

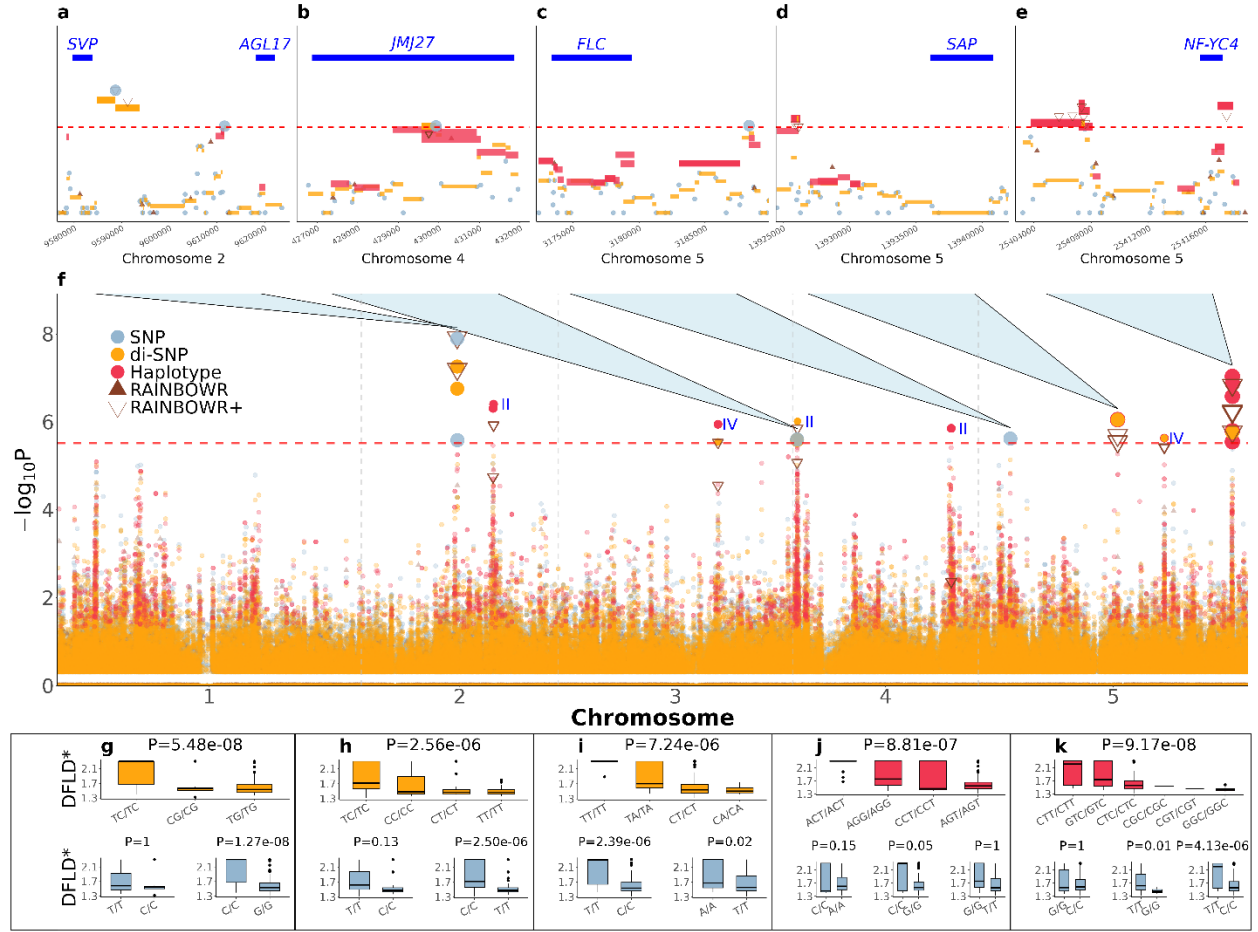
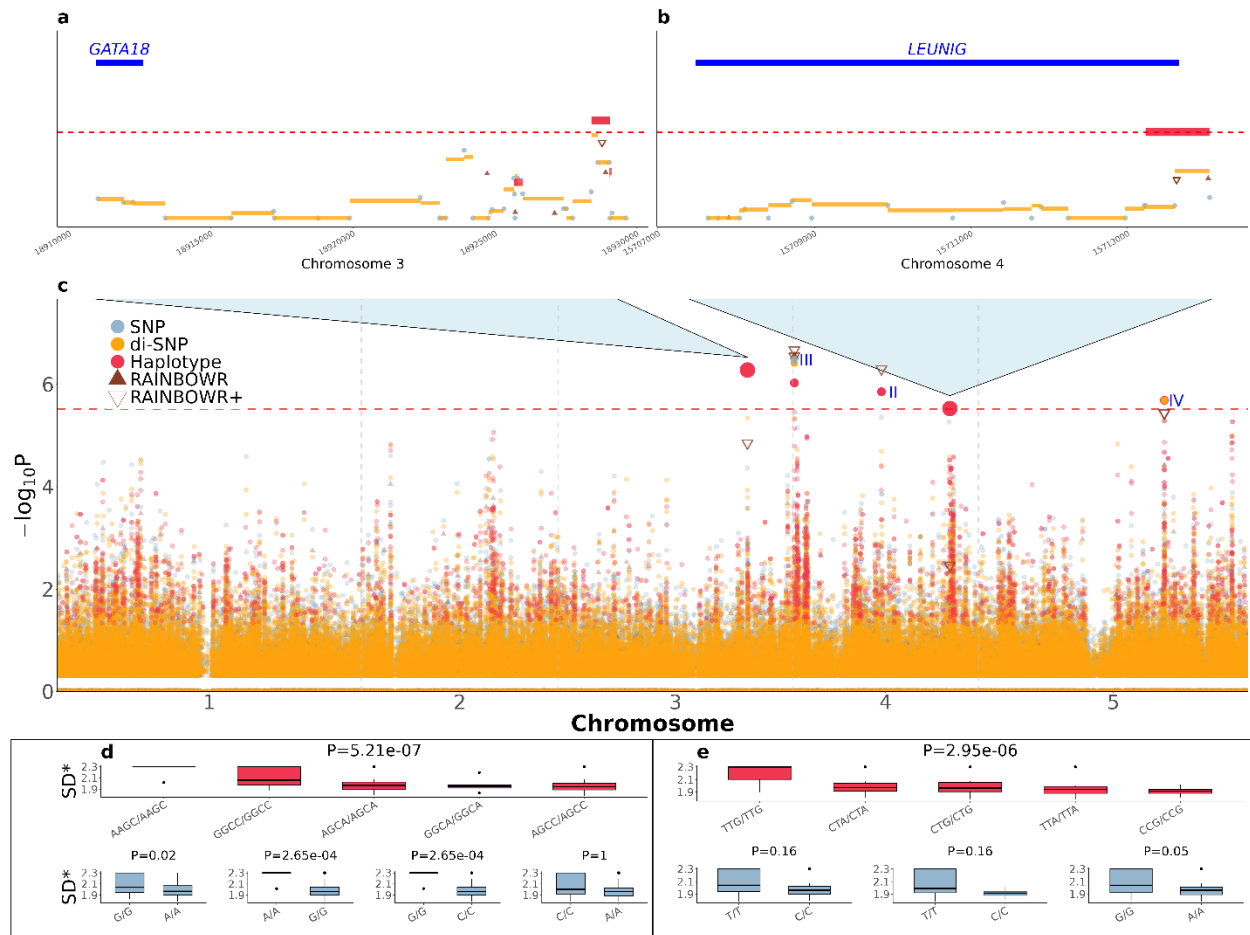


Figure S1. The results of analyzing an agronomic trait in Arabidopsis, days to flowering under long days (DFLD), where DFLD* represents the log-transformed DFLD. (a – e) Five zoomed-in loci and nearby genes on chromosomes 2, 4, 5, 5 and 5, respectively, detected using di-SNP & SNP (a and b), SNP only (a and c), and haplotype variants & di-SNP (d and e). In panel a, two di-SNPs and one SNP were assigned to SVP, whereas one SNP was assigned to AGL17. (f) Manhattan plot showing the results based on single SNPs (blue), di-SNPs (orange), haplotypes (red), and RAINBOWR analyses using PLINK-pre-selected (solid brown triangles) and CHAP-GWAS-selected haplotypes (hollow brown triangles). (g – k) Comparison of association strength with DFLD* between haplotype variables with the strongest signals and single SNPs at the three genomic loci corresponding to (a – e), respectively. The upper panels show the distribution of DFLD across haplotypes, along with the overall p-values. The lower panels show the distribution of DFLD between the two genotypes at each SNP locus within the detected haplotype variants, together with the corresponding p-values. In Figure S1 f, Roman numerals I, II, III, and IV denote variant clusters corresponding to four distinct scenarios: I – only SNPs detected; II – only haplotypes detected; III – SNPs overlapping with di-SNPs or haplotypes; IV – haplotypes overlapping with di-SNPs.



