Figure S1 Morphology of cauliflower Koroso_1401 (**a**) and pointed cabbage OX-heart_923 (**b**).
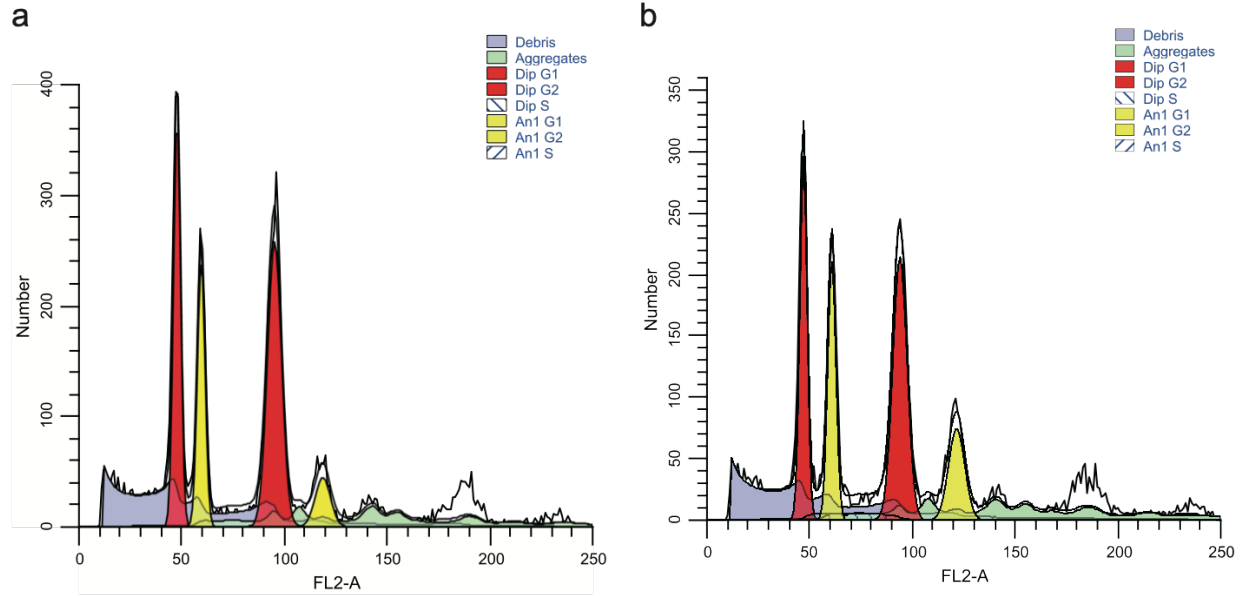
Figure S2 Genome size estimation using flow cytometry analysis for cauliflower Korso (**a**) and cabbage OX-heart (**b**). *B. rapa* Chiifu-401-42 was used as the reference. Red peaks represent the reference *B. rapa*, and yellow peaks represent Korso and OX-heart in (**a**) and (**b**), respectively. Genome sizes of Korso and OX-heart were calculated according to the relative positions of the peaks with the reference *B. rapa*.
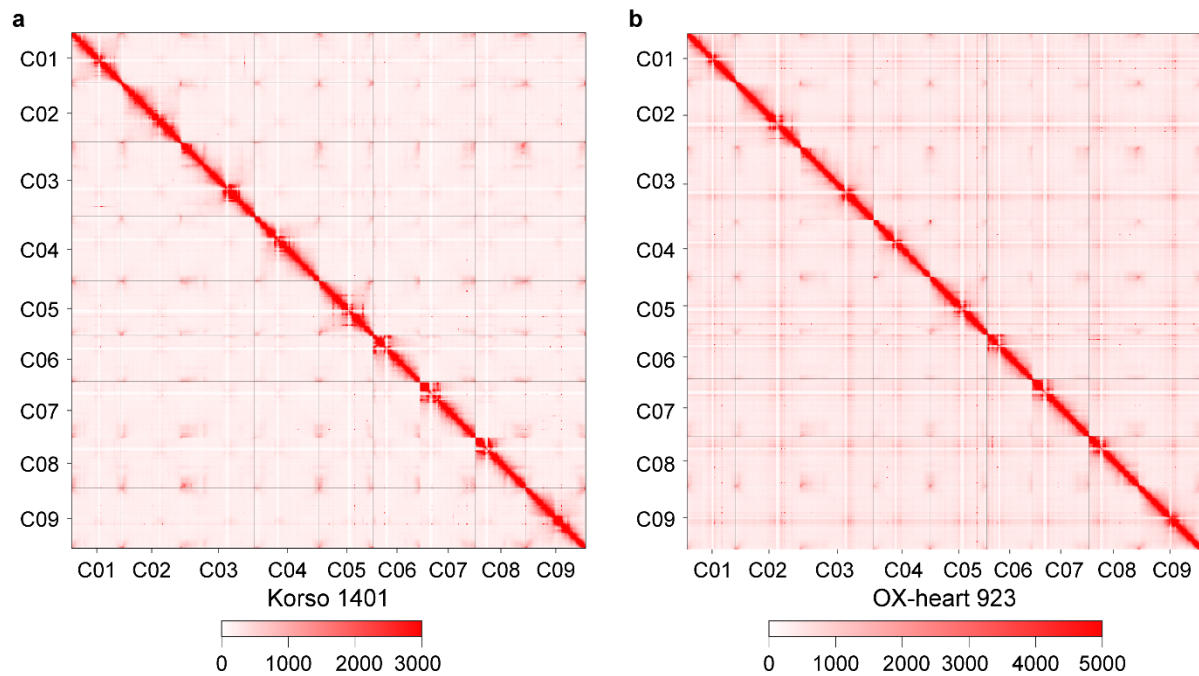
a

Korso 1401

0   1000   2000 3000

b

OX-heart 923

0   1000   2000 3000 4000 5000

Figure S3 Chromosome conformation capture of cauliflower Korso and pointed cabbage OX-heart. **a,b**, Hi-C interaction heatmaps of Korso (**a**) and OX-heart (**b**) genomes. The colored bars indicate the intensity of interaction, which represents the normalized count of Hi-C links between 1-Mb bins.
