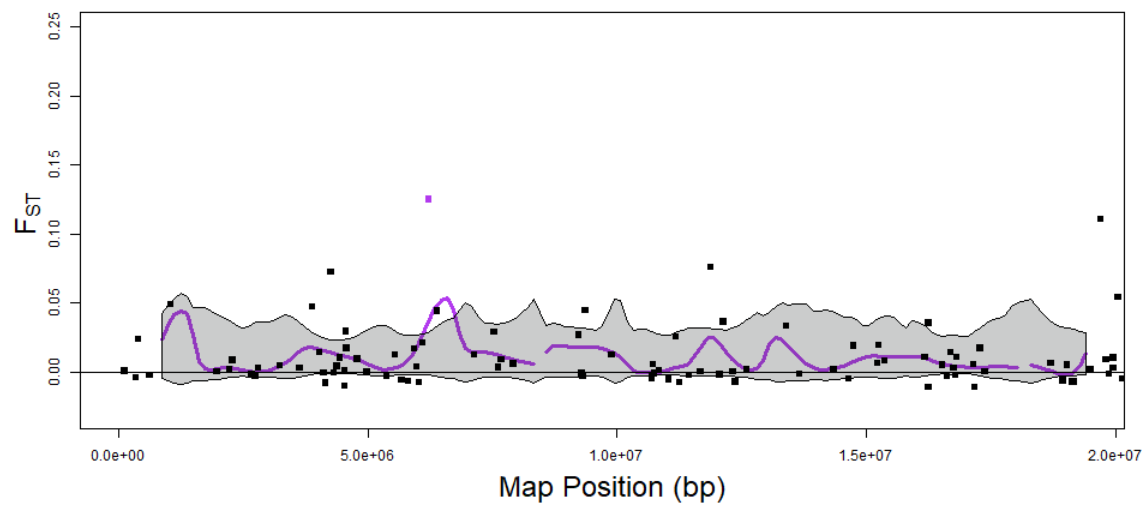
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LG21



LG22



LG23

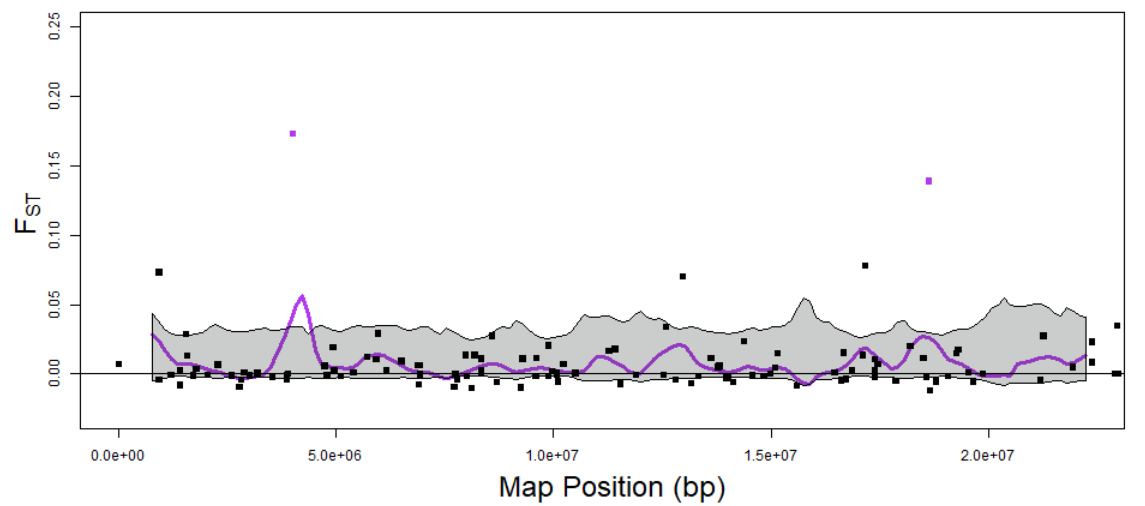
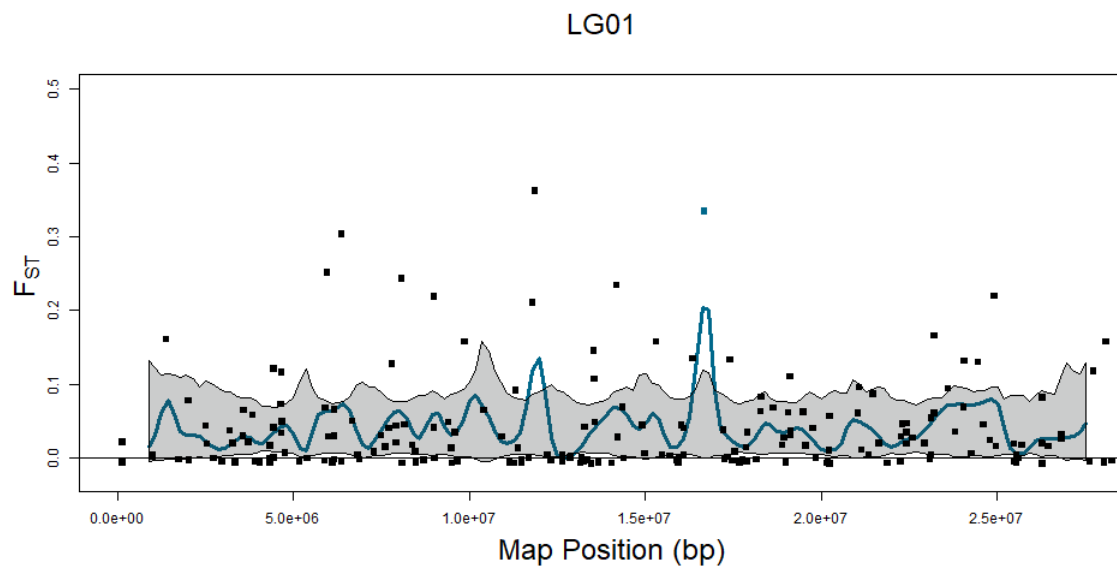
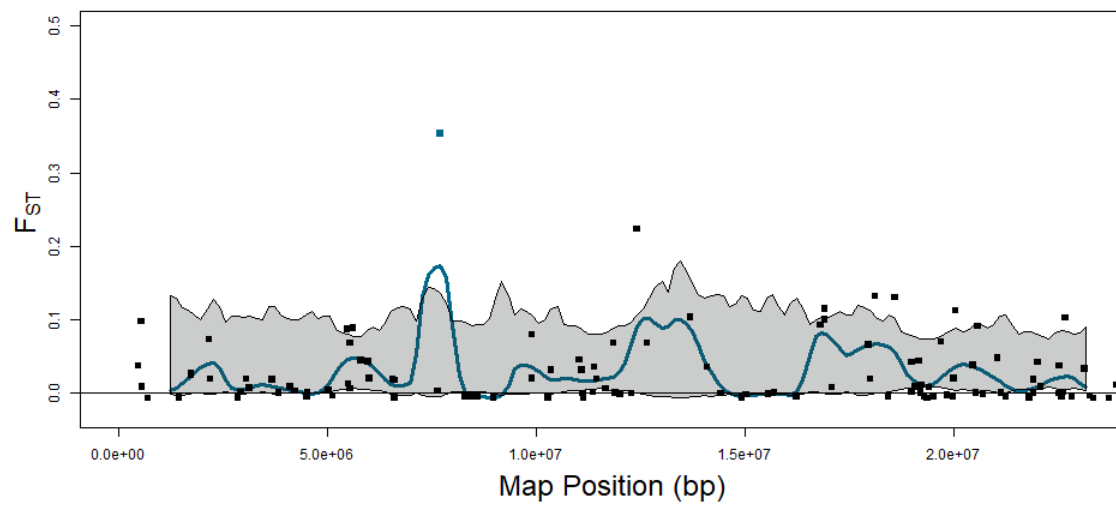


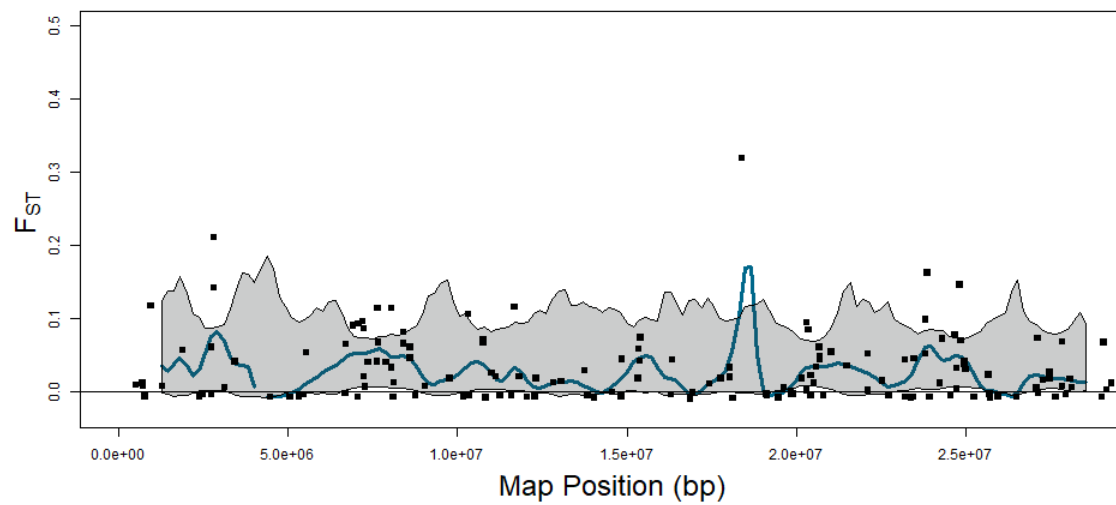
Figure S2.9. Kernel-smoothing average F_{st} in the western population, overlaid with per-locus F_{st} (black points). Points colored blue indicate an outlier locus. Gray shading indicates the limits of the 95% confidence interval. Each linkage group (1 – 23) was plotted on its own graph. Breaks in the kernel-smoothing average are the result of data removed during filtering for low marker density.



