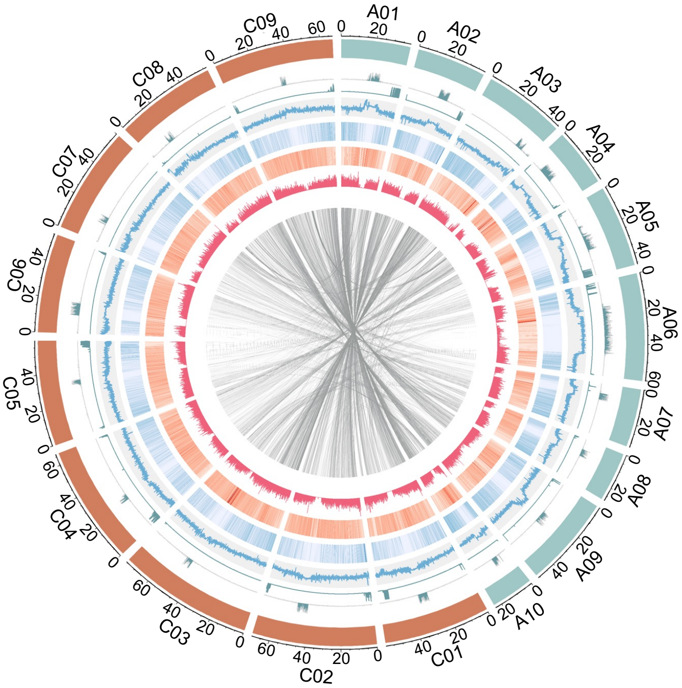
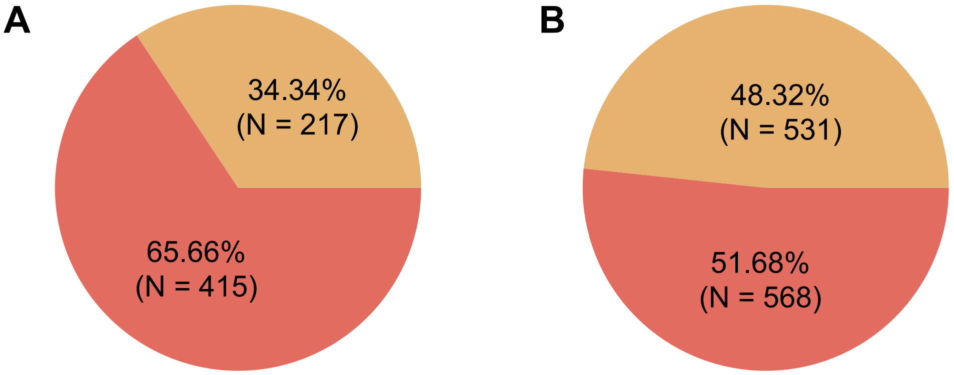
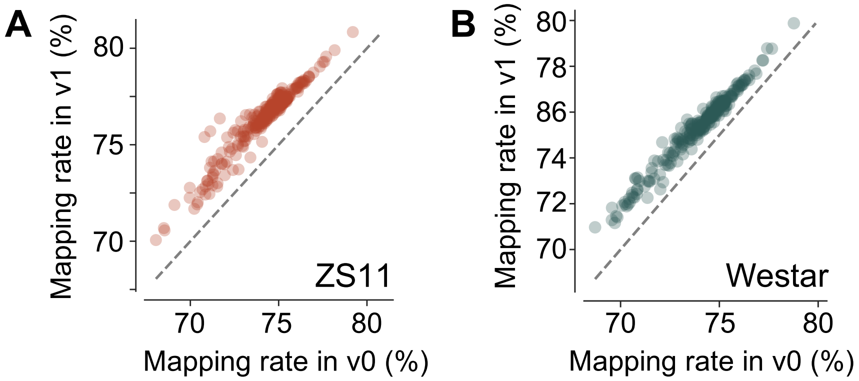


