

Additional file2: This excel file contains all of the additional Tables (Tables S1-S5).

Table S1 Primers pairs used for Quantitative Real-Time PCR

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Table S5. Mobile signals controlling photoperiod-dependent flowering

Table S1. Primers pairs used for Quantitative Real-Time PCR

Gene ID	Description	Primer	
		Forward (5'- 3')	Reverse (5'- 3')
Unigene49490	MADS-box transcription factor 50-like	GTCGCGCTCGTCGTCTTC	ACATTGTCGGTATCGGCTGAT
Unigene57034	zinc finger CCCH domain-containing protein 55-like	AGGGCGAGGTAAAGGCAGAA	AGCAGGTCCTCCGGATGTT
Unigene108692	flower development related protein	GGTCGCGCTCATCGTCTT	CGATTTGCCTGGTCTCCAAT
Unigene32545	Ethylene-forming enzyme	TCGCTCTCCATGGACTTGAAG	GGCGTATCCCAAGTTCGTGTT
Unigene114564	zinc finger protein CONSTANS-LIKE 13-like isoform X2	GGGTCCCCGAGTTTGAGAAG	GGAAGCCATGGCAGGAAGT
Unigene120387	putative 29 kDa ribonucleoprotein A, chloroplast precursor	AGCCGTGGATTTGGATTTCG	CCCTCAGAGCTCTTCCTTGAAA
Unigene103892	light harvesting chlorophyll a-b binding protein 2-1	CGGAGATCCTGTCCAAGA	GGTAAACCTTGTCGAGCC
Unigene104205	heat shock protein 70	CTTCTCCACCTACTCGGACAAC	CTCAAACCTTGCCCAGCAGGTT
Unigene109097	ribulose biphosphate carboxylase/oxygenase activase, chloroplastic-like	CAGCGAGTTCCCTGACTCAATC	CCAAACCAAGCTCTGGACTTCT
Unigene110315	protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic-like	AGGATGAAAGGACAGCAAGGAGT A	TGCAACTTTTTTCGGCCAACT
Unigene130058	chlorophyllase-2, chloroplastic-like	CGGAGATGGACACCTTGGT	GCCCTCAGCTTTACACGATAT
Unigene137345	17.8 kDa class II heat shock protein-like	TGTCCATGTCGGCGTTCTC	TCAAGGTGCAGGTGGAGGA
Unigene30387	photosystem I reaction center subunit IV, chloroplastic-like	GATCCGTCGTACAGTTGAT	GTCCAGGGCGTAGTTGTTG
Unigene32039	chlorophyll a-b binding protein CP24 10B, chloroplastic-like	GCTTGCCAATGCCTCATCAGT	TGAACTCGGCGTTCGCTCTT
Unigene33763	putative UVB-resistance protein (UVR8)	TGATTGCTGCTGGTGCTGAG	CGCCATCCACATGCAACAAG
Unigene36923	probable protein arginine N-methyltransferase 6.1-like	GGCACTGGGCTACGATCATC	TCACGACCCTCAATCTCAACCT
Unigene39652	MADS15 protein	CTGAAGCGGATCGAGAACAAG	CGTCGCAGAGGACGGAGAT
Unigene28224	cytokinin receptor CRE1b, putative, expressed	AGTTCTTGTCAACTGTTTCTCATG	GGGTTGTCTTTAGTTCTGTGCCT AA
EF1 α	Reference gene	GTTGTTACCTTTGGTCCCAGCGG	TGGCAGGGTCATCCTTGGAGTTG

Table S2. Expression of the same clump of *D. latiflorus* flowering biomarkers in floral transition. FPKM, fragments per kilobase of exon per million fragments mapped. Genes with ratio values less than unity show increased expression during early stages of floral development; genes with ratio values greater than unity show increased expression during later stages.

GENE ID	Function description (GO)	e-value	FPKM (L1)	FPKM (L2)	FPKM (L3)	L2:L1	L3:L2
Continue increase in the gene expression							
Unigene39652	MADS14 protein	3.00E-86	0.6	9.84	43.1	16.4	4.38
Unigene138210	loosening and extension of plant cell walls	e-150	0.06	3.19	13.7	53.17	4.29
Unigene43312	loosening and extension of plant cell walls	e-145	0.2	3.46	15.56	17.3	4.50
Unigene10723	Regulates floral architecture and leaf development	4.00E-55	0.01	0.67	3.32	67	4.96
Unigene114865	Probable transcription factor involved in plant development PREDICTED: scarecrow-like protein 14-like [<i>Setaria italica</i>]	0	0.01	0.48	2.5	48	5.21
Unigene111037	Abscisic acid 8'-hydroxylase 3	6.00E-11	0.01	0.34	6.8	34	20
Continue decrease in the gene expression							
Unigene38555	Promotes plant stress tolerance such as heat, chilling, salinity and methylviologen	6.00E-67	39.36	3.31	1.2	0.08	0.36
Unigene41907	FAR1-RELATED SEQUENCE 5	5e-25	1.98	0.19	0.01	0.10	0.05

