

Fig.Suppl

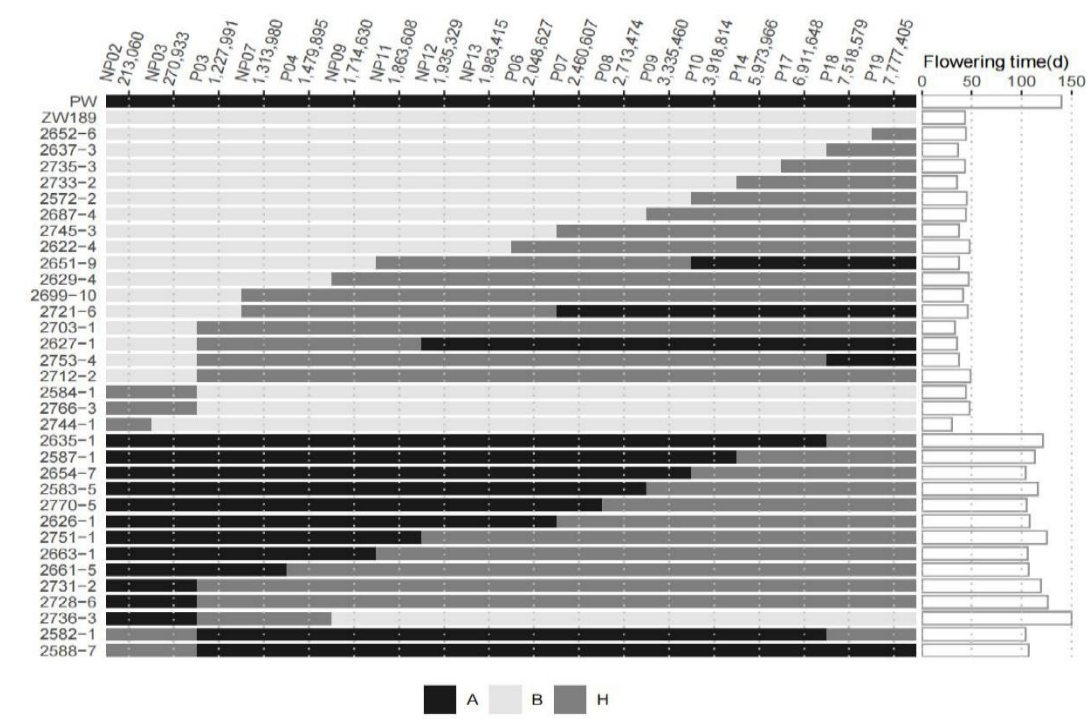


Fig. S1 Candidate genomic interval associated with *BnaC08cqDTF* from 2.5 Mb to the 957 kb flanked by the markers NP02 to P19 on chromosome C08 of spring *B. napus*