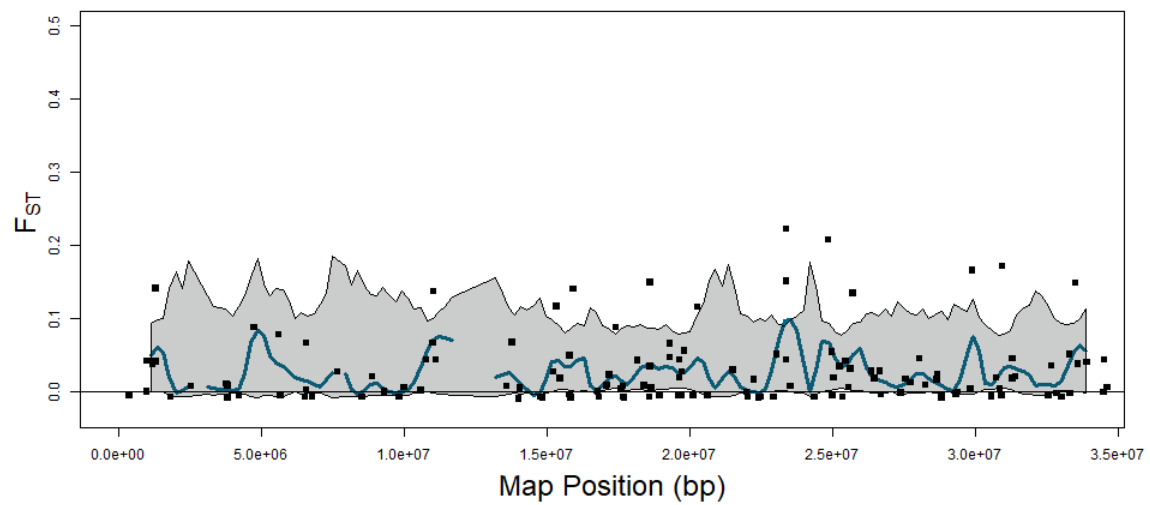
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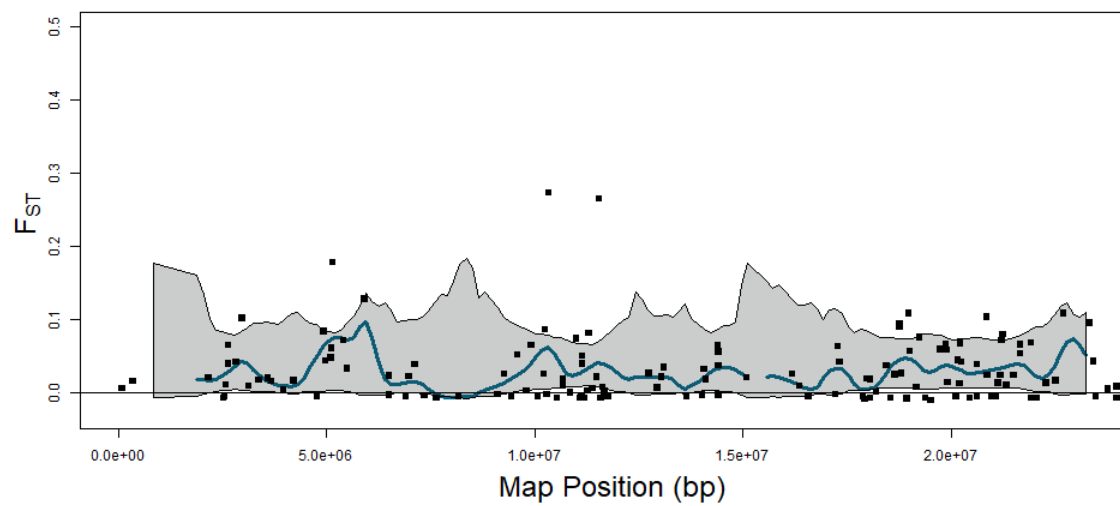
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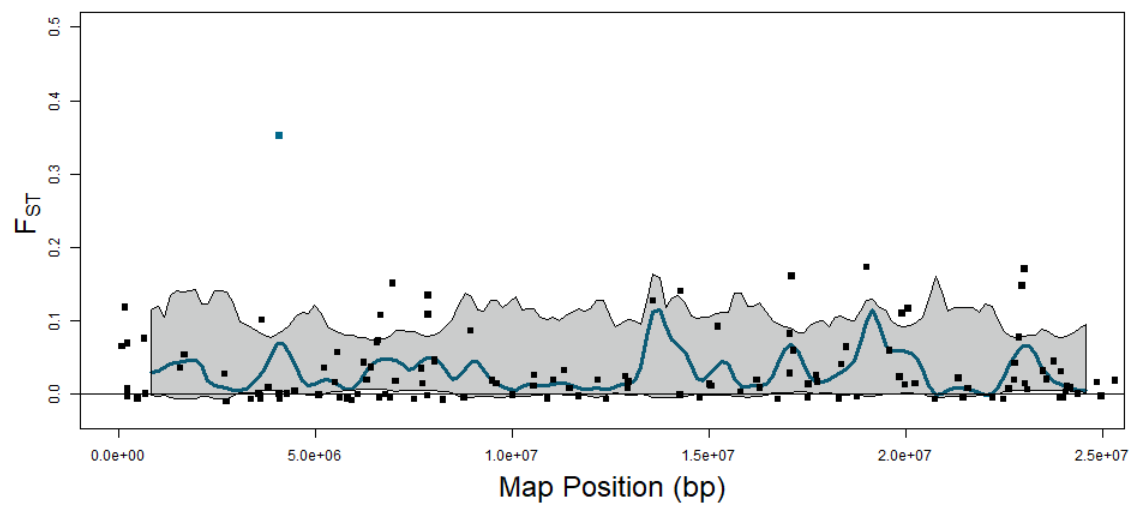
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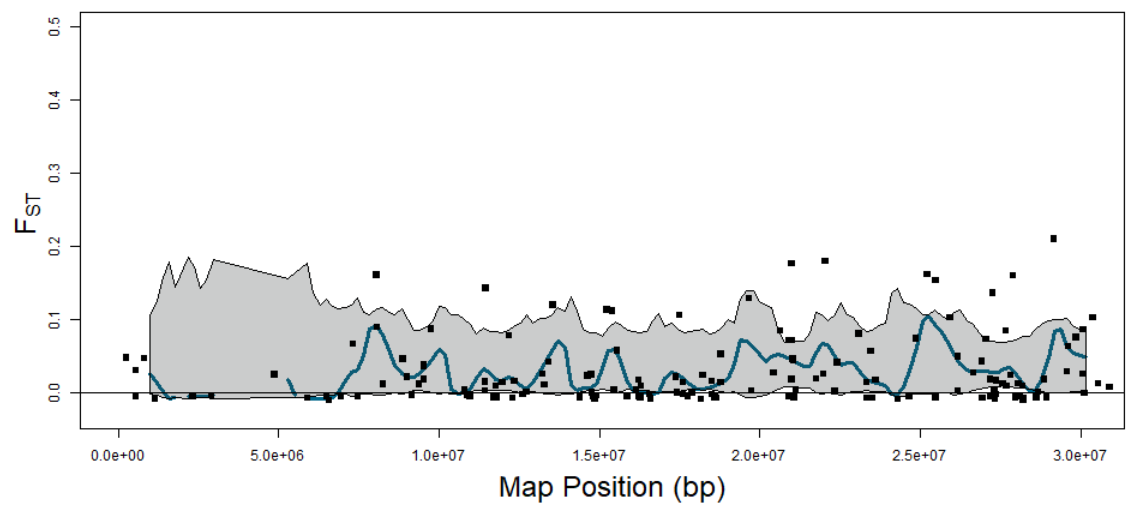
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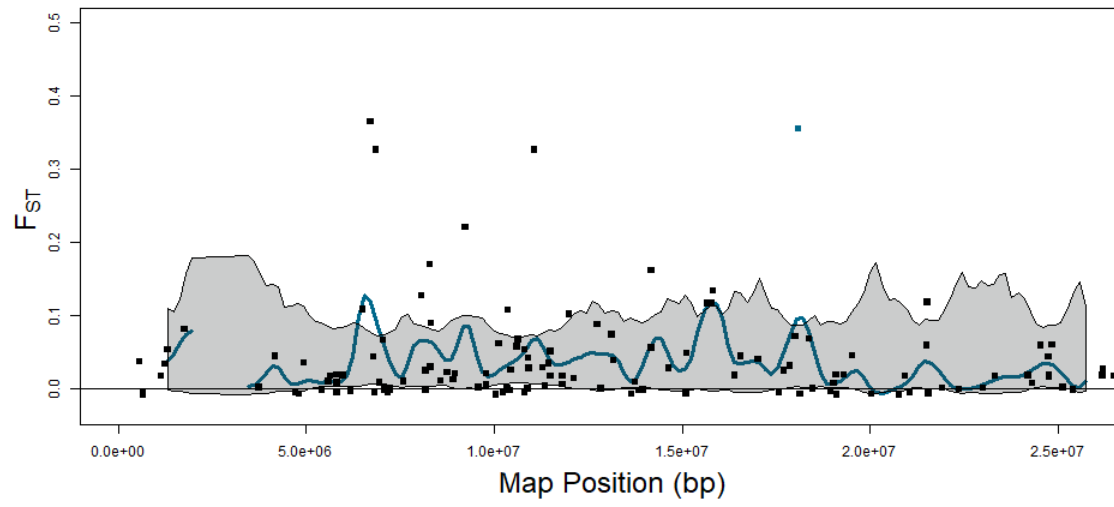
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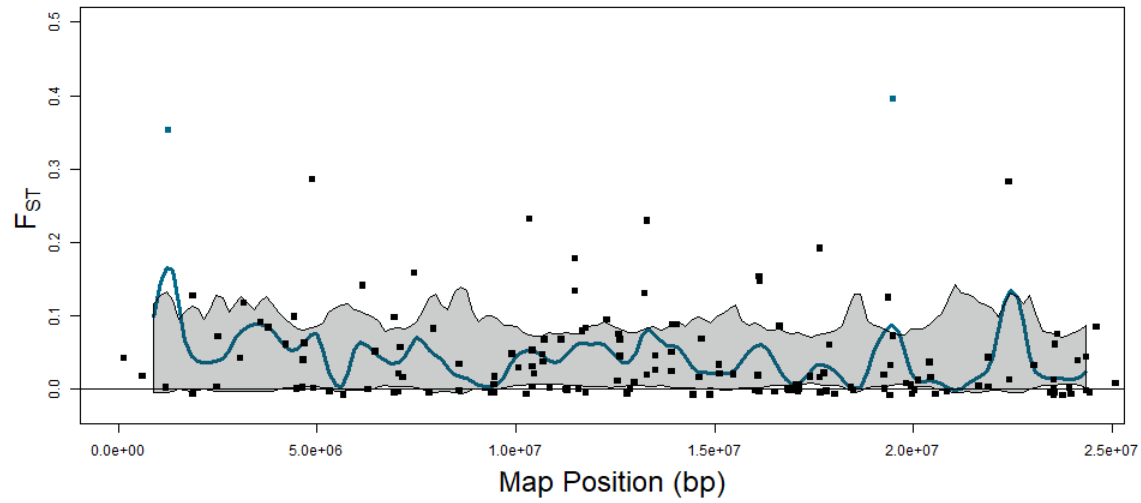
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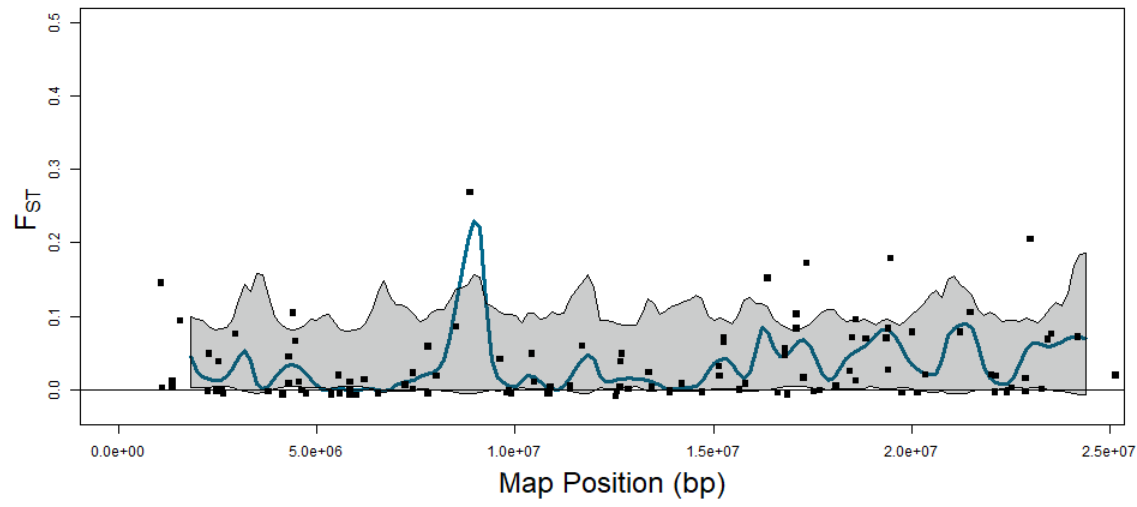
