

Figure S1 Genomic survey of NY7 and its pedigrees with *K*-mer distribution

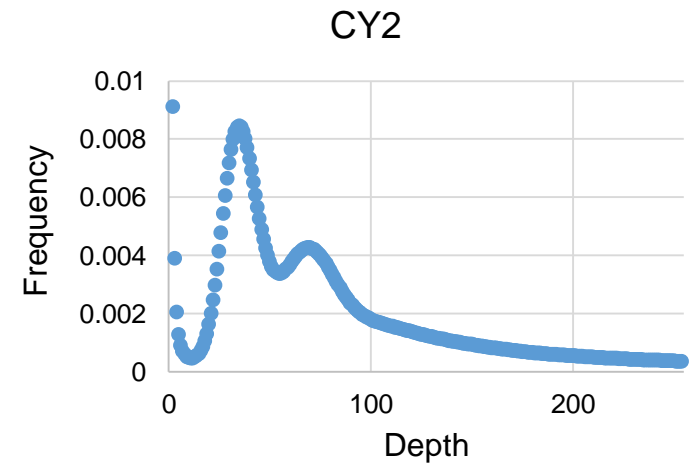
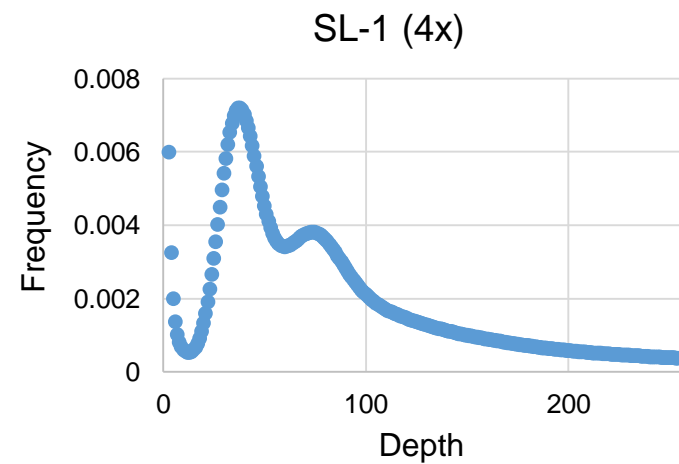
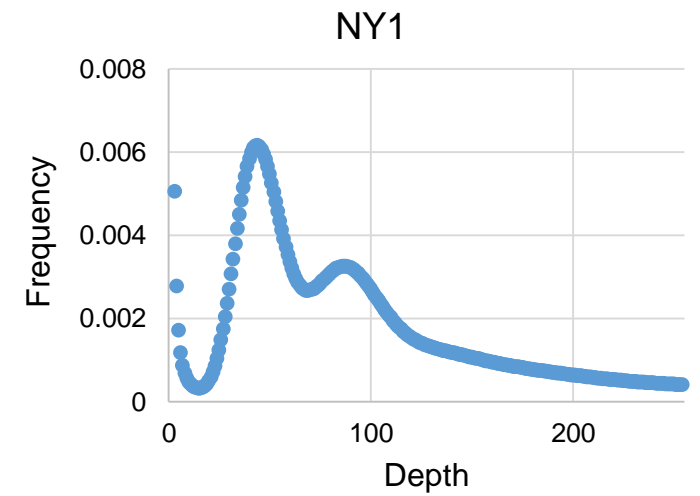
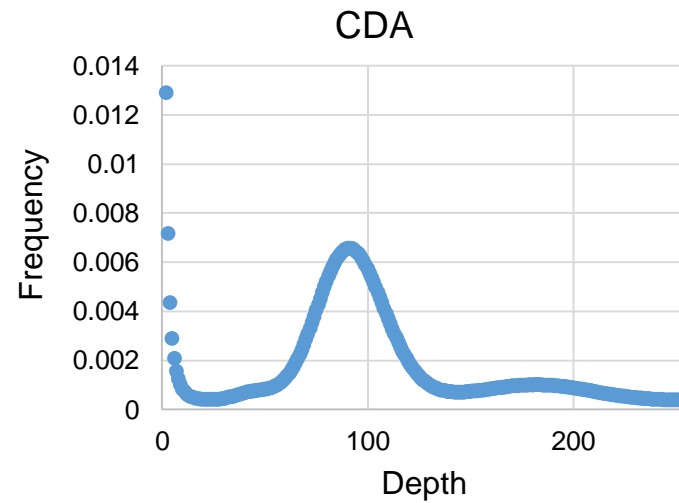
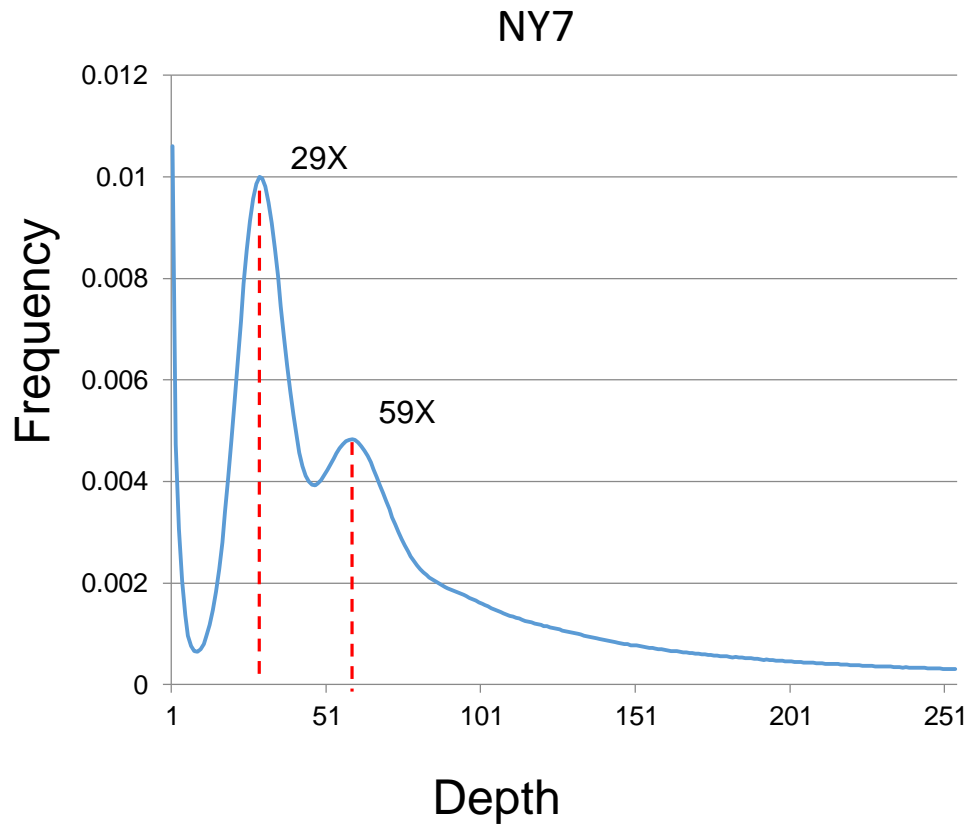


