

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

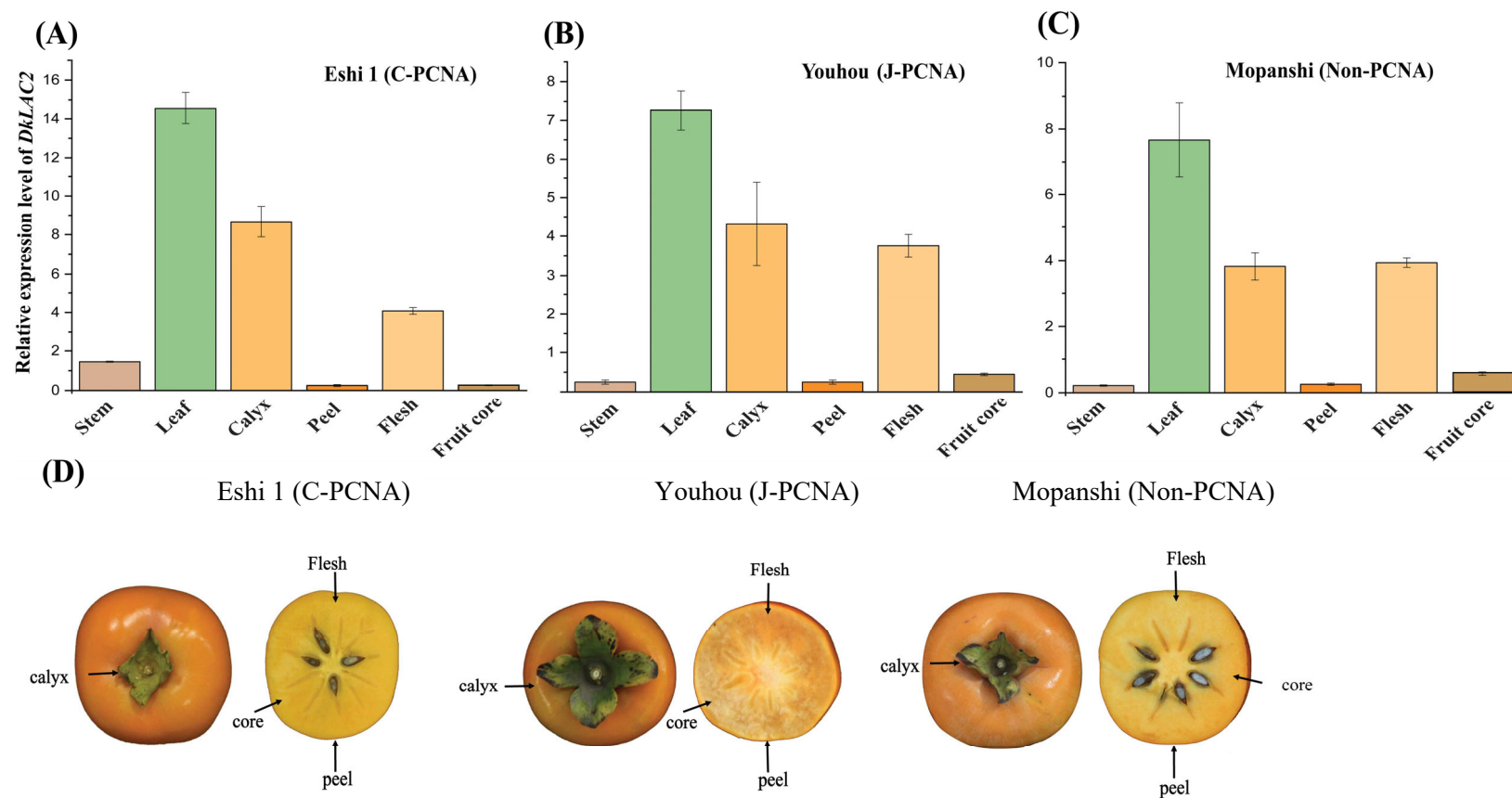


Figure S2: Expression of *DkLAC2* in different tissues of three persimmon varieties.