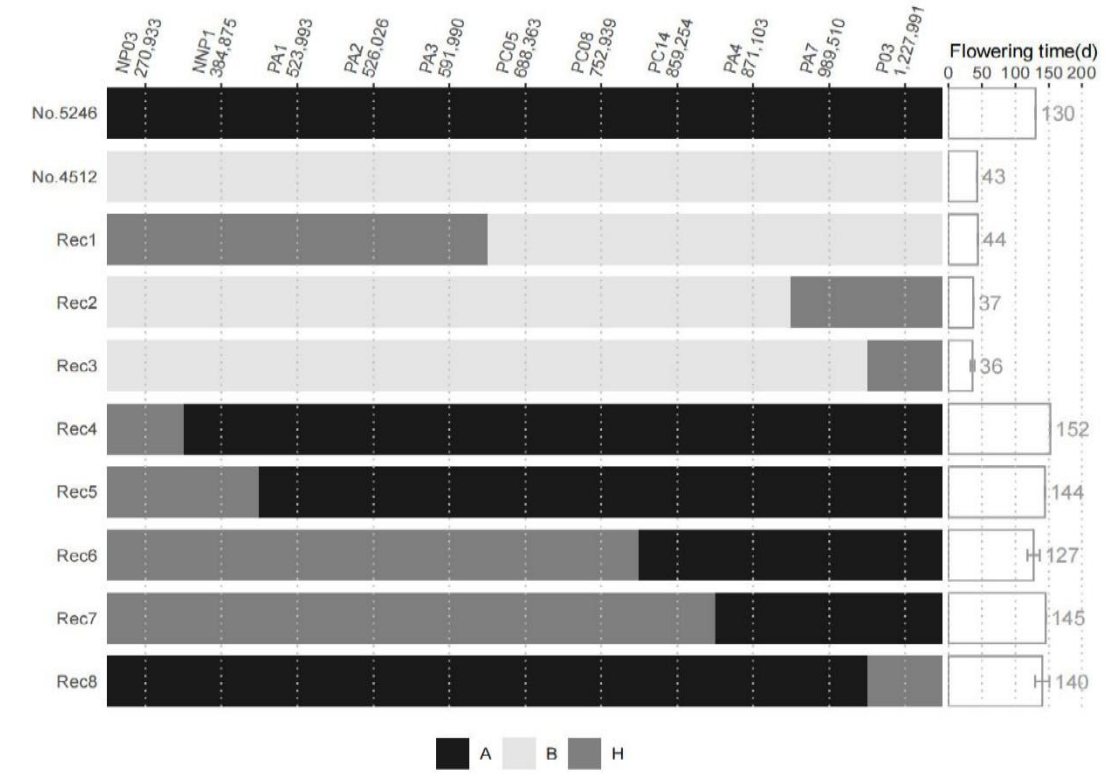


Fig. S2 Candidate genomic interval associated with *BnaC08cqDTF* from 957 kb to the 130 kb flanked by the markers NP03 to P03 on chromosome C08 of spring *B. napus*