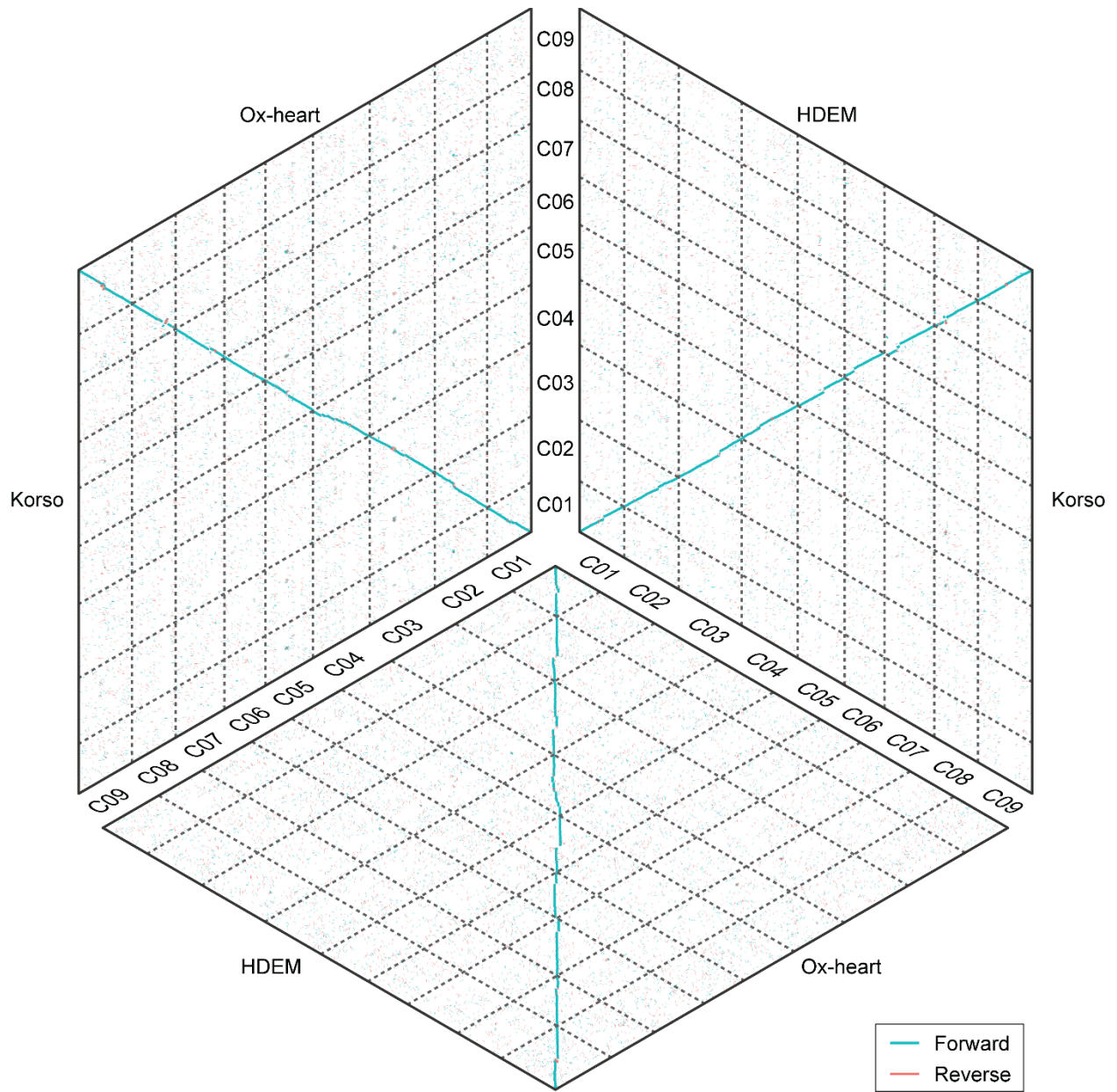
Figure S4 Pairwise comparisons of the pseudo-chromosomes among cauliflower Korso, cabbage OX-heart and broccoli HDEM.