DkLAC2MQFGGRKNFILILLGFLLVDCFVHCH.ARTTHTYTTFTVREVPYTRLCSSKAILLVNS.FPGELIKAHKGKXIYVNVQNRASYNTIMHWHGVQCFERNFWSGDFVYITQCFIRPGGK 112
 ATLAC15MSHSFFNLFLISLFLYNN.CIAHTHTYTTFTVREVPYTRLCSTKAILLVNSQFPGEIIVKHKGDTIYVNVQNRASENIMHWHGVQCFERNFWSGDFEYITQCFIRPGSD 105
 OsLAC1MGIAKIPALLWELLAGLVLAVALVNPAGHAKTRHYDFFITEINNYTRLCHEKSIILVNGQFPGETIYARKGDFIYVNVHNNGNKNITIHWHGVQCFERNFWSGDFEYITQCFIRPGGN 115
 ATLAC14 MEFLKNIPNTIITKLTQITVFFLFVLLAFQIAE.AEIHHTFKIKSKAYTRLCNTNKILVNGEFPGETIKAYRGKLIYVNVNNANYNTILHWHGARGIRNFWSDGFEYVITQCFIRPGES 119
 GaLAC1MGLQQLGLVTFWVGVLFLSTLLLSN.ADVHTYEFFVRESNETRLCNTITILLVNDSPGGEIRVHRGDTVEVNVHNCQNGYGETIHWHGVQCFERNFWSGDFEYITQCFIQPGTN 111
 Consensus h f t lc l vn pgg gd vn v n t hwhg q rnpwsdgp tqcpi pg

 DkLAC2 FKQKIFLSIEGTLWWHAHSCWSEAHVHGAIIIYFKHGTGYEFPKPFDEEVEIILG.....DWKKS.GVMSVLEEFVQTGGAFNDSDAFTINGQEGDLVY.CSKFPGTFK 213
 ATLAC15 ELYKVFIESIDITVWWHAHSSWTRATVHGLIFVYHPPFQILFFPKRADHEVPIILG.....DWKKR.DVREVVEEFVRTGGAPNVSDALTINGHEGFLYF.CSKSDTFH 206
 OsLAC1 ETYQVILFEDEGTLWWHAHSCDFDRATVHGAIIVHFKRGTIFLFRKLDKEIEVILGNQFCITISILQCDAMQCQWVND.DVEHVLDAKAKRIGGDVEFSDNTINGQEGDMFELCSRDDTFK 234
 ATLAC14 VVYRIDLVDEGTLWWHAHSCNRRATVHGAFIVYFKRGSSYEFPKPFHREIPLILG.....DWKKKENIMHIPGKANKTGGEPAISDSYTINGQEGYLYF.CSKFETFK 221
 GaLAC1 ETYEIVLSIEGTLWWHAHSCNRRGSHGAFVILFAKKETYEFPFADQTIILLES.....WYDG.DYKQIIDDALAGVSPRQPSAYAISCHVGDYTG.CFNDTIFR 212
 Consensus e t wwhahs r vhg p f il w g 1 g g c f

 DkLAC2 LNVHGGKTYLIRIVNAAMNTILFFSIARHSLTVVGAGSYGWVATREKAKNPGVWLMHCHLBRHLTWGMEVVEIVKNGEEYSFLVVGWCSGNYP.KKDF.LKYNLVDPFLLNTVAVFKN 325
 ATLAC15 LTVKGGKTYRIRMVNAAMNLPFFAIANESLTVVSAGHYGWATREKAKNPGVWFMHCHLBRHLTWGMNVVFIKNGREFSFYVVGWCSGNYNISEDFSSRYNLDPEYKNTMTVFRN 321
 OsLAC1 VAVQQGNTYLRIVNAGLINDMFFAIAGHSLTVVGIDARYSWATREKAKNPGVWFMHCHLBRHLTWGMNTVFIKNGKFTFYVVGWCSGTFDE.RRDF.ATYNLVDPFQNTVSVFKN 354
 ATLAC14 ITVVRGRYLLIRIVNAVDEELFFAIANHSLTVVAKGDFYGWATREKAKNPGVWLMHCHLBRHLTWGMNTVFIKNGDPTYNFYVVGSGSGNFDR.RKDF.LRYNLVDPFEETTVGVFRN 333
 GaLAC1 MQVDSEKIYLLIRIVNAAMNEHFFAIANHSLTVVACDASYRWATREKAKNPGVWFMHCHLBRHSSWGMNTVILVRNGKTSFYVVGTCRGNFNN.KTDF.RTYNLVDPFLINTVHVEGR 322
 Consensus v y r na ff ia h ltvv d y w a r f a npgvw hch rh wgm iv g f vg g g dp ynl dpp t vp

