

Supplemental Figure S1. Verification of the sampling by expressions of marker genes.

Semi-quantitative RT-PCR was performed using cDNA prepared from total RNAs extracted from each sample. The marker genes of *P. densiflora* (e.g., *PdeNAC2*, *PdeMYB46*, and so on) are homologous to *Arabidopsis* genes involved in the transcriptional regulator, cellulose biosynthesis, lignin monomer biosynthesis and lignin polymerization. And *PdeUBI* was used as a loading control.

Supplemental Figure S2. Characteristics of DEGs in CW and OW by seasonal changes.

(a) Identification of DEGs both up or down-regulated in CW and OW. DEGs were found by comparison of Spring and Fall or Summer and Fall, respectively. (b) Venn diagram shows the number of DEGs in CW vs. OW. in relation to season. (c) Gene Orthology (GO) analysis for Biological Process of up- or down-regulated genes in (a). Top significance GO terms was plotted with the negative logarithmic adjusted p-value of enrichment. CW (Compression Wood), OW (Opposite Wood), SP (Spring), SM (Summer), FA (Fall).

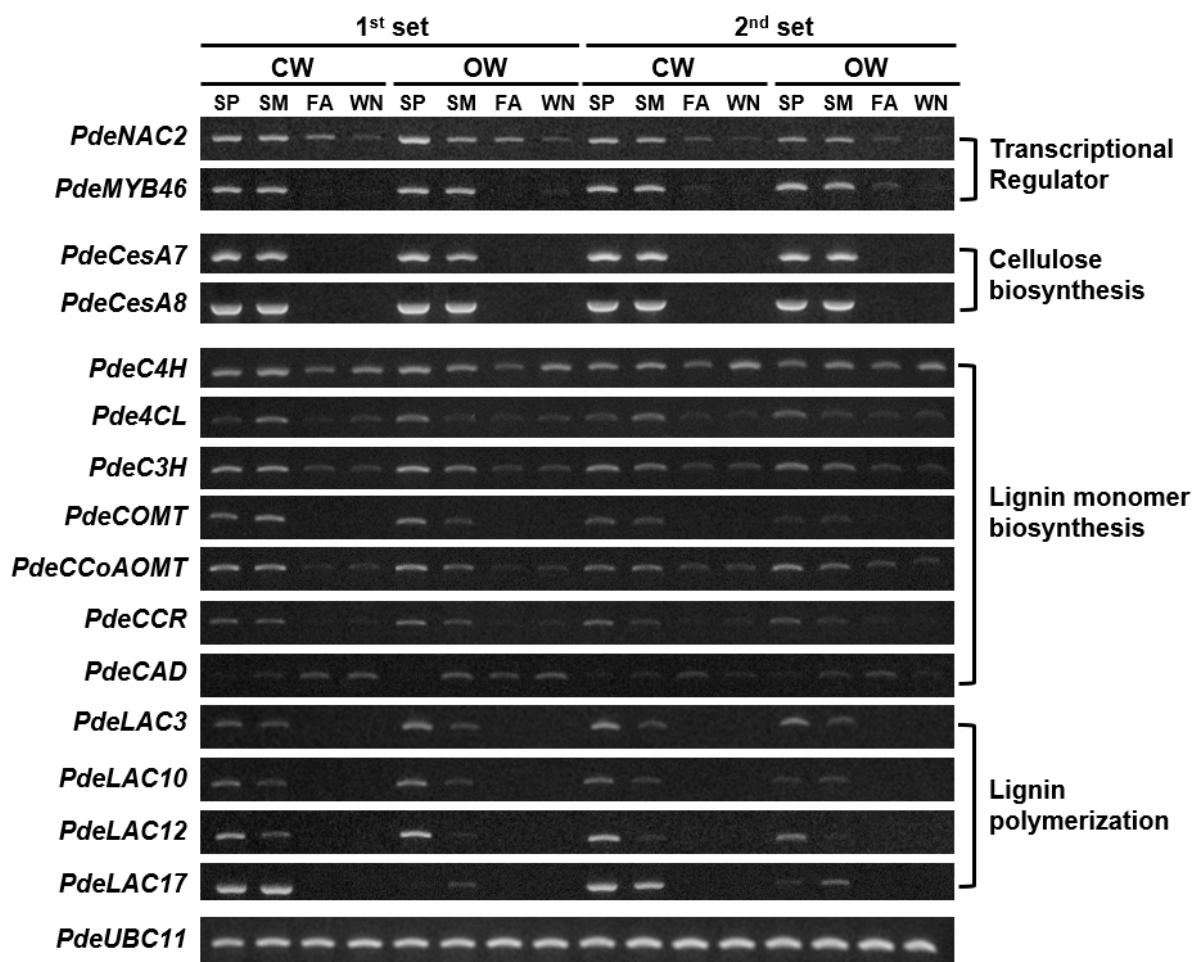
Supplementary Figure S3. Expressional changes of significant transcript involved in the wood formation (CW and OW) over four seasons in two consecutive years.

