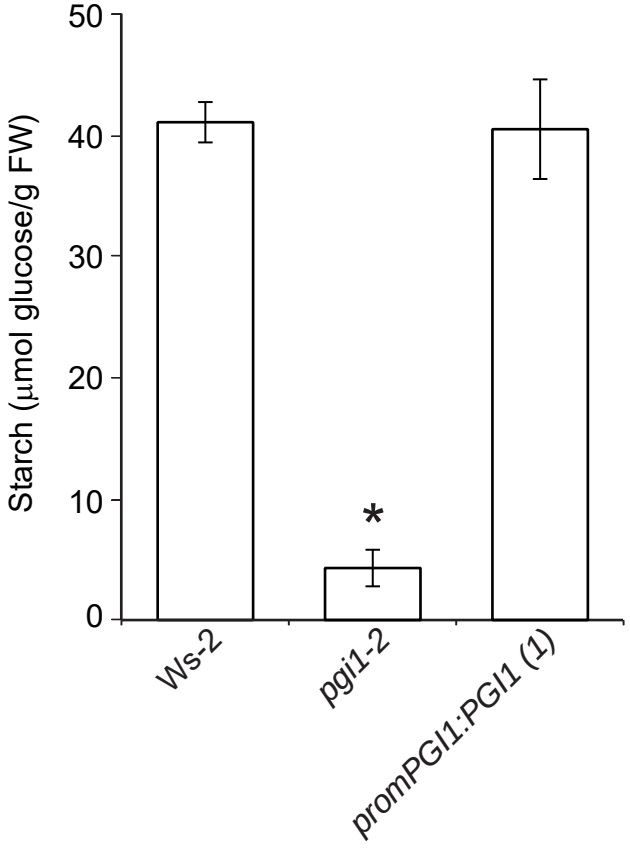
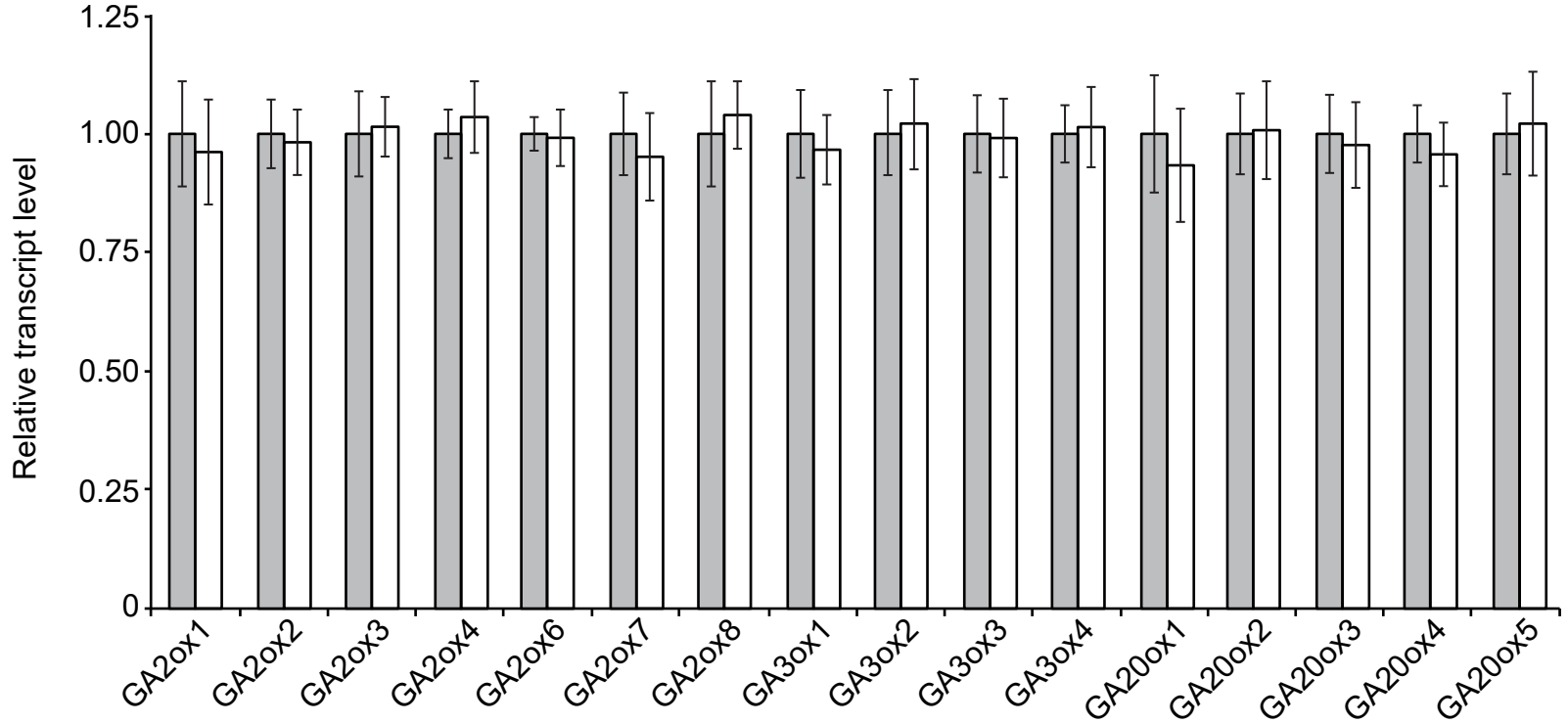
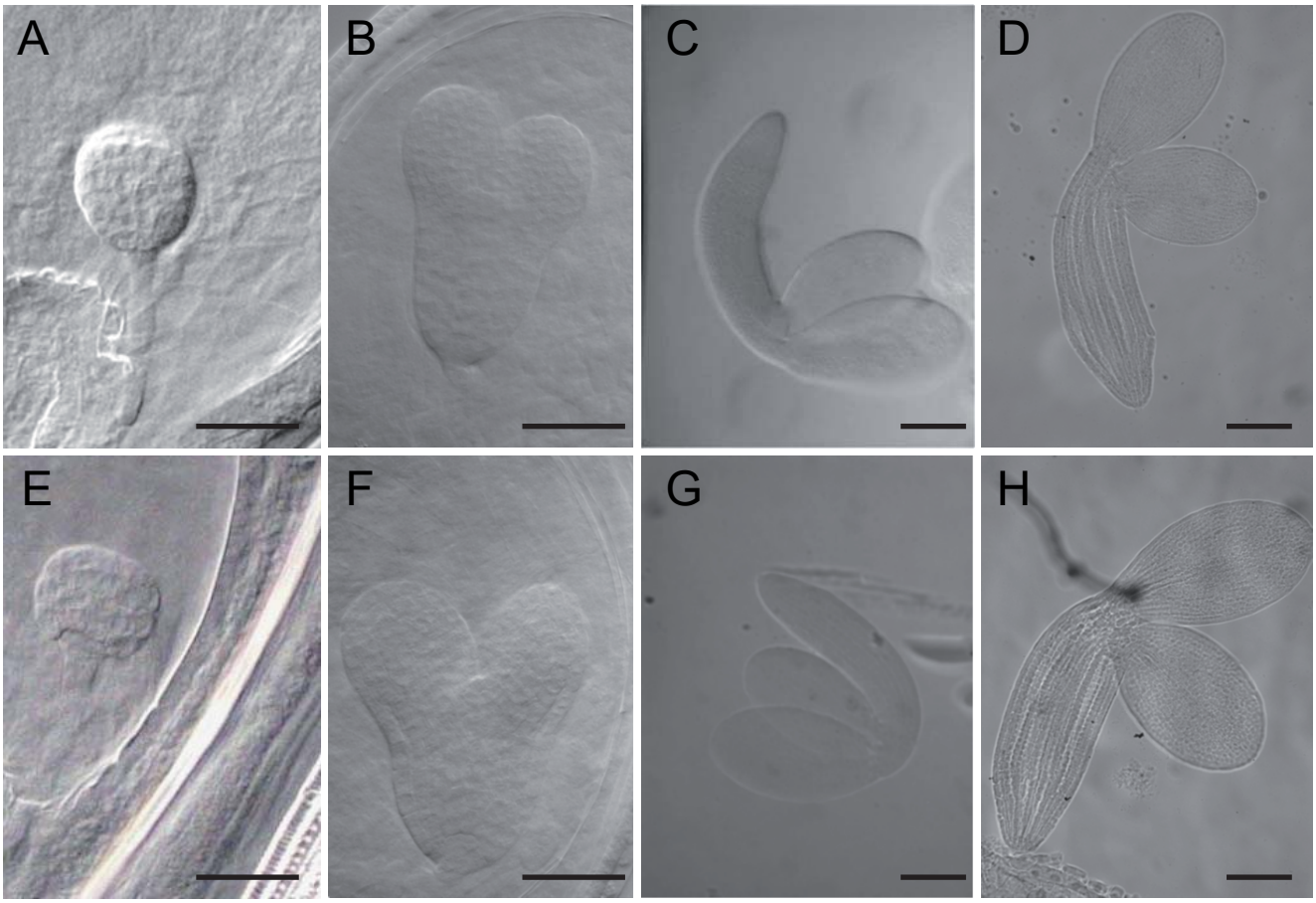


