Supporting Information

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SI Text

Transgenic Lines Carrying the −152 to +67 Fragment of the *Lhcb1*2* Promoter. The −152 to +67 fragment, and the 4-bp substitution to CCCC in the context of this fragment of *Lhcb1*2* were obtained by PCR with specific primers bearing a *Hin*dIII tail at its 5′ end using a pUC19-derived plasmid bearing the −152 (*Hin*dIII) to +67 (*Bam*HI) fragment of the *Lhcb1*2* promoter as template. The amplified fragments were cut with *Hin*dIII and *Bam*HI and subcloned in the pBI101.2 vector, containing the *gusA* reporter gene (1), and sequenced. The fragments were introduced into *A. thaliana* accession Columbia by way of *Agrobacterium tumefaciens*, using the floral dip method (2). Lines homozygous for the *Lhcb1*2* promoter fusion to *gusA* were selected by kanamycin resistance. The nature and integrity of the transgene were verified by PCR. The activity of the promoter was normalized to the values observed in seedlings treated with hourly R pulses because this was unaffected by the substitutions [average GUS activity, (nmol 4-MU mg^{-1} min^{-1}) under R: control = 0.97 ± 0.07; −145 = 0.95 ± 0.04; −143 = 0.95 ± 0.03; −139 = 0.82 ± 0.07; −135 = 0.98 ± 0.04; −131 = 0.97 ± 0.12; −127: 1.01 ± 0.09; −123: 0.89 ± 0.13].

Transgenic Lines Carrying the −453 to +67 Fragments of the *Lhcb1*2* Promoter. The 6-bp substitution in the context of the −453 to +67 fragment of *Lhcb1*2* were obtained as described for the −152 to +67 fragment. The following substitutions (italics) were introduced into the WT promoter sequence (TCTTGGAAAATTGATGGATTACAA): −143 TCTT*TCTAGA*TTGATGGATTACAA; −139 TCTTGGAA*GGTACC*TGGATTACAA; −135: TCTTGGAAAATT*GGTACC*TTACAA; −129: TCTTGGAAAATTGATGGA*GGTACC*. For each line, activity was normalized to the values under R pulses, which were unaffected by the substitutions [average GUS activity, (nmol 4-MU mg^{-1} min^{-1}) under R: −453: 1.7 ± 0.2; −143: 1.0 ± 0.2; −139 = 1.3 ± 0.2; −135: 1.3 ± 0.3; −129: 1.4 ± 0.2]. For some experiments the −135 transgene was introduced into the *blh1* mutant background and into the WT seedlings obtained from the population segregating the Salk-089095 T-DNA insert (see below). For each line, activity was normalized to the values under R pulses, which were unaffected by the substitutions or *blh1* mutation [average GUS activity, (nmol 4-MU mg^{-1} min^{-1}) under R: −453 *BLH1* = 3.2 ± 0.2; −453 *blh1* = 3.3 ± 0.1; −135 BLH1 = 3.2 ± 0.2; −135 *blh1* = 3.2 ± 0.1].

Experiments to Measure GUS Activity Driven by the *Lhcb1*2* Promoter. One hundred seeds were sown on 3 mL 0.8% agar in clear plastic boxes (40 mm × 33 mm × 15 mm height). The boxes were incubated 5 days at 4 °C, transferred to 22 °C, and exposed to 4 h R (to induce germination) followed by darkness. Two-day-old seedlings were exposed to 3-min hourly pulses of FR (60 μmol m^{-2} s^{-1}), 3-min hourly pulses of R (20 μmol m^{-2} s^{-1}) or continuous FR for 24 h or remained in darkness as controls. The seedlings were harvested under dim green light and used for measurements of GUS activity using 4-methylumbelliferyl-b-D-glucuronide (Sigma) as substrate (1). The standard curves were prepared with 4-methylumbelliferone (Sigma).

Electrophoretic Mobility Shift Assays. EMSA reactions contained nuclear extract buffer (3), supplemented with 100 ng poly(dIdC)poly-(dIdC) and 0.1 ng of ^{32}P end-labeled probe (10^8 cpm/μg). The binding reaction (final volume 10 μL) was incubated at room temperature, loaded onto a 5% polyacrylamide gel (30:0.8) and run at 10 V/cm with 0.5× TBE buffer. The gel was dried on DE81 Whatman paper and autoradiographed. The coding region of *BLH1* (1.5 kb) was cloned from pACT-BLH1 as *Xho*I fragment into pGEX-4T-1 plasmid (Amersham Biosciences). To extract recombinant protein, 5 mL overnight cultures of BL21(DE3, pLys; Novagen) carrying plasmids pGEX-BLH1 were used to inoculate 500 mL LB medium containing 200 μg/mL ampicillin and 50 μg/mL chloroamphenicol and grown at 37 °C to an optical density at 600 nm of 0.5. Next, protein synthesis was induced by the addition of solid IPTG to final concentration of 1 mM and cultures were grown for 4 h at 29 °C. The harvested cells were suspended in 20 mL PBS and frozen in liquid nitrogen. After thawing on ice, the bacteria were lysed by sonication (8 × 10 s burst; 5-s pause between bursts), centrifuged (at 18,000 rpm for 30 min at 4 °C), and the supernatant was filtered through a 0.45-μm membrane. Protein purification was performed using PolyPrep Chromatography columns (731–1550; Bio-Rad Laboratories) containing 0.5 mL settled Glutathion-Sepharose 4B beads (Amersham Biosciences). Columns were first washed 2 times with 10 mL PBS before bacterial extract was passed through. After binding, columns were washing with 10 mL PBS and bounded proteins were eluted in 2.5 mL (10 × 0.25 mL) glutathion elution buffer (100 mM glutathione, 500 mM Tris-HCl, pH 8.0). Eluted protein was concentrated using Microcone Centrifugal Filter devices (Millipore) according to manufacturer's protocol, and the protein content was determined by the method of Bradford.

The probes used in EMSA experiments were:

HIRa 5′-GGCCGCTGATGGATTACAAAGTGCCATGTAGATCTT,

HIRa m 5′-GGCCGCTGACCCCTTACAAAGTGCCATGTAGATCTT,

HIRb 5′-GGCCGCGGAAAATTGATGGATTACAAAGTAGATCTT, and

HIRb m 5′-GGCCGCGGAAAATTGACCCCTTACAAAGTAGATCTT.

Yeast Transformation and Library Description. The *Arabidopsis* cDNA expression library was obtained from ABRC [accession CD4–22; (4)] and is derived from mRNA isolated from the 3 days-old etiolated seedlings, which after conversion into cDNA is cloned into λACT. The auxotrophic marker on the pACT vector is *LEU2* and cDNAs are cloned as translational fusions with the transcription activation domain of Gal4p. The screening of the library was carried out on histidine-lacking medium with 2 mM 3-AT, a competitive inhibitor of His3p. Putative positive yeast colonies were isolated and restreaked in the presence of different concentrations of 3-AT. Finally, pACT plasmids were isolated from yeast by using the Y-DER Yeast DNA Extraction Reagent kit (Pierce), and the cDNA region was sequenced using primer pACT-Fw 5′-CCCACCAAACCCAAAAAAAG-3′.

Genotyping of *blh1* Mutants. Seedlings homozygous for the *blh1-1* or *BLH1* alleles were screened in the segregating population by using the LBb1 primer (ABRC) and 5′-TTTCCAGCCGCTTAAGCATACA-3′ or the latter primer and 5′-AGCCCAATGGCGGACACTAAT-3′, respectively. The Ds insertion in the *blh1-4* allele was amplified with primers Ds5–1 5′-GAAACGGTCGGGAAACTAGCTCTA-3′ and 5′-GTGTTGTTGATGATGTTGCTGTT-3′, and the WT allele was amplified with the latter and 5′-TATCAATCCAGGTTCTTCATCTTTT-3′. The *blh1-5* or BLH1 alleles were screened in the segregating population by using

the Spm32 (JIC SM) 5′-TACGAATAAGAGCGTCCATTTTA-GAGTGA-3′ and 5′-TACTAAGTTTTGCTTTCTTCATCTG-TATTT or the latter primer and 5′-CAACTACTAATTATA-CATAGATGGCTGCTT-3′, respectively.

Experiments to Measure Hypocotyl Growth Inhibition, Cotyledon Unfolding, Anthocyanin Levels, and Cotyledon Angle. Fifteen (hypocotyl growth, cotyledon angle, and hypocotyl orientation) or 50 (anthocyanin) seeds were sown on 3 mL 0.8% agar in clear plastic boxes (40 × 33 × 15 mm height). In hypocotyl-angle experiments (randomization of growth orientation) all of the seeds were sown on the same line, approximately 10 mm above the 40 mm side of the box. The boxes were incubated 5 days at 4 °C, transferred to 22 °C and exposed to 4 h R (to induce germination) followed by darkness. One-day-old seedlings were transferred to the different light or dark conditions for 3 days before measurements. The seedlings were exposed to 3-min hourly pulses of FR (60 μmol m^{-2} s^{-1}), 3-min hourly pulses of R (20 μmol m^{-2} s^{-1}), or continuous FR of the fluence rate indicated in the figure legends. Hypocotyl length was measured to the nearest 0.5 mm with a ruler. Only the 10 longest hypocotyls of each box were averaged and used as a replicate for statistics, to avoid seedlings with defects. Inhibition of hypocotyl growth relative to dark controls was calculated as (length in darkness - length under a given condition)/length in darkness. Cotyledon angle was measured with a protractor. For hypocotyl angle experiments, the position of the boxes containing 1-day-old seedlings was shifted to place the agar plane normal to the horizontal plane. Then the boxes were transferred to the different light or dark conditions for 3 days. The angle of the hypocotyl with respect to the vertical position was measured by placing the box on a protractor. For the measurement of anthocyanin levels, the seedlings were harvested for extraction with 1 mL 1% (wt/vol) HCl methanol. Absorbance at 530 nm was measured and corrected for chlorophyll absorption by subtracting 0.25 absorbance at 657 nm.

Analysis of Gene Expression by Quantitative PCR. Total RNA was extracted using RNeasy Plant Mini Kit columns (Qiagen). One microgram RNA was reverse-transcribed into cDNA by using the SuperScript III Reverse Transcriptase (Invitrogen). The cDNA was purified by alkaline degradation (NaOH, 65 °C for 30 min) and precipitated with ethanol. The OliGreen ssDNA Reagent (Molecular Probes) was used to quantify the single-stranded cDNA. Primers, SYBR Green, ROX, and cDNA were mixed with the TaqDNA Polymerase Recombinant (Invitrogen), and the reaction was carried out in a Stratagene Mx 3005 System. The cycling conditions were: 95 °C for 10 min, followed by 40 cycles of 95 °C for 30 s, 57 °C for 1 min, and 72 °C for 1 min. Raw data were analyzed with Stratagene Mx 3005 software to extract Ct values. Relative expression of each gene was calculated according to the $2^{-\Delta\Delta Ct}$ method (5), setting the average value of the control in darkness as 1. The *A. thaliana* Polyubiquitin 10 (*UBQ10*) gene was used for normalization (reference) and centered to the mean Ct calculated for the 3 biological replicates. The *Lhcb1*1* plus *Lhcb1*2* primers were:

5′-TCTCACTCACAAGTTAGTC-3′ and 5′-TGTCACACG-GCCGCTTCCA-3′.

