

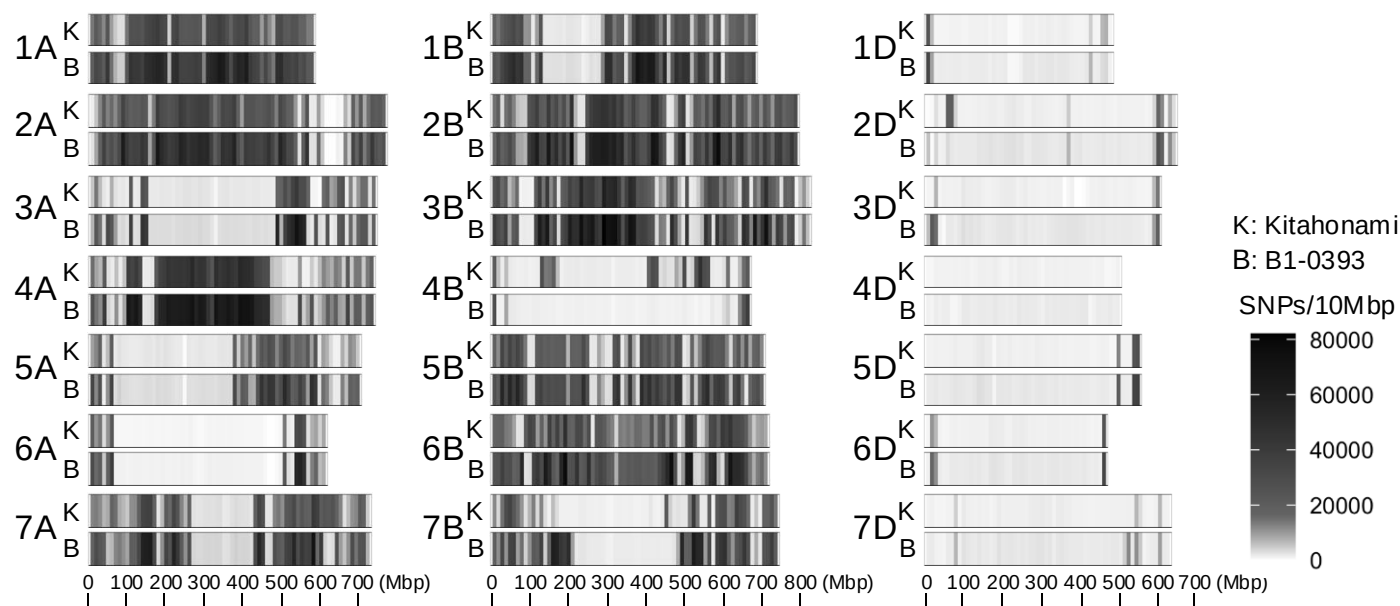


Figure S1 Distribution of SNPs of wheat cultivars 'Kitahonami' and the 'B1-0393' over the chromosomes. SNP density was estimated by counting the number of SNPs per 10 Mbp. The SNP density is displayed as the gradation color from white to black. The higher the density, the blacker it is.