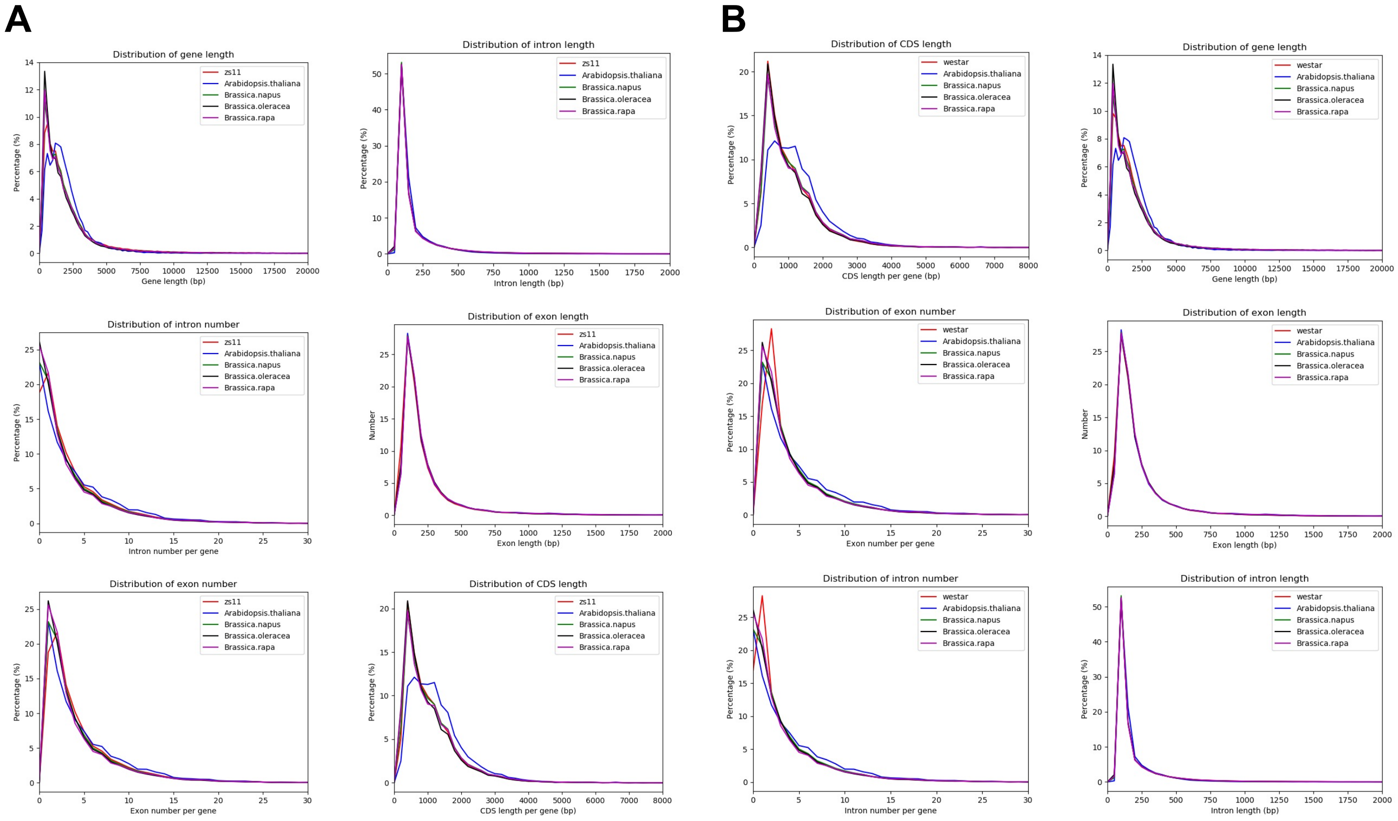
Supplementary Figure 1. Overview of the Westar v1 genome. Tracks from outermost to innermost represent centromere-specific repeats, telomere-specific repeats, GC content, gene density, transposon density, tandem repeats, and covariate blocks between subgenomes. Darker colors in the heatmap indicate higher densities.