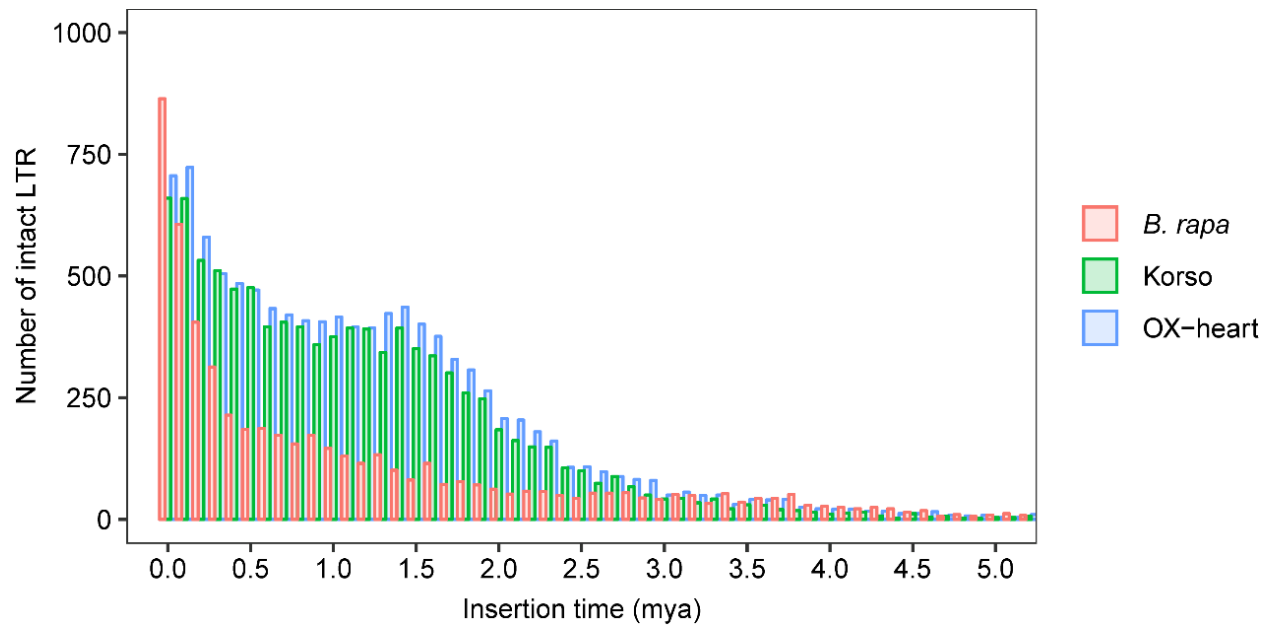
Figure S5 Distribution of estimated insertion times of intact LTR retrotransposons in Korso, OX-heart and *B. rapa* (v3.0) genomes. MYA, million years ago.
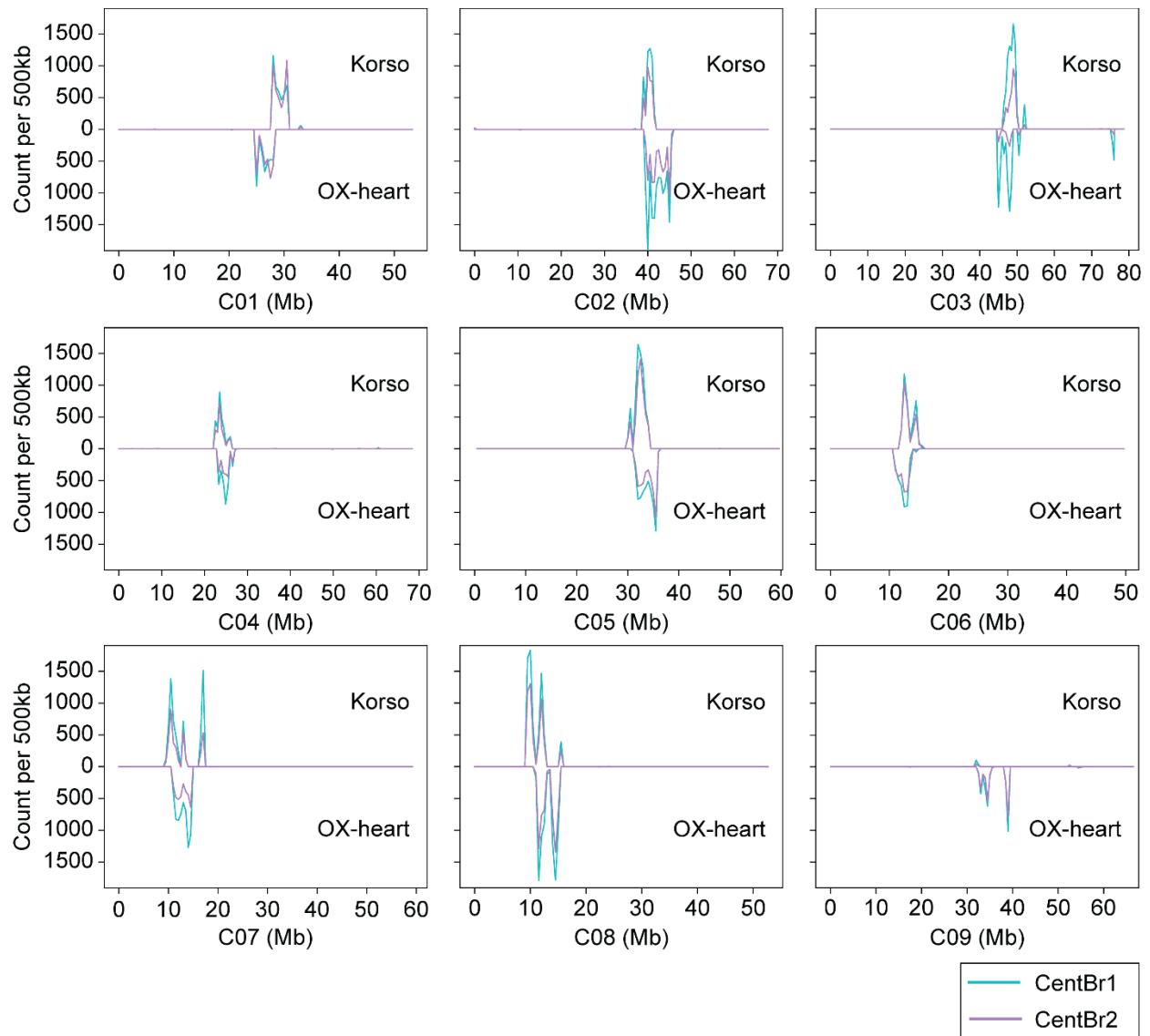
Figure S6 Distribution of centromeric satellite repeats CentBr 1 and CentBr 2 on the nine chromosomes of Korso and OX-heart.