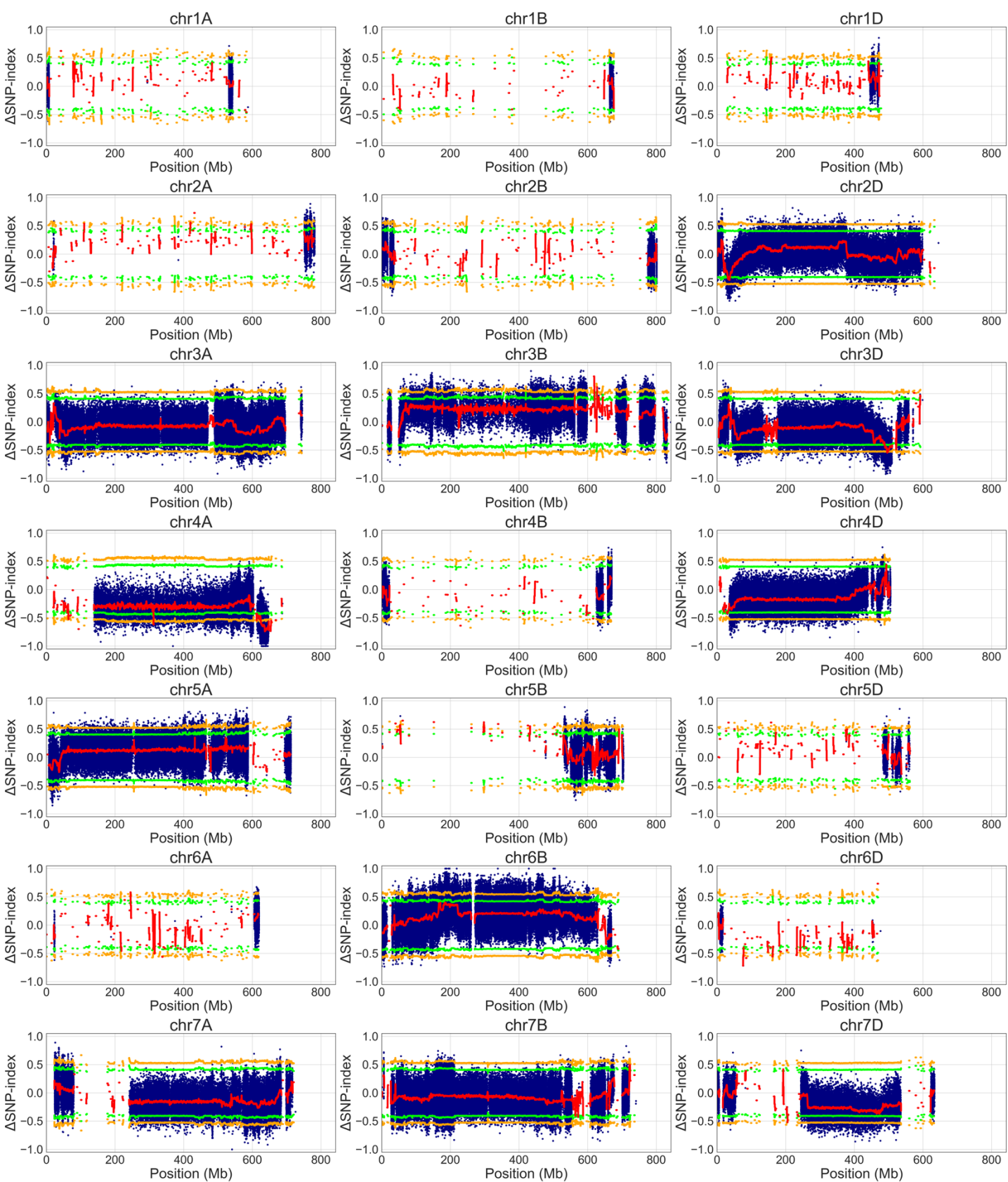
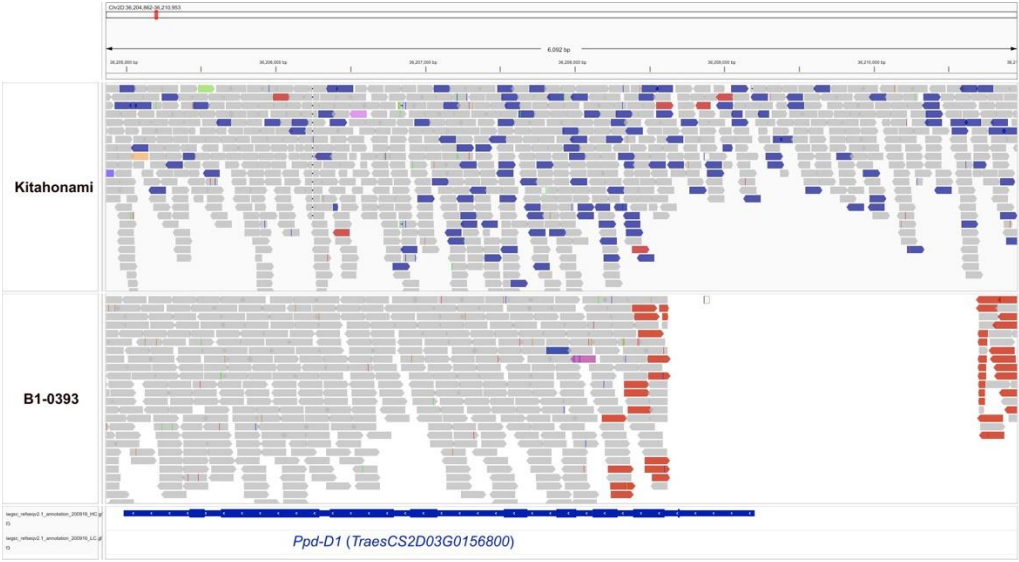


