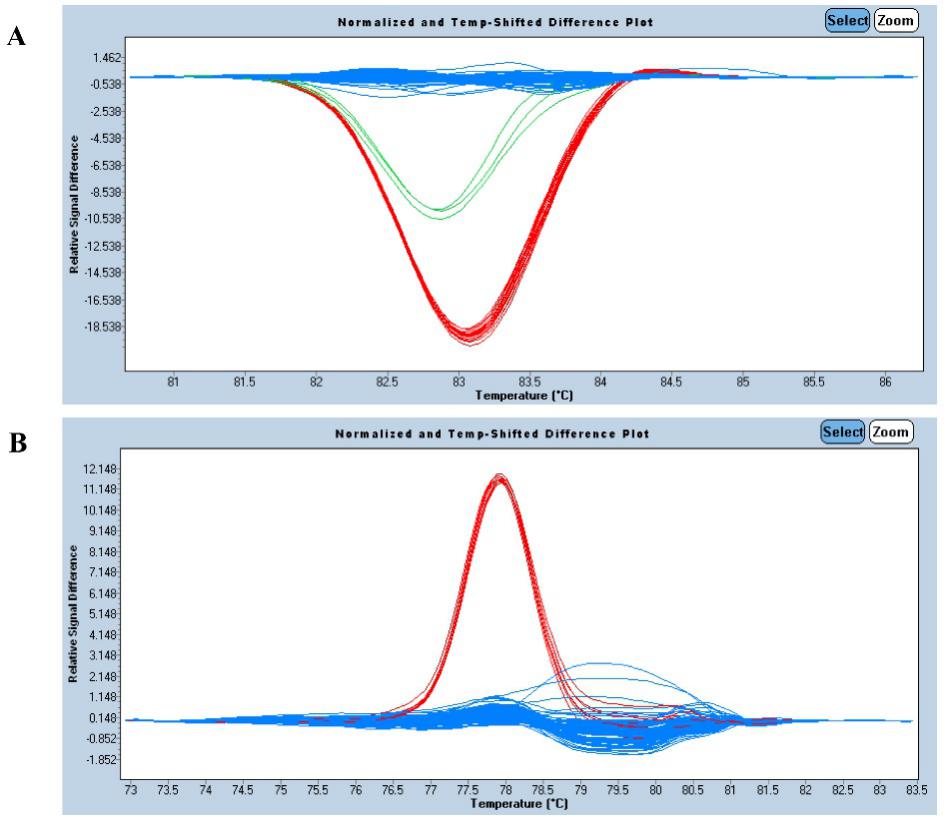
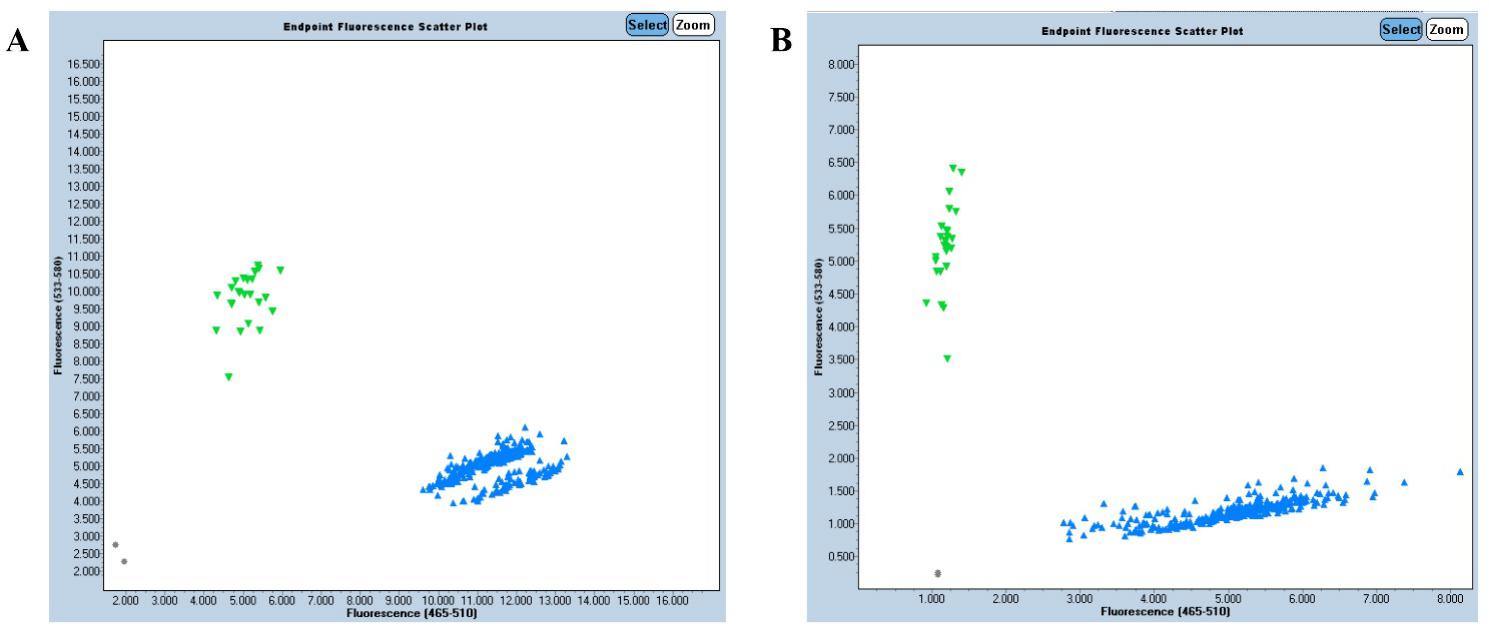
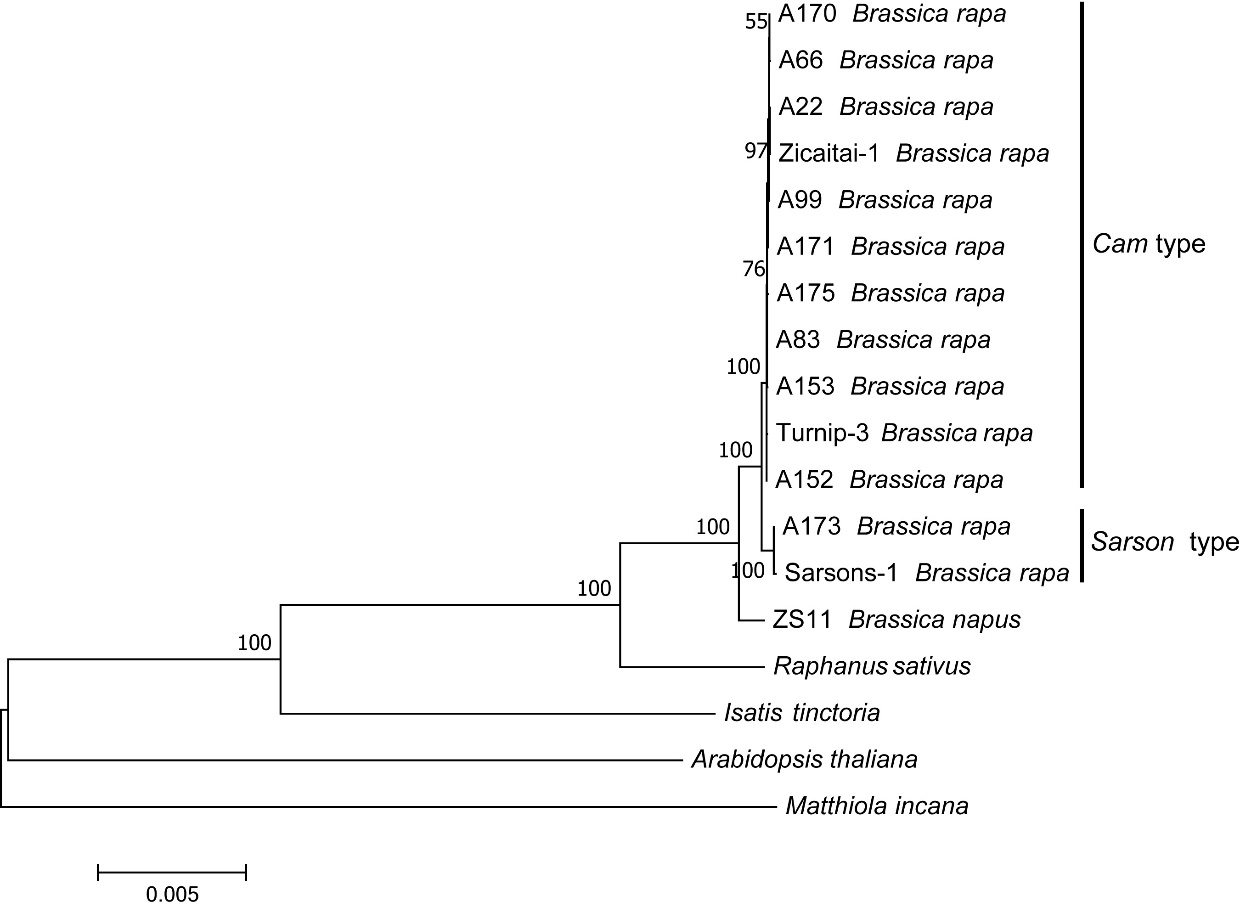
# Supplementary Figures:



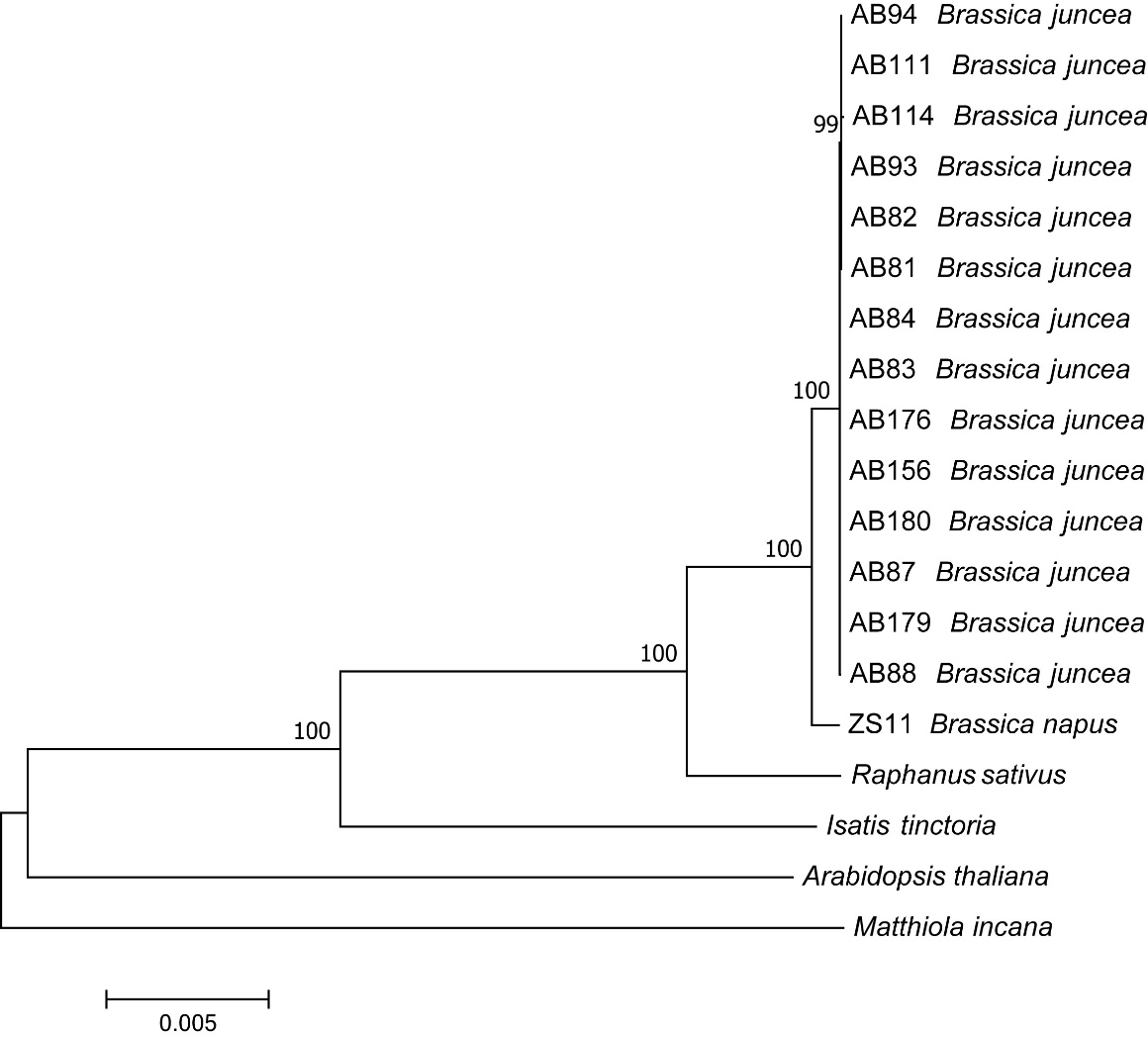
**Figure S1.** Representative genotyping results by HRM analysis. (A) The normalized and temperature-shifted difference plot indicated that three site-specific haplotypes were identified in a plate of 96 plant DNA samples using HRM407 primers. (B) The normalized and temperature-shifted difference plot showed that two site-specific haplotypes were identified in a plate of 96 plant DNA samples using HRM727 primers.