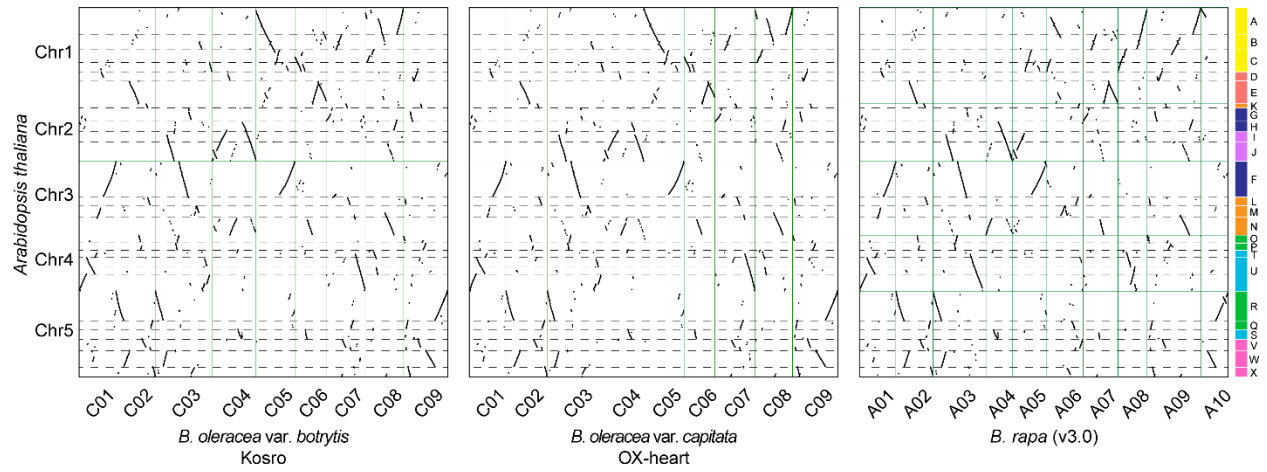
Figure S7 Segmental collinearity between the *A. thaliana* genome and genomes of Korso, OX-heart and *B. rapa*. The conserved collinear blocks labeled A to X are color-coded by inferred ancestral chromosomes according to Wang et al. (2011).
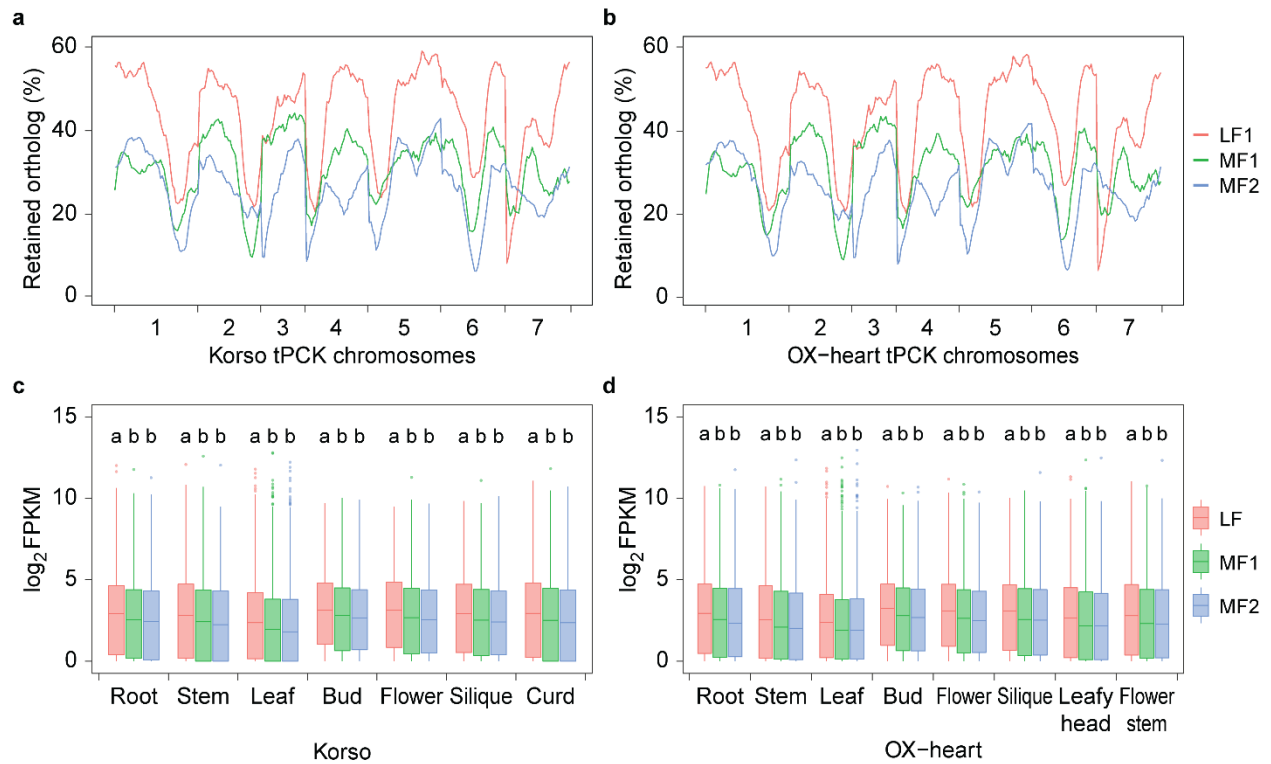
Figure S8 Subgenomes in Korso and OX-heart. **a**,**b**, Percentage of retained gene orthologs in the three subgenomes (LF, MF1 and MF2) of Korso (**a**) and OX-heart (**b**). The x axis denotes the seven supposed translocated Proto-Calepine Karyotypes (tPCK1-7). **c**,**d**, Expression of genes with orthologs identified in all three subgenomes in different tissues of Korso (**c**) and OX-heart (**d**). Group labeled with different letters indicate significant difference at $P < 0.05$ (Tukey's HSD test).
