



Figure S7. Gene tree of *C. kanehirae*, *L. chinense*, and *A. montana*. **a.** The gene tree of WGD events meet the condition “The ancient gene pairs of *C. kanehirae* can be aligned with the gene pairs of the *L. chinense*”. **b.** The gene tree of WGD events meet the condition “The ancient gene pairs and the recent gene pairs of *C. kanehirae* can be aligned with the gene pairs of *L. chinense*”. All K_s values of *C. kanehirae* were equivalent to the peak value of the gene pair protein of *C. kanehirae* itself (last K_{S1} , ancient K_{S2}), which is aligned to that of *L. chinense* by BLASTP (E-value $< 1e^{-5}$). Based on the alignment results, genes that met one of the following two conditions were selected, the protein sequence was built with software raxml (parameter -m PROTGAMMAJTT), and the outgroup gene was fixed to *Amborella trichopoda* (*emm_27.model.AmTr_v1.0_scaffold00106.118*). Conditions: 1. The ancient gene pairs of *C. kanehirae* can be aligned with the gene pairs of *L. chinense*; 2. The ancient gene pairs and the recent gene pairs of *C. kanehirae* can be aligned with the gene pairs of *L. chinense*. The results show that ten groups met condition 1 and two groups met condition 2. The results indicate that after *C. kanehira* and *L. chinense* differentiated, *L. chinense* experienced one WGD event and *C. kanehira* experienced two WGD events.