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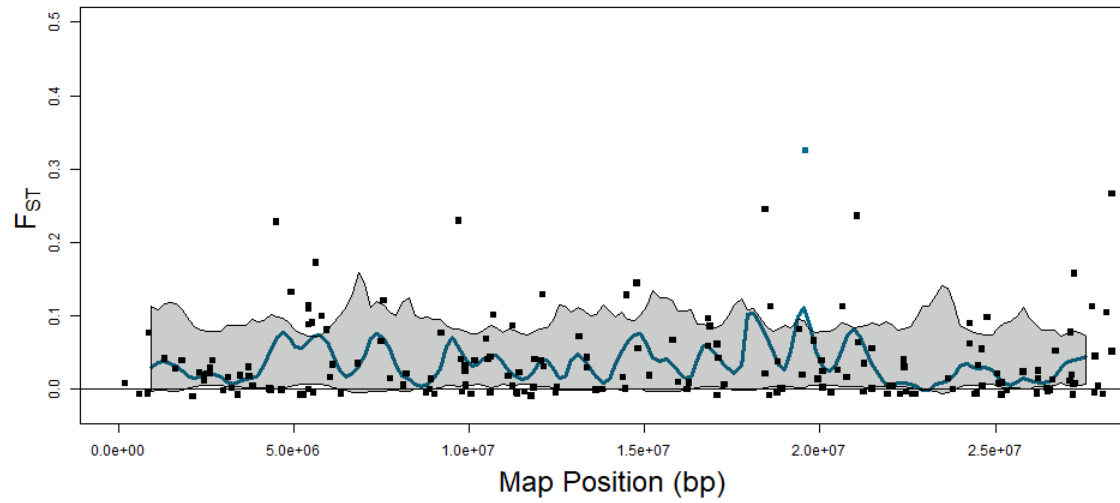
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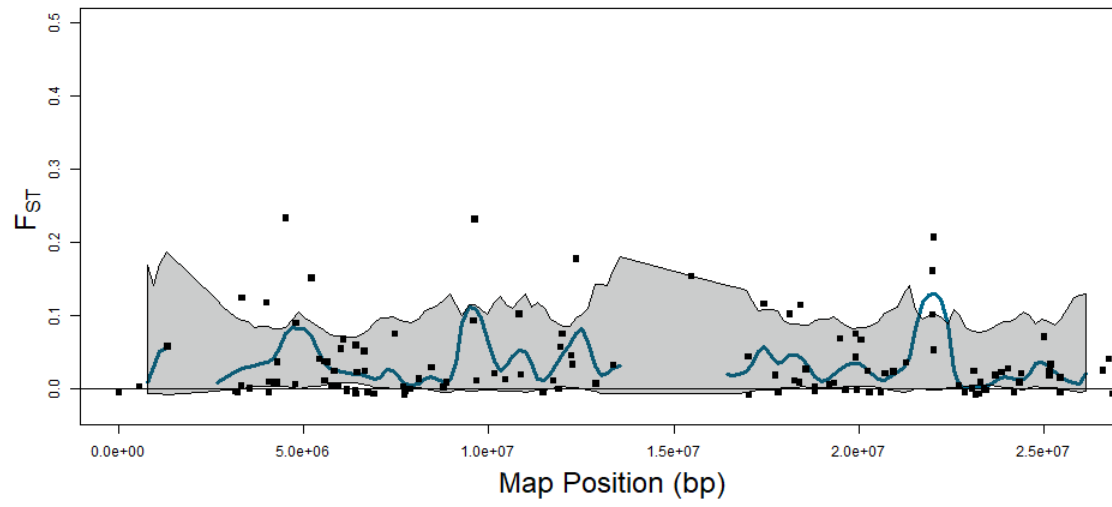
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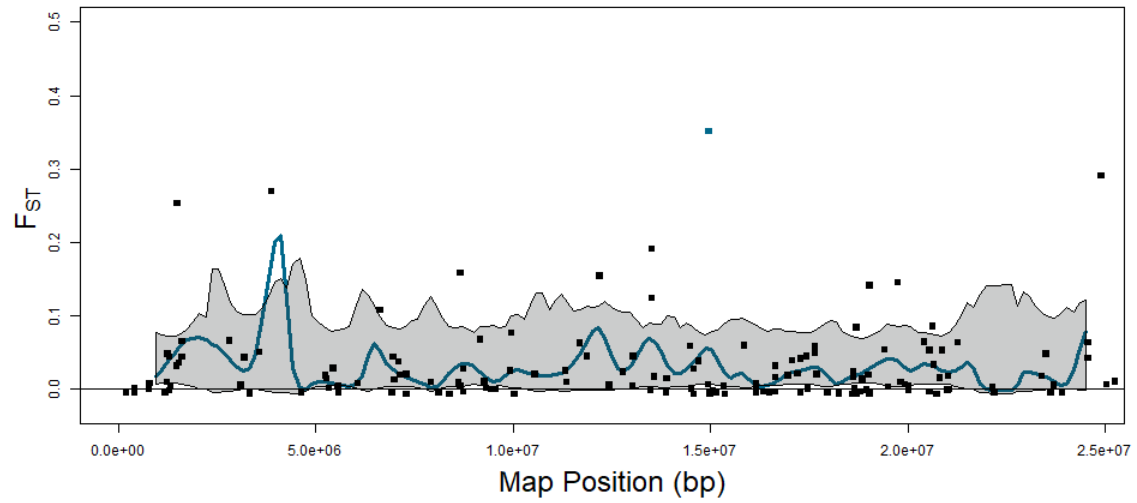
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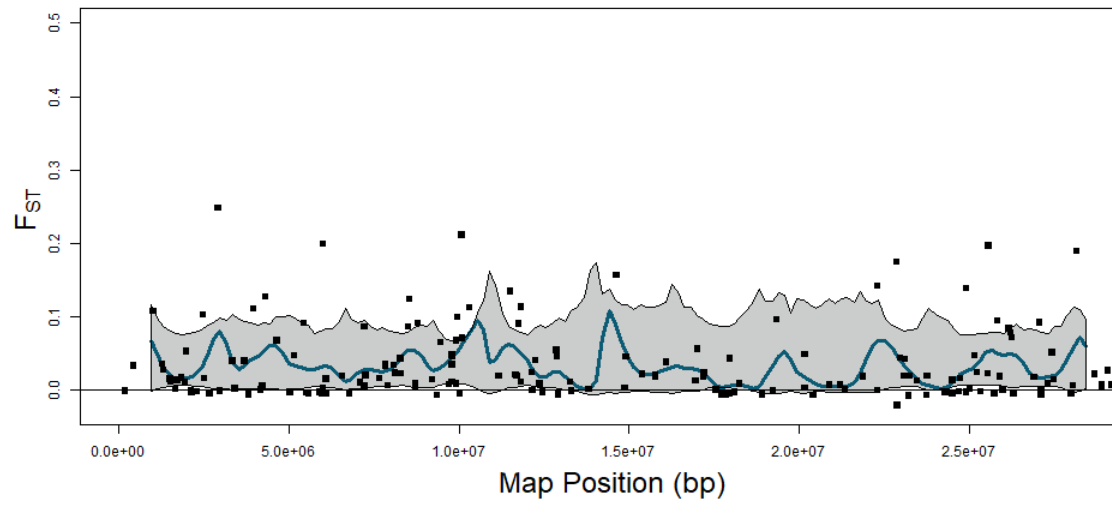
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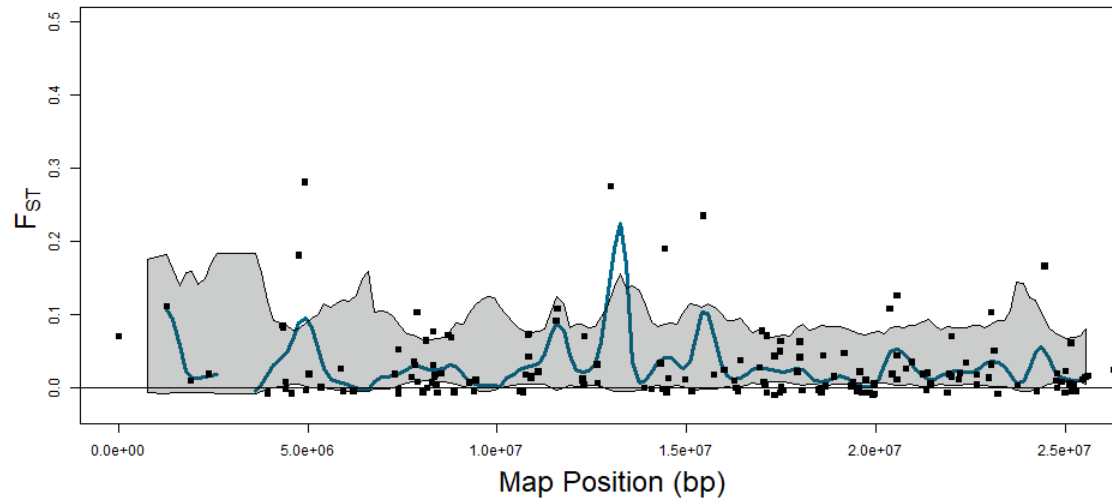
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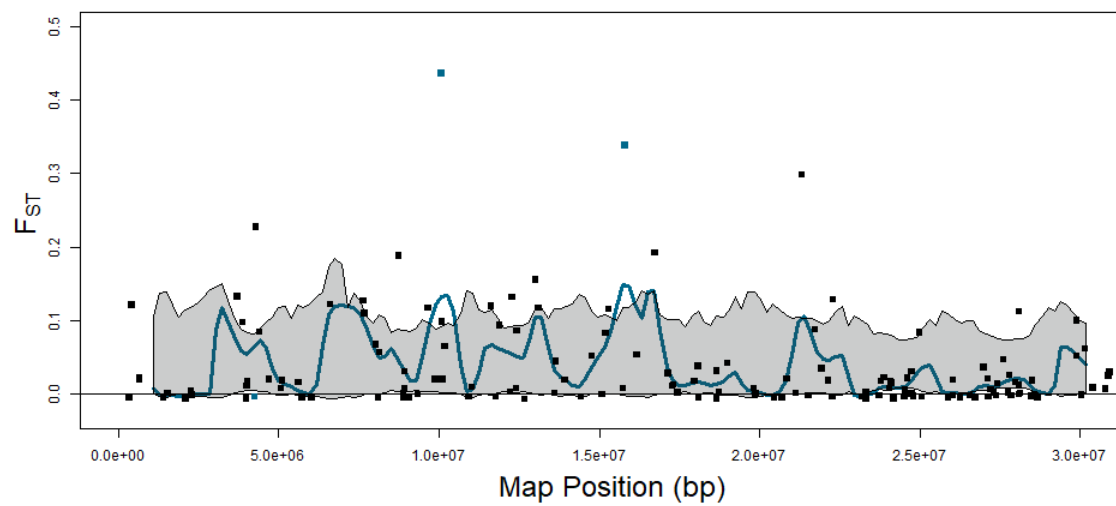
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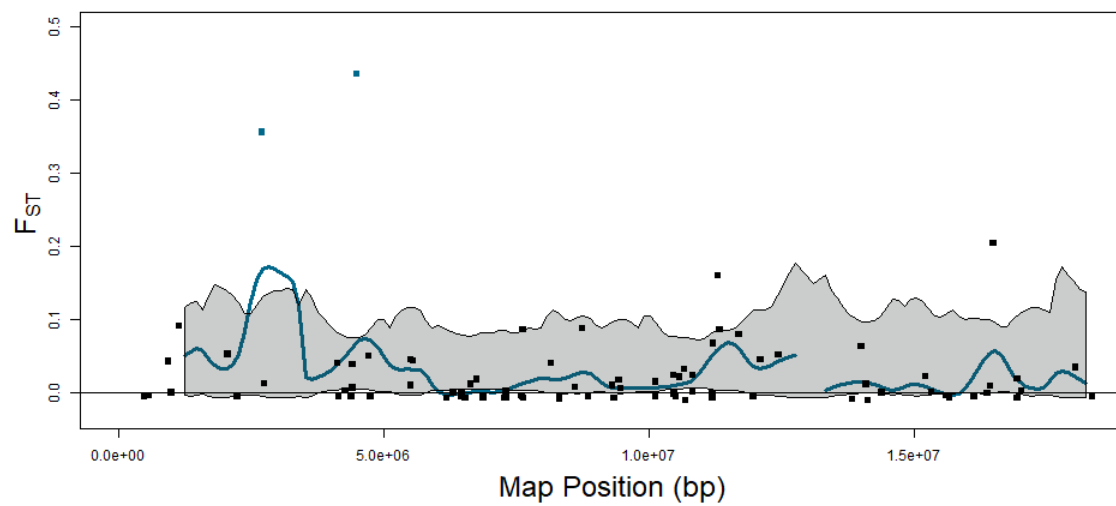