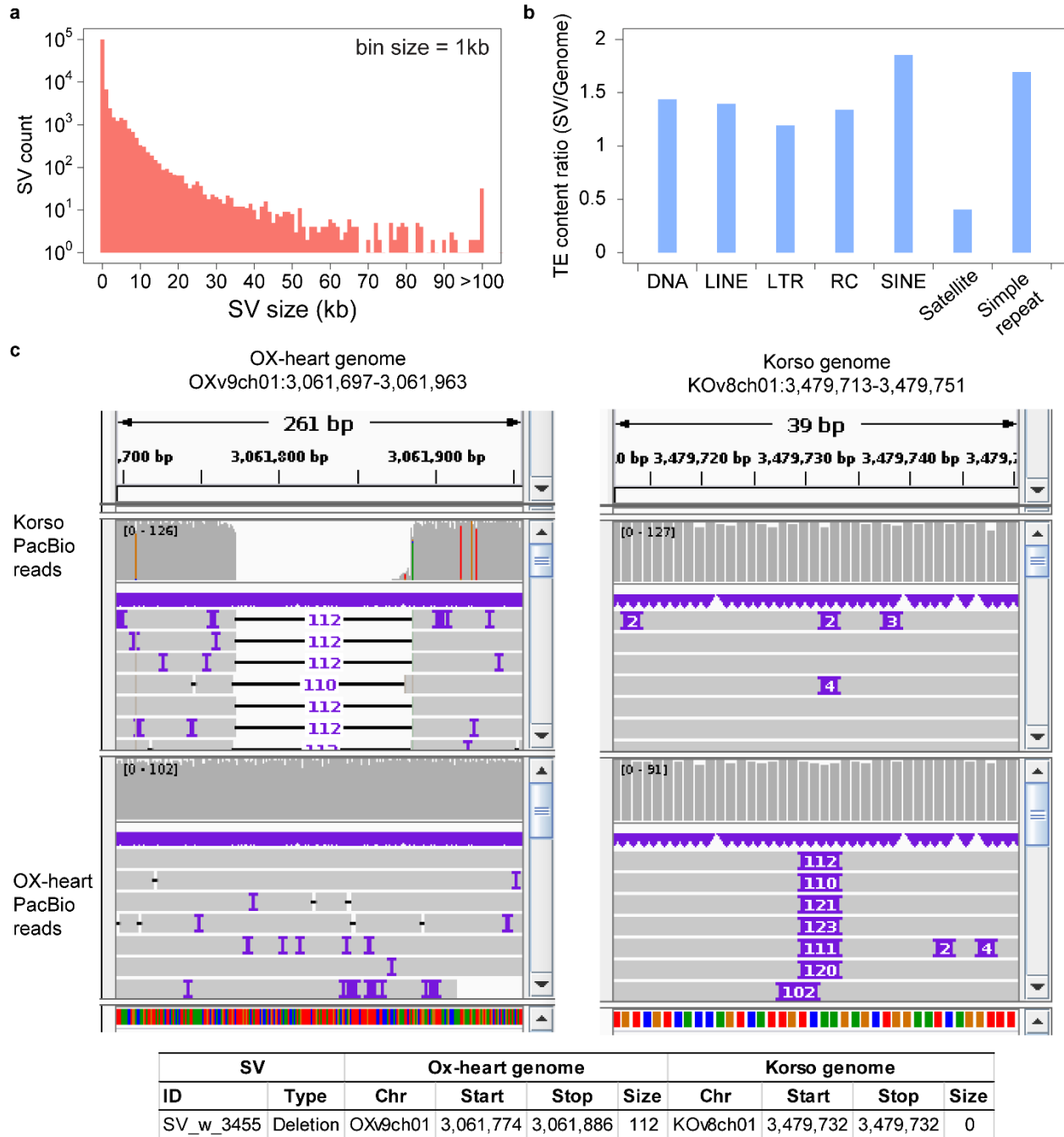
SV		Ox-heart genome				Korso genome			
ID	Type	Chr	Start	Stop	Size	Chr	Start	Stop	Size
SV_w_3455	Deletion	OXv9ch01	3,061,774	3,061,886	112	KOv8ch01	3,479,732	3,479,732	0

Figure S9 Detected SVs between the genomes of Korso and the OX-heart. **a**, Size distribution of detected SVs. **b**, Ratios of transposable element contents in SV regions to those in the entire genomes. **c**, Integrative Genomics Viewer (IGV) screenshots showing an example of the detected SV supported by the PacBio reads. PacBio reads from Korso and OX-heart were aligned to OX-heart (left) and Korso (right) genome, respectively. The expected deletion can be seen on the alignments of Korso reads on OX-heart genome (top left), whereas the expected insertion appears on that of OX-heart reads on Korso genome (bottom right). We manually checked 250 randomly selected SVs and confirmed 245 (98%) of them under IGV.