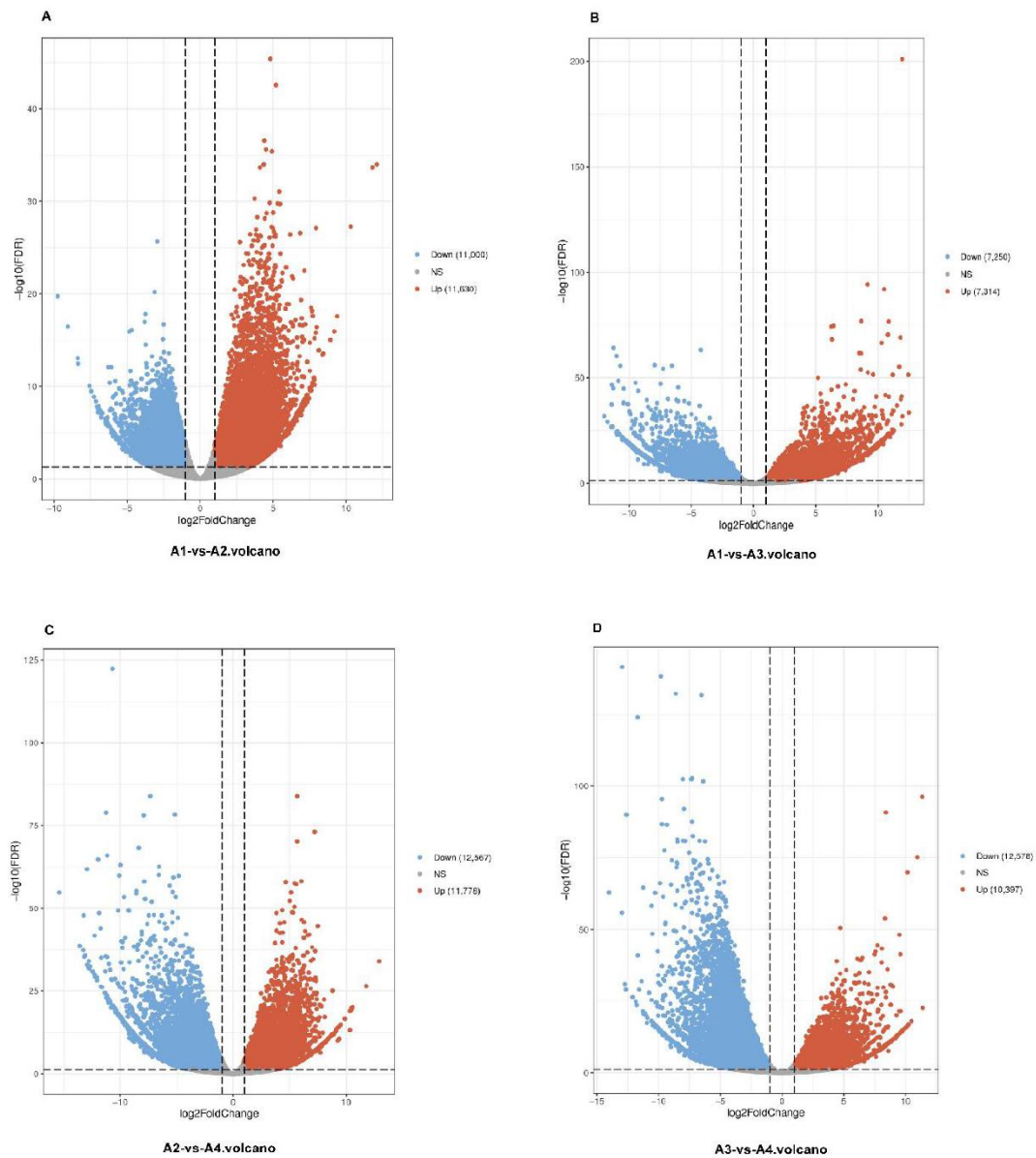


Fig.S3 Comparison of gene expression levels in the young leaves and SAMs of No. 4512 and No. 5246 a-d Volcano plot of DEGs in the young inflorescences of No. 4512 compared with those of No. 5246, with $-\log(\text{padj}) > 0$ as the significance threshold

