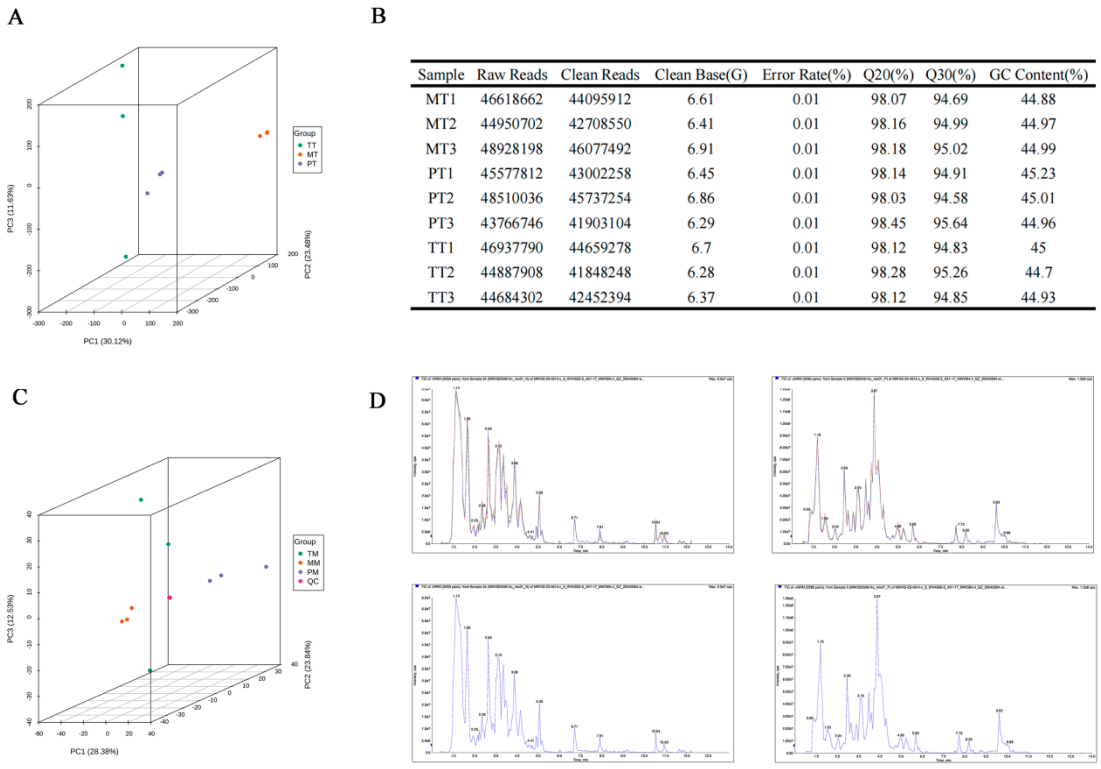
Supplementary Material

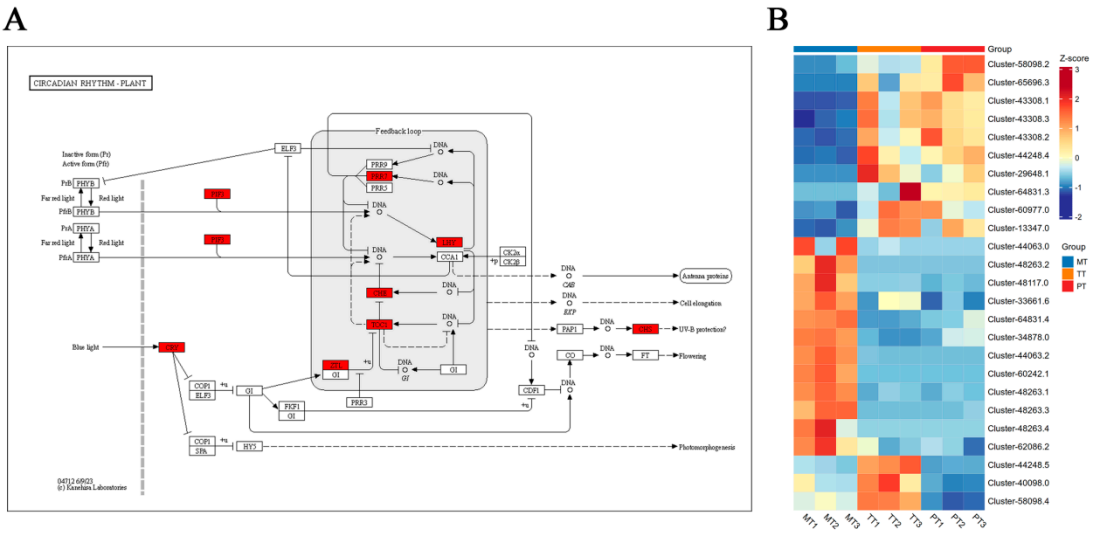
Supplementary Table S1. Primer sequences used for qRT-PCR.