Figure S2 Distribution of Δ SNP-index using F_3 early and late heading bulks. Blue plots indicate Δ SNP-index at each position of SNPs. The moving average of Δ SNP-index is shown in the red line. Green line and orange line show 95% confidence interval and 99% confidence interval, respectively.

(a)



(b)

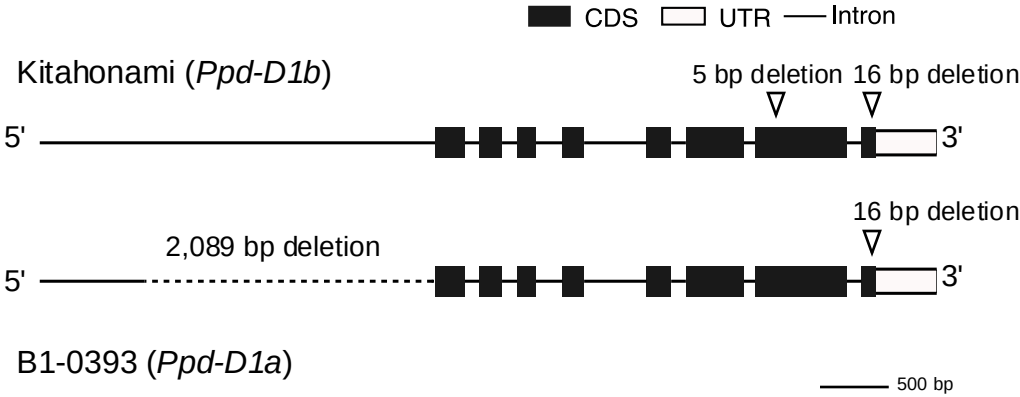


Figure S3 (a) Coverage of short read to *Ppd-D1* locus visualized by IGV alignment viewer (Robinson et al. 2011). (b) Schematic representation of *Ppd-D1* structure in 'Kitahonami' and 'B1-0393.'

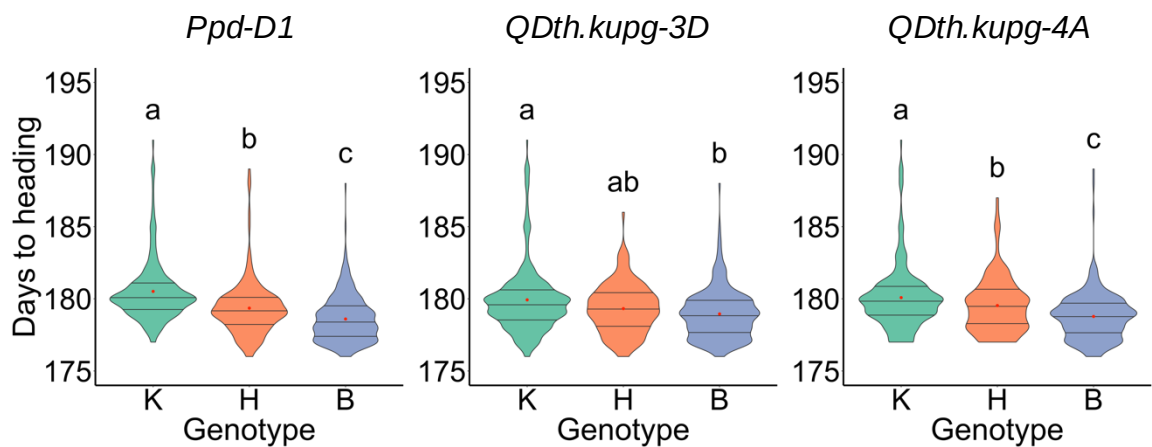
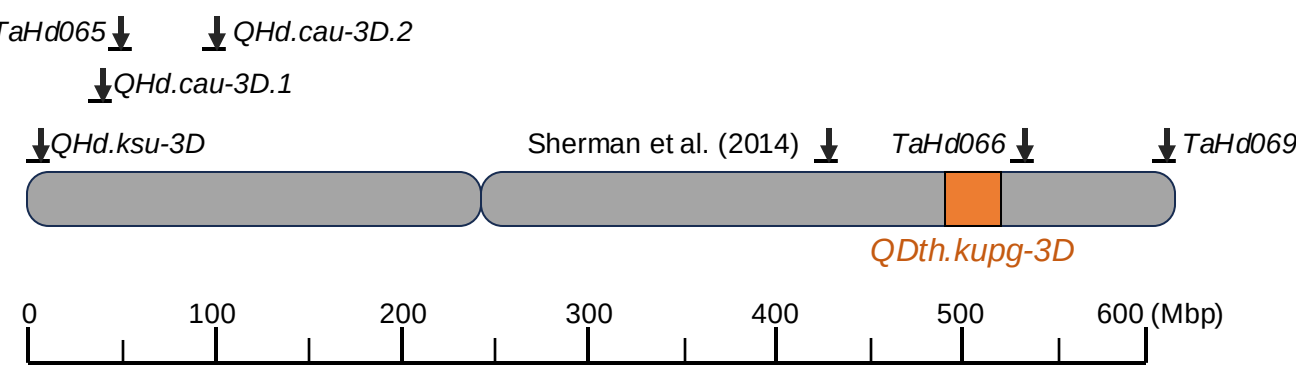