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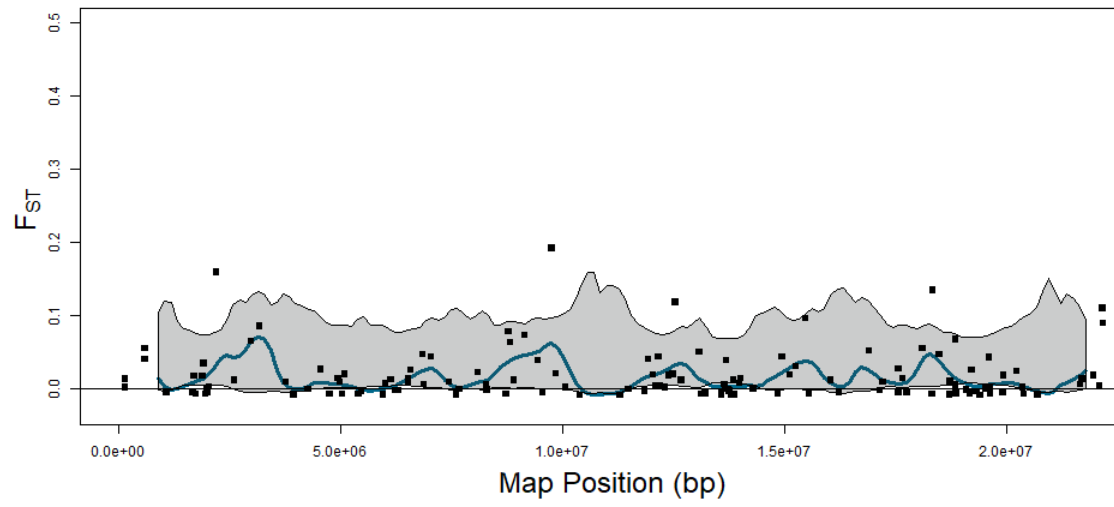
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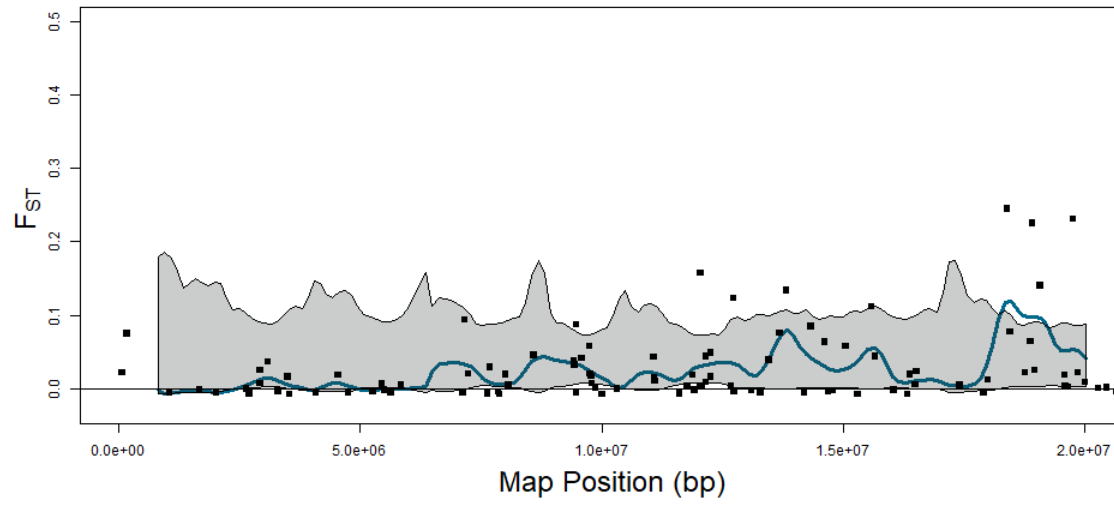
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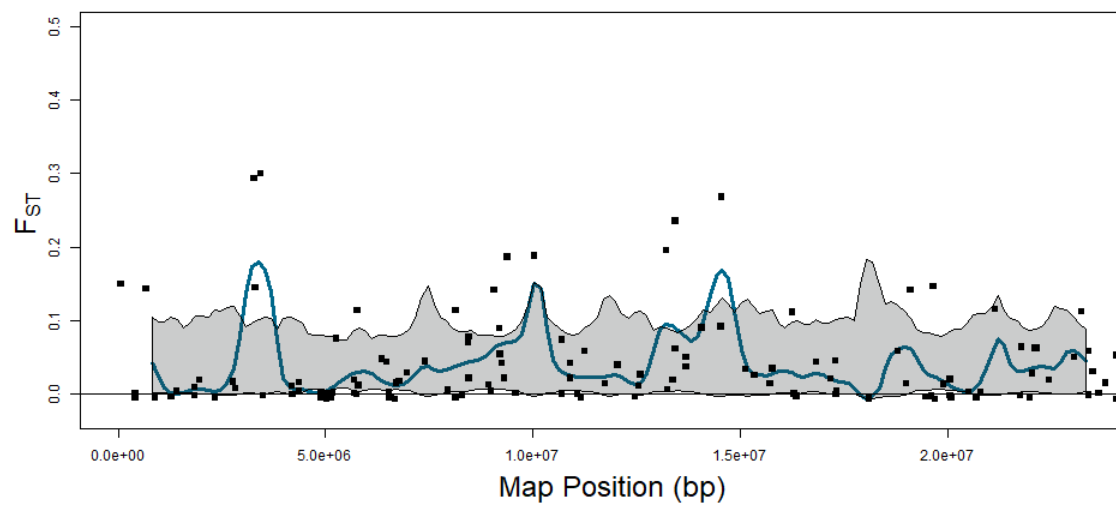
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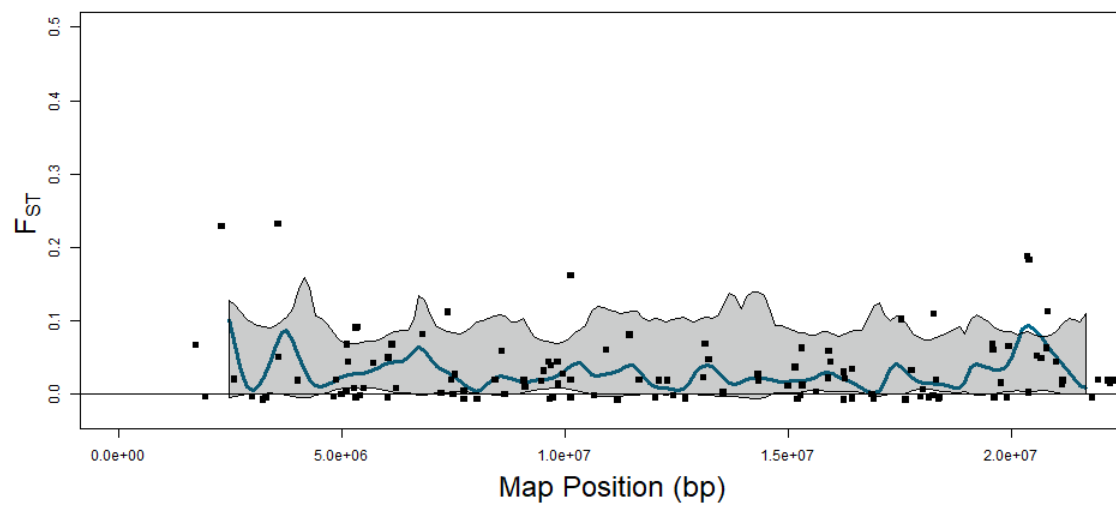
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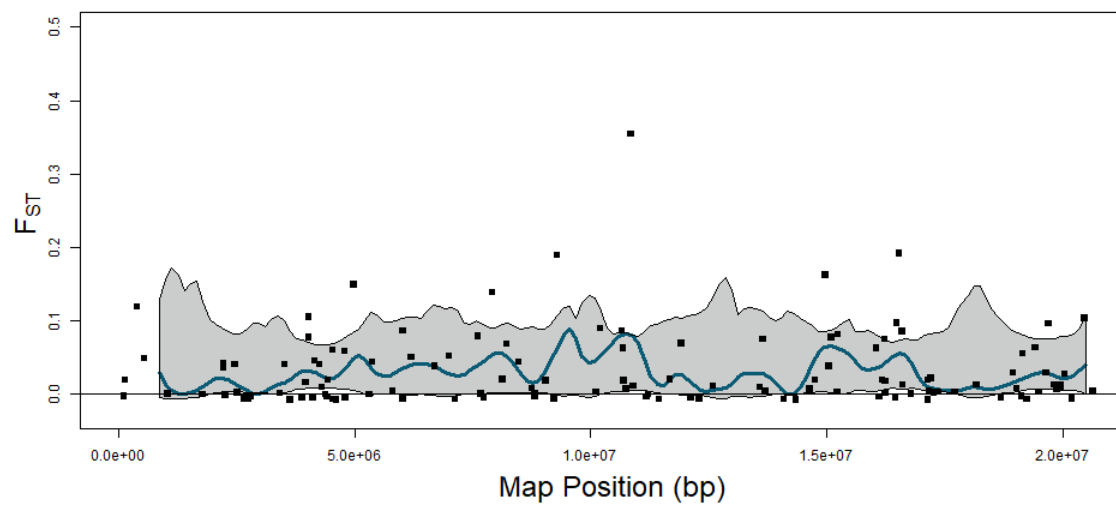
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LG21



LG22



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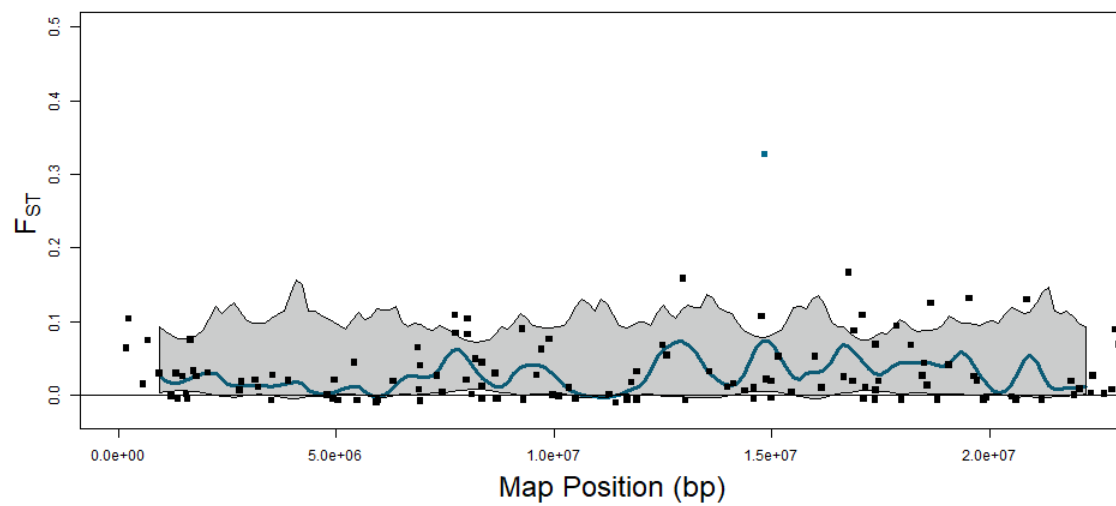