The *BLH1* primers were:

5′-CACGATGAAGATTCTAGAACGGCAAGGG-3′

5′-CGGTTTCTCCTTCGAGAGAGATGGGTTTATGC-3′.

Analysis of *BLH1* expression in transgenic plants bearing the full-length promoter fused to GUS. The full-length *BLH1* promoter including the 5′-UTRs of 2.5 kb (−1800 to +725) was PCR-amplified using the genomic DNA of *A. thaliana* accession Columbia as template with primers 5′-*Hin*dIII 5′-CCGAAGCT-TCATGAACTTAAACACTCTTTGC and 3′-*Bam*H1 5′-CCGGGATCCTGTTACACACGAATGAAAACGAC.

The amplified promoter fragment was cloned into the CHF1 vector in the *Hin*dIII-*Bam*H1 sites. Plant transformation and GUS measurements were as described above. For in vivo GUS staining transgenic seedling were incubated at 37 °C for 60 min in staining solution as described (6).

Analysis of Microarray Data. Microarray data were standardized to the sum of all of the values of each microarray (7) and analyzed by factorial ANOVA with BLH1/*blh1* and FR/dark as main factors. We selected the genes showing significant effects of treatments at $P < 0.05$, a false discovery rate (8) q <0.03 and a "present" flag in the 2 samples of at least 1 condition. Within these genes, we selected and used for clustering (9) 518, showing significant interaction between the main factors ($P < 0.05$). Of these genes, 287 formed 9 clusters with a required probability of genes belonging to cluster of 0.75 and a minimum of 14 genes. Five of the 9 clusters (214 of the 287 genes) showed reduced response to FR in the mutant and were used in subsequent functional analysis. Functional classification was conducted according to (10). For this purpose, the 3 clusters with expression promoted by continuous FR were grouped, and the same procedure was applied to the 2 clusters showing reduced expression in response to continuous FR.

Analysis of Overrepresented Sequences. Genes were selected when the effects of treatments were significant ($P < 0.05$, q <0.03), the effect of *blh1* and/or the interaction between *blh1* and FR treatment was significant ($P < 0.05$), and the expression ratio between the mutant and the WT is >1.2 or <0.8 (using more stringent mutant to WT ratios does not change the conclusions). A 6-bp frame defines 3 possible sequences of the promoter that contain the TGGA motif: GATGGA, ATGGAT, and TG-GATT. We analyzed the promoter elements (500 bp upstream of the start codon) of the selected genes using the "Motif Analysis in Promoter/Upstream Sequences" tool available at the TAIR web site (www.arabidopsis.org) to investigate if these 3 6-bp sequences were overrepresented.

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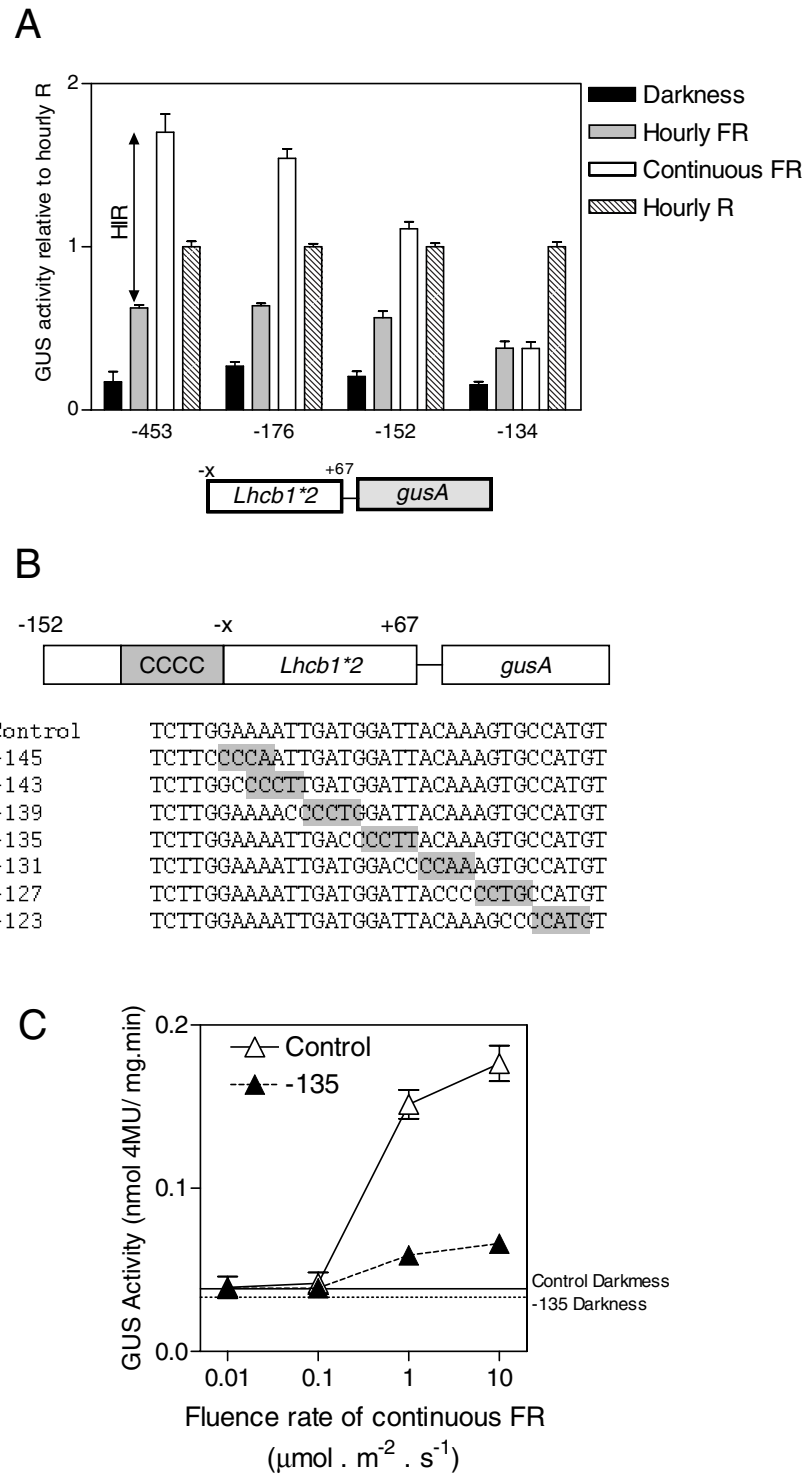


Fig. S1. *Lhcb1*2* promoter deletion from −453 to −134 eliminates the HIR. (*A*) Etiolated seedlings were exposed to hourly pulses of FR, continuous FR, or hourly pulses of R or remained as dark controls. Data are means and SE of at least 5 independent transgenic lines. For each line, activity was normalized to the values under R pulses [average GUS activity, (nmol 4-MU mg^{-1} min^{-1}) ± SE under R: −453 = 1.39 ± 0.09; −176 = 1.07 ± 0.07; −152 = 1.06 ± 0.08; −134 = 1.08 ± 0.08]. (*B*) Promoter substitutions used in Fig. 1*A*. (*C*) Reduced dependency of the −135 *Lhcb1*2* promoter activity on the fluence rate of continuous FR. Data are means and SE of 3 replicate samples from 1 control and 1 −135 transgenic lines selected for their similar levels of expression in darkness. Two-way ANOVA followed by Bonferroni post-tests indicates significant differences between promoters ($P < 0.001$) for 1 and 10 μmol m^{-2} s^{-1}. Other independent transgenic lines bearing the −135 *Lhcb1*2* promoter also showed severely reduced fluence rate dependency.

