Supplementary information for construction of plasmids

Generation of PKL peptides

To generate the N-terminal fragment of PKL, the relevant portion of the *PKL* ORF was amplified with Platinum *Pfx* DNA polymerase (Invitrogen Corp., Carlsbad, CA) using the primers of JOPR488 (5'-GTCGGGATCCGATGAGTAGTTTGGTGGAGAG-3') and JOPR489 (5' – CCGCAAGCTTATGGATGTAACAAGCCTTTGA-3'). The PCR product was cloned into the *Eco*RV site of pBS II SK (Stratagene, La Jolla, CA) generating pJO844 and the identity of the product was confirmed by determination of the nucleotide sequence. The PKL N-terminal region was subsequently ligated as a *Bam*HI-*Hind*III fragment into the expression vector pET21b+ (Novagen, Madison, WI) cut with *Bam*HI and *Hind*III. This expression vector was designated pJO857.

An expression vector that carried the C-terminal region of PKL was generated as described above except that the primers used for amplification were JOPR490 (5'-GTCGGGATCCGGGATTCTTAAAGGCTTTCAA-3') and JOPR491 (5'-CCGCAAGCTTAATCAACGACCATGTTCTTTG-3'). The expression plasmid carrying the cloned C-terminal *PKL* fragment was designated pJO862.

Production of full-length PKL in E. coli and yeast

*Cla*I and *Sph*I were added to 5' and 3' terminus of PKL cDNA by PCR and cloned into a modified version of pBluescript that contains an altered MCS generating pJO971. The sequence of the junction of the resulting PKL cDNA cassette at the start codon is 5'-TGGGTACCTTCGAAATCGATGAGTAGTTTGGTGGAGA-3' where PKL cDNA sequence is bolded and the *Cla*I site is underlined. The junction sequence at the stop codon is 5'-ATGGTCGTTGATTGAGCATGCCCATGGCTAGC-3' where PKL cDNA sequence is bolded and the *Sph*I site is underlined. The final product has been validated by DNA sequencing.

To express PKL protein in *E. coli*, we first modified pET-21b (Novagen, San Diego, CA) to eliminate the T7 tag. A 5.4 kb *Nhe*I-*EcoR*I fragment of pET-21b+ was ligated to an adaptor formed by annealing the oligos 5'-AATTCGCTAGCGGAATCAAGGGA-3' and 5'-CTAGTCCCTTGATTCCGCTAGCG-3' to generate pJO1076. A 7.1 kb *Nhe*I-*Nde*I fragment from pJO971 carrying *PKL* cDNA was then ligated to a 5.4 kb *Nhe*I-*Nde*I fragment from pJO1076 to generate pJO1079, resulting in *PKL* cDNA being placed downstream of the T7 *lac* promoter.

To express PKL protein in yeast, we first modified pPC86 (Invitrogen Corp., Carlsbad, CA) to remove the GAL4 activation domain. A 6.7 kb *Hind*III-*Sal*I fragment of pPC86 (Invitrogen Corp., Carlsbad, CA) was ligated to an adaptor formed by annealing the oligos 5'-TCGACGCTAGCGTCCAAAGTCCATCGATA-3' and 5'-AGCTTATCGATGGACTTTGGACGCTAGCG-3' to generate pJO1080. A 7.1 kb *Nhe*I-*Cla*I fragment from pJO971 carrying *PKL* cDNA was then ligated to 6.7 kb *Nhe*I-*Cla*I fragment of pJO1080 to generate pJO1081, resulting in *PKL* cDNA being placed downstream of the *ADH* promoter.

PKL:eGFP characterization

The transcriptional and translational *PKL:eGFP* fusions are both flanked by the genomic sequences that flank *PKL*: a 1.1 kb upstream fragment (bounded by a *BstB*I site and the start codon of *PKL*) and a 1.4 kb downstream fragment (bounded by the stop codon of *PKL* and an *Nco*I site). For the *PKL:eGFP* transcriptional fusion, *Cla*I and *Sph*I restriction sites were introduced at the start and stop codon of both *PKL* and e*GFP* by PCR. *PKL* sequences were amplified from genomic DNA whereas the eGFP fragment was amplified from pEGAD (Cutler et al., 2000) All resulting PCR products (and those described hereafter) were subcloned into pBluescript and sequenced. The sequence of the junction of the resulting transcriptional fusion at the start codon is 5'-*tgtgtgcagaaa*atc*gatg*gtgagcaaggg-3' where the *PKL* genomic sequence is italicized, the *eGFP* sequence is bolded, the ATG is italicized and bolded, and the *Cla*I site is underlined. The sequence of the junction of the resulting transcriptional fusion at the stop codon is 5'-cgagctgtacaag*tag*catg*ctcaactggt*-3' where the *eGFP* sequence is bolded, the *PKL* genomic sequence is italicized, the termination codon is italicized and bolded, and the *Sph*I site is underlined.

For the *PKL:eGFP* translational fusion, the *PKL* genomic sequence between the start and the stop codon was replaced with full-length *PKL* cDNA by PCR. *Cla*I and *Sph*I sites were introduced by PCR prior to the termination codon of *PKL* such that it is possible to generate translational fusions with *Cla*I-*Sph*I fragments. The resulting vector (containing 1.1 kb of *PKL* upstream sequence, *PKL* cDNA, *Cla*I, *Sph*I, and 1.4 kb of *PKL* downstream sequence) is referred to as pJO981. A *Cla*I site and an $(Ala)_9$ linker were introduced at the ATG of eGFP and an *Sph*I site was introduced at the 3' terminus by PCR. The *Cla*I-*Sph*I fragment spanning the resulting *eGFP* product was then cloned into pJO981, generating pJO1027. The sequence of the resulting junction and the 3' end of the *PKL* ORF is 5'- *ggtcgttgat*atcgat[gccgctgcggcagcggctgcggccgcttcg]atggtgagca-3' where the *PKL* cDNA sequence is italicized, the *eGFP* sequence is bolded, the $(Ala)_9$ linker sequence is bracketed, and the *Cla*I site is underlined. The sequence of the junction at the termination codon of the translational fusion is as described above for the transcriptional fusion.

