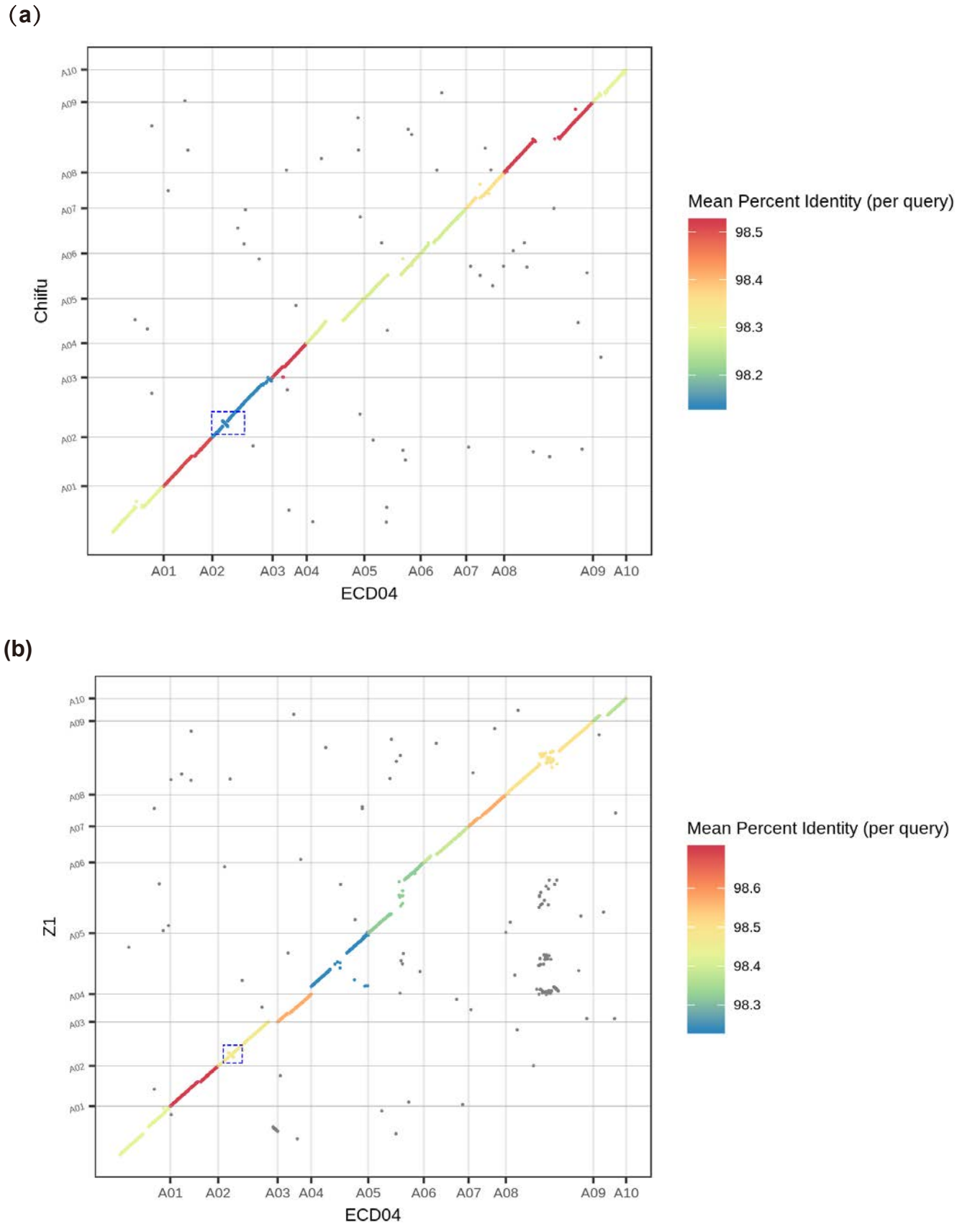


Figure S1. Genome alignment between the Chiifu-ECD04 and Z1- ECD04 genomes. (a) Genome alignment between Chiifu and ECD04. The x axis is the position in ECD04 and the y axis is the positions in Chiifu genome. **(b)** Genome alignment between Z1 and ECD04. The x axis shows the position in ECD04 genome and the y axis is the position in Z1 genome. The color of dots represents the identity of alignments. The blue boxes represent a large inversion with the length of ~3.5 Mb on the A03 chromosome of the ECD04 genome (6.9 Mb-10.4 Mb).