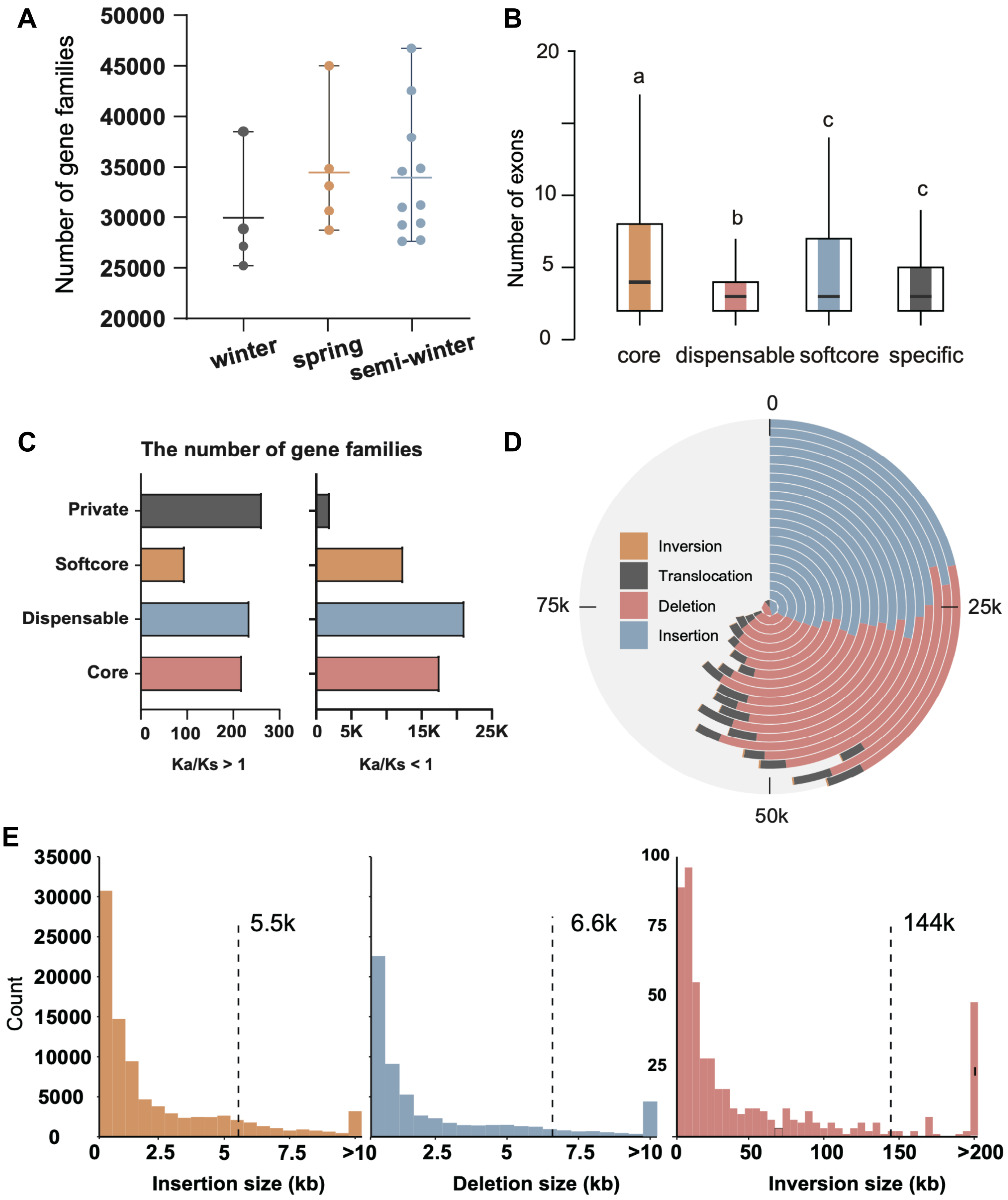
Supplementary Figure 2. Number and proportion of genes expressed in the centromere region of the ZS11 genome. (A) is ZS11 v0 genome, and **(B)** is ZS11 v1 genome.