PKL:GR inducible lines

PKL:GR is a C-terminal fusion of PKL with the ligand-binding domain of the rat glucocorticoid receptor (GR). Similar to the *PKL:eGFP* translational fusion described above, *PKL:GR* is derived from pJO981. A *Cla*I site and a small linker were introduced at the 5' terminus of the ligand-binding domain of *GR* and an *Sph*I site was introduced at the 3' terminus by PCR amplification of pBI-△GR (Lloyd et al., 1994). The *Cla*I-*Sph*I fragment spanning the resulting *GR* product was then cloned into pJO981, generating pJO1002. The sequence of the resulting junction and the 3' end of the *PKL* ORF is 5'- *ggtcgttgat*atcgat[gctctagaggttcct]gaagctcgaa-3' where the *PKL* cDNA sequence is italicized, the *GR* sequence is bolded, the linker sequence is bracketed, and the *Cla*I site is underlined. The sequence of the junction of the resulting transcriptional fusion at the stop codon is 5'-tcatcaaaa*tga*gcatg*ctcaactggt*-3' where the *GR* sequence is bolded, the *PKL* genomic sequence is italicized, the termination codon is italicized and bolded, and the *Sph*I site is underlined.

Supplementary information for qRT-PCR:

Oligonucleotide primer sequences and primer concentrations used for qRT-PCR are available in Table S2. Relative expression values of genes were calculated from critical threshold values as described in ABI User Bulletin #2, part # 4303859B available at http://docs.appliedbiosystems.com/search.taf?_UserReference=6E00E667F6CFB2C43DE24701. Table S2 lists the critical threshold values for Table 1 from the manuscript.

Table S1. Relative transcript levels for Type I MADS-box transcription factors in *pkl* mutants. Transcript levels were determined for *pkl* and wild type plants at 50% radicle emergence (50% germination), in young seedlings (4-day-old seedlings) and in 21 day-old leaves (21-day-old rosette). 18s rRNA was used as a standardization control. Expression levels in *pkl* plants are normalized relative to wild-type plants. N/D indicates transcript not detected.

	50% germination		4-day-old seedlings		21-day-old rosette	
AGI code	WT	*pkl-1*	WT	*pkl-1*	WT	*pkl-1*
At1g01530	1	2.20	1	1.49	1	2.04
At1g17310	1	0.51	1	0.69	1	0.39
At1g18750	1	0.08	1	1.22	1	0.73
At1g22130	1	1.50	1	4.43	1	0.54
At1g22590	1	0.52	1	0.45	1	0.22
At1g28450	N/D	N/D	1	4.35	N/D	N/D
At1g28460	1	2.33	1	1.19	N/D	N/D
At1g31140	N/D	N/D	1	1.02	1	0.24
At1g31630	1	0.78	1	0.54	N/D	N/D
At1g31640	N/D	N/D	1	1.59	1	1.09
At1g47760	1	3.47	1	2.21	1	0.57
At1g48150	1	0.57	1	1.94	1	0.72
At1g60880	1	0.63	1	0.38	1	0.87
At1g60920	1	2.83	1	0.27	N/D	N/D
At1g65300	1	1.81	1	40.04	1	21.41
At1g65330	1	2.24	1	161.27	1	184.82
At1g65360	N/D	N/D	N/D	N/D	1	0.83
At1g69540	1	1.19	1	0.99	1	0.78
At1g72350	1	0.60	1	0.32	N/D	N/D
At1g77950	1	0.88	1	0.72	N/D	N/D
At1g77980	N/D	N/D	1	0.28	N/D	N/D
At2g03060	1	1.25	1	1.27	1	1.30
At2g24840	N/D	N/D	1	2.27	N/D	N/D
At2g26320	N/D	N/D	1	0.86	N/D	N/D
At2g26880	1	1.56	N/D	N/D	N/D	N/D
At2g28700	N/D	N/D	1	17.15	1	3.15
At2g34440	1	1.44	1	0.73	1	2.09
At2g40210	1	1.92	1	1.85	N/D	N/D
At3g04100	N/D	N/D	N/D	N/D	N/D	N/D
At3g05860	1	3.66	1	3.34	N/D	N/D
At3g66656	1	37.53	1	1.28	N/D	N/D
At4g14530	N/D	N/D	1	0.93	N/D	N/D
At4g36590	N/D	N/D	N/D	N/D	N/D	N/D
At5g04640	N/D	N/D	1	0.92	N/D	N/D
At5g06500	N/D	N/D	N/D	N/D	N/D	N/D
At5g26580	1	0.87	1	0.99	1	2.52
At5g26630	1	5.08	1	0.57	1	0.74
At5g26650	1	1.56	N/D	N/D	N/D	N/D
At5g26950	1	3.05	1	0.92	1	2.10
At5g27130	N/D	N/D	1	1.63	1	0.19
At5g27960	N/D	N/D	N/D	N/D	N/D	N/D
At5g38620	N/D	N/D	N/D	N/D	N/D	N/D
At5g48670	1	1.64	1	1.01	1	0.23
At5g49420	1	2.08	N/D	N/D	1	0.19
At5g49490	N/D	N/D	1	2.13	N/D	N/D
At5g55690	N/D	N/D	1	3.30	N/D	N/D
At5g58890	N/D	N/D	1	0.82	N/D	N/D
At5g60440	1	0.28	1	0.35	1	0.41
At5g38620	N/D	N/D	N/D	N/D	N/D	N/D
At5g48670	1	1.64	1	1.01	1	0.23
At5g49420	1	2.08	N/D	N/D	1	0.19
At5g49490	N/D	N/D	1	2.13	N/D	N/D
At5g55690	N/D	N/D	1	3.30	N/D	N/D
At5g58890	N/D	N/D	1	0.82	N/D	N/D
At5g60440	1	0.28	1	0.35	1	0.41

Table S2. Primer information for qRT-PCR.

