

Community Resources to Study Switchgrass Adaptation Using Genome-Wide Association

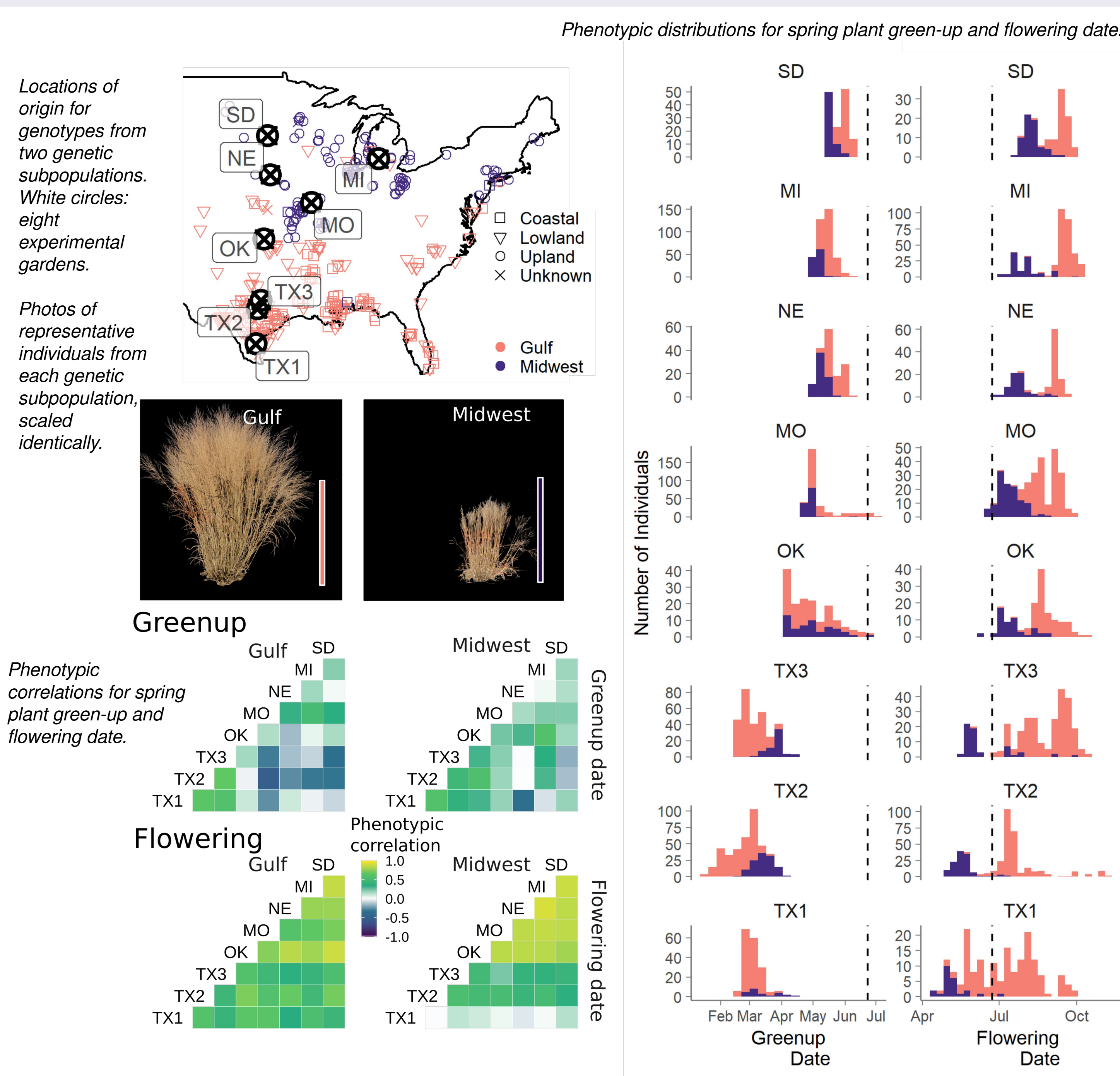
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Why Switchgrass?

BIOFUELS: Switchgrass (*Panicum virgatum*) is the model herbaceous bioenergy crop; it has high biomass yields and is productive on marginal lands; its ethanol yield can exceed that of maize on a per acre basis.

GENETIC DIVERSITY: Natural switchgrass populations are found across North America east of the Rocky Mountains. These populations are morphologically and genetically divergent and have distinct environmental adaptations. Genetic differences in flowering date and photoperiod response will be an early point of exploitation in biomass crop breeding.

1. Continent-Scale Adaptation Using Common Gardens



Take-home message

The switchgrassGWAS R package allows genetic mapping of genetic and genotype-by-environment effects in the switchgrass diversity panel.

