

## Article

# Comparative Transcriptome and Pigment Analyses Reveal Changes of Gene Expression Associated with Flavonol Metabolism in Yellow Camellia

**Supplementary Table S1.** Sequences of primers used for the qRT-PCR.

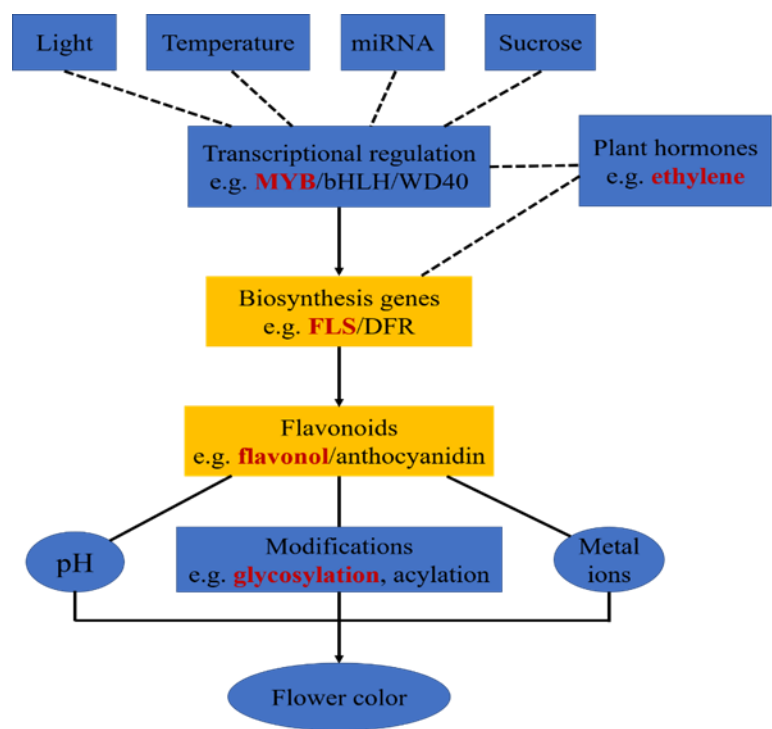
Target	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>GAPDH</i>	CTGTCGATGTCTCAGTGGTTGAC	TGATCTCATCATAGGAAGCCTTCTT
<i>c114511.graph_c1(FLS1)</i>	GGTGGATTTTCGTCGTCGAT	ACAAGGAGACAACAAGAATGTCATG
<i>c132672.graph_c1(FLS2)</i>	AGGAGAGAGTGCAAGCCATTG	TTGTTCGATCCTGGCTGTTCA
<i>c136629.graph_c1(GT74D1)</i>	AATGGCAGAGGCCCTAAAGC	TGATGTCTCCTCCACGAAACC
<i>c103558.graph_c0(GT83A1)</i>	CTCCCCATAGGCCCACTTCT	GATGTTGATCGAGCCATTCCA
<i>c125858.graph_c0(GT86A1)</i>	CCTTAATCGCCTTCTTCAACGT	TTGTGCGATAAGAGACCGATCA
<i>c125858.graph_c6(GT86A2)</i>	TGGGCATAGCTACCGAAGGA	AACCGGGTTCACCAAAAAGC
<i>c136900.graph_c1(GT72B1)</i>	CAGCTCCCTCGCCTTTTGT	CTTGTGTCGTCGTAAGAAATCG
<i>c136900.graph_c2(GT72BL)</i>	AATAGACCCAACCCCCCTCTT	GGAGCCCAGCTAAGGATGGT
<i>c114749.graph_c0(GT90)</i>	TGATTGGTGCCTTTGTTTGC	CGGAGATGTGATGGAAGTTATGG
<i>c131595.graph_c0(GT8)</i>	CATGGGTTGGGTGGTGACA	TCAACCATGGCTTACCTTTGC
<i>c138052.graph_c0(GT90L)</i>	TGGGCTTGTCATGCAATC	CGAGCAATGTTACGTTTG
<i>c134185.graph_c1(MYB1R1)</i>	CCGCCAAATGCCATTCT	CCATGGTGGTTGGGAAAATT
<i>c140967.graph_c2(MYB3)</i>	TTCTTTGTGGCCTTTGACCTTT	CATGCTCCCTCCCTCTCAAG
<i>c140113.graph_c1(ACS1)</i>	CTAAAGCCAGGAAAACCCATGT	GCCTCCCCACTTCACTAGCA
<i>c132432.graph_c1(ACS7)</i>	TGTTTCATGGCTTGTCAGTGT	GTGGAGGACCGCGTAAAG
<i>c147573.graph_c0(ACS12)</i>	CAGAAGCAGCCGCAGTTGA	ACCAGGTCCTGAAGCATTCTG
<i>c95148.graph_c0(ACO1)</i>	TCATTGTCATGGAGAATCTTAATGG	GCCCCAGAACTCACAAGAATCT
<i>c128783.graph_c0(EIN2)</i>	ACATTGAAGGCAAGAGCTCCTT	GCTTGAGCTGAACTGCAAAGTG
<i>c128783.graph_c1(EIN2L)</i>	AAGCCAAAGCATCAAACAAAGC	ATGTGGGCAGTAGCACGTCTCT
<i>c140267.graph_c1(EIN3)</i>	AGTGCAAGCCCCGTGATG	TCTGATGGCTGCTTCTCTTC
<i>c108582.graph_c1(ERF109)</i>	GCTCGGATGGGTTCCAAATT	ACCCAGGACCAGGAGTTCTTC
<i>c127403.graph_c0(ERF109L)</i>	AGTGCCCTTTTTGTCCTCTTGA	AACGCCCTCTATTCCCAGTTC
<i>c138285.graph_c0(ERF017)</i>	GCCCGGTGGATCATTTGATA	TGGGAGAAGCTGACGTCACA
<i>c96422.graph_c1(ERF1b)</i>	CCCCTCTCCATGCTATACCT	CTTATGATCAAGCCGCTTTTCG