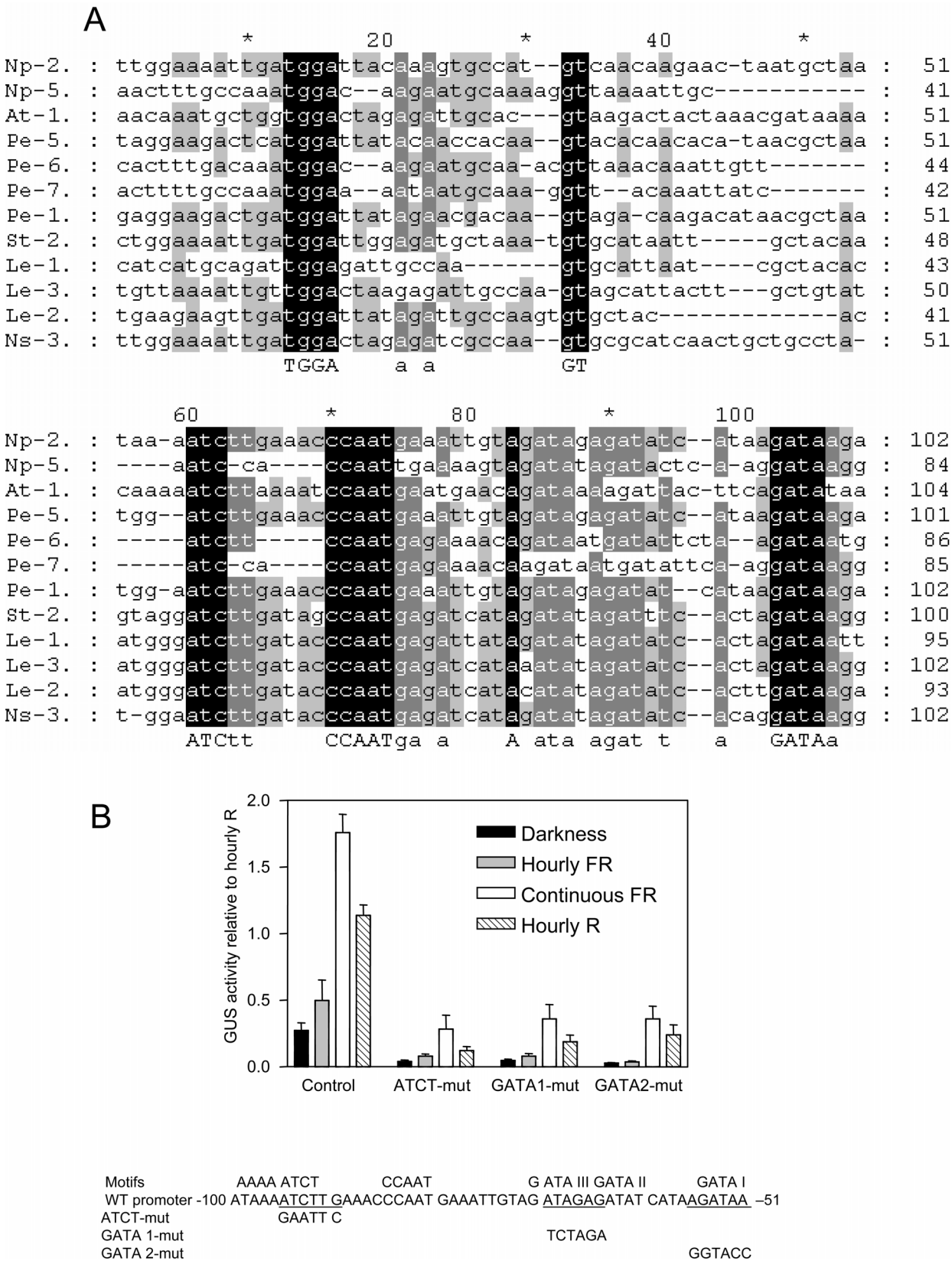
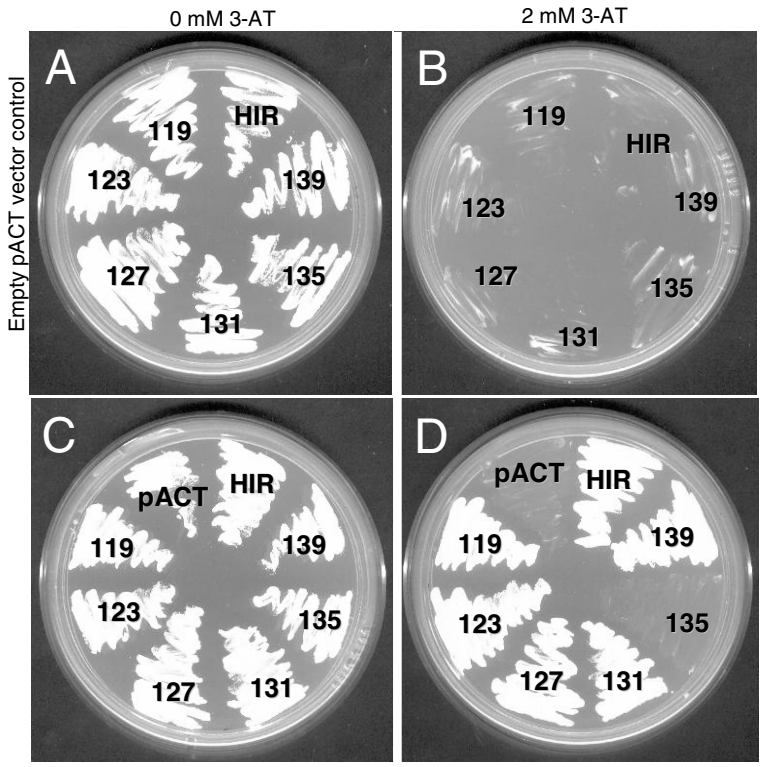


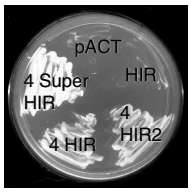
Fig. S2. The TGGA motif in the context of other sequences involved in the control of gene expression by light. (*A*) Presence and relative position of the TGGA motif in the promoters of *Lhcb* genes from *Nicotiana plumbaginifolia* (Np), *Arabidopsis thaliana* (At), *Petunia* (Pe), *Solanum tuberosum* (St), *Solanum lycopersicon* (Le), and *Nicotiana sylvestris*. The number given after the species abbreviation completes the denomination *Lhcb1*_*. (*B*) Mutations of other motifs of the *Lhcb1*2* promoter with large effects on light responses do not eliminate the HIR (i.e., the differential effect of hourly and continuous FR). Data are means and SE from 3 independent transgenic lines for each promoter.



E

HIR	GGCCGCTGATGGATTACAAAGTGCCATGTAGATCTT
-139	GGCCGCCCCCTGGATTACAAAGTGCCATGTAGATCTT
-135	GGCCGCTGACCCCCTTACAAAGTGCCATGTAGATCTT
-131	GGCCGCTGATGGACCCCCAAAGTGCCATGTAGATCTT
-127	GGCCGCTGATGGATTACCCCCTGCCATGTAGATCTT
-123	GGCCGCTGATGGATTACAAAGCCCCATGTAGATCTT
-119	GGCCGCTGATGGATTACAAAGTGCCCCCCAGATCTT

F



HIR	GGCCGCTGATGGATTACAAAGTGCCATGTAGATCTT
HIR2	GGCCGC 4X (TGATGGATTACAATAATCCATCA) AGATCTT
4HIR	GGCCGC 4X (TGATGGATTACAAAGTGCCATGT) AGATCTT
4 Super HIR	GGCCGC 4X (TGATGGAGGTCAAAGTGCCATGT) AGATCTT

Fig. S3. Controls of the yeast-1-hybrid experiment shown in Fig. 1*B* (relevant Fig. 1*B* data are repeated here for completeness) and DNA sequences used as bait reporter strains. (*A*) Yeast strains transformed with an empty pACT vector grow in medium lacking histidine. (*B*) Yeast strains transformed with an empty pACT vector fail grow in medium lacking histidine in the presence of 2 mM 3-AT. (*C*) Yeast strains transformed with pACT-BLH1 grown in the absence of histidine. (*D*) Yeast strains transformed with pACT-BLH1 fail to grow in the absence of histidine and the presence of 2 mM 3-AT if the bait reporter construct carries a TGGA to CCCC substitution between −138 and −135 bp. (*E*) DNA sequences used in the bait reporter strains. (*F*) Enhanced binding of the Super HIR sequence.

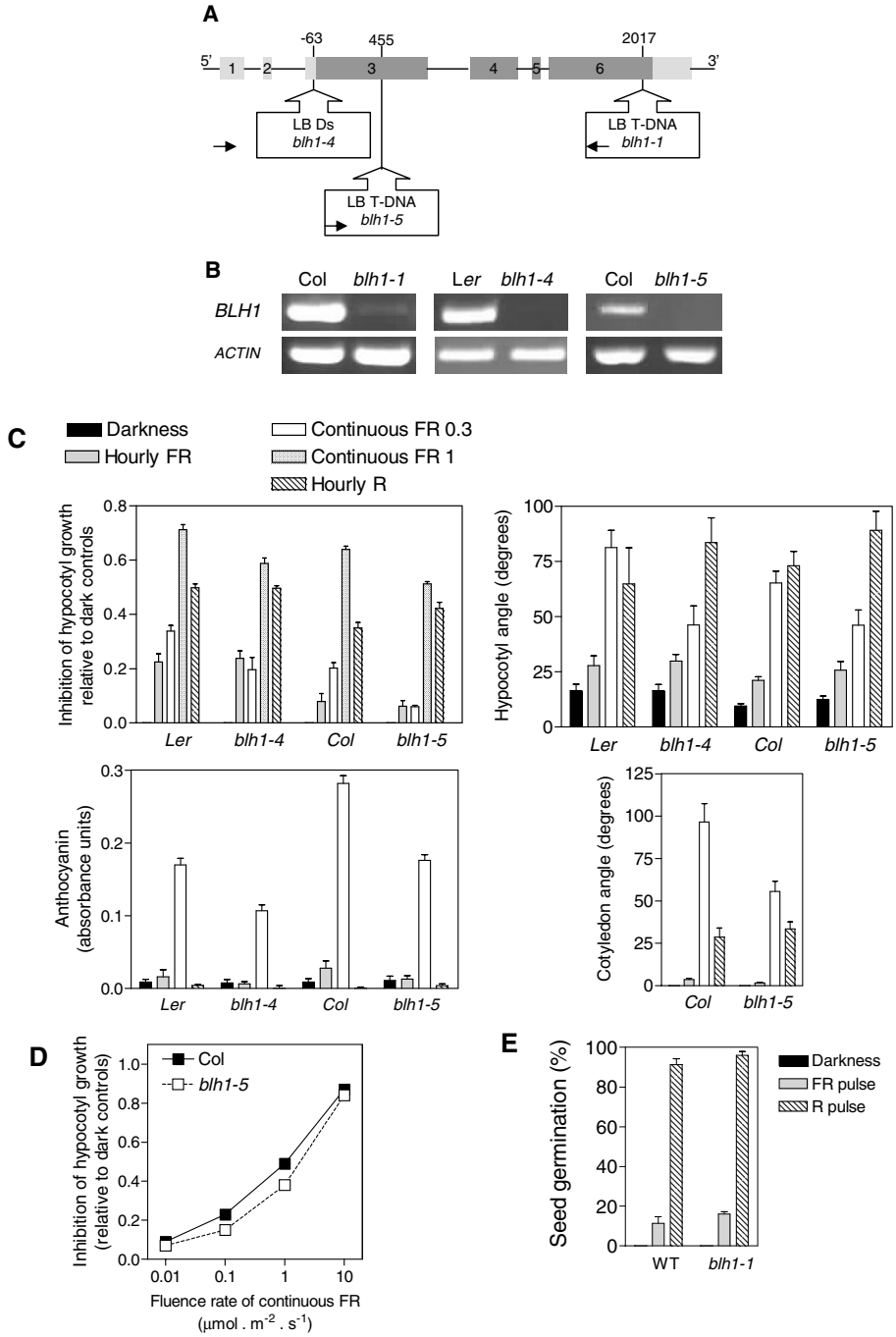


Fig. S4. Deficient HIR and normal VLFR in *blh1* mutants. (*A*) *blh1* mutant alleles: Position and orientation of the T-DNA insert (arrowed box) in the *blh1* (At2g35940) alleles. The genomic regions surrounding the insertions were sequenced to confirm the position. Lines represent introns, and boxes indicate exons (lighter fill correspond to 5′ and 3′ UTR). LB, left border junction sequence. (*B*) Expression of *BLH1* determined by RT-PCR. Seedlings were grown for 3 days in darkness followed by 6 h under continuous FR before harvest. (*C*) Hypocotyl growth inhibition relative to the length in dark controls (the mutations did not affect hypocotyl length in darkness), hypocotyl angle, anthocyanin levels, and cotyledon angle in additional alleles of *blh1*. The VLFR pathway contributes significantly to cotyledon unfolding under continuous or pulsed FR in the Landsberg erecta background, therefore the HIR of cotyledon unfolding was not tested in *blh1-4*. One-day-old seedlings were grown for 3 days under various light conditions before measurements. Data are means and SE of 3–4 replicate boxes. (*D*) Fluence response curve of hypocotyl growth inhibition under continuous FR. ANOVA followed by Bonferroni post-tests indicate significant effects of *blh1* under 0.1 ($P < 0.05$) and 1 ($P < 0.001$) μmol m^{-2} s^{-1}. (*E*) Normal VLFR of seed germination in *blh1* (seed germination shows no HIR in *Arabidopsis* and germination in darkness was nil). For germination tests, 25 seeds per box were sown on agar, given a pulse of long-wavelength FR, incubated 5 days in darkness at 4 °C, transferred to 22 °C, and (1 h later) given a 5-min pulse of long-wavelength FR or of R, or left as dark controls, and incubated 3 days in darkness before counting germinated seeds. Data are means and SE of 3 replicate boxes.