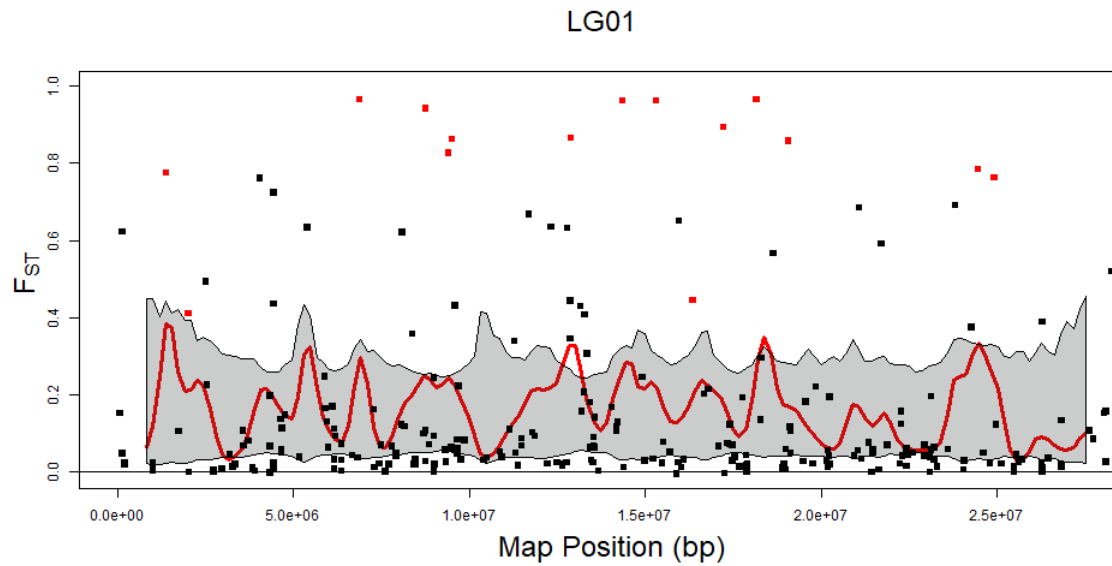
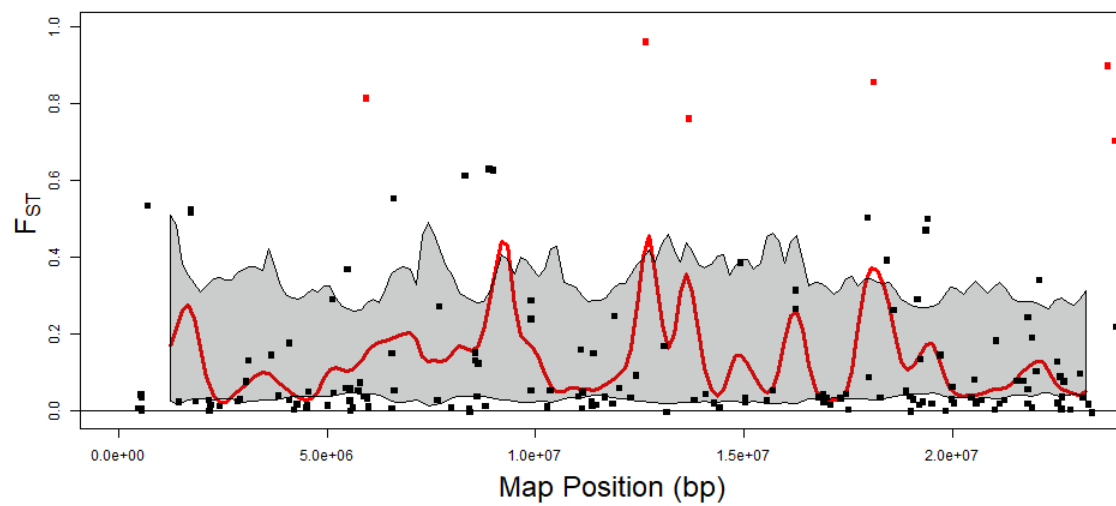


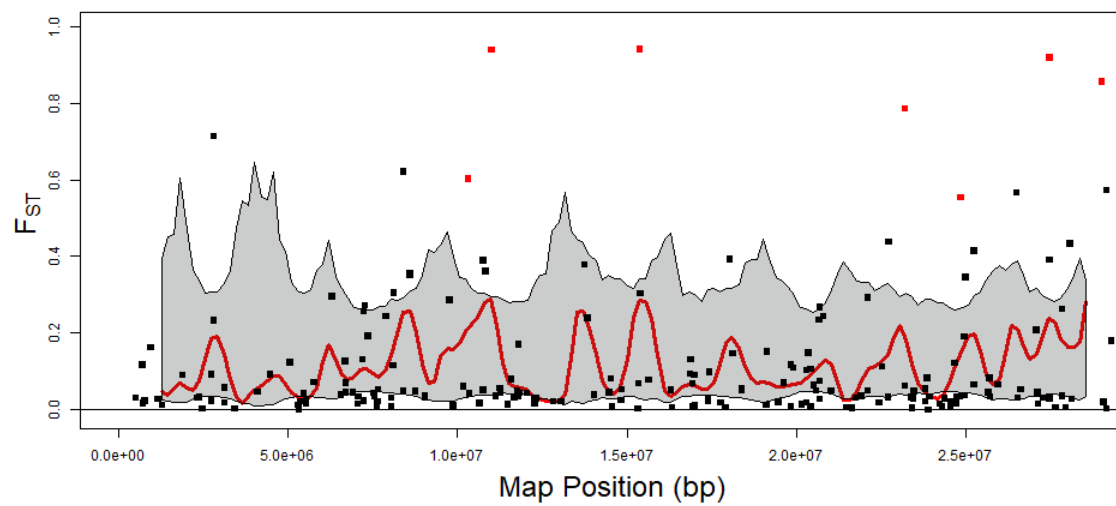
Figure S2.10. Kernel-smoothing average averages F_{st} across the full data set, overlaid with per-locus F_{st} (points). Points colored red indicate an outlier locus identified by both Bayescan and PCAdapt methods. Gray shading indicates the limits of the 95% confidence interval. Each linkage group (1-23) was plotted on its own graph. Breaks in the kernel-smoothing average are the result of data removed during filtering for low marker density.