 DkLAC2 ILQYSGNIIGGLRNLASKSHPIITIELINKFIPIELEIIPRRGTEVKVLKYNSTVEMVLQG...TNLVAGIFVNPSIDILQAYYKHINGVFGTRFPSVE.PLVFNFTAKYL 433
 ATLAC15 ILSYISSQIGGLRNLASKSHPIITIELINKFIQCNRAS..RGTEVKVLKYNSTVEMVLQG...TNLVAGIFVNPSIDILQAYYKHINGVFGTRFPSVE.PLVFNFTAKYL 440
 OsLAC1 IIVETD..IGGLRNLASKSHPIIACIALKFIPIELEIIPRRGTEVKVLKYNSTVEMVLQG...TNLVAGIFVNPSR..LCHEKSIINGVFGTRFPSVE.PLVFNFTAKYL 432
 ATLAC14 ILQYKGD..IGGLRNLASKSHPIITIELINKFIKILQEIPRRGTEVKVLKYNSTVEMVLQG...TNLVAGIFVNPSIDILQAYYKHINGVFGTRFPSVE.PLVFNIPNTII 441
 GaLAC1 IIFETNSTIIGGLRNLASKSHPIITIELINKFIPIELEIIPRRGTEVKVLKYNSTVEMTKLCNTITILLVVGIFVNPSIDILQAYYKHINGGLVTVWVGVL.PLVFNFTAKYL 438
 Consensus i y igglrnlaskshpi l kfi rgtevkvlkynstvem t lv fvnps l in t f v plvfn

 DkLAC2 PLELEIIPRRGTEVKVLKYNSTVEMVLQG...TNLVAGIDPLLNTVAVTNLVAGIDHFMHLHG'HCHLBRHLTWGMEVVEIVKNNHCHLBRHLTWGMEVVEIVKNGEE 554
 ATLAC15 PQNRAS..RGTEVKVLKYNSTVEMVLQG...TNLVAGIDPLLNTVAVTNLVAGIDHFMHLHG'HCHLBRHLTWGMNVVFIKNGRE 548
 OsLAC1 PLELEIIPRRGTEVKVLKYNSTVEMVLQG...TNLVAGID.QFPGPTITNLVAGIDHFMHLHG'HCHLBRHLTWGMNTVFIKNGKFTFYVVGWCSGTFDE 584
 ATLAC14 KTLQEIPRRGTEVKVLKYNSTVEMVLQG...TNLVAGIDPLLNTVAVTNLVAGIDHFMHLHG'HCHLBRHLTWGMNTVFIKNGKFTFYVVGWCSGTFDE 554
 GaLAC1 PLELEIIPRRGTEVKVLKYNSTVEMTKLCNTITILLVVGIDPLLNTVAVTNLVAGIDHFMHLHG'HCHLBRHSSWGMNTVILVRNGKTSFYVVGTCRGNFNN 548
 Consensus rgtevkvlkynstvem t lv tnlvagidhfmhlhg'hch rh wgm iv hch rh wam iv a

Figure S3: Alignment of the deduced amino acid sequences of DkLAC2, AtLAC14 (At5g09360, *Arabidopsis thaliana*), AtLAC15 (At5g48100, *A. thaliana*), GaLAC1 (AAR83118, *Gossypium arboreum*) and OsLAC1 (NP_918753, *Oryza sativa*) by DNAMAN.