Unigene21870	Sugar transport protein 11	2e-10	16.7	2.67	0.01	0.16	0.004
Unigene49486	Regulates shoot apical meristem (SAM) initiation and maintenance	9e-24	1.46	0.54	0.01	0.37	0.02
Unigene112435	negatively regulates salicylic acid- (SA-) dependent defense responses, abscisic acid (ABA) signaling, and ethylene-induced senescence	3e-21	1.31	0.36	0.05	0.27	0.14
Unigene133805	Modulates plant transpiration efficiency	0	1.23	0.28	0.01	0.23	0.04
Unigene14850	Transcription factor bHLH13	6e-67	2.97	0.82	0.36	0.28	0.44
Unigene14377	Glutamate synthase 1 [NADH], chloroplastic	0	0.82	0.29	0.05	0.35	0.17
Unigene137525	Outer envelope protein 61, chloroplastic	0	4.8	1.71	0.89	0.36	0.52
Unigene12963	C-terminal processing peptidase, chloroplastic	2e-65	1.14	0.48	0.15	0.42	0.31
Unigene99180	Involved in the regulation of stomatal aperture	0	0.98	0.38	0.01	0.39	0.03
Unigene27191	May be involved in oxidative stress response	e-113	10.81	6.13	2.41	0.57	0.39

Table S3. The pathway and the products involved in the pathway of plant hormone signal transduction

Pathway	Product	Pathway ID
Tryptophan metabolism	Auxin/IAA	Ko00380
Zeatin biosynthesis	Cytokinin	Ko00908
Diterpenoid biosynthesis	Gibberellin	Ko00904
Carotenoid biosynthesis	Abscisic acid	Ko00906
Cysteine and methionine metabolism	Ethylene	Ko00270
Brassinosteroid biosynthesis	Brassinosteroid	Ko00905
α -Linolenic acid metabolism	Jasmonic acid	Ko00591
Phenylalanine metabolism	Salicylic acid	Ko00360

Table S4. The unigenes that share homology with CONSTANS-like genes

Gene ID	Gene length	UniprotKB-ID	Nr-ID
Unigene105685	2689	sp Q8LG76 COL6_ARATH	gi 226499562 ref NP_001148229.1
Unigene105693	738	sp Q940T9 COL4_ARATH	gi 21667485 gb AAM74069.1 AF490474_1
Unigene111712	799	No hits	gi 349500574 dbj BAL02998.1
Unigene114564	2191	sp Q9C7E8 COL15_ARATH	gi 357119825 ref XP_003561634.1
Unigene118524	1788	sp Q8RWD0 COL16_ARATH	gi 514814470 ref XP_004982006.1
Unigene129223	573	sp Q9SK53 COL3_ARATH	gi 21667485 gb AAM74069.1 AF490474_1
Unigene148512	1331	sp O50055 COL1_ARATH	gi 514794585 ref XP_004973094.1
Unigene148539	1318	sp Q9FHH8 COL5_ARATH	gi 226508042 ref NP_001148275.1
Unigene65187	659	sp Q9FHH8 COL5_ARATH	gi 514709130 ref XP_004951711.1
Unigene108408	1211	sp Q9SK53 COL3_ARATH	No hit
Unigene108407	1244	sp O50055 COL1_ARATH	No hit
Unigene114558	2887	sp O82256 COL13_ARATH	No hit
Unigene39936	1130	sp Q9SK53 COL3_ARATH	No hit
Unigene65996	1362	sp O82256 COL13_ARATH	No hit
Unigene84956	1310	sp Q940T9 COL4_ARATH	No hit