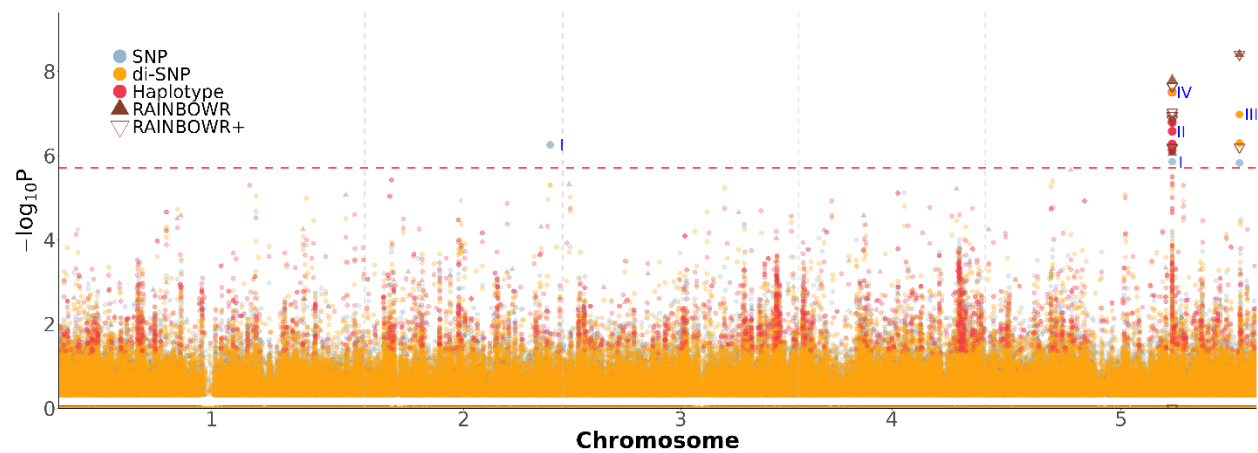


Figure S3. The results of analyzing an agronomic trait in Arabidopsis, days to flowering under long days with vernalization (LDV). Manhattan plot showing the results based on single SNPs (blue), di-SNPs (orange), haplotypes (red), and RAINBOWR analyses using PLINK-pre-selected (solid brown triangles) and CHAP-GWAS-selected haplotypes (hollow brown triangles). In Figure S3 a, Roman numerals I, II, III, and IV denote variant clusters corresponding to four distinct scenarios: I – only SNPs detected; II – only haplotypes detected; III – SNPs overlapping with di-SNPs or haplotypes; IV – haplotypes overlapping with di-SNPs.

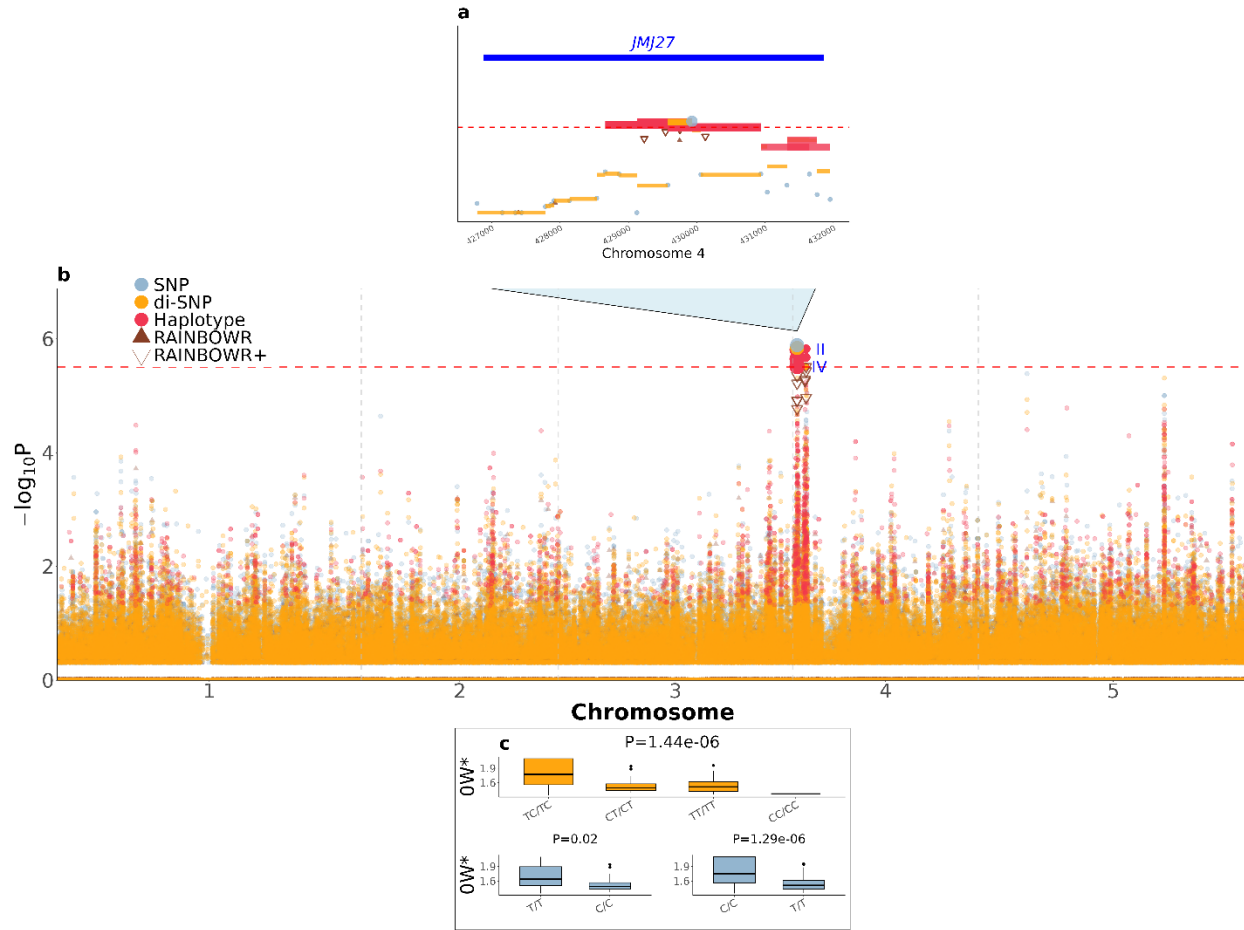


Figure S4. The results of analyzing an agronomic trait in *Arabidopsis*, days to flowering under long days with no vernalization (OW), where OW* represents the log-transformed OW. (a) One zoomed-in loci and nearby gene on chromosomes 4, respectively, detected using SNP, di-SNP and haplotype variants. (b) Manhattan plot showing the results based on single SNPs (blue), di-SNPs (orange), haplotypes (red), and RAINBOWR analyses using PLINK-pre-selected (solid brown triangles) and CHAP-GWAS-selected haplotypes (hollow brown triangles). (c) Comparison of association strength with OW* between haplotype variables with the strongest signals and single SNPs at the three genomic loci corresponding to (a), respectively. The upper panels show the distribution of OW across haplotypes, along with the overall p-values. The lower panels show the distribution of OW between the two genotypes at each SNP locus within the detected haplotype variants, together with the corresponding p-values. In Figure S4 b, Roman numerals I, II, III, and IV denote variant clusters corresponding to four distinct scenarios: I – only SNPs detected; II – only haplotypes detected; III – SNPs overlapping with di-SNPs or haplotypes; IV – haplotypes overlapping with di-SNPs.