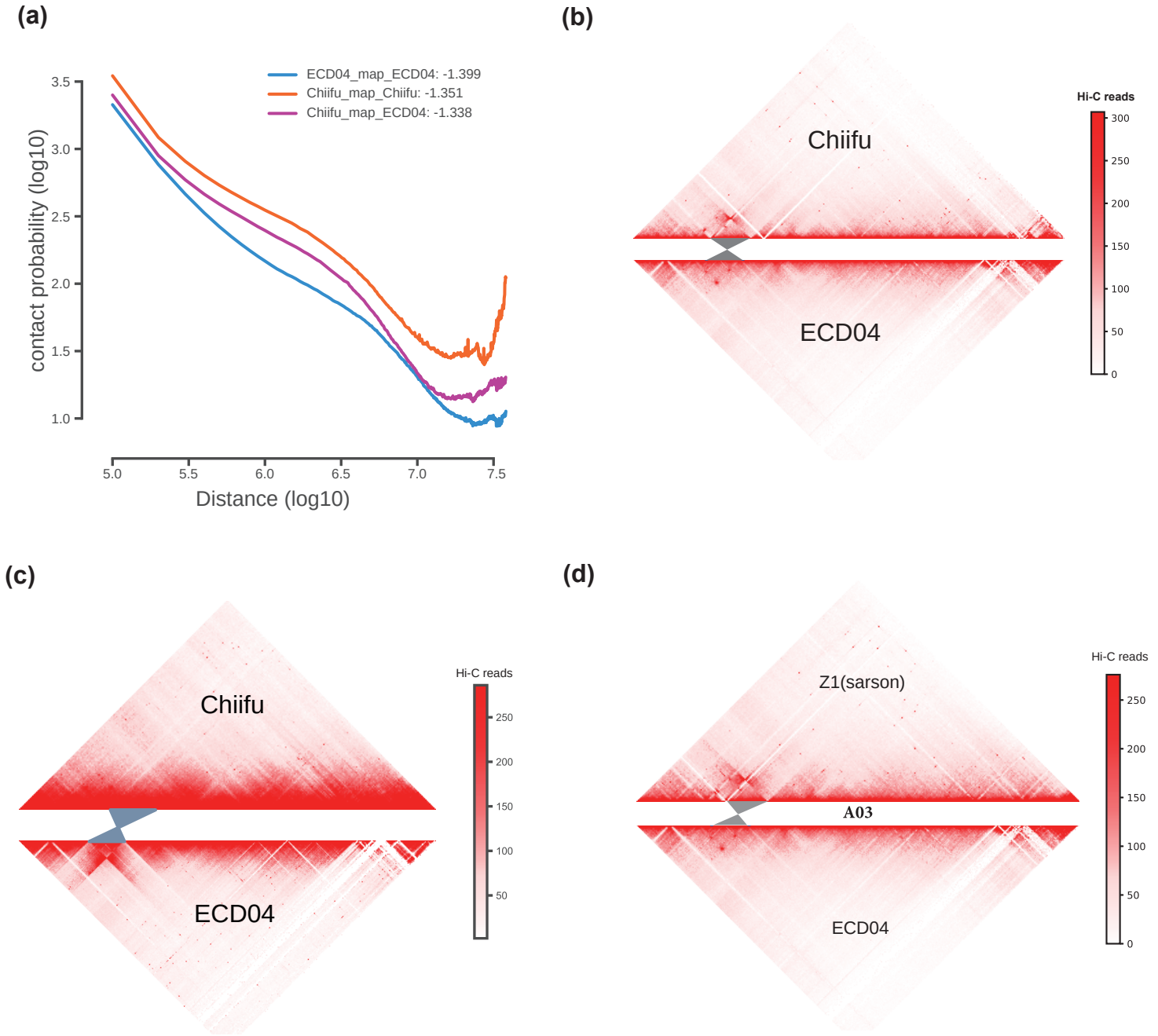


Figure S2. Hi-C data analysis of ECD04. (a) The relationshiop between probability of contact and genomic distance on genome at 100kb resolution. Blue line represents the interaction decay curve of the ECD04 reads mapped to ECD04 genome(interaction decay exponent (IDE) = -1.399); orange line represents the interaction decay curve of the Chiifu reads mapped to Chifu genome (IDE=-1.351). Purple line represents the interaction decay curve of the Chiifu reads mapped to ECD04 genome (IDE=-1.338). **(b-d)** The Hi-C data validation of a large inversion in the A03 chromosome. **(b)** The Hi-C heatmap of ECD04 reads mapped to the ECD04 and Chiifu genomes. There is an abnormal interaction region in the Chiifu genome. **(c)** The Hi-C heatmap of Chiifu reads mapped to the ECD04 and Chiifu genomes. There is an abnormal interaction region in ECD04 genome. **(d)** The Hi-C heatmap of ECD04 reads mapped to the ECD04 and Z1 genomes. There is an abnormal interaction region in A03 chromosome of Z1 genome.

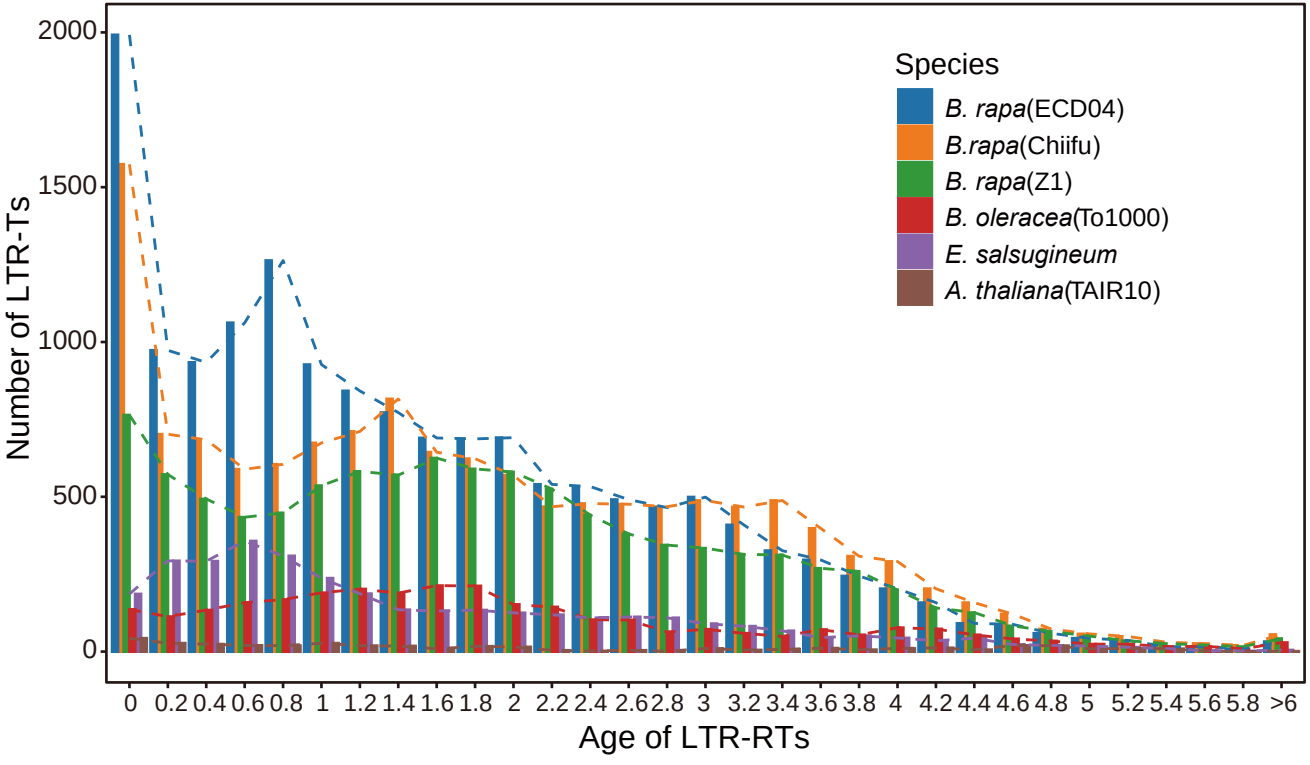
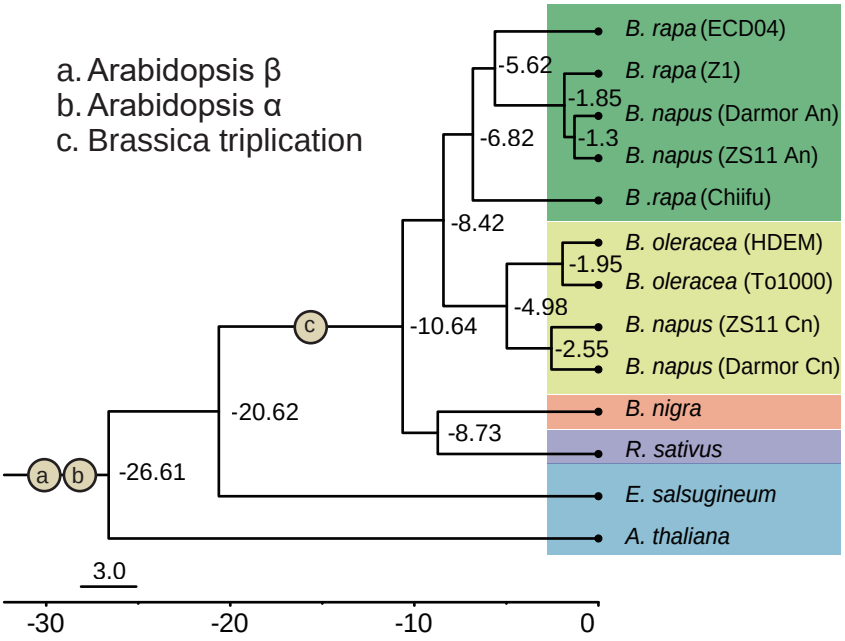