Primer name	Primer sequence(5′-3′)	
	Forward primer	Reverse primer
Cluster-49792.0	CACTGCCTCTACGACATCACTGGG	CATCCAAACAACTGCTGCTCCAC
Cluster-53279.0	CCCAATTAGTCGTCTCATCGCTTAC	GAACCCTGTCCTTCCCTTCAAAA
Cluster-34553.0	GGGGTCAAGCTACAGACAGTCAC	TTGCCAGTCATCTTATCACAACC
Cluster-54898.1	TACGCCAAATGGTGTCAGTGTCT	CCAAACTTGAAGTAAGGGCAAAC
Cluster-54049.4	TCTTGCCCTACCTTAAATCTCAA	CTCATAGCCATTCTCACATCCTC
Cluster-44248.4	ATGGGTAGCAATTCAAAAACCATTG	CAATGGTTTTTGAATTGCTACCCAT
Cluster-66385.1	GATTCGGATGACTTTATGGAGAA	CATTGTGGAGGTCTTTGATCTTT
Cluster-64831.3	CTTCGCTAACGAGCCTGAGGACG	CATCAATCACTTCTCCACCAAACAA
Cluster-43308.2	AGCATTCCAACCCTTGGGCATCT	TGGTCCGAACCCGAATAGCACTC
Cluster-51029.0	ACCAACTTCTTGAAATGGAGGCA	GGTAAATTCATAGCCAAGTACACTCAT
Cluster-65584.0	TTGGAGGGCGACAAAGGACTGAA	CCAAACCAGCCACAACCACTAAA
Cluster-48263.1	ATGGATAGCTTGGGTTGGGATGGCA	TGCCATCCCAACCCAAGCTATCCAT
Cluster-11963.1	TTGTCCCTTTGCCTCACTATAACT	TGATCTTGATGACTTCCCTCCAT
Cluster-30153.1	TCATCATAGTCATCATGGGTCTG	GATCTTTGGGTCCAGTTGGTTAA
Cluster-23067.0	CGGAAGAACGGATAACGAGATTA	TTGCCATAGGATGACATGAATGA
Cluster-19707.0	TCAAGCCCTCTGTGAAGAACCCA	ATGCCATAGCTGAAAGATCATCACCAT
Cluster-31575.0	ATGACGGTGAAAGGAGGCACTAGCC	GGCTAGTGCCTCCTTTCACCGTCAT
Cluster-42627.0	CCAAATCGACCTCTACCACGCTAA	TGCTCGTAATTCCGCAACATCTC
Cluster-53862.2	ATGGAAAACAAGGATGAGGATTGTC	GACAATCCTCATCCTTGTTTTCCAT
Cluster-16228.0	CCCTGGTAGAACAGACAATGAAG	CCGTGGGAAGTTATGGAGAAAGC
GAPDH	GGGAATCCTTGGTTACACTGAG	ACCCCATTCGTTGTCATACC