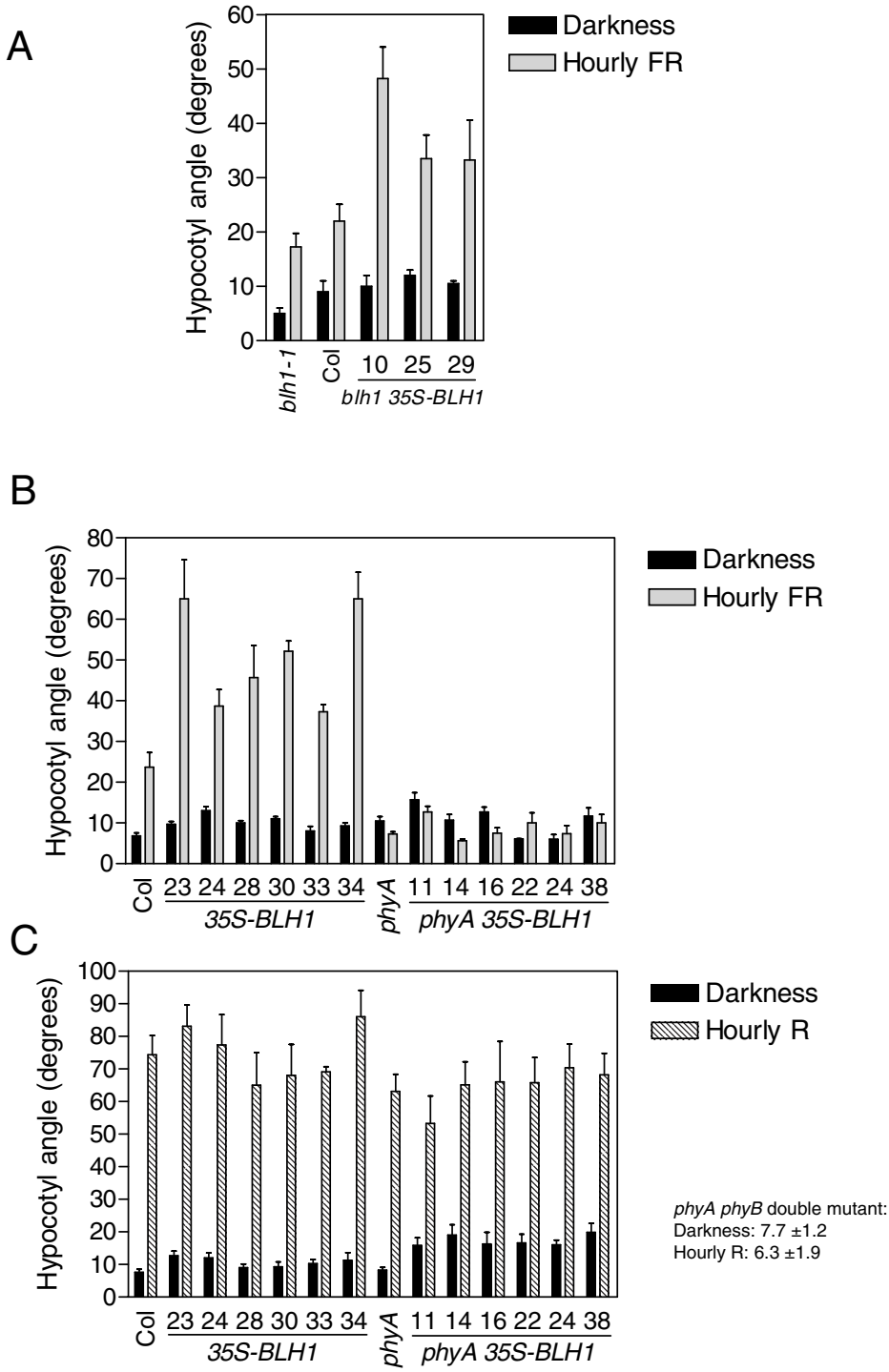


Fig. S5. Overexpression of *BLH1* enhances the response to hourly pulses of FR. (*A*) Overexpression of *BLH1* enhances hypocotyl angle under hourly pulses of FR. One-day-old seedlings were grown for 3 days either in darkness or under hourly pulses of FR before measurements. The transgenic lines show higher response to pulses of FR than the WT Col ($P < 0.05$). Data are means and SE of 3 replicate boxes. (*B*) BLH1 enhances hypocotyl angle under hourly pulses of FR when overexpressed in the WT Col background but not when overexpressed in the *phyA* mutant background. Each number in the *x* axis indicates an independent transgenic line. One-day-old seedlings were grown for 3 days either in darkness or under hourly pulses of FR before measurements. Data are means and SE of 3 replicate boxes. All of the transgenic lines in the WT Col background show significantly higher hypocotyl angle ($P < 0.01$) than the WT under hourly pulses of FR and normal angle in darkness. (*C*) Overexpression of BLH1 has no effect under hourly pulses of red light.

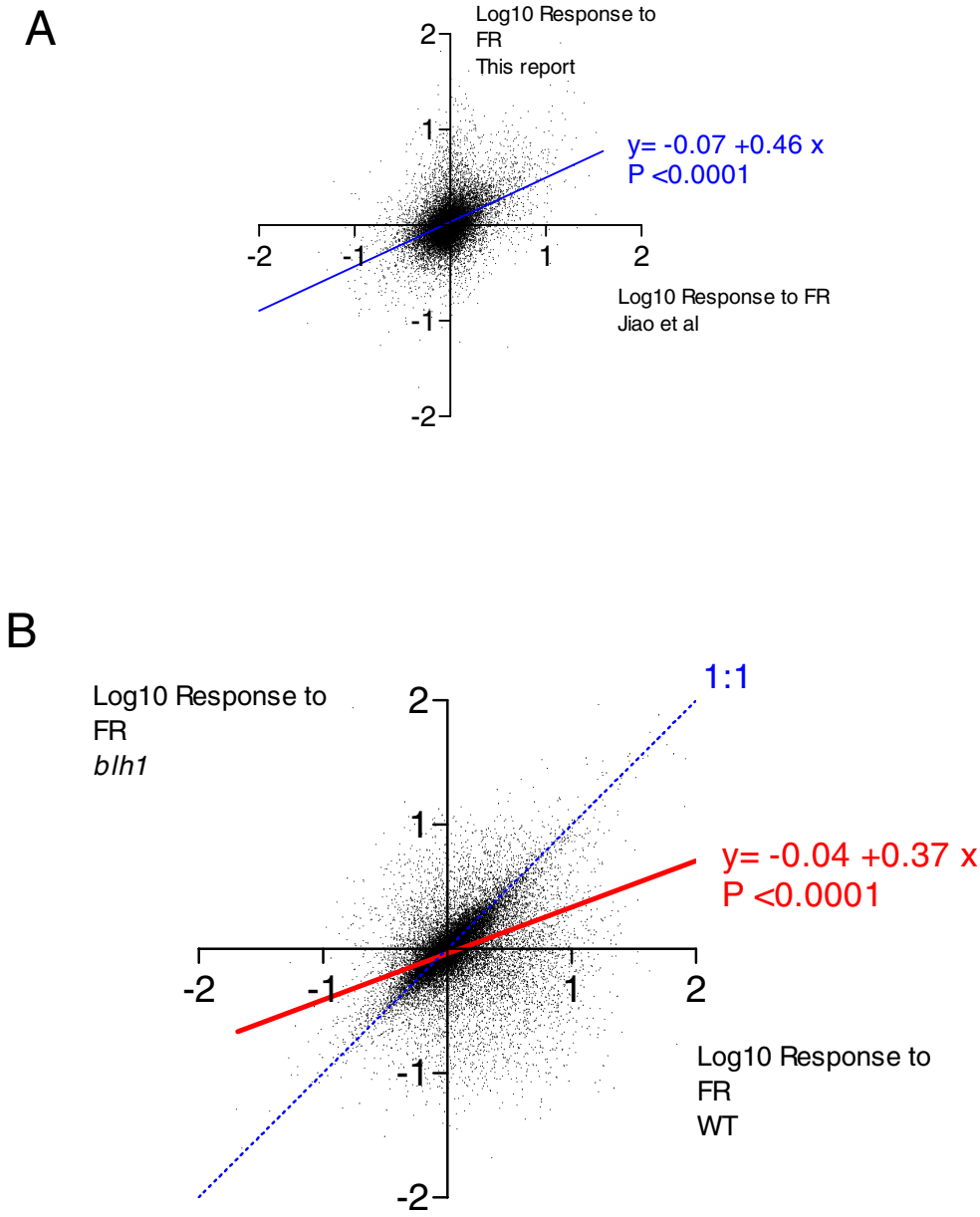


Fig. S6. Overview of the microarray data. (*A*) High coincidence of the microarray data presented here and those published by Jiao et al. (11). The $\log_{10}$ of the ratio between the expression under continuous FR and in darkness was calculated for all of the genes present in both microarray platforms (Affymetrix). ATH1 used here and the 70-mer oligonucleotide microarray based on 26,090 unique 70-mer oligonucleotides of the *Arabidopsis* Genome Oligo Set version 1.0, Operon used by Jiao et al. (11). Despite the different growth media and the very different time frames (in the current work the seedlings were grown on agar and exposed to FR for only 6 h, while Jiao et al. (11) present data from seedlings grown on agar plus sucrose for 6 days under FR), there is a strong overlap indicated by the highly significant positive correlation between the response to FR in each study. (*B*) The overview of the *blh1-1* transcriptome phenotype indicates an average 60% reduction in the response to 6 h of continuous FR (60 μmol $m^{-2} s^{-1}$) compared to the Col WT. The $\log_{10}$ of the ratio between the expression under continuous FR and in darkness was calculated for WT and *blh1* for all of the genes present in the microarray. The slope of the relationship is significant, indicating that the genes that respond to FR (promotion or inhibition) in both genotypes tend to be the same. However, the slope (0.37) is significantly lower than 1 ($P < 0.001$), indicating that the average extent of response is much weaker in the mutant.