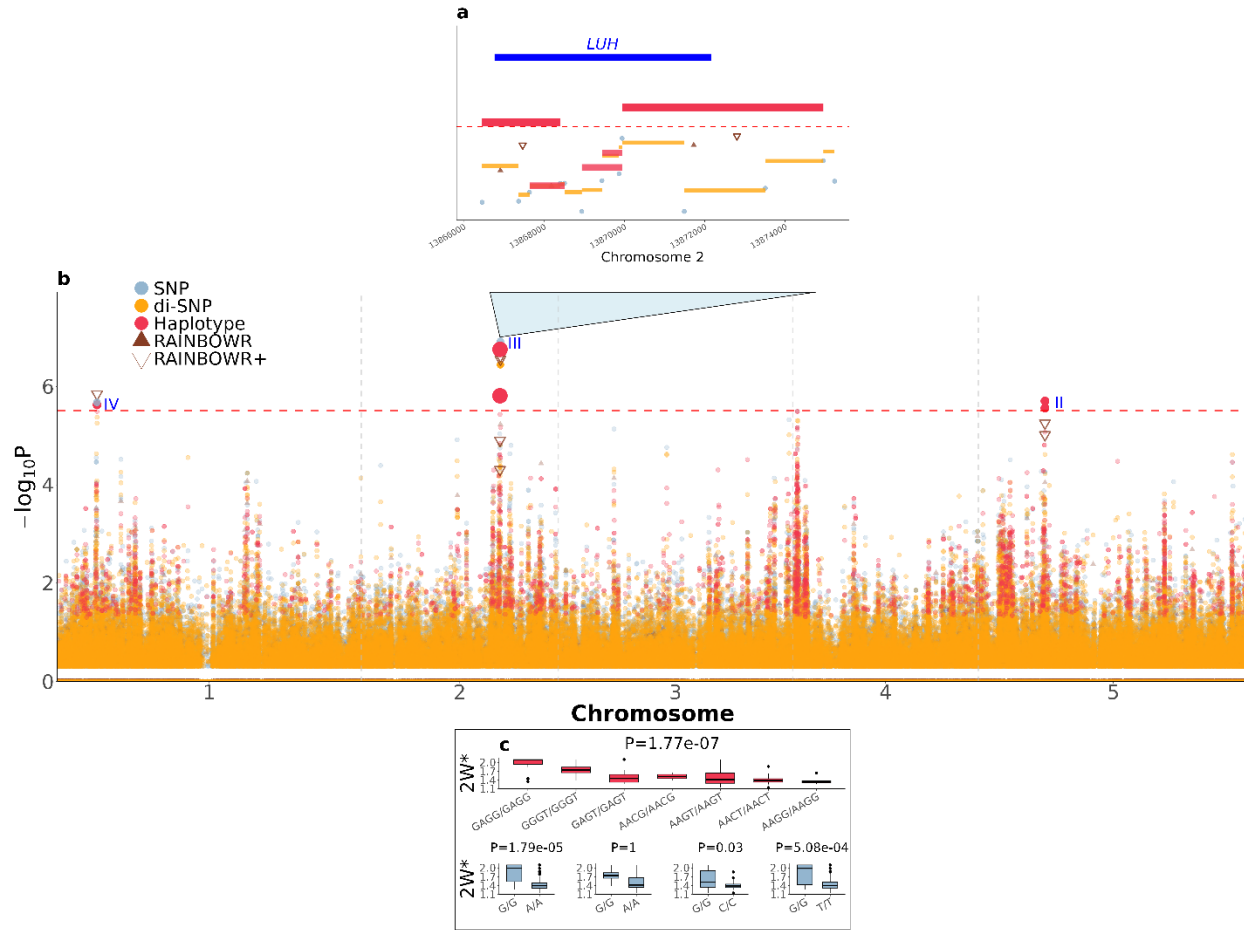


Figure S5. The results of analyzing an agronomic trait in Arabidopsis, days to flowering under long days for two weeks vernalization (2W), where 2W* represents the log-transformed 2W. (a) One zoomed-in loci and nearby gene on chromosomes 2, respectively, detected using haplotype variants only. (b) Manhattan plot showing the results based on single SNPs (blue), di-SNPs (orange), haplotypes (red), and RAINBOWR analyses using PLINK-pre-selected (solid brown triangles) and CHAP-GWAS-selected haplotypes (hollow brown triangles). (c) Comparison of association strength with 2W* between haplotype variables with the strongest signals and single SNPs at the three genomic loci corresponding to (a), respectively. The upper panels show the distribution of 2W across haplotypes, along with the overall p-values. The lower panels show the distribution of 2W between the two genotypes at each SNP locus within the detected haplotype variants, together with the corresponding p-values. In Figure S5 b, Roman numerals I, II, III, and IV denote variant clusters corresponding to four distinct scenarios: I – only SNPs detected; II – only haplotypes detected; III – SNPs overlapping with di-SNPs or haplotypes; IV – haplotypes overlapping with di-SNPs.