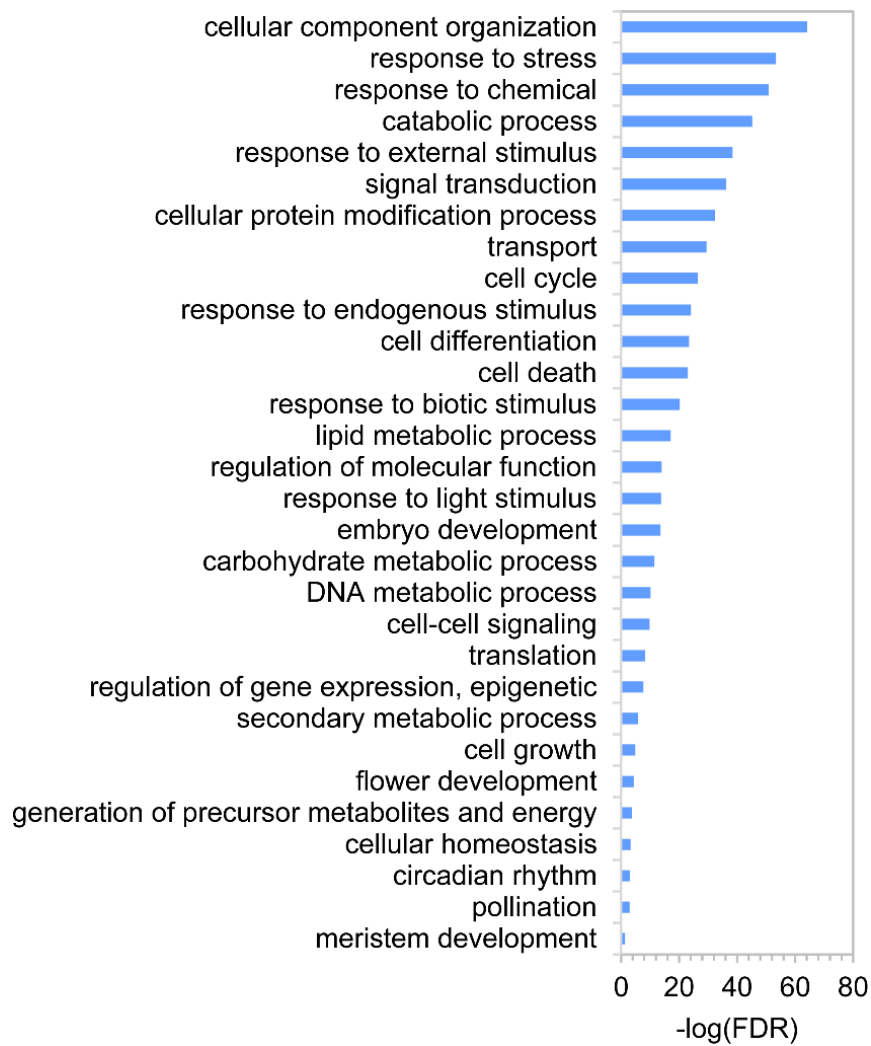
9

Figure S10 Significantly enriched GO terms in genes overlapping with detected SVs in their gene body and/or promoter regions
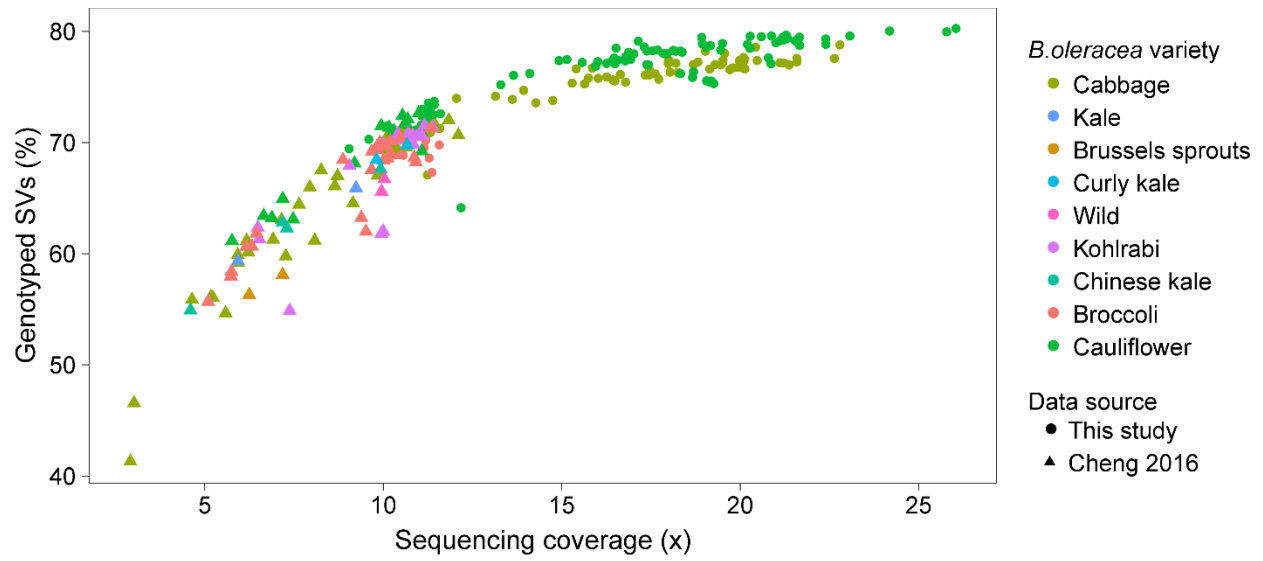
Figure S11 Distribution of SV genotyping rates in 271 *B. oleracea* accessions.