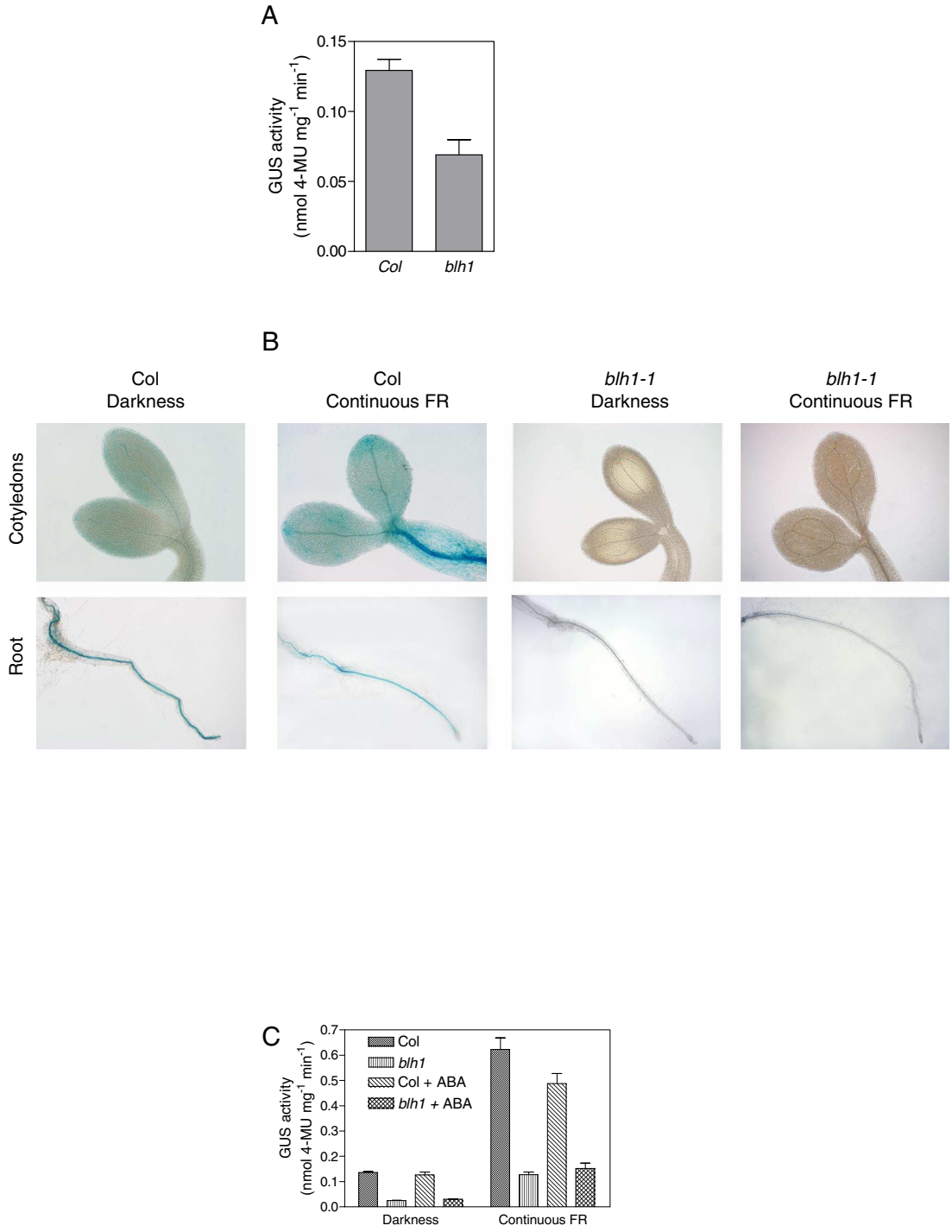


Fig. S7. BLH1 and continuous FR enhance the activity of *BLH1*::*GUS*. (*A*) GUS activity in transgenic seedlings of the WT Col and the *blh1-1* mutant background bearing the *BLH1*::*GUS* fusion. Transgenic seedlings bearing *BLH1*::*GUS* were grown in darkness for 3 days before harvest. The difference is significant at $P <$ 0.0001 according to a *t*-test. Data are means and SE of 15–14 independent transgenic lines. (*B*) Histochemical analysis of GUS activity under the control of *BLH1*::*GUS* in seedlings of the WT and of the *blh1-1* mutant background grown in darkness or continuous FR. Transgenic seedlings bearing *BLH1*::*GUS* were grown in darkness for 2 days and then exposed to continuous FR (60 μmol m^{-2} s^{-1}) or no light for 24 h before harvest. (*C*) Abscisic acid (ABA), previously reported to promote *BLH1* expression in 4-week-old light-grown *Arabidopsis* plants (12) does not promote *BLH1*::*GUS* activity in young seedlings. Transgenic seedlings bearing *BLH1*::*GUS* were grown in darkness for 2 days and then exposed to continuous FR (60 μmol m^{-2} s^{-1}) or no light for 24 h before harvest. The seedlings were sprayed with 300 μM ABA or water 60 min before the beginning of the 24-h period as described (13).

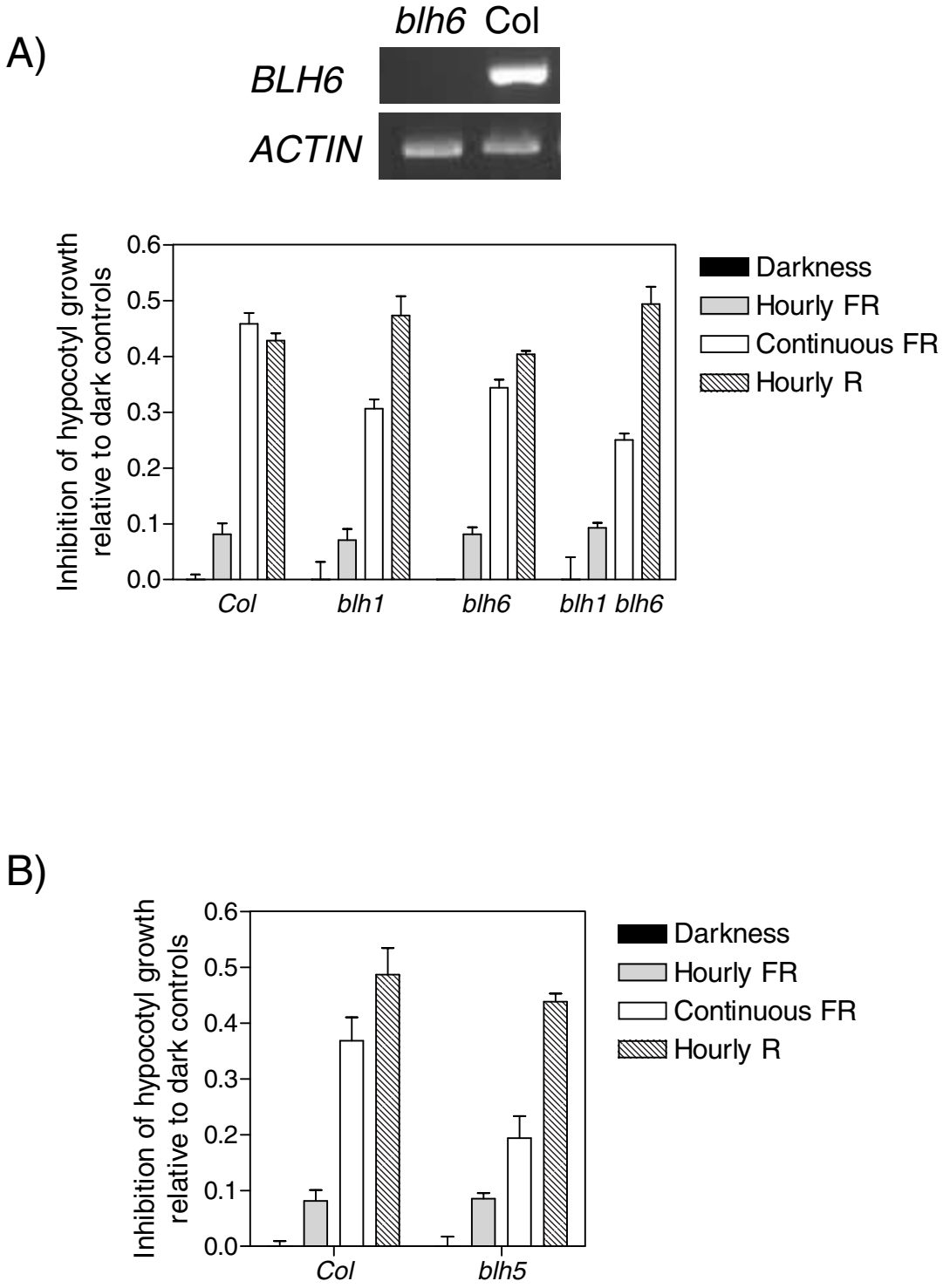


Fig. S8. Deficient HIR of hypocotyl growth inhibition in the *blh6* and *blh5* mutants. (*A*) Seedlings of the WT, the *blh1* and *blh6* single mutants, and *blh1 blh6* double mutant. The expression of *BLH6* in WT and *blh6* is shown at the top to characterize this previously unreported *blh6* allele (Salk_011023). Factorial ANOVA indicates that under continuous FR, the effects of *BLH1* versus *blh1* and *BLH6* versus *blh6* are significant ($P < 0.001$), and the interaction is not significant. There are no significant effects under hourly R or FR pulses. (*B*) Seedlings of the WT and of the *blh5* mutant kindly provided by Dr. Venkatesan Sundaresan (University of California, Davis, CA) and previously described in (14). One-day-old seedlings were grown for 3 days either in darkness or under continuous FR (1 μmol m^{-2} s^{-1}) before measurements of hypocotyl length. The inhibition of hypocotyl growth is shown relative to the length in dark controls (the mutations did not affect hypocotyl length in darkness). Data are means and SE of 3–4 replicate boxes. A *t*-test indicates significant differences ($P < 0.05$) between the WT and *blh5* under continuous FR. There are no significant effects under hourly R or FR pulses.