Gene		Oligonucleotide Primer Sequences		primer number (JOPR####)		Concentrations used (nM)	
name	AGI code	Forward primer sequence	Reverse primer sequence	Forward	Reverse	Forward	Reverse
	At1g01530	TGATCAAAACGGAAACTCTACTTCTG	GCTGGTGTGCGATTCATAACA	2595	2596	900	900
	At1g17310	GGTAACGATCGGACGGTTGA	GGTTTCCATCCCATCACATTG	2597	2598	900	900
	At1g18750	AACTCTTGCCAATAGAATGTGCAA	TTACCTCCCATCGCCATAGG	2599	2600	900	900
	At1g22130	TGCCAGCTCAGCAGAGTGATA	GTCGGAGACTTCATGATCAACTTG	3127	3128	900	900
	At1g22590	CGGTCAGAGTGGCTTGCA	TTCTCTACCGGAAGTTCGCTTAA	2603	2604	900	900
	At1g28450	TCAAGAAAATTGAAAAAGACGAAGAC	AGAGAATGGAAAGCTCAATGATCA	3129	3130	900	900
	At1g28460	ACACTTTTGGCAGTCCATCCTT	AGGCATCGCCGTTGAGAA	2607	2608	900	900
	At1g31140	CGATGTCCACCTTGGTCTCA	TGCTGGTAGAGTTGGAGCAGAA	2609	2610	900	900
	At1g31630	CAGTGGTGTGGCCGTCAA	CCGGCCTCTCCATAAACATG	2611	2612	900	900
	At1g31640	ACAGTCCGTTCGAGAATCCAA	GAACTCCGAAATCACCTCTTGAA	2613	2614	900	900
	At1g47760	CGAAAGGAAAGCGACGTTTT	CGCGAGTTCATCAGCCTTCT	2615	2616	900	900
	At1g48150	TTGAAATTGAGAAACGCATGACTAAA	AGTGTGGGACGGCGTTTG	3131	3132	900	900
	At1g60880	GCAATCTTAGCGGCTCCTATGA	CGACAGAGGAATGACCGAAAG	2619	2620	900	900
	At1g60920	GGCAGTCGATGCGGTTTC	TGCTCTTCACGGCATCATCTA	2621	2622	900	900
PHE2	At1g65300	GATGACGAAGAAACTAACCGAGCTA	GGGATCGAGTTGAACGGACTATAG	3133	3134	50	300
PHE1	At1g65330	CATCTGTCCCAATCGGTTTTG	TGGAATTGAACCGGCTCTTG	2623	2624	900	900
	At1g65360	TTCAAATGCTCAACAAATCCTACAC	GCCCGCGACTGCTTATTC	3135	3136	900	900
	At1g69540	GGGAAAGGCTTCAATTTGCA	GGAGAGAGTTGAGCAAACTTAGCA	2629	2630	900	900
	At1g72350	CCCGAAGGCAAGTGACGTT	CTTAATTCTGCCGCTTTTTTGAA	2631	2632	900	900
	At1g77950	TCTTTTCCGGTCAAACAAGGA	CTCTTTCTTGATCAGGAAGATTGATG	2633	2634	900	900
	At1g77980	TGGGTGGGCCTTTTGGA	CTTCGTTAGGCCCATTTTCAGT	2635	2636	900	900
	At2g03060	GTCGAGTGCTCAGCGAGTTCT	TCAGGAGATTTCCCTGTTCCA	2637	2638	900	900
	At2g24840	TCGCTACGTGTCTCGAAACAA	TGCAGGGCTTCCTTGCA	2639	2640	900	900
	At2g26320	CCCACCGAGAAGCCTACAGTT	GCATGCAAAACCTCTCAAGGA	2641	2642	900	900
	At2g26880	AAGAAGTTTGATTTCATGCAGCAT	CGACTTGCACCTCGAATGG	2643	2644	300	300
	At2g28700	CTGGAAACATGGCAACAACTGTA	AGGAGGAACTCCCTTCAGCAA	2645	2646	900	900
	At2g34440	GGACATGAACACACGACAGGTT	AACTCGCTCGCCTTCTTGAA	2647	2648	900	900
	At2g40210	CCCCGATAAGGTTGGACCAT	CGAAAAATTCGTCTAGGAGACCAT	2649	2650	300	900
	At3g04100	CAGACCCCTCGTCGAAGCT	TCGAGCGCCTCCATTTTTT	2651	2652	900	900
	At3g05860	CGTTCTCTGCGGAATCGAA	GCCAGACTTCAGGGTTTGAGTT	2653	2654	900	900
	At3g66656	GAGCGAGCTTGCGACTCTGT	CGGTTTGTTTCCTGGAGAAAAG	2655	2656	300	300
	At4g14530	TCGGAGGATTCGGAGGAGTT	CCAATTCCTTCAGATCTCTCAACA	2657	2658	300	300
	At4g36590	CACATTAAGTGGTGCAGAGATTCTG	TGGATGGCCAAAAGAAAACAC	2659	2660	900	900
	At5g04640	TCTCTCCGATGCACAAATTGC	GCCAAAGGTGTAGAAAGAAACGTT	2661	2662	900	900
	At5g06500	GCCCTGAGGGCTTCGAAT	CTTCCAGTTTCCATCATGTTTAACC	2663	2664	900	900
	At5g26580	TGGCCGATACGACTCATTTTC	AGCCTGGTATTGAACCTGATTCA	2665	2666	900	900
	At5g26630	TGTCGTCAACAGTCCGTACGA	CCTGGTTCGCAGCCTCTCT	2667	2668	900	900
	At5g26650	TGAATCCGATGGTGGAACAA	TAGCAGTTTCCGTCCACGAAA	2669	2670	900	900
	At5g26950	TTTTCCTCCTCAGATGCAGACA	GATTCCATGGCGCAAACTG	2671	2672	900	900
	At5g27130	AGAGCAACGAGCCGTGACTT	GAGATCGGCGGCTTTGG	2673	2674	300	900
	At5g27960	TTCTTGCGGGCGATATGAC	CTGGGAGCAGTTACCGCATT	2675	2676	900	900
	At5g38620	TGTTCACGGAACTCAAGATCAAA	GATTTTCAGGGATGCAACAAACT	2677	2678	300	300
	At5g48670	CCAACATCAGATCCATGACGAA	CAGGGATGATGCTGCTTGAGT	2679	2680	900	900
	At5g49420	GACGAGGGAGGACGTTGGTA	CGTCGTTCCACCAAAAACCT	2681	2682	900	900
	At5g49490	CGAGATTGAGAGATTATGGCTTTCA	CCACAGCGACGGTTTTTGTT	2683	2684	900	900
	At5g55690	CCTCAAATACTGCGGAAGTGTCT	AGCTTTGCCCGTTCGCTAT	2685	2686	900	900
	At5g58890	AAACCAACGTGGAGACTTTCGT	TCACGCTTCACTCTCTTTTTAGTCA	2687	2688	900	900
	At5g60440	GACAAAAGCCCTTGGGAATTG	AACCCCTCGAGTTGAGATAACG	2689	2690	900	900
18S		GGTCTGTGATGCCCTTAGATGTT	GGCAAGGTGTGAACTCGTTGA	997	998	300	900
LEC1	At1g21970	AAGCCGGCATTCCGTTAAT	GGTCGTCGGGTCAAGATGAA	868	869	300	50