The Midwest and Gulf genetic subpopulations flower in response to distinct environmental cues: only Gulf genotypes are photoperiod responsive.

2. switchgrassGWAS R Package

<https://alice-macqueen.github.io/switchgrassGWAS/>

1. Run Genome-Wide Association with `pvdiv_standard_gwas`
2. Conduct multivariate analysis using mash with `pvdiv_bigsnp2mashr`, `mash_standard_run`, `mash_plot_effects`.

Associated with the article published in the 18-February 2021 issue of *Nature*:
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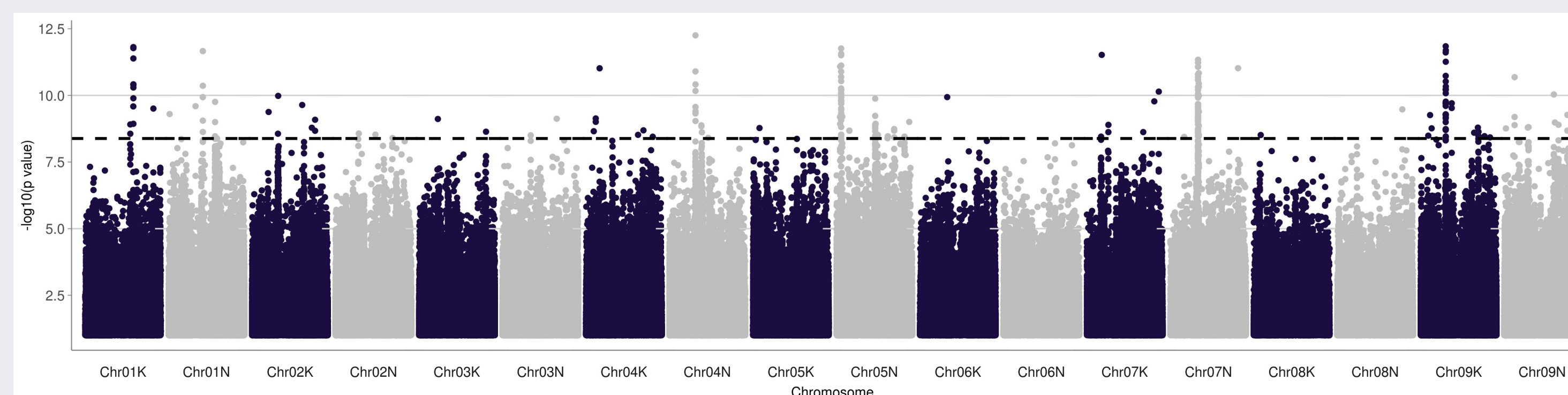