Figure S2 The Hi-C contact maps for NY7 whole genome and NY7 chrA03

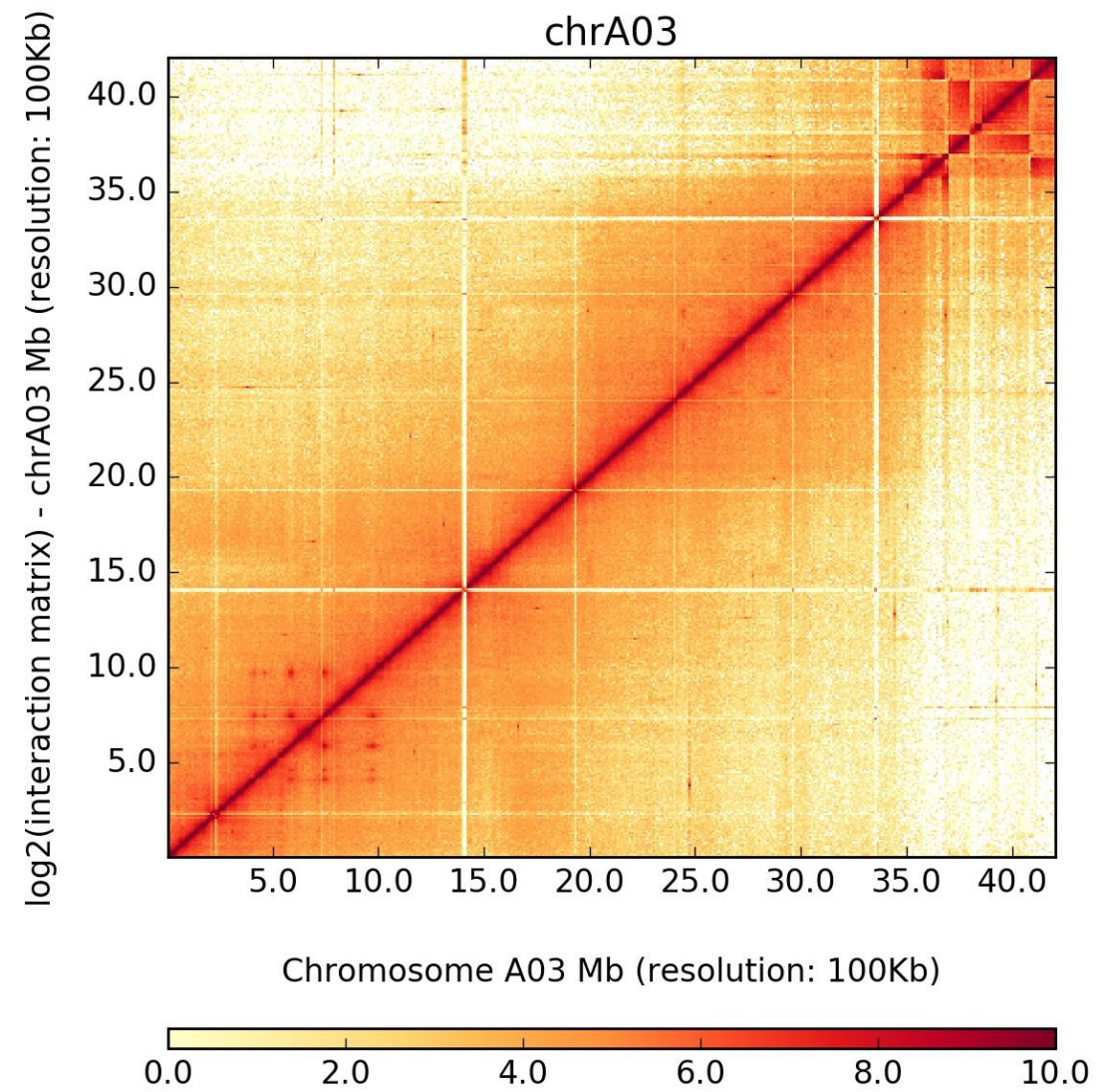
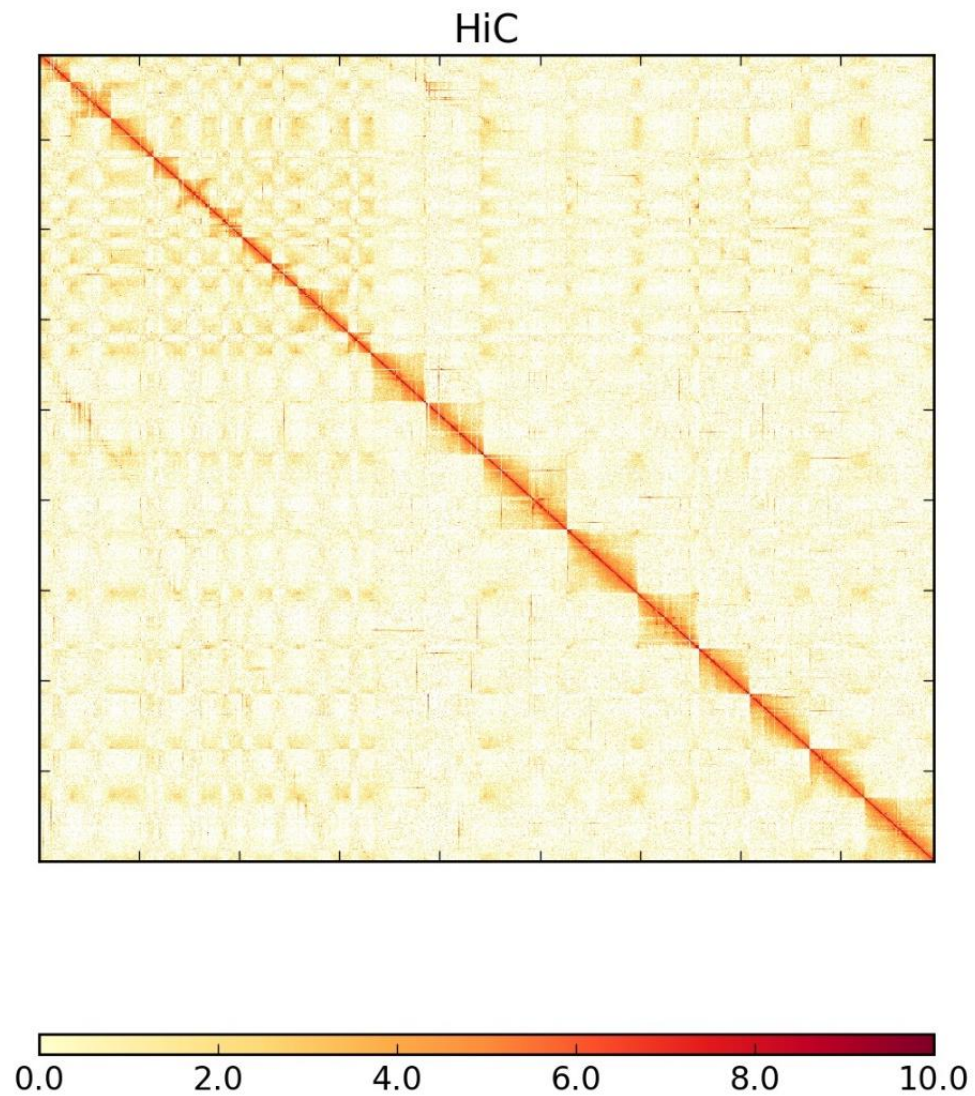


Figure S3 The collinearity between three *B. napus* genetic maps and the NY7 genome assembly

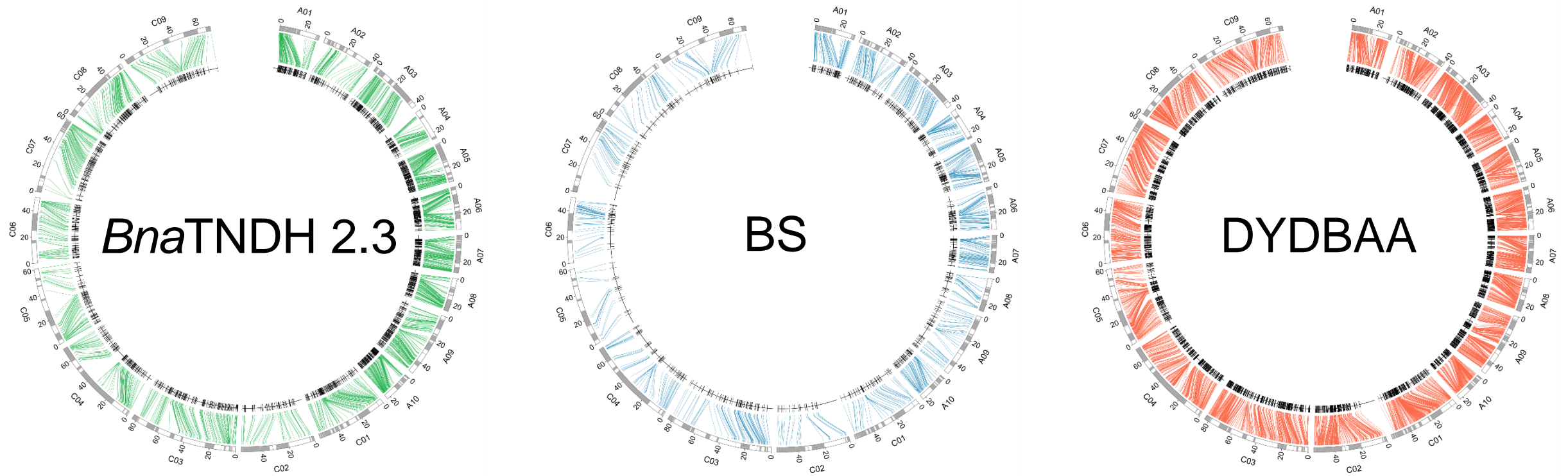


Figure S4 The pipeline for genome assembly and pseudo-chromosome construction for NY7

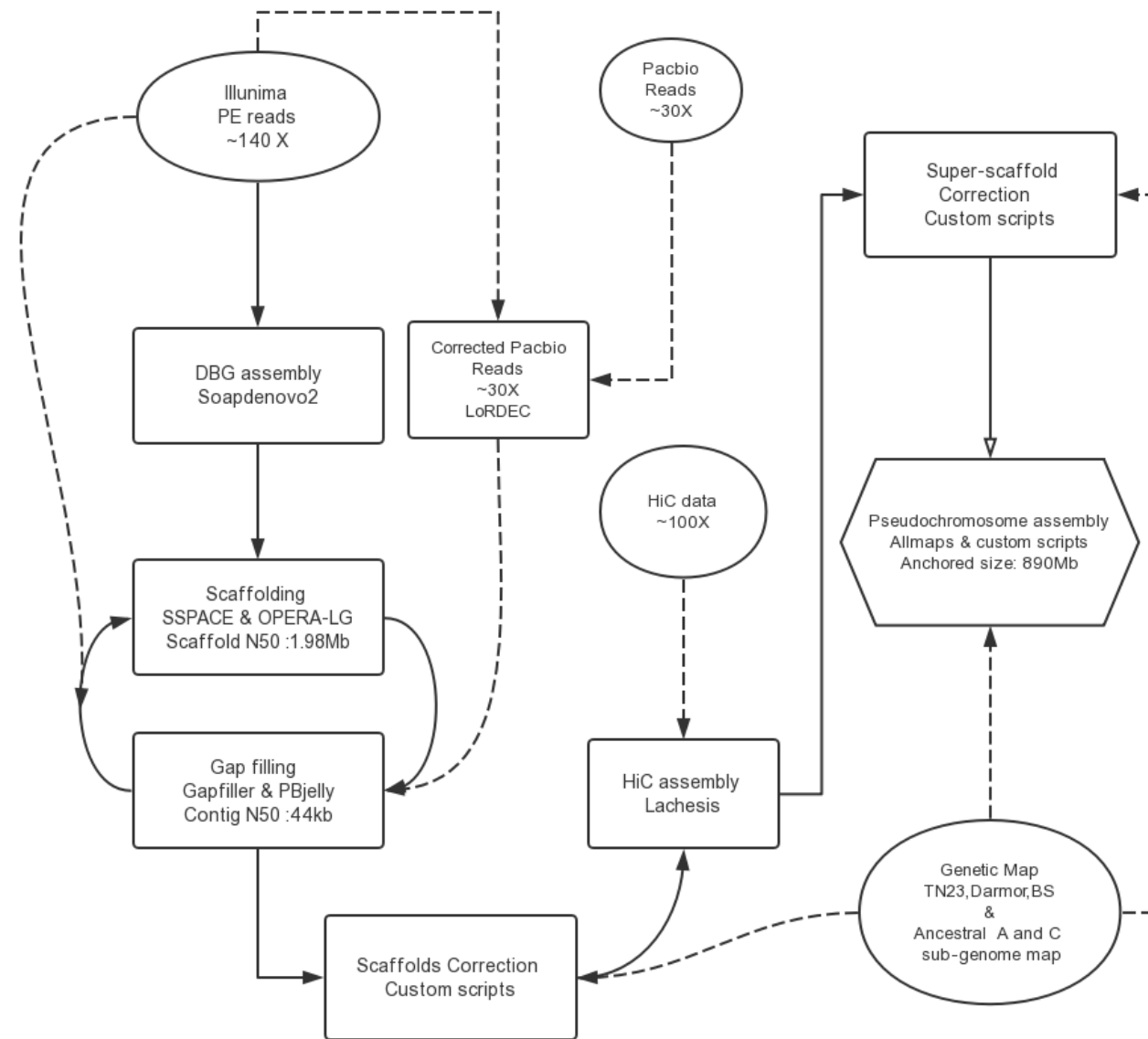


Figure S5 The genomic synteny between NY7 and other *de novo* assembly of *B. napus* and two diploid progenitors