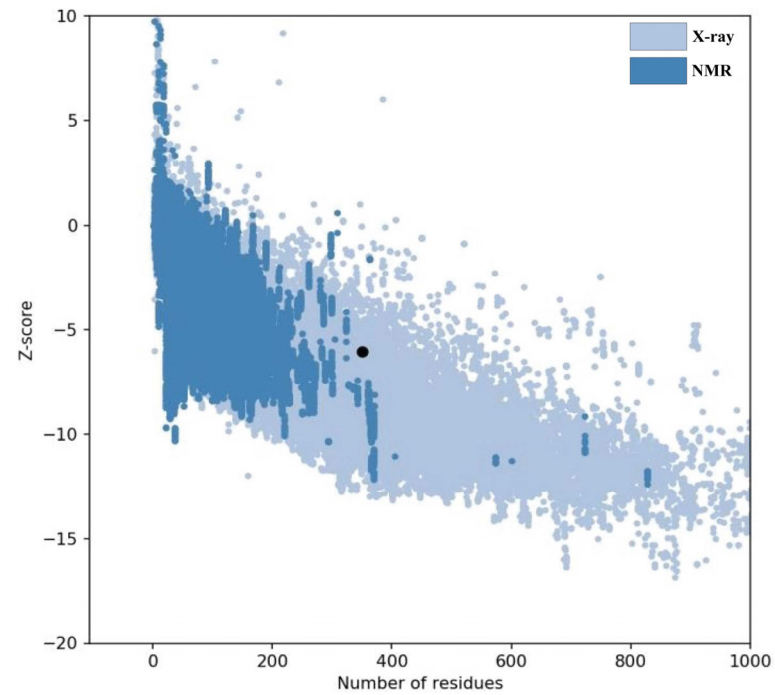


Figure S4: The Z-score represents the model quality score of predicted DkLAC2 protein by “ProSA web server”. The black dot indicating the score of protein model.