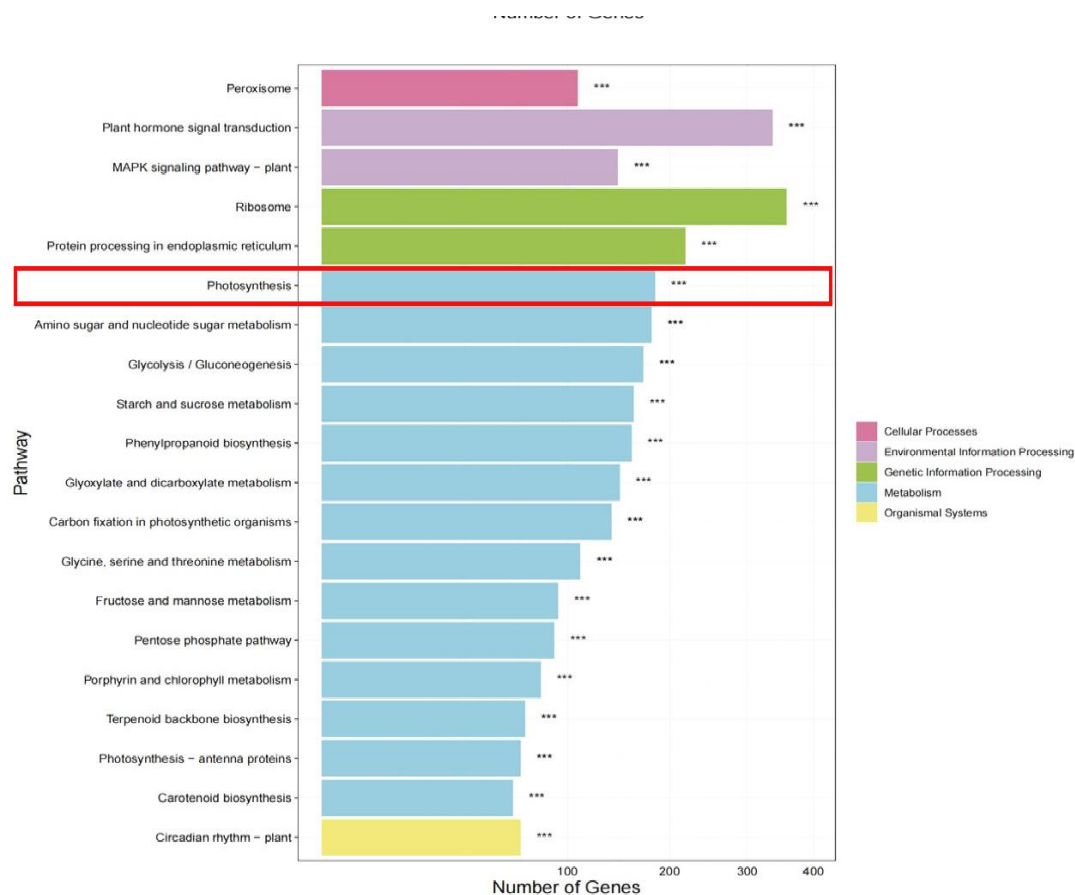


Fig. S4 Most significantly enriched DEGs involved photosynthesis DEG in metabolism

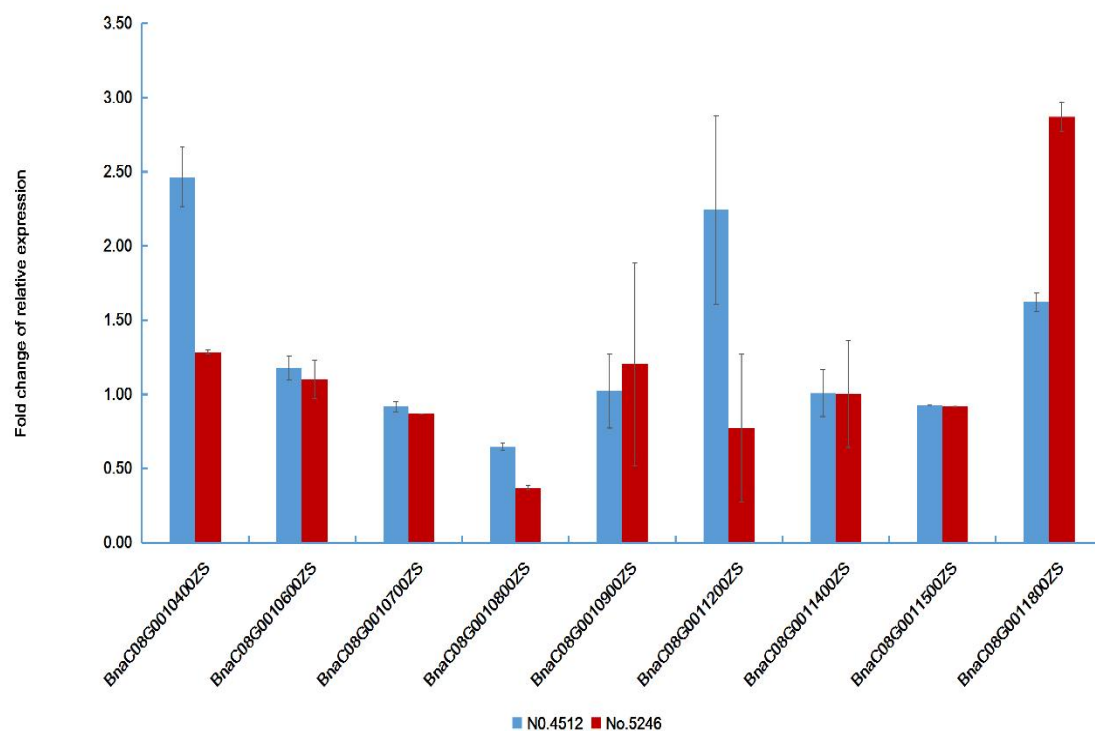


Fig. S5 Expression levels of 9 candidate genes within an 86-kb region according to qRT-PCR in the leaves of the early-flowering parent (No. 4512) and Late-flowering parent (No. 5246)