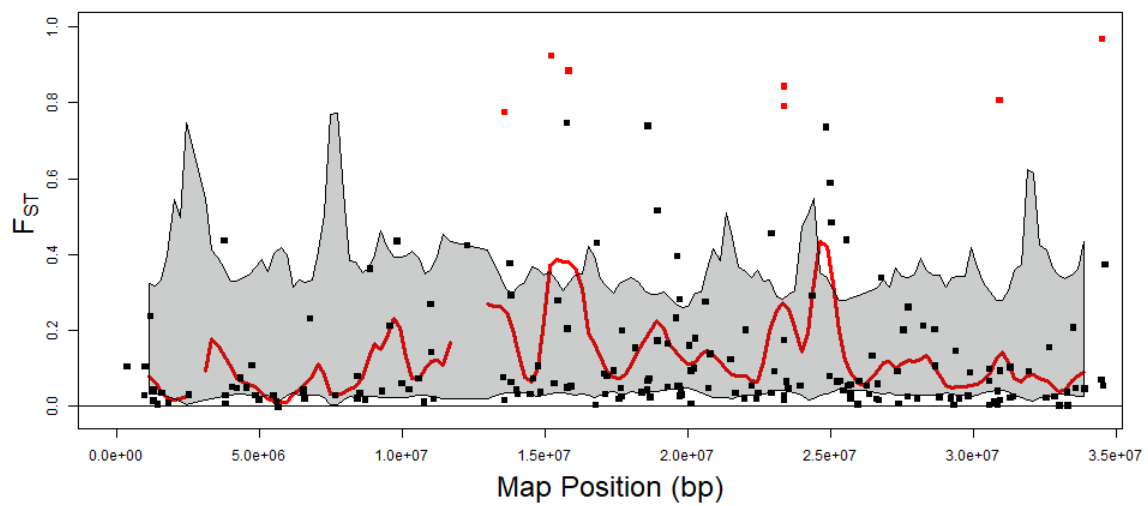
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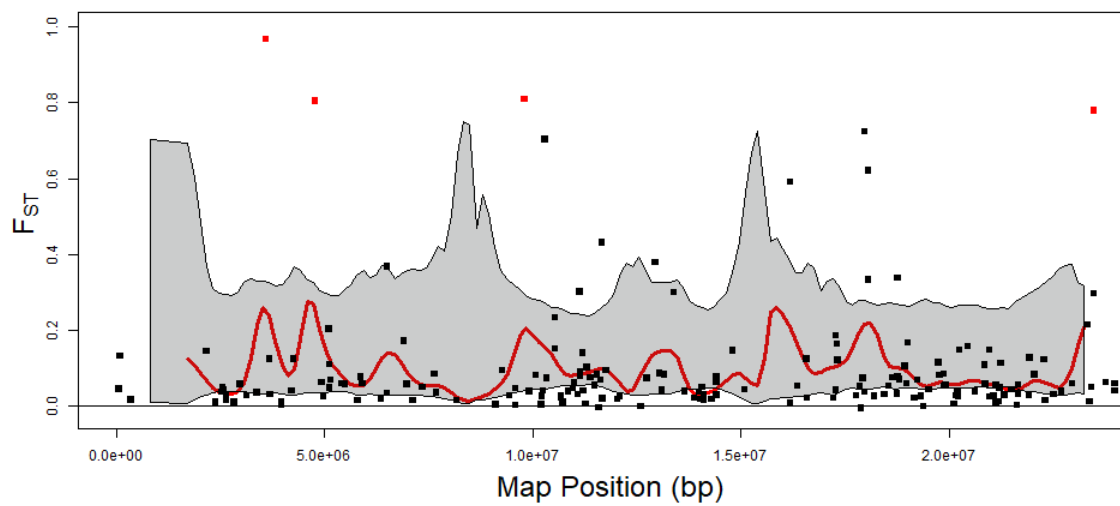
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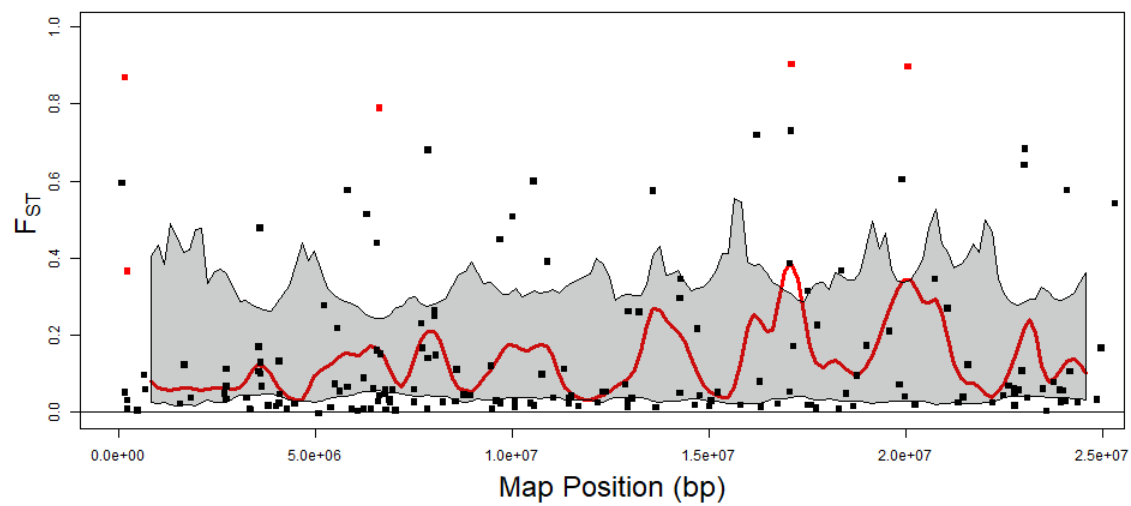
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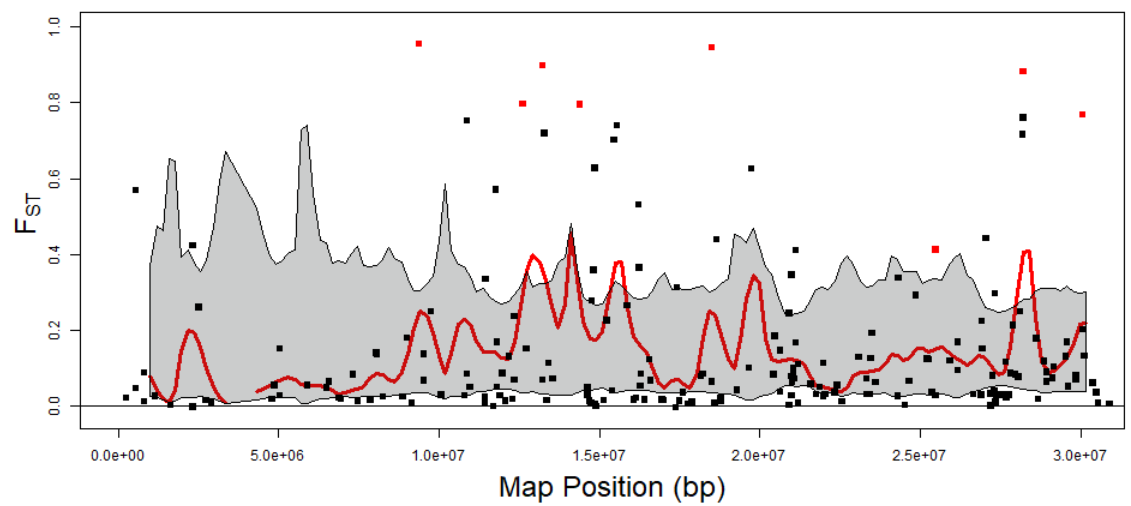
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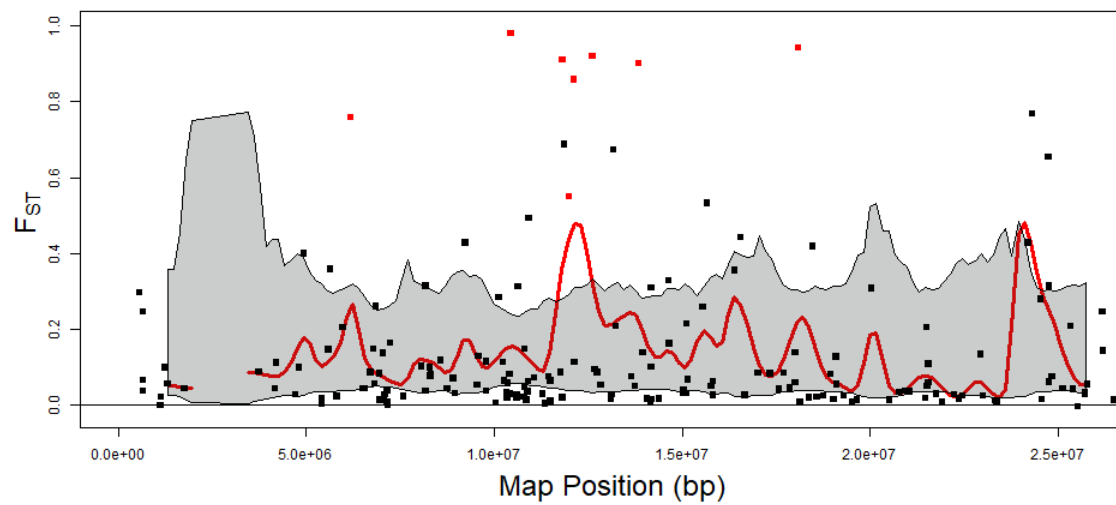
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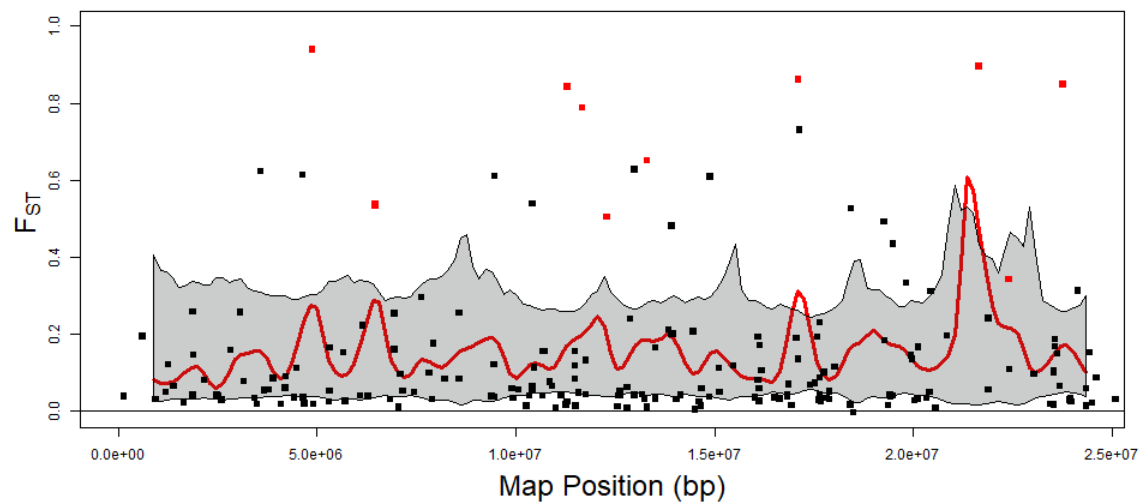
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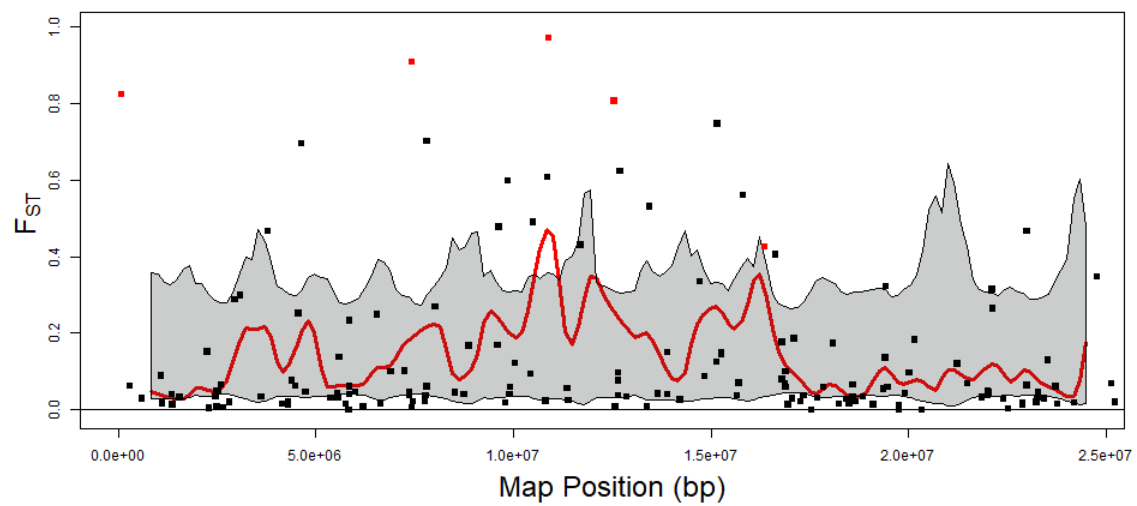