Figure S3. The insert time of intact LTR retrotransposons in the ECD04 genome. The frequency distribution of LTR-RT insertion times in six genomes. ECD04 genome underwent three waves (0~0.4 Mya, 0.6~1 Mya and 2.8~3.2 Mya) of LTR-RT expansion since it diverged from *B. oleracea* (approximately 3.9 Mya), which are not exactly the same as those in Chiifu genome (0~0.4 Mya, 1.0~1.4 Mya and 3~3.4 Mya) . The synonymous replacement rate r is chosen to be $1.5*10^{-8}$ mutations site/year.

(a)



(b)

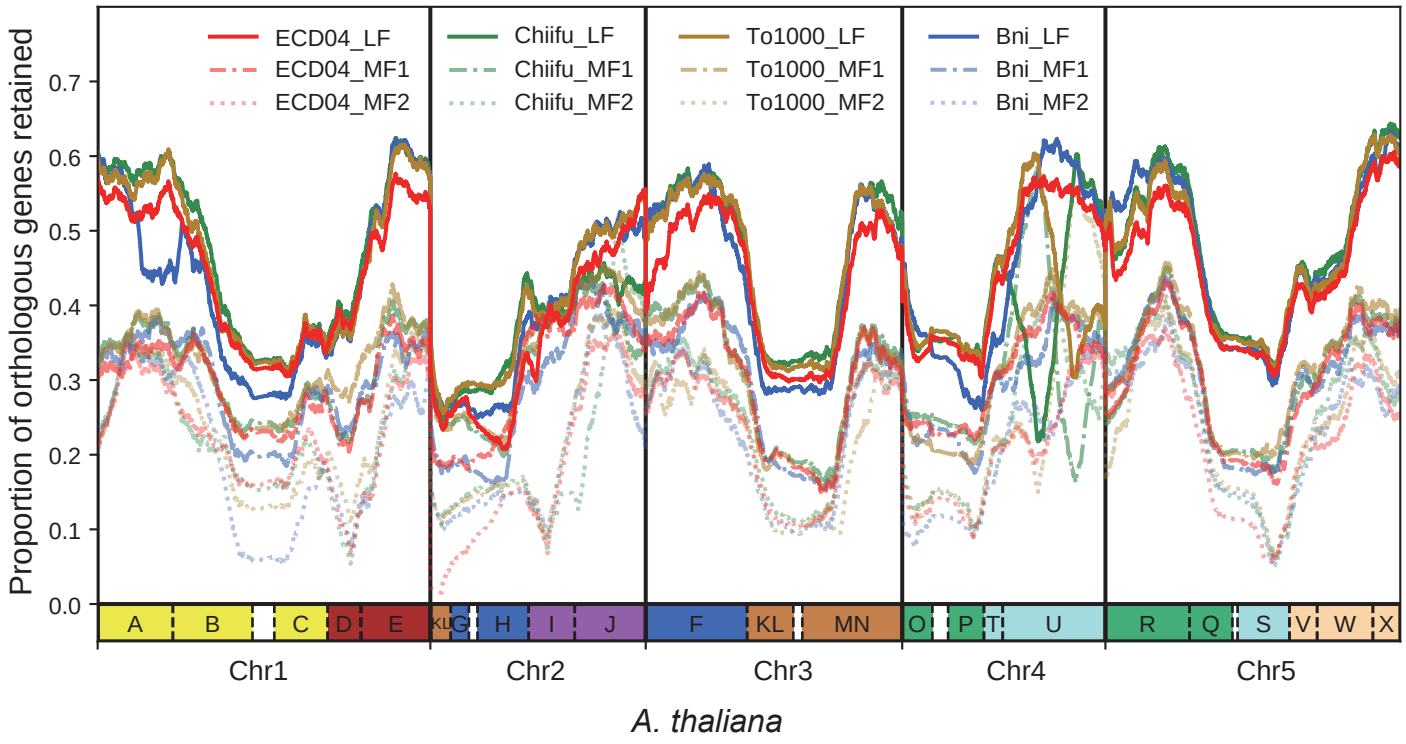


Figure S4. Phylogenetic tree of ECD04 and retention of ancestral genes in ECD04 genome. (a) Phylogenetic tree of ECD04. **(b)** Proportion of retained ancestral genes in four genomes. Red lines represent ECD04 genome; green lines represent Chiifu genome; brown lines represent To1000 genome and blue lines represent *B. nigra* genome. Solid lines represent LF subgnome; dot dash lines represent MF1 subgenome and dashed lines represent MF2 subgnome. The squares with different colors at the bottom represent the distribution of 22 ancestral crucifer karyotype blocks (A–X) in *A. thaliana* genome.