Article



News & Views

3. Genome-Wide Association Studies

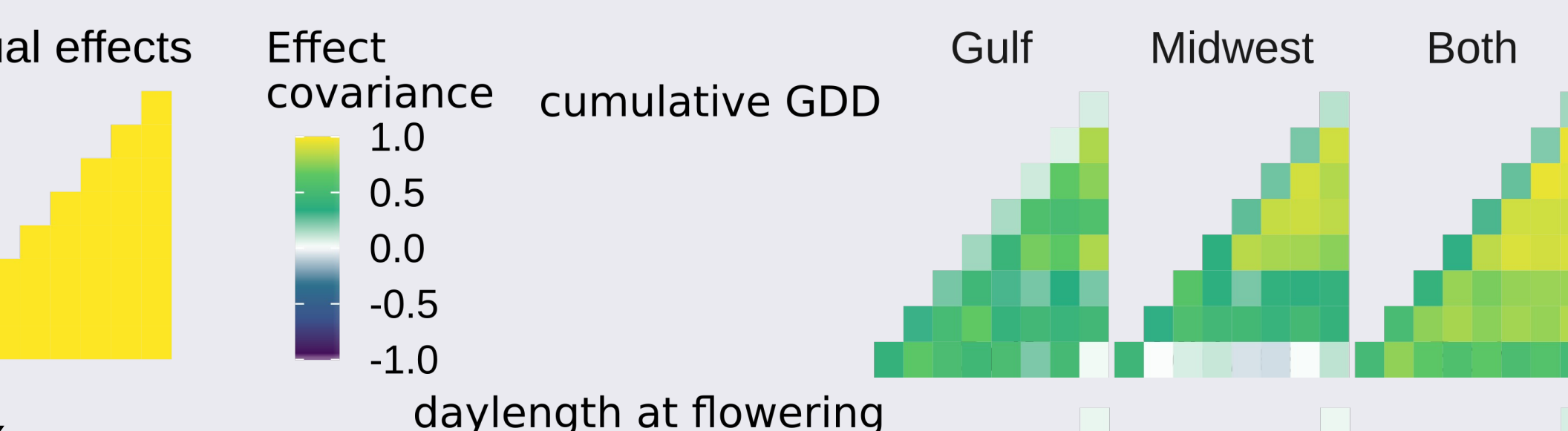
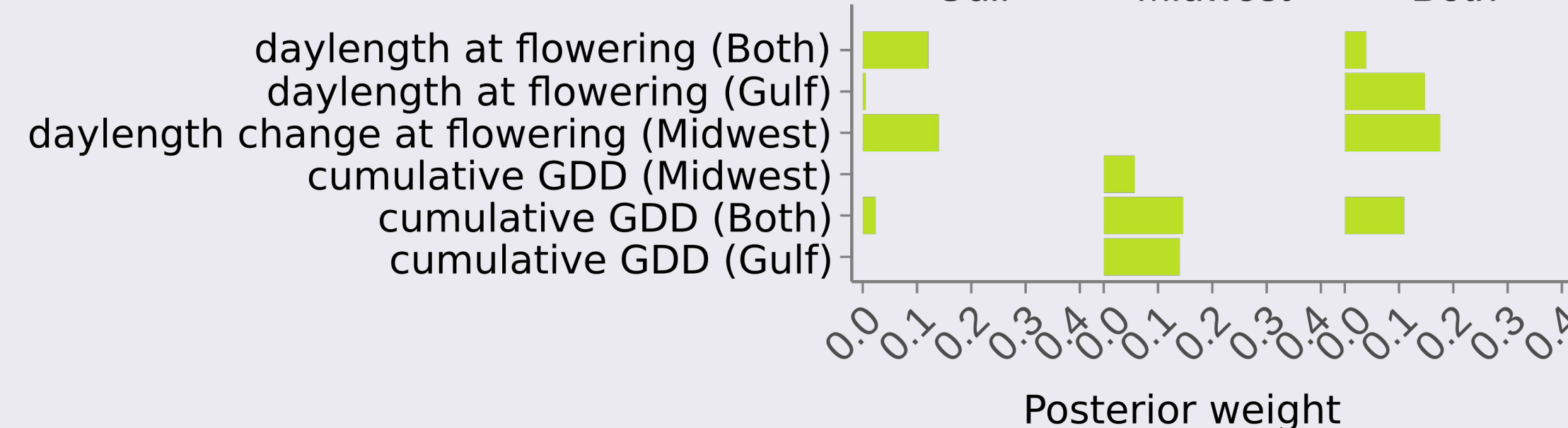


Manhattan plot showing genome-wide association results for flowering date in MI for both the Gulf and Midwest genetic subpopulations. Effect size estimates for the most significant SNPs are used for multivariate analysis with mash (Urbat et al 2019 Nat. Gen.).

