DOI: 10.17957/IJAB/15.1840 (IJAB-21-0128)

Supplementary material

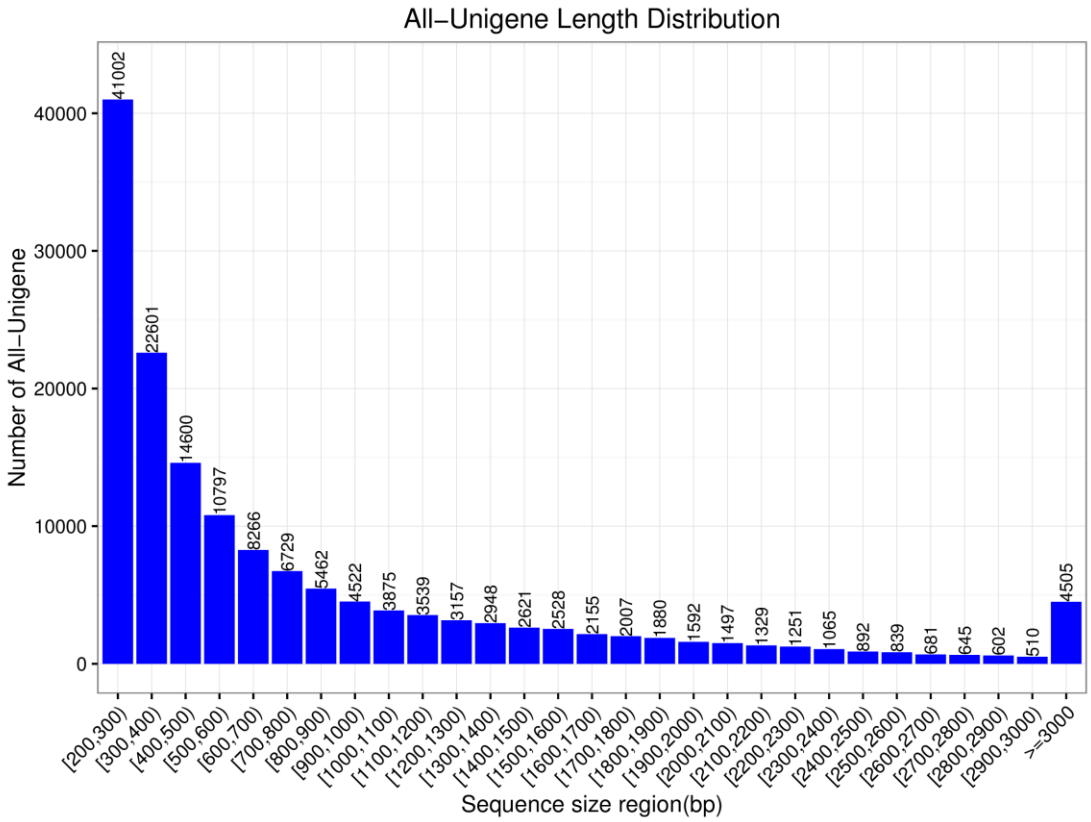


Fig. S1: Length distribution of the *Camellia sinensis* unigenes

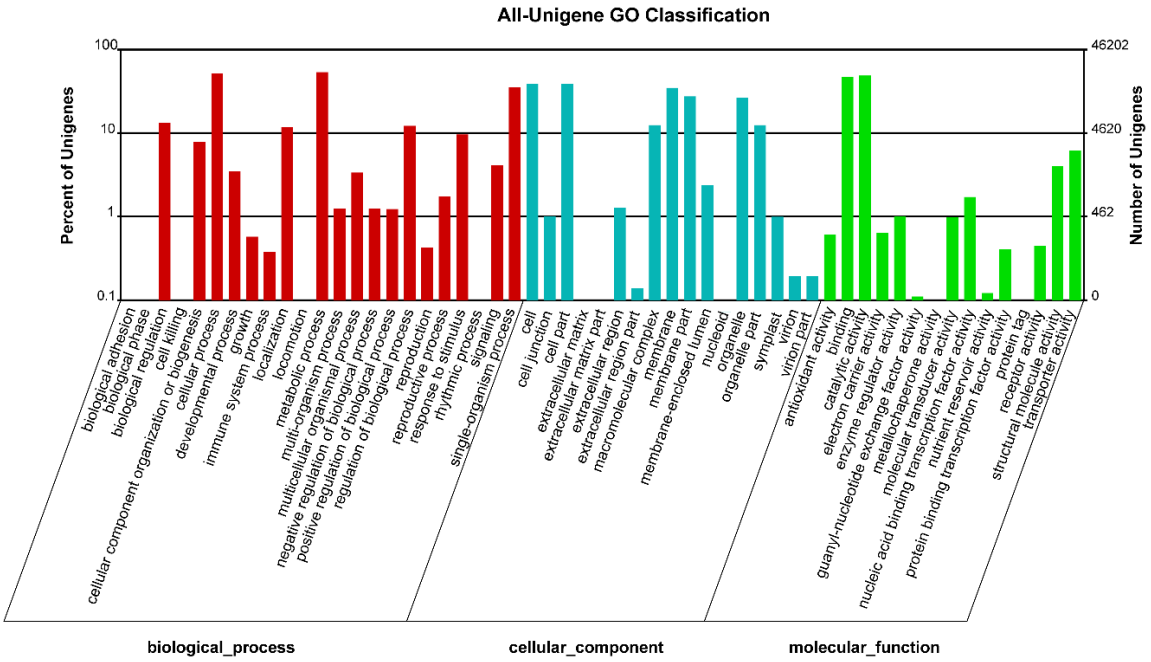