All the significantly expressed transcripts of the genes involved in cellulose, hemicellulose, lignin biosynthesis, and PCD which described in Figure 4 were plotted to confirm the differences in CW and OW for two years.

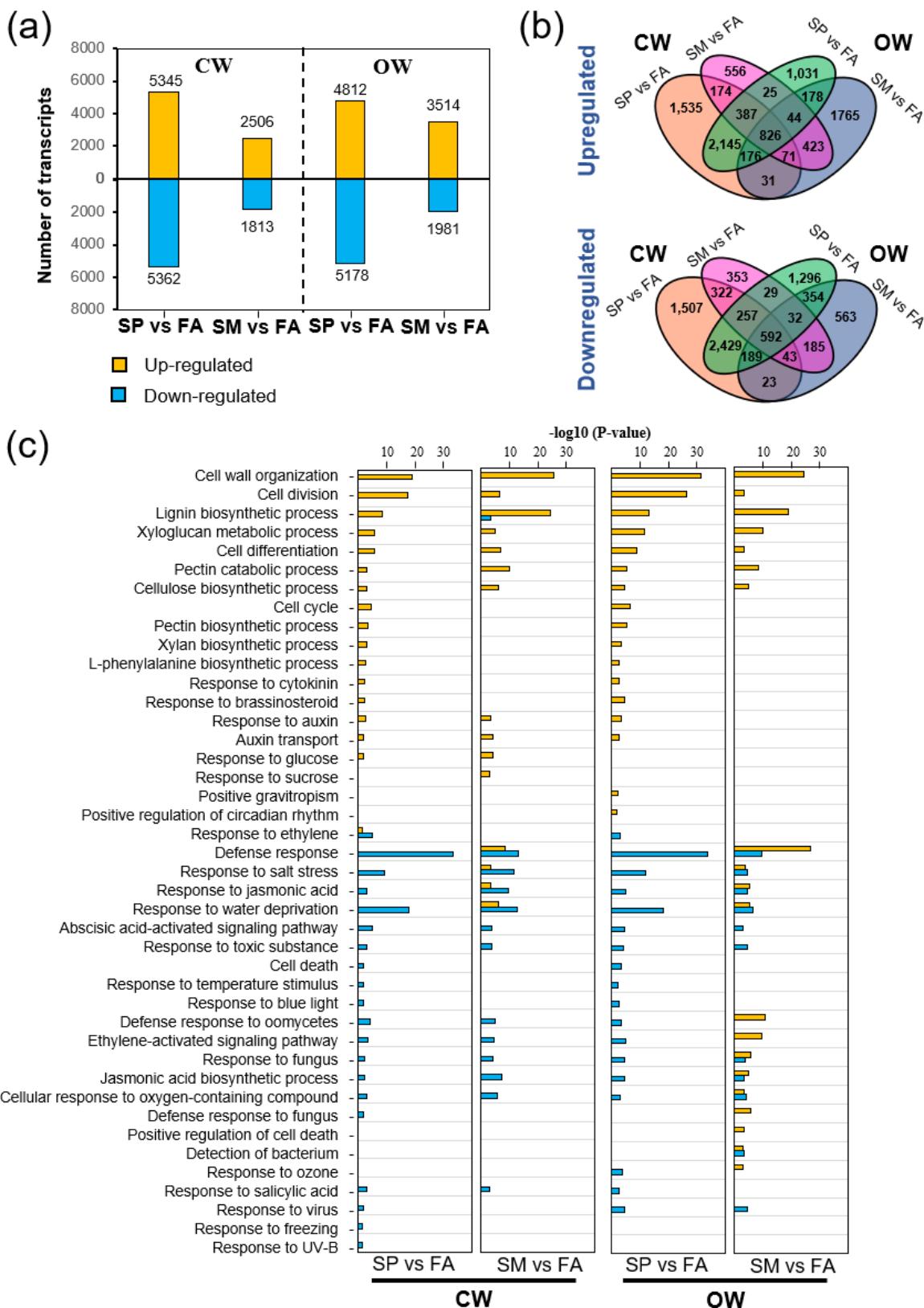
Supplementary Figure S4. Differentially expressed genes (DEGs) categorization of the CW in the growth season (SP and SM).