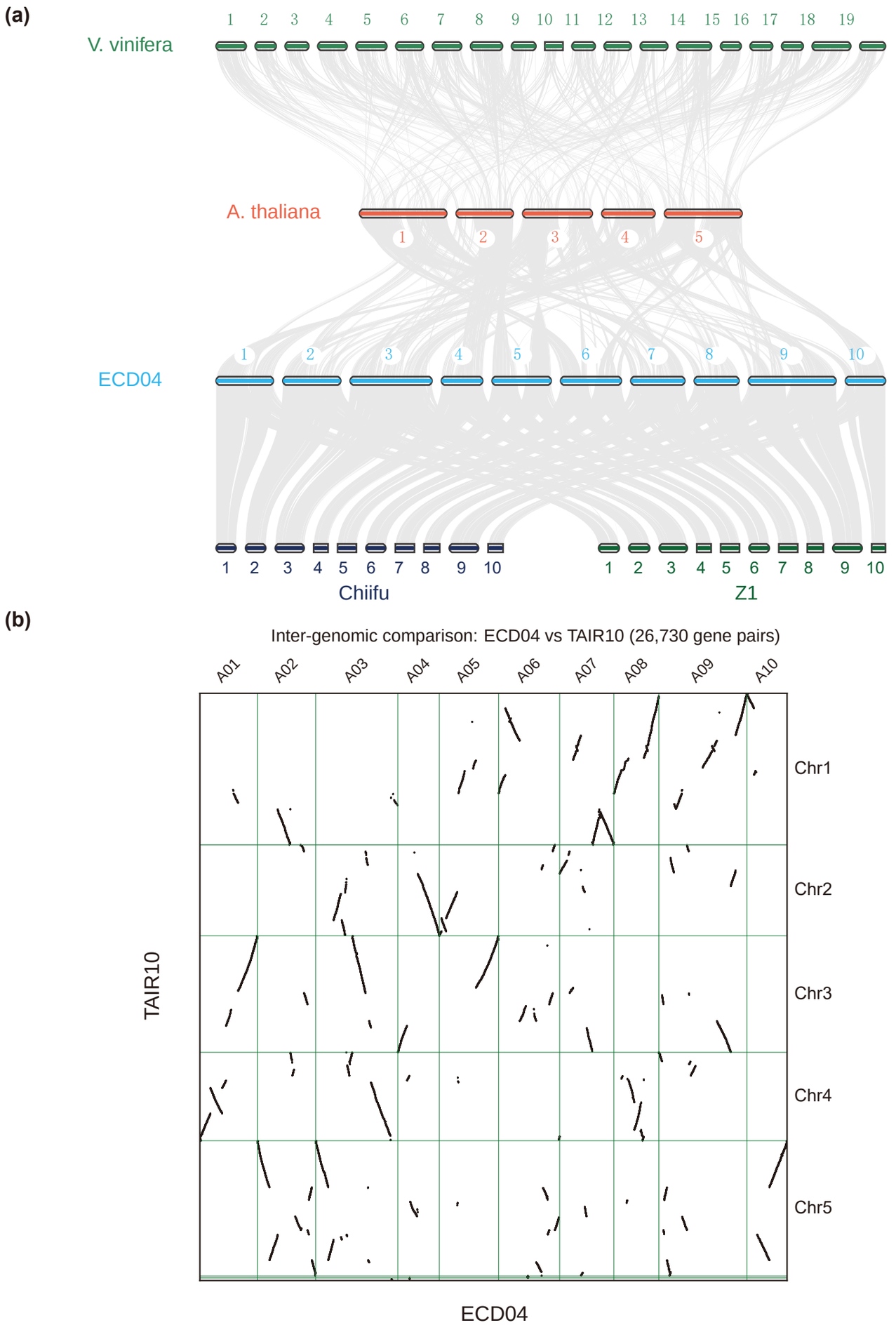


Figure S5. The evolution process of the *B. rapa* (ECD04) genome. (a) Evolutionary scenario and genome duplication of *B. rapa* (ECD04). *A. thaliana* experienced two round WGDs relative to *V. vinifera*, and then *B. rapa* experienced a WGT event. **(b)** Retention of paralogs in *B. rapa* after *Brassica* WGT.