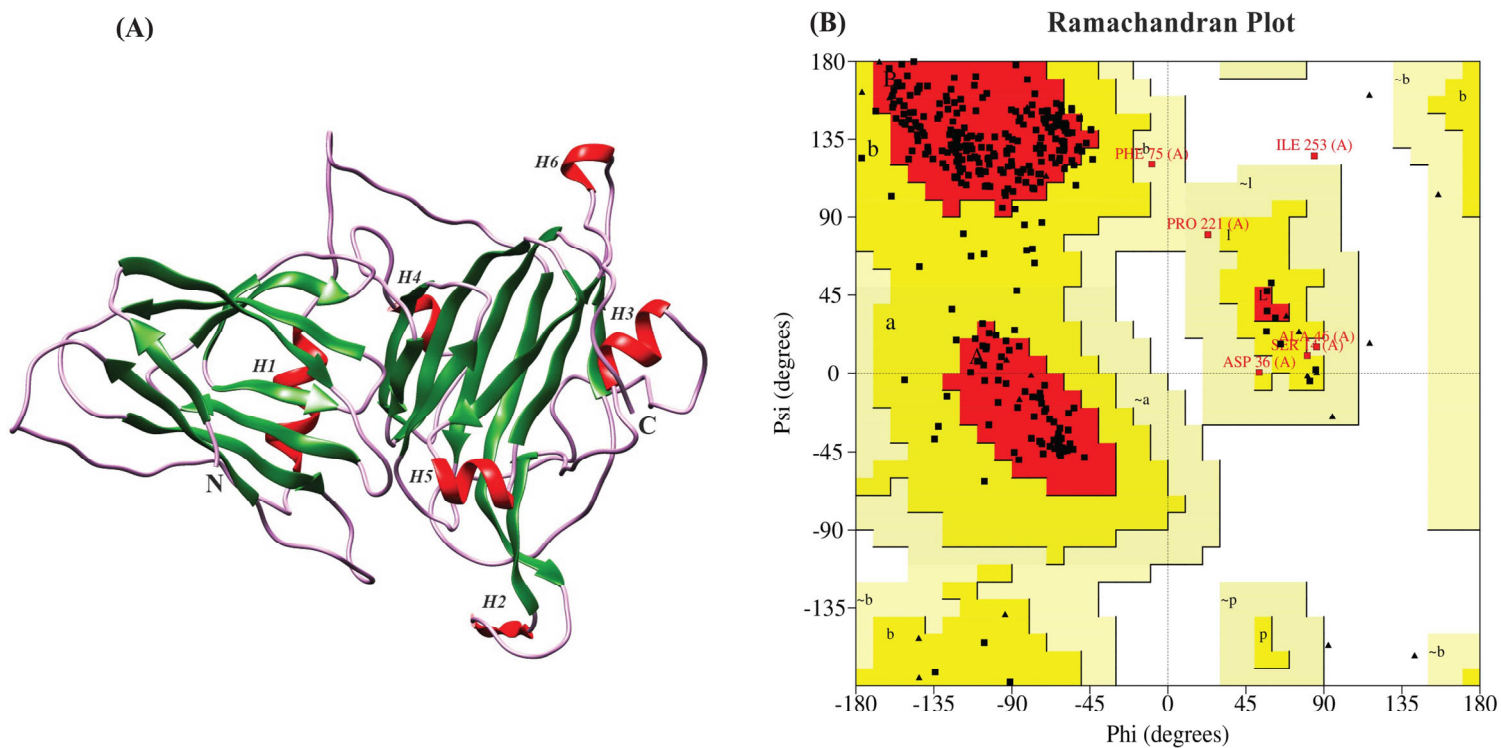


Figure S5: Three-dimensional structure of the DkLAC2 and assessment of DkLAC2 structure. (A) Ribbon representation of DkLAC2 protein. Red color: Helices (H); Green color: β -Sheets; Pink color: connecting loops; (B) Ramachandran plot suggesting the good quality of model. Red dots indicates the distribution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

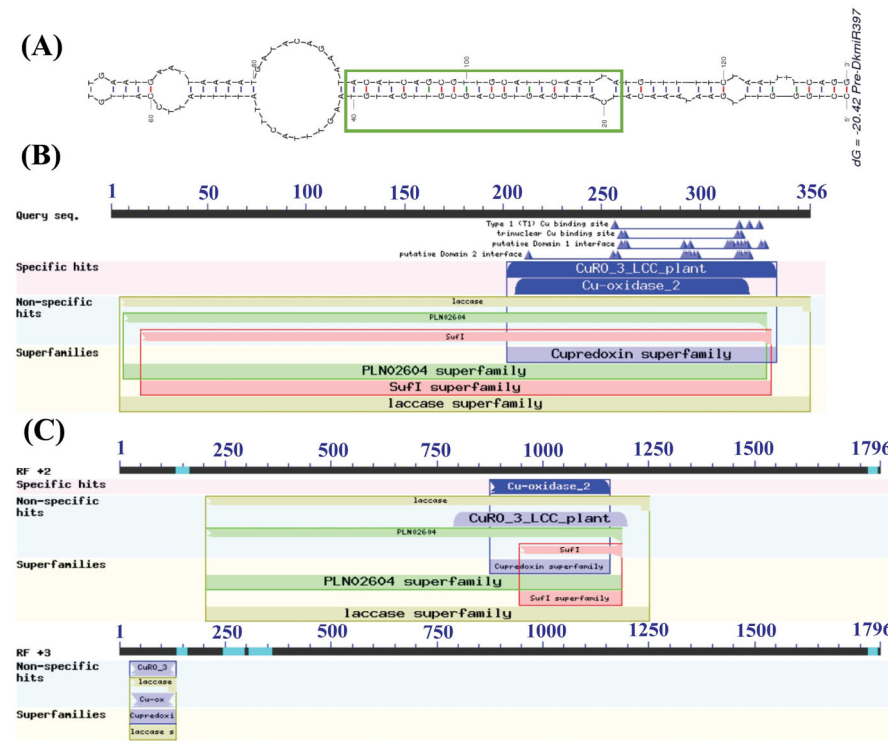


Figure S6: The secondary structure of *DkmiR397* precursor and characterization of *DkLAC2*. (A) Secondary structure of *DkmiR397* precursor. The mature sequence in green box. (B) Gene structure of *DkLAC2*. *DkLAC2* has typical copper ion domain and his rich conservative domain, which are typical characteristics 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.