(a) Venn diagram shows the number of DEGs in growth season (SP and SM). (b) Gene Orthology (GO) analysis for Biological Process of SP, SM specific and SP-SM commonly expressed DEGs which classified in (a). Top significance GO terms was plotted with the negative logarithmic adjusted p-value of enrichment analysis. CW (Compression Wood), OW (Opposite Wood), SP (Spring), SM (Summer), FA (Fall).

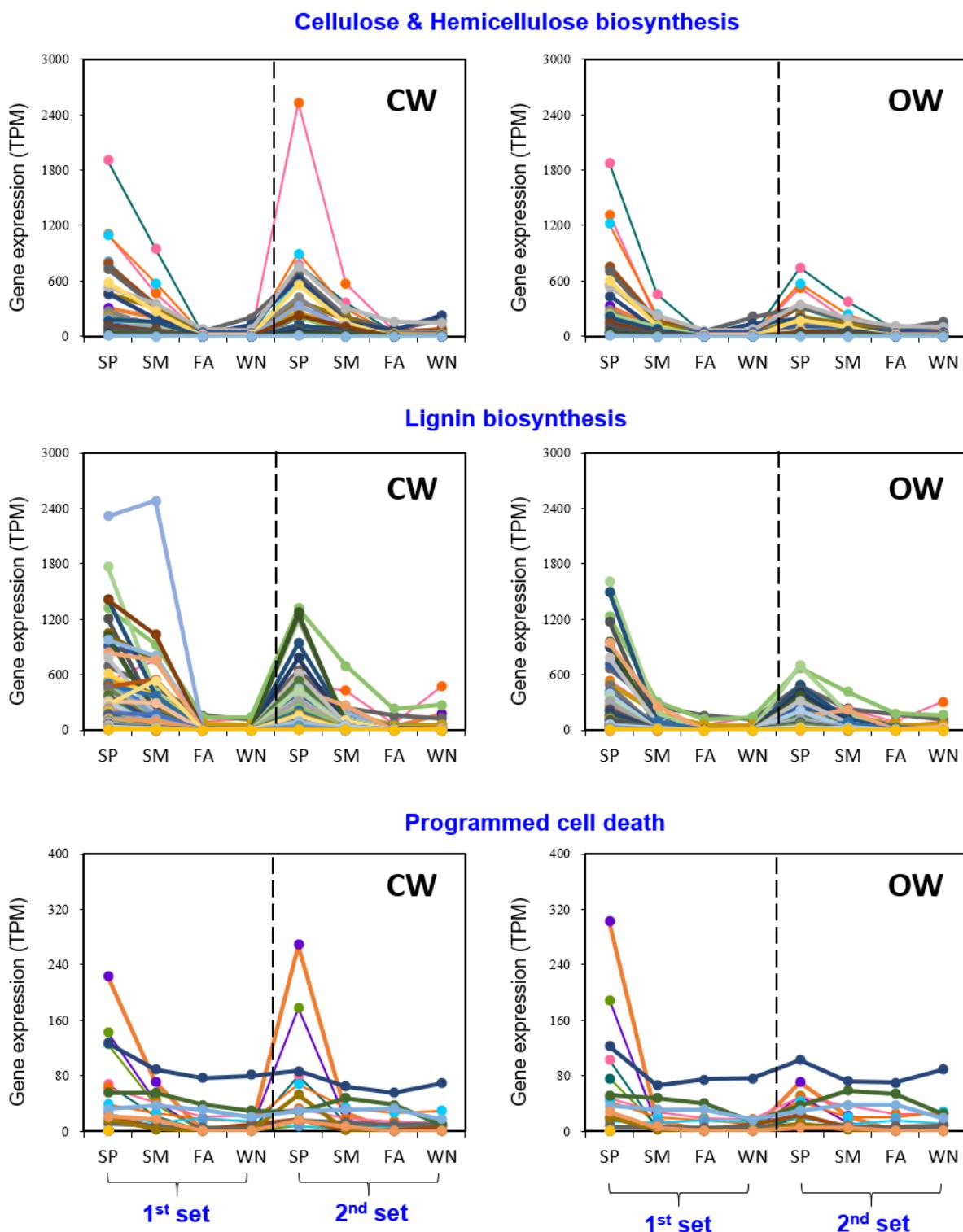
Supplementary Figure S5. Coding sequences of *Pde ERF4* and *PdeMYB106*