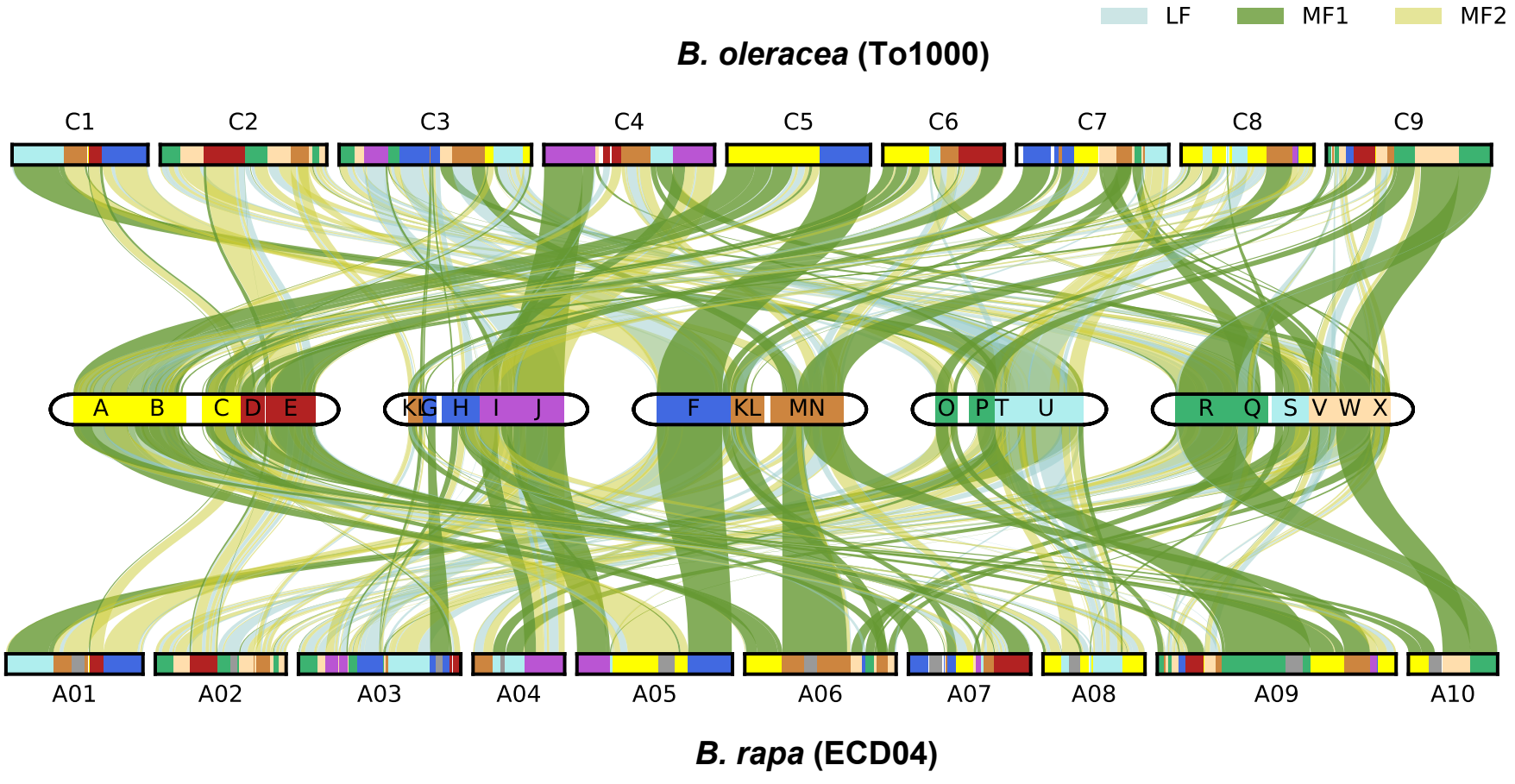


Figure S6. ACK blocks in the *B. rapa* (ECD04) and *B. oleracea* (To1000) genomes. 22 syntenic blocks are defined and labeled from A to X (colored) previously reported in *A. thaliana*. Light blue, green, light yellow stripes represent syntenic blocks of LF, MF1, and MF2 subgenomes in the ECD04 and To1000 genomes.

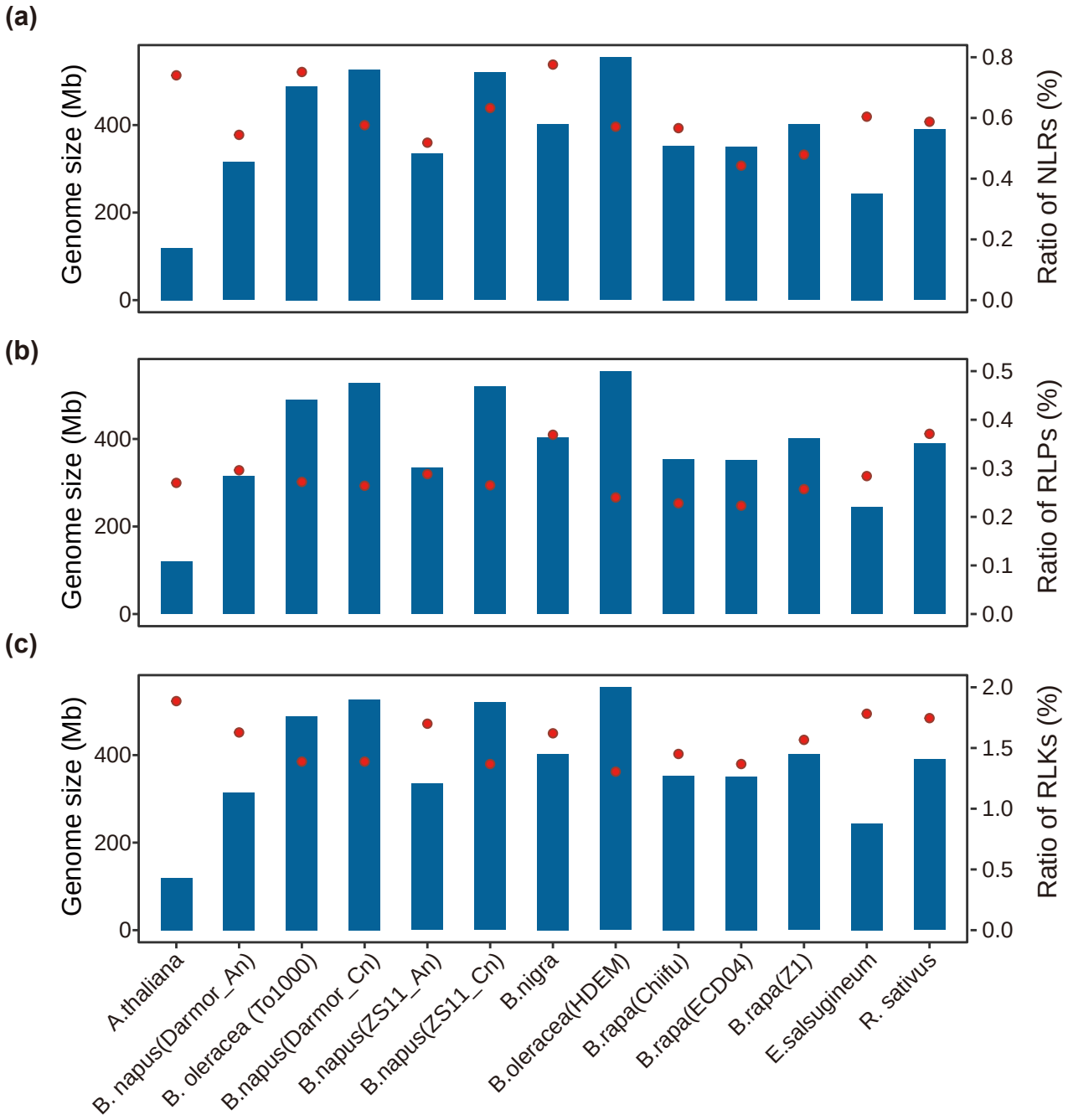


Figure S7. Comparison of R gene ratios and genome sizes. No clear relationship between the genome size and the ratio of R genes was found.