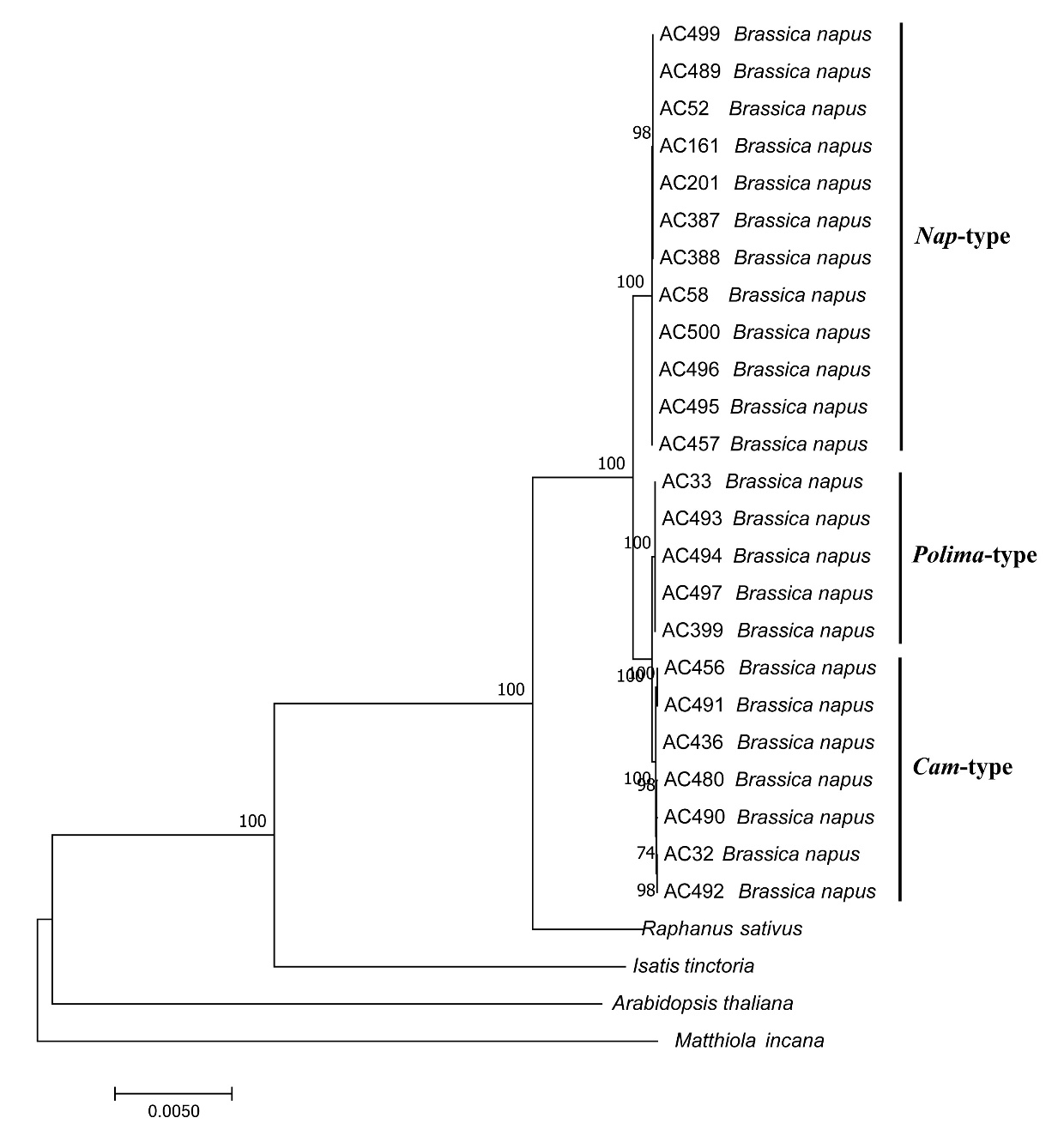
**Figure S2.** Representative genotyping results in a plate of 384 plant DNA samples by KASP analysis for primers mP1858 (A) and cP1225 (B).