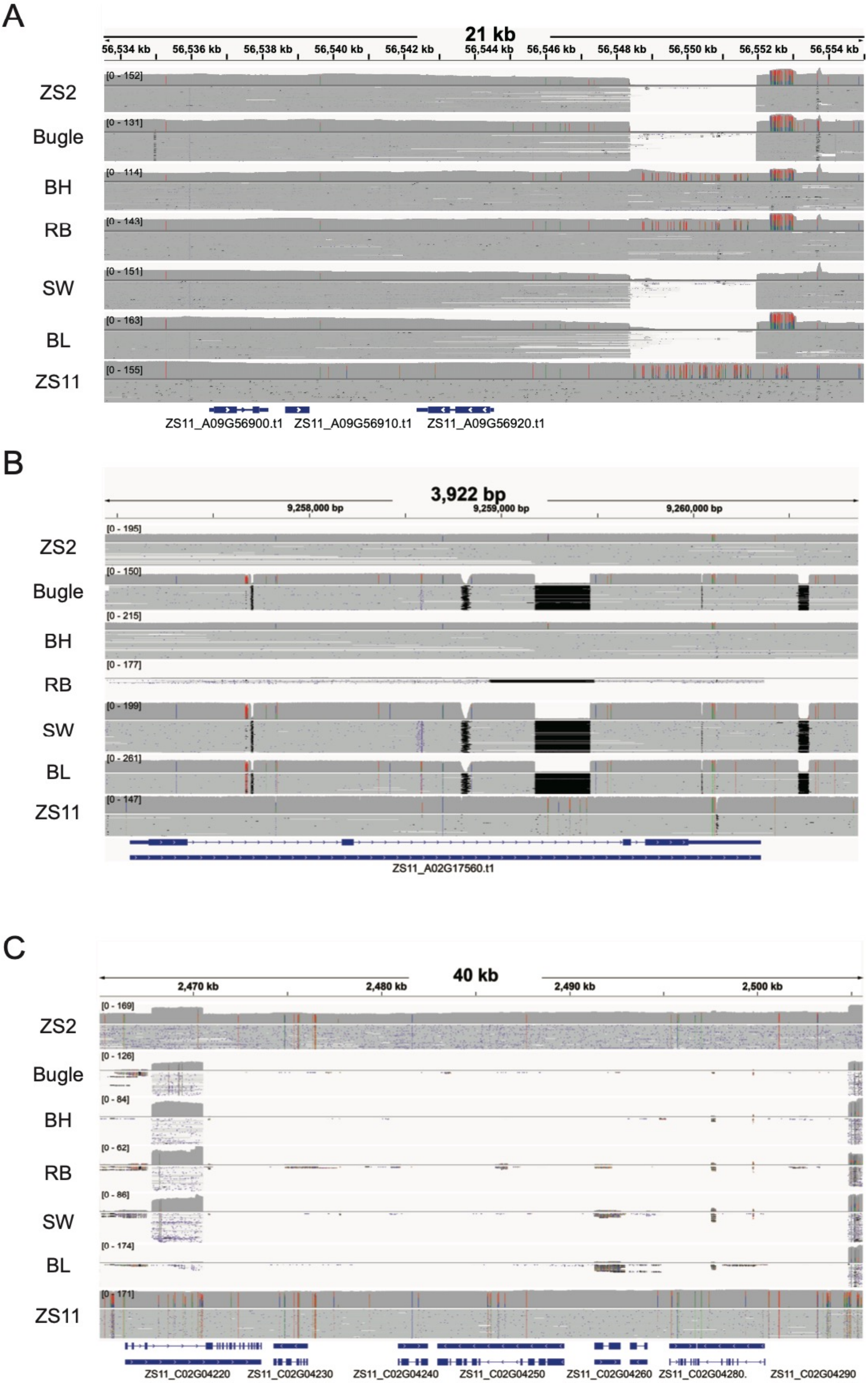
Supplementary Figure 3. The RNAseq mapping rates in the ZS11 and Westar genome. The axes represent RNAseq mapping rates for the v0 and v1 genomes of ZS11 (**A**) or Westar (**B**), with each point indicating an RNAseq sample.