**Supplementary Table S2.** Summary of sequencing reads.

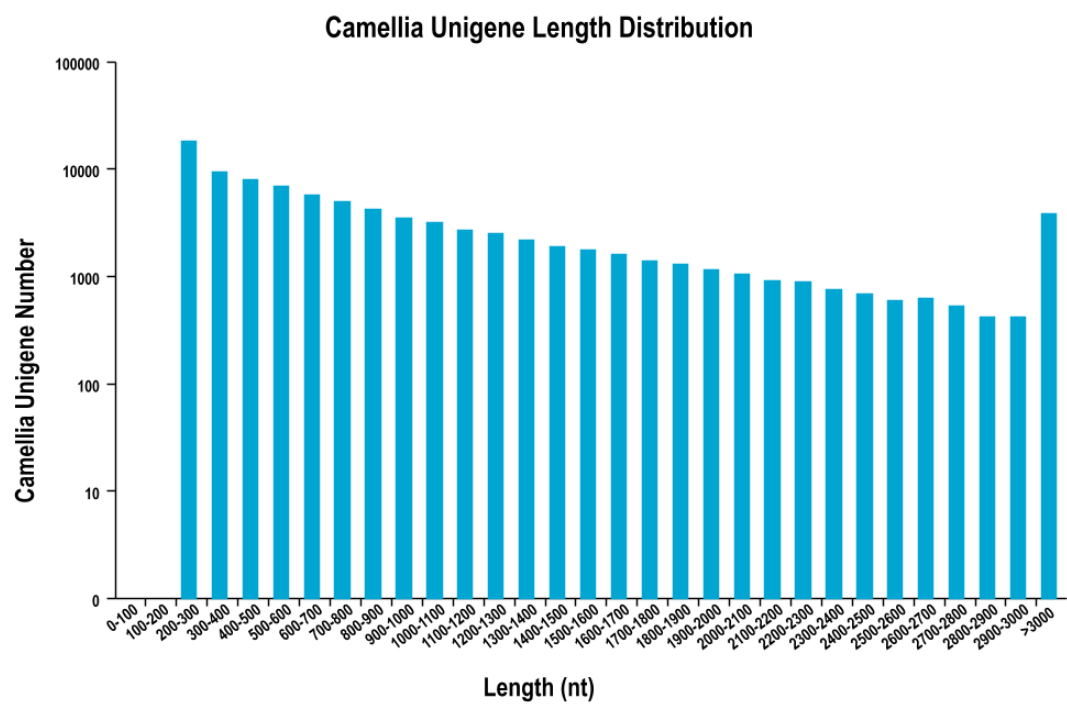
Sample	Clean Reads	Clean Base (G)	Clean Reads Ratio (%)	Q30 (%)	GC Content (%)	Mapped Ratio (%)
CN-1	24492072	7.32	98.50	92.48	45.73	58.99
CN-2	26621922	6.97	98.66	93.24	44.70	61.26
CN-3	25021699	7.49	98.68	93.36	44.45	60.06
ZHQ-1	23291183	6.97	98.87	91.55	45.02	60.39
ZHQ-2	26535549	7.94	98.92	91.78	45.14	61.21
ZHQ-3	24595056	7.36	98.87	91.66	45.24	61.50
HXL-1	24476951	7.33	98.74	93.74	45.25	59.81
HXL-2	243250094	6.96	98.65	94.23	45.04	59.71
HXL-3	22711885	6.79	98.89	93.58	46.30	61.83
XSL-1	25784479	7.71	98.72	91.14	45.33	58.98
XSL-2	24934847	7.46	98.75	91.17	45.11	59.33
XSL-3	24781860	7.41	98.69	91.31	45.12	59.62

Supplementary Table S3. Summary of the functional annotation results of unigenes.