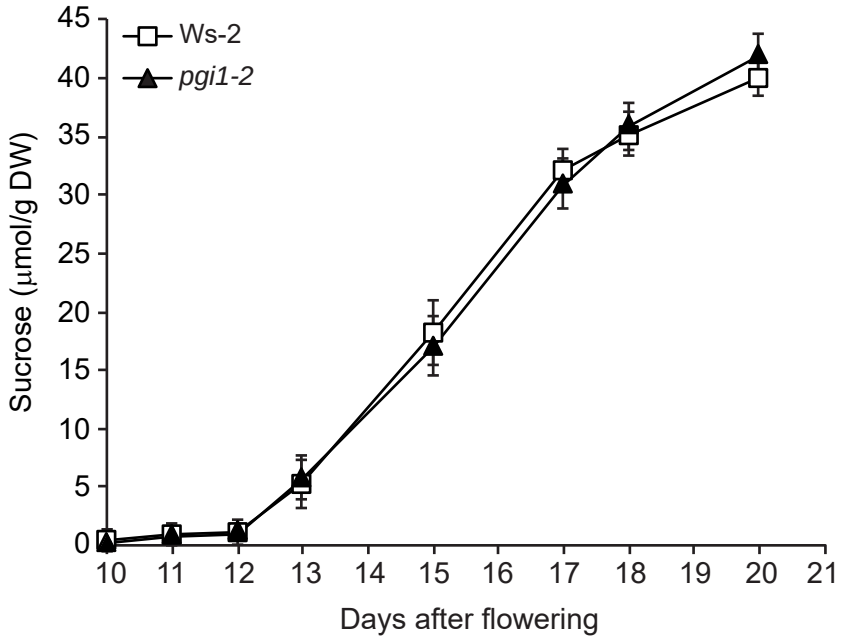
Supplemental Figure 1: Starch content in mature leaves of Ws-2, *pgi1-2* and *promPGI1:PGI1(1)*) plants. Values represent the means ± SE of four biological replicates obtained from four independent experiments, each biological replicate being a pool of mature leaves from four plants. Leaves were harvested after 12 h of illumination. The asterisk indicates significant differences from WT leaves according to Student´s t-tests ($p<0.05$) (**Supports Figure 1**).



Supplemental Figure 2: Expression levels of different *GA2ox*, *GA3ox* and *GA20ox* genes in WT (Ws-2) and *pgi1-2* shoots (gray and white bars, respectively). mRNA levels are set to 1. Values represent the means ± SE of three independent experiments, each consisting of four biological replicates corresponding to a pool of four shoots. Leaves were harvested after 12 h of illumination (**Supports Figure 3**).

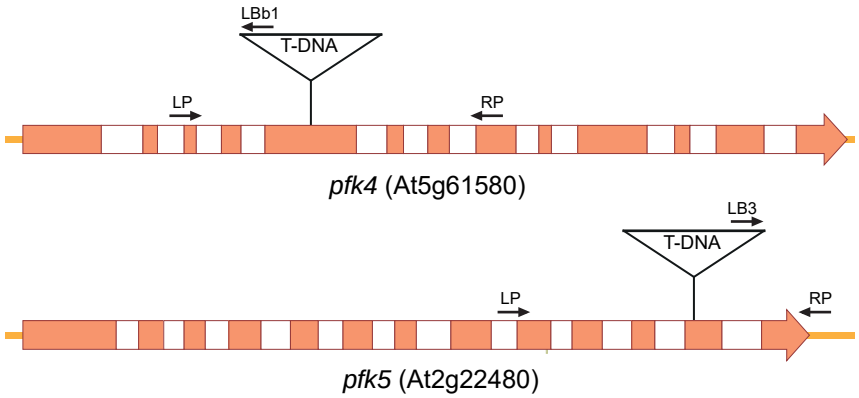


Supplemental Figure 3: Embryo development in WT (Ws-2) **(A–D)** and *pgi1-2* **(E–H)** embryos at: **A** and **E**, globular embryo stage; **B** and **F**, heart stage; **C** and **G**, mid-torpedo stage; **D** and **H**, mature embryo stage. Bars = 10 µm in **A** and **E**; 20 µm in **B-D** and **F-H** (**Supports Figure 4**).



Supplemental Figure 4: Time-course of sucrose content in developing Ws-2 and *pgi1-2* seeds. Values represent the means ± SE of three biological replicates obtained from three independent experiments, each biological replicate being a pool of 50 seeds from four plants (**Supports Figure 4**).