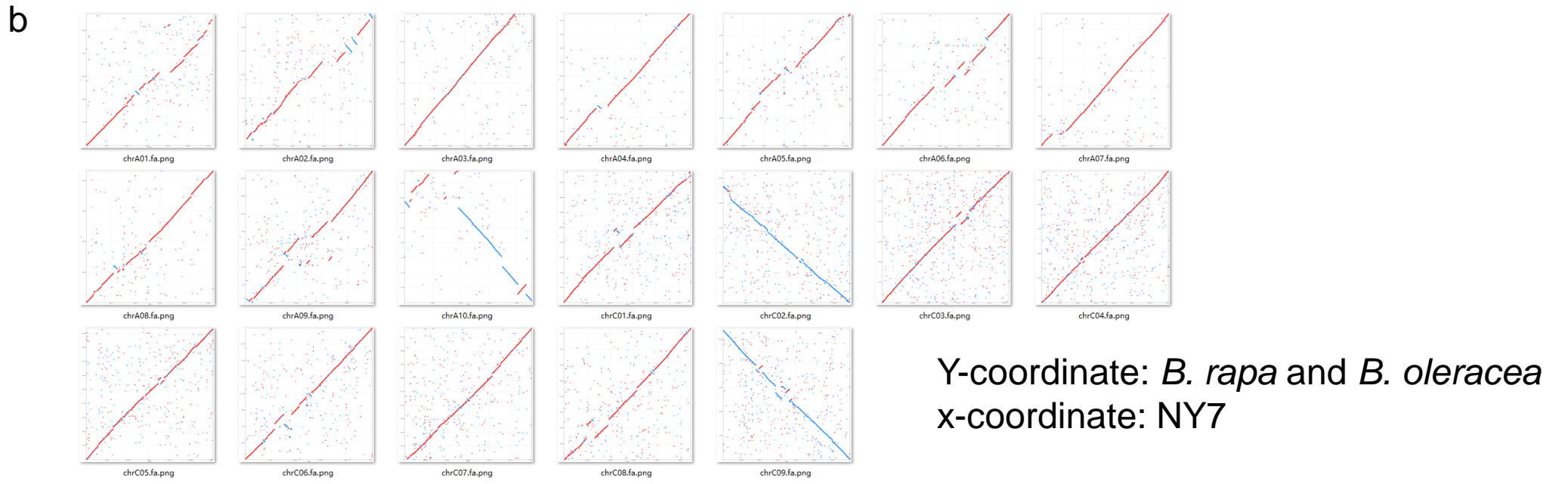
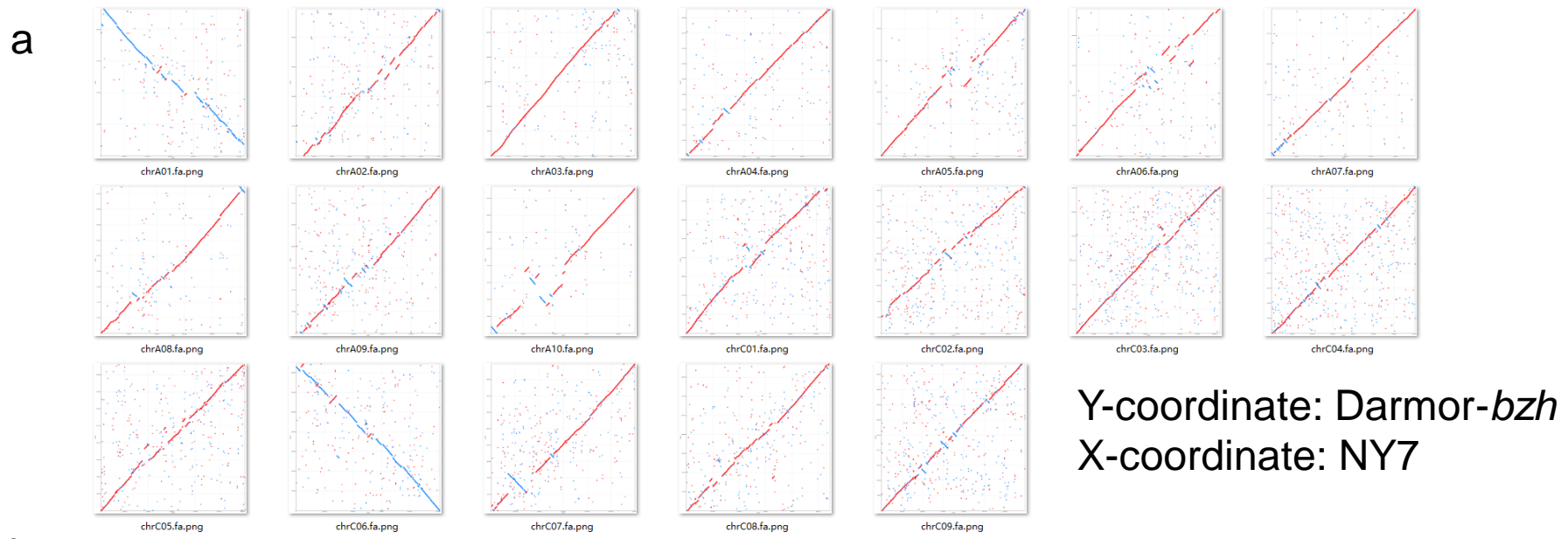


Figure S5 The genomic synteny between NY7 and other *de novo* assemblies of *B. napus* and two diploid progenitors

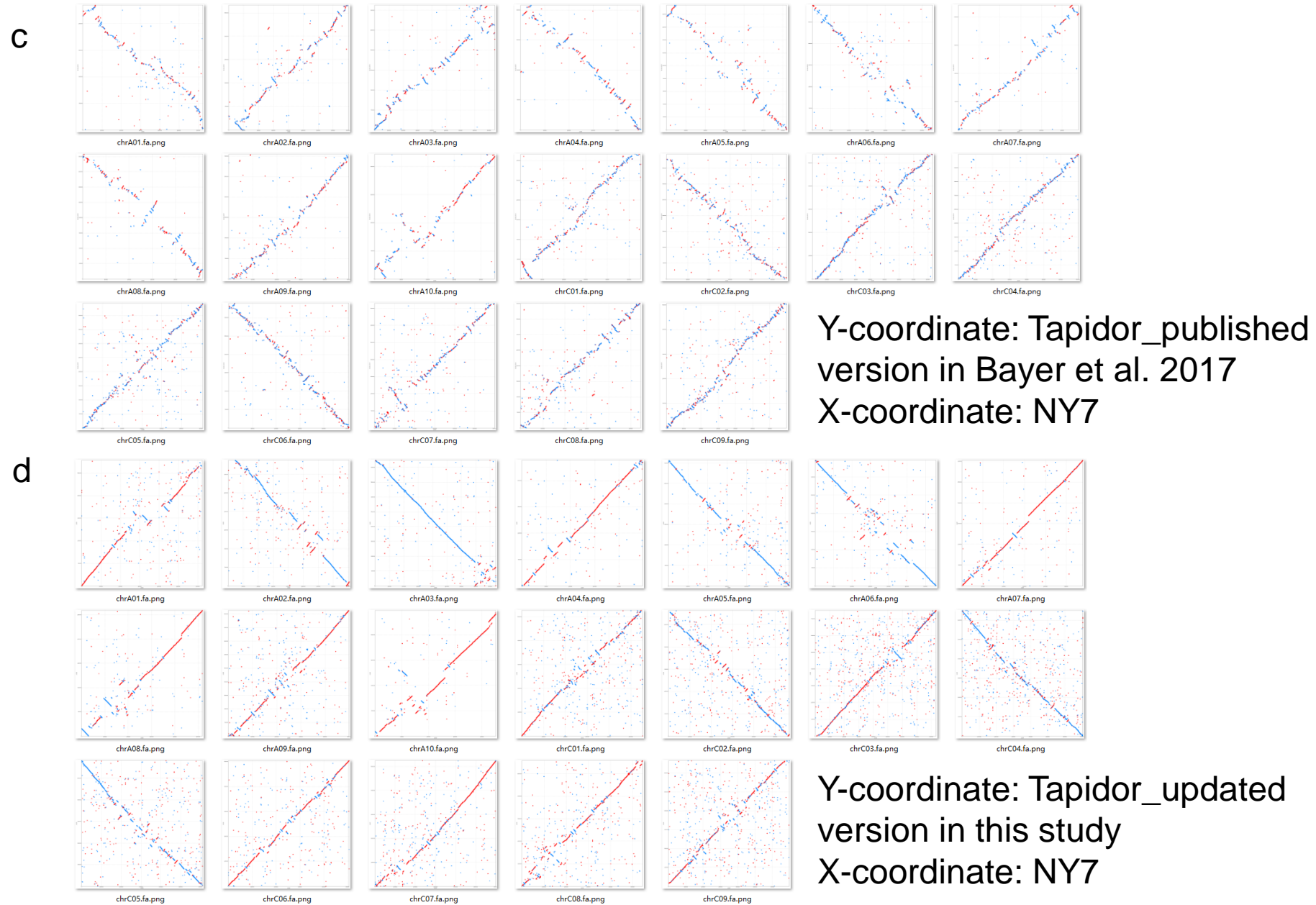


Figure S5 The genomic synteny between NY7 and other *de novo* assemblies of *B. napus* and two diploid progenitors