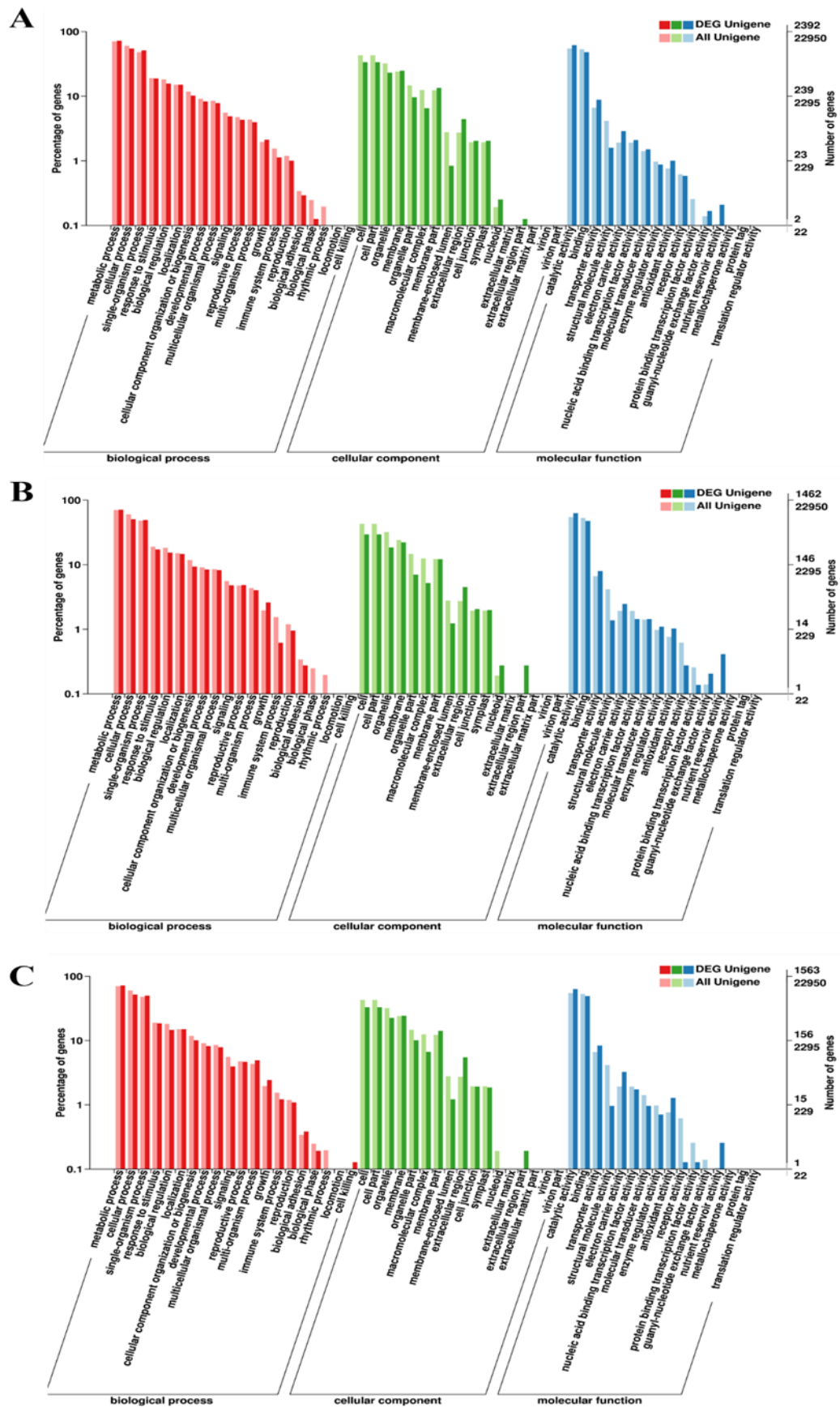
Database	Annotated number	Annotated percentage (%)
NR	38864	49.78
SwissProt	24308	31.14
GO	22950	29.40
COG	10907	13.97
KOG	21940	28.11
eggNOG	36574	46.85
KEGG	13792	17.67
Pfam	24481	31.36
Overall	39886	51.09