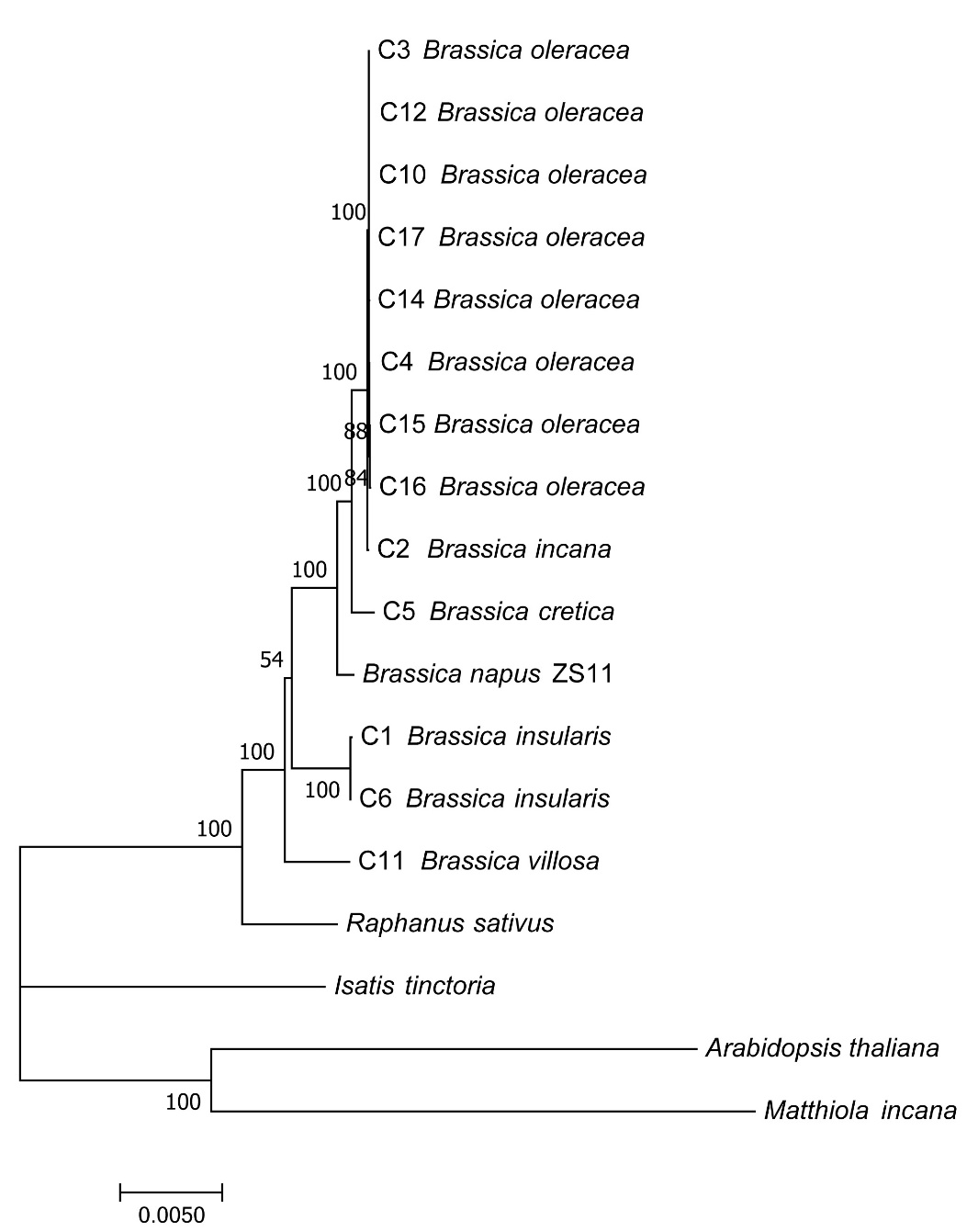
**Figure S3.** Phylogenetic tree of *Brassica* *rapa*. This tree structure was inferred using Maximum Likelihood method based on the entire chloroplast genomes from representative *B. rapa* materials. The sequence data for materials Zicaitai-1, Turnip-3 and Sarsons-1 from Li et al. (2017) were added.