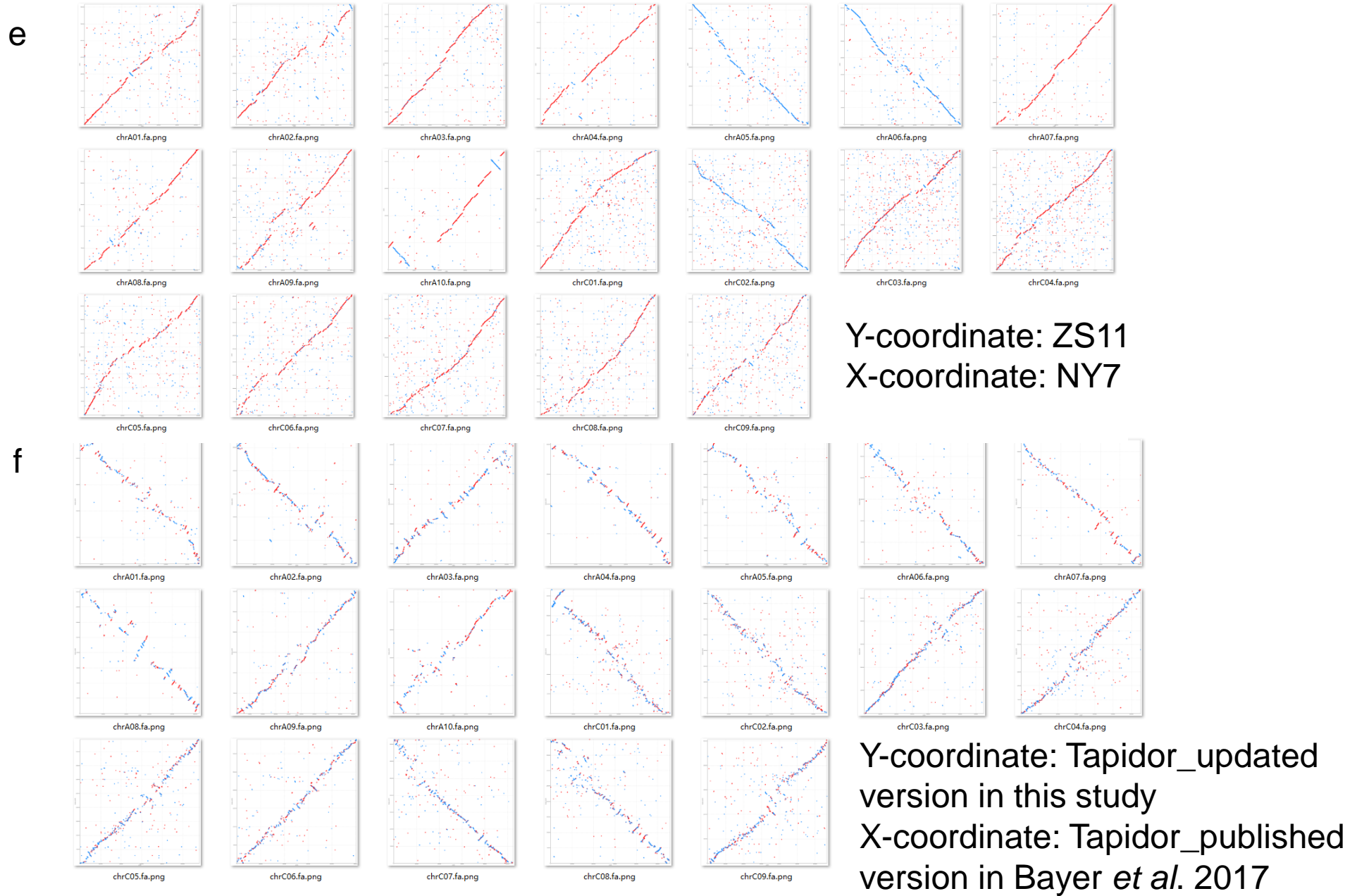
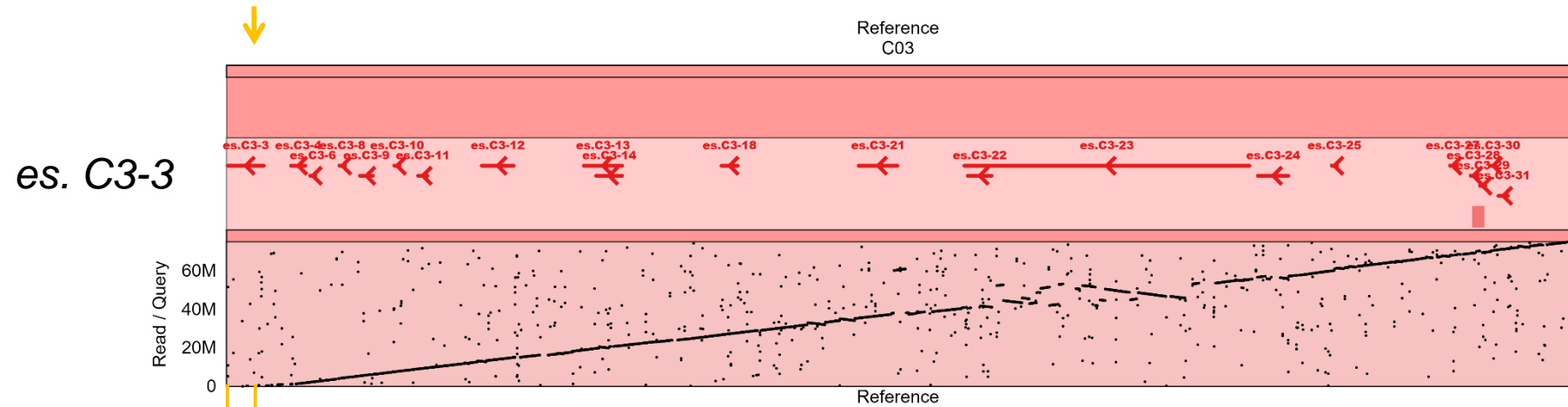


Figure S6 Demonstration of a QTL located at the genomic divergent region between the NY7 and Tapidor genome

Genomic alignment view of the Tapidor assembly to NY7 reference on chromosome C03. All of the QTLs identified in C03 were labelled with 'es.' at the top. The arrow shows a QTL (*es. C3-3*) region with present and absent sequence variation between Tapidor and NY7. Significantly high read coverage in the NY7 genome was found in the QTL (*es. C3-3*) region.



es. C3-3

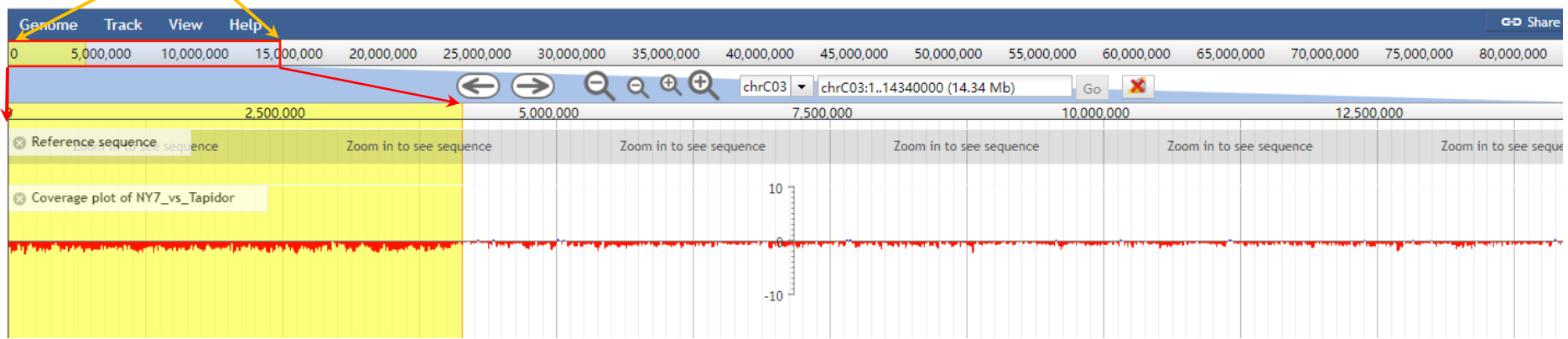


Figure S7 Phylogenetic trees for *B. napus* accessions based on SNPs found in both the A and C subgenomes

The EU, AS_DL, AS_DH represent the European rapeseed (*B. napus*), Asian rapeseed (*B. napus*) with double-low and double-high traits, respectively.