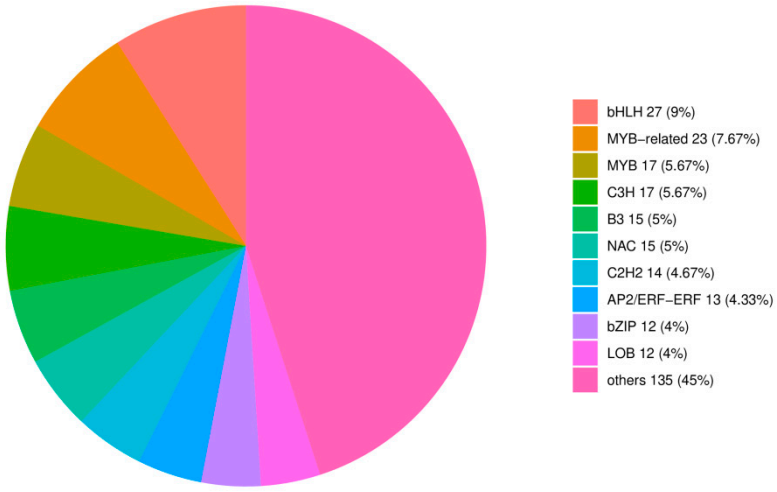


Sample	Raw Reads	Clean Reads	Clean Base(G)	Error Rate(%)	Q20(%)	Q30(%)	GC Content(%)
MT1	46618662	44095912	6.61	0.01	98.07	94.69	44.88
MT2	44950702	42708550	6.41	0.01	98.16	94.99	44.97
MT3	48928198	46077492	6.91	0.01	98.18	95.02	44.99
PT1	45577812	43002258	6.45	0.01	98.14	94.91	45.23
PT2	48510036	45737254	6.86	0.01	98.03	94.58	45.01
PT3	43766746	41903104	6.29	0.01	98.45	95.64	44.96
TT1	46937790	44659278	6.7	0.01	98.12	94.83	45
TT2	44887908	41848248	6.28	0.01	98.28	95.26	44.7
TT3	44684302	42452394	6.37	0.01	98.12	94.85	44.93

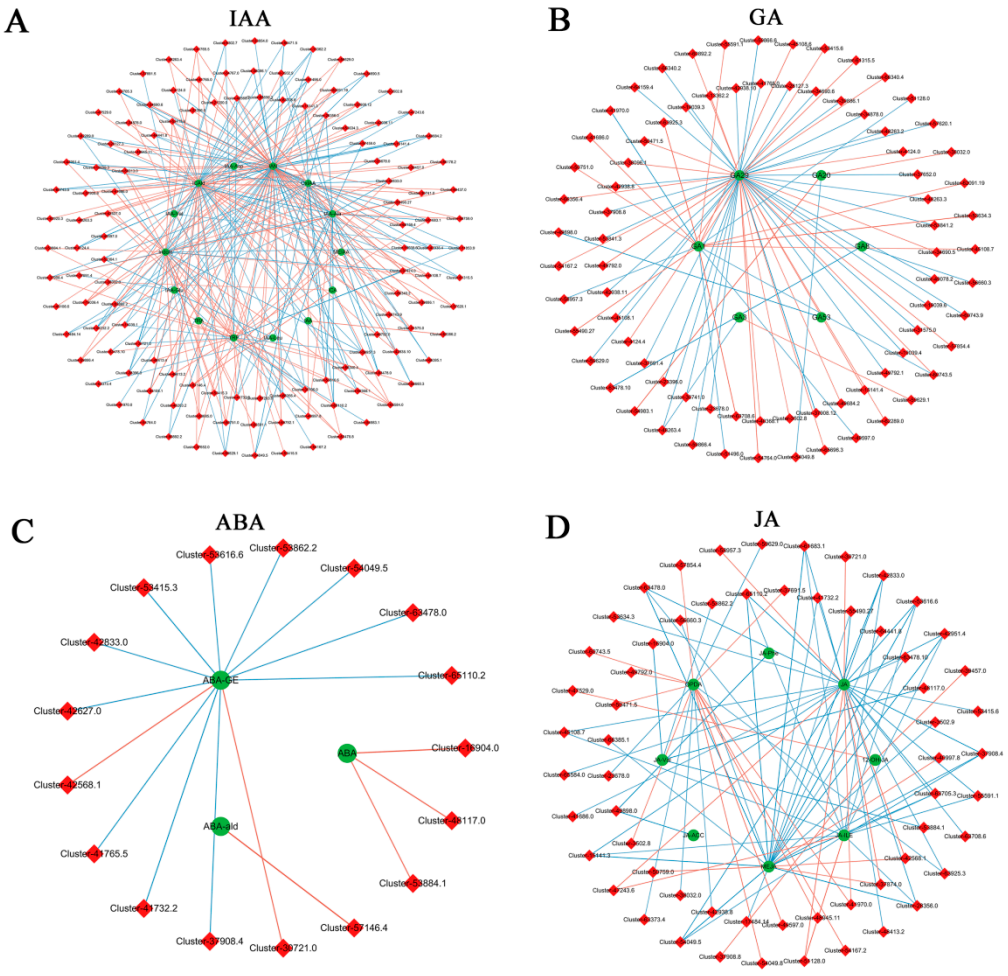
Supplementary Figure S1. Transcriptome and metabolome data quality control. (**A**) Principal component analysis (PCA) of transcriptome samples; (**B**) Quality control of transcriptome data; (**C**) Principal component analysis of metabolome samples; (**D**) Mixed sample quality spectrum analysis total ion flow map and tandem mass spectrometry detection TIC overlap diagram. The negative ion mode was remarked by N on the left, while the positive ion mode was remarked by P on the right.