A



B

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RSTFCLKMRS PTEDFVGGYP SDEEWHGYIN NNDRVLLKVI SYSSPTSAGA
ECLDHDCSWV EQWIHRAGPR EKIYFRPEEV KAAIITCGGL CPGLNDVIRH
IVITLEIYGV KNIVGIPFGY RGFSDKDLTE MPLSRKVVQN IHLSGGSLLG
VSRGGPSVSE IVDSMEERGI NMLFVLGGNG THAGANAIHN ECRKRKIKVA
VVGVPKTIDN DILHMDKTFG FDTAVEEAQR AINSAYIEAH SAYHGIGVVK
LMGRNSGFIA MQASLASGQV DICLIPEVPF NLHGPNGVLK HLKYLIETKG
SAVICVAEGA GQNFLEKTNA KDASGNAVLG DFGVYIQQET KKYFKEISTP
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HYAYLPITEV IAYPKSVDPN SRMWHRCLTS TGQPDFI*
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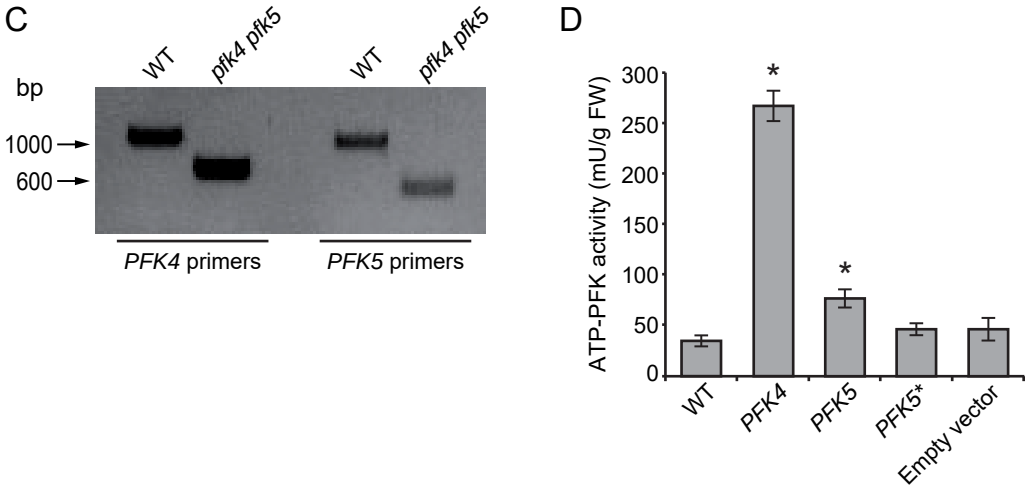
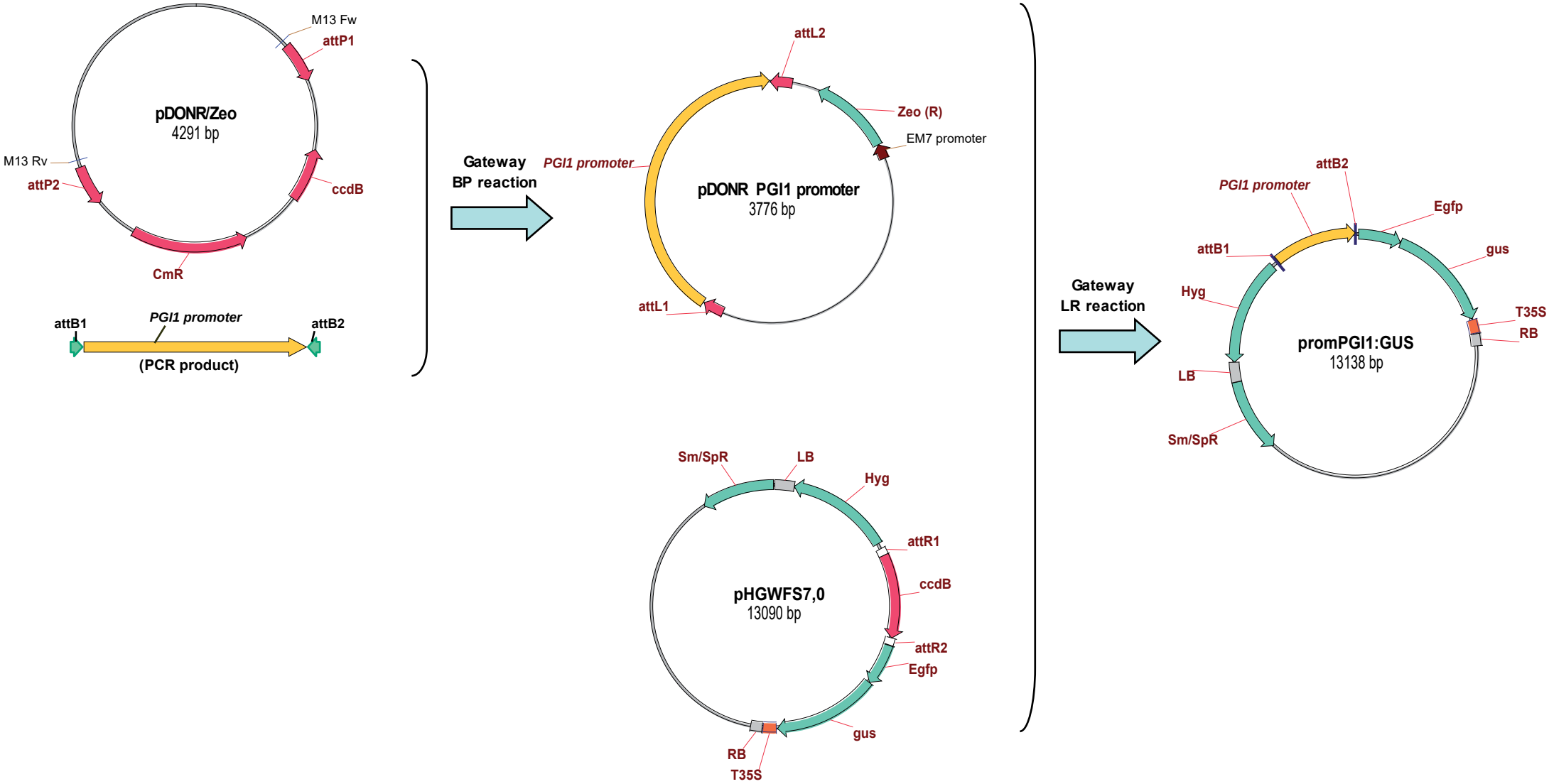
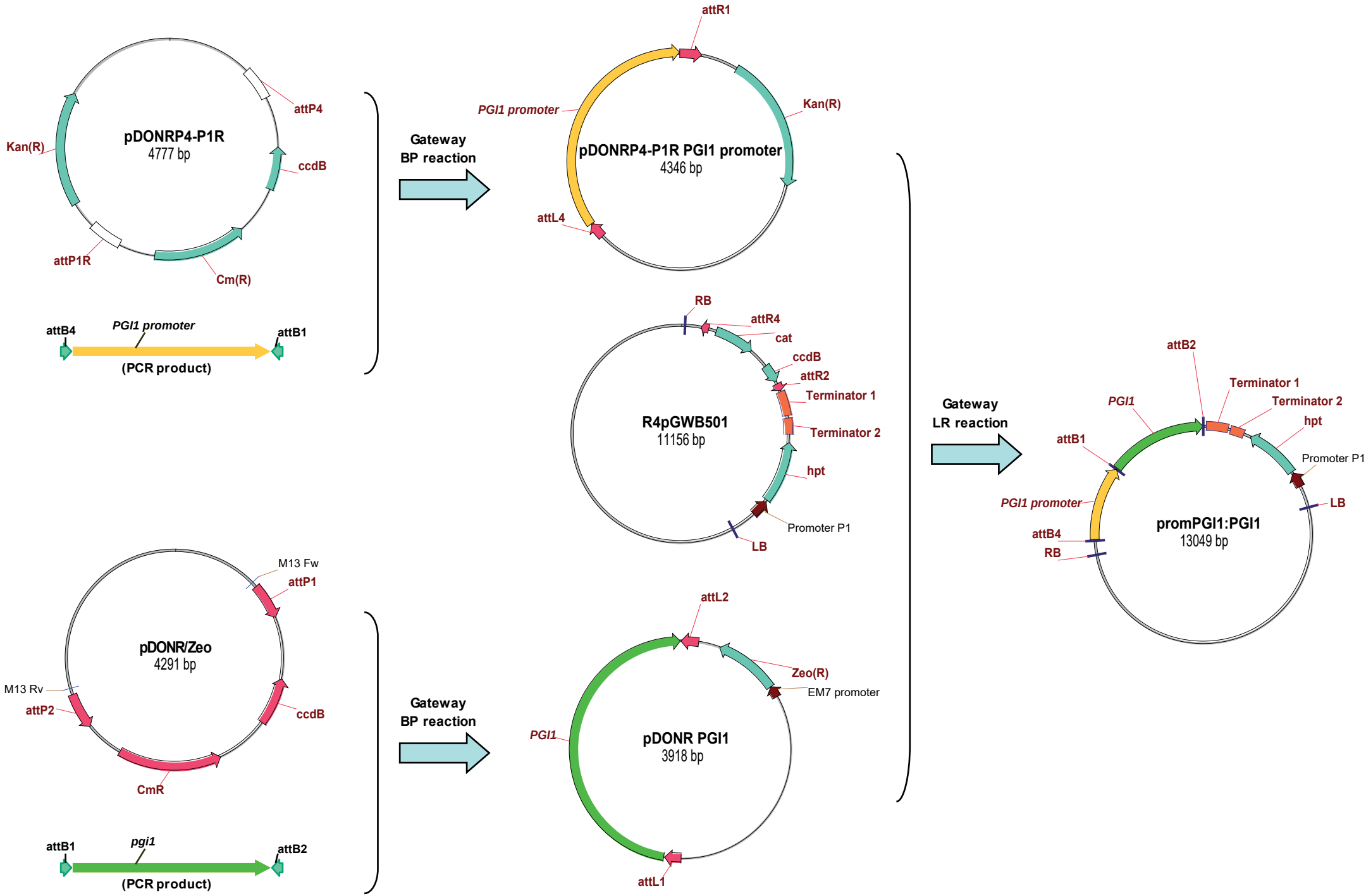