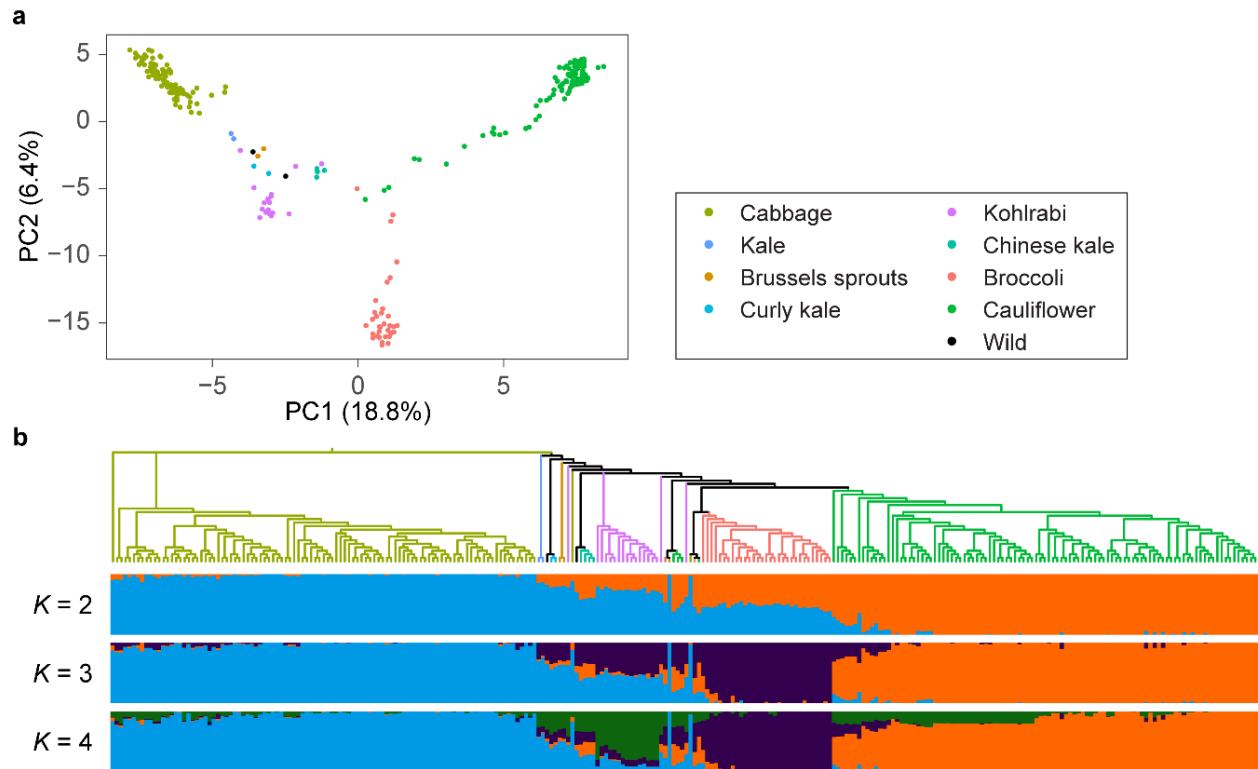
Figure S12 Population analysis of the 271 *B. oleracea* accessions using SNPs. **a,** Principal component analysis of *B. oleracea* accessions. **b**, Neighbor joining phylogenetic tree and population structure of the 271 *B. oleracea* accessions. Branch colors of the tree indicate different morphotypes as in **a**. *K*, number of ancestral kinships.