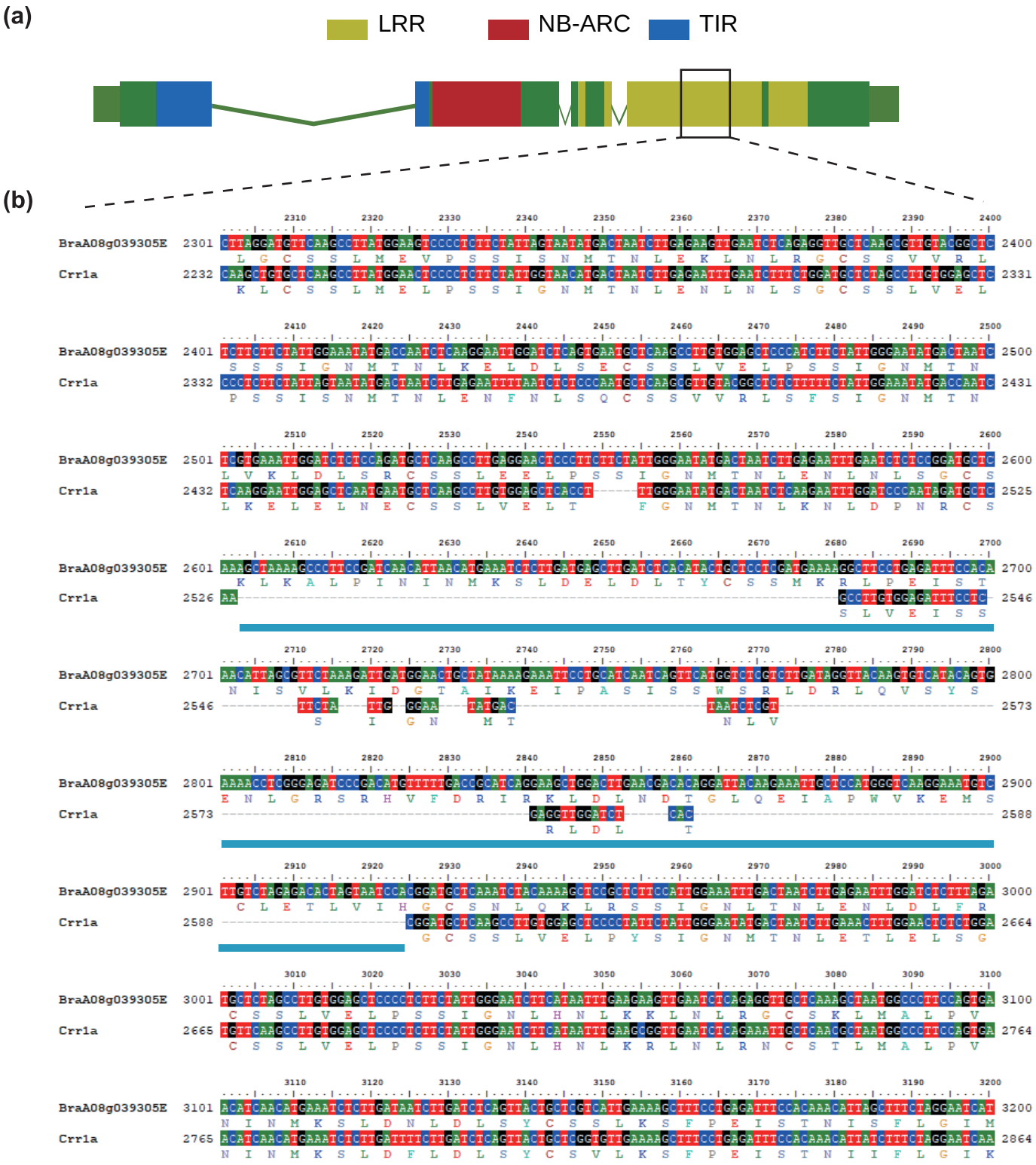


Figure S8. Sequence alignment of *BraA08g039305E* (*CRA8.2.4*) and *Crr1a*. (a) Gene structure of *BraA08g039305E* (*CRA8.2.4*). **(b)** Sequence alignment in LRR domain between *BraA08g039305E* and *Crr1a*.

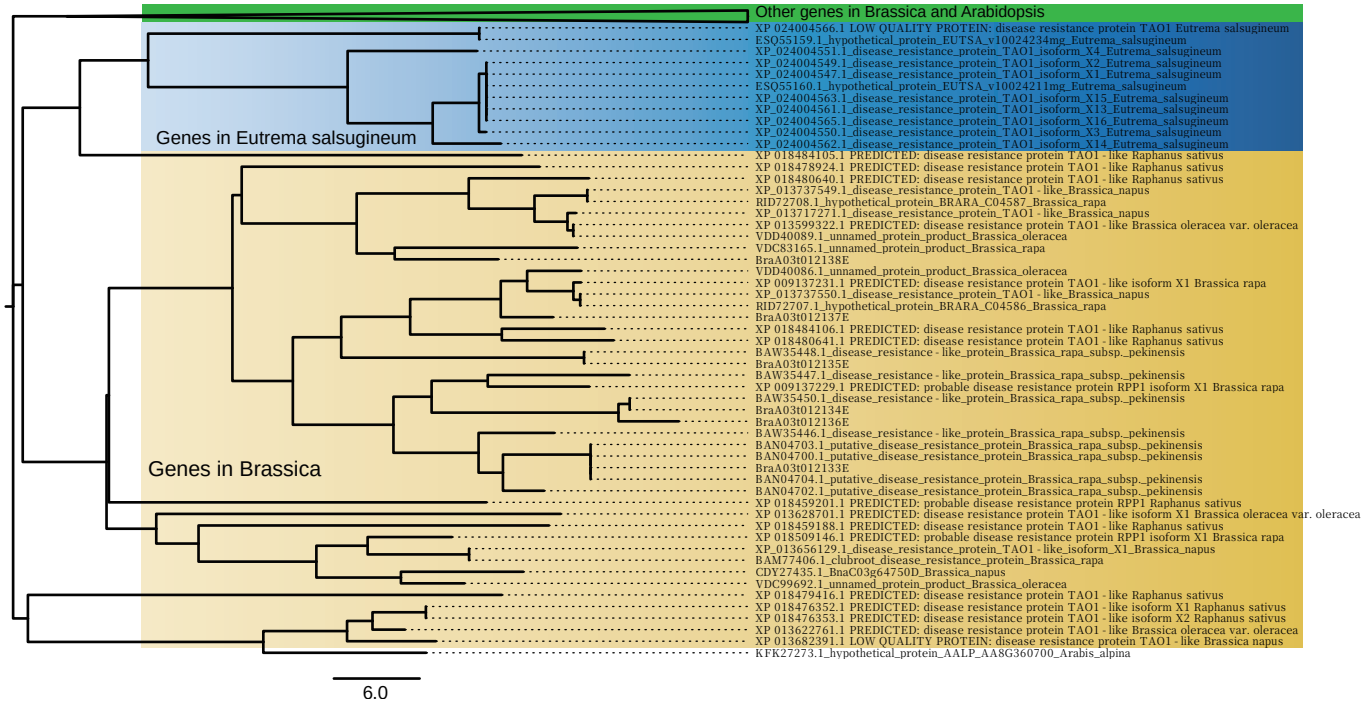


Figure S9. Neighbour-joining tree of homologous genes of CR genes. The green background represents homologous genes in *A. thaliana*; the blue background represents homologous genes in *E. salsugineum* and the yellow background represents homologous genes in *Brassica* species.