Fig. S2: Histogram presentation of GO classification. The results are summarized in three main categories, cellular component, molecular function, and biological process. The left y-axis indicates the percentage of genes in a category, and the right y-axis indicates the number of genes in a category.

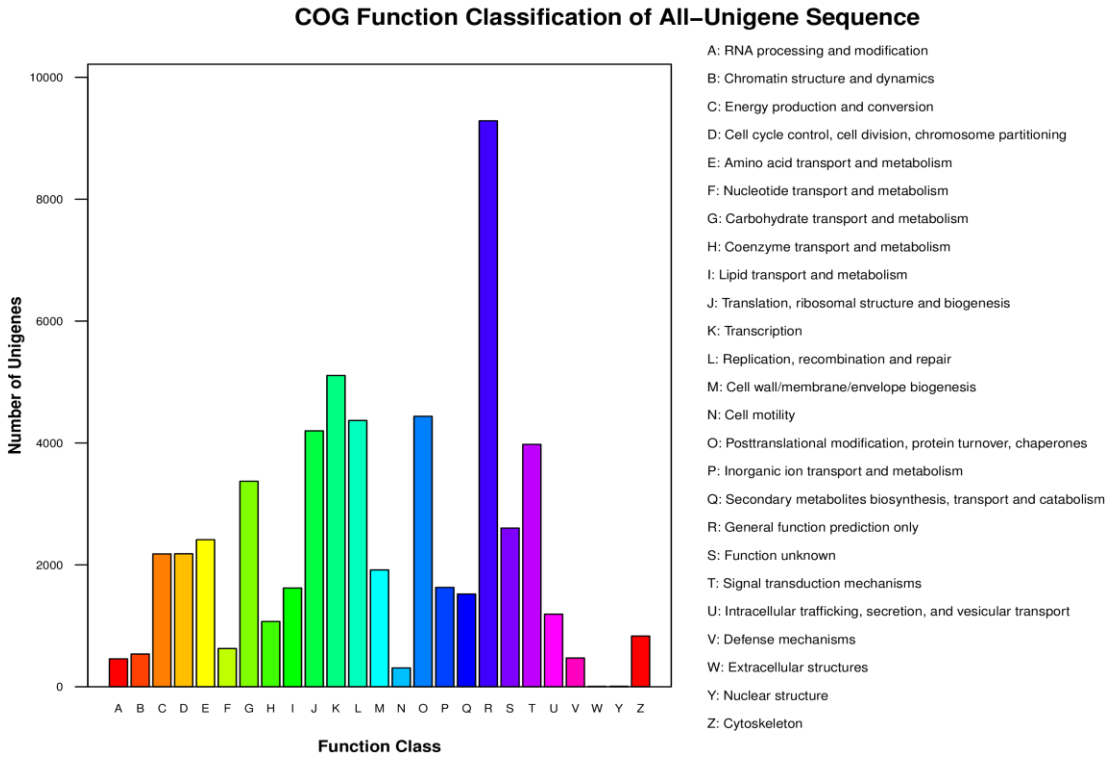
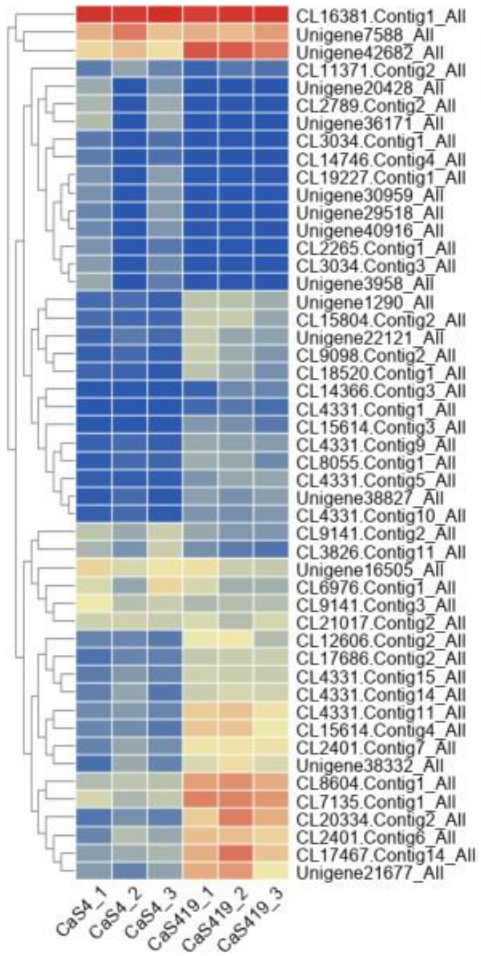