Figure S4 Segregation analysis of *Ppd-D1*, *QDth.kupg-3D*, and *QDth.kupg-4A* for days to heading using F_3 population generated from a cross between 'Kitahonami' and 'B1-0393.' K, H, and B indicate plants with homozygous for the 'Kitahonami' allele, heterozygous, and homozygous for the 'B1-0393' allele, respectively. The red points indicate mean of heading dates. Different letters designate significant differences between the means in Steel-Dwass test ($P < 0.05$).

Chromosome 3D



Chromosome 4A

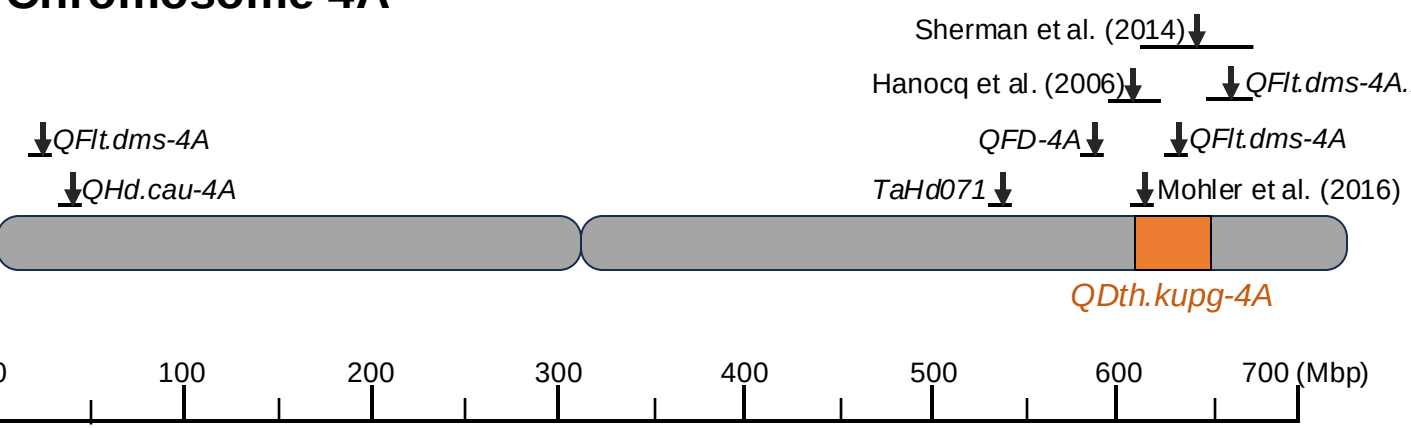


Figure S5 Schematic diagram of QTL loci with previous studies for days to heading in wheat on chromosomes 3D and 4A. Arrows and lines indicate the previously reported QTL loci. Orange areas represent the position of *QDth.kupg-3D* and *QDth.kupg-4A*.