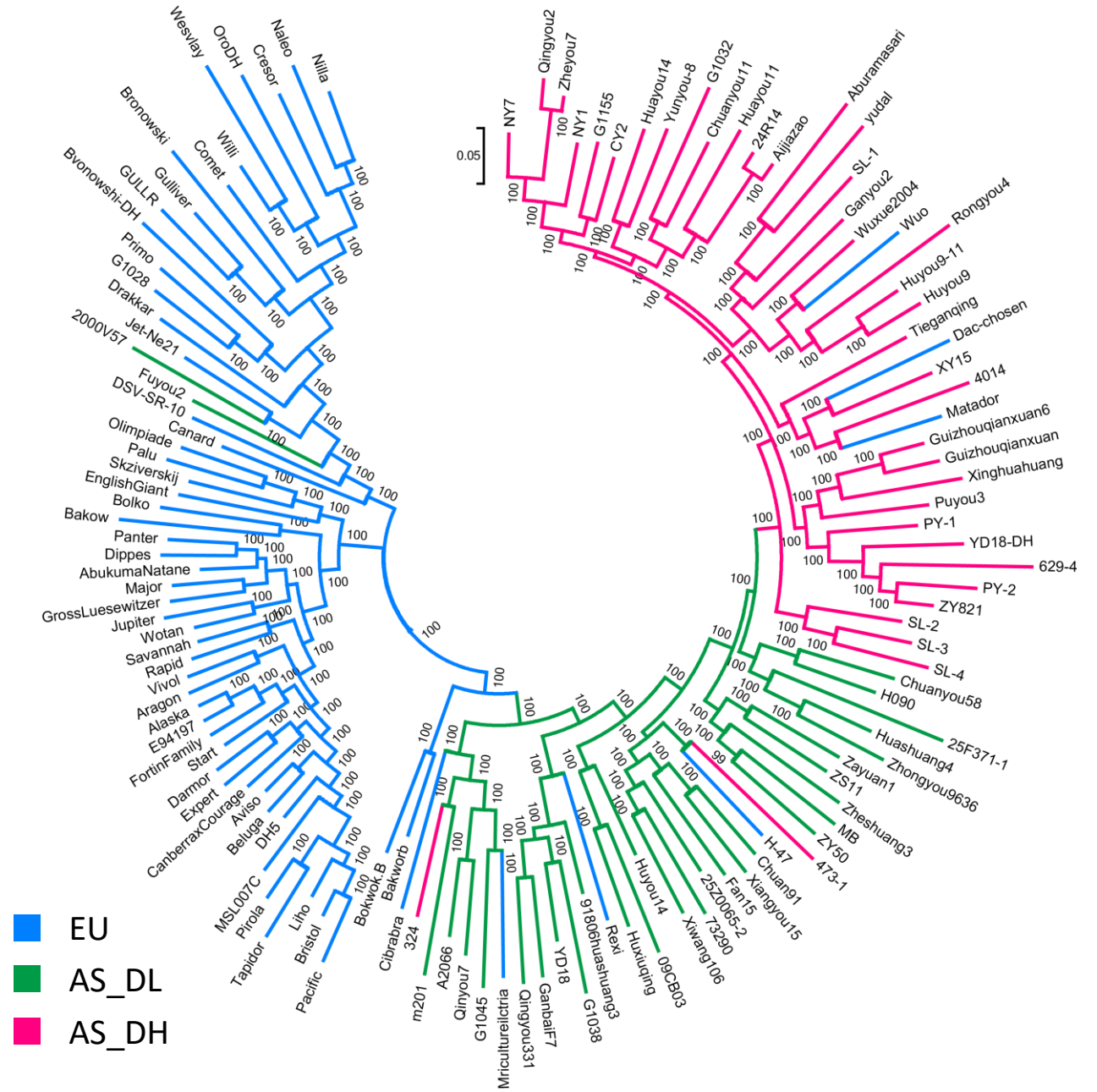


Figure S8 Genetic diversity (π) of different chromosomes in different populations. EU and AS represent the European rapeseed (*B. napus*) and Asian rapeseed (*B. napus*), respectively. The EU, AS_DL, AS_DH represent European rapeseed, Asian rapeseed with double-low and double-high seed-quality traits, respectively

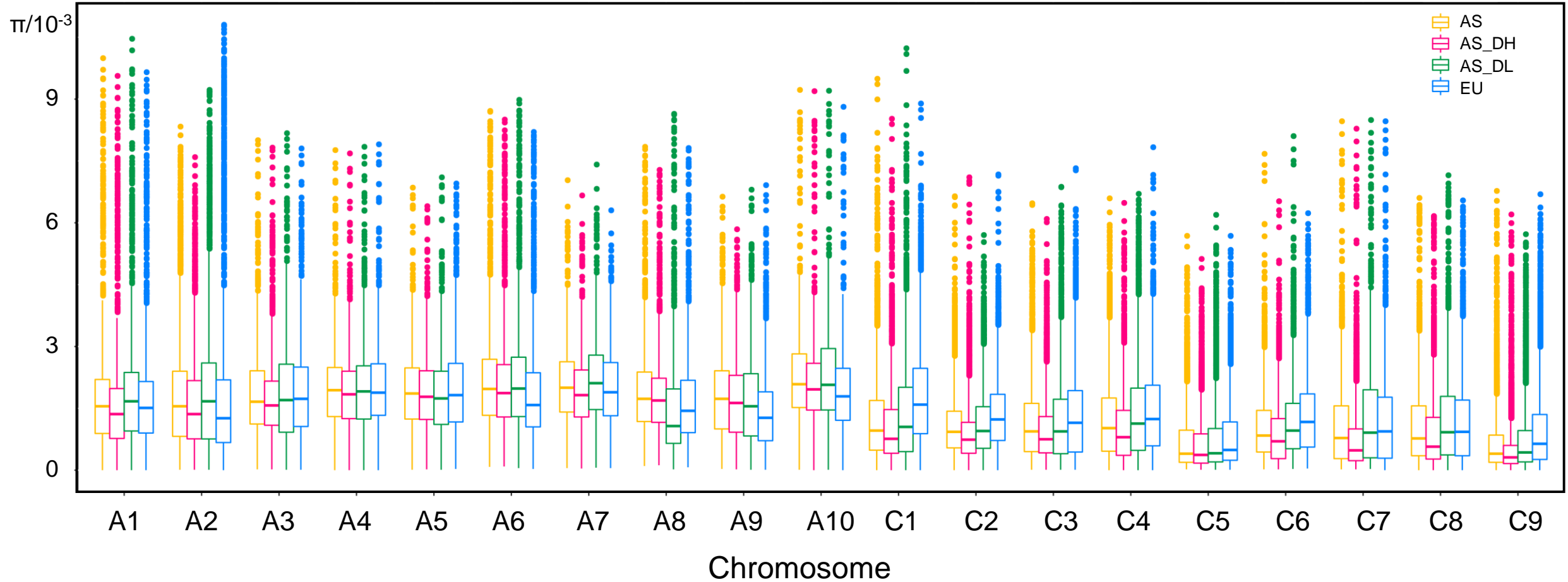


Figure S9 Linkage disequilibrium of European and Asian rapeseed populations

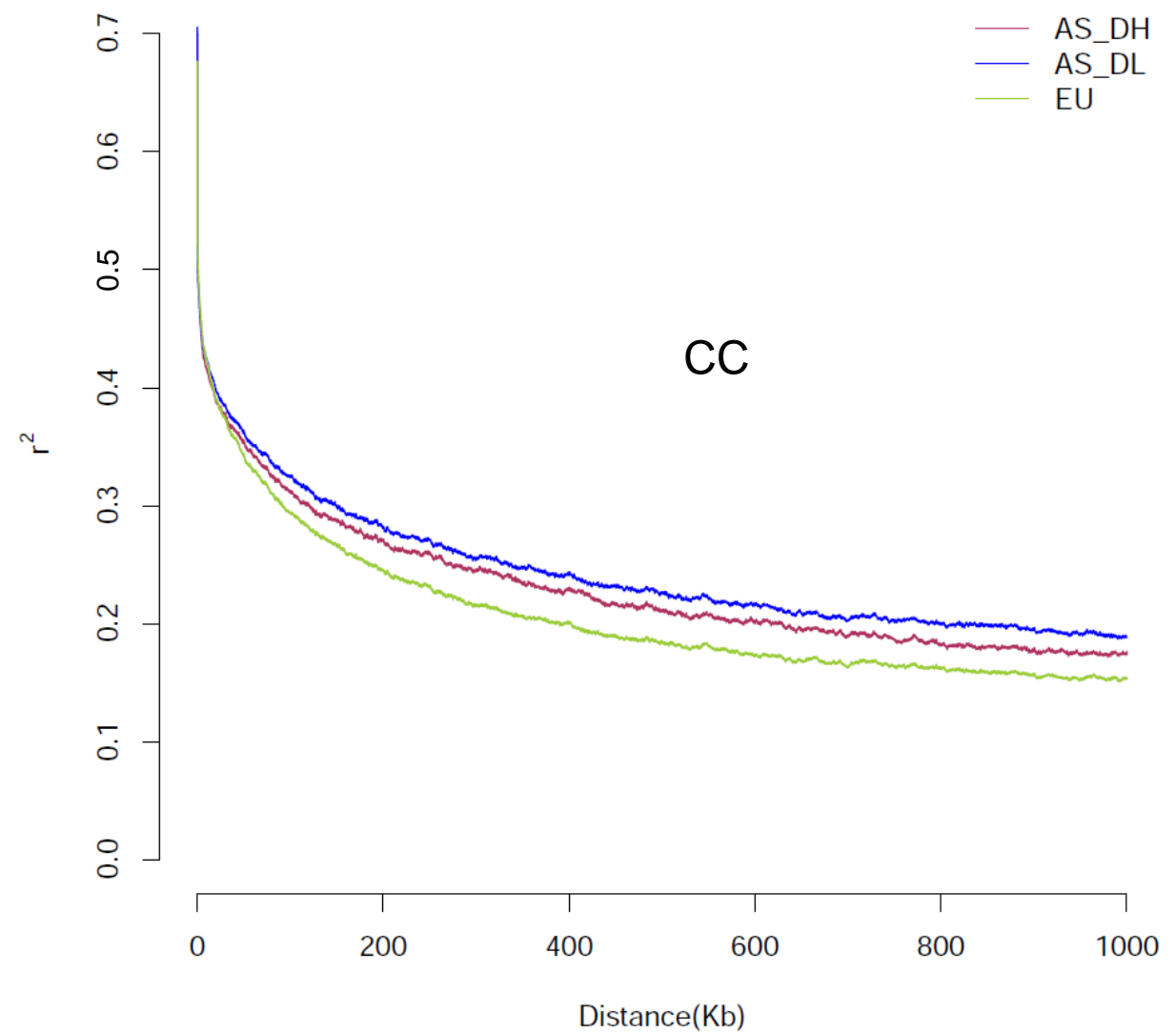
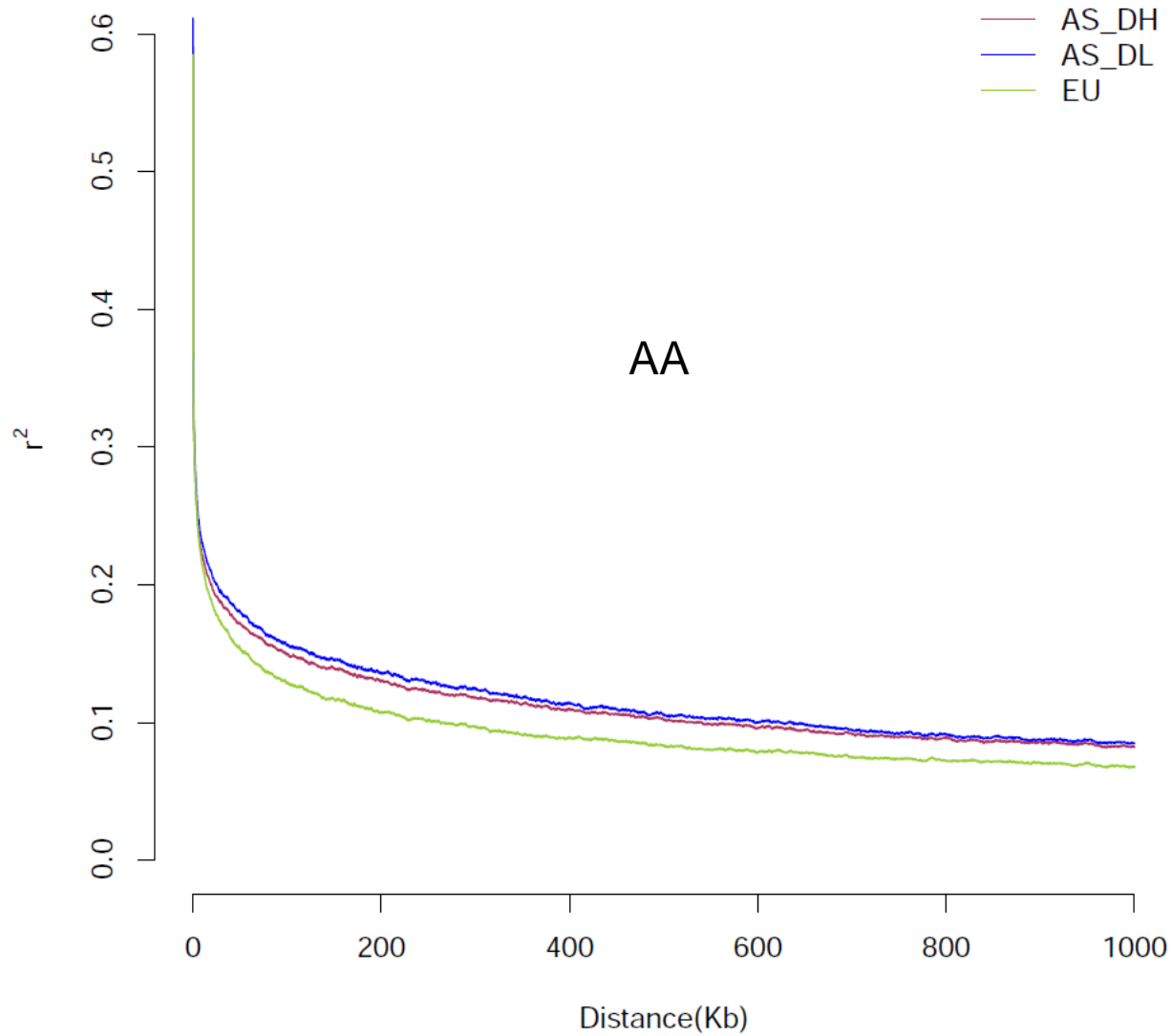


