

Figure S1: Expression analysis of the structural gene involved in PA biosynthesis during the persimmon development phase in three varieties.

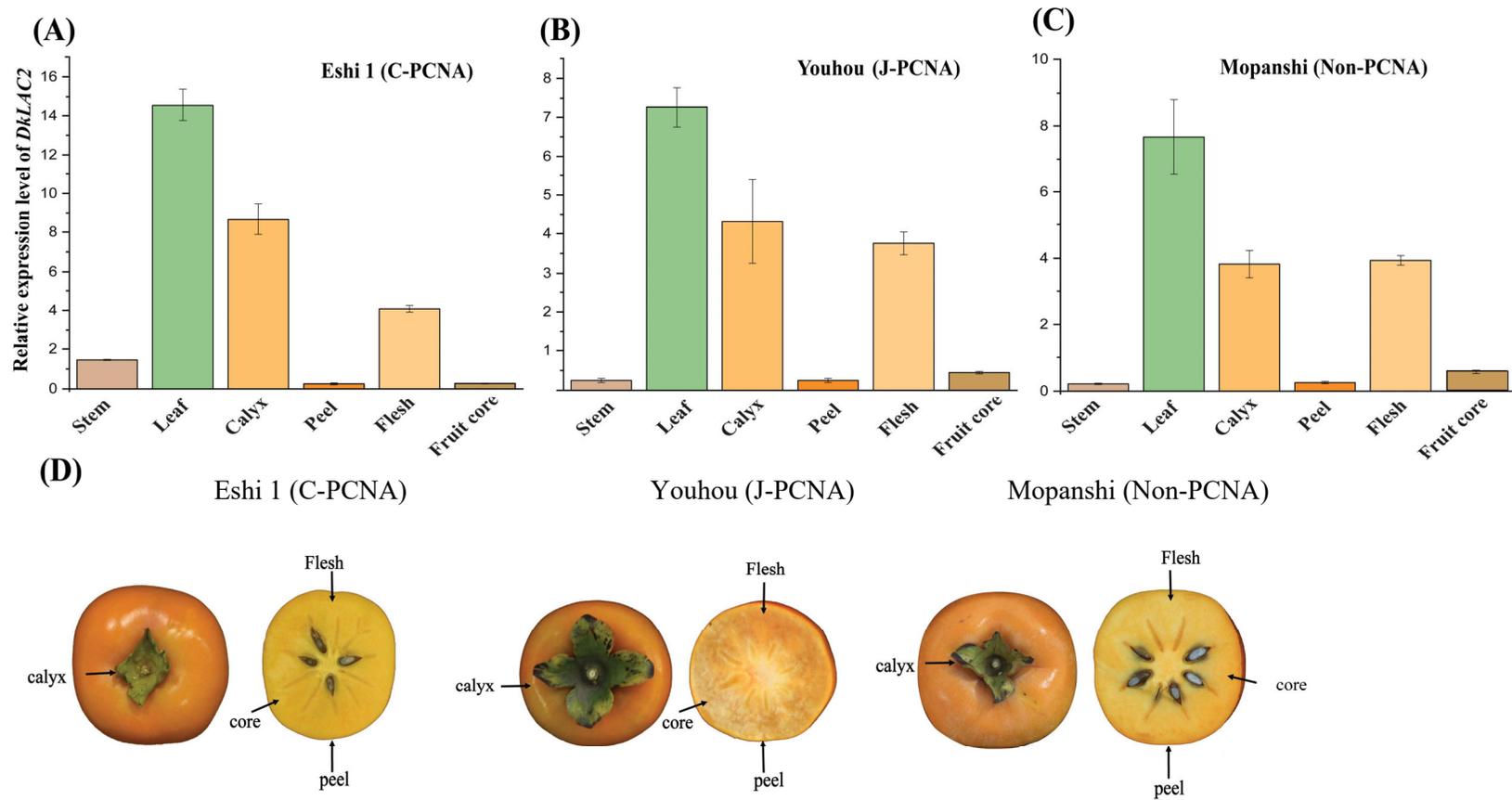


Figure S2: Expression of *DkLAC2* in different tissues of three persimmon varieties.