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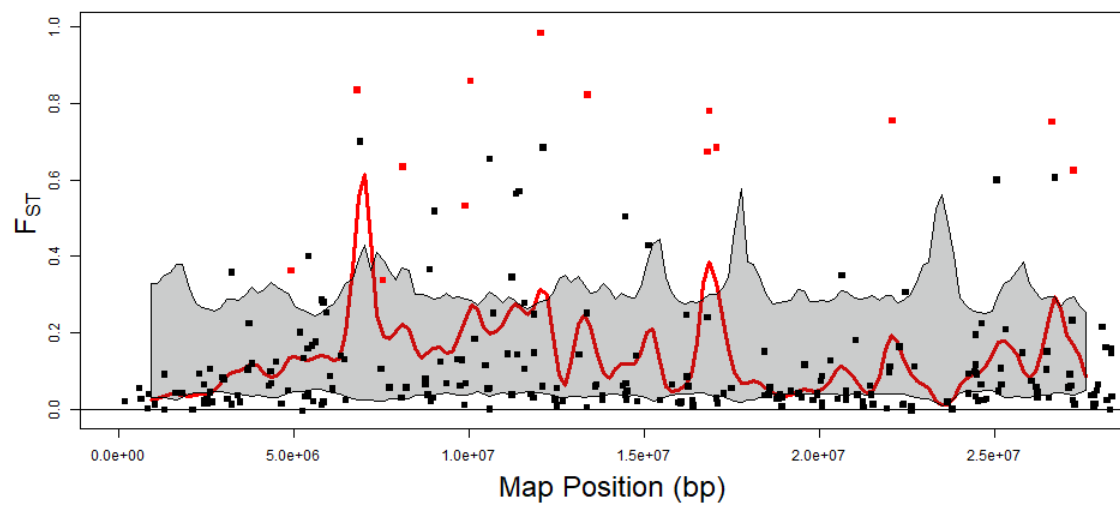
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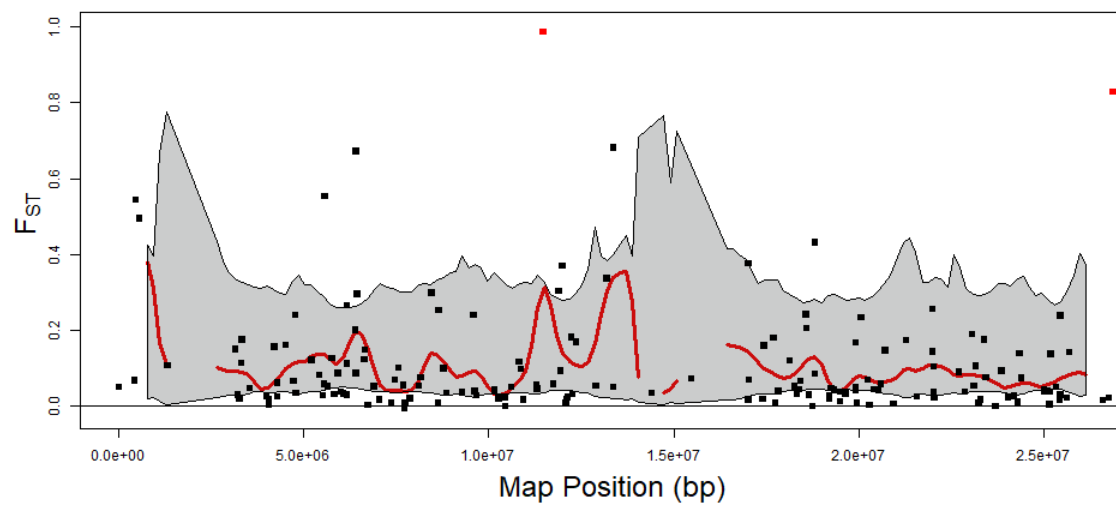
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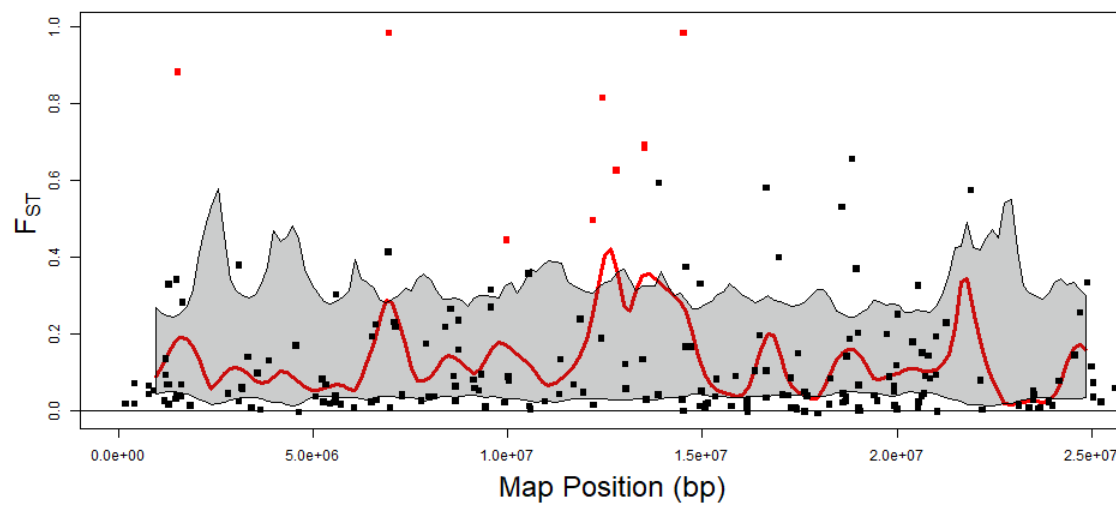
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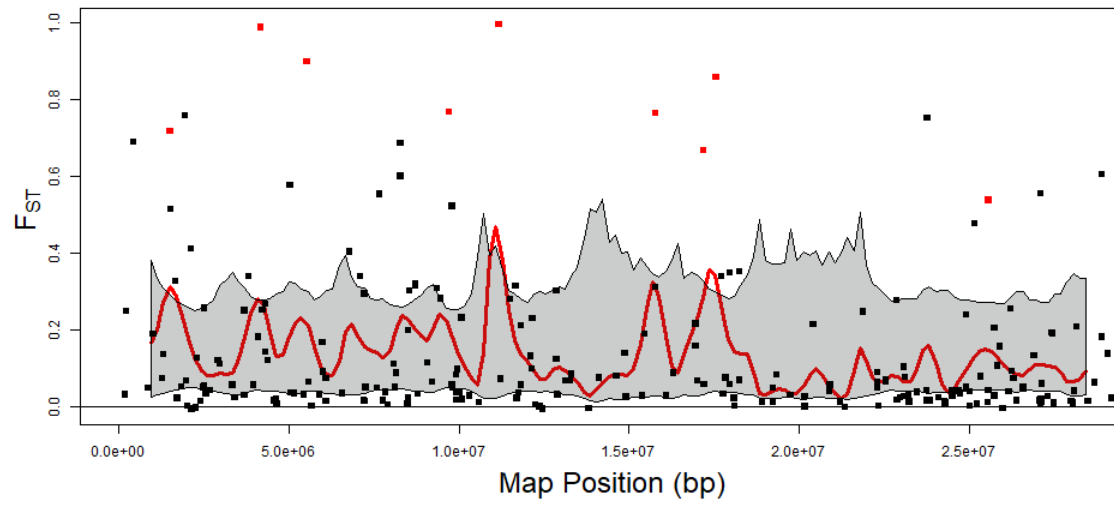
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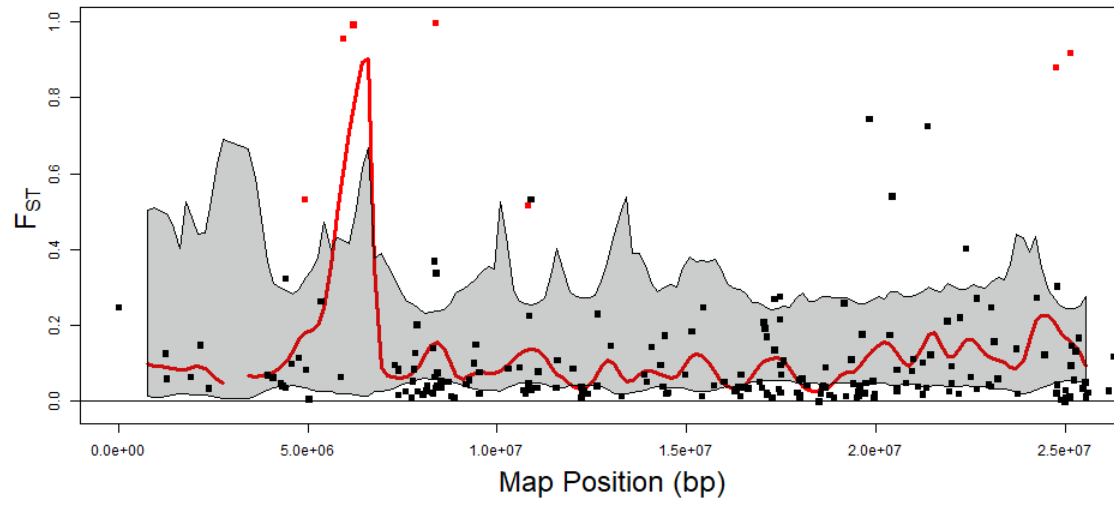
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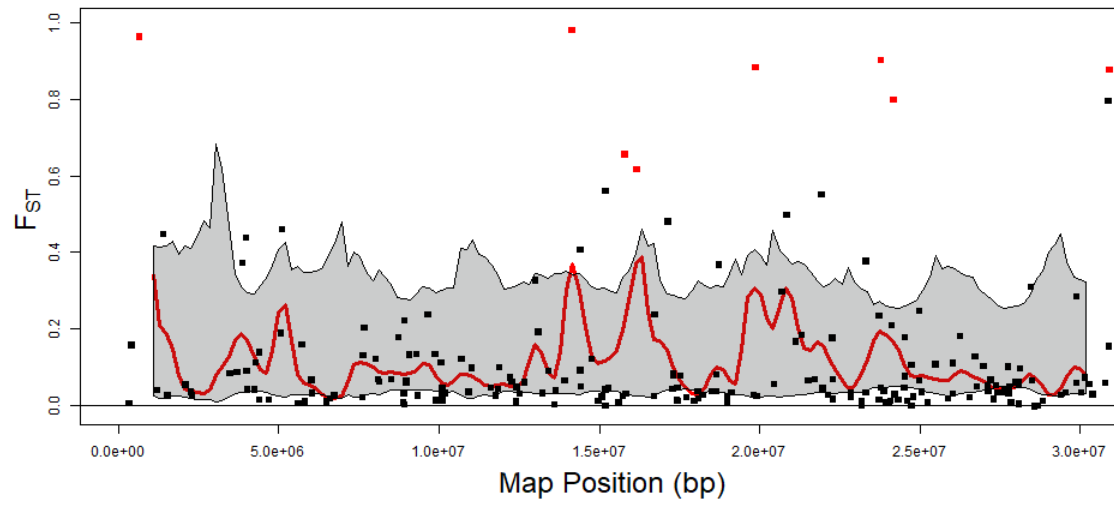