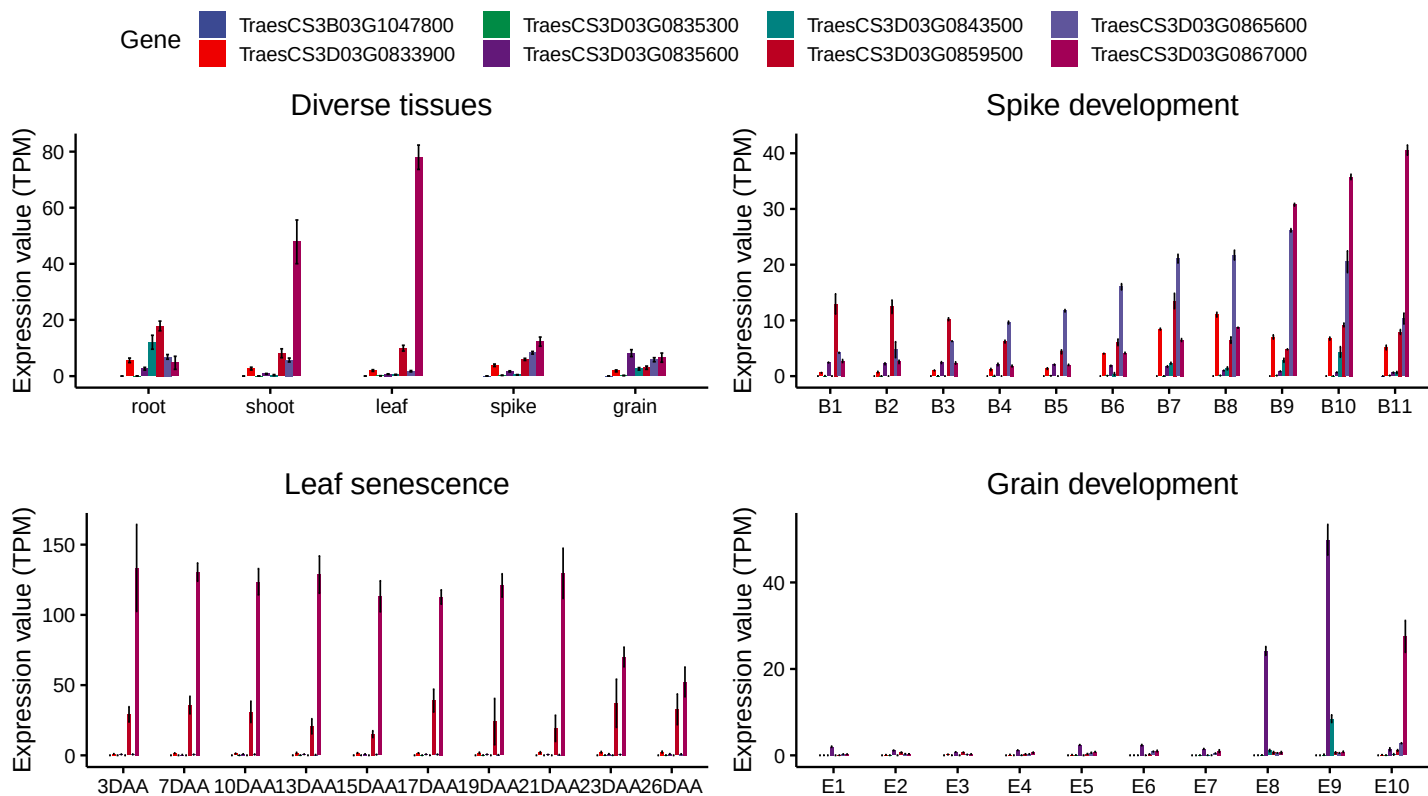


Figure S6 Predicted gene expression levels of genes with missense mutations in *QDth.kupg-3D*. Gene expression levels were predicted through wGRN (Chen et al. 2023).

References in supplementary materials

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