

Figure S1. Frequency of *G. jasminoides* fruit unigenes

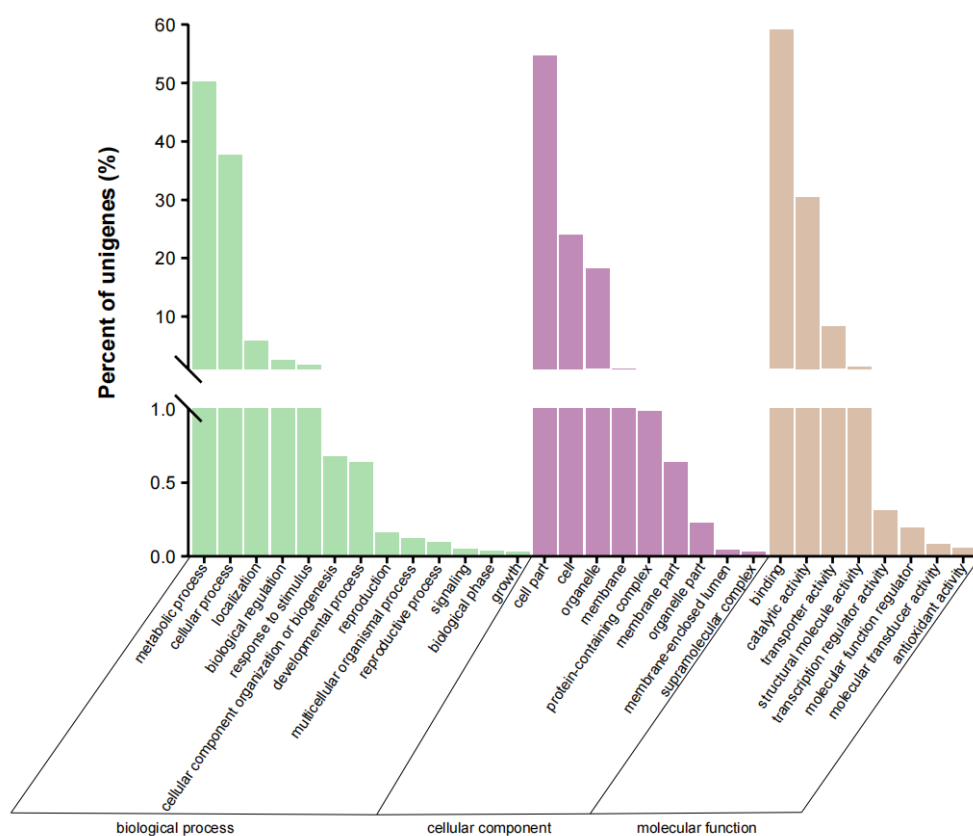


Figure S2. Gene Ontology ( GO ) pathways of *G. jasminoides* fruit unigenes

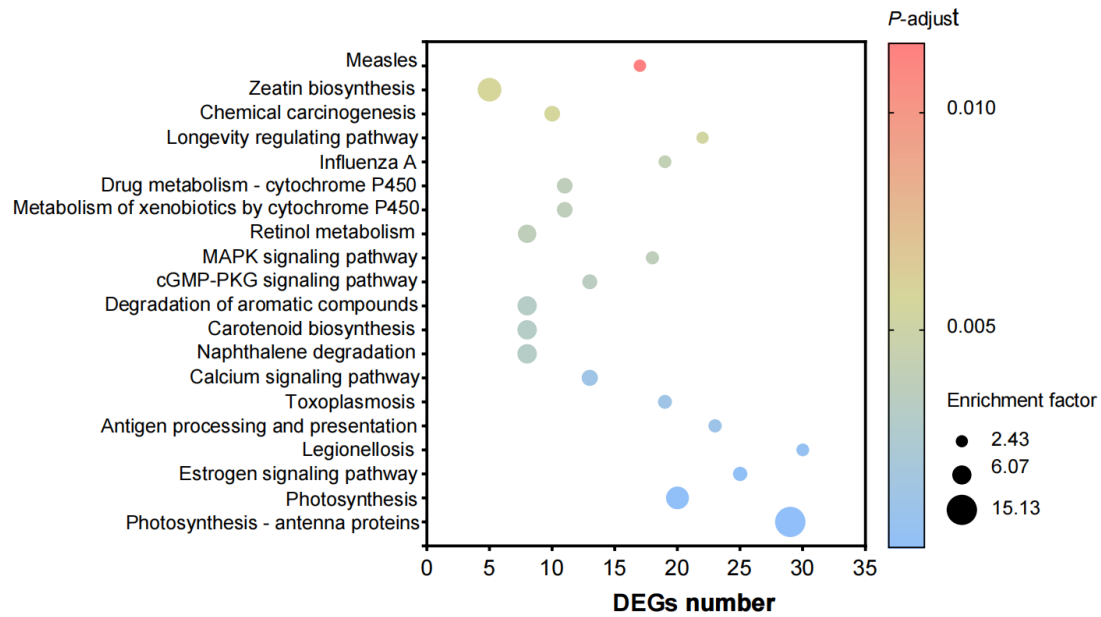


Figure S3. DEGs annotated by KEGG enrichment analysis in ' T1 vs T2 '

Table S1 qRT-PCR validation primer sequences

Gene ID	Forward (5'-3')	Reverse (5'-3')
DN80963_c0_g1_i1	CATGGTGGTGATGGCTCCTT	CCCTCTCGGATAACGGAAGC
DN79822_c0_g2_i1	GTGGATGGCCAATTCAGGGA	TATAGCTCCACACGCAGCAG
DN78530_c1_g1_i2	GATGGGGATGTGTTGCTCCA	ACGGAGCGCCTTTCCATTTA
DN85606_c3_g3_i1	TCGATGGAAGGTGCTGTTCT	GCTTGCCTCAGGTATCCTCT
DN81253_c0_g1_i1	TGGCATGGAGACCTTACTGAA	GCATGGCAAGCTCTCCTAGT
DN84511_c2_g4_i1	GTCACTGCTCTGCTGCTACA	GAAGCAGAGGAAGACTCGCA

Table S2. Assembling of the sequencing data

Statistics	Number	Total length ( bp )	Average length ( bp )	N50 ( bp )	N90 ( bp )
Transcripts	384 421	321 711 569	836	1859	288
Unigenes	298 869	152 447 815	510	567	246

Table S3. Functional annotation of *G.jasminoides* fruit in public protein databases

Annotated Databases	Total of Unigenes	Number of Unigenes	Percentage (%)
Annotated in NR	298 869	152 647	51.07%
Annotated in Swiss_prot	298 869	92 529	30.96%
Annotated in pfam	298 869	91 287	30.54%
Annotated in GO	298 869	23 358	7.82%
Annotated in KEGG	298 869	46 940	15.71%