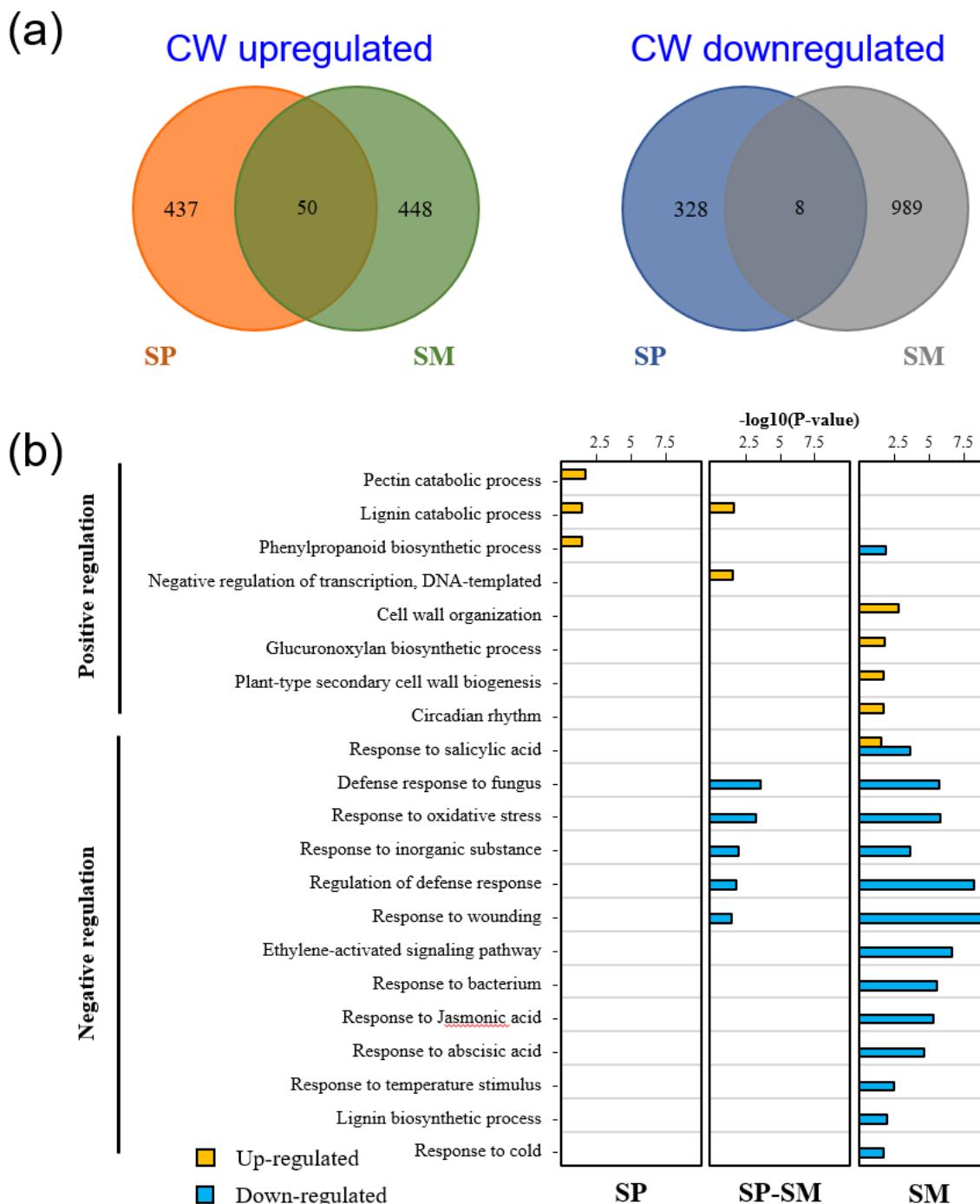
Supplemental Figure S1. Verification of the sampling by expressions of marker genes.