Table S3. Critical threshold values for Tables 1, 2, and S1. "AGI Code" provides the AGI number for the analyzed gene. "Sample" describes the sample collected. Sample codes: W=wt, P=pkl, G=germination, S=4d seedling, R=21d rosette. "Average CT" is average critical threshold of three measurements, and "STDEV" is the standard deviation associated with the average critical threshold. 18S was used as a control. "GOI" indicates values for gene of interest (designated by AGI code in first column). N/D indicates not detected.

AGI code		18S		GOI			18S		GOI	
	Sample	Avg CT	STDEV	Avg CT	STDEV	Sample	Avg CT	STDEV	Avg CT	STDEV
At1g01530	WG1	7.18	0.27	35.02	0.08	PG1	7.82	0.32	34.52	0.41
At1g17310	WG2	6.83	0.12	33.65	0.20	PG2	6.91	0.09	34.70	0.46
At1g18750	WG3	9.24	0.05	31.35	0.58	PG3	9.29	0.05	34.97	0.62
At1g22130	WG4	8.15	0.05	37.61	0.32	PG4	8.21	0.05	37.08	0.33
At1g22590	WG5	7.36	0.07	28.16	0.07	PG5	7.43	0.06	29.15	0.12
At1g28450	WG6	6.38	0.08	34.92	N/D	PG6	6.45	0.08	34.14	N/D
At1g28460	WG7	7.36	0.07	37.95	0.21	PG7	7.43	0.06	36.79	0.91
At1g31140	WG8	6.82	0.16	35.60	N/D	PG8	6.98	0.16	38.81	N/D
At1g31630	WG9	6.82	0.16	35.52	N/D	PG9	6.98	0.16	36.03	N/D
At1g31640	WG10	7.18	0.08	N/D	N/D	PG10	6.85	0.01	N/D	N/D
At1g47760	WG11	7.68	0.10	26.81	0.14	PG11	7.90	0.16	25.23	0.26
At1g48150	WG12	7.68	0.10	33.70	0.48	PG12	7.90	0.16	34.73	0.57
At1g60880	WG13	6.82	0.16	34.02	0.01	PG13	6.98	0.16	34.84	1.01
At1g60920	WG14	7.30	0.09	35.84	0.65	PG14	7.46	0.15	34.50	0.62
At1g65300	WG15	7.50	0.17	37.09	N/D	PG15	8.06	0.06	36.80	0.12
At1g65330	WG16	7.18	0.08	36.09	0.40	PG16	6.85	0.01	34.60	0.56
At1g65360	WG17	6.24	0.16	39.65	N/D	PG17	6.40	0.12	38.39	N/D
At1g69540	WG18	7.97	0.16	32.89	0.36	PG18	8.14	0.04	32.80	0.14
At1g72350	WG19	7.97	0.16	37.73	2.18	PG19	8.14	0.04	38.64	1.41
At1g77950	WG20	6.59	0.17	28.80	0.15	PG20	6.80	0.13	29.20	0.15
At1g77980	WG21	6.59	0.17	N/D	N/D	PG21	6.80	0.13	36.58	1.19
At2g03060	WG22	8.19	0.08	27.52	0.08	PG22	8.25	0.10	27.25	0.13
At2g24840	WG23	8.19	0.08	N/D	N/D	PG23	8.25	0.10	38.12	0.10
At2g26320	WG24	8.19	0.08	38.92	N/D	PG24	8.25	0.10	N/D	N/D
At2g26880	WG25	8.26	0.11	35.79	0.67	PG25	8.78	0.41	35.66	0.00
At2g28700	WG26	8.17	0.08	N/D	N/D	PG26	8.58	0.54	37.85	N/D
At2g34440	WG27	7.66	0.02	33.44	0.30	PG27	7.98	0.21	33.24	0.51
At2g40210	WG28	7.18	0.27	36.02	0.37	PG28	7.82	0.32	35.72	0.43
At3g04100	WG29	7.43	0.46	N/D	N/D	PG29	8.19	0.20	38.13	N/D
At3g05860	WG30	6.66	0.08	34.20	0.45	PG30	7.05	0.17	32.73	0.62
At3g66656	WG31	7.66	0.02	38.34	1.00	PG31	7.98	0.21	33.44	0.50
At4g14530	WG32	7.50	0.17	35.66	0.22	PG32	8.06	0.06	36.00	N/D
At4g36590	WG33	9.17	0.07	36.84	0.60	PG33	9.47	0.13	37.52	N/D
At5g04640	WG34	7.43	0.46	35.87	0.26	PG34	8.19	0.20	36.76	N/D
At5g06500	WG35	7.84	0.16	38.24	1.44	PG35	8.34	0.37	36.04	0.14
At5g26580	WG36	7.05	0.40	37.48	0.43	PG36	7.22	0.71	37.86	1.19
At5g26630	WG37	6.15	0.13	37.39	1.40	PG37	6.38	0.11	35.28	0.19
At5g26650	WG38	7.43	0.46	36.67	0.25	PG38	8.19	0.20	36.79	0.79
At5g26950	WG39	6.71	0.18	34.81	0.41	PG39	6.71	0.06	33.21	0.18
At5g27130	WG40	7.43	0.46	39.47	N/D	PG40	8.19	0.20	36.14	0.47
At5g27960	WG41	6.71	0.18	35.44	0.25	PG41	6.71	0.06	35.48	N/D
At5g38620	WG42	6.71	0.18	36.59	N/D	PG42	6.71	0.06	35.94	N/D
At5g48670	WG43	6.71	0.18	32.76	0.26	PG43	6.71	0.06	32.06	0.35
At5g49420	WG44	7.67	0.43	36.85	1.03	PG44	7.77	0.75	35.89	0.64
At5g49490	WG45	7.67	0.43	35.99	0.22	PG45	7.77	0.75	N/D	N/D
At5g55690	WG46	6.48	0.12	34.80	0.33	PG46	6.86	0.21	35.04	N/D
At5g58890	WG47	7.56	0.06	35.98	N/D	PG47	7.93	0.28	36.51	0.87
At5g60440	WG48	7.43	0.14	34.07	0.15	PG48	7.86	0.20	36.34	0.92

