**A red dots and lines on a black background

Description automatically generated**

**Figure 1.** Frequency of effect alleles across populations for significant SNPs identified in the single-SNP LMM analysis (GEMMA and GMMAT), as well as the multi-SNP BSLMM analysis, all of which surpassed the genome-wide significance threshold (1 × 10⁻³) for the Vegetation Period Duration (VPD) trait. The analysis also includes SNPs meeting the same threshold in the multivariate GWAS. The corresponding SNPs are detailed in Table 3 and Table 5 of the manuscript.

A blue circles and lines on a black background

Description automatically generated**Figure 2.** Frequency of effect alleles across populations for significant SNPs identified in the single-SNP LMM analysis (GEMMA and GMMAT), as well as the multi-SNP BSLMM analysis, all of which surpassed the genome-wide significance threshold (1 × 10⁻³) for the Beginning of Flowering (BOF) trait. The analysis also includes SNPs meeting the same threshold in the multivariate GWAS. The corresponding SNPs are detailed in Table 3 and Table 5 of the manuscript.

A green dots and dots on a black background

Description automatically generated**Figure 3.** Frequency of effect alleles across populations for significant SNPs identified in the single-SNP LMM analysis (GEMMA and GMMAT), as well as the multi-SNP BSLMM analysis, all of which surpassed the genome-wide significance threshold (1 × 10⁻³) for the Beginning of Sprouting (BOS) trait. The analysis also includes SNPs meeting the same threshold in the multivariate GWAS. The corresponding SNPs are detailed in Table 3 and Table 5 of the manuscript.

A chart of dots and lines

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**Figure 4.** Frequency of effect alleles across populations for significant SNPs identified in the single-SNP LMM analysis (GEMMA and GMMAT), as well as the multi-SNP BSLMM analysis, all of which surpassed the genome-wide significance threshold (1 × 10⁻³) for the Flowering Period Duration (FPD) trait. The analysis also includes SNPs meeting the same threshold in the multivariate GWAS. The corresponding SNPs are detailed in Table 3 of the manuscript.