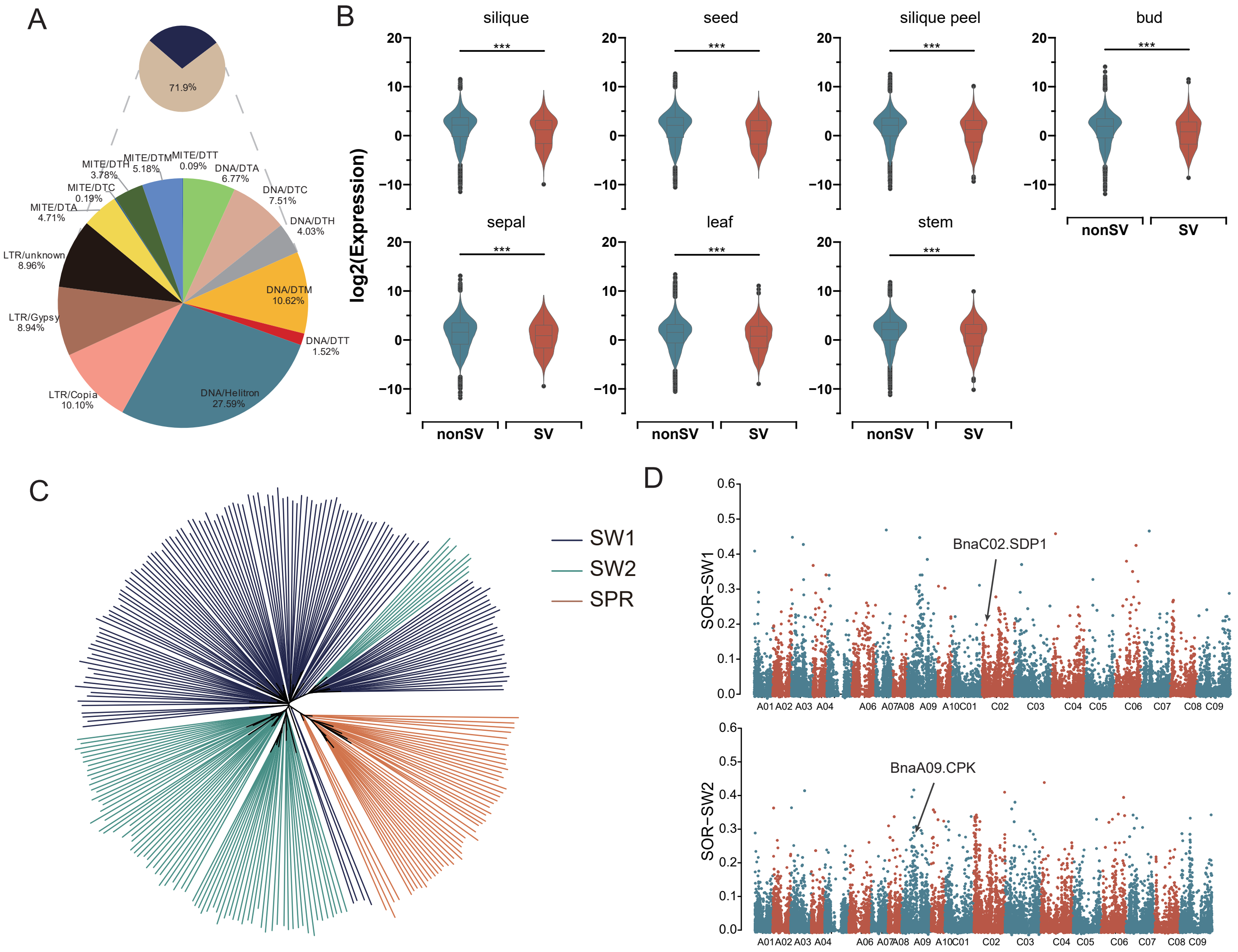
Supplementary Figure 4. Characterization of genes of ZS11, Westar with other closely related species. (A) is ZS11 v1 genome, and **(B)** is Westar v1 genome.



