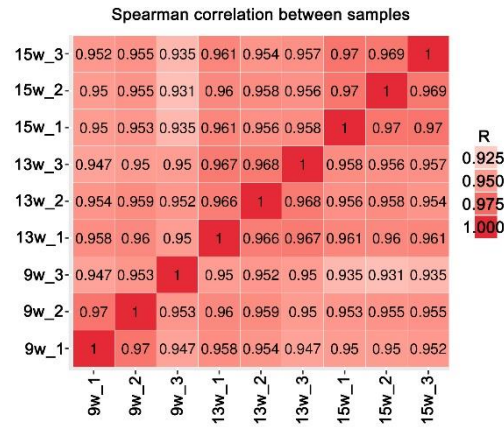
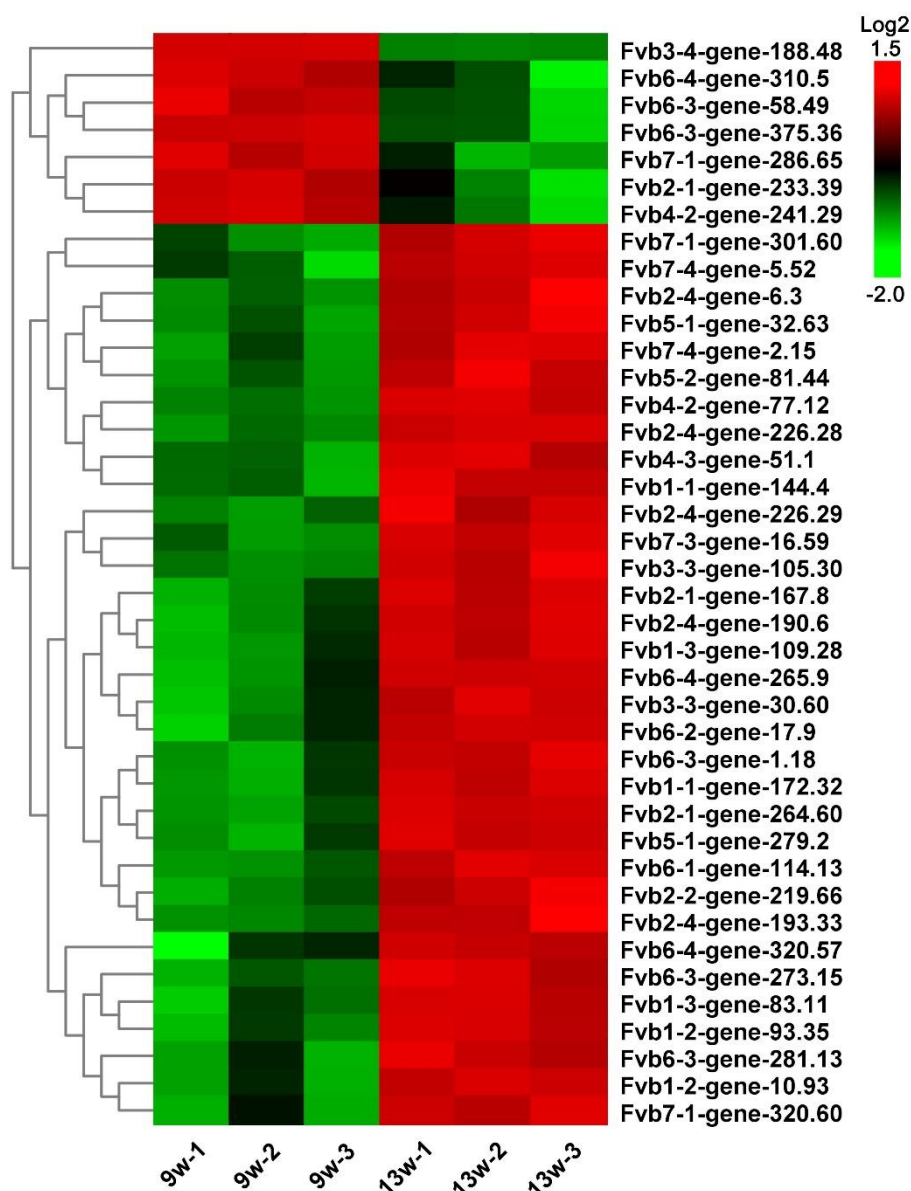