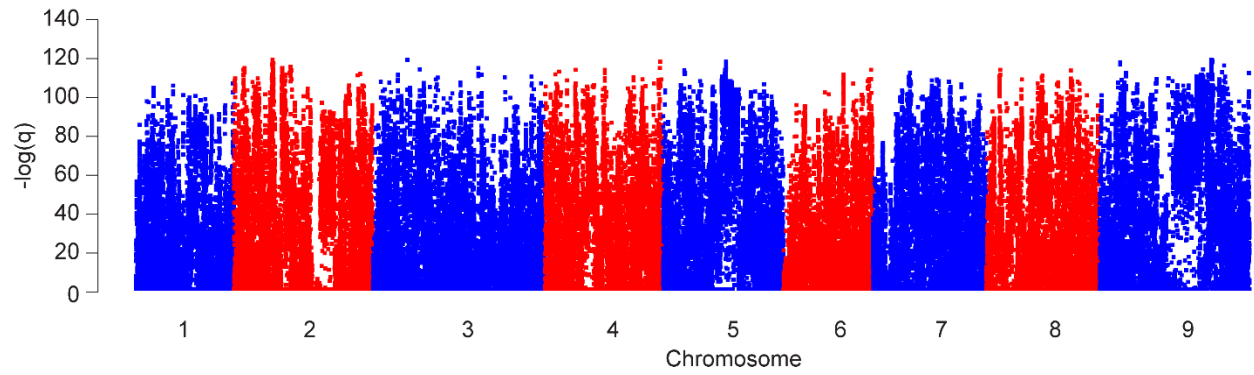
Figure S13 Manhattan plot displaying the -log(q-value) of allele variations between cabbage and cauliflower for SVs across the Korso genome. q-value, Bonferroni-corrected p value of Fisher's exact test.
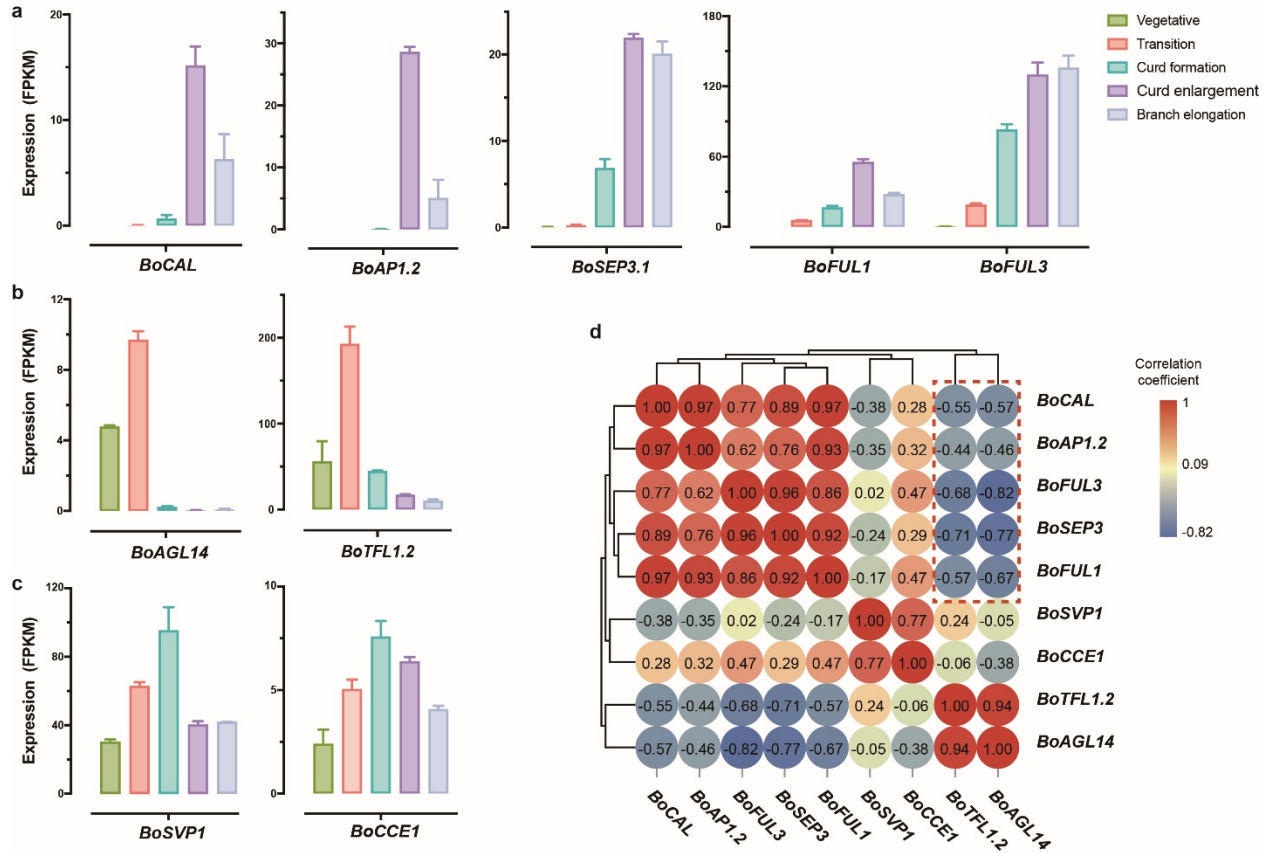
Figure S14 Expression profiles of genes potentially involved in curd maintenance and floral arrest. **a**, Expression profiles of FMI genes *BoCAL*, *BoAP1.2*, *BoSEP3.1*, *BoFUL1* and *BoFUL3*. **b**, Expression profiles of the IMI gene *BoTFL1.2* and its positive regulator *BoAGL14*. **c**, Expression profiles of the putative floral arrest genes *BoSVP1* and *BoCCE1*. **d**, Correlation heatmap of the gene expression profiles during curd development. The red dash square highlights the negative correlation between *BoAGL14*, *BoTFL1.2* and the FMI genes.