Table S3. (*Cont'd*)

AGI		18S		GOI			18S		GOI	
code	Sample	Avg CT	STDEV	Avg CT	STDEV	Sample	Avg CT	STDEV	Avg CT	STDEV
At1g01530	WS1	7.23	0.07	32.86	0.10	PS1	7.36	0.07	32.41	0.36
At1g17310	WS2	6.44	0.08	30.99	0.25	PS2	7.21	0.07	32.30	0.05
At1g18750	WS3	9.60	0.10	31.81	0.28	PS3	9.70	0.10	31.63	0.23
At1g22130	WS4	7.39	0.21	37.12	0.28	PS4	8.01	0.07	35.59	0.16
At1g22590	WS5	6.44	0.08	24.15	0.01	PS5	7.21	0.07	26.07	0.11
At1g28450	WS6	7.59	0.14	36.58	0.17	PS6	7.74	0.18	34.60	0.11
At1g28460	WS7	6.44	0.08	36.16	0.93	PS7	7.21	0.07	36.69	0.14
At1g31140	WS8	7.33	0.11	33.86	0.62	PS8	7.69	0.22	34.19	0.54
At1g31630	WS9	6.44	0.08	32.84	0.54	PS9	7.21	0.07	34.51	0.76
At1g31640	WS10	7.39	0.21	35.84	0.64	PS10	8.01	0.07	35.80	0.74
At1g47760	WS11	6.44	0.08	25.34	0.03	PS11	7.21	0.07	24.97	0.04
At1g48150	WS12	7.33	0.11	33.47	0.79	PS12	7.69	0.22	32.87	0.42
At1g60880	WS13	7.33	0.11	34.25	0.33	PS13	7.69	0.22	36.00	0.07
At1g60920	WS14	6.44	0.08	32.90	0.38	PS14	7.21	0.07	35.57	0.25
At1g65300	WS15	7.39	0.21	35.60	0.59	PS15	8.01	0.07	30.90	0.34
At1g65330	WS16	6.49	0.12	31.41	0.14	PS16	6.69	0.36	24.27	0.02
At1g65360	WS17	6.49	0.12	35.27	0.08	PS17	6.69	0.36	34.48	N/D
At1g69540	WS18	6.49	0.12	31.74	0.16	PS18	6.69	0.36	31.94	0.62
At1g72350	WS19	7.58	0.06	34.93	0.40	PS19	7.68	0.42	36.65	0.87
At1g77950	WS20	7.03	0.03	30.38	0.09	PS20	7.75	0.07	31.58	0.16
At1g77980	WS21	6.44	0.08	35.30	0.33	PS21	7.21	0.07	37.89	0.47
At2g03060	WS22	6.54	0.09	25.46	0.07	PS22	6.71	0.08	25.29	0.04
At2g24840	WS23	6.13	0.09	36.72	1.52	PS23	6.87	0.14	36.28	1.03
At2g26320	WS24	5.61	0.19	36.03	0.27	PS24	6.33	0.19	36.97	0.08
At2g26880	WS25	7.59	0.05	N/D	N/D	PS25	7.85	0.23	N/D	N/D
At2g28700	WS26	6.54	0.09	34.47	1.05	PS26	6.71	0.08	30.54	0.07
At2g34440	WS27	8.09	0.03	32.43	0.36	PS27	8.09	0.41	32.88	0.24
At2g40210	WS28	7.59	0.05	37.67	0.76	PS28	7.85	0.23	37.05	0.04
At3g04100	WS29	6.45	0.01	39.57	0.03	PS29	7.21	0.07	36.73	N/D
At3g05860	WS30	6.44	0.22	29.61	0.27	PS30	6.79	0.41	28.23	0.26
At3g66656	WS31	7.59	0.05	33.57	0.31	PS31	7.85	0.23	33.48	0.22
At4g14530	WS32	7.18	0.12	35.16	0.14	PS32	7.41	0.11	35.49	2.21
At4g36590	WS33	7.06	0.02	33.89	0.66	PS33	7.72	0.01	38.52	0.47
At5g04640	WS34	6.44	0.22	38.80	0.28	PS34	6.79	0.41	39.27	0.54
At5g06500	WS35	6.44	0.22	37.24	N/D	PS35	6.79	0.41	34.81	0.47
At5g26580	WS36	7.02	0.06	36.61	0.29	PS36	7.37	0.12	36.98	0.26
At5g26630	WS37	7.02	0.06	32.91	0.48	PS37	7.37	0.12	34.07	0.69
At5g26650	WS38	7.02	0.06	N/D	N/D	PS38	7.37	0.12	N/D	N/D
At5g26950	WS39	6.45	0.01	33.68	0.55	PS39	7.18	0.03	34.52	0.38
At5g27130	WS40	8.08	0.01	33.97	0.24	PS40	8.77	0.01	33.95	0.60
At5g27960	WS41	7.02	0.06	35.44	N/D	PS41	7.37	0.12	35.80	N/D
At5g38620	WS42	7.02	0.06	37.27	N/D	PS42	7.37	0.12	N/D	N/D
At5g48670	WS43	6.45	0.01	30.02	0.15	PS43	7.18	0.03	30.73	0.31
At5g49420	WS44	7.02	0.06	34.06	0.23	PS44	7.37	0.12	36.76	2.26
At5g49490	WS45	6.45	0.01	36.71	0.98	PS45	7.18	0.03	36.35	0.49
At5g55690	WS46	7.39	0.21	36.86	0.99	PS46	8.01	0.07	35.76	0.42
At5g58890	WS47	5.49	0.04	33.86	0.45	PS47	6.29	0.09	34.95	0.25
At5g60440	WS48	6.45	0.01	30.98	0.23	PS48	7.18	0.03	33.23	0.11