Supplemental Figure 5: Confirmation of the knock-out status of the *pfk4 pfk5* mutant**. (A)** Schematic illustration of the sites of T-DNA insertion in the *pfk4* (SALK_012602) and *pfk5* (SAIL_297_F05) alleles. **(B)** Deduced amino acid sequence of PFK5. The sequence that is not expressed in *pfk5* is highlighted in red. **(C)** PCR analyses of the *pfk4/pfk5* mutant. *PFK* LP and RP specific primers, and T-DNA specific primers used are listed in **Supplemental Table 1.** Annealing positions of *PFK* LP and RP specific primers, and T-DNA specific primers are shown in panel A. **(D)** ATP-PFK activities of tobacco leaves transiently expressing PFK4, PFK5 or PFK5*. Values represent the means ± SE obtained from three independent experiments, each consisting of three biological replicates corresponding to a pool of 4 agro-infiltrated tobacco leaves. Asterisks indicate significant differences from WT leaves according to Student´s t-tests (p<0.05). Note that PFK5 has weak activity, relative to PFK4, in accordance with findings by Mustroph et al. (2007). Note also that the truncated PFK5* form totally lacks ATP-PFK activity (**Supports Figure 8**).



Supplemental Figure 6: Stages in construction of the promPGI1:GUS, 35S:PGI1 and promPGI1:PGI1 plasmids used to produce *promPGI1:GUS*-, *35S:PGI1*- and *promPGI1:PGI1*-expressing plants. Plasmid constructs were produced using Gateway technology and confirmed by sequencing. Complete PGI1-encoding cDNA was obtained from the RIKEN Arabidopsis cDNA collection (Seki et al., 1998; 2002). To construct *promPGI1-GUS* a 1.7-kb fragment of the *PGI1* upstream region was amplified by PCR and subcloned in front of the GUS reporter gene. Primers used for PCR amplification of *PGI1* cDNA, *GUS* and the *PGI1* promoter are listed in **Supplemental Table 2** (**Supports Figure 1**).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attP4
ccdB
Cm(R)
attP1R
Kan(R)
attB4
PGI1 promoter
attB1
(PCR product)
Gateway
BP reaction
attR1
PGI1 promoter
Kan(R)
pDONRP4-P1R PGI1 promoter
4346 bp
attL4
RB
attR4
cat
ccdB
attR2
Terminator 1
Terminator 2
R4pGWB501
11156 bp
hpt
Promoter P1
LB
Gateway
LR reaction
attB2
Terminator 1
PGI1
Terminator 2
hpt
attB1
Promoter P1
PGI1 promoter
LB
promPGI1:PGI1
13049 bp
attB4
RB
M13 Fw
attP1
pDONR/Zeo
4291 bp
M13 Rv
attP2
ccdB
CmR
attB1
pgi1
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(PCR product)
Gateway
BP reaction
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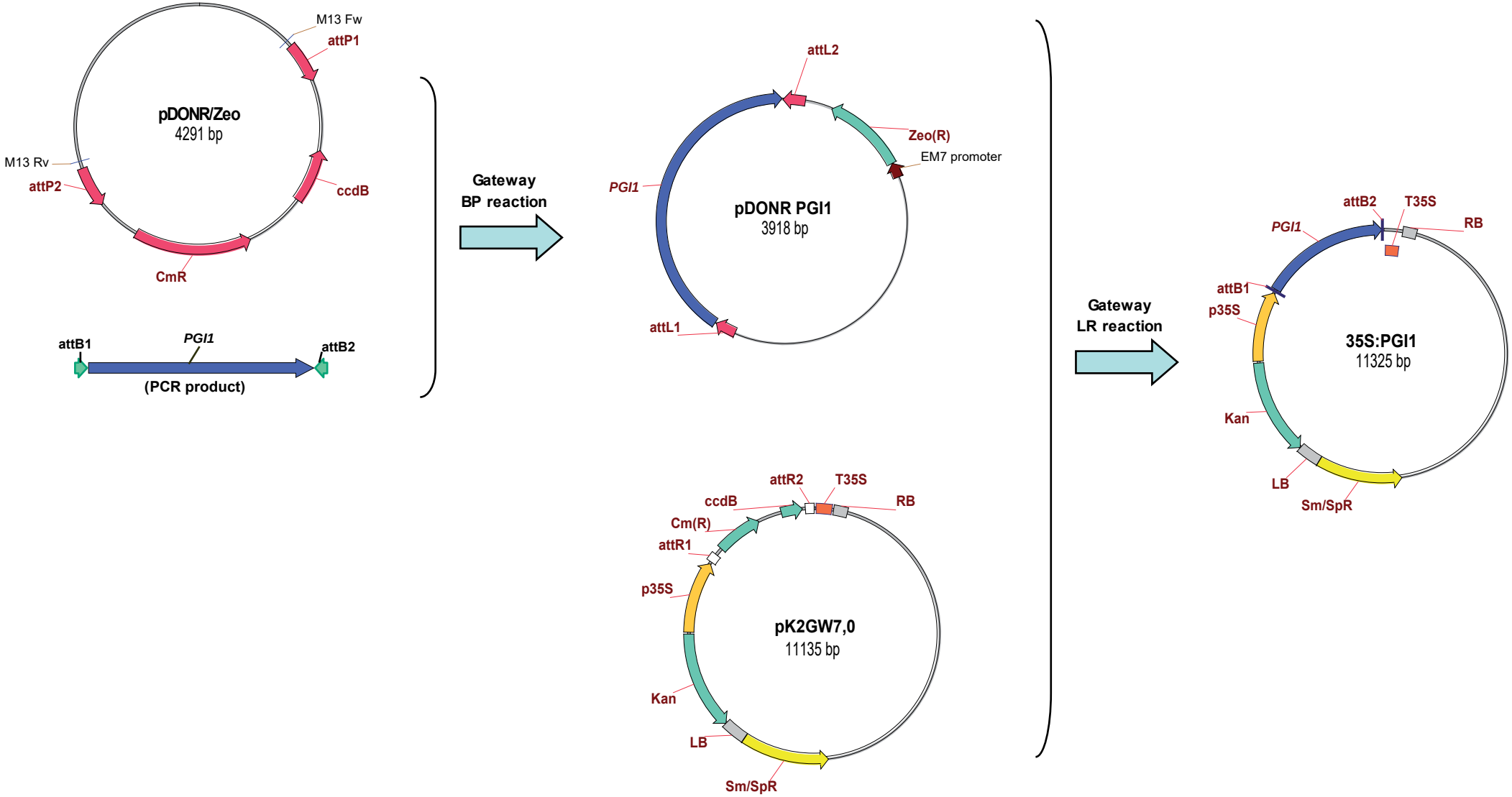
Zeo(R)
EM7 promoter
PGI1
pDONR PGI1
3918 bp
attL1