Supplemental Figure S2. Characteristics of DEGs in CW and OW by seasonal changes.



Supplementary Figure S3. Expressional changes of genes involved in the wood formation (CW and OW) over four seasons in two consecutive years.



Supplementary Figure S4. Histogram of differentially expressed genes (DEGs) categorization of the CW in the growth season (SP and SM).

>PdeERF4_DN57342_c0_g1_i2_813bp

ATGGCGGCTCACAGACATAGAAATGGGGATGGCATAGCGAGATCCTCGGCATTGTGATGCTCATG
TGGTTAAAGAAGTGCATTATAGAGGCCAGGAGGAGGCCTGGGTCGATATGCAGCAGAGATCAC
AGACCCATTAACGAAAAAACGTAAGTGGCTGGCACTTCGACACAGGCAGGAGGCAGCCAGGGC
CTATGACAAAGTCGCCAGAAATATGAGAGGAGCCAACGCCAAAACCAACTTCCGGTGCCTCCGTC
CAGAGCGAAGCCTCGGCATCCAGAGCGGCACGATCTCATTGCTACCAGTCTCCAGATCCTCCGCT
TTCCTCTACGTCTCGAATGATTGTAAAATAAAAACAAGGTGTGCCAGTTGGCTAGCTAAAC
AAGGGAAACCATGCACGCCATTACGTGAATGAGGGAGTGGGATGACAACATGAATCGCACTGC
TACTGCCATTCTGGACTACGCTACTCTCTGGAGAAGCTACCTATGGGGTGTGTTAGGGAGAT
TGTGGATCTCAGATGATCAACAGACACGGAGGCCATGATTGGATGGAGTAGGGTTAGTGAACAAAT
TTGCTTACTGCAACCCGAAGTCAAGCGTTGCGATTACCTCATCTCGGGCTTCGTTGACACACAA
CTCTCCTCCACCTCTGCAAACGAAAACGCCACGCTGCAGTCAATCGATTGAATGAAGATGAGCG
TCCCCGCTCTGACTCTTGATACGATTCTGAACAAATTCTGTGTGGATACAAGGATTAG

>PdeMYB106_DN63531_c0_g3_i10_985bp

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AAAAGCTCCTCGTTACATACAGGAGCACGCCATGGCAGCTGGAGGGCTCGCTCAGAAAGCTGG
GTTGCTGAGATGCCGGAAAAGCTGCAGATTGCGTTGGCTAACTATCTAAGGCCAGATATCAAGCGG
GGAAAGTTCAGCACACAGGAAGAACAGACGATTATTCAACTTCATGCCCTCTGGAAACAGGTGGT
CCACCATGCCACTCACCTCTAACCGAACTGACAACGAAATCAAGAAACTACTGGAATACCCATCTG
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CAGTTGCCCTCAGTCGCTAATGGTCGTCGAATCTGAGCCATATGGCGCAGTGGAGAGCGCGCG
CTGGAAGCCGAATCGAGGTTGGCGCGAGTCCAAGCTCAGGGCCAGGGCTATGCCCTGGTCCA
TGAGAAACCTAATGTGAACTCAGATATACTTACTAGATTGCGTTAGCCAGTCAAGGATTGATTCC
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GGAAGTTCCCTCAGAGGTATAATCCACTGGAGAATGTTCATAGCGCGGACCGAGCCAGTAACACAA
GTTATCTCAGCCTCTGCAACAAGCCATGTGCTCTGCTCAAGGCAGCAAATTCTGTACAATGAGG

CCAAGAACGCTGATGGAGAACCAAGAAGAACCGAGATAATGTAACGCCACCCTTATAATGTCCA

CCAACCTCATGGAAAATTGCAGTGAAAGCAAGCATCTATGA

Supplementary Figure S5. Coding sequences of *Pde ERF4* and *PdeMYB106*