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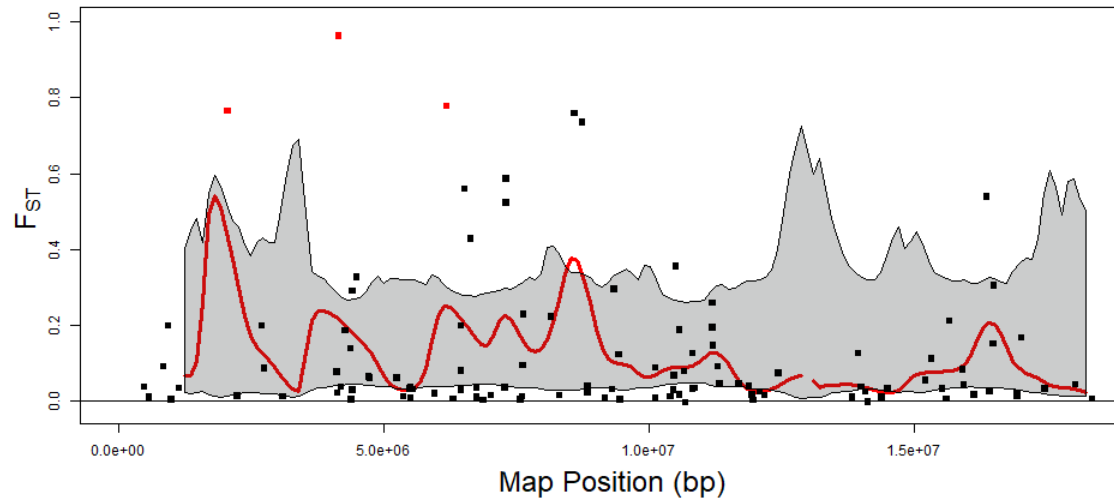
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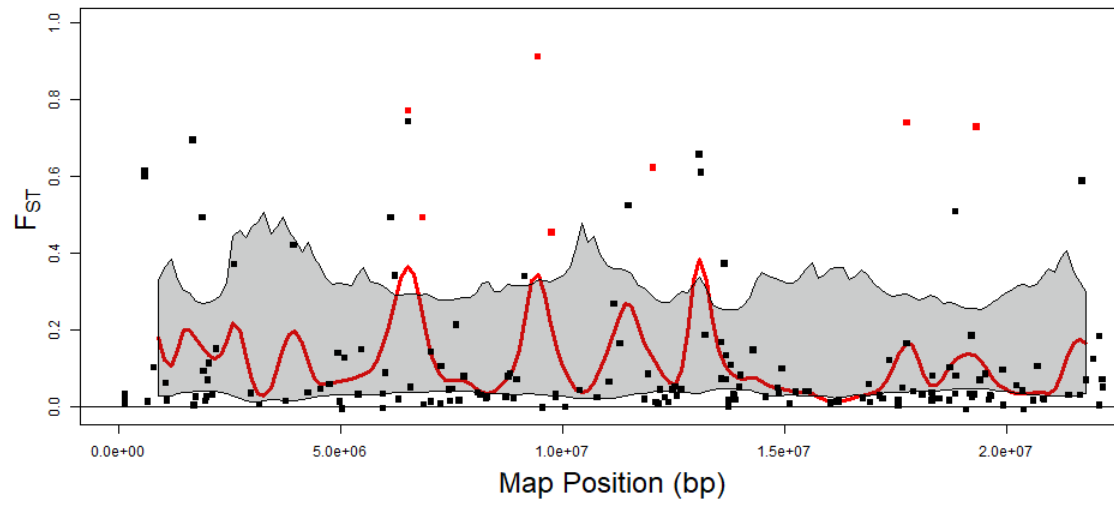
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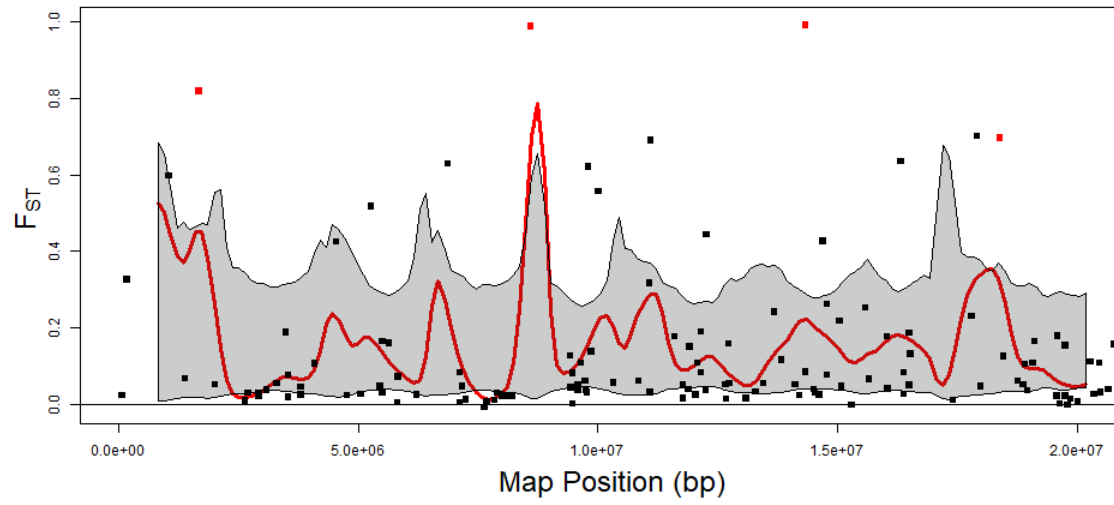
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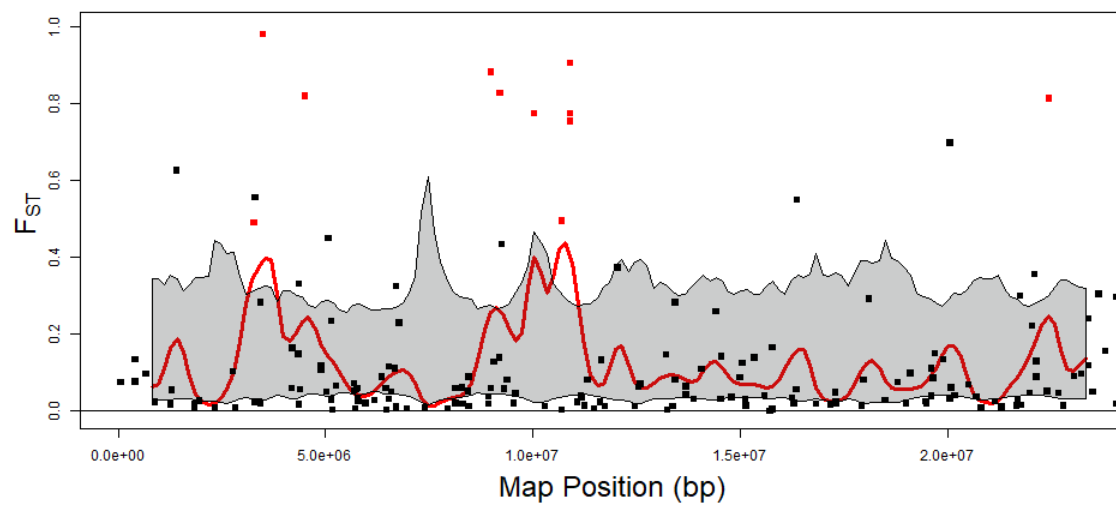
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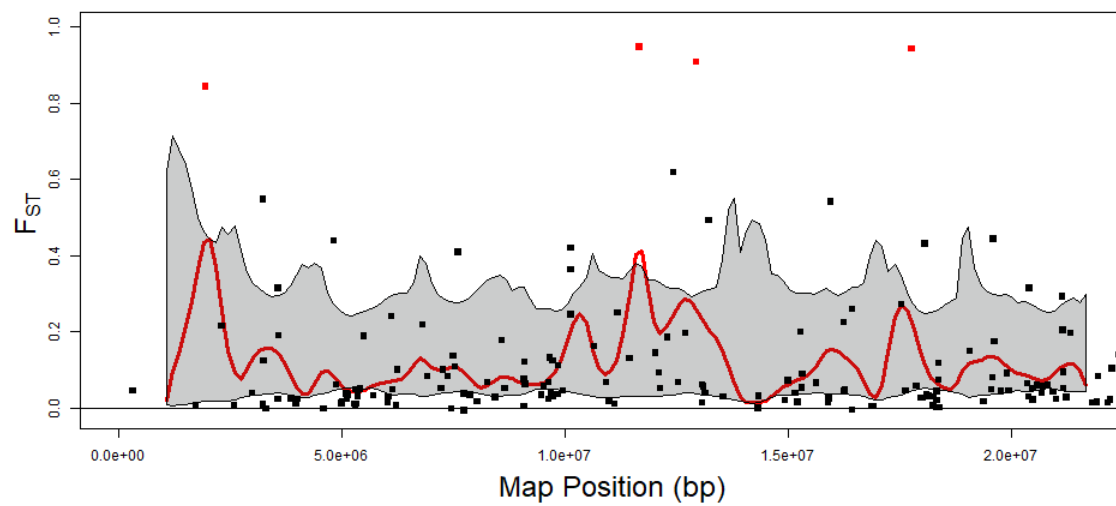
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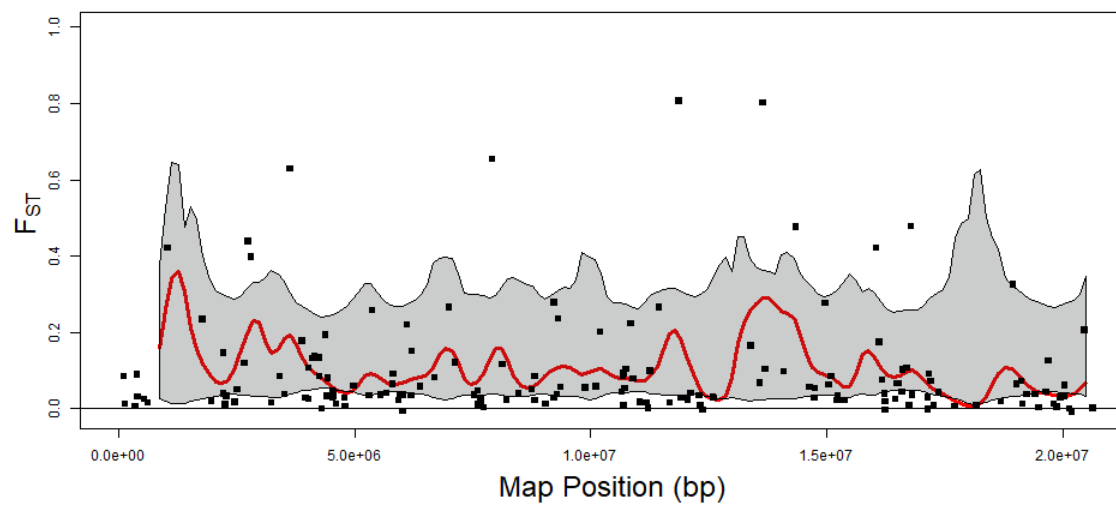
LG20



LG21



LG22



LG23