Figure S10 Demographic models of the origin of Asian rapeseeds

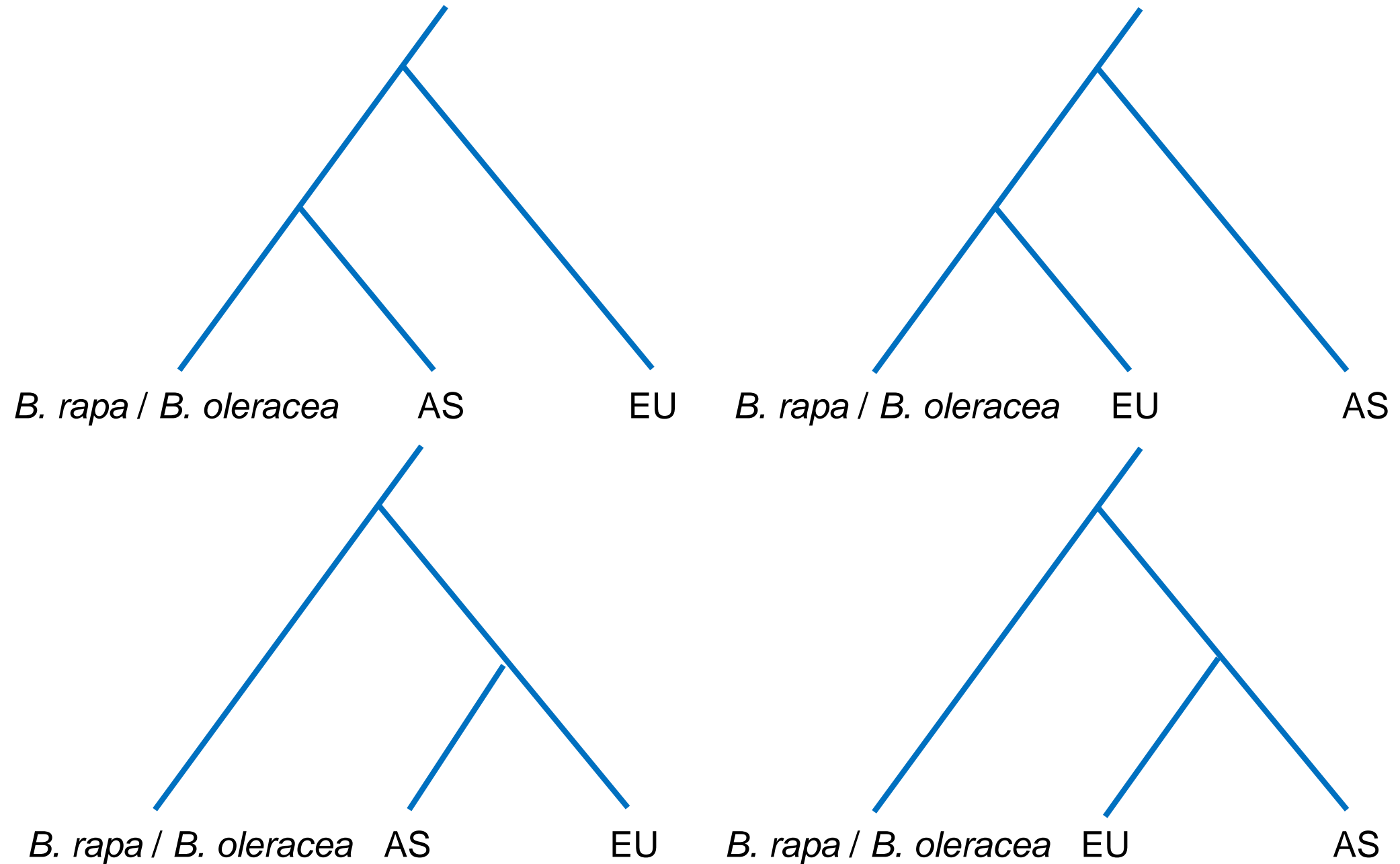


Figure S11 Demographic models of the origin of Asian double-low rapeseeds

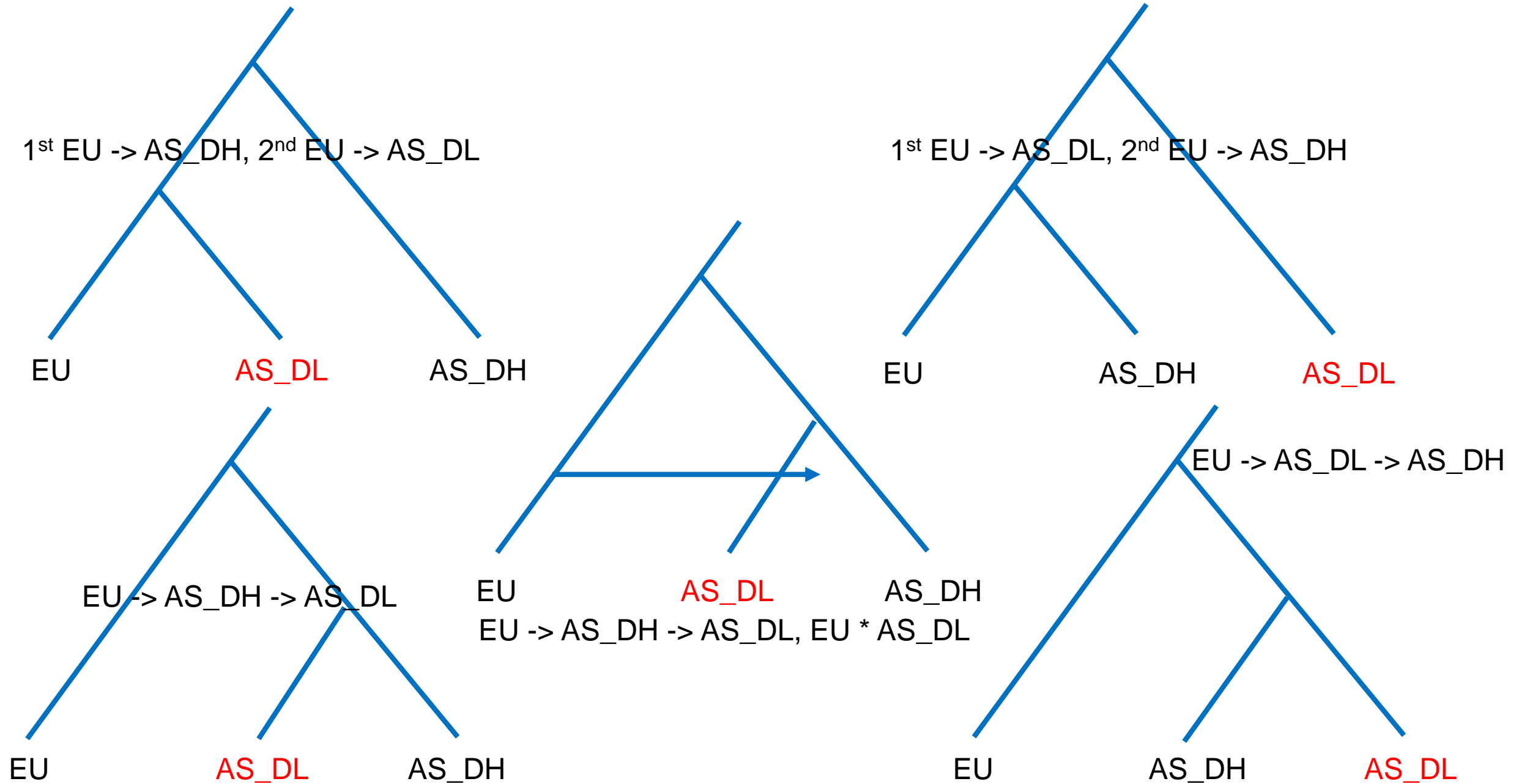


Figure S12 A genomic view of the read mapping information for *CDF2* homologue in the parental lines of NY7

