

Table S1 Statistics of transcriptome sequencing quality of *wt* and *ym*

Samples ID	Raw Base (bp)	High-quality Rate (%)	Clean Base (bp)	Q20 (%)	Q30 (%)	Clean Reads	Mapping reads (Mapping Rate) (%)
<i>wt_1</i>	6,599,985,900	92.43	6,100,861,800	98.05	94.58	40672412	33305419 (81.89%)
<i>wt_2</i>	5,847,663,000	92.23	5,393,373,600	97.97	94.36	35955824	29114898(80.97%)
<i>wt_3</i>	6,135,290,100	93.02	5,707,457,700	97.86	93.86	38049718	31966031(84.01%)
<i>ym_1</i>	6,665,650,500	93.11	6,206,678,100	98.09	94.65	41377854	36222391 (87.54%)
<i>ym_2</i>	6,254,909,700	92.96	5,815,113,300	98.03	94.58	38767422	34719318 (89.56%)
<i>ym_3</i>	6,499,759,500	93.14	6,054,097,500	97.74	93.86	40360650	35306479 (87.48%)

'\_1, \_2, \_3' represent three replicates.

Table S2 qRT-PCR primer sequences of reference gene, 19 DEGs and *Lut 5*

Gene ID	Forward primer	Reverse primer
UBQ	AAGTGCAGAGGCTCAGGAAG	ACATCAATCACCACCGGCAG
DCAR_032504	CTATGGTTCGGGTCTTTAGCAGG	TCAAAAAAAGGGGAATGTCAACG
DCAR_029630	TCCCCATCATTCGCAGGGA	TCTGCGAGCCAGCTTTGAAC
DCAR_027950	AGGAAGTCTGTCAAGGCCCC	CACCAGTGAGGTAAGACGGC
DCAR_019192	TCCCTGCATCCCCTACATGG	TGCATCAGCTACGTCAGGGT
DCAR_027951	CTTTGGCCGGAAGGCAGTC	GGCAAAAGTCTCGGGGTCTAG
DCAR_031498	GAAAGTGAGCAAAATGCGGGG	GTCTCCAACCTTGCCCATC
DCAR_007901	CTTCGCCATCATTCGCTGGA	TGAACCACACAGCTTCTCCG
DCAR_029209	AATGGTCTGGGTTCATCTTTTTTG	CCGTGGATTAGCTCAGCTTCTC
DCAR_009633	AAAAGATCAAACTGACAGCCCT	GTATCCGTCGACATTAGCACCA
DCAR_027952	AGGAAGTCTGTCAAGGCCCC	CCGGAGAATGGCCCCAAGTA
DCAR_023434	CTGGCACTGGACGTATTGGG	CAAGCTAACCCGCGAGAAA
DCAR_003942	GAGACCTTTGCCAAGAACCGT	GCCCAAGTAGTCAAGTCCACCC
DCAR_003943	GTTGTTGACCCCTTTACCCC	CTCCAATGGACCCTTTCTGT
DCAR_015960	GTGAGGTCTCGTTCAAGCCG	CAGCTAGCGCCAAAGGATCA
DCAR_018610	CTCCAGTGACATCGAGCCCA	GGCAAGACCAACCTCCACTC
DCAR_007902	GCTCTTGGCTGTGTCTTCCC	GCATCTCTGCTGTGTGACCC
DCAR_005105	ATCACAGATCTTTAGCGAGGGTG	TGTGTAGCCCAGATGGCAAG
DCAR_007169	TGGGGCACAAGGTCATTCT	ATTGCATTGGTCATGTCCTGGG
DCAR_003120	GACCCTTCACTAGCCACCCAAAGA	TGAACCAGTGTCTGCCATCAGC
DCAR_021059	CCGATGGCACCAAATCCCAA	GCCACCCCGTACCATTTCAG
DCAR_004826	CGAACCTACTGCGGGACATCACTT	GCCAGCATTAGCCACCAATTCC
DCAR_023843	ACCCAACCCAAATGAGACCAACCA	CTCTGCTGTAAGTCTGGAGGTGT
DCAR_005572	GCTTCTAGCGCCGTTCAAGT	TCAAAGGGTAGCCGGGTCT
DCAR_025914	TCTTCTTGTCTGAACGACGAATCA	CAGTTCCCAGGGTGAAAGCA

Table S3 Information of total reads, resequencing data quality and sequence variation of *wt* and *ym*

Samples ID	Raw Base(bp)	High-quality Rate (%)	Clean Base(bp)	Q20 (%)	Q30 (%)	Total SNP	Non-synonymous mutant SNP	Non-synonymous mutant gene
<i>wt</i>	18,553,191,518	90.46	16,782,627,630	96.66	92.79	4,407,439	-	-
<i>ym</i>	16,379,439,006	90.73	14,860,701,931	96.73	92.94	5,500,413	216,984	22,889

Q20, Sequencing base quality values, when base quality is 20, sequencing error rate is 1%.