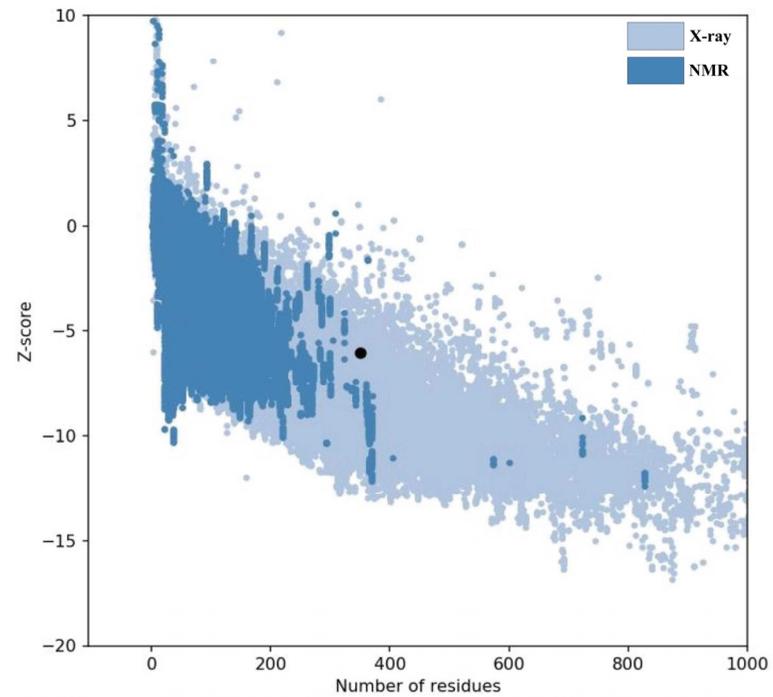


Figure S4: The Z-score represents the model quality score of predicted DkLAC2 protein by “ProSA web server”. The black dot indicating the score of protein model.