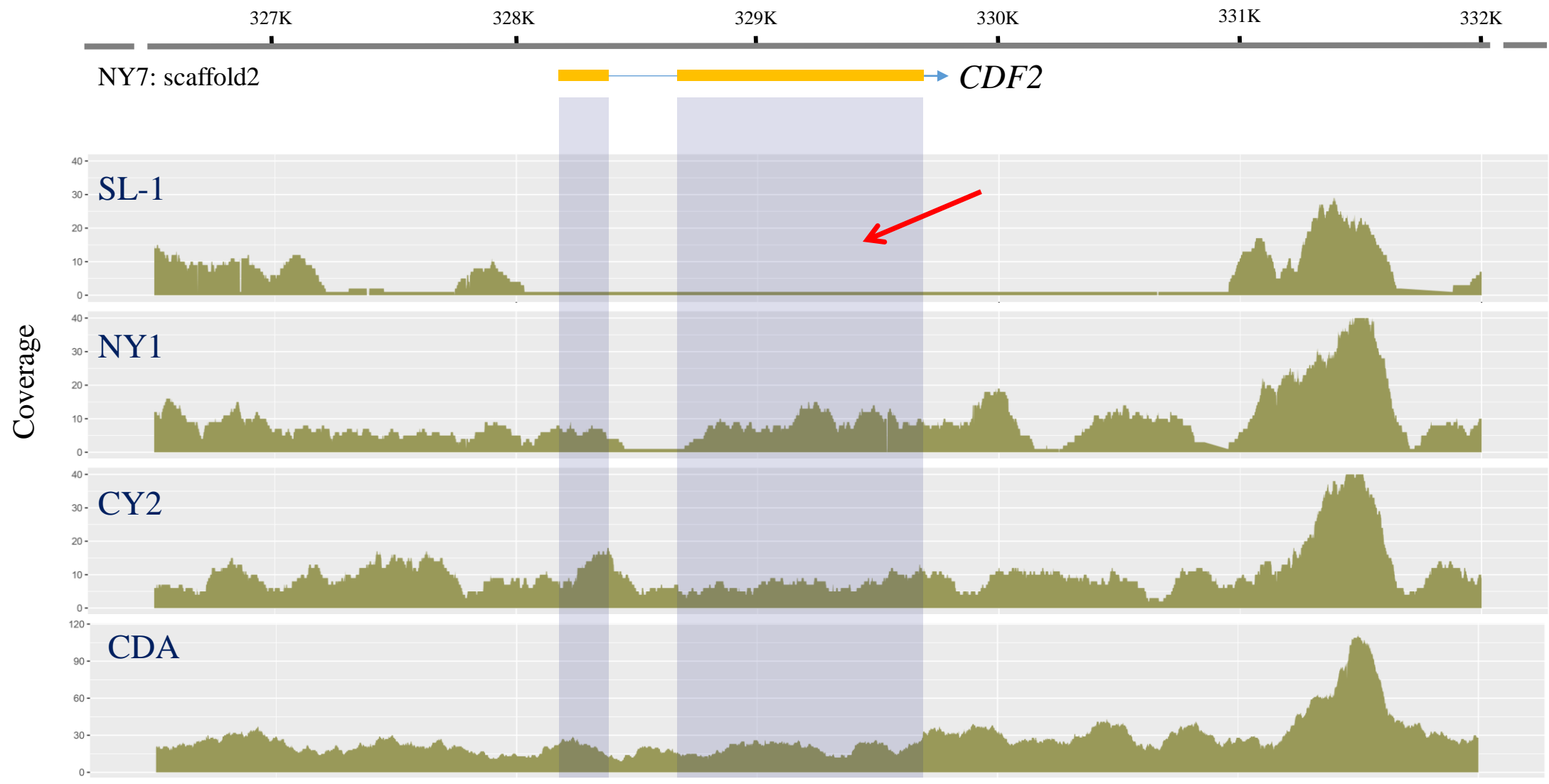


Figure S13 The frequency distribution of deleterious SNPs (dSNPs) and neutral intergenic SNPs (iSNPs) in (a) the NY7 pedigree (b) the Cn genome of the Asian and European populations

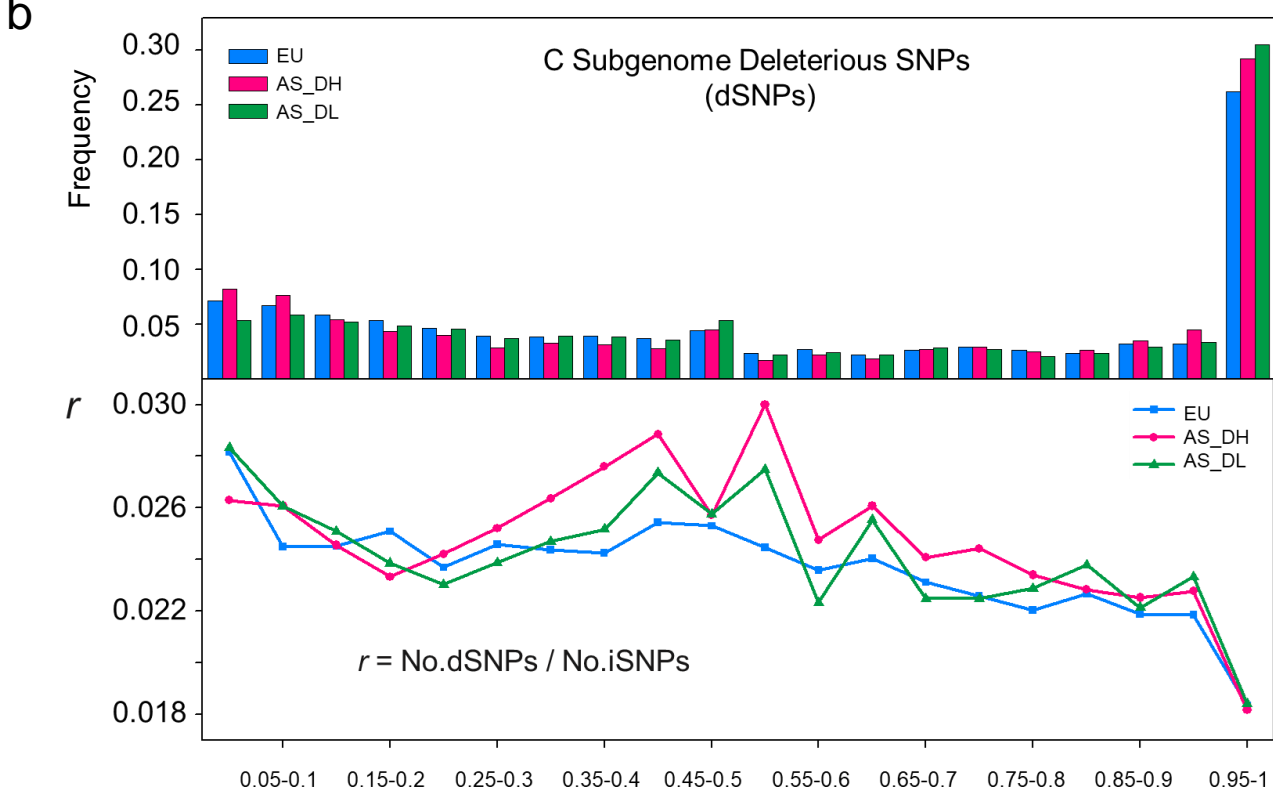
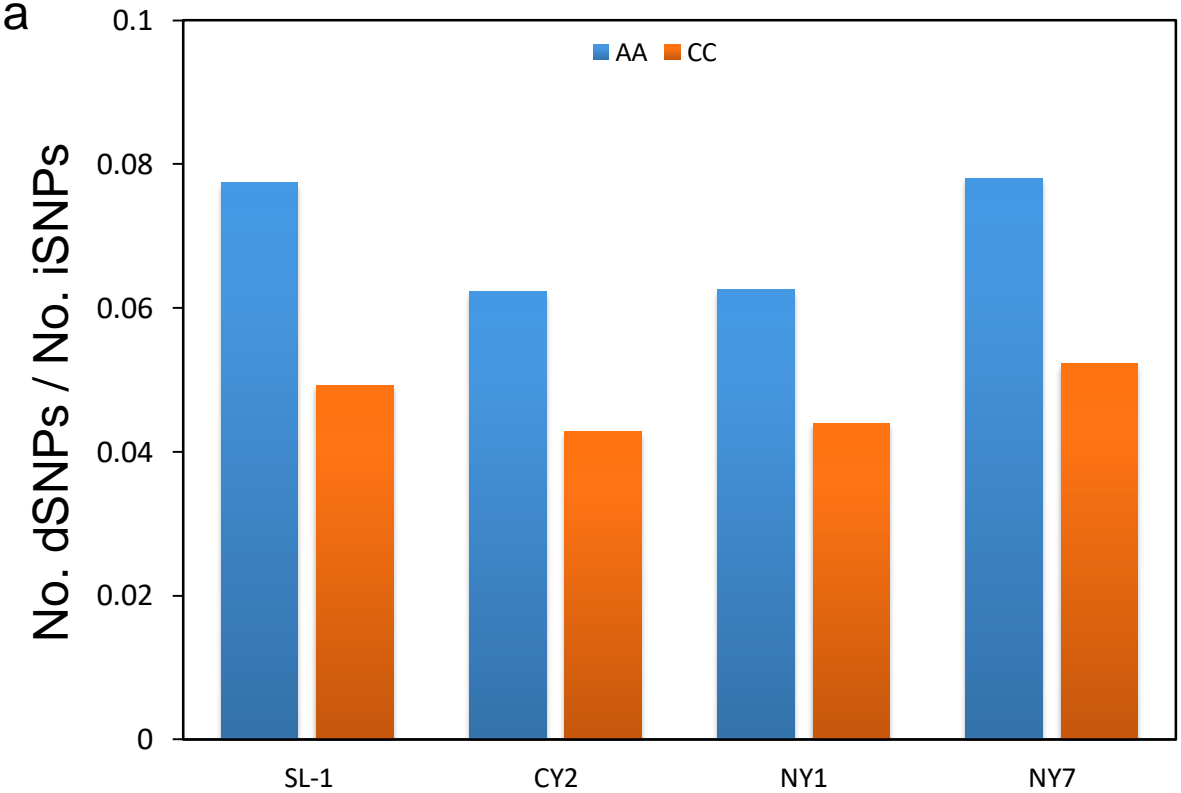