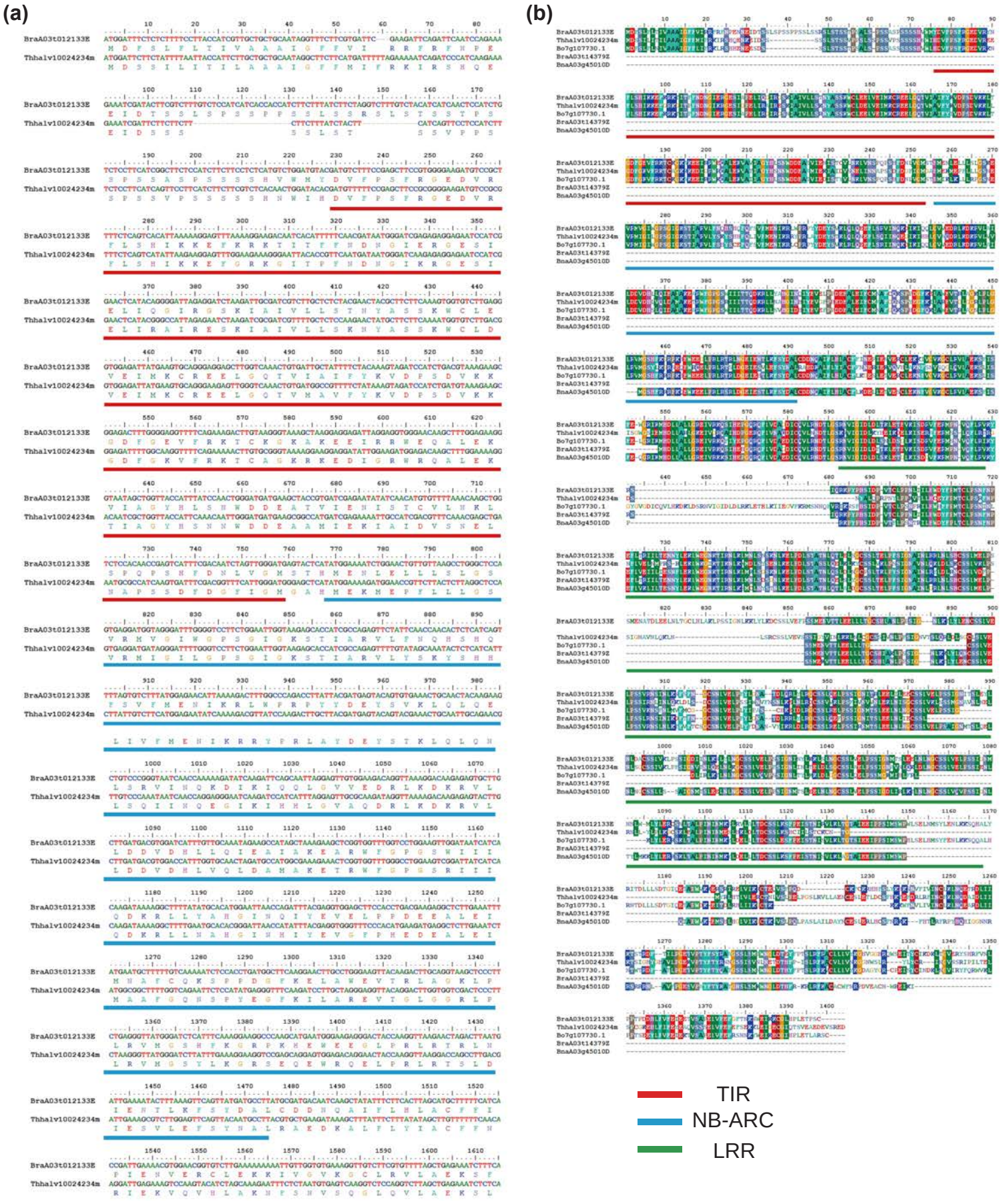


Figure S10. Sequence alignment of homologous genes of *CRA3.7.1*. (a) Comparison of *CRA3.7.1* (*BraA03g012133E*) in ECD04 and *Thhalv10024234* in *E. salsugineum*. **(b)** Sequence alignment of CDS of homologous genes of *CRA3.7.1*.