Table S3. (*Cont'd*)

AGI code	Sample	18S		GOI		Sample	18S		GOI	
		Avg CT	STDEV	Avg CT	STDEV		Avg CT	STDEV	Avg CT	STDEV
At1g01530	WR1	7.25	0.20	30.51	0.24	PR1	7.38	0.22	29.61	0.14
At1g17310	WR2	7.25	0.20	34.08	0.01	PR2	7.38	0.22	35.58	0.14
At1g18750	WR3	7.25	0.20	14.28	0.13	PR3	7.38	0.22	14.86	1.79
At1g22130	WR4	7.25	0.20	33.96	0.31	PR4	7.38	0.22	34.98	0.46
At1g22590	WR5	7.25	0.20	26.09	0.24	PR5	7.38	0.22	28.37	0.11
At1g28450	WR6	7.25	0.20	35.09	0.01	PR6	7.38	0.22	34.98	N/D
At1g28460	WR7	7.04	0.21	37.21	3.71	PR7	7.29	0.20	34.56	N/D
At1g31140	WR8	7.04	0.21	34.80	0.73	PR8	7.29	0.20	37.09	2.60
At1g31630	WR9	7.04	0.21	36.48	N/D	PR9	7.29	0.20	38.48	N/D
At1g31640	WR10	7.04	0.21	37.54	1.59	PR10	7.29	0.20	37.66	0.99
At1g47760	WR11	7.04	0.21	28.36	0.43	PR11	7.29	0.20	29.42	0.11
At1g48150	WR12	7.04	0.21	32.00	0.45	PR12	7.29	0.20	32.72	0.27
At1g60880	WR13	7.04	0.21	36.56	1.54	PR13	7.29	0.20	37.00	2.22
At1g60920	WR14	7.04	0.21	35.92	0.24	PR14	7.29	0.20	39.03	N/D
At1g65300	WR15	7.04	0.21	37.14	0.12	PR15	7.29	0.20	32.97	0.21
At1g65330	WR16	7.04	0.21	29.78	0.15	PR16	7.29	0.20	22.49	0.13
At1g65360	WR17	7.04	0.21	29.47	0.23	PR17	7.29	0.20	29.98	0.11
At1g69540	WR18	7.04	0.21	31.97	0.57	PR18	7.29	0.20	32.57	0.32
At1g72350	WR19	7.04	0.21	36.81	1.73	PR19	7.29	0.20	N/D	N/D
At1g77950	WR20	7.04	0.21	35.42	N/D	PR20	7.29	0.20	N/D	N/D
At1g77980	WR21	7.04	0.21	35.16	N/D	PR21	7.29	0.20	N/D	N/D
At2g03060	WR22	6.82	0.43	26.90	0.46	PR22	7.13	0.04	26.85	0.12
At2g24840	WR23	6.82	0.43	36.25	N/D	PR23	7.13	0.04	37.30	0.71
At2g26320	WR24	6.82	0.43	N/D	N/D	PR24	7.13	0.04	N/D	N/D
At2g26880	WR25	8.61	0.43	36.97	N/D	PR25	8.96	0.07	37.74	N/D
At2g28700	WR26	6.82	0.43	35.52	0.38	PR26	7.13	0.04	34.18	0.35
At2g34440	WR27	6.82	0.43	32.21	0.37	PR27	7.13	0.04	31.46	0.01
At2g40210	WR28	6.82	0.43	37.33	N/D	PR28	7.13	0.04	35.26	N/D
At3g04100	WR29	6.82	0.43	35.06	0.86	PR29	7.13	0.04	34.95	N/D
At3g05860	WR30	6.82	0.43	37.80	0.47	PR30	7.13	0.04	35.37	0.21
At3g66656	WR31	6.82	0.43	34.84	N/D	PR31	7.13	0.04	35.38	N/D
At4g14530	WR32	6.82	0.43	34.60	1.08	PR32	7.13	0.04	33.30	N/D
At4g36590	WR33	8.61	0.43	36.33	0.08	PR33	8.96	0.07	37.06	N/D
At5g04640	WR34	6.82	0.43	N/D	N/D	PR34	7.13	0.04	N/D	N/D
At5g06500	WR35	6.82	0.43	37.15	N/D	PR35	7.13	0.04	N/D	N/D
At5g26580	WR36	6.82	0.43	36.88	0.29	PR36	7.13	0.04	35.86	0.33
At5g26630	WR37	7.10	0.60	31.92	0.18	PR37	7.13	0.33	32.38	0.68
At5g26650	WR38	7.10	0.60	37.82	N/D	PR38	7.13	0.33	N/D	N/D
At5g26950	WR39	7.10	0.60	35.39	0.17	PR39	7.13	0.33	34.35	0.04
At5g27130	WR40	7.10	0.60	34.95	0.18	PR40	7.13	0.33	37.37	0.78
At5g27960	WR41	7.10	0.60	35.41	0.06	PR41	7.13	0.33	N/D	N/D
At5g38620	WR42	7.10	0.60	37.27	N/D	PR42	7.13	0.33	36.37	0.53
At5g48670	WR43	7.10	0.60	32.38	0.35	PR43	7.13	0.33	34.54	0.30
At5g49420	WR44	7.10	0.60	35.84	0.80	PR44	7.13	0.33	38.24	1.06
At5g49490	WR45	7.10	0.60	39.63	0.26	PR45	7.13	0.33	N/D	N/D
At5g55690	WR46	7.10	0.60	34.58	0.66	PR46	7.13	0.33	N/D	N/D
At5g58890	WR47	7.10	0.60	35.43	0.05	PR47	7.13	0.33	35.50	N/D
At5g60440	WR48	7.10	0.60	30.33	0.38	PR48	7.13	0.33	31.65	0.47