Fig. S3: Histogram presentation of the COG classification of all unigenes. In total, 56,330 unigenes showing significant homology to the COGs database are grouped into at least 25 categories. The capital letters in x-axis indicate the COG categories as listed on the right and the y-axis indicates the number of unigenes in each category.

A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CL3034.Contig1_All
CL14746.Contig4_All
CL19227.Contig1_All
Unigene30959_All
Unigene29518_All
Unigene40916_All
CL2265.Contig1_All
CL3034.Contig3_All
Unigene3958_All
Unigene1290_All
CL15804.Contig2_All
Unigene22121_All
CL9098.Contig2_All
CL18520.Contig1_All
CL14366.Contig3_All
CL4331.Contig1_All
CL15614.Contig3_All
CL4331.Contig9_All
CL8055.Contig1_All
CL4331.Contig5_All
Unigene38827_All
CL4331.Contig10_All
CL9141.Contig2_All
CL3826.Contig11_All
Unigene16505_All
CL6976.Contig1_All
CL9141.Contig3_All
CL21017.Contig2_All
CL12606.Contig2_All
CL17686.Contig2_All
CL4331.Contig15_All
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CL4331.Contig11_All
CL15614.Contig4_All
CL2401.Contig7_All
Unigene38332_All
CL8604.Contig1_All
CL7135.Contig1_All
CL20334.Contig2_All
CL2401.Contig6_All
CL17467.Contig14_All
Unigene21677_All
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CaS4_2
CaS4_3
CaS419_1
CaS419_2
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1.00
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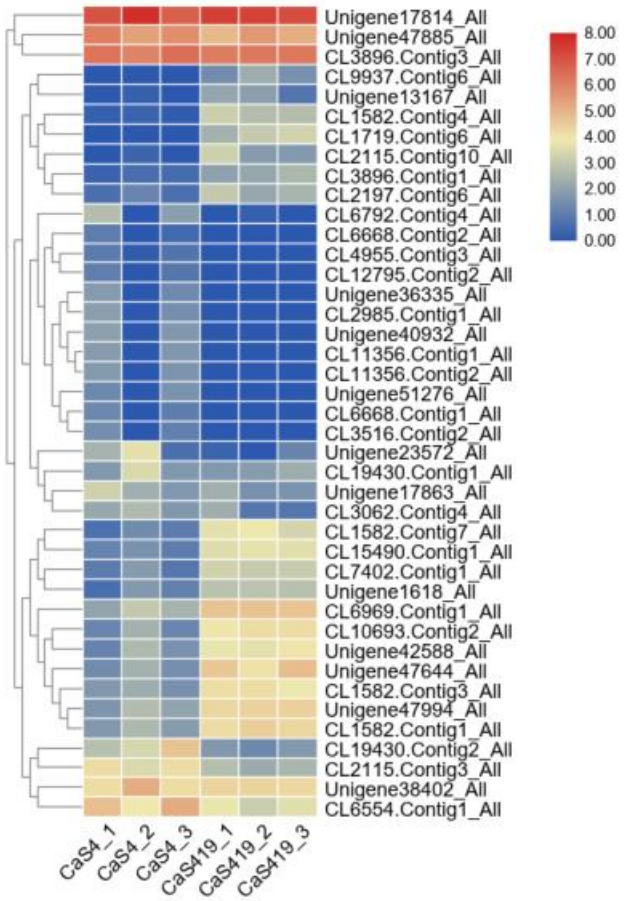
B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CL2197.Contig6_All
CL6792.Contig4_All
CL6668.Contig2_All
CL4955.Contig3_All
CL12795.Contig2_All
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CaS4_2
CaS4_3
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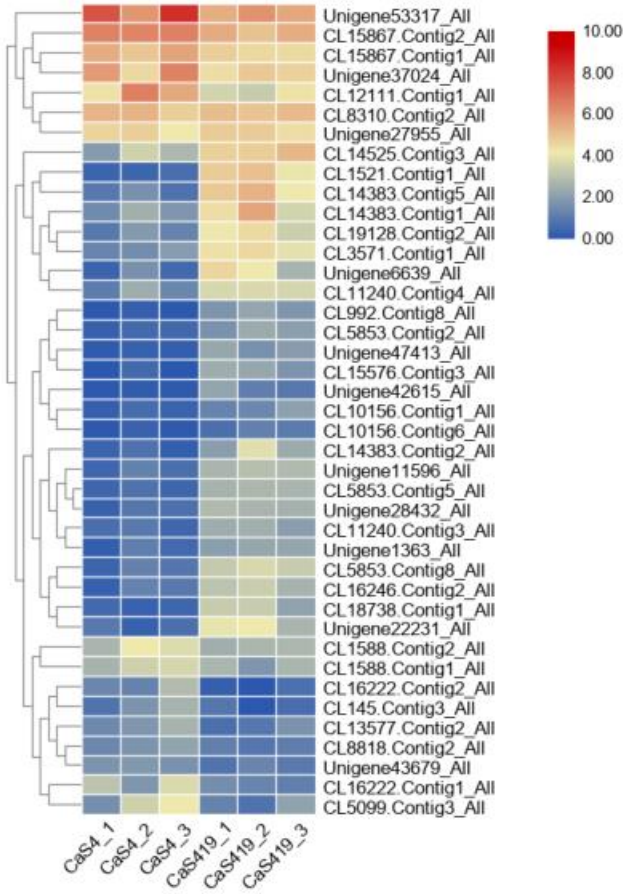
0.00