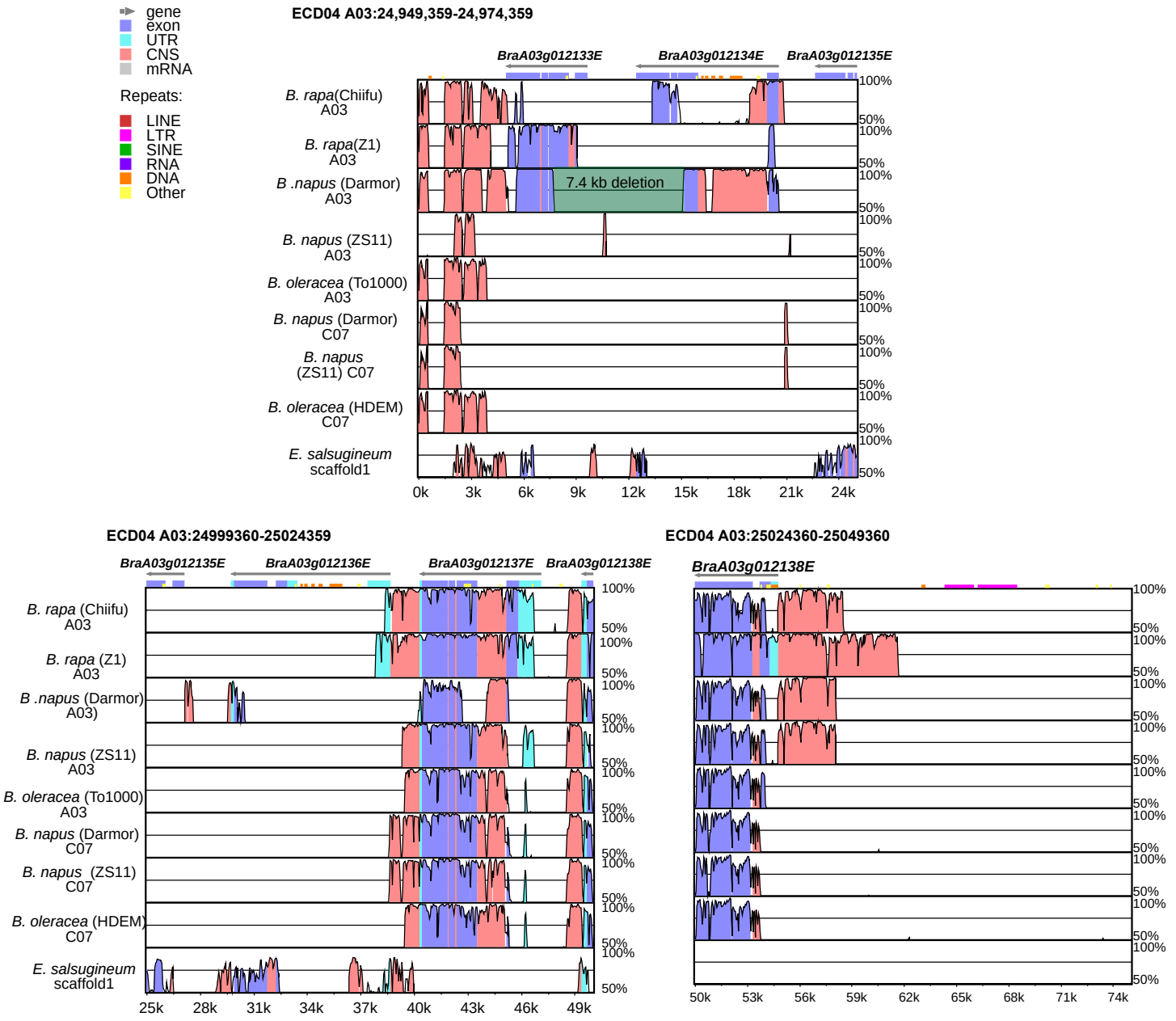


Figure S11. Sequence alignment of genomic regions in *CRA3.7.1* and its homologs using the mVISTA program with "ECD04" as a reference. Gray arrows above the alignment indicate the transcriptional directions of genes. Genome regions are color coded as exons, UTRs and conserved non-coding sequences (CNSs). The identity cutoff of 50% was used for the plots. The Y-axis indicates the percent identity between 50 and 100%. Compared with ECD04, a 7.4 kb deletion (green region) in A03 chromosome of Darmor results in the fusion of *BraA03g012133E* (*CRA3.7.1*) and *BraA03g012134E* (*CRA3.7.2*).

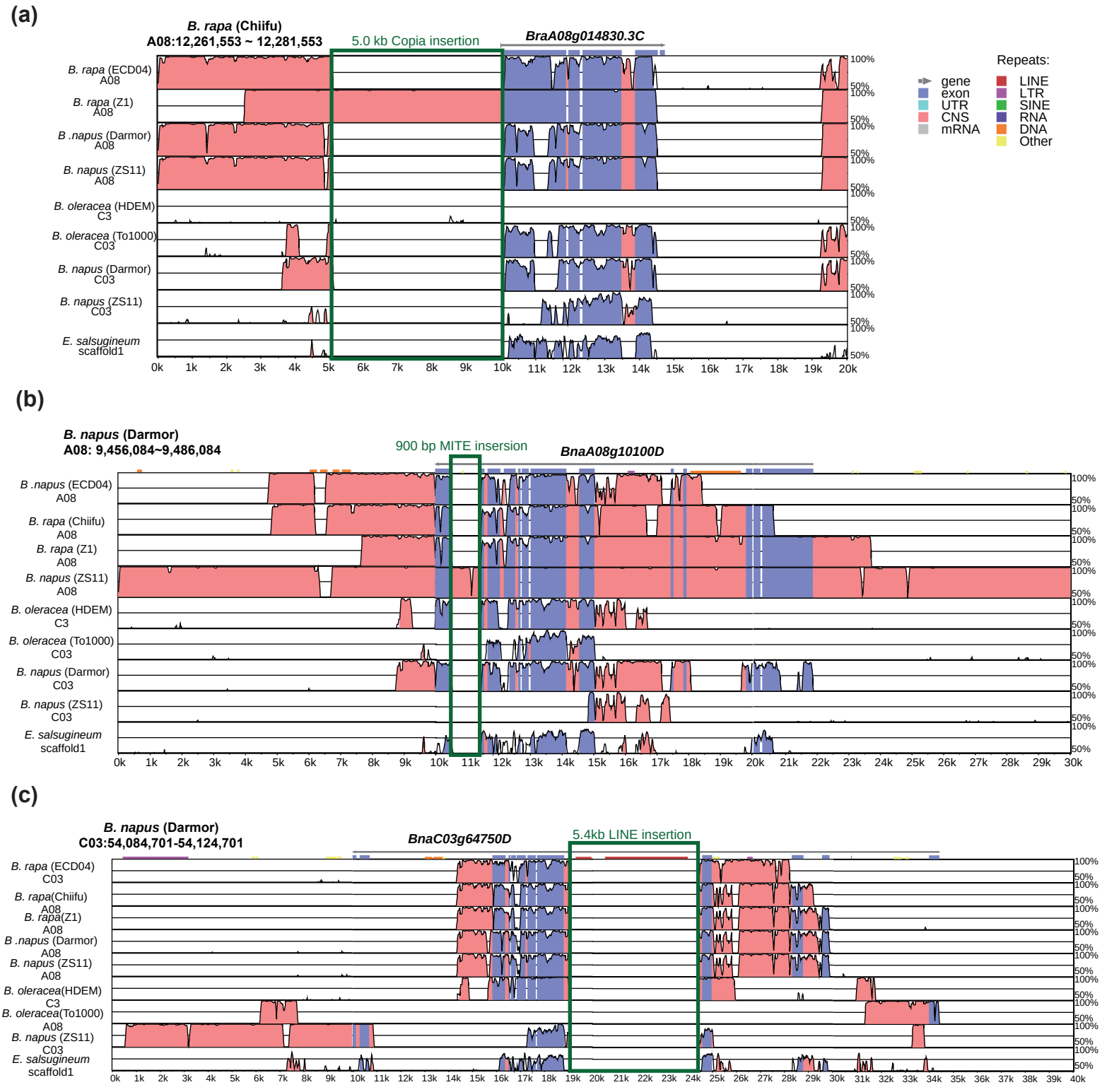


Figure S12. Sequence alignment of genomic regions in *CRA8.2.4* and its homologs. The top gray arrows indicate the transcriptional directions of genes and rectangles with different colors indicate exons of genes and repeats. Genome regions are color coded as exons (purple), UTRs (blue) and conserved non-coding sequences (CNSs) (orange), respectively. The identity cutoff of 50% was used for the plots. The y-axis indicates the identity between sequences. **(a-c)** Sequence alignment with Chiifu **(a)**, "Darmor An" **(b)** and "ZS11 An" **(c)** as a reference.