Figure S14 (a) Local ancestry inference of the introgression of *B. rapa* for Asian rapeseed. On the top of each box, the red signals represent the conserved blocks with introgression from *B. rapa*. (b) Local ancestry inference of the introgression of European lineage (blue) in Asian double-low cultivars

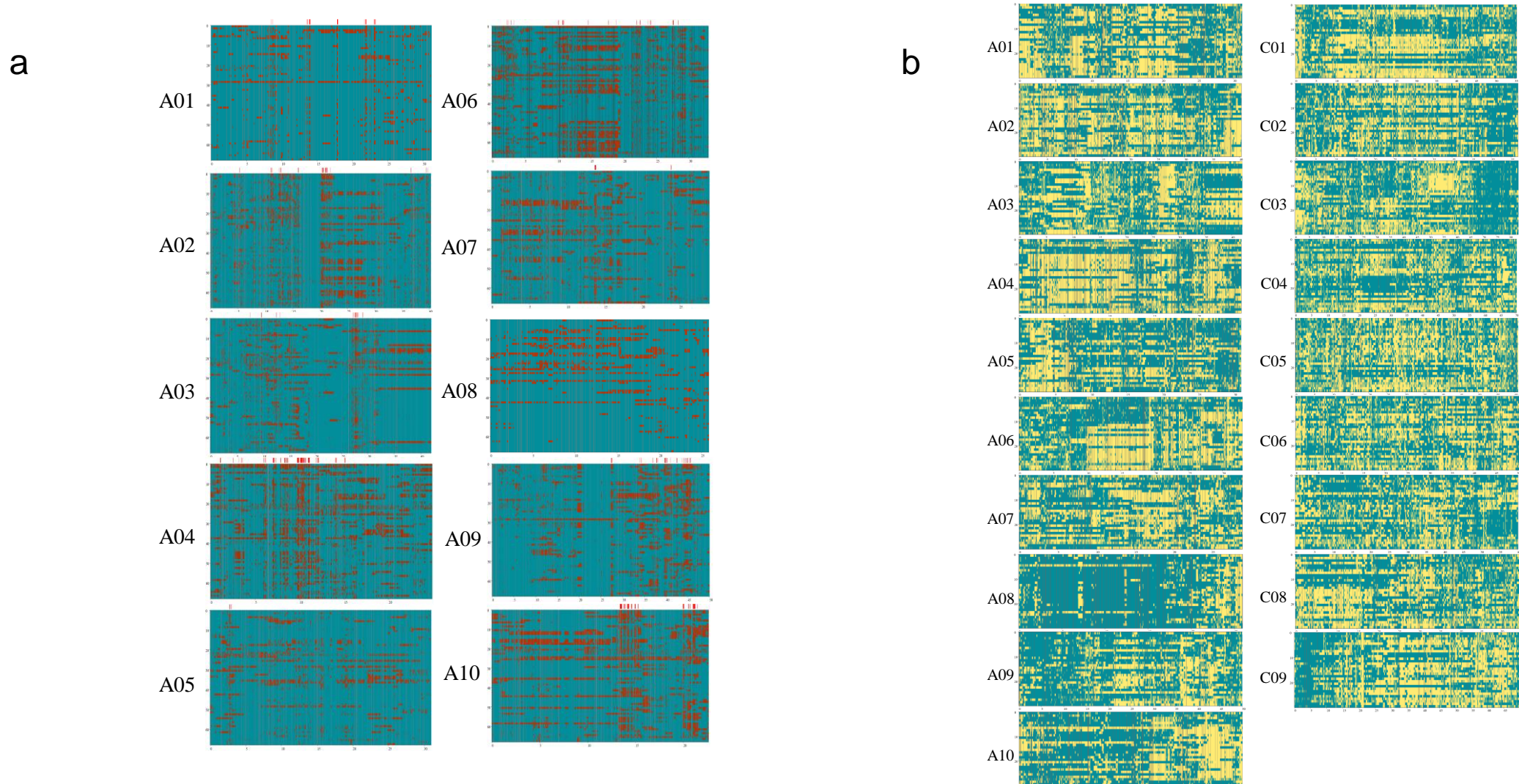


Figure S15 (a) A genomic view of NY1 reads in the homoeologous chromosome pair A01 and C01 with two diploid ancestors (*B. rapa* and *B. oleracea*) as references. (b) A genomic view of NY1 and CY2 reads in the homoeologous chromosome pair A09 and C09 with two diploid ancestors (*B. rapa* and *B. oleracea*) as references.

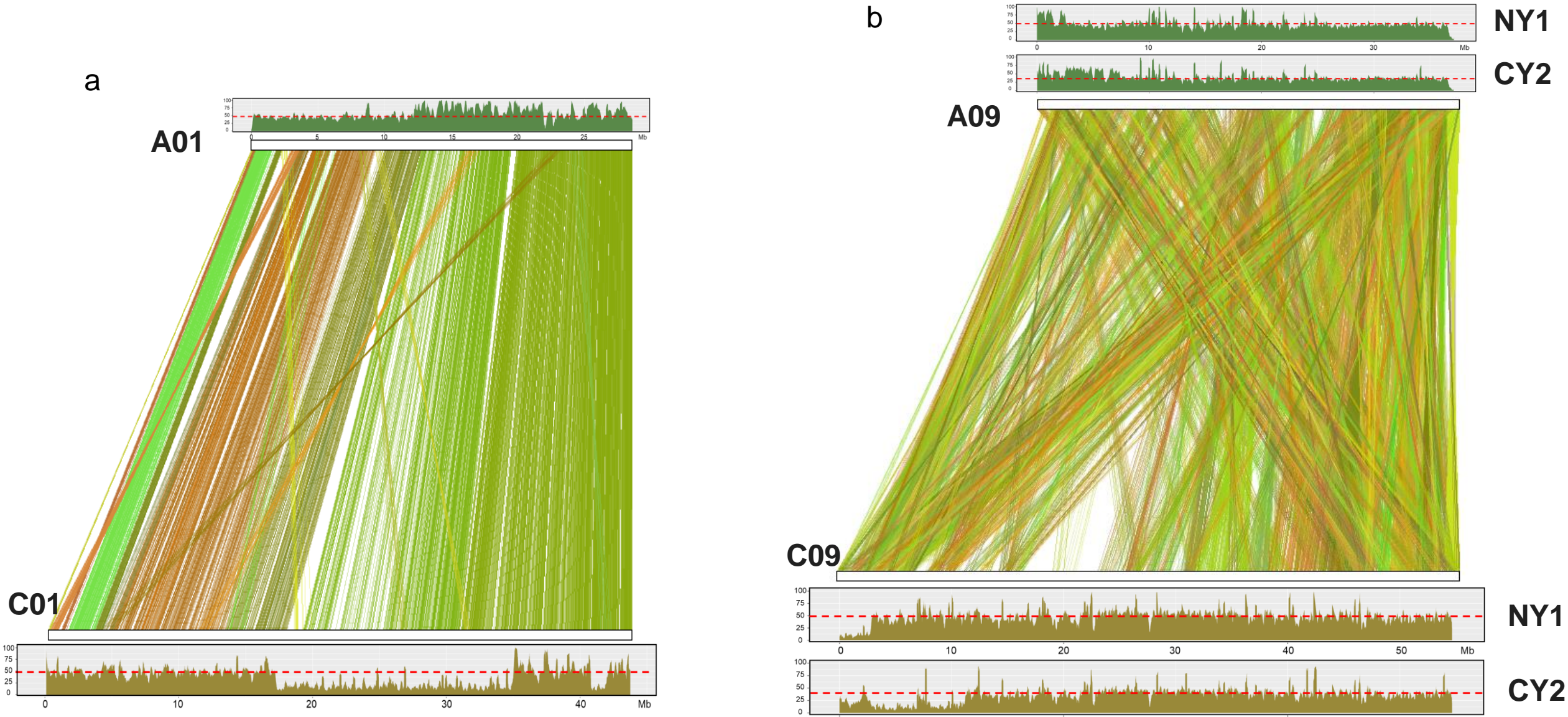


Figure S16 A summary of the origin and breeding history of Asian rapeseeds and the dynamic changes of genomic diversity and deleterious SNP (dSNP) accumulations in the two stages of the Asian local breeding history. The Asian genomes were significantly re-shaped by two genetic introgression events contributed by *B. rapa* and double-low European *B. napus*