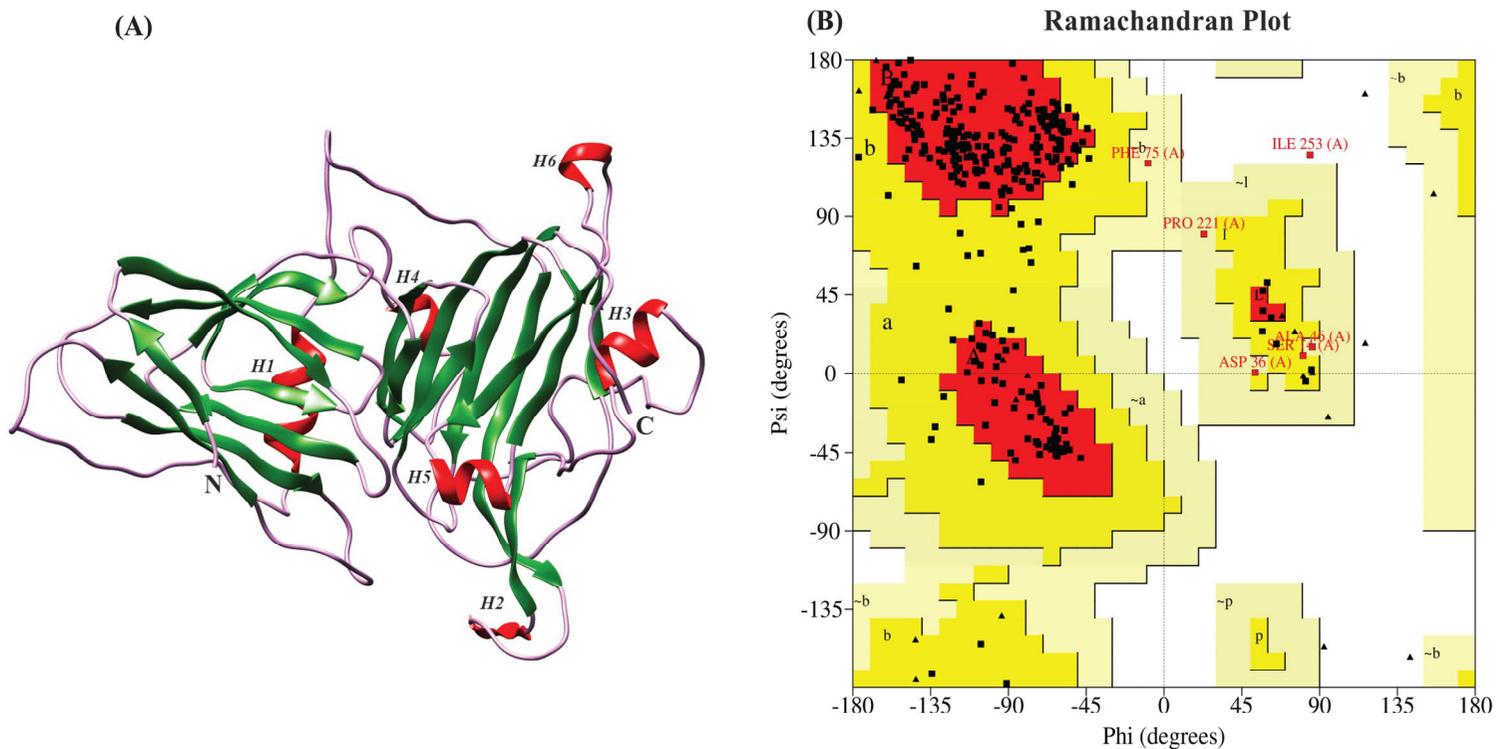


Figure S5: Three-dimensional structure of the DkLAC2 and assessment of DkLAC2 structure. (A) Ribbon representation of DkLAC2 protein. Red color: Helices (H); Green color:  $\beta$ -Sheets; Pink color: connecting loops; (B) Ramachandran plot suggesting the good quality of model. Red dots indicates the distribution of residues. The first quadrant and third quadrant represent the allowed region while second and fourth quadrant indicating the disallowed region

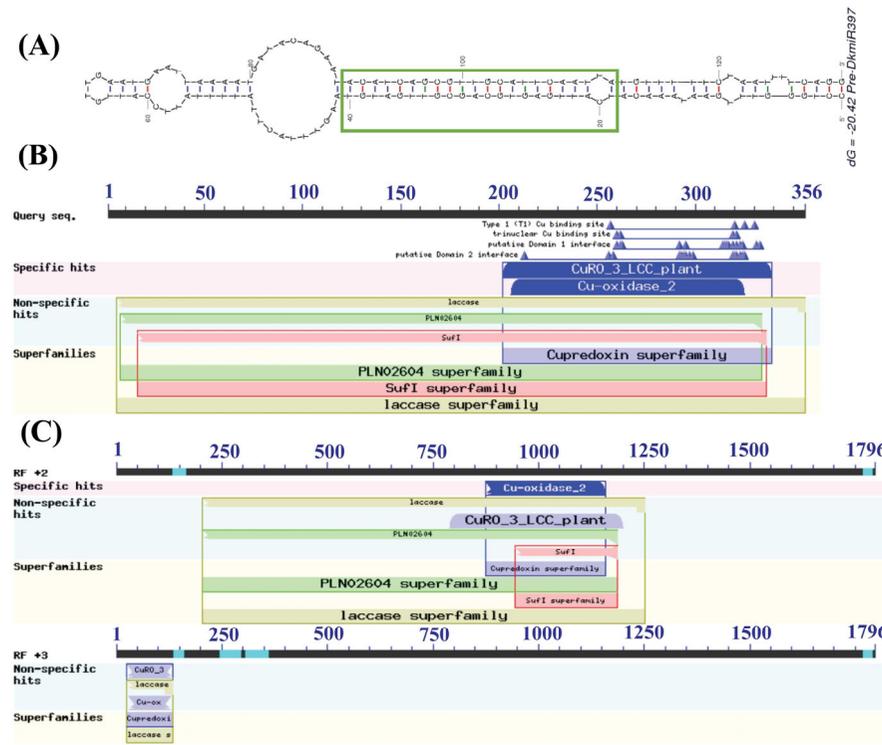


Figure S6: The secondary structure of *DkmiR397* precursor and characterization of *DkLAC2*. (A) Secondary structure of *DkmiR397* precursor. The mature sequence in green box. (B) Gene structure of *DkLAC2*. *DkLAC2* has typical copper ion domain and his rich conservative domain, which are typical characteristics of multi copper oxidation family. Sequence analysis showed that the size of *DkLAC2* was 1794 bp. (C) *DkLAC2* was predicted to encode a protein of 356 amino acids.