4. Multivariate analysis assigns environmental drivers to SNP effect patterns

1. Make covariance matrices based on environmental cues (shown here are matrices for flowering date).

2. Assign SNPs posterior weights on each covariance matrix using maximum likelihood.



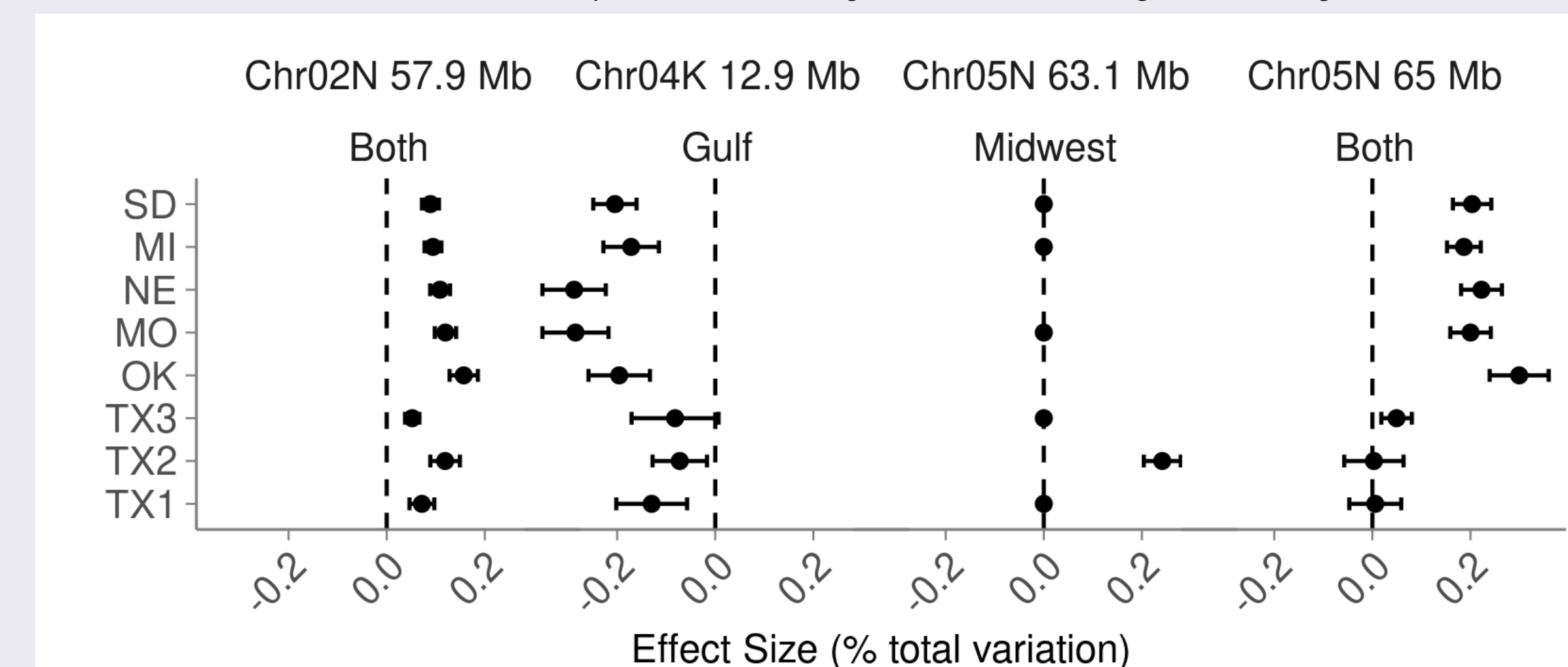
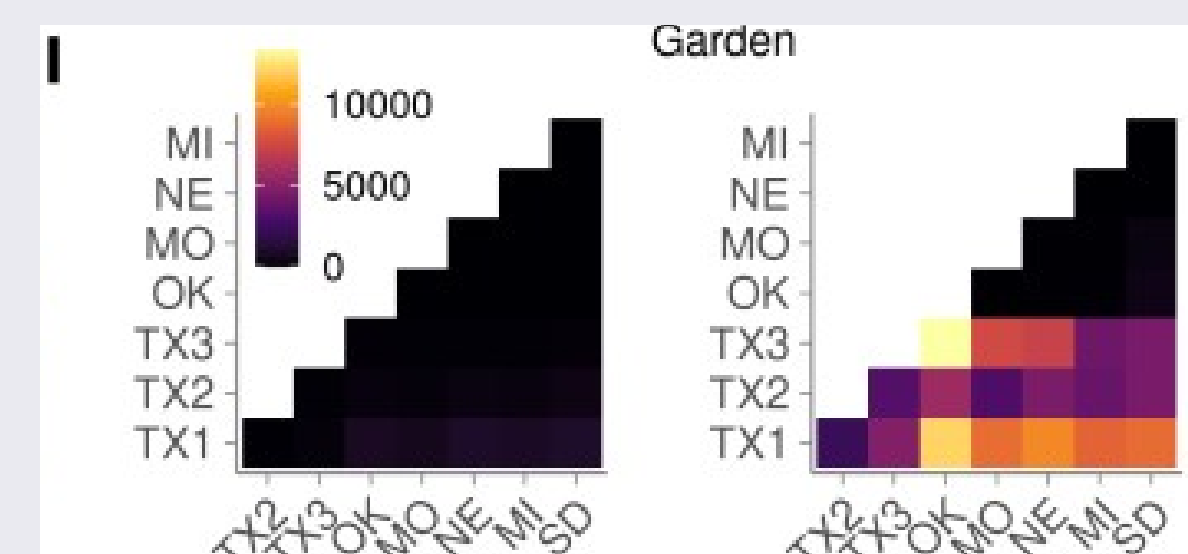
Gulf genotype effects have high posterior weights on flowering daylength covariance matrices; Midwest genotype effects have high posterior weights on cumulative GDD covariance matrices.

Patterns of highly significant SNP effects across eight common gardens. These SNPs were also in significant quantitative trait loci for flowering date in an independent F2 cross grown at the same eight common gardens in 2019.

3. Find significant SNP effects that covary with particular environmental drivers using multivariate adaptive shrinkage (mash).

4. Explore overall patterns of SNP effects, including those not affected by any hypothesized environmental driver.

Number of SNPs with sign changes (antagonistic pleiotropy) and magnitude changes (differential sensitivity) for flowering date between pairs of common gardens



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