

Comparative Transcriptomic Analysis Reveals a Series of Single Nucleotide Polymorphism between Red- and White-fleshed Loquats (*Eriobotrya japonica*)

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Electronic Supplementary Material (ESM)

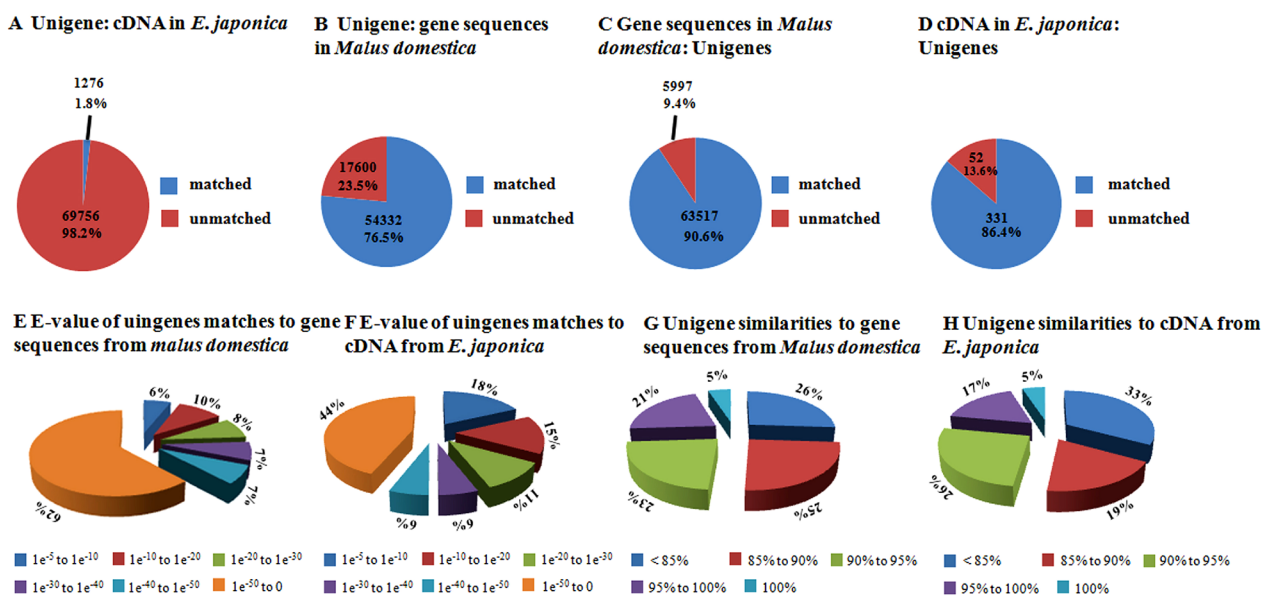


Figure S1. Summary of the nucleotide BLAST results between *de novo* assembled transcripts and cDNA sequence from loquat (*Eriobotrya japonica*) as well as gene sequences from the apple (*Malus domestica*) genome: (A) percentage of assembled transcripts matched with EST sequence from loquat; (B) percentage of assembled transcripts matched with gene sequence in the apple genome; (C) percentage of gene sequences in the apple genome matched with assembled transcripts; (D) cDNA sequences from loquat matched with assembled transcripts; (E) E-value of assembled transcripts matched to gene sequences of the apple genome; (F) E-value of assembled transcripts matched to cDNA sequences from loquat; (G) assembled transcript similarities to gene sequences of the apple genome; (H) assembled transcript similarities to cDNA sequences from loquat