M13 Fw
attP1
pDONR/Zeo
4291 bp
M13 Rv
attP2
ccdB
CmR
attB1
PGI1
attB2
(PCR product)
Gateway
BP reaction
attL2
Zeo(R)
EM7 promoter
PGI1
pDONR PGI1
3918 bp
attL1
attR2
T35S
RB
ccdB
Cm(R)
attR1
p35S
pK2GW7,0
11135 bp
Kan
LB
Sm/SpR
Gateway
LR reaction
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RB
PGI1
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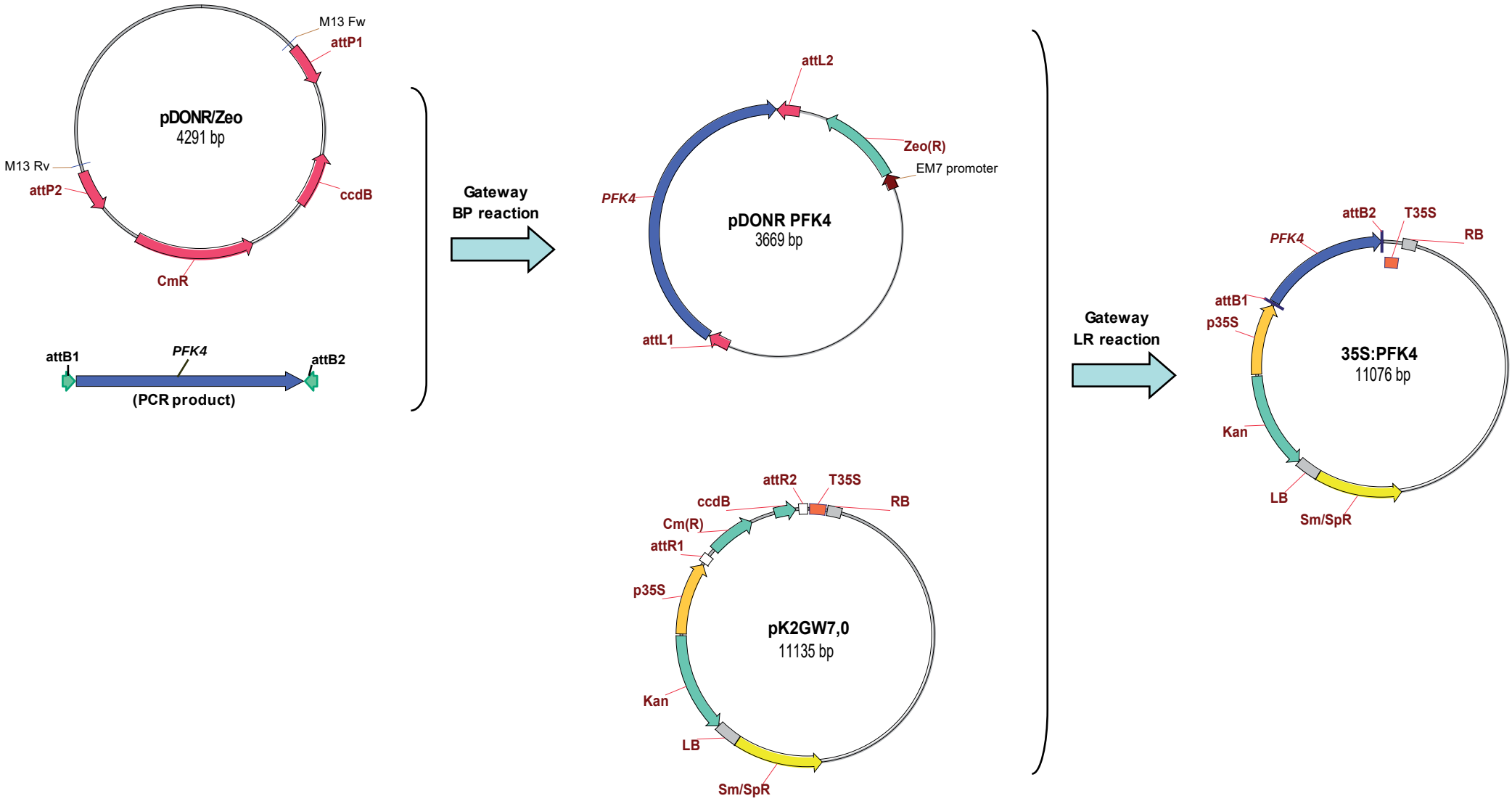
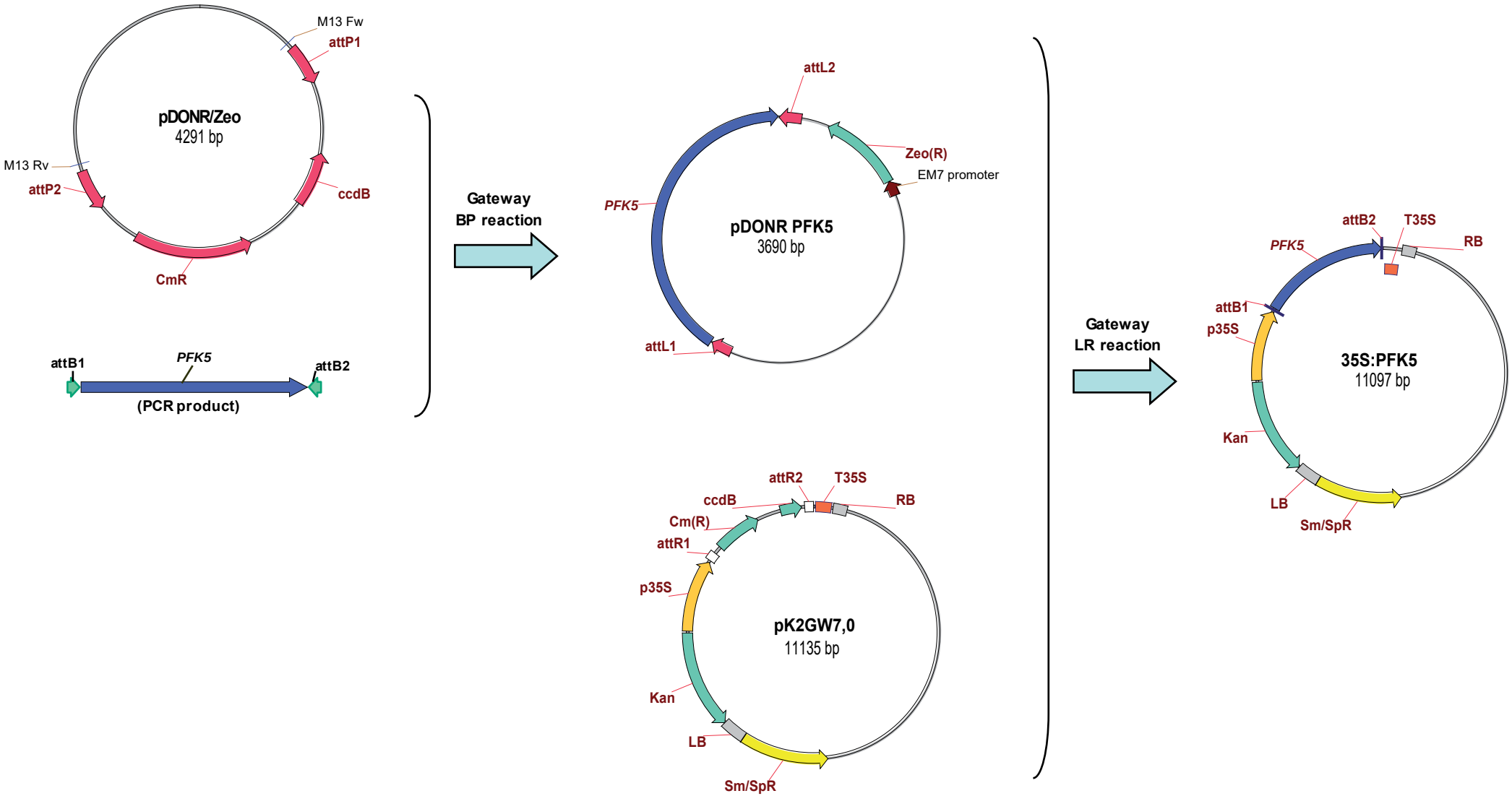
Kan
LB
Sm/SpR