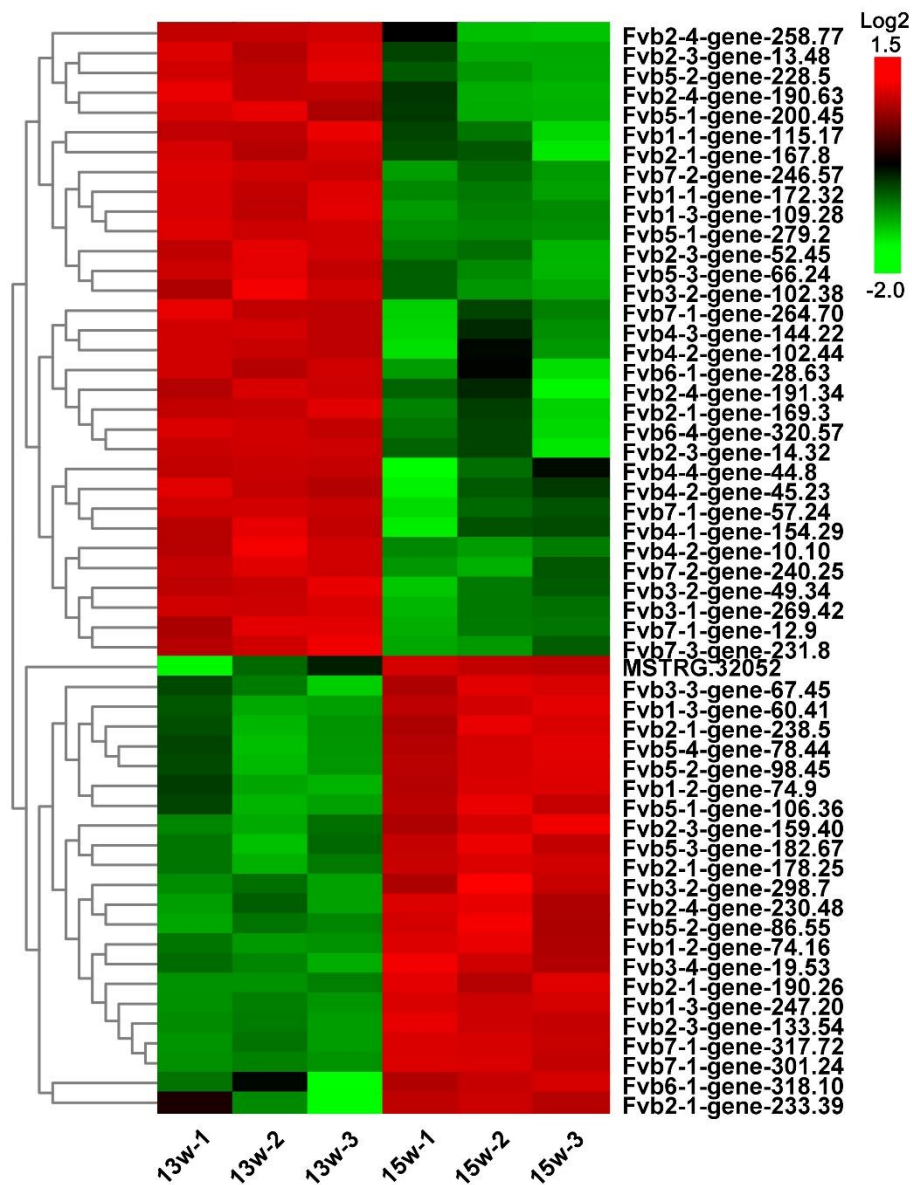
**Figure S1. Temperature and daylight length in Beijing from June to September 2018.** The daughter plants were rooted at 2018/6/6, which is recorded as 0w. The purple square indicates the sampling time interval, and the first time of sampling was at 8w.



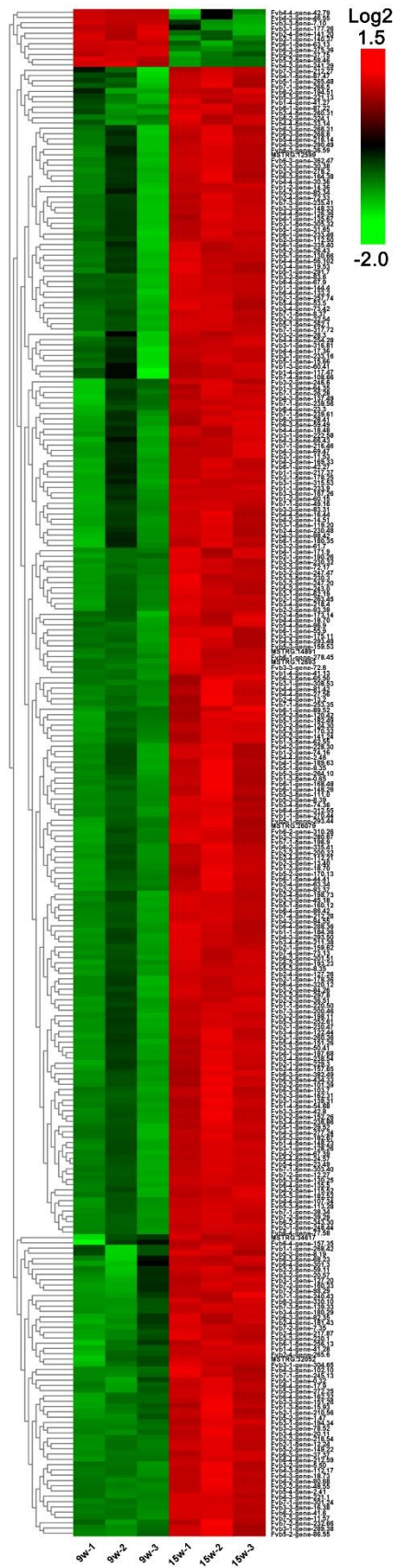
**Figure S2.** Hierarchical cluster diagram of gene expression levels in the nine samples.