Table S4. Critical threshold values for Figure 6A. “AGI Code” provides the AGI number for the analyzed gene. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype” indicates the type of plant collected, whereas ”Tissue” describes the sample collected. “Growth Conditions” indicates the presence or absence of Dex. 18S was used as a control.

Gene	AGI code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
18S		8.39	0.30	pkl-1	21day seedlings	Dex
18S		8.02	0.02	pkl-1	21day seedlings	no Dex
18S		8.05	0.02	PKL::GR	21day seedlings	Dex
18S		8.05	0.01	PKL::GR	21day seedlings	no Dex
PHE1	At1g65330	23.61	0.18	pkl-1	21day seedlings	Dex
PHE1	At1g65330	23.41	0.03	pkl-1	21day seedlings	no Dex
PHE1	At1g65330	24.79	0.24	PKL::GR	21day seedlings	Dex
PHE1	At1g65330	23.11	0.08	PKL::GR	21day seedlings	no Dex

Table S5. Critical threshold values for Figures 6B and 6C. “AGI Code” provides the AGI number for the analyzed gene. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype” indicates the type of plant collected, whereas ”Tissue” describes the sample collected. “Growth Conditions” indicates Dex regimen. 18S was used as a control.

Gene	AGI code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
18S		10.09	0.22	pkl-1	10.5 day seedlings	10 days on Dex5 to 0.5 day on Dex5
18S		10.08	0.01	pkl-1	10.5 day seedlings	10 days on Dex5 to 0.5 day on no Dex
18S		10.13	0.01	pkl-1	10.5 day seedlings	10 days on no Dex to 0.5 day on no Dex
18S		9.91	0.05	pkl-1	10.5 day seedlings	10 days on no Dex to 0.5 day on Dex5
18S		10.39	0.18	pkl-1	11 day seelings	10 days on Dex5 to 1 day on Dex5
18S		10.04	0.05	pkl-1	11 day seelings	10 days on Dex5 to 1 day on no Dex
18S		10.29	0.09	pkl-1	11 day seelings	10 days on no Dex to 1 day on no Dex
18S		10.09	0.07	pkl-1	11 day seelings	10 days on no Dex to 1 day on Dex5
18S		9.24	0.21	pkl-1	13 day seedlings	10 days on Dex5 to 3 day on Dex5
18S		8.60	0.04	pkl-1	13 day seedlings	10 days on Dex5 to 3 day on no Dex
18S		8.46	0.02	pkl-1	13 day seedlings	10 days on no Dex to 3 day on no Dex
18S		8.73	0.04	pkl-1	13 day seedlings	10 days on no Dex to 3 day on Dex5
18S		10.27	0.23	PKL:GR	10.5 day seedlings	10 days on Dex5 to 0.5 day on Dex5
18S		9.87	0.01	PKL:GR	10.5 day seedlings	10 days on Dex5 to 0.5 day on no Dex
18S		10.16	0.04	PKL:GR	10.5 day seedlings	10 days on no Dex to 0.5 day on no Dex
18S		10.34	0.15	PKL:GR	10.5 day seedlings	10 days on no Dex to 0.5 day on Dex5
18S		10.21	0.23	PKL:GR	11 day seelings	10 days on Dex5 to 1 day on Dex5
18S		10.21	0.06	PKL:GR	11 day seelings	10 days on Dex5 to 1 day on no Dex
18S		10.19	0.02	PKL:GR	11 day seelings	10 days on no Dex to 1 day on no Dex
18S		10.04	0.10	PKL:GR	11 day seelings	10 days on no Dex to 1 day on Dex5
18S		8.62	0.22	PKL:GR	13 day seedlings	10 days on Dex5 to 3 day on Dex5
18S		8.88	0.07	PKL:GR	13 day seedlings	10 days on Dex5 to 3 day on no Dex
18S		9.35	0.03	PKL:GR	13 day seedlings	10 days on no Dex to 3 day on no Dex
18S		9.31	0.14	PKL:GR	13 day seedlings	10 days on no Dex to 3 day on Dex5
PHE1	At1g65330	27.99	0.08	pkl-1	10.5 day seedlings	10 days on Dex5 to 0.5 day on Dex5
PHE1	At1g65330	27.67	0.06	pkl-1	10.5 day seedlings	10 days on Dex5 to 0.5 day on no Dex
PHE1	At1g65330	27.91	0.13	pkl-1	10.5 day seedlings	10 days on no Dex to 0.5 day on no Dex
PHE1	At1g65330	28.35	0.14	pkl-1	10.5 day seedlings	10 days on no Dex to 0.5 day on Dex5
PHE1	At1g65330	27.14	0.13	pkl-1	11 day seelings	10 days on Dex5 to 1 day on Dex5
PHE1	At1g65330	27.05	0.16	pkl-1	11 day seelings	10 days on Dex5 to 1 day on no Dex
PHE1	At1g65330	27.65	0.13	pkl-1	11 day seelings	10 days on no Dex to 1 day on no Dex
PHE1	At1g65330	27.80	0.18	pkl-1	11 day seelings	10 days on no Dex to 1 day on Dex5
PHE1	At1g65330	25.34	0.07	pkl-1	13 day seedlings	10 days on Dex5 to 3 day on Dex5
PHE1	At1g65330	25.19	0.02	pkl-1	13 day seedlings	10 days on Dex5 to 3 day on no Dex
PHE1	At1g65330	25.68	0.18	pkl-1	13 day seedlings	10 days on no Dex to 3 day on no Dex
PHE1	At1g65330	25.71	0.14	pkl-1	13 day seedlings	10 days on no Dex to 3 day on Dex5
PHE1	At1g65330	30.61	0.17	PKL:GR	10.5 day seedlings	10 days on Dex5 to 0.5 day on Dex5
PHE1	At1g65330	30.21	0.13	PKL:GR	10.5 day seedlings	10 days on Dex5 to 0.5 day on no Dex
PHE1	At1g65330	28.45	0.13	PKL:GR	10.5 day seedlings	10 days on no Dex to 0.5 day on no Dex
PHE1	At1g65330	28.83	0.15	PKL:GR	10.5 day seedlings	10 days on no Dex to 0.5 day on Dex5
PHE1	At1g65330	29.13	0.08	PKL:GR	11 day seelings	10 days on Dex5 to 1 day on Dex5
PHE1	At1g65330	28.43	0.26	PKL:GR	11 day seelings	10 days on Dex5 to 1 day on no Dex
PHE1	At1g65330	27.16	0.06	PKL:GR	11 day seelings	10 days on no Dex to 1 day on no Dex
PHE1	At1g65330	28.59	0.12	PKL:GR	11 day seelings	10 days on no Dex to 1 day on Dex5
PHE1	At1g65330	27.09	0.06	PKL:GR	13 day seedlings	10 days on Dex5 to 3 day on Dex5
PHE1	At1g65330	25.81	0.15	PKL:GR	13 day seedlings	10 days on Dex5 to 3 day on no Dex
PHE1	At1g65330	26.60	0.10	PKL:GR	13 day seedlings	10 days on no Dex to 3 day on no Dex
PHE1	At1g65330	28.85	0.25	PKL:GR	13 day seedlings	10 days on no Dex to 3 day on Dex5