Supplemental Figure 7: Stages in construction of the 35S:PFK4, 35S:PFK5 and 35S:PFK5* plasmids used for transient expression in tobacco leaves. Plasmid constructs were produced using Gateway technology and confirmed by sequencing. Complete PFK4- and PFK5-encoding cDNAs were obtained from the RIKEN Arabidopsis cDNA collection (Seki et al., 1998; 2002). Primers used for PCR amplification of *PFK4, PFK5* and *PFK5** are listed in **Supplemental Table 2** (**Supports Figure 8**).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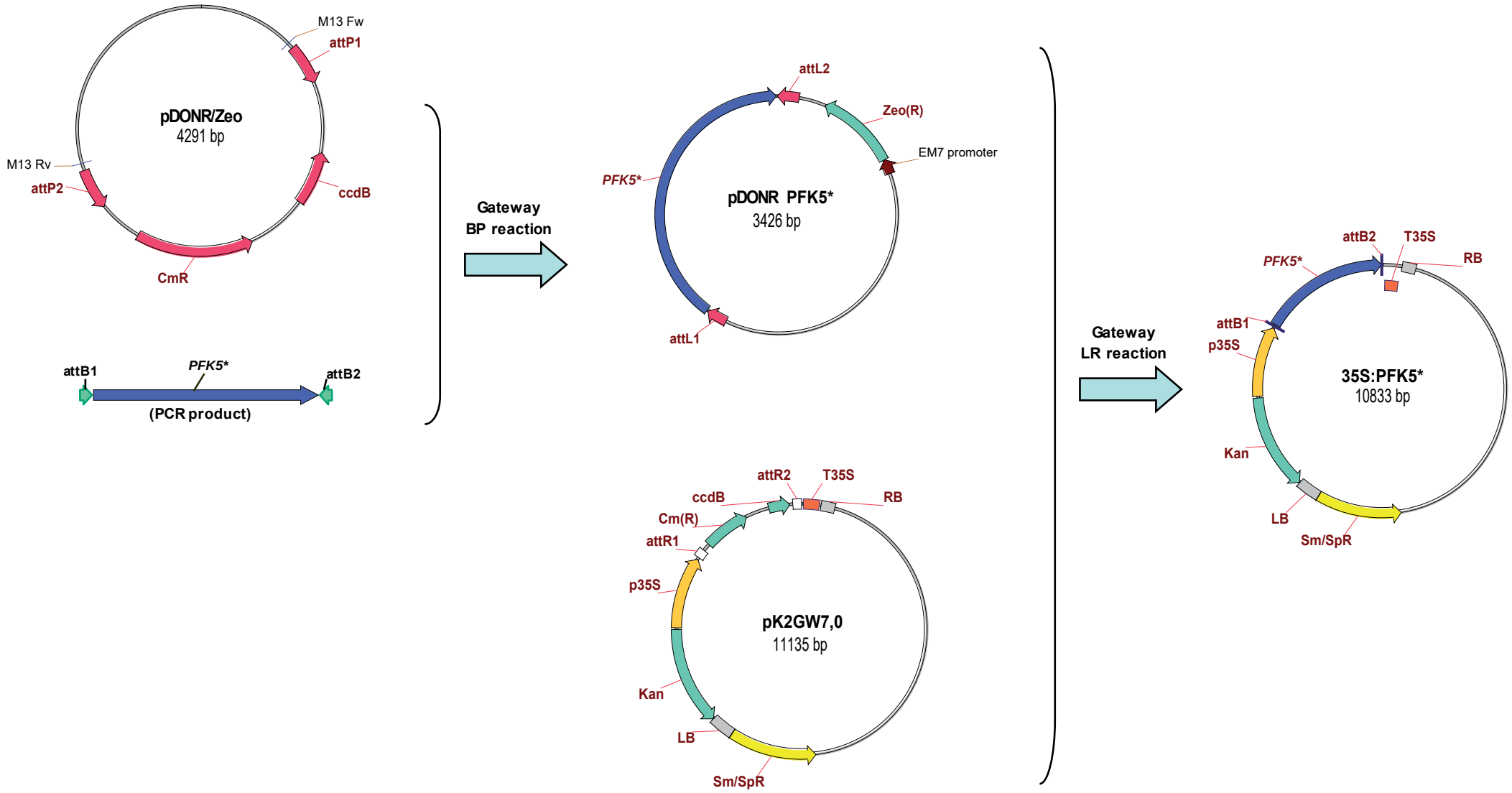
pDONR/Zeo
4291 bp
M13 Rv
attP2
ccdB
CmR
attB1
PFK5
attB2
(PCR product)
Gateway
BP reaction
attL2
Zeo(R)
EM7 promoter
PFK5
pDONR PFK5
3690 bp
attL1
attR2
T35S
RB
ccdB
Cm(R)
attR1
p35S
pK2GW7,0
11135 bp
Kan
LB
Sm/SpR
Gateway
LR reaction
attB2
T35S
RB
PFK5
attB1
p35S
35S:PFK5
11097 bp
Kan
LB
Sm/SpR


M13 Fw
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pDONR/Zeo
4291 bp
M13 Rv
attP2
ccdB
CmR
attB1
PFK5*
attB2
(PCR product)
Gateway
BP reaction
attL2
Zeo(R)
EM7 promoter
PFK5*
pDONR PFK5*
3426 bp
attL1
attR2
T35S
ccdB
RB
Cm(R)
attR1
p35S
pK2GW7,0
11135 bp
Kan
LB
Sm/SpR
Gateway
LR reaction
attB2
T35S
PFK5*
RB
attB1
p35S
35S:PFK5*
10833 bp
Kan
LB
Sm/SpR

Supplemental Table 1. Primers used for PCR screening of the *pfk4 pfk5* mutant.

Mutant	**Primer**	**Sequence**
pfk4 (SALK_012602)	RP (*pfk4*)	5′ AGGCGAACTTTTGTCAGTTCC 3′
	LP (*pfk4*)	5′ ACCACTGTATCTGCCCATGAG 3′
	LBb1 (T-DNA)	5′ GCGTGGACCGCTTGCTGCAACT 3′
pfk5 (SAIL_297_F05)	RP (*pfk5*)	5′ TTTTAGATGAAATCGGGTTGG 3′
	LP (*pfk5*)	5′ TTTGGGCCTTCTGTATTAGGC 3′
	LB3 (T-DNA)	5′ TAGCATCTGAATTTCATAACCAATCTCGATACAC 3′

Supplemental Table 2. Primers used to produce the promPGI1:GUS, promPGI1:PGI1, 35S:PGI1, 35S:PFK4, 35S:PFK5 and 35S:PFK5* plasmids. Primer sequences for attB sites (see **Supplemental Figures 6 and 7**) are indicated in bold.

Primer	Sequence
promPGI1:GUS	
attB1 *PGI1* promoter	5′ **GGGGACAAGTTTGTACAAAAAAGCAGGCTTA**CTTTATATGATCCGATTCAATCTAAAC 3′
attB2 *PGI1* promoter	5′ **GGGGACCACTTTGTACAAGAAAGCTGGGTA**AAATTCTTGGCTCATTGAGAAGG 3′
promPGI1:PGI1	
attB4 *PGI1* promoter	5′ **GGGGACAACTTTGTATAGAAAAGTTGCT**CTTTATATGATCCGATTCAATCTAAAC 3′
attB1R *PGI1* promoter	5′ **GGGGACTGCTTTTTTGTACAAACTTGC**AAATTCTTGGCTCATTGAGAAGG 3′
attB1 *PGI1*	5′ **GGGGACAAGTTTGTACAAAAAAGCAGGCTTA**ATGGCCTCTCTCTCAGGC 3′
attB2 *PGI1*	5′ **GGGGACCACTTTGTACAAGAAAGCTGGGTA**TTATGCGTACAGGTCATCCAC 3′
35S:PGI1	
attB1 *PGI1*	5′ **GGGGACAAGTTTGTACAAAAAAGCAGGCTTA**ATGGCCTCTCTCTCAGGC 3′
attB2 *PGI1*	5′ **GGGGACCACTTTGTACAAGAAAGCTGGGTA**TTATGCGTACAGGTCATCCAC 3′
35S:PFK4	
attB1 *PFK4*	5′ **GGGGACAAGTTTGTACAAAAAAGCAGGCTTA**ATGGAAGCTTCGATTTCGTTTC 3′
attB2 *PFK4*	5′ **GGGGACCACTTTGTACAAGAAAGCTGGGTA**TTAGATAGAAGAGATCTTCATGTT 3′
35S:PFK5	
attB1 *PFK5*	5′ **GGGGACAAGTTTGTACAAAAAAGCAGGCTTA**ATGGATGCTCTTTCTCAGGCG 3′
attB2 *PFK5*	5′ **GGGGACCACTTTGTACAAGAAAGCTGGGTA**TTAGATGAAATCGGGTTGGCC 3′
35S:PFK5*	
attB1 *PFK5*	5′ **GGGGACAAGTTTGTACAAAAAAGCAGGCTTA**ATGGATGCTCTTTCTCAGGCG 3′
attB2 *PFK5**	5′ **GGGGACCACTTTGTACAAGAAAGCTGGGTA**TTAAGTACTTATTTCTTTGAAATACTTC 3′

