

Supplementary Materials:

Table S1. Summary of transcriptome sequencing data.

Sample	Raw Reads	Clean Reads	Clean Base (Gb)	Q20 (%)	Q30 (%)	Clean Reads Ratio (%)
Nonspot-A	55,765,564	44,632,028	6.69	98.03	93.91	80.04
Nonspot-B	57,355,802	45,110,536	6.77	97.93	93.61	78.65
spot-A	57,715,006	45,380,086	6.81	98.03	93.91	78.63
spot-B	57,355,434	44,434,116	6.67	97.91	93.53	77.47

Q20 (%): the ratio of bases with Phred values greater than 20 to the total base. Q30 (%): the ratio of bases with Phred values greater than 30 to the total base.

Table S2. Summary of mapping ratio.

Sample	Total Mapping Ratio	Uniquely Mapping Ratio
Nonspot-A	51.71%	29.83%
Nonspot-B	55.81%	32.16%
spot-A	58.38%	33.90%
spot-B	55.98%	32.18%

Table S3. Functional Annotation in NR, KEGG, GO database.

Total	NR	GO	KRGG
22,188	17,871	15,588	19,864

Table S4. The KEGG analysis of DEGs and the most enrichment pathway (top 20).

NO.	Pathway	Gene_N umber	Background_Gene_ Number	RichFactor	Q-value
1	Photosynthesis - antenna proteins	12	18	0.6666667	2.62×10^{-13}
2	Phenylpropanoid biosynthesis	45	512	0.0878906	2.94×10^{-10}
3	Metabolic pathways	191	4806	0.039742	1.37×10^{-7}
4	Biosynthesis of secondary metabolites	109	2430	0.044856	2.31×10^{-6}
5	Photosynthesis	16	116	0.137931	2.31×10^{-6}
6	Flavonoid biosynthesis	12	105	0.114286	5.28×10^{-4}
7	Glycerolipid metabolism	19	266	0.0714286	2.14×10^{-3}
8	Porphyrin and chlorophyll metabolism	11	123	0.0894309	7.44×10^{-3}
9	Starch and sucrose metabolism	34	701	0.0485021	1.11×10^{-2}
10	ABC transporters	15	235	0.0638298	2.23×10^{-2}
11	Plant-pathogen interaction	36	797	0.0451694	2.23×10^{-2}
12	Amino sugar and nucleotide sugar metabolism	19	341	0.0557185	2.48×10^{-2}
13	Regulation of autophagy	10	156	0.0641026	8.79×10^{-2}
14	Terpenoid backbone biosynthesis	9	137	0.0656934	9.90×10^{-2}
15	Stilbenoid, diarylheptanoid and gingerol biosynthesis	7	100	0.07	1.40×10^{-1}
16	Phenylalanine metabolism	8	132	0.060606	1.90×10^{-1}
17	Cyanoamino acid metabolism	9	159	0.0566038	1.93×10^{-1}
18	Tryptophan metabolism	5	66	0.0757576	2.02×10^{-1}
19	Limonene and pinene degradation	5	73	0.0684932	2.68×10^{-1}
20	Glycerophospholipid metabolism	10	202	0.049505	2.68×10^{-1}

Table S5. Summary of miRNA transcriptome sequencing data.

Sample	Raw Tag	Clean Tag	Clean Base Ratio (%)
Nonspot-A	26,663,561	23,352,936	87.58
Nonspot-B	26,865,118	24,896,769	92.67
spot-A	28,739,122	26,605,438	92.58
spot-B	27,644,225	25,926,370	93.79

Table S6. Summary of mapping ratio of clean tag.

Sample	Clean Tag	Total Mapped Tag	Percentage (%)
Nonspot-A	23,352,936	18,062,942	77.35

Nonspot-B	24,896,769	19,039,072	76.47
spot-A	26,605,438	21,395,134	80.42
spot-B	25,926,370	19,516,924	75.28

Table S7. mRNA QPCR primer.

Primers	Primer Sequences (5'-3')
PeAct4 real F	TTGTGAGCAACTGGGATGACAT
PeAct4 real R	GCCACGCGAAGTTCATTGT
PeMYB2 real F	ATGGTTGTTACCTTCCTGATGATGAGAAC
PeMYB2 real R	TTCCACCAGTCCTCCTCCTTC
PeMYB7 real F	CAAGGGAGCATGGACCAAGGAAG
PeMYB7 real R	TTTGAGATCGGGACGGAGGTAAT
PeMYB12 real F	AACAAAAGTAGACGCAGCACTACCAAC
PeMYB12 real R	TTGGGACGGATCATTTCAGCC
PeMYB16 real F	ACTTTCCTCAGCAGCATCTACC
PeMYB16 real R	GGCTTCCAGCTTGGCTATTATCT
PeCHI real R	GGTGATAAAGGAGATCAAGGGTT
PeCHI real R	GCTGTAGAAGAAGTTGCAGGAAA
PeF3H real F	TCATTACCTGAGCAACGGTCGG
PeF3H real R	AACGCCCGCATCGAAAGCC
PeDFR real F	TTGAGGATATGTTTGATGATGCTATTAAG
PeDFR real R	TTCTCAGTGTGGCGGTAAGAG
PeANS real F	TGCCACAGCGTTCTTACCG
PeANS real R	AAACCGCCACGAGATCCGTAC
PeC4H real F	TGCTGCCATTGAGACAACCCTGTG
PeC4H real R	GCGATGGATGTCCGGCTCTGTGA
PeFLS real F	GAGTACGGGAGGCAGATGGTGAG
PeFLS real R	CGGGTTGCGGGCATTTAGGATAG
PeF3'H real F	GCCCTGCTGGCTTGGCTTGATT
PeF3'H real R	TCCACCATTGACTTCGCCGTTCT
Pe4CL real F	GGGCCAGTGCTATCAATGTGCTT
Pe4CL real R	CCAGGCTGATTGTAGCCAAGGGA
Pe4CL2 real F	GGGTACGTGGATGATGACGAGGAG
Pe4CL2 real R	GAGACTACGGCAGAATCGGCTATGTT
PebHLH real F	TCAACTCCACAATGGCTAATGGCAAG
PebHLH real R	ATTTATTTCACGAATGCTGGCTCTC

Table S8. miRNA QPCR primer.

Primers	Primer Sequences (5'-3')
PeU6_F	CATCCGATAAAAATTGGAACGA
PeU6_R	TTTGTGCGTGCATCCTTGCG
PemiR858_F	GCGGGCTTTCGTGTCTGTT
PemiR858_R	GTGCAGGGTCCGAGGT
PemiR858-RT	GTTGGCTCTGGTGCAGGGTCCGAGGTATTTCGCACCAGAGCCAACAAGGTC
PemiR156g_F	GCGGGCGCTCTCTAGACTTCT
PemiR156g_R	GCTCTCTAGACTTCTGTTCATC
PemiR156g-RT	GTTGGCTCTGGTGCAGGGTCCGAGGTATTTCGCACCAGAGCCAACCATGAC