C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CL1521.Contig1_All
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CL19128.Contig2_All
CL3571.Contig1_All
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CL11240.Contig4_All
CL992.Contig8_All
CL5853.Contig2_All
Unigene47413_All
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CaS4_2
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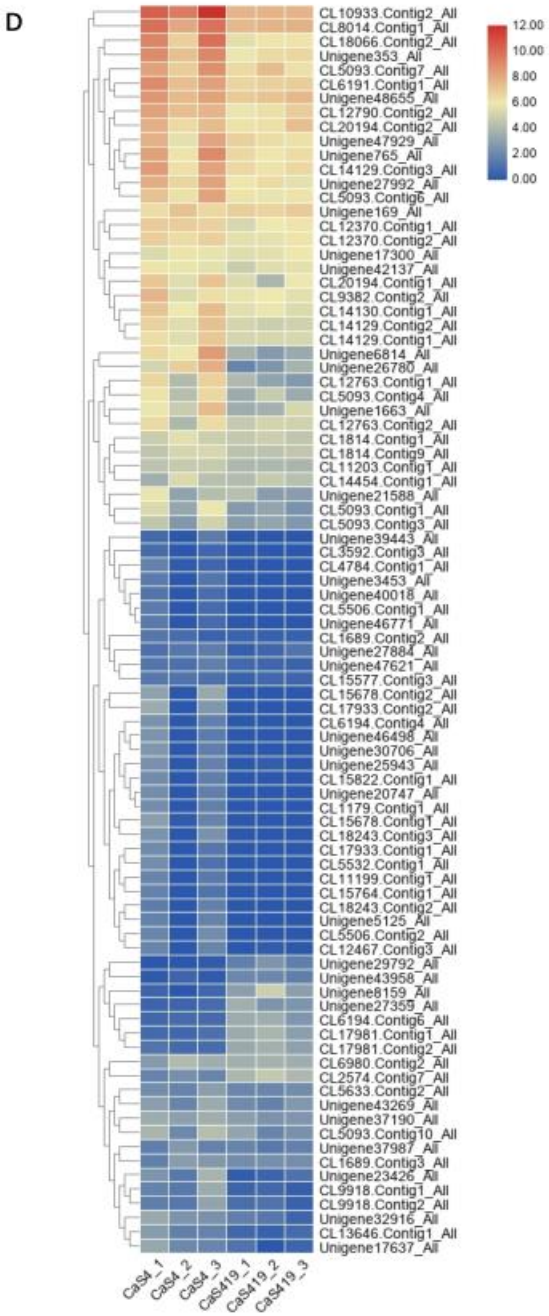

Fig. S4: All DEGs encoding the WRKY (A), bZIP (B), MYB(C) and ERF (D). Transcription factors were hierarchically clustered and mapped using the FPKM values. Colours indicate log2 transformed FPKM values. Green indicates low expression, and red indicates high expression.

Table S1: The primer sequences and amplicon characteristics used for qRT-PCR

Unigene ID	Forward primer (5'-3')	Reverse primer (5'-3')
CL182.Contig14_All	TACTCTGGCATTCGGTTCG	TTGAGCGTTTCTCCGTTGG
CL15670.Contig2_All	CAAGCGAAAGCATCCAAGG	CCCGACGAATAAGGTAGCG
CL1377.Contig9_All	ACACCCAGCGTCTACTTTT	TCACGAGCCAGCCGTCCAG
CL10933.Contig2_All	GCGGTAGACATTGACGGAG	AAAGCAGGGAACTGGGCAT
CL15867.Contig2_All	TCCGAAGACGAGGAAACAC	TCCTCTGCCGTCCTTCCTG
CL11642.Contig3_All	GGCTTCATTTGGGAGTTCA	GGCTTCATTTGGGAGTTCA
CL14810.Contig2_All	TTGCTCCCATAGAGTCCCA	CCAACGAAAACCACCTGAT
Unigene32202_All	CGGTAGTTCCGTAGCAGGTT	GCCCCAAGAAGCATCAAACAT
CL938.Contig2_All	TCGGTGACTTTGTGGTGGA	TGAGGATGAAGGCGGTGGT
CL290.Contig15_All	CCGCTGTCTGTCTCCTTAC	TCGTCTATGGTAACGCCTC

Table S2: Summary for the *Camellia sinensis* transcriptome

Parameters	Values
Total number of raw reads	318,515,326
Total number of clean reads	317,609,528
Total number of clean nucleotides (bp)	47,641,429,200
Average Read Length (bp)	150
Total number of contigs	154,097
Total length of contigs (bp)	127,232,652
Mean length of contigs (bp)	825
Total number of unigenes	154,097
Total length of unigenes (bp)	127,233,270
Mean length of unigenes	826
N50	1,349