Supplemental Table 3. Primers used in qRT-PCR analyses

Gene	Direction	Sequence
EF-1α RNA	Forward	5´ TTCTTGACAACACCGACAGC 3´
At1g07940	Reverse	5´ AAGCCCATGGTTGTTGAGAC 3´
PGI1	Forward	5´ GCTGCGTTTAAGGCTATGGA 3´
At4g24620	Reverse	5´ GGCTTAGGTGCGAGCTTAGA 3´
GA2ox1	Forward	5´ CCAAGTCTTCTCAAAAGCCCG 3´
At1g78440	Reverse	5´ GTACTCTTCCAATGCGTTTCTGAA 3´
GA2ox2	Forward	5´ GGTTCCGGTTCTCACTTCCC 3´
At1g30040	Reverse	5´ GGATCGGCTAGGTTGACGAC 3´
GA2ox3	Forward	5´ AGCCAGCCAGTTTTGATAGCA 3´
At2g34555	Reverse	5´ GCGGTTTGCATTTTGGATTAAC 3´
GA2ox4	Forward	5´ CTTTGCTAAACCGGCTCACG 3´
At1g47990	Reverse	5´ GGCTGGTTAACTGGTCGGAC 3´
GA2ox6	Forward	5´ GATCCTTTCAAGTTCAGCTCGG 3´
At1g02400	Reverse	5´ TCTAACCGTGCGTATGTAATCATTC 3´
GA2ox7	Forward	5´ ATGGACAATGGATCAGCGTAAA 3´
At1g50960	Reverse	5´ TGTTGACTGTAAGGGCTTCCAA 3´
GA2ox8	Forward	5´ CATGGAGCAATGGCATGTACA 3´
At4g21200	Reverse	5´ GGTTCGTCATCACACGGTGTT 3´
GA3ox1	Forward	5´ CCATTCACCTCCCACACTCT 3´
At1g15550	Reverse	5´ AGCGGAGAAGAGGAGATCGT 3´
GA3ox2	Forward	5´ CTGCCGCTCATCGACCTC 3´
At1g80340	Reverse	5´ AGCATGGCCCACAAGAGTG 3´
GA3ox3	Forward	5´ CGCTACACTCTTATGGCCCG 3´
At4g21690	Reverse	5´ TCCATCACATTGCAGAACTCG 3´
GA3ox4	Forward	5´ GATCACACCAAGTACTGCGGTATAA 3´
At1g80330	Reverse	5´ TTCCATTTCGTCCACGTATTCTT 3´
GA20ox1	Forward	5´ CTTCCATCAACGTTCTCGAGC 3´

At4g25420	Reverse	5´ GGTTTTGAAGGTCGATGAGAGG 3´

GA20ox2	Forward	5´ AGAAACCTTCCATTGACATTCCA 3´
At5g51810	Reverse	5´ AGAGATCGATGAACGGGACG 3´
GA20ox3	Forward	5´ ACTCGTCTCAAAGGCTGCAAC 3´
At5g07200	Reverse	5´ GAGGCTCTCATCGACACCATG 3´
GA20ox4	Forward	5´ CTATCCAAAATGCAAGCAACCA 3´
At1g60980	Reverse	5´ CAGTGAGGCCCCGTACCTAGT 3´
GA20ox5	Forward	5´ GCCACCCCATGTTGTTGAAG 3´
At1g44090	Reverse	5´ CGATGGTTGCCTAGCCTTGA 3´

Supplemental Data. Bahaji et al. Plant Cell (2018) 10.1105/tpc.18.00312.

Supplemental Table 4. ANOVA Tables

Figure 3

df = degrees of freedom; Mean Sq = Mean Squares; Sum Sq = Sum of Squares

GA1

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	5.33571	5.33571	50.51	0.0004***
Residual	6	0.6338	0.10563		
Total	7	5.9695			

GA4

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.23823	0.23823	9.09	0.0236*
Residual	6	0.15729	0.02621		
Total	7	0.39552			

GA5

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0	0	5.41e-05	0.9944
Residual	6	0.03864	0.00644		
Total	7	0.03864			

GA6

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.00122	0.00122	0.08	0.7932
Residual	6	0.09726	0.01621		
Total	7	0.09847			

GA7

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.00002	0.00002	0.01	0.907
Residual	6	0.00833	0.00139		
Total	7	0.00835			

GA8

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	8.4912	8.49122	18.49	0.0051**
Residual	6	2.7557	0.45919		
Total	7	11.2464			

Supplemental Data. Bahaji et al. Plant Cell (2018) 10.1105/tpc.18.00312.

GA9

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.09103	0.09103	0.09	0.7721
Residual	6	5.94785	0.99131		
Total	7	6.03888			

GA15

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.06504	0.06504	14.01	0.0096**
Residual	6	0.02785	0.00464		
Total	7	0.09289			

GA19

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.01987	0.01987	0.05	0.8354
Residual	6	2.5335	0.42225		
Total	7	2.55338			

GA20

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	1.82745	1.82745	6.54	0.0431*
Residual	6	1.67781	0.27964		
Total	7	3.50527			

GA24

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	1.30947	1.30947	1.1	0.3344
Residual	6	7.13448	1.18908		
Total	7	8.44395			

GA29

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	50.9593	50.9593	68.12	0.0002***
Residual	6	4.4886	0.7481		
Total	7	55.4479			

Supplemental Data. Bahaji et al. Plant Cell (2018) 10.1105/tpc.18.00312.

GA34

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.00161	0.00161	0.69	0.4371
Residual	6	0.01393	0.00232		
Total	7	0.01553			

GA44

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.20416	0.20416	0.56	0.481
Residual	6	2.17092	0.36182		
Total	7	2.37508			

GA51

	df	Sum Sq	Mean Sq	F-value	P-value
Treatment	1	0.90201	0.90201	3.55	0.1086
Residual	6	1.52578	0.2543		
Total	7	2.42779			

SUPPLEMENTAL REFERENCES

Mustroph, A., Sonnewald, U., and Biemelt, S. (2007). Characterization of the ATP-dependent phosphofructokinase gene family from *Arabidopsis thaliana*. FEBS Lett. 581: 2401-2410.

Seki, M., Carninci, P., Nishiyama, Y., Hayashizaki, Y. and Shinozaki, K. (1998) High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated CAP trapper. Plant J. 15: 707-720.

Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., and Shinozaki K (2002) Functional annotation of a full-length Arabidopsis cDNA collection. Science 296: 141-145.