Q30, Sequencing base quality values, when base quality is 30, sequencing error rate is 0.1%.

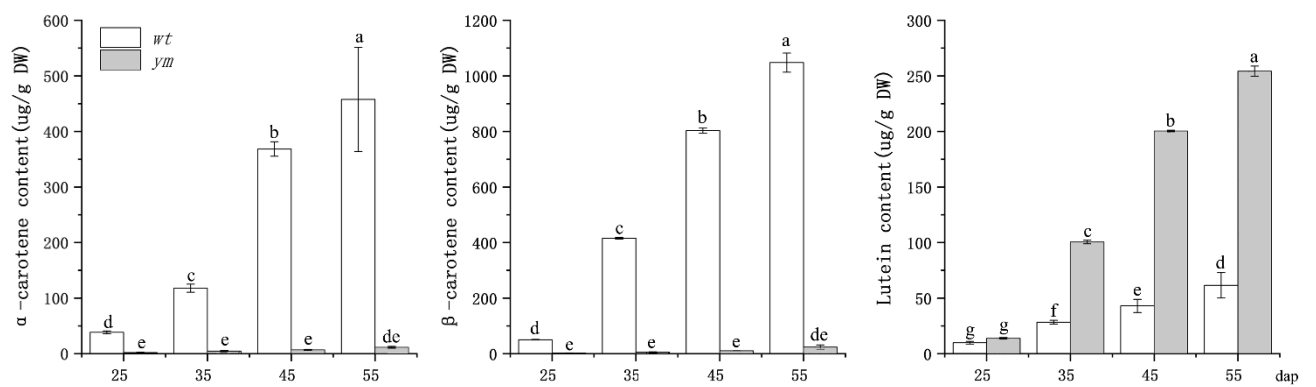


Figure S1: Carotenoid compositions of the root of *wt* and *ym* at different development stages. Means ( $\pm$ standard errors) per unit of DW. Lowercase letters indicate significant differences at the 0.05 level

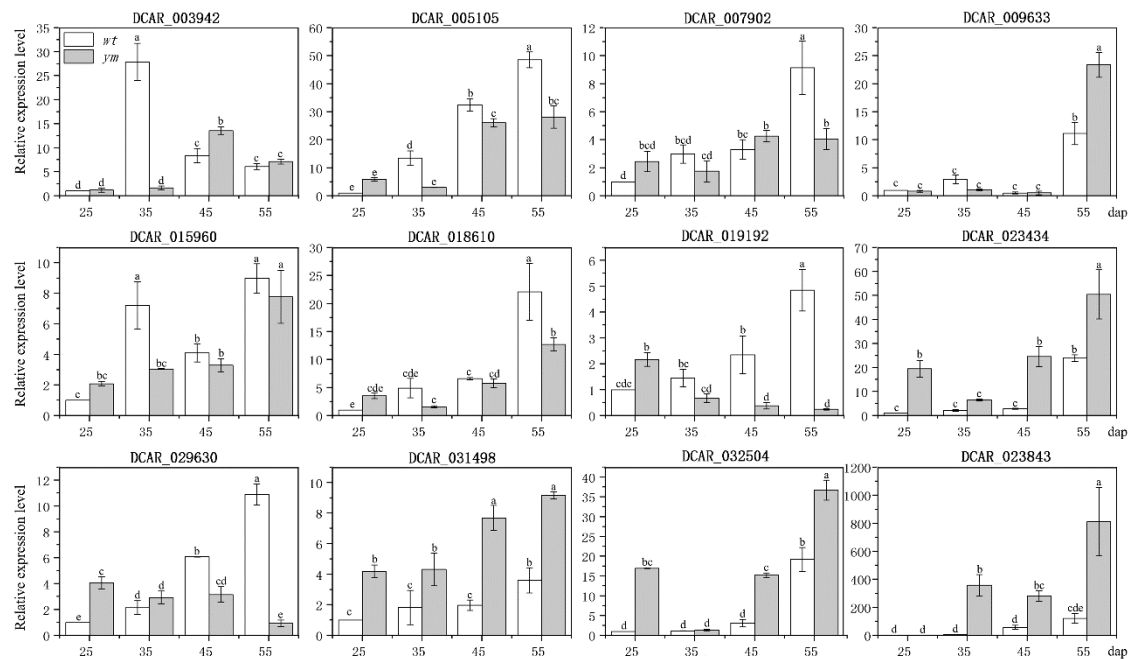


Figure S2: Expression level of 11 DEGs significantly associated with lutein content and *Lut 5* by quantitative real-time PCR. Lowercase letters indicate the least significant difference at 0.05 between *wt* and *ym* at different development stages. Values are the mean  $\pm t * SE$ , with *t* value from a student-*t* table