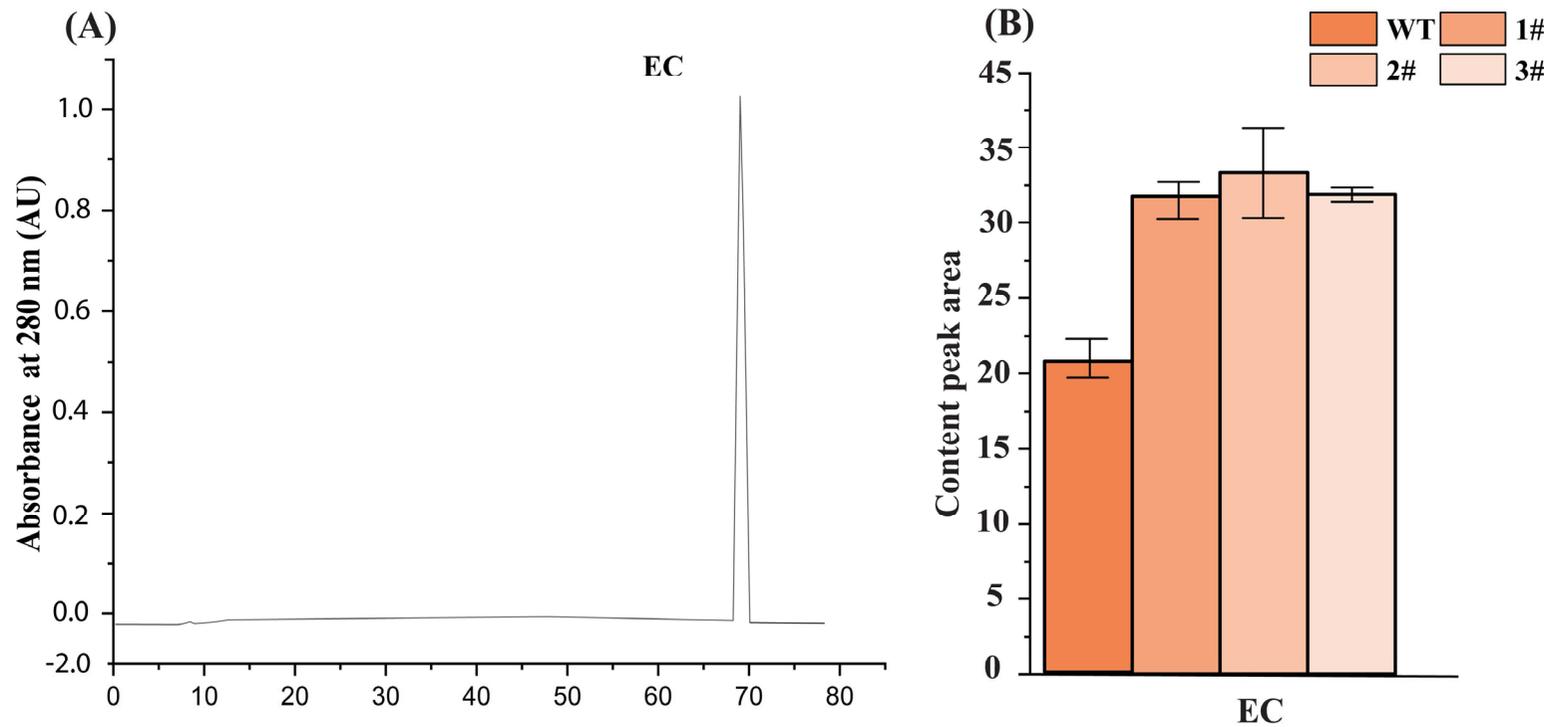


Figure S7: Detection of proanthocyanidin precursor epicatechin (EC) standard (A) and epicatechin contents measurement of *DkLAC2* transgenic *Arabidopsis* lines and wild-type seeds (B).