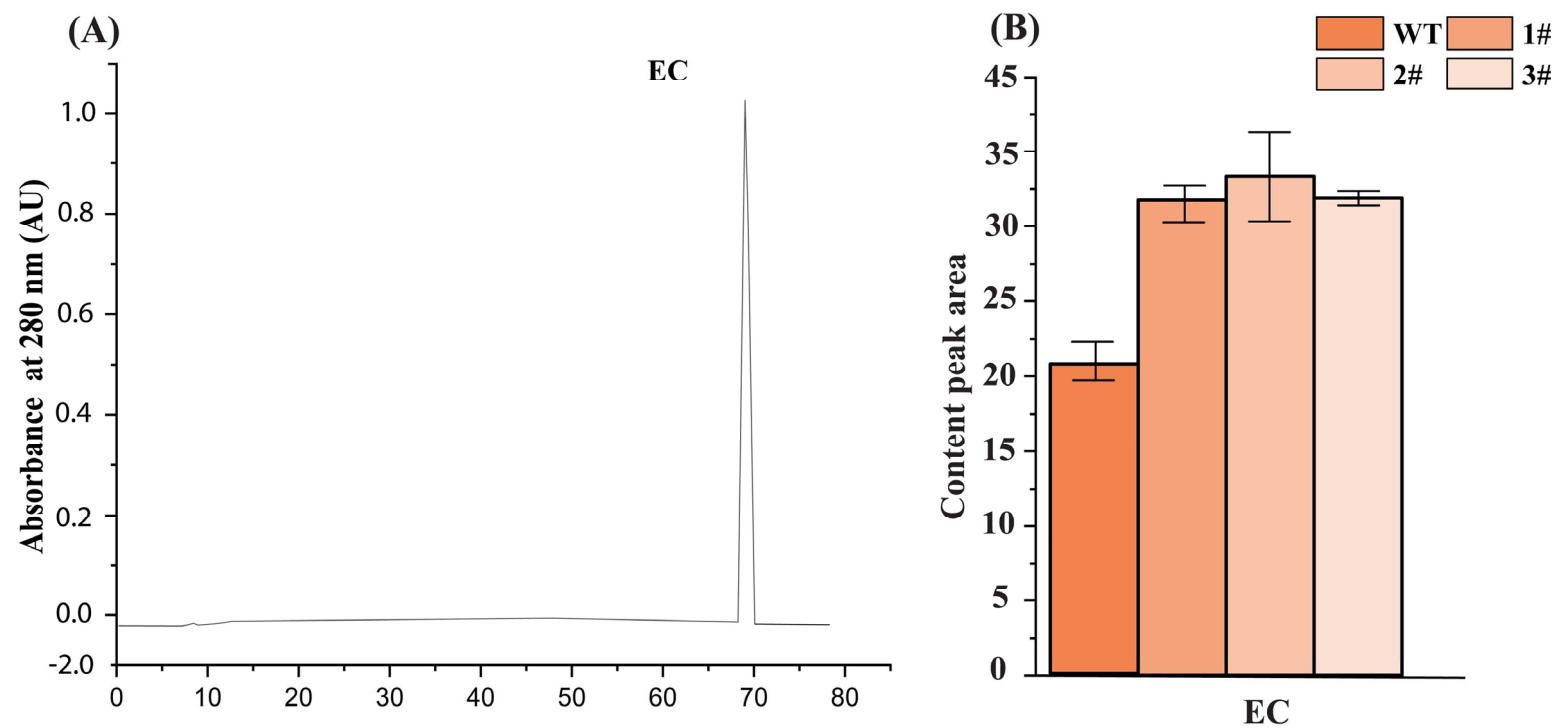


Figure S7: Detection of proanthocyanidin precursor epicatechin (EC) standard (A) and epicatechin contents measurement of *DkLAC2* transgenic *Arabidopsis* lines and wild-type seeds (B).