Table S6. Critical threshold values for Figure 7A. “AGI Code” provides the AGI number for the analyzed gene. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype” indicates the type of plant collected, whereas ”Tissue” describes the sample collected. “Growth Conditions” indicates absence or presence of Dex. 18S was used as a control. Data are presented separately as the samples were analyzed on two separate plates.

Gene	AGI code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
18S		6.52	0.19	pkl-1	50% germination	no Dex
18S		6.58	0.02	pkl-1	50% germination	Dex
18S		6.58	0.11	PKL::GR	50% germination	no Dex
18S		6.59	0.07	PKL::GR	50% germination	Dex
LEC1	At1g21970	27.88	0.22	pkl-1	50% germination	no Dex
LEC1	At1g21970	28.56	0.16	pkl-1	50% germination	Dex
LEC1	At1g21970	28.64	0.11	PKL::GR	50% germination	no Dex
LEC1	At1g21970	31.09	0.13	PKL::GR	50% germination	Dex

Gene	AGI code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
18S		8.05	0.04	pkl-1	50% germination	no Dex
18S		8.21	0.08	pkl-1	50% germination	Dex
18S		8.23	0.18	PKL::GR	50% germination	no Dex
18S		8.70	0.23	PKL::GR	50% germination	Dex
PHE1	At1g65330	31.38	0.27	pkl-1	50% germination	no Dex
PHE1	At1g65330	31.15	0.08	pkl-1	50% germination	Dex
PHE1	At1g65330	32.29	0.21	PKL::GR	50% germination	no Dex
PHE1	At1g65330	33.28	0.21	PKL::GR	50% germination	Dex

Table S7. Critical threshold values for Figure 7B. "AGI Code" provides the AGI number for the analyzed gene. "Average CT" is average critical threshold of three measurements, and "STDEV CT" is the standard deviation associated with the average critical threshold. "Genotype" indicates the type of plant collected, whereas "Tissue" describes the sample collected. "Growth Conditions" indicates absence or presence of Dex. 18S was used as a control. Data are presented separately as the samples were analyzed on two separate plates.

Gene	AGI code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
18S		6.56	0.04	pkl-1	75% germination	no Dex
18S		6.78	0.04	pkl-1	75% germination	Dex5
18S		6.75	0.14	PKL::GR	75% germination	no Dex
18S		6.81	0.09	PKL::GR	75% germination	Dex5
LEC1	At1g21970	27.38	0.11	pkl-1	75% germination	no Dex
LEC1	At1g21970	27.63	0.10	pkl-1	75% germination	Dex5
LEC1	At1g21970	29.69	0.02	PKL::GR	75% germination	no Dex
LEC1	At1g21970	30.31	0.16	PKL::GR	75% germination	Dex5
PHE1	At1g65330	25.25	0.05	pkl-1	75% germination	no Dex
PHE1	At1g65330	25.53	0.09	pkl-1	75% germination	Dex5
PHE1	At1g65330	28.57	0.16	PKL::GR	75% germination	no Dex
PHE1	At1g65330	27.05	0.14	PKL::GR	75% germination	Dex5