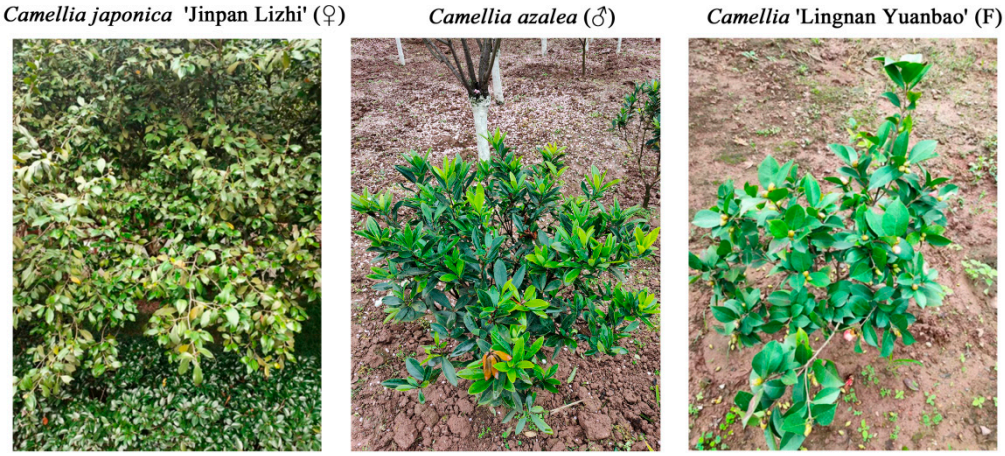
Supplementary Figure S2. Analysis of DEGs related to plant circadian rhythm pathway. (**A**) Schematic representation of plant circadian rhythm pathway; (**B**) Heatmap of DEGs involved in plant circadian rhythm pathway.



Supplementary Figure S3. Classification pie chart of TFs in TT vs MT and PT vs MT.



Supplementary Figure S4. The correlation analysis of the transcriptome and the targeted plant hormones. (**A**) Correlation network diagram for IAA; (**B**) Correlation network diagram for GA; (**C**) Correlation network diagram for ABA; (**D**) Correlation network diagram for JA.



Supplementary Figure S5. *Camellia* germplasm sampled for sequencing analysis