Table S5. Mobile signals controlling photoperiod-dependent flowering

Gene name	Annotation	Gene ID	Nr ID	UniprotKB-ID
ARF2	Auxin response factor 2	Unigene11110	No hit	sp Q94JM3 ARFB_ARATH
GA2OX	Gibberellin 2-beta-dioxygenase	Unigene121361	No hit	sp O04706 GAO1B_WHEAT
		Unigene33009	No hit	sp O04705 GAO1D_WHEAT
		Unigene13852	No hit	sp Q39111 GAOX2_ARATH
		Unigene50654	No hit	sp Q39110 GAOX1_ARATH
CYP735A2	cytokinin hydroxylase	Unigene44120	No hit	sp Q9ZW95 C7352_ARATH
ABA	Abscisic acid	Unigene108262	gi 115454105 ref NP_001050653.1	sp Q02066 AAIP_WHEAT
		Unigene111035	gi 115479545 ref NP_001063366.1	sp Q0J185 ABAH3_ORYSJ
		Unigene111042	gi 115479545 ref NP_001063366.1	sp Q0J185 ABAH3_ORYSJ
		Unigene11612	gi 514718583 ref XP_004954028.1	sp Q9C5Q2 AI5L3_ARATH
		Unigene32213	gi 473986639 gb EMS51712.1	sp Q9C5Q2 AI5L3_ARATH
		Unigene65317	gi 115450859 ref NP_001049030.1	No hit
		Unigene65667	gi 115461512 ref NP_001054356.1	sp Q02066 AAIP_WHEAT
SAI	salicylic acid-induced protein	Unigene51767	gi 115489522 ref NP_001067248.1	No hit
		Unigene130045	No hit	sp F4IMK4 MES19_ARATH
		Unigene27802	No hit	sp Q6RYA0 SABP2_TOBAC
		Unigene40690	No hit	sp Q6RYA0 SABP2_TOBAC
Ethylene	Ethylene-forming enzyme	Unigene106135	gi 514743219 ref XP_004960335.1	sp Q9FH95 TOE3_ARATH
		Unigene106137	gi 514743219 ref XP_004960335.1	sp Q9SK03 RAP27_ARATH
		Unigene11640	gi 514795194 ref XP_004973240.1	No hit
		Unigene116402	gi 357158484 ref XP_003578142.1	sp Q94AN4 AP2L1_ARATH
		Unigene118502	gi 115441921 ref NP_001045240.1	No hit
Ethylene	Ethylene-forming enzyme	Unigene129023	gi 114229339 gb ABI58288.1	No hit
		Unigene140590	gi 514747439 ref XP_004961367.1	No hit

		Unigene154974	gi 514813004 ref XP_004981291.1	sp Q9FK12 CRF3_ARATH
		Unigene18244	gi 357134855 ref XP_003569031.1	sp Q9SK03 RAP27_ARATH
		Unigene20985	gi 514814582 ref XP_004982062.1	sp O82436 ETR1_CUCMN
		Unigene28980	gi 514708773 ref XP_004951621.1	sp O80339 ERF82_ARATH
		Unigene32545	gi 148886766 sp A2Z1W9.1 ACCO1_ORYSI	No hit
		Unigene51069	gi 514813004 ref XP_004981291.1	sp Q9FK12 CRF3_ARATH
		Unigene68341	gi 514730325 ref XP_004956913.1	sp Q6K7E6 ERF1_ORYSJ
		Unigene76465	gi 350534422 ref NP_001234140.1	No hit
		Unigene8137	gi 115481754 ref NP_001064470.1	No hit
		Unigene121361	gi 148886766 sp A2Z1W9.1 ACCO1_ORYSI	No hit
BRs	BRASSINOSTEROID	Unigene9068	gi 115486225 ref NP_001068256.1	sp Q94F62 BAK1_ARATH
	INSENSITIVE 1-associated	Unigene117976	gi 226493335 ref NP_001147917.1	sp Q94F62 BAK1_ARATH
	receptor kinase 1	Unigene17567	gi 108710634 gb ABF98429.1	sp Q94F62 BAK1_ARATH
		Unigene17569	gi 41469446 gb AAS07247.1	sp Q94F62 BAK1_ARATH
		Unigene9068	gi 115486225 ref NP_001068256.1	sp Q94F62 BAK1_ARATH
		Unigene96090	gi 115486225 ref NP_001068256.1	sp Q94F62 BAK1_ARATH
		Unigene96100	gi 115486225 ref NP_001068256.1	sp Q94F62 BAK1_ARATH
SUS	Sucrose synthase	Unigene100130	gi 514819488 ref XP_004984440.1	sp Q10LP5 SUS4_ORYSJ
		Unigene12672	gi 108708059 gb ABF95854.1	sp Q10LP5 SUS4_ORYSJ
Tre6p	Trehalose-6-phosphate	Unigene118660	gi 328864181 gb AEB53177.1	No hit