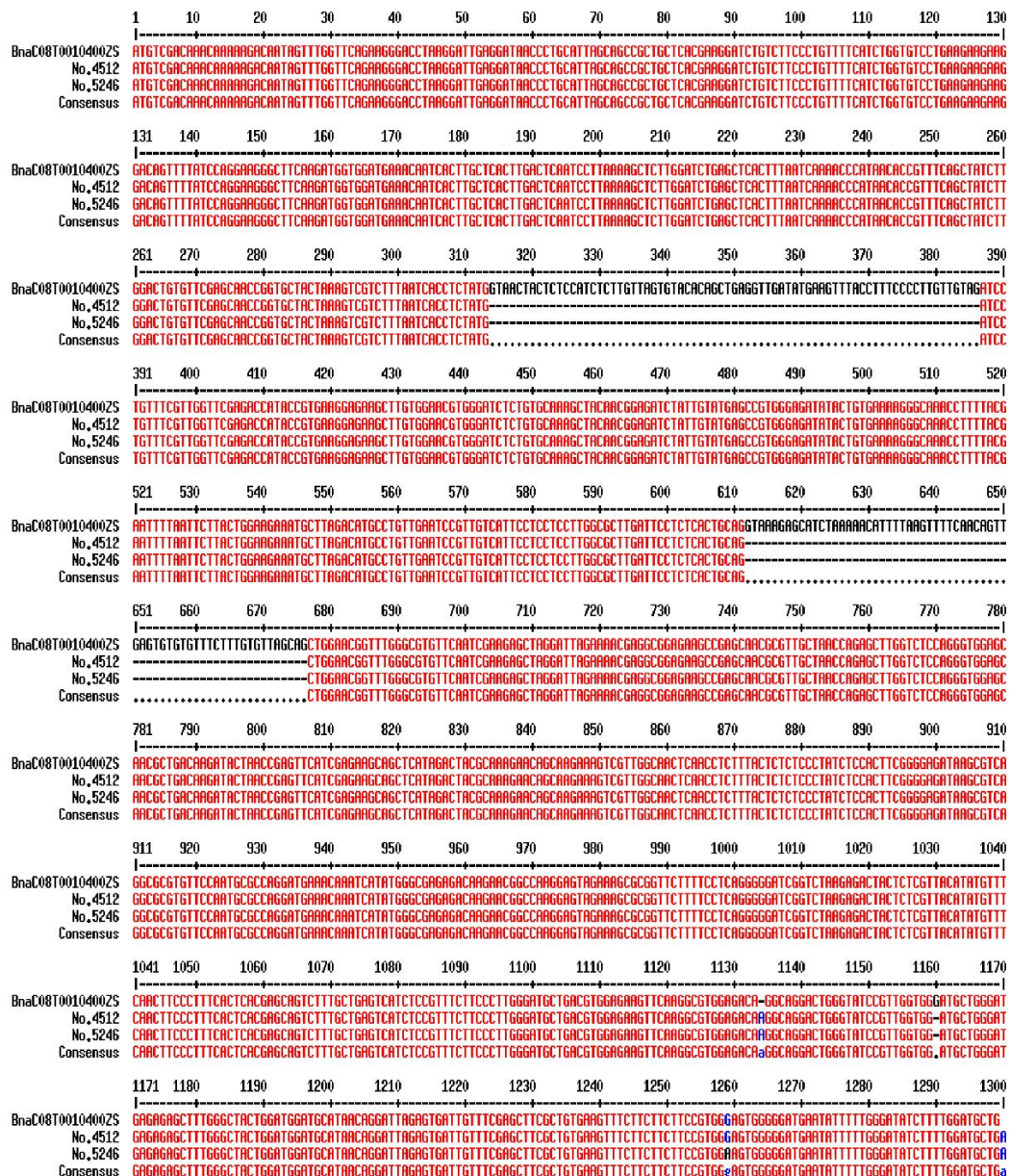


Fig. S8 Differences between CDSs of *BnaC08G0010400ZS* from the early-flowering parent (No. 4512) and late-flowering parent (No. 5246) with that cloned from the reference genome ZS11

