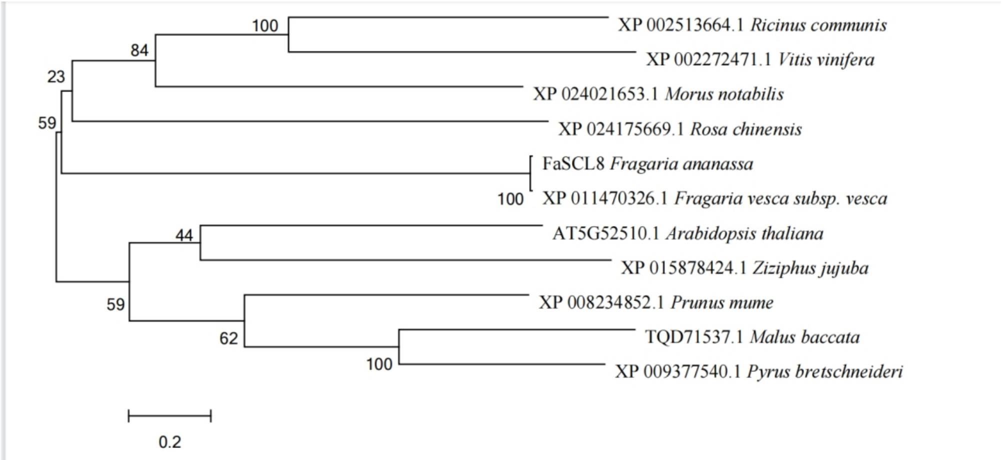

Supplemental Figure 3 Phylogenetic analysis of FaSCL8 and its homologs in plants.
Distances were estimated using the neighbor-joining algorithm. The numbers at the nodes (100) represent the percentage of 1000 bootstraps. The scale bar indicates the average number of amino acid substitutions per site. The phylogenetic tree was based on the full-length protein sequence of FaSCL8 and its homologous proteins in Fragaria vesca, Arabidopsis thaliana, Rose (Rosa chinensis), jujube (Ziziphus jujuba), mulberries (Morus notabilis), grape (Vitis vinifera), castor (Ricinus communis), apricot (Prunus mume), crab apple (Malus baccata), and pear (Pyrus bretschneideri).

301x138mm (144 x 144 DPI)