Table S1. Clusters of genes with reduced response to continuous FR (6 h, 60 μmol m-2 s-1) in the *blh1–1* mutant

			Darkness				Continuous FR				Statistics			
Cluster	Locus	Descriptions	WT		*blh1*		WT		*blh1*		*P*	*q*	*P* (inter.)	TGGA
I	AT1G12900	putative calcium-binding protein, calreticulin	420	434	394	364	3765	3869	3002	2926	1.8E-13	3.9E-10	2.7E-04	
I	AT4G03100	putative rac GTPase activating protein	35	31	31	30	146	154	101	100	4.6E-11	2.0E-08	3.9E-04	+
I	AT5G46420	unknown protein	219	238	249	245	439	450	358	354	1.1E-09	9.4E-08	6.9E-04	+
I	AT2G04039	predicted protein	115	113	103	100	220	225	167	153	4.9E-09	2.4E-07	2.7E-03	+
I	AT3G10050	threonine dehydratase/deaminase (OMR1)	64	66	61	69	185	188	141	149	6.0E-10	7.4E-08	2.8E-03	+
I	AT1G18730	unknown protein	117	147	153	130	466	448	332	324	5.4E-09	2.5E-07	3.0E-03	+
I	AT2G34460	unknown protein	71	59	80	78	340	321	277	270	1.7E-10	3.8E-08	4.1E-03	+
I	AT3G04870	putative zeta-carotene desaturase precursor	255	243	247	258	548	568	474	451	9.6E-10	9.1E-08	4.5E-03	+
I	AT1G14120	dioxygenase-like protein	187	198	210	184	391	384	313	304	1.5E-08	4.2E-07	4.7E-03	+
I	AT3G15520	hypothetical protein	75	72	78	67	247	227	170	177	8.2E-09	3.1E-07	5.9E-03	+
I	AT3G61870	hypothetical protein	169	194	157	197	926	934	699	606	6.8E-09	2.8E-07	6.5E-03	+
I	AT1G02080	unknown protein	395	412	419	400	602	618	539	523	3.0E-08	6.8E-07	7.3E-03	+
I	AT4G17000	hypothetical protein	11	9	18	21	56	56	45	36	5.4E-07	4.5E-06	8.9E-03	+
I	AT1G18060	unknown protein	115	126	99	111	488	510	408	382	2.9E-10	4.9E-08	9.1E-03	+
I	AT5G05390	laccase (diphenol oxidase)	7	11	8	13	46	42	29	28	2.2E-07	2.6E-06	9.6E-03	+
I	AT5G47840	putative protein contains similarity to adenylate kinase	291	321	293	277	619	617	509	527	1.4E-09	1.1E-07	1.4E-02	+
I	AT5G01530	chlorophyll a/b-binding protein CP29	1740	1825	1921	1718	5827	6168	5211	5118	2.7E-10	4.8E-08	1.4E-02	+
I	AT1G71500	unknown protein	345	343	398	394	673	702	630	664	3.3E-09	2.0E-07	1.4E-02	+
I	AT2G31400	unknown protein	396	429	411	373	1185	1145	1010	974	2.3E-10	4.8E-08	1.4E-02	+
I	AT5G29771	ribosomal protein S1	1130	1197	1056	1161	2700	2621	2220	2298	7.3E-10	8.0E-08	1.4E-02	
I	AT2G42600	phosphoenolpyruvate carboxylase	350	341	354	318	780	748	629	654	3.0E-09	1.9E-07	1.5E-02	+
I	AT4G02770	putative photosystem I reaction center subunit II precursor	929	942	1054	923	3790	3742	3494	3362	1.1E-11	9.4E-09	1.5E-02	+
I	AT2G45770	putative signal recognition particle receptor (alpha subunit)	68	65	64	72	185	169	131	142	7.9E-08	1.3E-06	1.7E-02	+
I	AT1G27120	unknown protein	44	52	49	52	114	103	83	74	1.9E-06	1.1E-05	1.7E-02	+
I	AT4G02530	predicted protein	219	230	205	229	809	814	743	715	7.9E-12	8.6E-09	1.8E-02	+
I	AT4G16985	Expressed protein	336	293	265	357	1938	1970	1528	1675	6.6E-10	7.8E-08	1.8E-02	
I	AT4G18240	starch synthase-like protein	92	100	102	105	169	176	156	146	1.2E-07	1.7E-06	1.8E-02	+
I	AT3G47470	CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR (LHCI TYPEIII CAB-4)	1113	1083	1211	1142	5792	6045	5292	4888	2.8E-10	4.8E-08	2.0E-02	+
I	AT5G37310	multispanning membrane protein	164	169	183	167	236	241	215	215	7.4E-07	5.6E-06	2.1E-02	+
I	AT5G13410	putative protein peptidyl-prolyl cis-trans isomerase	108	94	92	91	235	211	164	159	3.2E-07	3.2E-06	2.1E-02	+
I	AT5G51560	receptor-like protein kinase	146	146	142	143	302	300	264	240	1.5E-08	4.2E-07	2.1E-02	+
I	AT5G39210	hypothetical protein	80	91	84	95	151	141	114	118	6.5E-06	2.6E-05	2.3E-02	+
I	AT1G74730	unknown protein	131	197	126	154	1582	1553	1332	1396	1.5E-11	1.1E-08	2.3E-02	+
I	AT1G73590	auxin transporter splice variant b	34	38	29	46	104	99	65	71	3.5E-06	1.6E-05	2.4E-02	+
I	AT4G25080	magnesium-protoporphyrin IX methyltransferase - like protein	707	653	684	627	1588	1638	1418	1426	2.7E-10	4.8E-08	2.4E-02	+
I	AT1G50450	hypothetical protein	64	75	65	84	281	235	165	177	2.0E-06	1.1E-05	2.4E-02	+
I	AT1G20810	putative FKBP-type peptidyl-prolyl cis-trans isomerase	115	86	108	112	227	214	170	142	1.9E-05	5.7E-05	2.6E-02	+
I	AT1G66430	putative similar to fructokinase	114	119	114	133	272	253	224	216	1.1E-07	1.7E-06	2.6E-02	+
I	AT4G14210	phytoene dehydrogenase precursor (phytoene desaturase)	201	252	221	201	600	556	450	435	1.1E-07	1.7E-06	2.8E-02	+
I	AT3G56010	putative protein CHLOROPLAST 30S RIBOSOMAL PROTEIN S20	160	207	209	206	316	338	250	267	4.1E-05	9.8E-05	2.8E-02	+
I	AT4G24120	putative protein	29	29	29	24	56	55	43	44	2.5E-07	2.7E-06	2.9E-02	+
I	AT2G41820	putative receptor-like protein kinase	178	192	199	185	312	315	271	236	5.7E-06	2.4E-05	3.0E-02	+
I	AT4G34240	putative aldehyde dehydrogenase aldehyde dehydrogenase (NAD+)	150	137	120	124	305	278	221	203	3.3E-07	3.3E-06	3.0E-02	+
I	AT5G17170	unknown protein	342	352	325	328	864	784	667	603	1.7E-07	2.2E-06	3.0E-02	+
I	AT4G12310	flavonoid 3,5-hydroxylase -like protein	31	44	34	35	111	121	85	80	3.7E-07	3.5E-06	3.1E-02	+
I	AT1G67740	putative photosystem II Core Complex	1015	1020	995	1141	3319	3151	2924	2929	2.7E-10	4.8E-08	3.2E-02	+
I	AT1G63420	hypothetical protein	61	58	51	63	112	111	89	79	2.9E-06	1.4E-05	3.4E-02	+
I	AT4G36180	putative receptor protein kinase Cf-2.1 leucine rich repeat protein	74	91	95	85	200	190	167	169	9.8E-08	1.6E-06	3.7E-02	+
I	AT4G39970	putative protein	99	131	116	114	270	296	220	194	2.8E-06	1.4E-05	3.7E-02	+
I	AT2G30950	FtsH protease (VAR2) identical to zinc dependent protease	674	631	631	670	1959	1857	1694	1547	7.8E-09	3.0E-07	3.9E-02	+
I	AT5G55520	putative protein	12	4	25	9	77	68	53	52	4.2E-06	1.9E-05	4.0E-02	+
I	AT1G07880	MAP kinase, putative	10	11	10	9	33	35	26	20	1.6E-06	9.5E-06	4.1E-02	+
I	AT4G30950	chloroplast omega-6 fatty acid desaturase (fad6)	1184	1266	1168	1141	2132	2079	1886	1880	7.5E-10	8.0E-08	4.1E-02	+
I	AT2G46820	unknown protein	736	801	777	784	1974	2024	1867	1758	5.9E-10	7.4E-08	4.4E-02	+