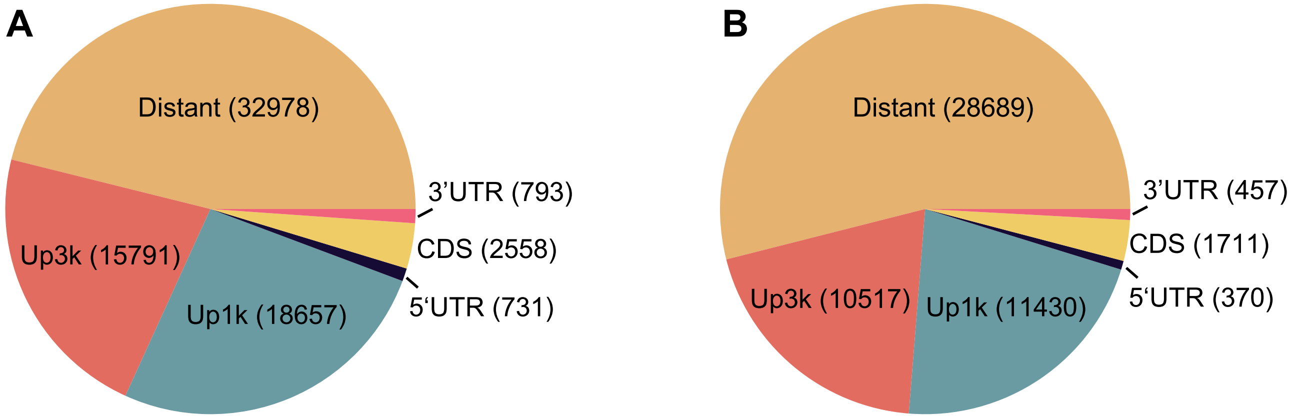
Supplementary Figure 5. Pan-genome and structure variation of *B. napus*. A. Gene families in different ecotype genomes in the pan-genome. **B.** Number of exons of genes in different clustered gene families. **C.** The number of gene families of different types with average Ka/Ks >1 (or Ka/Ks <1). **D.** Number of different variant types of SV in 2 genomes. **E.** Length of insertions, deletions, and inversion SVs across the genome.



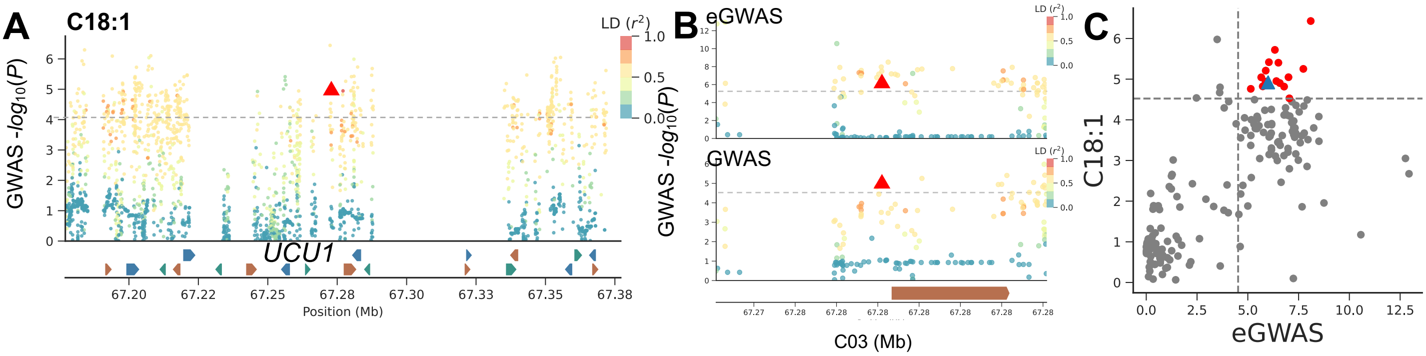
Supplementary Figure 6. Validation of *BnaA09.CYP78A9*(A), *BnaA02.FT*(B) and *BnaC02.FLC*(C) structural variation using raw long reads mapped to the ZS11 genome. A. A 3.9-kb CACTA-like ET inserted upstream of the *CYP78A9* promoter region in ZS11 (Song *et al.*, 2020). **B.** A 200-bp PAV was found in different ecotypes. **C.** A large deletion including the region of *BnaC02.FLC* was detected in ZS11 and ZS2 ecotypes (Song *et al.*, 2020).



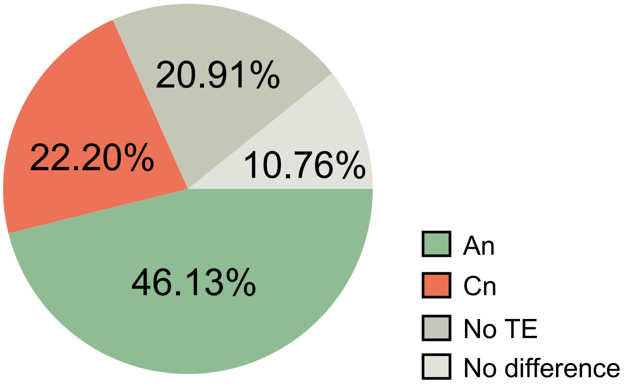
Supplemental Figure 7. The effects of TEMSV on gene expression and the differential distribution of SVs in subpopulations. A. The summary of TE-medicated SVs. **B.** Expression level of SV associated and non-SV gene in different tissues (p-value < 0.001, two-tailed Student's t-test for TPM). N (nonSV) = 107,640; n (SV) = 4,064. **C.** Neighbor-joining tree of 505 accessions of three ecotypes were constructed based on SVs. **D.** Genetic differentiation index F_{st} of spring accessions and different semi-winter accessions.