**Figure S3. Heat maps of highly differentially expressed genes ( $|\text{Log2FC}| \geq 2$ ,  $p < 0.001$ ) between 13w and 9w.** The genes are clustered by FPKM value, with red indicating high expression genes and green indicating low expression genes.

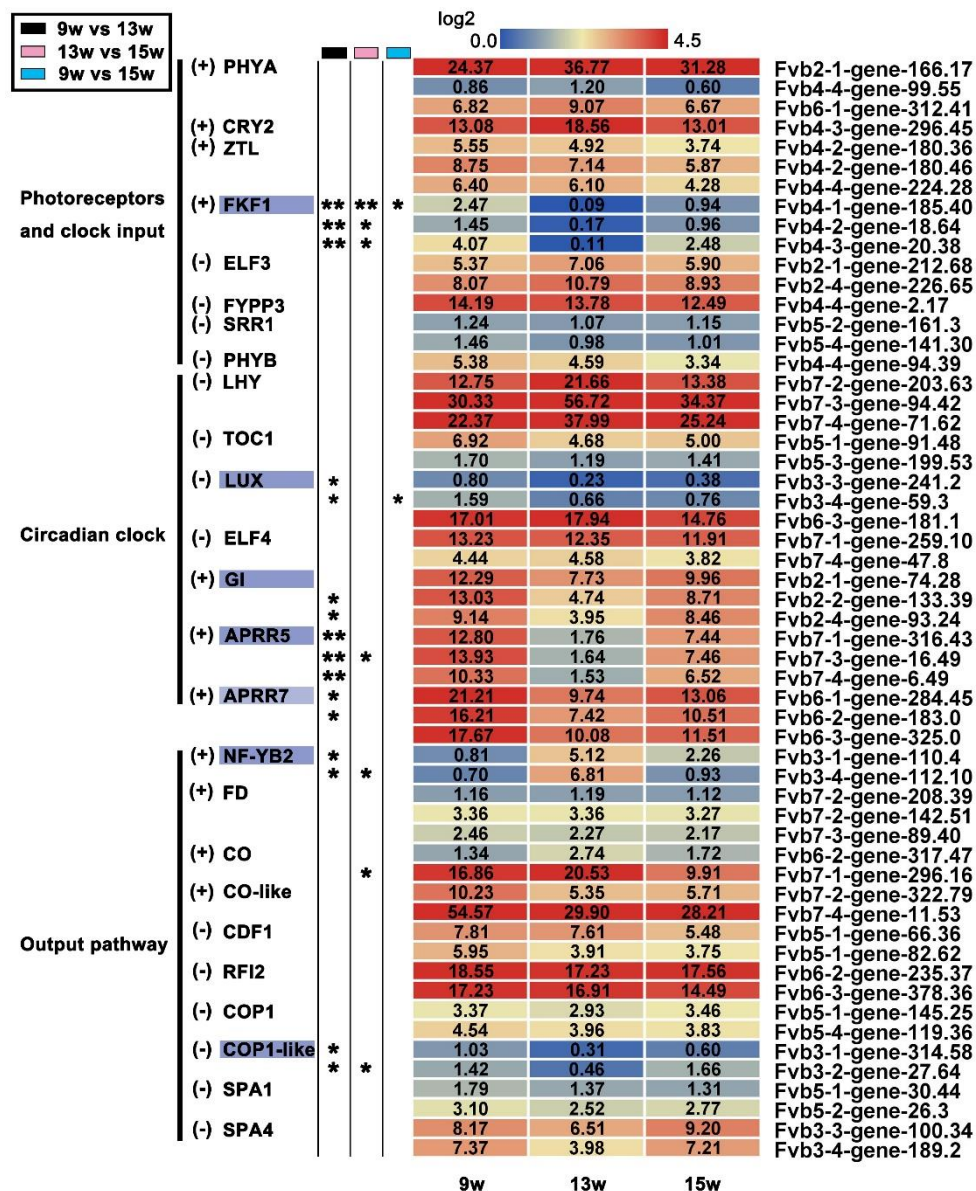


**Figure S4.** Heat maps of highly differentially expressed genes ( $|\text{Log2FC}| \geq 2$ ,  $p < 0.001$ ) between 15 w and 13 w. The genes are clustered by FPKM value, with red indicating high expression genes and green indicating low expression genes.