			Darkness				Continuous FR				Statistics			
I	AT5G19370	peptidyl-prolyl cis-trans isomerase - like protein	246	309	287	321	587	557	480	492	1.3E-06	8.1E-06	4.5E-02	+
I	AT5G51010	unknown protein	270	318	301	330	746	688	630	600	1.2E-07	1.7E-06	4.6E-02	+
I	AT3G01500	carbonic anhydrase, chloroplast precursor	402	398	270	345	5807	6073	5057	4265	8.0E-09	3.1E-07	4.7E-02	+
I	AT5G04140	ferredoxin-dependent glutamate synthase	210	234	178	189	1505	1329	1133	1002	4.3E-08	9.1E-07	4.8E-02	+
I	AT4G28680	aromatic amino-acid decarboxylase - like protein tryptophan decarboxylase	17	14	17	20	84	77	69	56	3.3E-07	3.3E-06	4.8E-02	+
I	AT2G20020	hypothetical protein	40	48	45	49	87	104	74	67	2.7E-05	7.2E-05	4.8E-02	
I	AT5G35210	putative protein	193	210	200	184	445	430	390	387	8.9E-10	8.8E-08	4.8E-02	+
I	AT5G02830	putative protein	28	6	38	33	217	156	118	107	3.3E-05	8.3E-05	4.8E-02	+
I	AT2G32590	hypothetical protein	17	21	18	14	81	84	65	52	3.3E-07	3.3E-06	4.8E-02	+
I	AT1G52230	photosystem I subunit VI precursor	587	689	583	505	5365	5108	4695	4367	1.5E-10	3.6E-08	4.9E-02	+
II	AT5G64840	ABC transporter protein 1-like	131	143	165	168	289	271	205	176	2.3E-06	1.2E-05	2.9E-03	
II	AT1G28340	unknown protein	192	184	203	192	306	285	215	192	7.5E-06	2.9E-05	4.2E-03	+
II	AT5G28300	GTL1 - like protein GTL1	259	244	273	255	322	324	272	261	2.4E-05	6.8E-05	6.0E-03	+
II	AT2G23840	unknown protein	4	1	3	11	41	35	16	16	3.9E-06	1.8E-05	6.2E-03	+
II	AT1G60230	hypothetical protein	41	39	50	43	72	75	60	55	2.4E-06	1.3E-05	6.3E-03	+
II	AT5G63780	putative protein	226	242	213	211	459	414	293	288	4.0E-07	3.7E-06	6.8E-03	+
II	AT1G31460	unknown protein	23	19	26	28	51	45	34	28	2.2E-05	6.2E-05	7.4E-03	+
II	AT5G47760	4-nitrophenylphosphatase-like protein	94	105	109	102	130	127	104	99	1.4E-04	2.5E-04	8.6E-03	+
II	AT1G30210	hypothetical protein contains similarity to cyc1A protein	63	64	75	69	106	99	83	73	3.4E-05	8.6E-05	9.7E-03	+
II	AT1G04200	unknown protein	101	99	104	104	139	131	114	103	4.3E-05	1.0E-04	1.1E-02	+
II	AT1G24706	unknown protein	71	69	82	67	110	103	72	79	2.0E-04	3.2E-04	1.6E-02	+
II	AT3G20280	hypothetical protein	28	32	27	38	65	58	33	39	1.3E-04	2.3E-04	1.9E-02	+
II	AT1G73970	unknown protein	77	80	78	79	89	86	79	79	1.9E-04	3.1E-04	1.9E-02	+
II	AT4G08150	KNAT1 homeobox-like protein	307	304	374	314	522	492	419	376	5.9E-05	1.3E-04	2.0E-02	+
II	AT3G50790	putative LEA protein Picea glauca late embryogenesis abundant protein (EMB8)	51	60	78	65	131	110	92	82	1.1E-04	2.1E-04	2.2E-02	+
II	AT3G16350	putative MYB family transcription factor	29	19	26	32	44	51	26	29	7.4E-04	8.6E-04	2.4E-02	+
II	AT1G65950	hypothetical protein contains similarity to ABC transporter	73	71	57	62	129	130	90	69	8.4E-06	3.2E-05	2.5E-02	+
II	AT2G20240	unknown protein	38	46	50	41	78	72	48	55	1.7E-04	2.9E-04	2.7E-02	+
II	AT3G18390	unknown protein	142	175	178	150	312	286	217	221	1.7E-05	5.2E-05	2.7E-02	+
II	AT1G22460	hypothetical protein similar to axi 1-like protein	8	9	10	15	24	22	16	10	8.7E-04	9.8E-04	2.7E-02	+
II	AT2G44440	hypothetical protein	69	89	80	98	166	145	104	74	6.9E-04	8.2E-04	2.8E-02	+
II	AT2G31530	putative preprotein translocase SECY protein	57	65	62	65	97	86	67	71	2.1E-04	3.3E-04	3.1E-02	+
II	AT3G16260	hypothetical protein	69	82	71	80	113	108	77	86	2.1E-04	3.3E-04	3.3E-02	+
II	AT5G40630	putative protein	53	46	72	49	111	85	50	56	2.6E-03	2.3E-03	3.3E-02	+
II	AT3G43610	putative protein gamma-tubulin interacting protein	95	92	82	96	161	172	118	85	1.8E-04	3.0E-04	3.4E-02	+
II	AT5G17250	unknown protein	35	34	41	39	57	48	41	42	9.1E-04	1.0E-03	3.5E-02	+
II	AT4G21060	putative protein	47	42	47	42	88	71	53	46	3.0E-04	4.3E-04	3.5E-02	+
II	AT1G63640	kinesin-like protein	70	80	82	88	157	126	78	100	9.4E-04	1.0E-03	3.6E-02	+
II	AT2G24960	hypothetical protein	32	18	40	38	80	66	55	38	7.4E-04	8.6E-04	3.6E-02	+
II	AT5G25580	putative protein	20	22	17	23	43	38	26	20	2.0E-04	3.3E-04	3.6E-02	+
II	AT4G12980	putative protein	68	60	68	60	135	112	86	78	8.9E-05	1.7E-04	3.6E-02	+
II	AT1G08960	hypothetical protein	62	53	52	63	88	92	60	68	2.1E-04	3.4E-04	3.9E-02	+
II	AT1G06670	DEIH-box RNA/DNA helicase	87	105	100	108	156	148	95	122	1.1E-03	1.2E-03	4.0E-02	+
II	AT5G11380	1-D-deoxyxylulose 5-phosphate synthase - like protein	56	63	64	72	108	89	75	72	8.7E-04	9.7E-04	4.0E-02	+
II	AT4G32660	protein kinase AME3	151	158	179	156	226	203	181	158	2.4E-03	2.1E-03	4.5E-02	+
II	AT1G55540	hypothetical protein	28	35	37	36	73	56	32	44	2.0E-03	1.9E-03	4.6E-02	+
II	AT5G16180	putative protein	36	44	40	35	72	68	52	42	9.2E-05	1.8E-04	4.6E-02	+
II	AT3G52640	hypothetical protein	170	157	163	164	227	210	181	190	5.2E-05	1.2E-04	4.8E-02	+
II	AT1G53670	transcriptional regulator	228	266	304	261	627	488	396	347	2.9E-04	4.3E-04	4.8E-02	+
III	AT3G14920	hypothetical protein	142	146	156	157	186	177	146	138	8.8E-06	3.3E-05	1.3E-03	+
III	AT1G70430	Ste-20 related kinase SPAK	12	9	19	16	31	39	8	13	4.1E-05	9.8E-05	3.1E-03	+
III	AT2G31450	putative endonuclease	53	53	57	55	67	68	56	50	3.8E-05	9.3E-05	4.2E-03	+
III	AT4G10710	putative transcriptional regulator	180	198	200	206	271	252	196	177	6.7E-05	1.4E-04	5.4E-03	+
III	AT2G20080	unknown protein	27	25	32	26	42	47	21	25	1.1E-04	2.0E-04	6.7E-03	+
III	AT3G02130	putative protein kinase	92	87	86	91	104	108	84	83	3.9E-05	9.5E-05	7.7E-03	+
III	AT1G12260	unknown protein similar to NAM like protein	25	22	30	26	52	37	19	14	8.7E-04	9.8E-04	1.5E-02	+
III	AT3G54320	aintegumaenta-like protein ovule development protein aintegumenta	19	13	29	14	38	37	11	5	1.3E-03	1.3E-03	1.6E-02	+
III	AT2G29390	putative C-4 sterol methyl oxidase	259	260	259	267	312	299	241	268	7.4E-04	8.6E-04	2.3E-02	+
III	AT2G27600	putative ATPase skd1 family	668	662	658	698	729	729	671	645	1.9E-03	1.7E-03	2.5E-02	+
III	AT3G07330	unknown protein similar to putative glucosyltransferase	130	138	131	135	155	146	128	122	7.9E-04	9.1E-04	2.5E-02	+
III	AT4G31150	putative protein	66	56	60	74	82	84	44	58	3.4E-03	2.8E-03	2.6E-02	+

			Darkness				Continuous FR				Statistics			
III	AT2G22630	putative MADS-box protein AGL17	8	14	14	16	24	20	12	7	5.1E-03	3.8E-03	2.8E-02	+
III	AT5G65780	branched-chain amino acid aminotransferase	229	245	245	244	285	284	237	194	3.0E-03	2.5E-03	2.9E-02	+
III	AT5G03550	putative protein	6	13	10	11	26	20	8	8	1.1E-03	1.1E-03	3.0E-02	+
III	AT4G17120	hypothetical protein	87	75	90	77	102	113	77	64	2.2E-03	2.0E-03	3.0E-02	+
III	AT5G10950	putative protein cylicin II	33	27	33	44	57	47	35	23	7.9E-03	5.3E-03	3.5E-02	+
III	AT3G61960	serine/threonine-protein kinase-like protein	201	230	221	232	253	292	210	183	5.2E-03	3.8E-03	3.7E-02	+
III	AT2G36790	putative glucosyl transferase	18	29	29	22	41	35	18	19	4.6E-03	3.5E-03	3.7E-02	+
III	AT5G61830	carbonyl reductase - like protein	72	70	73	68	92	81	63	67	1.9E-03	1.8E-03	3.7E-02	+
III	AT5G45900	ubiquitin activating enzyme E1-like protein	93	99	89	116	131	116	84	82	7.0E-03	4.8E-03	3.9E-02	+
III	AT2G45680	putative PCF2-like DNA binding protein	43	50	44	51	55	61	38	44	5.5E-03	4.0E-03	4.8E-02	+
IV	AT2G33730	putative U5 small nuclear ribonucleoprotein	283	292	266	263	215	212	235	229	2.9E-08	6.7E-07	1.8E-03	+
IV	AT5G59880	actin depolymerizing factor 3 - like protein	2156	2092	2055	2080	1499	1494	1680	1663	1.4E-09	1.1E-07	2.8E-03	+
IV	AT2G28120	nodulin-like protein	108	110	84	96	67	68	84	85	6.4E-06	2.6E-05	3.4E-03	+
IV	AT3G43300	guanine nucleotide-exchange - like protein	229	220	188	187	167	169	169	181	3.0E-06	1.5E-05	4.7E-03	+
IV	AT2G04305	hypothetical protein	123	119	101	102	61	61	65	75	5.6E-08	1.1E-06	5.2E-03	+
IV	AT3G20130	cytochrome P450	148	139	109	98	74	67	76	73	4.7E-07	4.2E-06	5.6E-03	+
IV	AT5G59530	1-aminocyclopropane-1-carboxylate oxidase - like protein	60	56	38	28	6	10	14	10	5.6E-07	4.6E-06	6.6E-03	+
IV	AT4G21610	Lsd1 like protein zinc-finger protein	132	130	118	122	59	64	72	80	1.0E-08	3.5E-07	6.8E-03	+
IV	AT2G25560	putative DnaJ protein	129	130	111	104	94	88	94	101	6.7E-06	2.7E-05	7.3E-03	+
IV	AT5G18690	proline-richh protein	246	221	192	182	133	117	158	158	7.0E-06	2.8E-05	7.4E-03	+
IV	AT1G34190	NAM(no apical meristem) protein	495	484	450	439	312	335	347	346	3.3E-08	7.3E-07	7.5E-03	+
IV	AT4G36480	serine C-palmitoyltransferase like protein	215	213	207	202	118	122	178	156	9.2E-07	6.5E-06	7.7E-03	
IV	AT1G76090	S-adenosyl-methionine-sterol-C-methyltransferase	831	810	690	732	426	388	443	464	1.8E-08	4.9E-07	8.1E-03	+
IV	AT5G43040	CHP-rich zinc finger protein-like	57	64	36	45	15	23	32	37	4.2E-05	1.0E-04	9.0E-03	+
IV	AT5G43190	F-box protein family, AtFBX6 contains similarity to unusual floral organs (UFO)	228	241	193	192	115	128	124	118	2.4E-08	5.8E-07	1.1E-02	+
IV	AT3G44400	disease resistence - like protein RPP1	21	23	13	17	2	7	13	13	1.2E-04	2.2E-04	1.3E-02	+
IV	AT4G08980	F-box protein family	440	436	427	428	286	305	333	353	1.1E-07	1.7E-06	1.4E-02	+
IV	AT4G32600	putative protein ring finger protein	203	206	183	181	152	167	166	170	2.3E-05	6.4E-05	1.7E-02	+
IV	AT2G20560	putative heat shock protein	141	136	99	122	58	73	93	90	5.8E-05	1.3E-04	1.8E-02	+
IV	AT5G09920	15.9 kDa subunit of RNA polymerase II	395	396	377	370	265	257	271	290	2.0E-08	5.3E-07	1.8E-02	+
IV	AT3G08890	unknown protein	160	149	145	138	98	113	131	128	8.2E-05	1.7E-04	2.1E-02	+
IV	AT3G01260	putative aldose 1-epimerase	291	308	197	227	133	137	110	121	2.3E-07	2.6E-06	2.1E-02	+
IV	AT1G15170	hypothetical protein	108	103	97	104	55	49	66	71	2.5E-07	2.8E-06	2.1E-02	+
IV	AT3G13320	low affinity calcium antiporter CAX2	208	213	189	174	154	163	177	164	1.2E-04	2.1E-04	2.1E-02	+
IV	AT5G13890	putative protein	196	209	185	194	132	126	146	147	4.9E-07	4.3E-06	2.1E-02	+
IV	AT2G19800	unknown protein	39	44	34	37	26	29	34	33	3.8E-04	5.2E-04	2.2E-02	+
IV	AT5G04410	putative protein NAC2	506	512	486	477	386	383	385	402	1.9E-08	5.1E-07	2.2E-02	+
IV	AT5G41320	unknown protein	29	26	20	13	5	5	7	10	2.4E-05	6.7E-05	2.3E-02	+
IV	AT3G03860	unknown protein	419	444	336	340	226	284	350	289	4.7E-04	6.1E-04	2.3E-02	+
IV	AT4G11260	putative protein phosphatase like protein	705	607	488	519	348	360	402	380	1.9E-05	5.8E-05	2.4E-02	+
IV	AT1G22300	14–3–3 protein GF14epsilon (grf10)	3318	3260	2980	2900	2189	2066	2139	2349	3.8E-07	3.6E-06	2.4E-02	+
IV	AT5G59680	serine/threonine-specific protein kinase	51	56	40	31	25	25	24	30	3.9E-05	9.5E-05	2.4E-02	+
IV	AT5G64190	putative protein	28	27	16	19	3	4	11	4	1.2E-05	4.0E-05	2.5E-02	+
IV	AT1G70330	unknown protein	1168	1134	1023	1128	723	750	858	862	2.3E-06	1.2E-05	2.5E-02	+
IV	AT3G12760	unknown protein	1007	949	938	943	650	661	725	770	4.6E-07	4.1E-06	2.5E-02	+
IV	AT2G42570	unknown protein	432	421	408	405	179	175	191	214	4.1E-10	5.6E-08	2.6E-02	+
IV	AT3G51330	putative protein	243	230	173	193	123	125	110	117	1.9E-07	2.3E-06	2.6E-02	+
IV	AT1G76920	F-box protein family	536	490	486	470	318	290	370	362	2.1E-06	1.2E-05	2.7E-02	+
IV	AT1G17230	putative leucine-rich receptor protein kinase	72	76	65	62	34	39	43	38	4.1E-07	3.8E-06	2.8E-02	+
IV	AT5G39190	germin-like protein (GLP2a) copy2	34	36	35	33	11	11	16	16	5.7E-09	2.6E-07	2.9E-02	+
IV	AT3G51895	sulfate transporter ATST1	155	157	117	132	59	48	51	61	1.3E-07	1.8E-06	3.1E-02	+
IV	AT2G41960	unknown protein	196	189	181	180	154	161	163	162	3.6E-06	1.7E-05	3.2E-02	+
IV	AT5G60660	mipC protein - like (aquaporin) mipC protein	3001	2738	2480	2498	549	589	650	599	1.0E-09	9.4E-08	3.2E-02	+
IV	AT3G04080	apyrase (Atapy1)	149	158	120	138	116	107	126	120	5.9E-04	7.3E-04	3.3E-02	+
IV	AT5G45070	putative protein contains similarity to disease resistance protein	109	125	78	103	18	42	66	62	1.5E-04	2.5E-04	3.4E-02	+
IV	AT1G54115	unknown protein	342	324	289	303	243	235	237	247	1.3E-06	8.4E-06	3.4E-02	+
IV	AT4G27040	SNF8 like protein	338	368	306	291	211	208	217	205	6.8E-07	5.3E-06	3.5E-02	+
IV	AT2G04500	unknown protein	32	40	24	24	13	19	18	22	5.2E-04	6.6E-04	3.5E-02	
IV	AT5G44340	tubulin beta-4 chain	3036	3008	2884	2896	2234	2089	2268	2400	4.0E-07	3.7E-06	3.7E-02	+
IV	AT5G40370	glutaredoxin -like protein	1284	1209	1138	1125	835	860	888	1000	1.6E-05	5.1E-05	3.8E-02	+
IV	AT4G14160	transport protein	519	507	464	504	346	380	428	410	3.1E-05	8.0E-05	3.9E-02	+
IV	AT1G64040	phosphoprotein phosphatase 1 i	680	726	695	707	446	463	532	524	1.1E-07	1.7E-06	3.9E-02	+