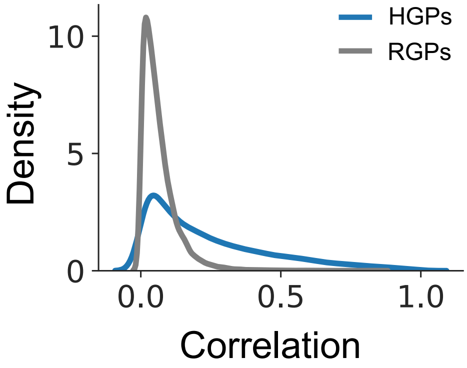
Supplementary Figure 8. Proportion of TEMSVs among subgenomes. (A) is An subgenome, and **(B)** is Cn subgenome.



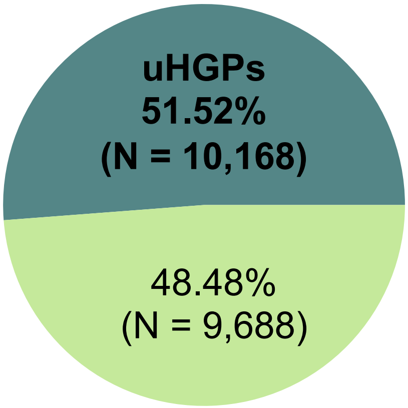
Supplementary Figure 9. *BnaC03.UCU1* are key candidate genes affecting C18:1. A. Manhattan plot of *BnaC03.UCU1* associated loci. The colors on the dots represent the LD between the variant and the Lead SNP, the bottom plot indicates the gene structure in the locus. **B.** *BnaC03.UCU1* localized eGWAS as well as GWAS results. Red triangles indicate 592 bp SV. bottom panel indicates the structure of *BnaC03.UCU1*. **C.** Horizontal coordinates indicate log-transformed *P* values of *BnaC03.UCU1* eGWAS variants in the C03 locus. Vertical coordinates indicate log-transformed *P* values for the C18:1 GWAS variant in the C03 locus. Blue triangles indicate 592 bp SV.



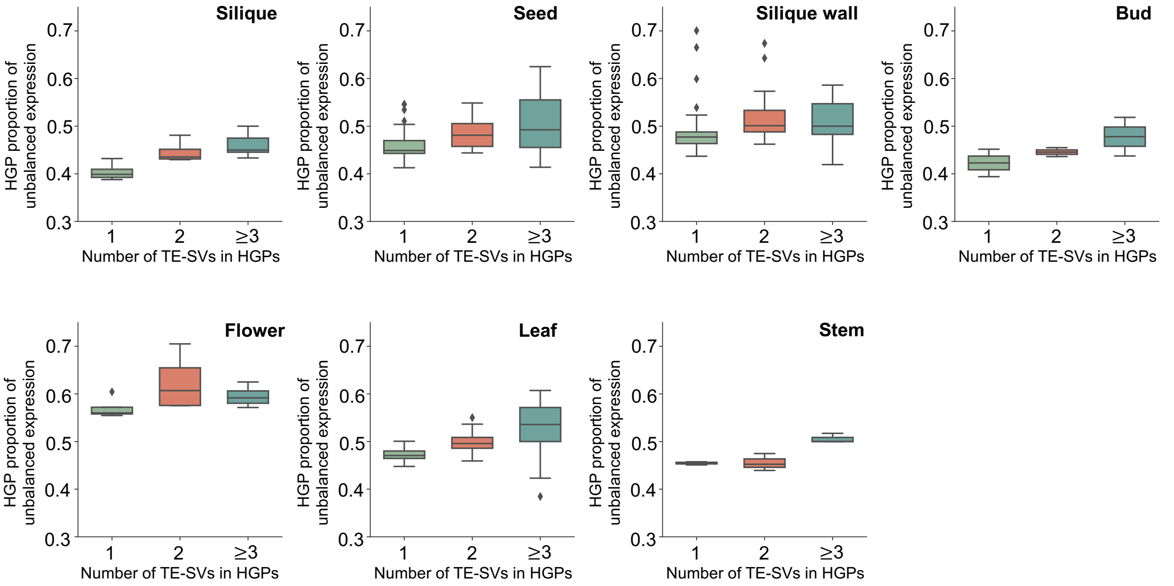
Supplementary Figure 10. Distribution of TEMSV in HGP. Red represents HGPs with a high number of gene TEMSVs in An, green represents HGPs with a high number of gene TE related SVs in Cn, light gray represents HGPs without TEs, and dark gray represents HGPs with no difference in the number of TEs between subgroups.