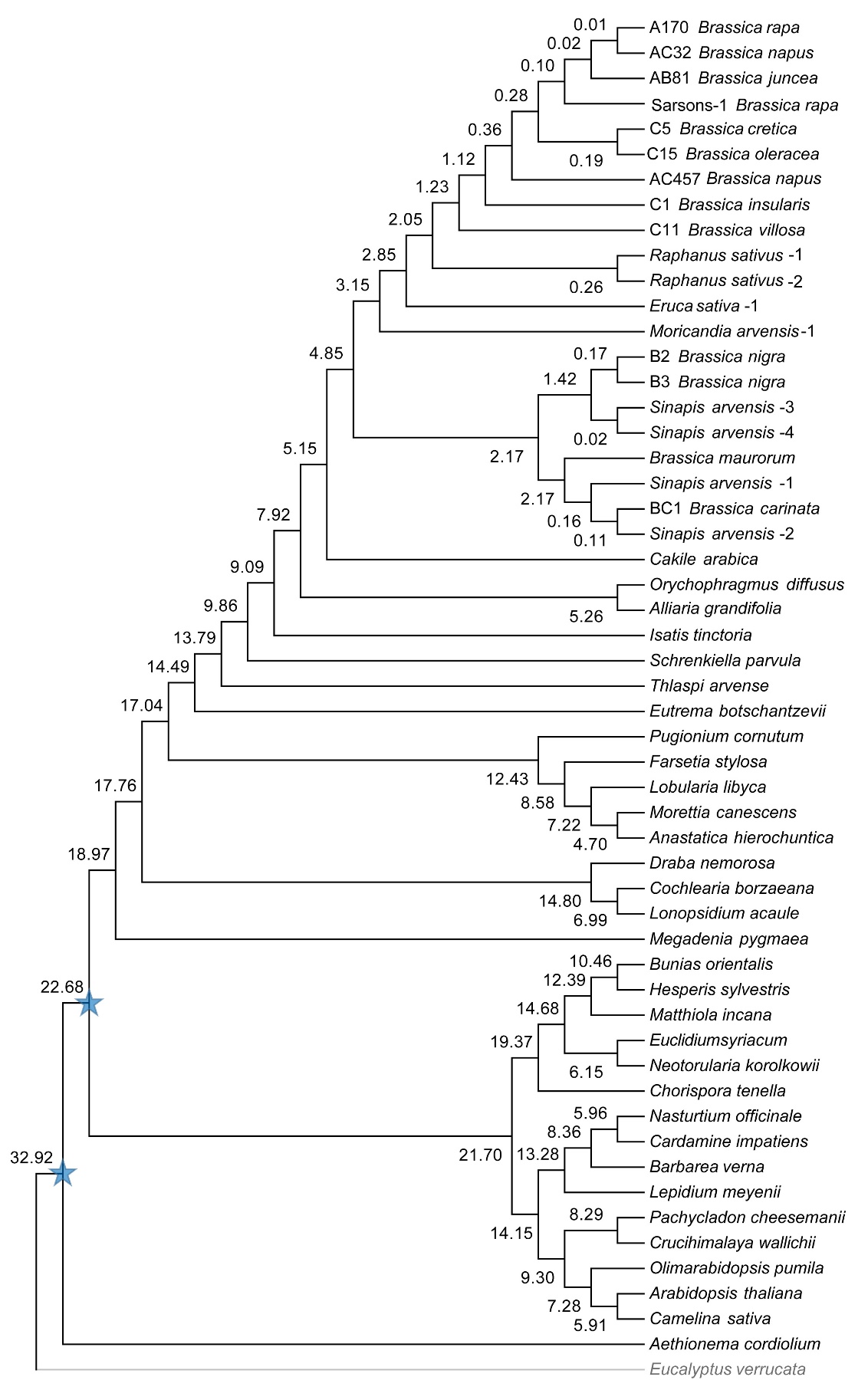
**Figure S4.** Phylogenetic tree of *Brassica* *juncea*. This tree structure was inferred using Maximum Likelihood method based on the entire chloroplast genomes from representative *B. juncea* materials.



**Figure S5.** Phylogenetic tree of *Brassica* *napus*. This tree structure was inferred using Maximum Likelihood method based on the entire chloroplast genomes from representative *B. napus* materials.



**Figure S6.** Phylogenetic tree of *Brassica* C-genome species. This tree structure was inferred using Maximum Likelihood method based on the entire chloroplast genomes from representative *B. oleracea* materials.



**Figure S7.** Timetree analysis using the RelTime method. The timetree was computed based on the phylogenetic tree of *Brassicaceae* family in Figure 4 using two calibration constraints labeled with blue stars and displayed only with topology. *Eucalyptus verrucata* labeled with lightgray was set as outgroup.