			Darkness				Continuous FR				Statistics			
IV	AT3G02240	unknown protein	70	57	38	34	5	24	35	21	8.1E-04	9.3E-04	3.9E-02	+
IV	AT2G43940	unknown protein	198	187	153	148	135	100	127	144	6.2E-04	7.6E-04	4.0E-02	+
IV	AT5G63600	1-aminocyclopropane-1-carboxylic acid oxidase-like protein	1873	1797	1467	1342	884	1064	890	883	9.7E-07	6.7E-06	4.2E-02	+
IV	AT1G01230	hypothetical protein	485	484	457	456	299	286	302	286	4.2E-10	5.6E-08	4.2E-02	+
IV	AT3G51550	receptor-protein kinase-like protein	859	894	834	836	655	635	794	704	9.1E-05	1.8E-04	4.2E-02	+
IV	AT1G18460	unknown protein	267	238	211	224	185	167	192	203	4.0E-04	5.4E-04	4.3E-02	+
IV	AT3G21700	putative SGP1 monomeric G-protein	66	74	62	67	35	31	52	42	2.2E-05	6.3E-05	4.4E-02	+
IV	AT1G66200	glutamine synthetase	3111	2603	2178	2174	1250	1328	1316	1410	8.4E-06	3.2E-05	4.4E-02	+
IV	AT4G23030	putative protein	117	132	111	91	44	49	59	59	7.5E-06	2.9E-05	4.5E-02	+
IV	AT2G25940	putative vacuolar processing enzyme	44	45	43	34	24	27	33	36	7.8E-04	9.0E-04	4.5E-02	+
IV	AT3G59990	putative protein ETHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18)	477	484	455	473	415	391	441	428	9.5E-05	1.8E-04	4.5E-02	+
IV	AT5G15830	bZIP DNA-binding protein-like	221	198	168	165	104	133	127	134	7.8E-05	1.6E-04	4.6E-02	+
IV	AT1G62880	unknown protein	102	101	95	85	43	55	70	59	2.5E-05	6.9E-05	4.7E-02	+
IV	AT2G21410	putative vacuolar proton-ATPase subunit	413	433	356	378	307	316	311	297	3.1E-06	1.5E-05	4.7E-02	+
IV	AT2G29700	unknown protein	926	850	767	818	626	619	704	652	5.1E-05	1.1E-04	4.7E-02	+
IV	AT2G40530	hypothetical protein	38	34	33	27	10	17	21	23	2.0E-04	3.3E-04	4.9E-02	+
V	AT1G53380	unknown protein	119	118	112	107	95	99	112	110	1.2E-05	4.0E-05	2.1E-03	+
V	AT4G30580	putative protein 2-acylglycerophosphoethanolamine acyltransferase	332	334	309	314	301	285	320	315	1.2E-04	2.2E-04	5.3E-03	+
V	AT1G28200	FH protein interacting protein FIP1 identical to FH protein interacting protein FIP1	434	443	404	433	325	350	408	412	5.5E-05	1.2E-04	9.7E-03	+
V	AT5G10780	putative protein HSPC184	682	724	668	666	624	621	689	665	1.5E-03	1.5E-03	2.0E-02	+
V	AT2G26830	putative choline kinase	181	189	165	178	150	153	176	168	8.9E-04	9.9E-04	2.1E-02	+
V	AT3G04120	glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)	4519	4499	4197	4449	3674	3930	4270	4516	1.2E-03	1.3E-03	2.4E-02	+
V	AT3G14100	oligouridylate binding protein	1207	1113	1031	1090	760	904	1043	1042	8.5E-04	9.6E-04	2.7E-02	+
V	AT1G16280	putative ATP-dependent RNA helicase	94	102	96	89	68	66	96	83	4.9E-04	6.3E-04	3.0E-02	+
V	AT1G67570	hypothetical protein	70	72	68	55	48	55	67	65	5.9E-03	4.2E-03	3.2E-02	+
V	AT2G01070	unknown protein	122	143	113	124	82	90	111	127	1.9E-03	1.8E-03	3.3E-02	+
V	AT3G57880	anthranilate phosphoribosyltransferase-like protein	225	225	175	217	163	152	195	197	2.3E-03	2.1E-03	3.4E-02	+
V	AT4G34460	GTP binding protein beta subunit	344	323	309	307	233	275	300	301	1.2E-03	1.3E-03	3.6E-02	+
V	AT2G36330	hypothetical protein	102	98	85	93	59	75	83	88	1.2E-03	1.3E-03	3.7E-02	+
V	AT3G25545	Expressed protein	111	125	118	106	84	84	117	106	1.5E-03	1.5E-03	3.8E-02	+
V	AT3G19760	RNA helicase	1010	998	1000	929	921	876	988	986	6.7E-03	4.7E-03	3.9E-02	+
V	AT4G26720	phosphoprotein phosphatase (PPX-1)	223	192	190	189	113	149	179	205	3.1E-03	2.6E-03	4.4E-02	+
V	AT2G17820	putative histidine kinase	118	129	114	104	97	91	120	104	6.5E-03	4.6E-03	4.4E-02	+
V	AT5G16760	Inositol 1,3,4-Trisphosphate 5/6 kinase	410	454	396	423	342	333	417	386	1.8E-03	1.7E-03	4.5E-02	+
V	AT4G27250	putative protein dihydrokaempferol 4-reductase	23	24	18	21	8	12	15	21	1.7E-03	1.6E-03	4.6E-02	+
V	AT5G50375	Expressed protein	310	310	253	317	188	209	269	322	4.4E-03	3.4E-03	4.6E-02	+
V	AT3G15120	chaperone-like ATPase	160	193	153	148	122	123	142	158	4.7E-03	3.6E-03	4.6E-02	+

Clusters I, II and III include genes with expression promoted by continuous FR (less promoted in *blh1–1*) and clusters IV and V include genes with expression reduced by continuous FR (less reduced in *blh1–1*). Biological replicates, P and *q* values for treatments and P values for interaction are shown for each gene. The presence of the TGGA sequence in the promoter is also indicated but not all these genes are predicted to be direct targets of BLH1. The closest homologues of the tobacco *Lhcb1*2* gene used in this paper are *AtLhcb1*1* (At1 g29920) and *AtLhcb1*2* (At1 g29910). At1 g29920 is not present in the ATH1 microarray. At1 g29910 is present but it showed no significantly reduced response to continuous FR, very likely because a single pulse of light is enough to induce am extreme promotion of the expression of these genes 6 h later (Anderson, S.L., Somers, D.E., Millar, A.J., Hanson, K., Chory, J., Kay, S.A. 1997. Attenuation of phytochrome A and B signaling pathways by the Arabidopsis circadian clock. Plant Cell 9: 1727–1743) leaving little room for a HIR. In agreement with the latter interpretation, reduced promotion of the *AtLhcb1*1* (At1 g29920) and *AtLhcb1*2* (At1 g29910) genes is observed in seedlings exposed to 24 h FR and analysed by real time PCR (see main text).