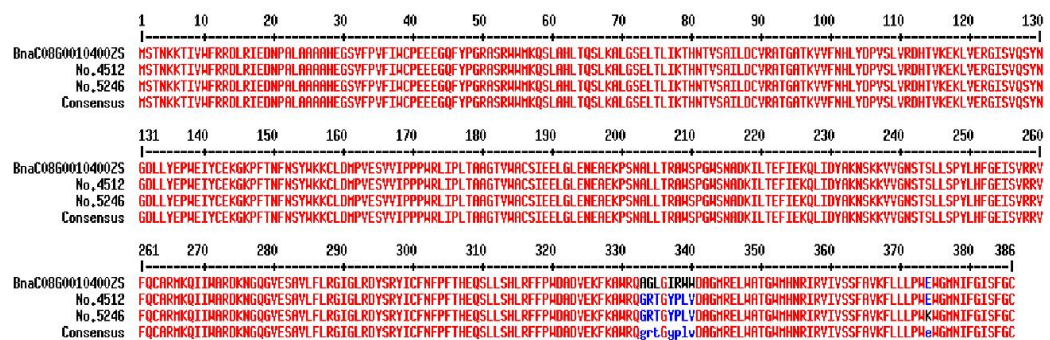


Fig. S9 Differences between CDSs of *BnaC08G0010400ZS* cloned from the early-flowering parent (No. 4512) and late-flowering parent (No. 5246) with that cloned from the reference genome ZS11

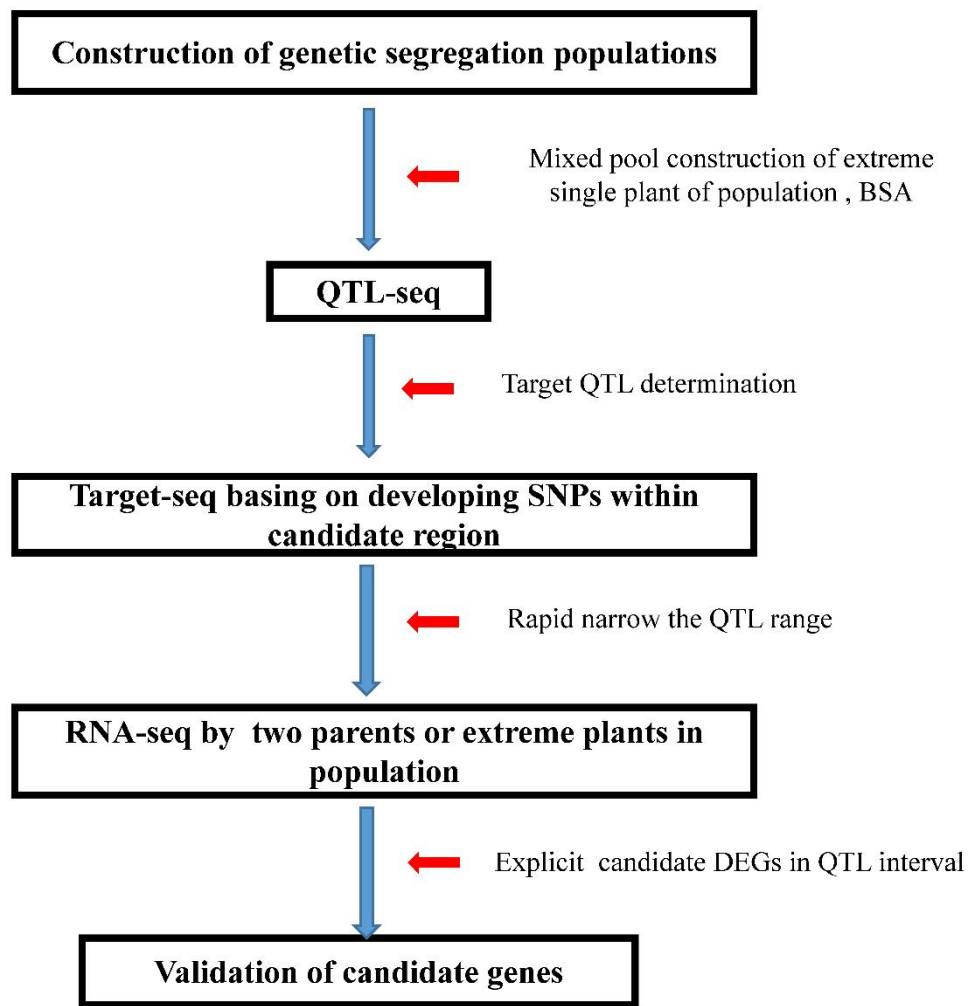


Fig.S10 A rapid fine mapping strategy of quantitative trait locus