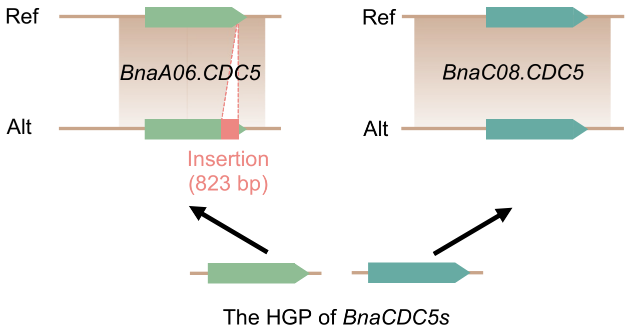
Supplementary Figure 11. Correlation distribution of HGP expression in seed at 20 DAF. The blue line indicates the distribution of absolute values of expression correlation between homoeologous copies in HGP. The gray line indicates the correlation distribution performed for 20,000 RGPs.



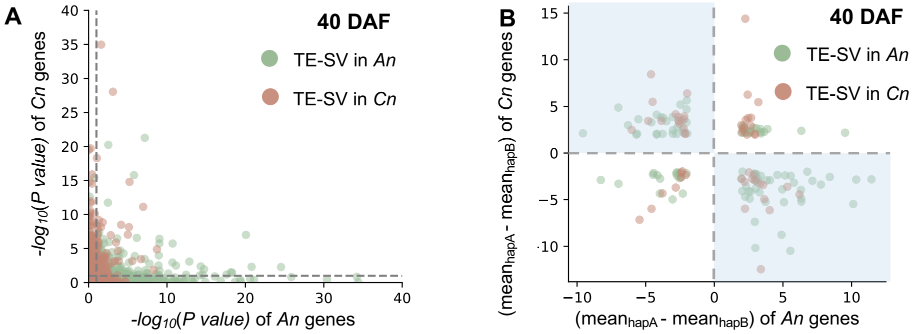
Supplementary Figure 12. Proportion of uHGPs in the ZS11 tissues.



Supplementary Figure 13. Effect of the TEMSVs number on the unbalanced expression HGPs in various tissues.



Supplementary Figure 14. Structural view of *BnaCDC5s*, showing a 823 bp insertion in *BnaA06.CDC5*.



Supplementary Figure 15. Changes in HGP are affected by TEMSV at 40 DAF. A. The degree of change in HGP expression at 40 DAF. Green dots indicate TEMSV located near the An copy of HGP. Red dots indicate TEMSV located near the Cn copy of HGP. The horizontal coordinate represents the *P* values for expression differences between An genes in HGPs with and without TEMSV, calculated by Student's t-test. The vertical coordinate represents the *P* values for expression differences between Cn genes in HGPs with and without TEMSV, calculated by Student's t-test. **B.** The direction of change in HGP expression at 40 DAF. Green dots indicate TEMSV located near the An copy of HGP. Red dots indicate TEMSV located near the Cn copy of HGP. The horizontal coordinate indicates the difference between the expression means in the HGP between An genes in HGPs with and without TEMSV. The vertical coordinate indicates the difference between the expression means in the HGP between Cn genes in HGPs with and without TEMSV. Shading indicates that homoeologous genes in HGP change in the opposite direction.