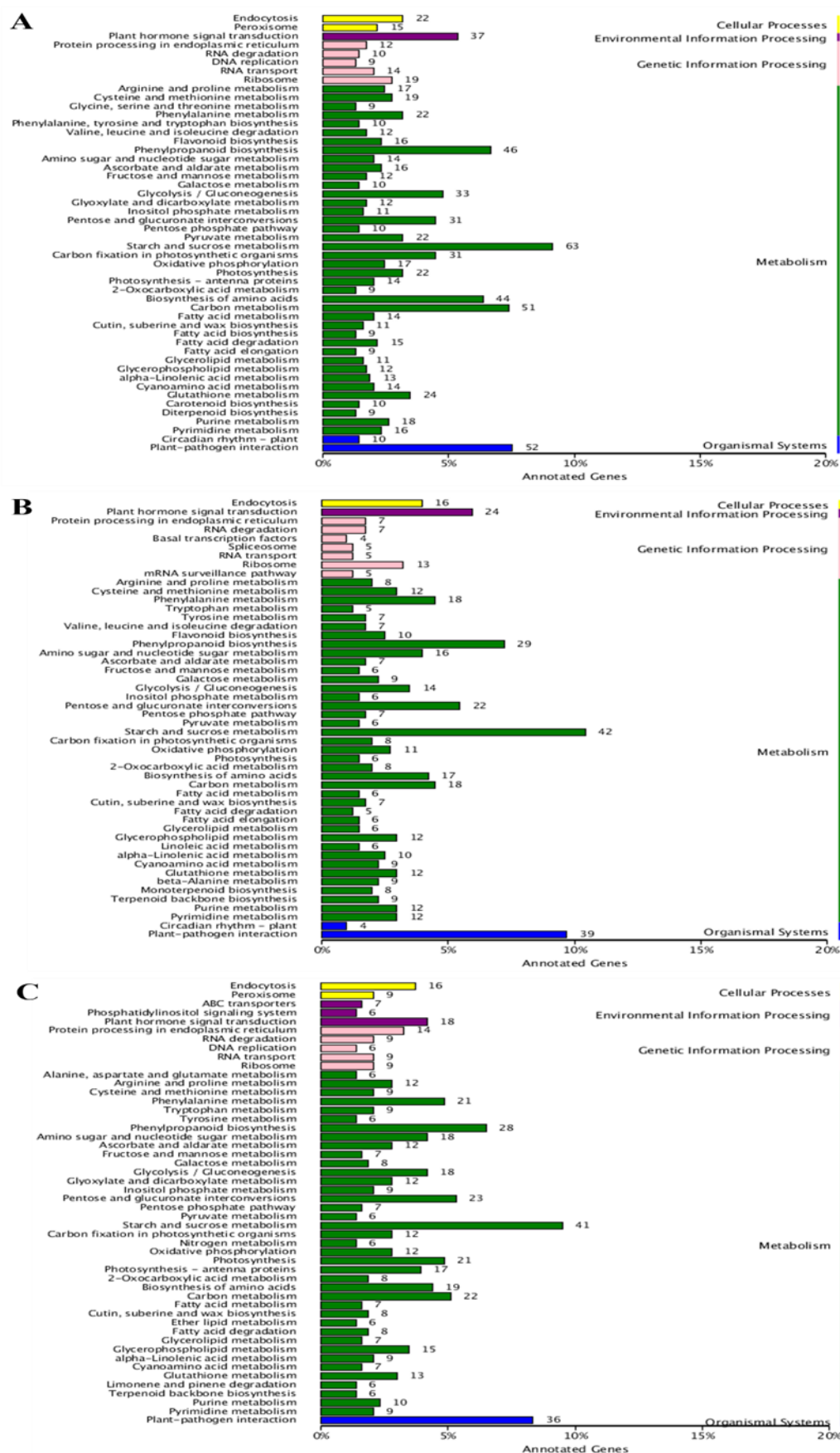
Supplementary Figure S1. Regulation of flower color in plants. In red are those factors related to this article.



Supplementary Figure S2. Distribution diagram of unigenes.



Supplementary Figure S3. Gene ontology (GO) analysis of CN vs ZHQ (A), CN vs HXL (B) and CN vs XSJ (C).



**Supplementary Figure S4.** KEGG and functional enrichment analysis of CN vs ZHQ (A), CN vs HXL (B) and CN vs XSJ (C).