wt	ATGGCTTCTTTCTCTCTGCACTCATGTCTTCCATCATCATCAATTACACACCTTGAAGCCCAACTCACAAAAAGCTTTGAT	80
ym	ATGGCTTCTTTCTCTCTGCACTCATGTCTTCCATCATCATCAATTACACACCTTGAAGCCCAACTCACAAAAAGCTTTGAT	80
wt	TTTTATTAGCCCAACACATGTTTCTTTCTTGAAAAACAACCTCAAAGCTTAGACTTGTCACTTCCTGTTCTGCAAAAGGATG	160
ym	TTTTATTAGCCCAACACATGTTTCTTTCTTGAAAAACAACCTCAAAGCTTAGACTTGTCACTTCCTGTTCTGCAAAAGGATG	160
wt	ACTCTGCTTCCTTCCTGCTGGAGATAACATCCCAAGCAATTTTGCATAATAGAAGGGCCGAAACTGTTCAAGATTTT	240
ym	ACTCTGCTTCCTTCCTGCTGGAGATAACATCCCAAGCAATTTTGCATAATAGAAGGGCCGAAACTGTTCAAGATTTT	240
wt	GTTTCAGATGCAAAACACAGGAAATCCAAGACAACATAAGGAGTAGGCGCAATAAAATATTTCTTCTCATGGAAGAGGTCCG	320
ym	GTTTCAGATGCAAAACACAGGAAATCCAAGACAACATAAGGAGTAGGCGCAATAAAATATTTCTTCTCATGGAAGAGGTCCG	320
wt	AAGGTTACGAGTACAACAACGCACCAACGTTTAAAGCATTGACAGTGATAGCATGGAGGAGAATGAGATGCCTGACA	400
ym	AAGGTTACGAGTACAACAACGCACCAACGTTTAAAGCATTGACAGTGATAGCATGGAGGAGAATGAGATGCCTGACA	400
wt	TTACATCAACTATTCCCTTCCTCTCTCGTATGACGCCAACTACATTGAAGCAGCTCTACCTGACAAGCTTTGCATTTGTA	480
ym	TTACATCAACTATTCCCTTCCTCTCTCGTATGACGCCAACTACATTGAAGCAGCTCTACCTGACAAGCTTTGCATTTGTA	480
wt	TCTGGAATCATCGTCTTTGGGGGTCTTCTCGCACCAGTTCCTTGAACATAAAATTGGGTATTGGCGGCACGTTGTATGAAGA	560
ym	TCTGGAATCATCGTCTTTGGGGGTCTTCTCGCACCAGTTCCTTGAACATAAAATTGGGTATTGGCGGCACGTTGTATGAAGA	560
wt	CTTCATCCGCAATATGCACCTTACCTATGCAGTTGAGTCAGGTGGACCCCATAGTAGCGTCTTTTTCAGGTGGAGCAGTGG	640
ym	CTTCATCCGCAATATGCACCTTACCTATGCAGTTGAGTCAGGTGGACCCCATAGTAGCGTCTTTTTCAGGTGGAGCAGTGG	640
wt	GGGTCATATCAACTTTAATGTTGATTGAAGCTAGTAATGTTGAGCAACAAGAGAAGAAAAGGTGCAAGTATTGCCATGGA	720
ym	GGGTCATATCAACTTTAATGTTGATTGAAGCTAGTAATGTTGAGCAACAAGAGAAGAAAAGGTGCAAGTATTGCCATGGA	720
wt	ACTGGGTACTTGGCTTGGCTCGCTGTTCTGCAAGTGGTGTGTGCTTAAATATTGAACCCATTTCAGAGTCCATGCTCTTC	800
ym	ACTGGGTACTTGGCTTGGCTCGCTGTTCTGCAAGTGGTGTGTGCTTAAATATTGAACCCATTTCAGAGTCCATGCTCTTC	800
wt	TGATCAACCATTACGGGCTCCCAACACAAAAAGGTGTACAAACTGCTCAGGAGCAGGAAAAGGTGATGTGCCCAACATGCC	880
ym	TGATCAACCATTACGGGCTCCCAACACAAAAAGGTGTACAAACTGCTCAGGAGCAGGAAAAGGTGATGTGCCCAACATGCC	880
wt	TGTGCACTGGAATGTTAATGGCAAGCGAACATGACCCCCGGTTTTATCCTTTTGATTA	938
ym	TGTGCACTGGAATGTTAATGGCAAGCGAACATGACCCCCGGTTTTATCCTTTTGATTA	938

Figure S3: Sequence alignment of *Or* gene between *wt* and *ym*.