**Figure S5. Heat maps of highly differentially expressed genes ( $|\text{Log2FC}| \geq 2$ ,  $p < 0.001$ ) between 15 w and 9 w.** The genes are clustered by FPKM value, with red indicating high expression genes and green indicating low expression genes.





**Figure S6. Heat maps showing the expression of genes involved in the photoperiod flowering pathway.** (+) indicates the positive regulators of flower bud differentiation in Arabidopsis, and (-) indicates negative regulator. The purple boxes indicate the genes in which expression was significantly changed by 9w VS 13w. 9w: vegetative stage, 13w: shifts to reproductive stage at gene level, 15w: reproductive stage. The column with the black boxes represents the student's *t* test analysis of DEGs by 9w VS 13w; The column with the pink boxes represents the student's *t* test analysis of DEGs by 13w VS 15w; The column with the blue boxes represents the student's *t* test analysis of DEGs by 9w VS 15w. (\* |Log2FC| ≥ 1, *p* < 0.05. \*\* |Log2FC| ≥ 2, *p* < 0.01).

**Table S1. Oligonucleotide primers used in this study.**

Gene ID	Gene name	Primers
Fvb7-1-gene-250.12	Actin	TGGGTTTGCTGGAGATGAT CAGTTAGGAGAACTGGGTGC
Fvb4-3-gene-20.38	FKF1	GCTCTGGAGCCCGATTGTCC GAACCGACAGTTGCGACCGA
Fvb6-2-gene-1.58	FLC	TCGTCCGCGTATGAGCAACC CTGGTTCTGCCCTTGGCGAT
Fvb7-3-gene-16.59	ATX1	TGCTAGCCACCGTAAGGACCA AGCGAACCCTAGTGAGAGCCT
Fvb4-3-gene-14.14	TSP10	GCAGCCGAGCATGGCTACTT AGCCATCTGTTCGCCTCGGTA
Fvb7-3-gene-128.14	SOC1	CCACGAGCCGTCAAGTCACC ATGAGCGCAACCTCGGCATC
Fvb3-2-gene-161.14	TFL1	TGCCGAGGCCAAACATAGGG AAGACAGCAGCCACCGGAAG
Fvb5-1-gene-7.60	AGL14	TGCGATGCTGAGGTTGCACT ACCATCACCAAGGAGCTTCCG
Fvb7-3-gene-145.26	SBP8	TCTCGACCACTACGCCACCA CGAGGCTGAGCATGGAGTGG
Fvb3-2-gene-130.24	GH3.6	CCTTGTGGCTCGTCCAGTCC GCGCCAACTCGGAGGACTAC
Fvb2-2-gene-155.6	AIP10A5	ACGGCAGACGGTTCATCGTG GGCTGGTTGGCGAAGCCATA
Fvb7-1-gene-105.29	SAUR36	ACGGCGACTTTCACCGTGTT CGGGCACGGTATGGTGATCC
Fvb4-4-gene-22.43	AHK4	GAGAGGGAGCCCTCACCCAT GCTCCTCCACGGTTGGGTTT
Fvb4-3-gene-131.37	ARR1-like	ATGGTGGCAGAGGGACAGGA AGGCTGGACATCCCTTGGGT
Fvb6-4-gene-76.12	PYL4	GTGGTCCGCCGCTTCGATAA CAGCACGTCCAGCCTCTCAG
Fvb7-2-gene-286.2	PP2C51	TGCCGGGAGAGGTTACACGA CAACCAGCTCCTCCGTCACC
Fvb1-4-gene-10.16	GAI-like	CGCTTCCGACGCCGTTATCT ATGGCGTCAGCGAAGTCGAG
Fvb2-4-gene-205.54	EBF1	TGTCTCTTGGTCGGCGTGTG TGCACAGGCACTCCTCTCCT

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Fvb1-3-gene-53.32	BZR1-like2	GCTGAAGCTGGTTGGGTCGT
		AGGACTGTGGGCTTGGTTGC
Fvb5-2-gene-57.31	MYC2-like	GGCCATTCCAGAGGCACCAG
		TTCCCATGGCCTGCAGCAAA
Fvb2-2-gene-218.4	PR1-like	GGGTGACGGAGAAGCCCAAC
		GCGCCAAACCACCTGGGTAT

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